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Book of abstracts

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The interplay of relevance and generalization in Biostatistics

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Abstract: In the development of mathematical methods, two contrasted, nearly contradictory logics are in action. This is particularly the case in Biomathematics, including Biostatistics and Statistical Ecology, which will be the main focus of my reflections and illustrations.

The logic of relevance stems from a full acceptation of biological questions, and then attempts at developing tools closely fitting these questions. After an initial tool is proposed, such as the probit model to analyse dose-response relationships, one generally see a proliferation of particularizations and variants, published one at a time, and often named from their author or by some exotic name. Many fields can serve as illustrations of this proliferation process: predator-prey models, capture-recapture methods, descriptive multivariate analysis ("data analysis"), etc… After an initial success, this proliferation of methods (and software) is often a source of confusion for users, with little help from a poor nomenclature. Another clear risk of the logic of relevance is of developing "ad hoc", statistically non optimal approaches to any particular question, that may become the dominant practices for years within a particular scientific community.

The logic of generalization comes from pure mathematics, and is based on the idea that, by generalizing an existing mathematical object, you will unavoidably visit new, unexplored, territories, discover unexpected links, and make valuable encounters. The use of the duality diagram as a prospective tool in descriptive multivariate analysis and of generalized linear models as a common frame for a variety of discrete data models are obvious examples of the logic of generalization. In face of the advantage of unifying existing approaches and opening new avenues of development, the clear risk is to use a sledgehammer to crack a nutshell, or, worse, to use a hammer to fit a screw. Using a fancy mixed logistic model for estimating survival from data on marked individuals, not accounting for incomplete detection which is the key feature of such data, would be an example of such a mismatch.

One can easily deduce from such premises that statistical Ecology, and biomathematics in general, could not have survived, developed, and be efficient and useful with only one of these two logics at work. I will show and illustrate how these two logics fit together in successive phases of development, each one needing an accumulation of material from the other one to be fully efficient. In a pluridisciplinary endeavour such as statistical ecology, the reflections should necessarily encompass the development of software and shared data bases. I will go on discussing the strategies of research and transfer of knowledge that can be thought of in such a framework.

Statistical methods for non-linear ecological dynamic models.

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Abstract: Highly non-linear, process based dynamic models are commonly used to describe pest insect populations and disease dynamics, but present challenges when used for statistical purposes. Naive application of standard Bayesian or frequentist methods fails as the dynamics of the system get close to the chaotic regime. In that case likelihoods, or the target distributions for Bayesian simulation, become highly multimodal or completely irregular. At the same time, the data from which to estimate such models is usually quite limited, so that efficient use of information is at a premium. Two main lines of attack are through controlled information reduction, such as ABC or Synthetic likelihood, or via working directly on the system state variables via filtering, for example. This talk compares and contrasts these strategies.

Mixture models for estimating population abundance using spatially non-random commercial fisheries data

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Keywords: abundance; monitoring of biodiversity.

Abstract: Reliable population abundance estimates are crucial for sustainable exploitation of fisheries resources as well as for monitoring impacts on vulnerable fisheries bycatch species such as sharks and rays. Using detailed haul-by-haul catch observations from an onboard fishing vessels observation program we compared two mixture models for estimating absolute population abundances. A crucial issue for these data is that not all individuals present will be caught by the fishing gear. This is commonly referred to as catchability and will tend to increase between-observations variability, e.g. between-hauls variability, and lead to excess zeros, given population density is sufficiently low. Assuming individuals are randomly distributed in space, we compared a hurdle model and a zero-inflated Poisson (ZIP) model for abundance and catchability estimation. To account for spatial trends and the non-random (preferential) nature of the observation locations, we used spatial grids where grid cell size decreased with increasing number of observations. Time trends were estimated by including period and grid cell as a factor for the non-zero model components. As the fishing method influences catchability, fishing method was included as an explanatory variable for the zero-components. The results were compared for several shark and ray species in European waters.

Large-scale monitoring of rare and elusive species combining capture-recapture with detection/non-detection data

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Keywords: abundance, Bayesian, double sampling, low detection probability, N-mixture, Orsini's viper.

Abstract: In the context of global species decline, the set-up of robust large scale monitoring is a central matter for any conservation or management purpose. The well-known problem of imperfect detection of a species which results in biased estimates of population parameters has been intensively studied over the last decades. However, while flexible and powerful statistical methods have recently been proposed for common and/or easily detectable species, they are of limited use when facing rare species with low and heterogeneous detection probability among sites. Here we introduce a double sampling strategy to estimate local abundance at a large number of sites. The method is based on two types of information: capture-recapture data at a particular site that is used to estimate the individual detection probability r; and repeated detection/non-detection data at any other site i to estimate the conditional – on abundance – probability of detecting the species at this site, noted p_i. The abundance N_i at any site i is given by the relation $p_i = 1-(1-r)^{N_i}$ (Royle and Nichols, 2003) and is easily calculated. We assessed the relevance of our approach using a regional scale monitoring dataset of the Orsini's viper, an extremely rare and elusive species. Using a large number of simulations we also explored how this approach performed compared to Royle N-mixture model (2004) for very low values of individual detection probability. The method and codes were developed in both frequentist and bayesian framework. We eventually sketched two examples of field protocols that could easily be applied to other situation such as monitoring of large mammals or birds.

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Estimating abundance from occurrence data

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Keywords: abundance; negative binomial; presence-absence map.

Abstract

The estimation of abundance from presence absence data is an intriguing problem in applied statistics. It can be viewed as an extension of the inverse birthday problem, which makes independence and random placement assumptions about the abundances. However, when applied in practice the random placement approach generally results in underestimation. We present an alternate estimator based on a simple paired negative binomial model. The proposed estimator is shown to be consistent and asymptotically normally distributed. In addition, a quadruple negative binomial version of the model is developed, which resolves a controversial issue in the literature. We examine the performance of the estimator in a simulation study and by estimating the abundance of 44 tree species in a permanent forest plot where the actual abundance is known.

The effect of model selection on point transect density estimation

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Keywords: distance sampling; abundance

Abstract: Many simulations have been done for testing the properties and robustness of distance sampling estimators. When data is generated from a particular model and fitted using the same model they seem to perform well. However, in a real life situations the true model is unknown. Therefore, the standard methods for fitting detection functions to distance sampling data (as described by Buckland *et al.* 2001) involve selecting among several classes of semi-parametric models, and it is recommended that this selection is performed using standard model selection techniques such as AIC.

Here, we check the performance of distance sampling estimators when data was analysed using model selection, comparing line and point transect estimators in a reasonable number of scenarios. As has been shown, point transect estimation is more difficult and model selection more critical, since the fit of the model to the distance data near the line or point is the most important and in point transects fewer distances are recorded. Initial results from our simulation study show that, point transect sampling can be highly biased (>30%) if the sample size is under the 75-100 observations recommended (Buckland *et al.* 2001). Moreover, under realistic circumstances and an adequate sample size, in some situations we still find around 10% bias, unless the sample size is very high.

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A Variational Bayes approach to the analysis of site-occupancy models.

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Keywords: logistic regression; species distribution model; variational Bayesian modelling

Abstract: Presence-absence data is often used to investigate the range and range shifts of animal populations using an occupancy model that contains covariates assumed to capture the probability of species occurrence as well as covariates assumed to capture the probability of species detection. To date, likelihood as well as Bayesian methods have been developed for the standard model (none-spatial) as well as the model that incorporates spatial random effects (spatial models). Bayesian models that include logistic link functions are often analysed using WinBugs or OpenBugs since Markov chain Monte Carlo methods are required to sample from the posterior distribution of the required parameters. In this article we develop a variational Bayes approximation to the posterior distribution of the parameters of a standard occupancy model which uses logistic link functions to model the probability of species occurrence at sites as well as species detection probabilities. A fast iterative algorithm that does not use Markov Chain Monte Carlo methods is developed. The effectiveness of the proposed technique is investigated via simulations and suggestions are made on how the technique could be extended to the case of the probit link function. Data extracted from Southern Africa Bird Atlas Project (SABAP) is used to illustrate the usefulness of the variational Bayes technique.

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Parameter redundancy of mixture models in mark recovery

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Keywords: mark-recovery, mixture model, identifiability.

Abstract: Mark-recovery methods are used to estimate the survival of marked wild animals, through the fitting of appropriate probability models to field observations. Of interest here are popular classes of mixture model, which may be both finite, infinite, or used in combination.

We focus on finite mixture models, which can introduce a large number of parameters that may require constraints to be applied in order for all the parameters to be estimated. This work is motivated by Pledger and Schwarz (2002). We provide for the first time a formal analysis of these models, using the methods of computational symbolic algebra introduced by Catchpole and Morgan (1997). This provides an illustration of the different steps that need to be carried out, using the recent developments of Cole et al (2010). We derive terms that define mixture model structures, called exhaustive summaries, and show how those terms are related to the number of estimable parameters.

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IMPROVING ABUNDANCE ESTIMATION BY COMBINING CAPTURE-RECAPTURE AND OCCUPANCY DATA

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SUMMARY: Abundance is a key quantity for conservation and management strategies but remains challenging to assess in the field. Capture-recapture (CR) methods are often used to estimate abundance while correcting for imperfect detection but these methods are costly. Occupancy, sometimes considered as a surrogate for abundance, is estimated through the collection of presence-absence data and is less costly while enabling to gather information at a large spatial scale. Building on the recent pieces of work on the combination of different data sources, we showed how abundance data can be complemented by presence-absence data and be analyzed conjointly to improve abundance estimates. Our approach relies on a hierarchical model that makes explicit the link between the abundance and occupancy state variables while formally accounting for imperfect detection. We used a population of Eurasian lynx in France monitored via camera-traps and a collection of presence signs as an illustration of our approach. Using a combination of capture-recapture and occupancy data, we demonstrate that we can efficiently improve abundance estimates without deploying a costly monitoring protocol. Combining different data sources has a great potential especially for monitoring elusive or species distributed over large areas and so difficult to monitor.

KEYWORDS: abundance, Bayesian approach, camera-trapping, population size**,** presence signs, site-occupancy.

Conditional spatially explicit simulations of strongly 0-inflated data to estimate biodiversity indices

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Keywords: Indicators of biodiversity, spatial ecology, monitoring of biodiversity, geostatistical simulations.

Abstract: Upscaling diversity indices is recognized as a problem as the diversity of a large region is not the average of the diversities of its sub-divisions. This led to the definition of the concept of β-diversity which corresponds to the difference between the mean of local α-diversities and the global γ-diversity. However, its expression is not known in practice which lets the problem unsolved unless some relationships between α- and γ-diversities are postulated. The non additivity of diversity indices makes it necessary to estimate them via indirect approaches where each species' distribution or presence is estimated before computing the index. Moreover, being non linear transformations of the species densities, these indices must be estimated on the basis of conditional simulations of species densities (and not on the basis of kriging maps). However, in marine ecosystems, the vast majority of species are rare or extremely rare (50% of the 139 species distributions get more than 95% of 0 in the present case study). This paper presents a general framework based on conditional simulation spatially consistent that allows producing accurate maps of diversity. A particular focus is devoted to the simulations of strongly 0-inflated distributions (Gibbs sampler with the variogram of the hidden Gaussian variable). Simulated data are used for demonstration purposes, but a case study is also presented where the Rao entropy is mapped over the Gulf of Lion (France) on the basis of scientific trawl survey data.

Beyond topographic habitats: wavelets and wombling identify meso-scale boundaries in $64km^2$ of lowland Amazon forest

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Keywords: spatial ecology, species distribution modelling, monitoring of biodiversity.

Abstract: Abrupt floristic changes are well documented across broad scale gradients (altitude/topographic/soil/geologic). Local scale floristic “patchiness” has been related to a variety of factors including below ground resources, random effects/ecological drift and dispersal limitation. However, not all groups are congruent with meso-scale (10^3 – 10^5 m) floristic patterns and it remains unclear to what extent meso-scale boundaries are driven by spatial/environmental gradients and/or species responses. Here we use a combination of spatial boundary modeling approaches (clustering, wavelet and wombling) to identify biologically meaningful “habitat” and “non-habitat” boundaries (regions with higher rates of change in density/species composition) associated with 22 taxonomic groups (ranging from Oribatid mites to canopy trees) in $64km^2$ of lowland Amazon forest. We then quantify spatial overlap in the identified boundaries to understand the spatial concordance between “habitat” and “non-habitat” boundaries. Our findings show that habitat categories that are commonly used in landscape ecology are not necessarily meaningful for understanding/representing the meso-scale spatial distribution of biological diversity in lowland Amazonia.

FIDEGAM: A novel method based on Generalized Additive Models for quantifying the sampling effort in biodiversity databases

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Keywords: monitoring of biodiversity; measures of biodiversity; survey design and analysis

Abstract: Biodiversity databases are the main source of information for a fast growing body of research in macroecology and conservation biology. However, such information is often severely biased (typically some areas, species or years have been more intensely sampled than others), compromising the accuracy of results and conclusions provided by classic and advanced analysis of biodiversity. The quantification of sampling effort plays a key role in the process for correcting this bias, and different methods based on species accumulation curves are the most widely adopted. Despite the availability of diverse completeness measures for describing the accumulative-sampling effort relationship, we still lack of an objective criteria to measure the capability for discriminating between well and bad sampled units. We explore the statistical pitfalls of the available methods, evaluate for the first time their discrimination capability, propose a new method, named FIDEGAM, based on the first derivative of the curve obtained from a fitted Generalized Additive Model (GAM, Hastie and Tibshirani 1990; Wood 2006)), and illustrate how our approach can account for sampling effort in biodiversity analyses. The discrimination capability of different methods is evaluated with ROC curves (Pepe 2003) and applied to databases with different degree of exhaustiveness: (a) the database of vascular flora of a mountain Spanish National Park (Ordesa-Monte Perdido; Pyrenees) and (b) a simulated database. The novel method FIDEGAM outperformed other methods in terms of discriminatory capability and regardless of the sampling exhaustiveness. Therefore, we propose the use of this method to improve the reliability of biodiversity analyses based on databases.
We show an application of this technique by incorporating FIDEGAM for modelling the alpha diversity of vascular plants in Ordesa-Monte Perdido National Park.

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Survey Design for Underwater Robots: Accomodating Autocorrelation and Constrained Sampling

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Keywords: Autonomous under water vehicle, AUV, Geostatistics, INLA, Model-based design, Temperate reef

Abstract: Autonomous underwater vehicles (AUV), which collect images of marine habitats, are now an established sampling tool. The use of AUVs is becoming more widespread as they offer a non-destructive method to survey substantial spatial areas. In this presentation, we investigate statistical aspects to AUV survey design for estimation of percentage cover of key benthic biota. In particular, we investigate the presence of spatial autocorrelation in AUV data and allow for it when evaluate different approaches to designing surveys. The design strategies varied in their statistical performance and nearly all strategies had short-comings. Design strategies that were consistently poor performers had: a) transects placed in parallel in a single spatial dimension, and b) made no attempt to spread-out the transects in space. The superior design types had more transect-to-transect separation (but not too much) and effectively spanned important covariates. The results give guidelines to researchers designing AUV surveys for biological mapping and for monitoring. In particular, we demonstrate that any spatial design should seek spatial balance, such as would be introduced by a systematic or stratified component within a randomised design. Knowledge of the system under study should be incorporated and, if possible, should be done so in a formal manner that is objective and repeatable.

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On turnover measures of species communities

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Keywords: beta diversity; temporal turnover.

Abstract: Ecological communities vary through time (and space). Measures of alpha diversity, for example species richness or Shannon diversity are widely used to capture spatial and temporal differences. However, beta diversity, a concept first introduced by Robert Whittaker, tracks shifts in species composition, and can be a more informative metric of community change. Here, we introduce a new statistical framework for many of the commonly used measures of beta diversity including those based on both presence/absence and abundance data. Using simulations and analyses of community time series we show how our framework illuminates the relationship between familiar metrics, enables the user to develop appropriate null models, and aids the interpretation of analyses of community change.

Simulating vegetation dynamics and an observation process to support monitoring and evaluation of public investment in biodiversity: A case study from Australia's *Biodiversity Fund*

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Keywords: monitoring of biodiversity; survey design and analysis

Abstract: Each year governments commission habitat protection and restoration through a variety of programs, but routinely fail to adequately demonstrate the ecological benefits obtained. The need to improve the way we measure and report on the outcomes of environmental investments has been made very clear in the literature, and yet major initiatives continue to be released without a coherent strategy to do so.

We simulated vegetation dynamics, and observation processes, for two biographic areas from southern Australia to inform a monitoring strategy for Australia's "Biodiversity Fund". Our aim was to identify the sampling design, data collection, and analytical framework that provides an acceptably precise estimate of hypothesised "true" outcomes of the Biodiversity Fund investment at the lowest cost.

The simulation models, implemented in R and JAGS, are informed by existing data from similar sites and ecosystems. We placed particular emphasis on two dimensions of the problem where investors often seek to minimise costs: i) obtaining control and contrast sites, and ii) distinct observation models associated with quantitative and pseudo-quantitative field assessments. Both are known determinants of power in statistical inference, but decision makers rarely confront an explicit trade-off of cost and inferential benefit.

Plausible changes to species richness and vegetation condition measures arising from ecological restoration works are unlikely to be discernible over the 3-5 years of investment given background variance and the sampling replication possible within the nominated monitoring budget. Conversely, the data that the program Investors required participants to supply as a condition of funding is unlikely to yield statistically compelling insight.

Like any *a priori* power analysis, our investigation will enable the Government to make informed decisions about how to allocate monitoring resources across their portfolio of investments. Importantly, through model-based extrapolation and predictions of outcomes based on available data, the models should also provide the basis for a whole-of-program estimate of impact that explicitly represents uncertainty.

Mapping diversity indices: a false simple question

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Keywords : map, diversity index, β-diversity, betagram, kriging procedure, species richness, quadratic entropy

Abstract: Mapping diversity is central to numerous research and applied fields in ecology. Mapping species diversity indices allows monitoring spatial and/or temporal variation in communities faced to environmental and human impacts, and helps identifying areas for effective conservation planning and management. Two approaches can be considered to map diversity: (i) the indirect approach, which consists in modeling individual species distributions, then stack the distributions of all species and map the desired diversity index and (ii) the direct approach which relies on mapping directly the desired diversity index. The latter approach is inaccurate because diversity indices are non additive. Therefore, the variance and some of its derivatives like the variogram are not appropriate tools to measure variability. β-diversity, which quantifies the turnover between locations, has thus been

investigated. More precisely, we integrated the variograms of β-diversity (i.e. the betagram) within the interpolation procedures. We then confronted results of this novel direct approach with the outcomes of i) the direct kriging estimation of α-diversity and ii) the indirect approach based on individual kriging maps. Two diversity indices were considered in this study: species richness and Rao's quadratic entropy that we applied on 18-years of surveys of the fish community in the northwestern Mediterranean Sea. We finally showed that none of the approaches performed well, for different reasons, and that further methodological development is still needed.

Choosing the right response: importance of time-scales in animal ecology

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Keywords: time-scale, double integration.

Abstract: Though essential, understanding how climate variability may influence ecosystems is no trivial endeavour. Climate is a dynamic assemblage of numerous parameters and choosing which parameters are likely to affect the ecosystem, and on which spatio-temporal scale to study them, are fundamental questions that need to be addressed at the start of any investigation. Here, we exemplify the issue of time scale using an inshore top predator, the little penguin, *Eudyptula minor*, as a model. Combining previously-published and new data, we revealed a paradigm that, depending on the time scale, different breeding parameters can respond in opposite directions when investigating climate effects. Indeed, we show that breeding success of little penguins was affected by mean sea surface temperature (SST) either positively when averaged over the entire breeding period, or negatively when investigating weekly patterns, in contrast to previously published results based on monthly SST values showing no direct relationship. Such findings highlight the need to study the effects of climate at ecologically relevant temporal scales, both long (*e.g.* the full breeding period) and short (*e.g.* the week). Using cumulative integrations on our decadal weekly dataset (DiLorenzo & Ohman 2013), we propose an interesting methodology to objectively investigate the time scale at which biological parameters (*e.g.* chick body mass changes, mortality, etc.) could respond to SST.

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Consistency of Bayesian and maximum likelihood inference in state-space models of ecological systems with strongly nonlinear dynamics

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Keywords: State-space models, hierarchical Bayesian models, chaotic dynamics, nonlinear dynamical systems

Abstract: Estimating population dynamics from data recorded with observation uncertainty is an important problem in ecology. Perretti et al. (2013) noted that standard Bayesian state–space solutions to this problem provide biased parameter estimates when the underlying population dynamics are chaotic. Consequently, forecasts based on these estimates show poor predictive accuracy, which lead Perretti et al. to conclude that "model-free" time-series methods are superior even to the correct mechanistic model when the latter is estimated in a Bayesian state-space framework. In Hartig & Dormann (2013), however, we showed that a simple modification to the standard state-space approach also suffices to remove the bias and reverse the previous results.

In this presentation, we will discuss in more detail when and why Bayesian and maximum-likelihood estimates fail when used for inference in nonlinear and chaotic dynamical systems. We will also discuss how to test for these conditions in real data, and what alternatives to the standard approaches for inference of state-space models are available that are robust under these conditions.

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Do dolphins alter their vocal behaviour in response to military sonar? A review of analytical methods

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Keywords: Cox point process; generalised estimating equations; Mahalanobis distances; presence-absence; state-space models

Abstract: The vocal repertoire of dolphins encompasses three categories of vocalisations – whistles, clicks and buzzes – which are used in different contexts, e.g. for socialising, under water echolocation or homing in on prey during foraging. Mid-frequency active sonar (MFAS) is used by military vessels for detecting objects. It involves the underwater emission of intense sound pulses that are often repeated. As the range of sound frequencies used for MFAS often overlaps that of dolphin vocalisations, we were interested in identifying any potential changes in the vocal behaviour that dolphins may exhibit in response to military sonar exercises. To identify such changes, we compare the vocal behaviour of dolphins from periods before the sonar exercises to the behaviour of dolphins from periods during or after the exercise at the same locations. We review some of the potential changes in vocal behaviour in response to military sonar using acoustic data collected with passive acoustic monitoring devices and the corresponding analytical methods: 1. do dolphins vocalise more or less in the presence of sonar? 2. given vocalisation, does the probability of using any of the vocalisation categories change in the presence of sonar? 3. do parameters describing the individual vocalisations, e.g. maximum frequency, change in the presence of sonar? For each question, we define a response variable which is modelled using factor, linear and smooth terms. Regardless of approach, we expect model errors to be correlated and potentially overdispersed. These issues may be addressed using generalised estimating equations or, alternatively, using stochastic processes such as state-space models or Cox point processes. We illustrate the approaches with acoustic data collected in the presence of vocalising dolphins and MFAS using Marine Acoustic Recording Units off the coast of Jacksonville, FL and in Onslow Bay, NC.

Estimation methods for nonlinear state-space models in ecology

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Keywords: AD Model Builder; Template Model Builder; theta logistic population model; BUGS

Abstract: The use of nonlinear state-space models for analyzing ecological systems is increasing. A wide range of estimation methods for such models are available to ecologists, however it is not always clear, which is the appropriate method to choose. To this end, three approaches to estimation in the theta logistic model for population dynamics were benchmarked by Wang (2007) and additional three approaches by Pedersen (2011). Similarly, we examine and compare the estimation performance of the three methods described in Pedersen (2011) with that of a novel tool called TMB. The first approach is to employ hidden Markov models (HMMs), which is a largely overlooked technique for problems of this type. The second and third method (the open source tools "AD Model Builder" [ADMB] and "Template Model Builder" [TMB]) use random effects via automatic differentiation the Laplace approximation. The fourth alternative is to use the popular Bayesian framework of BUGS. In simulation based estimation of the theta logistic population model all approaches give similar parameter estimates. However, ADMB is orders of magnitudes faster than BUGS and HMM, and the novel TMB framework is an order of magnitude faster than ADMB and with simpler source code due to automatic sparseness detection of the Hessian matrix.

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State space model selection and the many faces of DIC

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Keywords: state space model, model selection; DIC

Abstract: The Deviance Information Criterion (DIC; Spiegelhalter et al. 2002) is a popular means among ecologists for comparing the fits of Bayesian hierarchical models to data. Several studies have, however, raised concerns about the reliability of DIC in selecting an adequate model (e.g. Celeux et al. 2006). These concerns are closely related to the ambiguity in defining DIC: depending on which variables in a hierarchical model are considered parameters, and thereby what part of the model is viewed as constituting the likelihood and what part is considered the prior, different DICs are obtained. These DICs at different 'levels of focus' can behave very differently and if an inappropriate focus is chosen, model selection by DIC may even become nonsensical (Millar 2009). There are currently few, and conflicting, guidelines for which focus to choose in any particular situation and it appears likely that different types of models may require different guidelines. We investigate the role the choice of focus of DIC plays in selection among state space models of population processes. A simulation study is designed where a set of models that differ both in the observation process and in the underlying population process, are fit to simulated data. DICs and complexity penalties at several levels of focus are evaluated for the models and simulated data to see how they perform and compare in picking up model differences.

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Advances in modeling the spatial dynamics of Pacific bigeye population with the use of conventional tagging data.

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Keywords: abundance, integrated population models, population dynamics, species distribution models

Abstract: Adult bigeye tuna (*Thunnus Obesus*) has been exploited in the Pacific Ocean by large-scale longline fleets since the 1960s and since the early nineties the juvenile bigeye has been incidentally caught by the purse-seine fisheries targeting skipjack tuna in the tropical ocean. The recent reduction of longline catches raises the concern that the overall fishing mortality of this migratory species is too high and the stock may be depleted. We use the model SEAPODYM (Spatial Ecosystem And Populations Dynamics Model) to predict the spatio-temporal dynamics of bigeye tuna population under the influence of environment and fishing pressure. Describing the detailed spatial structure of the population this model provides also the estimate of the species abundance and can help us attributing the observed trends and stock variability to the impact of environment or exploitation. Using the maximum likelihood method to estimate the parameters of the model while incorporating catch and length frequencies data allowed significant improvement of the agreement between observations and model predictions. However the results were not fully satisfactory as not all model parameters could be estimated based on fishing data. Therefore we have integrated the fisheries-independent data into the maximum likelihood approach, namely the tagging data. Thanks to a considerable effort deployed in the Pacific Ocean for tagging tuna, 45 thousands of bigeye tuna were tagged with conventional tags and about 25% of them were recaptured. These data is the source of additional key information on movement, habitat distributions and stock age and spatial structure. In this talk we present the method employed to incorporate the individual tagging data within the Eulerian model and discussing the first results obtained on the basis of the integrated approach.

Derivation and inference on the bivariate age- and size-specific mortality.

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The term "senescence" refers to the physiological deterioration of an organism as it gets older, which results into a systematic increase in the age-specific risk of mortality and a decrease in the fertility rate with age. Evolutionary theories of aging all seem to agree that senescence is unavoidable in nature. However, species for which individuals keep growing as they get older (also known as "indeterminate growers") commonly show increases in fertility and declines in mortality with age. These species are thought to show negative senescence, a process that - in theory - entails physiological improvements through which individuals are capable of escaping senescence. Those opposing the notion of negative senescence argue that the real advantages behind larger sizes are only mechanical and not physiological, i.e. the actual mechanisms of senescence might still be at play, but they are overshadowed by the fact that larger individuals are less likely to be predated upon while they can produce more offspring because they have fewer physical constraints as they grow. The debate is far from solved; current mortality models cannot distinguish between the contributions of age and size to mortality since they tackle age- and size-specific mortality separately or as independent processes. We derive a model that expresses age- and size-specific mortality as a bivariate process from which the subsequent bivariate survival and probability density functions of ages and sizes at death can be calculated. We then constructed a Bayesian model to draw inference on these rates. Our results show that different effects of age and size on mortality can produce the impression of negative senescene where senescence is still present, while negative senescence can be masked by size effects. These methods should shed light into the debate and allow us to explore the existence and extension of negative senescence in wild populations.

Spatial cue-mixture models for estimating bird song rate and population density

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Keywords: abundance, capture–recapture, survey design and analysis

Abstract: Existing methods for the analysis of sound recordings to estimate bird population density rely either on distinguishing individuals or on independent estimates of the per capita song rate, the expected number of songs or other cues produced by one bird during a recording. When several individuals of a species sing simultaneously or sequentially on one recording the assignment of songs to particular individuals is difficult and somewhat subjective. Independent estimation of song rate is also difficult and prone to sampling bias. We show how to avoid these difficulties by analyzing recordings replicated in space using a hierarchical model in which song rate is a latent variable. We derive an expression for the distribution of the number of cues detected at an isolated microphone. Our data are the breeding-season songs of three warbler species in 10-minute recordings at each of 272 forested points in Maryland, USA. We also operated a 4-microphone array for 10 minutes at 66 of these points, allowing us to estimate distance-related sound attenuation and spatial detection probability for songs of these species. We obtained density estimates using either the first song of each putative recorded individual (Dawson and Efford 2009) or the hierarchical model applied to all songs. Results were consistent between the two methods. The best hierarchical model used a negative binomial distribution for the number of songs per bird per recording. The model allows for 'unavailable' birds that do not sing during the recording, corresponding to the zero class of the fitted distribution of songs per individual. The 2-phase design is easily scaled to survey birds across landscapes.

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Analysis of extended batch-marking studies

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Keywords: capture-recapture; abundance

Abstract: Batch-marking studies have been largely ignored by the capture-recapture community because of the loss of information due to using non-unique marks in the study design (Cowen et al., In press). However there are some instances when it is not possible to uniquely tag individuals uniquely, such as with juvenile fish or insects. Extended batch mark data arise when different batch marks are used for different batches, such as using different colours for each batch. We investigate an extended open-population batch-marking study of Pacific Sand Lance (Ammodytes hexapterus) and develop a hidden Markov model to model the observed capture process and the latent survival process. This work extends the modelling of Huggins et al. (2010) who presented a simplified, pseudo-likelihood, followed by model-fitting using estimating equations. In the case of the sand lance, not all unmarked fish that were captured were marked as fish could only be kept for a limited time before they had to be released.

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A spatial capture-recapture model for single catch trap data

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Keywords: density estimation, live traps, small mammal traps, mcmc, Bayesian framework

Abstract: Spatial capture-recapture models have been developed in the literature to estimate demographic parameters for spatially collected animal detection data. As it stands, a method to appropriately model data collected in single-catch traps is lacking. Single-catch trap designs, for example small mammal trap arrays, induce a complex dependence structure between animals. Currently, the standard approach is to ignore this dependence and treat the animals as independent; this approximation does well in a suite of conditions. However, we show that ignoring dependence between animals leads to bias and poor coverage when the size of the population is large relative to the number of traps. Here, we develop a fully-specified hierarchical model for single-catch trapping surveys analysed in a Bayesian framework. We present a simulation study, which shows that for single-catch data, the bias from a multi-catch model increases with trap saturation, while the single-catch model typically outperforms the multi-catch model in terms of bias, coverage and mean squared error. We apply this to a study on Microtus and show the differences in bias of relative abundance parameters between the commonly used approximation and our single-catch trap model. Additionally, we present an approach for trapping methods that may allow more than one individual on rare occasions. With the prevalence of single-catch traps, this model should be widely applicable to a number of studies and other techniques where the order of capture matters.

Flexible Density Surface Estimation for Spatially Explicit Capture-Recapture Surveys

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Keywords: abundance, spatially explicit, capture-recapture, spatial ecology.

Abstract: Although maximum likelihood methods for spatially explicit capture-recapture (SECR) survey were formulated by Borchers and Efford (2008) using a general nonhomogeneous Poisson process to model animal home range (or activity centre) locations, all published implementations of this SECR method to date assume a homogeneous Poisson process for locations - which implies uniform animal distribution in space. Although such a model is statistically convenient, in many applications a homogeneous Poisson process is likely be unrealistic, as animal density is seldom uniform in space.

Efford (2013) has implemented nonhomogeneous Poisson process models with parametric models for the dependence of density on explanatory variables, but this kind of model has limited scope for flexible modelling of animal density surfaces. In this talk I develop and illustrate maximum likelihood-based SECR methods with flexible nonhomogeneous Poisson process animal density models, using a generalized additive model formulation for the dependence of density on explanatory variables. I consider both additive univariate smooths and multivariate smooths of explanatory variables. The strengths and vulnerabilities of the methods are illustrated by application to a variety of SECR datasets.

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Abundance and demography via close-kin, from lethal- or non-lethal sampling of adults alone

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Keywords: abundance, population dynamics, capture-recapture, survey design and analysis

Abstract: Close-kin mark-recapture (CKMR) is a revolutionary tool for assessing absolute abundance, demographics, and spatial structure. It can avoid many difficulties of traditional mark-recapture, for example the expense of live-capture-and-release. The idea is to use "DNA profiling" to identify close relatives (e.g. parent-offspring pairs), then to apply mark-recapture principles to the number and pattern of relationships found. CKMR has been successfully used to estimate the absolute abundance of Southern Bluefin Tuna, but that situation is unusual (at least among fisheries) since known-age-juveniles as well as adults can be sampled. We have now generalized CKMR to a more common situation: capture of adults only. This talk shows how the precision of abundance and trend estimates is affected by study duration, availability of age data, lethal vs non-lethal sampling (where CKMR and conventional MR are combined), and of course sample size. We present two examples. The first uses non-lethal CKMR to dramatically improve the efficiency of a proposed mark-recapture study on blue whales. The second example concerns culling a species with basically no prior demographic information; can an excessive rate of culling be detected before it is too late, just from lethal samples collected during the cull?

Making R available to a wider audience: an example in power analysis software for capture-recapture studies

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Keywords: abundance; capture-recapture; population dynamics; survey design and analysis

Abstract: A question that many of us face is how to get our statistical developments to reach a wide audience. Although many ecologists are now using R, this tends to be on an occasional basis such that commands and syntax need to be re-learnt each time, representing a barrier to uptake even when statistical code is highly customised and easily available. Some new R tools, such as the Shiny package (RStudio and Inc. 2013), make it easy to create simple, interactive user interfaces to complex code. The interface opens in the user's web browser, and can also be run remotely. A simple user interface takes minimal effort to create and finalise, but things do get more complicated if subsequent options for display must depend upon previous choices made. I will demonstrate a user interface for new software 'CaPow' that we have developed for power analysis in capture-recapture studies, based on the 'POPAN' model (Arnason and Schwarz 1996). The primary focus is to determine whether the study design is likely to have the power to detect a specified rate of annual increase or decrease in population size. A typical question might be whether, given funding for six annual surveys, it is better to space them biennially (2014, 2016, . . . , 2024), or in two blocks of three (2014-2016, 2022-2024). The software allows users to simulate from any model they like, and fit any other model they wish, so that the impact of model misspecification can also be investigated. The interface design may be useful for many other applications in statistical ecology.

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Population dynamical effects of spring migration phenology in passerine birds

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Keywords: population dynamics, movement ecology, citizen sciences

Abstract: Migratory birds vary in their ability to adjust their timing of spring migration to earliness of spring. Negative correlations between spring arrival and population trends have been reported in earlier studies. A proposed explanation for this pattern is a temporal mismatch between food availability and requirement, which is thought to be of special concern in long distance migratory birds. To unravel possible drivers of population dynamics, we here study annual breeding population growth of 15 short distance and 12 long distance migratory passerines in southern Finland based on population indices estimated from standardized national monitoring data. Each species' phenological distribution of spring arrival is estimated using a non-linear negative binomial regression. The model fit is further used to obtain annual phenological covariates, which are applied in a density dependent population model with lags of zero and one. We hypothesize that phenological effects operating through reproduction (e.g., trophic mismatch) should be found with a one year lag, while variation in migration behaviour (e.g., climate induced prolonged migration) can cause correlation between phenology and local population densities without a lag. Results from naïve process error models and state-space models with predefined observation errors are analysed in parallel. In general, we found relatively little evidence for links between phenology and population growth. In contrast to what would be expected from earlier studies, most effects found were immediate, suggesting correlations between timing of migration and settling behaviour during migration, rather than effects on reproduction. We propose that boreal migratory birds might be better buffered against variation in spring earliness than previously thought.

Application of Bayesian integrated population models to national bird monitoring: a practical perspective

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Keywords: abundance, citizen sciences, integrated population models, monitoring of biodiversity, population dynamics.

Abstract: Many countries have instituted a national bird population monitoring scheme to track annual fluctuations in the abundances of widespread bird species over time. Understanding the environmental causes behind the fluctuations in a particular species, however, requires knowledge of variation in demographic rates: recruitment, survival and dispersal. These too may be monitored at large spatial scales, particularly through ringing and nest-recording schemes. Although each of these parameters may be analysed individually, much greater insight should come from analysing the data in combination, since each observed dataset may contain information on more than one parameter. We make use of recent developments in state-space (hidden-process) modelling to construct hierarchical population models for a number of species with a range of life-history and ecological strategies. We fit these models to combined census, productivity and survival datasets collected by volunteers participating in the BTO's national monitoring schemes, using MCMC estimation in JAGS. We introduce a scaling parameter into the models to account for unmeasured processes and assess to what extent this influences inference about population dynamics. We show that the models provide useful demographic insights and that by integrating the available datasets they enable one to explicitly assess the importance of unmeasured variables, which can be helpful in formulating conservation policies.

Designing volunteer based monitoring programs for Natura 2000 species in Flanders

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Keywords: citizen sciences; survey design and analysis; occupancy models

Abstract: European member states have to report every six years on the conservation status of Natura 2000 species in the framework of the Habitat and Bird Directive. The European Commission (EC) demand that this reporting is based on statistically sound data. The monitoring network should be able to detect a decline of the population with about one quarter in a period of 24 year. In Flanders, monitoring data will be mainly collected by volunteers. Therefore designing monitoring networks is not just a statistical exercise, but it also has a social dimension. Volunteers tend to prefer visiting sites closer to their homes and the more ‘interesting’ sites. It’s a challenge to find a good balance between optimal design from a statistical point of view and site preferences by volunteers.

We follow two complementary approaches to fill in information needs: (1) standardized monitoring networks for a set of priority species, and (2) analysis of unstandardized data using site-occupancy models. Standardized monitoring networks provide the best guarantee to obtain unbiased results but are quite expensive. We aimed at achieving a pragmatic design that both provides the necessary information and guarantees sufficient participation of volunteers. To guide this process we performed power analyses and closely involved volunteer organisations. This process revealed that it is not possible to develop monitoring networks for all species due to its high costs or practical constraints. Therefore, for a number of species we decided to rely on unstandardized data collected and reported by volunteers. The challenge is to analyse the data taking into account site selection bias and differences in observation effort between years. Site-occupancy models have been proven successful in deriving trends in occupancy while coping with differences in observation effort. Yet, we should be aware of its limitations.

Applying multiple imputation on waterbird census data

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Keywords: missing data; citizen sciences; monitoring of biodiversity; survey design and analysis

Abstract: The bulk of waterbird censuses are conducted by volunteers. Shifts in availability of volunteers leads to missing data. Missing data in waterbird censuses are commonly imputed using the method described by Underhill and Prys-Jones (1994). This method models the raw counts in terms of several covariates like site, month, year,... The missing data are imputed by the predictions of this model. Finally, the augmented dataset is analyzed.

Since this method uses the predicted values to impute to missing data, the variances of the parameters of the final analysis are likely to be underestimated. Two key factors play a role in this. Firstly, the apparent number of observation in the final analysis is higher than the true number of observations. Secondly, predicted values are less variable than raw counts. Therefore the imputation adds data with much smaller variation. Furthermore, the method potentially biases the parameters estimates, depending on the starting values of the imputation.

We compare this imputation method with a model-based multiple imputation (Rubin, 1987). A missing value is imputed by random number based on the distribution of the prediction for this value rather than the predicted value itself. The variance of the augmented dataset will increase depending on the uncertainty of the imputations and is most likely higher than when a complete dataset would have been available. Whereas imputing predicted values would result in a lower variance compared to a complete dataset. Next, we apply the same analysis to the augmented dataset. The results will off course depend on the randomly imputed numbers. We accommodate this by repeating the imputation and analysis process several times. The parameters of interest are averaged over the different imputations. Their standard errors are based on the standard errors of the individual imputations and the variance among the parameter estimates.

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Assessing the use of counts of migrating birds to estimate broad-scale population trends

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Keywords: citizen science; survey design and analysis; population trends

Abstract: A large part of the Canadian boreal forests lies north of human populated regions, and therefore beyond the northern extent of the North American Breeding Bird Survey. Daily counts of birds as they migrate through more populated regions *en route* to or from their breeding grounds is considered a potential alternative to conducting more intensive breeding surveys in those regions. However, migration count data are currently analyzed on a site-by-site basis, and different sites could be capturing different sub-populations with different underlying rates of population change. Using simulated migration count data with known constant rate(s) of population change, we assessed the value of a network of migration monitoring sites for estimating regional and national population trends by determining 1) what level of precision in estimated trends could be achieved with varying numbers of monitoring sites under ideal scenarios for a common and rarely detected species (i.e., model assumptions match simulated data); 2) how much bias might be expected in population trends if model assumptions do not match underlying data (e.g., population trends vary geographically, but model assumes they are the same, or vice versa); and 3) whether model selection procedures (AIC) are able to detect and model regional variation in trends with current or increased numbers of sites. Simulated data were fit using a log-linear regression model with Poisson distribution of counts and hierarchical terms to account for stochastic site, year by site, and day by site effects. Models that assumed a single rate of change were compared to models that allowed the slope of the trend to vary among regions. Results will be discussed in terms of their implication for using a network of migration monitoring sites for broad-scale population monitoring.

Spatial epidemiology of foulbrood diseases in honey bees

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Key words: K-functions, Cuzick-Edwards, apiary network, process-based modelling

Abstract: Foulbrood diseases remain a threat to the European honey bee (*Apismellifera*) due to a poor understanding of disease epidemiology. We present an analysis of the spatial ecology of European foulbrood disease, demonstrating that it is significantly clustered in space independent of the inhomogeneous arrangement of bee colonies in the UK apicultural network. We describe an individual-based model of foulbrood disease based on the spatial analysis of the apiary network, which accounts for local movement (via drifting and robbing) as well as global movement (via beekeeper behaviour). According to our model, factors influencing beekeeper behaviour can account for a large proportion of new infections of European Foulbrood disease, both in discovery of infection and in moving of disease to disparate parts of the apiary network. Consequently, improving links between beekeepers and regulatory agencies can potentially decrease disease incidence in the UK.

Comparing survival estimates from unmarked population- and individual-level data

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Keywords: integrated population model; abundance; population dynamics

Abstract: Models of population dynamics allow us to estimate population growth or decline and to predict responses to environmental change. Parameterizing these models typically requires demographic data at the individual level, collected by marking or - in some experimental settings - isolating individuals from the population. However, these methods can unintentionally alter demographic rates by reducing the fitness of marked individuals in the wild or changing their environment in isolation. Thus, there is a need for methods that enable the estimation of demographic rates without individual data.

Stage-structured N-mixture models were recently developed to enable the estimation of state-specific vital rates using repeated state-specific counts of populations of unmarked individuals (Zipkin et al. 2013). We extend the stage-structured N-mixture model to apply to a time series with uneven sampling intervals. Such uneven or irregular sampling periods often occur in long term monitoring programs.

We apply this method to an extensive laboratory experiment of soil mite populations. Individual vital rates were observed by isolating and monitoring individuals for 24 hour periods. Stage-specific population counts were done twice per week, creating uneven sampling times. Mites were observed eating other mites, but it is unclear if this behaviour was simply scavenging or killing. To test if mortality was higher in the population than for isolated individuals, possibly due to cannibalism, we compare estimates of daily mortality from the stage-structured N-mixture model to the individual data.

If time permits, we will present further extensions including covariates and comparison of multiple fitting algorithms.

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Ecological modelling in BUGS: Some tricks of the trade

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Keywords: Population dynamics, multispecies models, integrated population models

Abstract: The use of the BUGS programs (OpenBUGS and WinBUGS) is popular within the ecological community for analyses that use Markov chain Monte Carlo. Numerous books and papers have been written on the subject, covering topics including population dynamics, capture-recapture, hierarchical models and more. Despite its utility, the BUGS programs have a number of limitations. While the potential for long computational times is one of the most frustrating, there are also restrictions on the distributions available to users, and how the defined distributions can be implemented. This can be overcome by using the BlackBox Component Builder, which allows users to define their own distributions and functions. This requires some familiarity with coding in Component Pascal, and is a topic best learned in a computer classroom. An alternative to BlackBox is to use the statistical properties of distributions to approximate them within BUGS. I will use two case studies, hen harriers (*Circus cyaneus*) whose population dynamics model was part of a larger multispecies model, and golden eagles (*Aquila chrysaetos*) for which an integrated population model has been built, to discuss four distribution-related limitations in BUGS. I will approximate two distributions not available in BUGS, the double Poisson and discrete uniform, and two whose use can be restricted in BUGS, the multinomial and Dirichlet. In general, knowledge these and other approximations is important, because not only can it overcome limitations in BUGS, but it can also be used to improve the efficiency of the Markov chain simulations.

Estimation of time-varying selectivity in fish stock assessments using state-space models

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Keywords: Stock assessment; Selectivity; State-space models; Catch-at-age analysis

Abstract: Time-varying selectivity is one of the main challenges in single species age-based assessment models. In classical deterministic VPA-type models the fishing mortality rates are unfiltered representations of the observed catches. As a consequence the selectivity becomes time-varying, but this representation is too fluctuating, because it includes the observation noise. In parametric statistical catch at age models a common assumption is that the selectivity is constant in all years, although time-varying selectivity can be introduced by splitting the data period in blocks with different selectivity, or by using smoothing splines and penalized time-deviances. However, these methods require subjective choices w.r.t. the degree of time-varying allowed. A simple state-space assessment model is presented as an alternative, which among other benefits offers an objective way of estimating time-varying selectivity pattern. The fishing mortality rates are considered (possibly correlated) stochastic processes, and the corresponding process variances are estimated within the model. The model is applied to North Sea cod and it is verified from simulations that time-varying selectivity can be estimated.

Combining matrix models with life-history theory to improve estimation of intrinsic growth for data-poor populations

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Keywords: integrated population models; population dynamics

Abstract: We integrate matrix models with allometric life-history theory, allowing us to improve the precision of estimates of intrinsic growth ($r_{\max}$) for data-poor populations. This work is motivated by our research on marine megafauna (e.g. sharks, sea turtles, marine mammals, and seabirds) where better understanding of intrinsic growth is needed in order to understand the ability of these populations to withstand directed or incidental catch in fisheries. Commonly, estimation of $r_{\max}$ is done through the use of matrix population models or by modelling population trends over time. Data challenges and/or model assumptions for either approach are substantial, with empirical estimates of $r_{\max}$ being limited to a small subset of populations. An alternative approach based on life-history theory uses allometric relationships between body mass, generation time, and $r_{\max}$ to estimate intrinsic growth with few demographic parameters. The allometric approach provides estimates for many additional data-poor populations, requiring only age at first reproduction and optimal adult survival. While allometric estimates of $r_{\max}$ represent growth of average, rather than individual, populations, this approach has proven useful in conservation settings. However, for populations where survival estimates are poor (e.g. sharks), or where productivity estimates for individual, rather than average, populations are desired, none of the current methods are satisfactory. Integrating the two methods using available data, we can estimate intrinsic growth for either average or individual populations, even where survival is poorly understood. After describing the method, we apply it to sharks, particularly focussing on a species of population concern, the white shark (*Carcharodon carcharias*).

How much does the choice of process model matter when combining data from multiple surveys?

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Keywords: integrated population models, population dynamics

Abstract: We consider the consequences of including more or less biological detail in the process model component of an integrated population model. We consider three possible process models: a state-space time series model with vague biological detail, a purely biological model with vital rates estimated from a banding program, and a hybrid combination. We apply these models to annual data on Mourning Doves in the US Central Management Unit. Unknown parameters in the process models are estimated by combining four data sources: three surveys providing indices of population size and a harvest-based estimate of population size. Estimation was by two-stage MCMC using samples of secondary data. The choice of process model was evaluated by both DIC and the root-MSE-prediction of 2010 log population size from a model fit to 2003-2009 data. The hybrid approach was favored by both the DIC and root-MSE-prediction criteria. For these data, the state-space model tended to overestimate the log population size. The biological model and hybrid model tended to underestimate the log population size, probably because of poor estimates of some vital rates. The hybrid model is judged to predict better because estimates from it are less variable. Mourning dove management is based on the posterior distribution of trend estimates for the previous three years. The posterior distributions for the three process models are slightly different, but management conclusions are similar. The degree to which the choice of process matters depends on the analysis goal. If predicting future population size, the choice makes some difference; if predicting trend, the choice makes little difference, at least for these Mourning Dove data.

Metapopulation Dynamics in the *Cakile maritima-Alternaria brassicicola* Host-Pathogen Interaction

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Keywords: Abundance, Bayesian modelling, Disease ecology, Metapopulation dynamics, Multispecies model, Plant epidemiology, Spatial ecology

Abstract: Spatial structure is an important determinant of epidemiological dynamics in host-pathogen systems, and is therefore central to explaining observed patterns of disease. However, the characteristics of individual populations can counterbalance metapopulation processes. Our goal was to quantify how much of disease dynamics at the population level was explained by individual population characters *vs.* metapopulation structure. A total of 61 populations of *Cakile maritima* - *Alternaria brassicicola* dispatched into three distinct metapopulations along the cost south to Sydney (New South Wales, Australia) were surveyed during 5 years (42 observation times). At each observation time the abundances of healthy and diseased plants were recorded. Local environment was characterized by physical variables (*e.g.* beach size, exposure) and climatic variables (*i.e.* temperature and rainfall). In order to analyse this dataset, we developed a spatially explicit metapopulation model for two species in interaction. Inference was performed within a Bayesian framework. Plant dynamics were mainly local which is consistent with the dispersal mode of *C. maritima*. In contrast the pathogen dynamics were mainly driven by metapopulation processes. Plant exchanges among beaches were higher from small and rocky beaches, but colonization was easier and populations were more perennial in large and sandy beaches. Beach exposure played also an important role with exposed and open-to-sea beaches favoring plant exchanges but with sheltered beaches hosting more perennial plant populations. Monthly cumulative rainfall had a positive effect on the pathogen dynamics and a negative effect on the plant. Increase in temperature favored both the plant and the pathogen. The model we developed allowed us to assess correlations between demographic and environmental parameters while taking into account the spatial structure. This framework could be used to study the metapopulation dynamics and pattern of coexistence among interacting species.

NEW ANALYTICAL METHODS FOR CAMERA TRAP DATA.

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Keywords: abundance; integrated population models; capture-recapture; camera trapping and random encounter model.

Abstract: To monitor animal populations, camera traps use fix cameras, which are triggered by infra-red sensors to ‘trap’ images of passing animals. Camera traps are commonly used for animals with individually unique markings where capture-recapture models can be used. We consider how camera trap data can be used for animals without these unique markings. The Random Encounter Model (REM), developed by Rowcliffe *et. al* (2008), models the underlying process between animals and camera traps, without the need for individual recognition of the animals. The REM describes the rate of contact between animals and camera traps, from which an estimator for animal density can be derived. The REM of Rowcliffe *et. al (*2008) models the trapping rate data and assumes a fixed value for animal speed of movement data, which is estimated as the average of the available data. We developed a maximum likelihood framework to model both data sets simultaneously, as this gives a more unified approach to estimation. We illustrate this method using data from a camera trap experiment at Whipsnade Animal Park (July, 2005), focusing on four species: Wallaby, Water deer, Mara and Muntjac. The method will be improved by adding covariates such as climate – temperature and rainfall, detection zone and camera. As the success of this technique is clearly dependent on a reasonable number of photographs, we explored the effect of increasing sampling effort on the precision of density estimates using simulation. The method will be applied to a larger dataset from the tropical moist forest of the Baro Colorado Island, Panama.

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Chasing Shadows: Analysing Data from Camera Trap Studies

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Keywords: capture-recapture, spatially explicit capture-recapture (secr), camera traps, abundance, density

Abstract: Advances in technology have led to new ways of "capturing" animals including DNA analysis and camera traps that are especially useful for monitoring rare and elusive animals. Traditional capture-recapture (CR) and spatially explicit capture-recapture (SECR) models are based on a discrete sampling process that leads to well defined sampling occasions, but camera traps are continuous-time samplers which record the exact time of capture.

We develop continuous-time models for camera trap surveys, discuss their strengths and weaknesses relative to discrete-time models, and suggest aspects of the models that would benefit from further development. We use a continuous-time estimator to estimate jaguar density from a camera trap survey in Belize and investigate estimator properties by simulation.

Horvitz-Thompson Whale Abundance Estimation Adjusting for Uncertain Recapture, Smoothed Availability Trends and Interrupted Effort

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Keywords: abundance, capture-recapture

Abstract: We examine the use of an unusual Horvitz-Thompson type estimator developed for the estimation of total population abundance of the Bering-Chukchi-Beaufort Seas population of bowhead whales in 2011 based on visual sightings and acoustic locations obtained from ice-based visual observation stations and submersed marine acoustical units. What makes this analysis unique is the derivation of three estimated correction factors required to account for complexities presented by the survey protocol and resulting features of the dataset. The first factor adjusts for detectability using uncertain recapture data to estimate detection probabilities and their dependence on offshore distance, ice condition, and whale group size. The second correction adjusts for availability using the acoustic location data to estimate a time-varying smooth function of the probability that animals pass within visual range of the observation stations. The third correction accounts for missed visual watch effort. Uncertainty in the estimates of these corrections is propagated into the final abundance estimate and an associated estimate of population trend that incorporates a time series of past estimates. Although some of the particulars of the approach are closely connected to the bowhead application, adjustments for detection, availability and effort are common and some of the methods discussed here could be adapted for abundance surveys facing similar challenges. Aside from the novel statistical aspects of our approach, the results of its application to bowhead whales has played a crucial role in the safe management of subsistence hunting of this species under the guidance of the International Whaling Commission.

Partial stratification in two-sample capture-recapture experiments.

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Keywords: capture-recapture; abundance, survey-design and analysis

Abstract: Capture heterogeneity is known to case bias in estimates of abundance in two-sample capture-recapture (Lincoln-Petersen) experiments. Often this heterogeneity is related to observable fixed characteristics of the animals such a sex or size. If this information can be observed for each handled animal at both sample times, then it is straightforward to stratify (e.g. by sex) and obtain stratum-specific estimates. In many fishery experiments, it is more difficult, for example to sex all captured fish. In these cases, a sub-sample of the captured fish at each sampling occasion is selected and further, more costly, measurements (e.g. sex determination through sacrificing the fish) are made. Our data now consists of three parts – animals whose stratification variable is unknown, and sub-samples at each occasion where stratification variables are determined.

In this talk we develop and apply new methods for these types of experiments. Furthermore, given the relative costs of sampling for a simple capture and for processing the sub-sample, optimal allocation of effort for a given cost can be determined. We also develop methods to account for additional information (e.g. prior information about the sex ratio) and for supplemental continuous covariates such as length. These methods are applied to a problem of estimating the size of the walleye population in MilleLacs, MN.

Using AD Model Builder for spatially explicit capture-recapture inference with passive detectors

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Keywords: Abundance, Capture-recapture.

Abstract: AD Model Builder (ADMB) is a software suite designed to carry out efficient and stable numerical optimisation of a complex likelihood function. Although it was originally developed with fisheries stock assessment models in mind, it is beginning to gain popularity outside fisheries science. One such area in particular is that of animal abundance and density estimation; currently ADMB plays a significant role in both distance sampling and spatially explicit capture-recapture (SECR) software development. This talk will focus on the utility and performance of ADMB in the latter. SECR extends traditional capture-recapture methods by using known locations of traps where animals were (and were not) captured. This information is then used to account for between-animal heterogeneity in detection probability due to differences in individuals' home range centre locations. SECR also allows abundance and density estimates to be obtained from a single sampling session when animals are detected passively (e.g., acoustically or visually by microphones, cameras, or human detectors) rather than by physical capture. The R package `admbsecr` fits models to SECR data collected with passive detectors, and uses ADMB to obtain maximum likelihood parameter estimates. We illustrate by using `admbsecr` to estimate animal density from a number of different kinds of passive acoustic survey.

Estimating Red Snapper Harvest by Charter Boats in the Gulf of Mexico

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Keywords: abundance; capture-recapture

Abstract:

A year-long for-hire study conducted by the National Marine Fisheries Service of catch by charter boats in the Gulf of Mexico allowed for estimation of expected Red Snapper harvest from two data sources: logbook and dockside reports. The former contained information reported directly by vessel captains and the latter required hiring port officials to verify catch quantities. We defined an estimator for expected harvest, τ, where $\tau = N\psi\gamma$ is a function of the expected number of trips N, expected effort ψ in hours spent fishing, and the expected catch per unit of effort (cpue) γ in numbers. We employed a Bayesian approach to estimate τ and obtained 95% credible intervals directly from the quantiles of the posterior distribution. A posterior predictive distribution of τ was computed by multiplying samples from posterior predictive distributions of expected cpue, expected effort, and expected number of trips. Selecting a distributional form for effort was complicated by the presence of extreme values while the distributional form for cpue was complicated by a high peak in the data with scattered larger values present. Additional verification sampling was conducted to estimate the percentage of compliance for estimation of expected number of trips. Credible intervals of weekly and cumulative expected harvest during the Red Snapper harvest season, June 1^{st}-July 18^{th}, 2011, from logbook reports and dockside reports largely overlapped. Overall, logbook reports provided comparable results and narrower credible intervals to the more reliable dockside reports.

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SCGLR: a component-based multivariate regression method to model species distributions.

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Keywords: Tropical forests, species distributions, generalized linear models, regression, partial least square, Fisher scoring algorithm

Abstract: Understanding how environmental factors spatially impact species coexistence is of primary importance in ecology. Species distribution models are statistical or mathematical models combining observations of species occurrence or abundance with environmental factors. They are used to gain insights into ecological and evolutionary processes and to predict distributions across landscapes, sometimes requiring extrapolation in space and time. Generalized linear models (GLM) are frequently used for modeling species distributions. Nevertheless GLM can suffer from different limitations: (i) the classical approaches do not allow the simultaneous modeling of multiple species (ii) the level of model realism and the prediction robustness can be poor if relevant predictors are omitted. We propose a regularizing component-based technique, supervised component generalized linear regression (SCGLR), which extends the Fisher scoring algorithm by combining partial least square (PLS) regression with GLM estimation in the multivariate context. The proposed method can handle different types of dependent variables (occurrence, abundance, growth) and explanatory variables mixing different types, and account for additional covariates. We illustrate SCGLR and the associated R-package using a dataset built from the abundance of 27 common tree genera in the tropical moist forest of the Congo-Basin and 40 geo-referenced environmental variables collected in the CoForChange project[1].

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Do old-growth birds go to secondary forest? A multi-species hierarchical model of site occupancy by Amazon forest birds

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Keywords: multi-species model; zero-augmentation; site-occupancy; birds; bioacoustics; Amazon forest.

Abstract: Avoidance of an anticipated mass extinction of tropical forest species relies on whether old-growth species can survive in secondary forests. It has been established that old growth and secondary forest faunas become increasingly similar with time and do so faster at shorter distances between forest types; a tentative time window of 20-40 years has been proposed for full recovery of bird species richness. Here, we document the slow recovery of bird species richness in 25-year-old central Amazonian secondary growth and test predictions about which species are most likely to colonize disturbed forest habitats. Combining autonomous recording of bird vocalizations and multi-species hierarchical models developed in a Bayesian framework, we estimate site-occupancy parameters for 140 species in 151 secondary forest and old growth sites distributed over 350 square kilometers. Species richness, estimated with a zero-augmentation approach (Kéry and Royle 2009), was surprisingly similar between the two types of habitat: 15% higher in old growth than in secondary forest. Nonetheless, our species-specific *a priori* predictions of forest-type preference misrepresented a large number of species, partly due to detection failure. A majority of species occupies both forest types indifferently, but when they don't they are more likely to avoid than to favor secondary growth. Most of the species that were predicted to favor secondary forest are easier to detect there, but occupy both types of forest without distinction. Our results document a slow secondary-forest recovery through re-colonization from old growth, reflecting the irreplaceability of undisturbed forests but also stressing the potential value of secondary forest habitats for tropical forest species. This work illustrates the potential of combining a technological innovation in field sampling with multi-species hierarchical models to answer pressing applied questions at a very broad spatial and taxonomic scope.

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Bayesian modeling to identify and map multi-species change points in the North American population trends of avian aerial insectivores.

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Keywords: multispecies models; population dynamics; spatial ecology.

Abstract: Many North American populations of swallows, swifts, nightjars, and flycatchers (avian aerial insectivores, hereafter "AI"), are declining. There is some indication that the population trends of species in this group changed, for the worse, in the 1980s. That is, that the population trends of these species share a common change point, presumably as a result of some common response to a change in the environment. To test for a common change point across 18 species of AIs, I fit a Bayesian, penalized regression splines model, using estimated annual indices of abundance from the North American Breeding Bird Survey (BBS). To first generate annual indices from BBS data that would be suitable for this type of model—indices published annually are not suitable—I fit a spatial, Bayesian conditional autoregressive (CAR) model to BBS data from all routes in North America. The CAR model estimates population trajectories separately for each species, while sharing information among neighbouring spatial strata (intersections of Bird Conservation Regions and states/provinces/territories), within each year of the BBS time-series (1968-2011). The results of these models indicate that: 1) there is in fact, strong evidence for two common change points in the population trends of these North American aerial insectivores—one positive, one negative; and 2) the timings of the change points are geographically structured—earlier in the East, later in the West. Future studies to identify covariates that explain the temporal and spatial structure of these change points, may shed light on the causes of AI declines.

Design-based inference about community composition and interactions using multivariate abundance data

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Keywords: bootstrap; Bray-Curtis; generalised linear mixed models; model-based approach; multivariate analysis.

Abstract: Multivariate abundance data are commonly and often erroneously analysed using distance-based algorithms (or techniques related to correspondence analysis), to answer questions concerning change in community composition, or interactions between predictors in their effects on communities. But both composition and interactions are model-based notions and it is shown by example that reliable inference in such situations is not possible without use of a statistical model, and a model that captures key data properties. One key data property that is difficult to capture is correlation between different taxa, because there are typically many more possible pairwise correlations than there are observations in the dataset to estimate them. An alternative approach which can circumvent the issue is using design-based inference, and we will see how block-resampling of residuals constructed via the probability integral transform can ensure valid inference about composition and interactions even when species correlations cannot feasibly be modelled. The approach is quite general, and in the mvabund package, it has been implemented in a very flexible framework capable of handling many common types of predictive model. The approach will be illustrated by example, including study of how species traits mediate changes in environmental response across species (the "fourth corner problem").

Bayesian parameter estimation of a multi species size spectrum model of the North Sea

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Keywords: multispecies models; population dynamics

Abstract: Size spectrum models have been recognised as being a simple way of describing fish in a large community. They are complex ecological models that are solutions to partial differential equations which are driven by ecological rules and algorithms. Until Blanchard et al. (2013) fitted their model to 12 interacting fish species and a background resource community, which account for 90% of all species trawled in the North Sea, to time averaged data from 1985-1995 these models had not been applied to real data. They found that the difficult parameters to estimate were the maximum recruitment for each species, R_{max} and the level of background resource carrying capacity, κ. The authors found a point estimate of these parameters.

We are attempting to fit R_{max} and κ to data from 1967-2010 using time varying fishing effort, taken from CEFAS (2013), as input to the model in a Bayesian framework. The output of the model, given a particular parameter set, is difficult to estimate due to the sensitivity of the parameters. This, coupled with the high dimensional parameter space, means that emulation of the model is impossible and the only way to get the model output is to run the model which takes about 20 seconds for each parameter set. In addition to this, the posterior distribution is very multimodal which means that standard MCMC would get stuck in local modes and not explore the posterior distribution.

In this talk we will discuss the difficulties of this inference and how we got around these to perform Bayesian parameter estimation of R_{max} and κ. We will also compare results and interpretations between this work and the work of Blanchard et al. (2013).

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Borrowing information: Hierarchical multispecies distribution models

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Keywords: multispecies models; species distribution models; occupancy models

Abstract: There are not enough readily available data to accurately predict the distribution of rare or difficult to detect species using conventional species distribution modelling techniques. To fill this gap, I constructed a hierarchical, Bayesian, multispecies detection-occupancy model with functional trait-based hyper-distributions in order to 'borrow information' from common species to help predict distributions of rare species. Regression coefficients and intercepts vary for each species and are informed by trait-based hyper-distributions. The model accounts for imperfect detection as well as including random effects to account for residual variation. I compare performance of this multispecies distribution model to progressively simpler models, and those models to each other, along a species prevalence gradient for woodland-dependent birds of the highly-fragmented box-ironbark forests of southeastern Australia. I evaluate if, and by how much, model performance is improved with respect to accuracy, precision and bias by the addition of random effects, hierarchical structures, functional traits and detection-occupancy modelling. I ask: can species distributions be accurately and precisely predicted without bias in the absence of occurrence data? Overall, the addition of a hierarchical structure, without traits, improved accuracy and precision of the model. The subsequent addition of random effects decreased precision to lower than a basic logistic regression with all species modelled independently, a comparatively more honest representation of the confidence in the predictions. Before accounting for imperfect detection, low prevalence species occurrence probability tends to be well predicted by simpler models because of a potentially false high certainty of low probability of occurrence.

Incorporating species interactions into predictive species distribution models for invasive species

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Keywords: species distribution models, spatial ecology

Abstract: The field of species distribution modelling has become increasingly complex as models have advanced from modelling single species to incorporating interactions between species within a single model. Here, we develop a model that specifically incorporates interactions between competing pollinator species and their host plants. We utilize a generalized additive model as the basis for the species distribution model. This model is calibrated based on current environmental variables; however, to predict future species distributions, future scenarios of climate and land use change are used. The merits of including dispersal rate, environmental tolerance ranges and different environmental variables will be discussed. As a practical application, this model is applied to native honey bee (*Bombus occidentalis*) and introduced, invasive honey bee (such as *Apis mellifera*) species in North America, where competition has resulted in a decline in the native honey bee population.

Flexible spatial models and their relevance in ecology

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Keywords: spatial ecology.

Abstract:

Statistical models typically rely on a number of distributional assumptions, which might or not be met in practice - with all the implications on the validity of the conclusions drawn from the model. This is particularly relevant in ecology; however surprisingly few flexible methods are available that are directly linked to a standard model. The approach we discuss here explicitly incorporates deviation from a standard model into the modeling process. This is done within an extended family of models that has a basic standard model at is centre.

This family is constructed by introducing an additional flexibility parameter that controls the deviation from the basic model. Instead of parameterising the flexibility parameters directly, we base the distance between the base and the flexible model. Based on this distance we derive meaningful prior distributions for the flexibility parameters. These allow us to interpret the flexible model as a flexible version of the basic model. Shrinkage to the base model is warranted when supported by the data, but moderate deviations from the base model are properly captured if required.

Further, the approach can directly be integrated into the R-INLA software. Hence we are able to work with more flexible models without loosing the usual benefits of integrated nested Laplace approximation (INLA; Rue et al. 2009), i.e. short computation times and high accuracy. This extends the toolbox of models available in R-INLA and makes these models accessible to a wide audience of users. We illustrate the methodology with a number of relevant ecological examples.

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Variable Selection in Ecological Habitat Modelling

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Keywords: spatial ecology

Abstract: Habitat modelling in ecology is becoming increasingly relevant in population dynamics, biodiversity and conservation studies. A typical application of these models is to predict potential zones of specific conservation interest. The availability of many environmental covariates, measured *in situ* or with remote sensors, means that a large number of models can be investigated, which in turn often renders multi-model inference impratical. Model-averaging, however, is important to address model uncertainty and to prevent over-estimating effect size. Shrinkage regression deals with the identification and accurate estimation of effect size. In a Bayesian framework, we investigated the use of a recently proposed shrinkage prior, the Horseshoe prior (Carvalho *et al.* 2010) for variable selection in modelling the habitat of small pelagic fish in the Gulf of Lions, France. Using spatially-explicit generalized linear models on 5 different data sets from the `IFREMER` acoustic survey `PELMED 2011` and more than 10 environmental covariates, we compared the ability of a simple kriging model with no covariate, a saturated model with independent normal priors for regression coefficients and a saturated model with a Horseshoe prior for regression coefficients. Each model was calibrated on 80% of each data set, and the 20% remaining data was used for cross-validation. With respect to out-of-sample predictive ability the saturated model with a Horseshoe prior performed best, and the saturated model with independent normal priors worst. Overfitting and overestimated effect sizes were to blame: with an increasing number of covariates, extrapolation quickly became pervasive as we tried to predict from combinations of covariate values that were not in the calibration data. Shrinking regression coefficients toward zero with a Horseshoe prior avoided this problem and required only one model to be fitted to the data to obtain reasonable predictions.

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Ordinal Outlier Prediction Model for the Reconstruction of Badger Territories

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Keywords: spatial ecology

Abstract: In some areas of Great Britain, European badgers *(Meles meles)* can be a potential source of infection for cattle since they are a reservoir of the bovine tuberculosis which could cost £1bn over the next 10 years. The European badger is a territorial animal that uses indirect signs to mark its territory such as communal latrines. The aim of the research is to reconstruct maps of badger territories from data collected through bait-marking, where plastic markers placed in bait have been recovered after excretion and the spatial locations of latrines recorded. Latrines can be classified into three types: hinterland, boundary and outliers i.e. those from extraterritorial excursions. An Ordinal Outlier Prediction Model (OOPM) was developed to reconstruct the territories using cumulative logits to classify the type of latrine from information such as its location, types of other latrines in the same direction and other covariate information adjusting for neighbouring territories. This research extends previous work by estimating joint probabilities for different classification of latrines allowing the reconstruction of boundaries of territories with concave areas and quantifying the uncertainty in the reconstruction.

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Spatial spread of the brown rat resistance to rodenticides in Flanders

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Keywords: spatial ecology; survey design and analysis; correlated data

Abstract: Between 2003 and 2010 two 3-year screening periods (I and II) were conducted to monitor the brown rat resistance to rodenticides in Flanders. Resistance was assessed by means of genetic mutations. The aim of the study was to estimate the degree of resistance in Flanders, to test whether there are differences between the 12 river basins, and whether the resistance is increasing over time. Multiple rats per location were caught.

Several statistical analyses were performed on these data. On the one hand, aggregated results per location (presence/absence of resistance, defined in several ways) were analysed using logistic regression (glm), while on the other hand, mixed model logistic regression (glmm) was used on the rat-level to incorporate correlations between rats from a single location.

The level of resistance differed strongly between river basins, some being almost completely resistant, while in others resistance was nearly zero. Correlation was strongest between rats within a location, but variograms also showed a strong correlation between nearby locations ($<$6km).

The number of locations (resp. rats) per river basin ranged from 2 to 54 (resp. 2 to 151) for screening I, and from 4 to 65 (resp. 11 to 110) for screening II. Due to these small numbers, the estimate of resistance was inaccurate for some river basins. Also, evolution of resistance over time was not analysed, since data collection in both screening periods was not comparable. A more balanced follow-up monitoring program, with enough rats and locations per river basin, has been designed to answer all questions more accurately in the future.

Are ecologists divided? Reconciling conflicting views in spatial modelling

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Keywords:community structure and dynamics; multispecies models; spatial ecology; species distribution models

Organisms, along with their environments, present remarkable patterns of variation across space. Unravelling the multiple mechanisms behind the myriad, yet complex patterns that dominate in nature is one of the most important intellectual challenges in the science of ecology. Much as astronomers cannot perform planetary experiments, ecologists cannot easily manipulate most biodiversity patterns because these patterns occur at many different scales. Therefore, ecologists often need to use spatial analytical frameworks (models) to understand the processes that structure biodiversity patterns at large scales such as species distributions, species richness, and species co-occurrence across communities. Although spatial models can provide great insights into these processes, ecologists tend to see spatial autocorrelation as a nuisance that needs to be filtered out of data rather than an interesting property to be studied. Beyond the standard nuisance viewpoint, an alternative and less acknowledged perspective is that the spatial legacy of ecological data can help us challenge heuristic interpretation about ecological processes and improve our understanding of ecological phenomena. While these views can be reconciled, we need to understand well what are the implications of considering spatial structure on different modelling and analytical strategies. To reconcile these two views, I will present study cases and simulations showing how spatial models can be improved by considering spatial variation explicitly. As ecologists commonly, if not always, deal with autocorrelated data, we should see spatial complexity as an opportunity rather than the view in which modelling of spatial data provide difficult challenges. With this view in mind, I will present a number of guidelines and a new spatial framework that should be helpful in understanding and reconciling the two views.

Estimating abundance from multi-state closed capture-recapture data

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Keywords: Closed population; abundance; capture heterogeneity; Great crested newts

Abstract: The aim of this work is to estimate the size of a closed population from ecological capture-recapture data. Typical capture-recapture data is recorded in a binary form indicating on which capture occasions each individual was or was not captured. There are a number of models which can be fitted to capture-recapture data and in particular models have been developed to allow for heterogeneous capture probabilities which more accurately reflect the biological behaviour. However, in many cases the data is not recorded in a simple binary format and instead records the discrete state in which the individuals are observed, for instance, 'breeding' or 'not breeding'. In our case we consider data relating to great crested newts where the states relate to different ponds. We still assume that the population as a whole is closed but we allow individuals to move between ponds within the study period. The use of the additional state information can be justified by considering that state-dependent capture probabilities may be different and failure to account for this would result in biased population estimates. By allowing the capture probabilities to be state-dependent we need to model the transitions between states since the state of an individual will not be observed at every capture occasion (i.e. when we miss the individual). The multi-state model we develop here can be considered as a closed form capture-recapture equivalent of the Arnason-Schwarz model for open capture-recapture data and allows individuals to move between states with varying capture probability.

We use simulation to demonstrate how the estimate of population size can be biased when movement between the different states is not accounted for and to assess the performance of the multi-state model in comparison to existing heterogeneity models. We also consider the issue of state uncertainty before applying the multi-state model to an ecological data set on Great crested newts.

Density dependent mortality in a European eel population: A Bayesian integrated population modelling approach

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Keywords: Abundance, capture-recapture, density-dependence, mortality, population dynamics

Abstract: Density dependent processes can have a strong impact on the dynamic of populations through their effect on one or more vital rates such as growth, mortality or fecundity. Intra-specific competition in a population is a very common mechanism of density dependence caused by limited availability of an essential resource such as space or food.

The understanding of density dependent mortality is especially interesting for species that strongly compete for food and/or space. Traditionally, an estimate of density is obtained and used as a covariate in capture-recapture models to explain the temporal variation of survival probability. Because it neglects the errors made on the measurement of the covariate, this approach is known to underestimate the effect of density.

Here, we propose to combine in a single framework a standard open capture-recapture model to estimate survival probability and a depletion model to estimate density. As a case study, we consider the European eel, for which, despite compelling evidence that it is declining throughout its range, density in catchments still remains at high levels particularly in small coastal catchments of western France.

In this work, we analyzed density-dependent mortality of an eel population quantitatively sampled by electrofishing and individually marked using PIT (Passive Integrated Tags)-tags during 10 years (1996-2005) in the Frémur. We compare the results from our approach to those obtained by using the naïve approach. Besides, the accuracy of the integrated model and its potential use for other fish species is discussed.

Can we learn about the spatial pattern of species' abundance from its probability of presence?

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Keywords: abundance, occupancy models, species distribution models, survey design and analysis.

Abstract: Accurate measures of species' abundance across space are crucial to their effective conservation and management. Many sampling methods and statistical tools have been developed to estimate species abundance per unit area. While density is a desirable state variable to report, there are two main practical issues in estimating it. First, even when possible to measure accurately, large-scale density sampling is prohibitively expensive in many cases. Second, animal abundance estimation is sensitive to detectability, but survey methods seldom detect all individuals present in an area. Because collection of presence data is much simpler to implement, many research programs rely on it to obtain approximations to species abundance. Indeed, collecting presence-absence data at a series of locations has become a preferred method of evaluating ecological status and trends, with statistical models relating species' presence to environmental variables used to interpolate between (or extrapolate beyond) the locations where species' presence is known. However, the statistical analysis of presence-absence data and the ability to infer abundance from such data has been questioned, because detection is seldom perfect and occurrence probability may not be linearly related to density. Here we used statistical models and data on the spatial distribution of North Pacific Right Whale (*Eubalaena japonica*) from 19th century American whaling voyages, to investigate if probability of presence is representative of abundance in this species. Given the short exploitation period (<20 years, implying little natural replenishment) and the nearly species extinction, it is an excellent test case for testing this relationship, as both occupancy and abundance can be accurately estimated. We assessed the effect of data quantity and quality by performing calculations with different subsets of the data.

Accounting for selective reporting in occupancy-abundance models for fishery-dependent data on bycatch species

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Keywords: abundance; occupancy models; population dynamics.

Abstract: Data collected as part of fisheries monitoring programs are often the only regular source of information on occurrence of marine species that are widely distributed, owing to the high cost of fishery-independent surveys. These types of data are notorious for their propensity to contain time-varying biases due to changes in fishing behavior. Not surprisingly, trends in abundance of dolphin species estimated from data of tuna purse-seine observer monitoring programs in the eastern tropical Pacific Ocean (ETP) have a long and controversial history. In the ETP, yellowfin tuna (*Thunnus albacares*) is often found in association with spotted (*Stenella attenuata*) and spinner (*S. longirostris*) dolphins. Purse-seine vessels use this co-occurrence to locate the tuna by searching for dolphins, and associated birds, with high-power binoculars, high-resolution radar and helicopters. Indices of relative abundance were originally developed in the late 1980s based on line transect methodology when the primary method of detection was binoculars. However, trend estimation was discontinued in 2000 due to concerns about changes in reporting rates of dolphin school detections with increased use of helicopter and radar search. At present, as a result of a hiatus in fishery-independent surveys since 2006, fisheries observer data remain the only source of information with which to monitor dolphin population status. Analysis has shown that proportionally more helicopter detections lead to purse-seine sets, suggestive of an under-reporting of dolphin schools not associated with tunas by this search method. Using zero-inflated occupancy-abundance models we cautiously revisit trend estimation for spotted and spinner dolphins. Our main goal is to account for changes in dolphin sighting reporting rates with changes in detection platforms through zero-inflation. We present model results that are based on explicit modeling of selective reporting, using fisheries operational covariates to describe the process of zero-inflation.

'Mixing dynamics': Quantifying population mixing rate from individual movements using the squared displacement modelling approach

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Keywords: squared displacement; stationarity; mixing rate; population dynamics; animal movements; movement ecology.

Abstract: It has recently been pointed out (Morales et al. 2010) that to properly include the effects of movement on population dynamics, it is necessary to quantify how individual movements affect the mixing rate of a population and how this varies under environmental change and between population with a different stage structure. In fact any single movement event of an animal leads by definition to the displacement away from the point of departure, but over longer temporal scales often a stationary distribution emerges, whereby animals restrict their movements within confined spaces. Different behaviours and life-history events can lead to the emergence of different confined movement patterns over multiple temporal scales. Here I develop a theoretical framework to quantify the dynamics of stationarity and diffusivity in animal movements and show how a recent nonlinear hierarchical modelling approach (Börger & Fryxell 2012), based on the squared displacement statistic, can be used to fit the models to movement data over multiple scales (from annual to lifetime temporal scales) and derive estimates of population mixing rate from individual data. I use simulations to evaluate the robustness of the approach to missing data and location error and exemplify the inclusion in population dynamic models.

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Hierarchical Bayesian computing of 3-dimensional whale trajectories from electronic tags

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Keywords: Hierarchical Bayesian model; Multiple sensors; Dead reckoning

Abstract: Researchers mainly consider electronic tagging and passive acoustics to study the underwater behavior of whales in the field. Both approaches share the common features of processing noisy data collected on a network of sensors which are representative of the whale movements. A hierachical Bayesian model (HBM) has proven to be an efficient framework to compute 3-dimensional whale trajectories from passive acoustic recordings (Laplanche, 2012). We show that an identical approach can be used to compute 3-dimensional whale trajectories from electronic tag data. Such tags could include part or all of the following sensors: depth-meter, accelerometer, magnetometer, speedometer, gyroscope and GPS. This Bayesian approach has the advantages of efficiently merging different sources of data and of propagating errors from measurements to location estimates. We illustrate the capabilities of the approach by reconstructing 3-d trajectories of beaked whale from simulated and field tag data.

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Comparison of methods that estimate seed dispersal kernels from genotypes of established seedlings

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Keywords: spatial ecology, movement ecology, molecular ecology, seed dispersal

Abstract: The seed dispersal kernel is a major determinant of spatial population dynamics and spatial distribution of genetic diversity. Among the main methods to estimate it, Inverse modelling (IM) and Gene Shadow Model (GSM) rely on seed or seedling counts in traps whereas Competing Source Model (CSM) and Spatially Explicit Mating Models (SEMM) rely on compositions of seed or seedling pools. GSM, CSM and SEMM exploit genetic information from molecular markers whereas IM only exploit seed/seedling counts ignoring their origins. In presence of post-dispersal density-dependent mortality (DDM) the effective dispersal kernel, describing the spatial distribution of established seedlings relatively to the seed source, is notoriously different from the basic dispersal kernel, describing the spatial distribution of seed deposition sites relatively to the source. Using simulated datasets, we investigated whether IM, GSM, CSM and SEMM applied to established seedlings estimate the basic or the effective dispersal kernel. We demonstrated that CSM and SEMM estimate the basic seed dispersal kernel, independently on the presence of post-dispersal mortality. By contrast, GSM estimates the effective dispersal kernel. Besides, for all methods, seed migration was inflated in presence of DDM, due to lower mortality among randomly-distributed immigrants relatively to local seedlings.

It seems implicitly accepted in the literature that estimates based on seedlings or seeds provide effective or basic dispersal kernels respectively. Our results showed that it is not true for estimates obtained with CSM or SEMM because they rely on the composition of seed/seedling pools and not seed/seedling counts such as IM or GSM. This has important consequences for life-stage studies where the discordance of dispersal kernels estimated from different cohorts is used to investigate post-dispersal density-dependent mortality.

A novel framework for analyzing interaction between individuals: a case study using brown hyenas in Northern Botswana

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Keywords: modelling animal movement; movement ecology; spatial ecology

Abstract: New developments in GPS and related satellite tracking technologies have facilitated the collection of highly accurate data on moving objects, far surpassing the ability to analyze them. Interactions, for which the basic unit of observation is a pair of locations for two individuals, can be considered a second order property of movement but their social and psychological explanations and implications are far less generalizable. Within movement pattern analysis, human interactions have been studied far more extensively than any other type, and they are often based on detailed information such as 'travel diaries' from which activity spaces can be calculated and intersections of multiple activity spaces can be used to derive social interaction metrics.

The nature of interactions between individuals of an animal population is a fundamental aspect of a species' behavioral ecology and information on the frequency and duration of these interactions is vital to understanding mating and territorial behavior, resource use, and infectious disease epidemiology. However, the number of times an individual animal comes into contact with another is an extremely difficult parameter to estimate and preliminary research has shown that current interaction metrics produce quite variable results and do not facilitate meaningful interpretations of interaction rates in general (Miller 2012). The goal of this research is to develop a novel framework that can be used to analyze and interpret dynamic interactions between individuals and focuses on GPS collar data from sixteen brown hyena individuals in Northern Botswana as a case study.

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PREFERENTIAL SAMPLING AND INFERENCE FROM PRESENCE-ONLY DATA

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Abstract

Databases on species occurrence in space are often collated from various sources and result in presence-only datasets. The rate of false-negatives can be influenced by the environment: the sampling effort can co-vary with the predictors of species occurrence (preferential sampling). This work aims at inferring the probability of occurrence and the prevalence of a species, based on presence-only data biased by preferential sampling. The Bayesian Image Restoration (BIR) model allows inference based on an environmental mean model, a spatial neighborhood component, and a model of the sampling effort. The latter relies on the number of 'control species' (selected by expert advice) observed. An observed absence is more likely to be a false-negative when the environment is conducive, the neighboring grid cells are occupied, and the number of control species is small (low sampling effort). With an artificial species whose true prevalence is 0.31 and a realistic sampling scenario with an observed prevalence of 0.18, the modeled prevalence was 0.32 (0.30-0.34). The estimation was robust to a failure of the assumptions, even with a misspecified environmental mean model. The restored map was visually close to the true map. The method is fit for the purpose of restoring maps and drawing inference when data is biased by preferential sampling. The link between the sampling effort and the number of control species is crucial, and a sensitivity analysis of the sampling effort model is recommended. BIR applied to *Asarum europaeum* L. resulted in different results compared to a spatial model with no sampling effort, and a significant interaction between rainfall and temperature appeared to be an artifact of observer bias. Given the pervasiveness of imperfect sampling in ecology, the benefits of using a priori knowledge from experts on sampling bias and Bayesian estimation are expected to outweigh the risks of model-based inference.

Goal-oriented evaluation of species distribution models' accuracy: exploring the True Skill Statistic profile

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Keywords: AUC, Bayesian inference, MaxEnt, presence-only data, sensitivity, specificity, spatial ecology, species distribution models, TSS.

Abstract:

Despite the wide acceptance of some standard statistics to evaluate the performance of spatial models' predictions, there is a strong on-going debate as to their use. The "area under the curve" (AUC) is a popular measure used to evaluate species distribution models (SDM); however, it does not provide information about model accuracy or the spatial distribution of model errors. A replacement for AUC, the maximum True Skill Statistic (TSS), is gaining acceptance. However, evaluations of a model's accuracy solely based on this statistic may also be misleading.

I demonstrate and compare the advantages of alternative methods to evaluate the accuracy of SDM as continuous probability or presence-absence maps. I evaluate the performance of two SDM approaches (Bayesian logistic model and a machine learning algorithm - MaxEnt) by contrasting model predictions to additional validation datasets. I propose an alternative use of TSS estimated for the whole detection threshold range: the TSS profile. Despite both SDMs score the same high AUC value (0.92), their predictions were very different at the species distribution margins. Also, a high maximum TSS did not guarantee accurate predictions.

The TSS profile allows for a better understanding about how close predictions are to the observation dataset. The proposed TSS profile offer solutions for researchers and practitioners i) to evaluate the overall performance of SDMs and compare between them, ii) to identify the

main source of error, iii) to determine whether the model is suited for the study goal, and iv) to select a detection threshold depending on the maps intended use.

Spatial Pattern Analysis of Esca Grapevine Disease

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Keywords: spatial ecology; join count statistics; permutation test; plant disease

Abstract: Esca is a major fungal wood disease of grapevine in France, whose widespread distribution in vineyards leads to vine decline and to reduced productivity. Spatial dynamics have been studied in an exploratory analysis in order to obtain better insight into the epidemiology of this complex disease. A plot of 2000 contiguous vines planted in rows was monitored visually each year, from 2004 to 2011, for esca symptom foliar expression. The ensuing data were used for join count statistical analyses, based on the symptomatic vine pair counts in the same neighbourhood, in order to measure the spatial aggregation of esca expression vines.

The neighbourhoods have been defined in terms of different distances and/or orientations with four different tests being employed: Isotropic, Row, Off test and Elliptic-Neighbourhood. The first three tests are based on distance. The Elliptic-Neighbourhood test is based exclusively on neighbour order, and has been specifically designed on the basis of an ellipse neighbourhood definition adapted to the irregular grid vineyard data.

Employing a permutation test is a simple way to extract data characteristics which do not require assumptions about the underlying distribution. The permutation tests, applied to lattice data here, were combined with specifically designed join count statistics. The p-values of the permutation tests were computed using a corrected form in order to avoid singular values. The four types of tests concerning different orders or distances (1m to 15m) were performed annually. The results have been presented as decisions (acceptance/rejection) of those tests by years according to two significance levels, to show temporal evolution. The results of the Row and Isotropic tests were compared for all distances to determine propagation direction. These two tests were further distinguished by showing the exact p-values for Isotropic, Row and Off Row tests in the same graph.

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Continuous time capture-recapture models

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Keywords: capture recapture; continuous time; Bayesian

Abstract: Motivated by field sampling of DNA fragments, we describe a general model for capture-recapture modeling of samples drawn one at a time in continuous time. Our model is based on Poisson sampling where the sampling time may be unobserved. We show that previously described models correspond to partial likelihoods from our Poisson model and their use may be justified through arguments concerning S- and Bayes-ancillarity of discarded information. We demonstrate a further link to continuous-time capture-recapture models and explain observations that have been made about this class of models in terms of partial ancillarity. We illustrate application of our models using data from the European badger (*Meles meles*) in which genotyping of DNA fragments was subject to error.

Ecological Prediction with High-Frequency “Big Data” Covariates.

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Abstract: Time-frequency analysis has become a fundamental component of many scientific inquiries. Due to the improvements in technology, the amount of high-frequency signals that are collected for ecological and other scientific processes is increasing at a dramatic rate. Incorporating such information into traditional models is complicated by the inherent differences in temporal scales between the response and the predictors. Salient features of high-dimensional time-dependent outcomes and/or predictors may be difficult to discern through scientific or statistical examination in the time domain. Such features often become more pronounced and possibly more interpretable when considered from a time-frequency perspective. Critically, such time-frequency based representations can be considered analogous to spatial image processes, which can be effectively represented by common reduced-rank methods to deal with the inherent dependence between time-frequency “pixels.” When combined with efficient variable selection approaches, such representations can improve prediction, classification, and interpretation of spatial and temporal responses on different scales of resolution than the high-frequency covariates.

In order to facilitate the use of these data in ecological prediction and inference, we present a class of nonlinear multivariate time-frequency functional models that can identify important features of each signal as well as the interaction of signals corresponding to response variables. The proposed methods utilize various methods to estimate time-frequency “images”, rank reduction, and stochastic search variable selection to effectively reduce the dimensionality and to identify important time-frequency (and, hence, time-domain) features. The methods are demonstrated through various ecological and environmental examples, such as predicting phenotypic selection from insect communication signals, and predicting spawning success of shovelnose sturgeon on the Lower Missouri River from high-frequency data storage tag information.

The Well-Tempered Assemblage: Reducing Bias in the Estimation of Species Rank Abundance Distributions

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Abstract: Most plant and animal assemblages are characterized by a few common species and many uncommon or rare species. Understanding the mechanisms shaping the species abundance distribution (SAD) has long been a major research focus in ecology. Beginning with seminal work by R.A. Fisher in the 1940s, ecologists have fit simple statistical models such as the geometric series, log normal, and exponential series to species abundance data. This distribution-fitting approach is based on the use of the simple "plug-in" estimator $\hat{p}_i = n_i / N$, where $\hat{p}_i$ is the estimated relative frequency of species i , n_i is the number of individuals observed of species i, and N is the number of individuals in the sample. However, with incomplete sampling and undetected species, $\hat{p}_i$ is a biased estimator of the true relative frequency of the species in the sample, and the degree of bias increases with the relative rarity of each species. Using the concept of sample coverage and the theory of frequency estimation by I.J. Good and A. Turing, we estimated the true species abundance distribution (SAD) based on a random sample of individuals. We separately estimated relative frequencies for the set of species detected in the sample and for the set of species undetected in the sample. We then combined the two parts to obtain an estimated SAD in which the relative frequency for each species has been tuned or adjusted to minimize the bias inherent in the traditional plug-in estimator. To examine the performance of the tuned estimators, we created artificial data sets by randomly sampling from common statistical distributions, and by randomly sampling from large empirical distributions based on very thorough field censuses. With sufficient sample size or sample coverage, the tuned estimators closely matched the true SADs. These more accurate estimators of relative frequency should aid ecologists in understanding and modeling SADs.

Identifying wild vs stocking components in fish recruitment despite the absence of identification data: an application to Atlantic salmon 0+ juveniles.

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Keywords: abundance; Atlantic salmon; hierarchical Bayesian model; juveniles; stocking; density dependence.

Abstract:

Over the last decades, exploited fish population have been declining significantly due to environmental changes, overexploitation and human activities. This has been reflected in the decline or collapse of numerous stocks. Alongside with fisheries regulations and habitat restoration, stock enhancement is a recurrent management tool used to inverse these trends. These enhancement programs are costly so measuring their impact is key although they are often poorly monitored.

During the course of an enhancement programme, stocking intensity may have been varied, intentionally or not, according to spatio-temporal units, wild production fluctuates in space and time too. The objective of this study is to propose an approach which takes advantage of these spatio-temporal variations of stocking vs wild recruitment for estimating their relative contribution from abundance data when no identification of the wild and stocked fish are available. We use Bayesian hierarchical modelling as a template for taking into account the spatio-temporal structure, while explicitly acknowledging that the abundance data issue from a mixture of fish of wild and hatchery origins. We illustrate our approach by means of a case study on 0+ juvenile of Atlantic salmon (*Salmo salar*) densities in the Allier catchment, France.

Not unlike similar stock enhancement projects in salmonids, the Allier stocking program lacks identification data for monitoring the fish that are released in the catchment separately from their wild counterparts. However, abundance data are available at the 0+ juvenile stage in early fall. A Bayesian hierarchical model was developed for estimating 0+ juvenile densities at two spatial scales over the 37 years of the study period, while assessing the relative contribution of wild reproduction, stocked eggs and stocked 0+ juvenile to the total 0+ juvenile production was evaluated.

Implications of the grid spacing on the quality of spatially predicted species abundances

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Keywords: abundance; species distribution models; spatial ecology; generalised linear geostatistical modelling; grid spacing; zero-inflation

Abstract:

The effect of grid spacing on spatial prediction of species abundances was estimated. Data on counts of intertidal macrofauna (*M. balthica*) were collected in the Dutch Wadden sea over a grid of 500 × 500 m. The first step in the procedure was modelling of the zero-inflated data without taking spatial dependency into account. The problem of excess zeros was addressed through a mixture model (Lambert, 1992) which allowed to distinguish the point mass at zero through a Bernoulli process and the count component through a Poisson process. In the second step spatial correlation in both processes was then accounted for through generalised linear geostatistical model (GLSM) (Diggle et al., 1998; Christensen, 2004). Using simulations from the conditional distribution by MCMC a Monte Carlo approximation to the likelihood function was made. In the third step the two calibrated GLSMs were used to generate 100 pseudo-realities. This was done by conditional simulation from the original grid to the nodes of a fine prediction grid (100×100 m) supplemented with 1000 randomly selected validation points. The simulated pseudo-realities of the Bernoulli variable and the Poisson variable were combined into 100 pseudo-realities of a zero-inflated Poisson variable. In the fourth step each simulated pseudo-reality was repeatedly sampled by grid sampling with a varying spacing. Each sample was used to predict the study variable at the validation points by inverse distance weighted interpolation, and to estimate the Mean Squared Error (MSE). By averaging the MSEs over the pseudo-realities an estimate of the model-expectation of the MSE was obtained. The results showed that the decrease in resolution of the sampling grid (upscaling) had a clear effect on the precision of the predictions. This has direct implications for decisions with respect to sampling density for ecological monitoring programmes.

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Using ecological principles to develop statistical models for the prediction of species' distribution and abundance

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Keywords: abundance; species distribution models; movement ecology.

Abstract: The development of statistical models to predict species distribution and abundance continues to play an important role in ecology. The notion that the model should closely reflect underlying scientific understanding has encouraged ecologists to investigate complex statistical methods as they arise. In this study, we used ecological principles to guide the development of a Bayesian hierarchical model that relates multi-scaled environmental variables to the distribution and abundance of a single fish species. The model simultaneously quantified the hierarchy of environmental determinants of species' spatial distribution and spatiotemporal variation in abundance. We illustrate the model with a small-bodied, mobile species, the empire gudgeon (*Hypseleotris galii*), and a larger-bodied, sedentary species, the eel-tailed catfish (*Tandanus tandanus*) in the Mary and Albert Rivers, Queensland, Australia. Sampling occurred at 28 relatively undisturbed locations with local-scale habitat and large-scale environmental variables collected along with fish abundances. The model accounted for greater than 50% of the variation in the distribution and abundance of each species. Empire gudgeon had a distinct spatial distribution within each catchment with a higher probability of presence in mid-elevation reaches than lowland or headwater streams. However, there was considerable temporal variation in its distribution and abundance that could be explained by local-scale environmental variation. In contrast, eel-tailed catfish was present across the entire range of sampling and its abundance tended to co-vary with local-scale variables only. For both species, the extent of spatial autocorrelation was relatively low compared to the distances among sampling reaches. Our findings illustrate how Bayesian statistical modelling can provide a robust framework for statistical modelling that reflects our ecological understanding. This allows ecologists to address a range of ecological questions with a single unified probability model rather than a series of disconnected analyses.

Inferring animal abundance from associative behavior

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Keywords: Abundance Estimate; electronic tagging; aggregative behaviour

Abstract: Estimating the abundance of animal populations is a central issue in applied ecology and conservation issues. Despite the development of satellite, archival and acoustic tagging techniques that allow the tracking of animals in their natural environments, these technologies have so far been underutilized in developing abundance estimation of animal populations, both for marine and terrestrial species. We propose a new sampling theory for estimating species abundance that employs these technologies and that can be applied to species that aggregate at well-defined sites. Based on a behavioral model describing the associative behavior of animals, we relate the time that individuals spend associated at a particular aggregative site and out of it to their abundance. Taking the case study of tropical tuna associated with floating objects (which constitute aggregation points for several pelagic fish species), we implemented our approach using a data set obtained through acoustic tagging. Our method opens a new perspective, which is fisheries independent, for direct estimation of populations of tropical tuna. The same approach can be applied to obtain population assessments for any marine and terrestrial species that display associative behavior and from which behavioral data have been acquired using acoustic, archival, or satellite tags or even visual observations where individual animals can be recognized.

Using spatio-temporal models to infer ecological dynamics and estimate animal abundance from transect counts

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Keywords: Abundance, spatial ecology, survey design and analysis

Abstract: Ecologists often estimate animal abundance by fitting models to transect survey count data. Such models often require that animal density remains constant across the landscape where sampling is being conducted. This assumption is problematic for animals inhabiting dynamic landscapes or otherwise exhibiting considerable spatio-temporal variation in density, and may be an impediment to inference about how changes in environmental conditions affect animals' spatial distribution. A variety of models have been developed for analyzing spatio-temporal variation in count data, but there has been little comparison of the efficacy of alternative modeling approaches for estimating animal abundance. We review several concepts from the burgeoning literature on spatio-temporal statistical models, including the nature of the temporal structure (i.e., descriptive or dynamical) and strategies for dimension reduction to promote computational tractability. We also review several features as they specifically relate to abundance estimation, including boundary conditions, population closure, choice of link function, and extrapolation of predicted relationships to unsampled areas. We compare a suite of novel and existing spatio-temporal hierarchical models for animal count data that permit animal density to vary over space and time. Models varied by the nature of the temporal structure (i.e., descriptive or dynamical), and whether total expected abundance was assumed constant over time (a pseudo-closure assumption). We gauge the relative performance (bias, precision, computational demands) of alternative spatio-temporal models when confronted with simulated and real datasets from dynamic animal populations. For the latter, we analyze spotted seal counts from an aerial survey of the Bering Sea where the quantity and quality of suitable habitat (sea ice) changed dramatically while surveys were being conducted.

Spatial autocorrelation in abundance models accounting for imperfect detection

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Keywords: abundance, species distribution models, imperfect detection

Abstract: Reliable maps of abundance are fundamental tools in ecology and applied fields such as biodiversity monitoring and conservation. However, two common problems are (i) interpretational challenges due to the complex observation process (e.g. imperfect detection) underlying most ecological field data and (ii) residual spatial autocorrelation. These may jeopardise our ability to draw inferences about abundance and produce underestimates of uncertainty. To investigate the consequences of these problems we fit four different models on simulated datasets using a bayesian framework: a standard generalized linear model, an N-mixture model (Royle 2004), an N-mixture model accounting for spatial autocorrelation using an intrinsic conditional autoregressive (ICAR) prior and another N-mixture model also accounting for spatial autocorrelation using two-dimensional penalized splines of the geographic coordinates. Knowing the true abundance distributions we can compare the predictive abilities of the models using different statistical measures. We also investigate the coverage rates of the credible intervals of the coefficients. We then apply the same models to several species using replicated count data coming from a Swiss breeding bird dataset and make predictions for the whole of Switzerland. The models are compared and validated using an independent dataset, and uncertainty maps are also computed.

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Introducing a novel methodology for quantifying niche overlap

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Keywords: evolutionary ecology; spatial ecology; species distribution models

Abstract: Niche conservatism is defined as the retention of niche-related ecological traits over time (Wiens et al., 2010). Niche conservatism can be applied to a a wide range of questions, including invasive species, speciation processes and responses to global climate change. One method of testing for niche conservatism is by looking at the degree of niche overlap between sister pairs. Current methods for quantifying niche overlap present limitations such as the use of reciprocal tests for each sister pair (Warren et al., 2008), the restriction to two environmental variables (Broennimann et al., 2012), the arbitrary selection of 'background' regions and the underlying assumptions when constructing traditional ecological niche models (Warren et al., 2008 and Broennimann et al., 2012). We developed a novel methodology to quantify for niche overlap between two species which alleviates these key problems. The new test is multi-dimensional, unidirectional, requires no 'background' points and involves an innovative null biogeographic model which is distinct from traditional ecological niche models. We created virtual species occurrence data and climatic gradient layers to assess the metric's ability to quantify niche overlap. The new metric was capable of identifying different degrees of niche overlap and therefore we regard it as a suitable alternative for addressing questions on niche conservatism.

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The use of mixture models in ecology and evolution: some examples describing cohort effects in ungulates

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Keywords: evolutionary ecology; clustering; individual heterogeneity.

Abstract: Mixed models have become a common analytical method in ecology and evolution to account for repeated measures on individuals. One assumption behind these models is that the distribution of the random effects follows a normal distribution. This assumption can be easily violated as soon as some level of clustering occurs among individuals. As an alternative to mixed models, mixture models have been developed to account for this clustering. Here, we used simulated data to test the accuracy of these models. We found that both BIC and bootstrap methods were better criteria than AIC for determining the number of clusters in the data. We then illustrate how mixture models can allow us to objectively group cohorts in various populations of ungulates. We showed that, in some cases, differences among groups of cohorts remained throughout life, whereas in other cases compensatory or cumulative effects occurred. Our study therefore illustrates the value of using mixture models in ecology and evolution.

Bayesian inference in evolutionary ecology: random drift vs. selection

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Keywords: evolutionary ecology

Abstract: One central aim in evolutionary ecology is to understand the causes and consequences of phenotypic variation, and to partition such variation into its genetic and environmental components (and their interaction) at different spatial scales, in particular within and among populations. Key parameters and concepts related to such research include e.g. individual- and population-level coancestry coefficients, the matrices of environmental and additive genetic variances and covariances, heritability, selection gradients, and the rates of mutation and migration. Typical data sets used to measure these parameters consist of phenotypic data from natural populations or breeding experiments (the latter possibly involving artificial selection), genotypic data on neutral or non-neutral marker genes, or data stemming from genome wide genotype or expression profiling. I discuss recent advances in mathematical theory and related Bayesian methods in this field of research, focusing on methods that aim to disentangle signals of diversifying or stabilizing selection from the null hypothesis of random genetic drift. In particular, I illustrate the use of the sparse Bayesian factor approach in identifying correlations (at the levels of phenotype, genotype or expression) from high-dimensional data.

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An evolutionary perspective on reproductive individual heterogeneity in a marine vertebrate: how to tackle complex questions with real data in the presence of multiple sources of uncertainty?

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Key words: evolutionary ecology, population dynamics

Abstract: Individual heterogeneity in vital rates has been evidenced in several wild animal populations but its evolutionary consequences (fitness, heritability) have remained virtually unstudied. Addressing such aspects proves very challenging because large amounts of data are needed and different sources of uncertainty must usually be taken into account. In particular, when heterogeneity in vital rates is quantified through individual random effects, there is inherent uncertainty (demographic stochasticity, sampling variation) associated with these trait values. Here, using long-term monitoring data from Weddell seals, we addressed the fitness consequences of heterogeneity in female reproductive rate and quantified the heritability of this trait. Fitness consequences were assessed using data on offspring recruitment in combination with simulations, and heritability was estimated through a mother-daughter regression. The uncertainty associated with individual reproductive rate values was fully incorporated and accounted for in our inferences, by using the full posterior distributions previously obtained for these quantities, instead of point estimates. There was no evidence for a trade-off, at the among-individual level, between a female's reproductive rate and her offspring recruitment characteristics, but some heritability in female reproductive rates was

evidenced. These two results support the hypothesis of true variation in female ‘quality’. Besides its interest for evolutionary ecology, this study emphasizes the use of adequate modelling approaches to account for various sources of uncertainty. The adoption of similar approaches in other study systems could be beneficial by facilitating the investigation of equally complex ecological and evolutionary questions for a broader range of taxa.

How to use molecular data to account for non random mating in quantitative genetic estimates derived from family structured experiments

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Keywords: evolutionary ecology, survey design and analysis, quantitative genetics, pedigree-free methods

Abstract: Accurate estimates of heritability (h^2) of fitness-related traits are necessary to assess their adaptive response in changing environments. For plants, maternal families are often sampled to estimate h^2. Estimates thus rely on several assumptions about the mating system and the relatedness among mates (basically offspring are assumed to be half-sibs or unrelated). In particular, when mating events are impossible to observe and sample sizes are large, the paternal relatedness is often neglected, leading to bias in the h^2 estimates.

We performed a simulation study to investigate how molecular markers can be used to analyze more efficiently the family structured designs. We compared the simple method based on a maternal family model assumption with methods using marker-based relatedness coefficients, pedigree or hybrid genetic information (animal models) to account for paternal relatedness. We assessed the effect of unequal male reproductive success, inbreeding and maternal effects on h^2 estimates.

Results showed that in presence of unequal male reproductive success, neglecting the genetic relatedness between families led to bias the h^2 estimates derived from the family model. Regarding the animal model, the method using mean marker-based relatedness coefficients was efficient to deal with non-random mating system and ancestral inbreeding in the parental population. But this method was biased in presence of maternal effects. In such cases, only the use of finest genetic information, like pedigrees, allowed to improve the accuracy of the h^2 estimates. Using a hybrid approach, that uses both the pedigree and mean relatedness information, was efficient to deal with any departures from the family assumptions.

In conclusion, family structure designs are part of the experimental exceptions, with inbred samples, where pedigree-free, or partial pedigree-free (also called hybrid approach), methods can be used to get accurate h^2 estimates, at the condition that mean relatedness coefficients are used (estimated at the family/population level).

Resistance surface selection for landscape genetics based on the optimization of a Matrix Selection Function, a simple and iterative statistical approach

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Abstract: Landscape genetics, born of the association of genetics, ecology and spatial statistics, aims to "highlight the linkage between the spatial context of ecological dynamics and evolutionary processes, which is revealed in genetic signature that reflect the underlying forces shaping evolutionary and ecological trajectories". Gene flows and isolation by landscape resistance (IBR) are two important questions in landscape genetics and has been widely studied since the last 20 years. In most of these studies, least-cost path analysis is used as the standard approach to explain the genetic distance.

Several authors have discussed conceptual and methodological topics like the importance of the adequacy of spatial and temporal scales or the pertinence of the least-cost distance which assumes that gene flows are restricted to a single and optimal pathways. Nevertheless, the way to choose resistance values (also called friction or impedance values) stays the central problem. It must depend on the objectives of the study and on the conceptual meaning of these values. Moreover, sensitivity analysis showed that poor choices of resistance values can dramatically blur the results.

As far as we know, resistance values are mostly based on i) expert judgements, ii) massive try-and-error approaches or iii) resource selection functions (point and home range selection functions). However, these approaches present the defect of being arbitrary (i), CPU intensive (ii) and conceptually misleading (iii), respectively.

In this communication, we propose to use a simple and iterative statistical approach to choose resistance values based on the optimization of a Matrix Selection Function (Zeller et al., 2012). Our approach is expected to be less subjective, more CPU efficient and to be more adapted to the spatial dynamic of gene flows.

Two-dimensional line transect methods for active acoustic surveys of pelagic fish populations

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Keywords: distance sampling.

Abstract:

Active underwater acoustics, or echosounding, is a fisheries-independent method that is widely employed to estimate the biomass of commercially and ecologically important pelagic species. Typically, acoustic instruments look vertically downwards into the water column and are unable to detect animals above some minimum depth. They therefore miss that part of the target population that is above this depth. In addition animals may exhibit avoidance behaviour by the time they come abeam of the survey vessel and hence be missed by the echosounder. Neglecting these effects results in density estimates that are negatively biased by some unknown amount.

Animals at shallow depths can be surveyed by a horizontally scanning sonar. We develop two-dimensional line transect methods for the analysis of such data (the dimensions being forward as well as perpendicular distances). The models can be viewed as a type of survival model or as an extension of the ideas on which the hazard rate models of Hayes and Buckland (1982) were based. We develop two-dimensional line transect density estimators for animals that are too shallow to be detected by conventional echosounders, using data from horizontally scanning sonar, and investigate their properties, including their ability to accommodate avoidance behaviour without substantial bias. The methods are illustrated with data from a pelagic fish population survey.

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Effects of cetacean depth on acoustic distance sampling surveys

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Keywords: distance sampling; survey design and analysis.

Abstract: Passive acoustic monitoring is an increasingly popular survey approach for cetaceans. In general, acoustic monitoring equipment is either towed behind a vessel or fixed in the water column. In some circumstances, the collected acoustic data can be analysed using traditional density estimation methods such as distance sampling. However, monitoring vocalising marine animals poses particular challenges. Firstly, a volume of water is monitored by acoustic instruments, so three-dimensional distance sampling must be considered. Secondly, animals are unlikely to follow a uniform distribution with respect to depth (many cetacean species dive to particular depths to forage on specific prey species). Finally, locations of calling animals are often not available. Previous work on krill swarm density estimation (an analogous problem, as krill swarms also exhibit non-uniform depth distributions) relied on estimates of the vertical bearing and slant range to each detected krill swarm, which were obtained using active acoustic techniques (Cox *et al.*, 2011). In the case of passive acoustic cetacean surveys, such information is difficult to obtain – often a slant range is estimated with no vertical bearing, or *vice versa*. In this presentation, we will (1) discuss the modifications that we have made to distance sampling methods to analyse data from both towed and fixed passive acoustic surveys (specifically, information about the depth distribution of the study species is incorporated into the maximum likelihood estimator of the detection function parameters), (2) present simulation results, verifying the newly developed methods and (3) apply the methods to beaked whale survey data.

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Optimising your survey design using DSsim / Distance 7.0

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Keywords: Distance sampling; Survey design and analysis; Simulations.

Abstract: Every distance sampling survey is unique, being carried out in a specific region, on specific species and with its own set of unique challenges. Until now we have relied on general rules of thumb to formulate what we believe to be the best survey design for the specific circumstances. Such guidelines have been derived through experience and individually constructed simulations, with the hope that they are generally applicable.

We have developed a distance sampling simulation framework that allows people to generate simulated populations with particular characteristics in their specific region of interest. They can then investigate how the choice of survey design and sampling protocol affects the accuracy and precision of density / abundance estimates. We have used this simulation framework to demonstrate how easily bias can be introduced into surveys through the subjective selection of transect locations. We have also explored the bias and precision trade-off between a zigzag and systematic parallel line transect design based on equal survey budgets. While the zigzag line transect design in a convex hull can introduce some bias when applying standard analysis techniques, the parallel design suffers lower precision due to the increased off-effort transit time between transects.

The question of how to locate transects is one aspect of survey design for which the simulation framework can be applied. Other design questions, such as how best to stratify, or even the effects of different sampling protocols, such as deciding on the number and location of cut points for binned distance data, can also be investigated. This simulation framework will therefore enable each researcher to achieve the best quality data they can for the budget they have.

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Comparison of methods for spatially explicit impact assessment of marine renewables

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Keywords: spatial distribution models, survey design and analysis, distance sampling

Abstract: Three spatial modelling methods were identified for methodological comparison: Generalised Additive Models (GAM), Generalised Additive Mixed Models (GAMM) and Complex Region Spatial Smoother (CReSS; Scott-Hayward *et al.*, 2013) with spatially adaptive knot placement using SALSA (Spatially Adaptive Local Smoothing Algorithm; Walker *et al.*, 2011). Three simulated impact scenarios (no-change post impact, 30% decrease and post-impact redistribution) were based on offshore data collected from existing renewables developments. Data was generated for each case using both GAM and CReSS models to prevent favouring one in the comparison process. Five measures were used to assess performance; model choice, model fit to the underlying process, spatially explicit bias and coverage and spatially explicit post-impact differences.

We present results from the off-shore GAM generated, scenario along with a summary of the entire comparison process. GAMs fit the underlying surfaces well but were poor at assessing if impact-related effects were present and at locating spatially explicit change. GAMMs performed very poorly when assessing if impact-related effects were present but performed well at locating spatially explicit change. Similar to GAMs, CReSS performed well at approximating the underlying process. CReSS performed the best of the three methods at assessing if impact-related effects were present and at identifying spatially explicit change.

Our conclusion is that CReSS gives the best results for identifying the impact of marine renewables. For both developers and government licensing organisations it is important to identify any change in density or distribution of animals at marine renewables sites and if those changes can be attributed to the presence of renewables devices (Mackenzie *et al.*, 2013). An R package, `MRSea`, was developed to assist with this type of modelling and can be found at `http://creem2.st-andrews.ac.uk/software.aspx`.

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Strategies for correlated covariates in distance sampling

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Keywords: distance sampling

Abstract: Correlation between covariates in detection function models is an acknowledged but as yet unaddressed issue in the distance sampling literature. Covariates that affect detectability, such as search distance or sea state, are highly correlated with distance as well as each other. Inference drawn from models which contain highly correlated covariates may be spurious and such models may have optimisation issues. Variable selection and shrinkage methods for correlated covariates are well-covered topics in the linear modelling literature. Here methods commonly used in regression (such as ridge regression, lasso, principle components, etc) are explored for their utility in modelling detection functions. Particular attention is paid to the interpretability of resulting models.

Modeling animal epidemics: A penalized simulated maximum likelihood approach to estimate parametes for stochastic differential equations

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Abstract: We consider the problem of estimating parameters of stochastic differential equations (SDEs) with discrete-time observations that are either completely or partially observed. The transition density between two observations is generally unknown. We propose an importance sampling approach with an auxiliary parameter which improves approximation of the transition density. We embed the auxiliary importance sampler in a penalized maximum likelihood framework which produces more accurate and efficient parameter estimates. Simulation studies in three different models illustrate promising improvements of the new penalized simulated maximum likelihood method. The new procedure is designed for the challenging case when some state variables are unobserved and moreover, observed states are sparse over time, which commonly arises in ecological studies. We apply this new approach to two epidemics of chronic wasting disease in mule deer. This work is coauthored by Chihoon Lee and Libo Sun.

Demography of small populations: incorporating prior information in multistate capture-recapture models

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Keywords: multistate models; Bayesian statistics; capture-recapture

Abstract: Capture-recapture models are often used to estimate demographic parameters of populations in natura, such as survival probabilities and population size. Multistate capture-recapture models in particular allow the estimation of cause-specific mortalities while accounting for the fact that the detection probability of an individual at any given year may be lower than 1.

Despite their advantages, multistate capture-recapture models are data hungry and their application to small populations often leads to inaccurate estimates which, in turn, translate into uncertainty in viability models that are used to devise conservation strategies.

Here, we will illustrate the use of informative priors in order to improve the precision of multistate capture-recapture model parameters estimates by resorting to data from other ecologically similar populations. Our work is in line with recent results that promote the elicitation of prior information in ecological models (Gedir et al 2013, Martin et al 2013).

As a case study, we will study the French-Spanish population of brown bears (*Ursus arctos*) in the Pyrénées. We use as priors the results of analyses performed on the Austrian and Italian brown bear populations, which share similarities with the French-Spanish one.

The use of informative priors helps in reducing uncertainty in demographic estimates, like extinction probabilities or abundance.

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Synchronicity in survival of four insectivores
in a wetland in South Africa

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Keywords: capture-recapture; multispecies models; community-structure and dynamics.

Abstract: Mostdemographic studies focus on a single species, but species are part of an ecological community in which several sympatric species occupy similar niches. The populations of these species face the same environmental changes and utilize similar resources. What drives population dynamics of similar species within a community is still a subject of debate. Compensatory-dynamics states that population dynamics are driven by competition: one species declines and others increase (Houlahan*et al.*2007). This assumes that each species responds differently to environmental change - response asynchrony. If environmental change regulates population dynamics, species respond synchronously.

In Africa, data to estimate abundance are scarce (particularly for common, non-threatened species), but capture-recapture data to estimate survival are available through a public ringing scheme. We used ringing data (1999-2013) collected at Darvill Bird Sanctuary - a wetland near Pietermaritzburg in the east of South Africa - of four resident insectivores: Lesser Swamp-Warbler *Acrocephalusgracilirostris*, Levaillant'sCisticola*Cisticolatinniens*, Tawny-flanked Prinia*Priniasubflava*, and Spectacled Weaver *Ploceusocularis*. We investigated the (a)synchronicity in survival with a state-space model with a variance term per species and year (asynchronicity) and a commontemporal variance (synchronicity) following Lahoz-Monfort*et al.* (2011).

The common temporal variance was not substantially larger than the species-specific temporal variance for the species that depend all year round on wetlands/vicinity of water (logit scale: 0.61, 95% Credible Interval (CRI): 0.08-1.326; swamp-warbler - 0.42, 95% CRI: 0.02-1.24;cisticola- 0.54, 95% CRI: 0.02-1.49; prinia - 0.43, 95% CRI: 0.08-1.43). This suggests that their survival is influenced by both competition and an asynchronous response to environmental factors. Survival of the spectacled weaver appears to be less influenced by competition than the other species (temporal variance: 0.92, 95% CRI: 0.04-2.43).It prefers well-wooded areas with abundant cover and only breeds near water.

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Estimating spatial, temporal and individual variability in dolphin cumulative exposure to boat traffic using spatially-explicit capture-recapture methods

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Keywords: capture-recapture, spatial ecology.

Abstract: Appropriate management of the effects of human activities on animal populations requires quantification of the rate at which animals encounter stressors. Such activities are heterogeneously distributed in space, as are the individual animals in a population. This will result in a heterogeneous exposure rate, which is also likely to vary over time. A spatially-explicit analysis of individual exposure is therefore required. We applied Bayesian spatially-explicit capture-recapture models to photo-identification data to estimate the home range of each well-marked individual in a protected coastal population of bottlenose dolphins. Dolphins perceive boat traffic as a risk that can disturb their activities. Model results were therefore combined with the estimated distribution of boat traffic to quantify how exposure rates varied in time and space. Variability in exposure between individuals was also investigated using a mixed-effects model. The cumulative exposure of individuals to boat traffic varied between summers, depending both on the overall usage of the study area and the degree to which individuals moved around their activity centres. Despite this variability, the relative exposure in different parts of the study area was stable, and regions of higher risk could be identified. There were marked inter-individual differences in the amount of time dolphins were predicted to spend in the presence of boats, and individuals tended to be consistently over- or under-exposed across summers. Our study offers a useful framework to describe the temporal, spatial and individual variation in exposure to anthropogenic stressors when individuals can be repeatedly identified over time. It provides opportunities to map exposure risk in space and understand how this evolves in time at both individual and population level. The outcome of such modelling can be used as a robust evidence base to support management decisions.

Explicit integrated population modeling: Escaping the conventional assumption of independence

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Keywords: capture-recapture; integrated population models; population dynamics.

Abstract: Integrated population modeling is a relatively new development in statistical ecology that permits the joint analysis of different sources of data. Typically, the joint likelihood is obtained using an independence assumption so that it can be conveniently expressed as a product of the likelihoods of the respective datasets (Schaub and Abadi, 2011). In this talk, I present a new Bayesian model that can be used when the independence assumption is not suitable. A key aspect of the model is that it makes use of latent variables that keep track of the states of the marked and unmarked individuals separately while allowing unmarked individuals to become marked when so. I describe the situations in which this explicit model is preferable (e.g. large capture probabilities) over the usual model (based on an independence assumption). I also present the results of a simulation study that compare, under various scenarios, the explicit and independent models in terms of mean and standard error of the Bayes estimator. Finally, I apply the methods to capture-recapture and count data from a colony of Greater horseshoe bats (*Rhinolophus ferrumequinum*) in the Valais, Switzerland.

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Modelling species abundance across large spatial extents: opportunities and challenges

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Keywords: abundance; citizen science; species distribution models.

Abstract: Information about the relative abundance of species can reveal much about the patterns, processes and dynamics which may be underlying natural systems. To date, most species distribution modelling has been concerned with the presence or occurrence of species in space and time. Abundance data are often reduced to presence-absence data to estimate species distributions, resulting in loss of considerable information. When considering abundance data collected over wide spatial extents, a number of statistical challenges are often present, including zero-inflation, overdispersion, and non-stationarity. Species' behavioural characteristics such as seasonal aggregations can also lead to statistical problems. Here we discuss and present various parametric and machine learning models adapted for these challenges. We use data from eBird a large-scale citizen science project, which contains counts of bird species alongside location and search effort information. We examine the performance of the models, which also account for the inherent variability in effort that occurs with citizen science data. We consider suitable model validation metrics for abundance data. We show that modelling abundance reveals patterns and processes that are not evident when considering presence-absence data, which enables ecological research that is more detailed and mechanistic, and supports better informed conservation and management applications.

Process-based estimation of ecological niches and range dynamics from demographic data and large-scale abundance variation

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Keywords: Biogeography, hierarchical Bayesian statistics, metapopulation dynamics, niche theory, spatial demography, species distribution modelling.

Abstract:

The geographical distributions of species are determined by the dynamic interplay of reproduction, mortality and dispersal in a spatially and temporally heterogeneous environment. Yet, widely applied species distribution models (SDMs) take a phenomenological and static approach to the estimation of species' ranges and ecological niches.

Dynamic Range Models (DRMs) are a process-based alternative to SDMs (Pagel & Schurr 2012, Schurr et al. 2012). They statistically estimate of ecological niches and range dynamics from demographic and species distribution data. DRMs integrate Hutchinson's niche concept with spatial population dynamics in a hierarchical Bayesian state–space model to estimate the environmental response of demographic rates, local population dynamics and dispersal rates conditionally upon each other while accounting for various sources of uncertainty. The approach thereby jointly infers species' niches and spatio-temporal population dynamics from data and provides probabilistic forecasts of range dynamics under environmental change. Parameters of the model are related to demographic rates that can be measured in the field or in experiments. DRMs thus enable the quantification of niches and range dynamics from a combination of demographic measurements and biogeographical distribution data.

In a case study, we investigate niches and range dynamics of serotinous shrubs (Proteaceae) in the South African Fynbos. For the quantification of species' niches in terms of demographic response functions we assembled a dataset that describes how demographic rates (mortality, fecundity, recruitment) vary among more than 3000 populations across the ranges of 26 Proteaceae species. These field data are combined with information on long-distance seed dispersal and data on range-wide variation in population size from the Protea Atlas citizen-science project to estimate DRMs and to analyze how interactions between demographic response functions and spatial population dynamics drive the formation of species' ranges.

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Opportunistic data and estimation of species abundances in a habitat-structured space

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Keywords: Estimation of species abundances; habitat preferences; citizen sciences; standardized and opportunistic data; maximum likelihood.

Abstract:

Our aim is to estimate abundances of common species by combining standardized and opportunistic data, following the approach originated in Giraud et al. (2013). The space is divided into sites and we estimate the relative abundances of each species between any two sites. More specifically, our problem here is to consider a habitat-structured space and to take into account and distinguish the respective preferences of observers and of each observed species for habitats. On any site, each species has an unknown spatial distribution which is determined by its preferences for each habitat. The model for the behavior of observers is different for each dataset. We estimate abundances, habitat preferences and observation efforts, and study the role of opportunistic data in improving the accuracy of these estimations.

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Mixture models for multi-brooded butterfly species

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Keywords: abundance; citizen science; indicators of biodiversity.

Abstract: Butterflies respond sensitively and rapidly to changes in habitat and climate, hence their population status is a valuable indicator for changes in biodiversity and phenology. The main source of count data for UK butterflies is the UK Butterfly Monitoring Scheme, which is used to derive abundance indices which form one of the UK Government's 18 indicators of general trends in biodiversity.

Butterflies have multi-stage life cycles and hence count data fluctuate within each year in response to their emergence as adults. Many species are also multivoltine, with up to two or three broods of adults emerging in a given year. The current approach for describing the seasonal variation in count data involves fitting non-parametric curves to estimate missing values in the calculation of abundance indices (Dennis et al., 2013). We present a parametric approach via a stochastic mixture of Normal distributions. The estimation of new parameters relating to emergence date can be used to assess changes in phenology.

A hierarchical structure treats individual site effects as random effects and provides a new method for generating indices of abundance. The model also accommodates particular features which will vary between species, such as weather and covariate dependence and spatial or temporal variation in the number of broods. The model is fitted to data available for a sample of species, and comparisons are made with the prediction of alternative models.

By accounting explicitly for multiple broods within a year, the model produces new insights relevant to the monitoring and conservation of invertebrates, and produces more efficient and accurate abundance indices than the current approach.

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Estimation of demographic parameters of an insect pest in apple-orchards landscape, from genetic data

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In the context of agrosystem management in order to reduce the use of pesticides, we aim to understand population dynamics at the landscape scale of the codling moth (*Cydia pomonella*), an insect pest in apple orchards.
To analyse statistically the genetic markers data (22 microsatellites) obtained from a thousand georeferenced individuals (sampled in 51 different orchards), we developed a spatially explicit metapopulation model. The objective is to estimate population sizes and migration rates as functions of landscape factors (spatial heterogeneities). First the structure of homogeneous genetic groups are analysed from genetic marker data, according to numerical Bayesian approach, with a non-supervised clustering method (STRUCTURE). Second the estimated sub-populations allelic frequencies are used as inputs of a mechanistic-statistical model to estimate dispersion in the heterogeneous landscape. The model associates a reaction-diffusion model for the mechanistic description of insect movements with a population genetic model for the statistical modelling of marker data.

Keywords

Metapopulation dynamics, Spatial ecology, Molecular ecology, Landscape genetics

The impact of data quantity on decision making using a Bayesian stochastic patch occupancy model

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Keywords: occupancy model; metapopulation dynamics; survey design and analysis.

Abstract: Stochastic patch occupancy models or SPOMs are used to describe stochastic changes in the occurrence of populations due to local colonization and extinction. Data on occupancy turnover are used to fit these models. SPOMs are useful tools in environmental decision making, e.g. in modelling the effect of management actions on the extinction risk of endangered species. Managers aim to optimize spending between data collection and implementing management actions. Using more data is beneficial for model-fitting but not always necessary for better management decisions. The goal of this retrospective study is to investigate the effect of data quantity on parameter uncertainty and predictions of population viability of an endangered frog. In addition we aim to gain a better understanding of the optimal allocation of resources between data collection and management. A Bayesian SPOM was used to describe the metapopulation dynamics of the frog. Data on occupancy turnover and wetland characteristics were collected over six years. The management question was to determine the number of new wetlands that need to be created to offset population losses due to urbanisation. We investigated how gathering more information about metapopulation dynamics contributed to the management decision by estimating the parameters in MCMC runs with different amounts of data and subsequently predicting population viability through simulation based on those parameter values. By assuming particular costs for data collection and wetland creation, we evaluated the effect of data quantity on decision making. Results show that thorough temporal sampling is necessary to arrive at stable parameter estimates and that using all gathered data is necessary to enable making a reliable management decision. This is largely due to the low cost of data collection compared to the cost of management. Our approach illustrates how data quantity affects parameter estimates and downstream conclusions in environmental management.

A spatial occupancy model for predicting metapopulation extinction risk

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Keywords: metapopulation dynamics, occupancy models, spatial ecology, species distribution models

Abstract:

Many metapopulations are completely isolated from external sources of immigrants such that colonization is an internal process, determined by the distances to and occupancy status of *all* other sites within the metapopulation network. While internal colonization is an important component of modern metapopulation theory, it has been largely ignored in occupancy models that account for imperfect detection. As a result, these models predict that the metapopulation will reach a state of quasi-equilibrium in which permanent extinction is not possible. We present a spatial occupancy model that allows for internal colonization and hence can be used to predict metapopulation extinction risk. We applied the model to six years of data on the threatened Chiricahua leopard frog (*Lithobates chiricahuensis*) and estimated extinction risk of the metapopulation to be $> 5\%$ by 2020. We also used the model to generate colonization probability surfaces to identify optimal locations for establishing new sites and increasing metapopulation viability.

Estimating density-dependence in vital rates from spatially and temporally replicated counts of unmarked animals

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Keywords: apparent survival; recruitment rate; open N-Mixture model; state-space model

Abstract: The relative importance of density-dependence regulation is a central issue in theoretical ecology as well as conservation biology. Density dependence is defined as a general tendency of per capita growth rates to decrease when population size is large and increase when it is small. Density dependence influences population growth by affecting survival and\or reproduction. We extend the open N-mixture model of Dail & Madsen (Biometrics 2011) to include density dependence in either survival or recruitment rates alone or in both vital rates. We assess the reliability of our models by simulation. Data are simulated for several scenarios representing different kinds of life histories, population sizes, magnitudes of temporal fluctuation of abundance and density dependence in the vital rates. Beyond demography, environmental stochasticity contributes to the dynamics of a population over time. Hence, we investigate how environmental noise could affect the estimation of strength of density dependence in vital rates. The simulations show that the strength of density dependence in the demographic rates can be estimated. When the model is well specified regarding the different kinds of scenarios, the estimates of the strength of density dependence are more accurate. We apply our model to spatially and temporally replicated counts of Swiss breeding birds obtained from the breeding bird monitoring scheme.

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Modeling source and sink dynamics in the spread and subsequent eradication of an invasive non-native species

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Keywords: invasive species; lag-phase; spatial statistics; eradication.

Abstract: We investigate the role of source and sink dynamics in the spread and successful eradication of an invasive non-native population in heterogeneous landscape. Relatively few case studies exist with temporal and spatial data of non-native species distribution during spread and establishment as well as their decline by control. We use a 50 year time-series of ruddy duck (*Oxyura jamaicensis*) abundance in the UK to determine key site characteristics in the establishment phase and make inferences about the role of particular sites in the species spread. Population growth at some sites had a lag-phase, we use broken-stick regression models to determine how the length and duration of the lag phase correlate with site characteristics. We investigate how the spatial distribution of duck densities at sites changes through time and hypothesese which sites may act as source populations. Across the same landscape we analyse site level changes in bird numbers in response to a national control programme where ruddy duck numbers were reduced by 95% over 5 years. We model the spatial and temporal dynamics of ruddy duck distribution and cull regimes using bayesian regression models to test for spatially variable effects. We demonstrate that different sites may contribute to the national population as sinks or sources and these roles may differ from the establishment phase. We seek to determine where generalities may be derived from the eradication process, which could in turn inform policy decision making, in particular where to apply control effort to a spatially heterogeneous population.
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Probability distributions to model under-dispersed count data in a Bayesian regression context: evaluation of existing distributions and proposal of new ones to analyze biodiversity data.

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Statistical likelihood-based analysis of count data usually only allows over-dispersion relative to the Poisson distribution. Yet, as we show for a biodiversity data set, some situations might warrant the consideration of under-dispersed distributions as well. A literature review proposed two modifications of the Generalized Poisson distribution as the only appropriate existing probability distributions that allowed for under-dispersion and that were easily applicable in a Bayesian regression setting.

Here we propose relevant alternatives to these two distributions, which involve the Bernoulli, Pòlya or Poisson distribution. The application of these distributions to our biodiversity data set showed that all the ecological groups had an under-dispersed species richness at at least one scale. In these cases, models that allowed for under-dispersion gave more precise estimators of parameters or more accurate estimators of the variance of random effects than models that allowed only over-dispersion. No under-dispersed distribution outperformed the other ones in all situations.

These new families of distributions are very flexible since they allow for both under- and over-dispersion by including the Poisson and negative binomial distributions in the over-dispersed range.

Using Integrated Population Models to Monitor Game Species

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Keywords: abundance; integrated population models; population dynamics.

Abstract: Traditional harvest-based estimators of abundance for game species, especially white-tailed deer, lack measures of precision and make strong assumptions about mortality processes or accounting of mortality. Moreover, information on other population characteristics is oftentimes available, such as reproductive data obtained via embryo counts or adult:young ratios, but such data may not be readily incorporated into traditional estimators and usually are evaluated in an ad hoc manner. We developed an integrated population model in a Bayesian framework that provides measures of precision and incorporates multiple sources of data in a population dynamics model to make inferences about survival, harvest, and reproductive rates, abundance, and population trends. The model uses data collected on hunter harvest, reproductive rates, survival between hunting seasons, and adult male and female harvest rates as data inputs. These data are integrated via a simple population dynamics model to estimate abundance, survival rates, and harvest rates by sex-age class along with measures of precision. Oftentimes, rich data sets are available for game species that can be used in integrated population models to enable stronger inferences about population trends. Moreover, these models can be used to investigate the population dynamics of species, or estimate population parameters for which it is otherwise difficult to collect data (e.g., survival from birth to the first hunting season), because all available data are linked to a population dynamics model that is believed to describe the system.

Using hierarchical null models to study the assembly of fungal communities

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Keywords: abundance, community structure and dynamics, measures of biodiversity, monitoring of biodiversity

Abstract:

The study of assembly rules can inform us about the relative roles of dispersal, abiotic and biotic filters in structuring biological communities. The target of our work is arbuscular mycorrhizal fungi (AMF), a globally-distributed group of microorganisms that form an important symbiosis with most land plants. These organisms can be effectively identified from environmental samples using DNA-based methods, and their global taxonomic diversity appears to be low in comparison, for example, with that of their plant hosts. These characteristics allied to the fact that coarse global distribution data and a comprehensive phylogeny are available for AMF make analysis of the rules governing their assembly more tractable than for more mobile or abundant taxa.

We attempt to characterize the role of different processes influencing AMF community assembly using a series of hierarchical null models. The basis of the analysis is ‘site by species’ tables populated by counts of sequencing reads recorded for particular sample and fungal taxon combinations. The influence of different filters is assessed by generating randomized matrices corresponding to a null model (i.e. a null hypothesis). Here we discuss some assumptions of assembly rules (including phylogenetic assembly rules), decisions concerning the design and implementation of null models, and the ecological and biogeographical conclusions of the study.

The current status and the future of Baltic grey seal population

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Keywords: population dynamics, abundance, management, state space model

Abstract: The population size of Baltic grey seals (*Halichoerus grypus*) has substantially increased in recent years leading to a conflict between seals and coastal fisheries in the Baltic Sea. Grey seals damage fishing gear and catches and an unknown number of seals drown in fishing gear. This has led to the need for new management measures and, thus, a better understanding of the current status and future trend of the grey seal population under alternative management scenarios. We build a biologically consistent population dynamics model to estimate the temporal changes in the seal population and predict the development of the population under alternative management options. As the uncertainty related to the subject is high, modelling is conducted by using a probabilistic approach and Bayesian methods. This allows us to include data and prior information from several complementary sources to infer the parameters of the model. These include, for example, survey counts, by-catch estimates, fishing and hunting statistics, data from sampled individuals, expert interviews and literature. Our model is age-sex structured and we provide estimates, among others, for the population size and total by-catch in age-sex classes. The results indicate a clear difference in the hunting and by-catch mortality rates between males and females, and a clear effect of sea ice extent for pup survival. We forecast the population development under a few alternative management decisions related to hunting and by-catch, and different ice extent scenarios in the breeding areas that are based on climate warming scenarios.

On the Challenge of Fitting Scaling Laws in Ecology

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Keywords: abundance; community structure and dynamics; survey design and analysis

Abstract: Scaling laws appear in a wide range of natural phenomena (Newman 2005). We concentrate on the size distribution of tree stem diameters in tropical forests as a representative example of scaling laws (Enquist and Niklas 2001). Fitting such an empirical size distribution, for example with a power-law, a negative exponential or a Weibull distribution, is usually done using maximum likelihood estimation (MLE) and results in reliable estimation of the unknown parameters (Clauset et al. 2009). However, classification of field data and random measurement errors influence this statistical estimation. We compare three different types of MLE, the common one not accounting for uncertainties in the observation procedure and two modified versions accounting either for binning of data or for random measurement errors. Results show that the two modified MLE methods accounting for such uncertainties are much more robust than the common MLE.

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Effects of species' similarity and dominance on the functional and phylogenetic structure of a plant meta-community

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Keywords: abundance, community structure and dynamics, measures of biodiversity, spatial ecology

Abstract (297 words): Studies of functional and phylogenetic diversity patterns have provided important insights into the assembly rules that govern the spatial structure of meta-communities. However they often rely on a single diversity measure and thus implicitly choose how they account for species relative abundances and how species similarities are linked to phylogenetic or functional distances, thus potentially failing to identify certain assembly rules.

Recent reviews[1,2] put back in the spotlight the family of Hill numbers[3] and its ability to gradually scale the importance of dominance in communities (i.e. the weight given to dominant vs. rare species) back in the spotlight. Some authors further generalized these indices to account for species similarities[4]. We are going a step further and combine this framework with the tree transformations proposed by Pagel[5] in order to gradually scale not only the importance of dominance but also species similarity (the weight given to small vs. large similarities). We applied this new flexible framework to study functional and phylogenetic diversity patterns in an alpine plant meta-community and tested them with a null model of random assembly and evaluated the contribution of environment and space on inter-community pairwise diversities[6].

Functional diversities were significantly high when the same weight was given to dominant vs. rare species and to large vs. small species' similarities and were random otherwise. In contrast, phylogenetic diversities were significantly low when greater weight was given to dominant species and were random otherwise. This suggested that the environmental gradients filtered species according to their functional traits, while, at the same time, competition prevented the co-dominance of too closely related species.

Our results highlighted the importance of an multi-indices framework (including our methodology) that, by utilizing the full extent of information provided by the structure of meta-communities, are able to disentangle patterns generated by multiple assembly rules.

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Nonlinear modelling of rodent population cycles: constrasting the roles of direct vs. delayed density dependence

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Keywords: population dynamics; cycles; growth rates

Abstract: Population cycles in voles and lemmings are often thought to require one-year delayed density-dependence of the annual population growth rate (Lambin et al. 2006), with specialist predators causing crashes. Re-analysing controversial data from French common voles, and replacing popular log-linear autoregressive models with non-linear ones, we show that direct density-dependence (DD) is less stabilising than previously thought, and that delayed DD can have a different role than suggested by the classic theory (Turchin 2003). Sum of squares and leave-one-out cross-validation (Turchin 2003) are used to rank models, with our best models including cycle phase. We highlight the importance of good practice in communicating results (e.g., what exact timescales are considered to define density-dependence of the population growth rate?), and conclude that the observed population cycles in France are in-between what Turchin (2003) calls first- and second-order cycles.

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Incorporating landscape attributes into dynamic population models.

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Keywords: population dynamics; occupancy models; community structure and dynamics

Abstract: Dynamic populations models such as the Lotka-Volterra model have been widely studied from both a mathematical perspective and in ecological applications. They are effective at giving researchers insights into how changes in various population parameters will influence the changes in the population dynamics. One area of interest is how the model parameters change across some ecological gradient. We propose using a hierarchical Bayesian framework model the influence across the ecological gradient. Furthermore, and possibly more importantly, be able to understand how future changes in the environment will affect the population dynamics with associated uncertainty quantification. This will be illustrated using two simulated datasets: one concerning the standard Lotka-Volterra predator-prey model and another concerning growth rates and carrying capacities. Using a dataset from the Daly river in Australia we show how impactful this type of analysis can be.

Estimating temporal changes in parameters of stochastic population models

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Keyword: population dynamics

Abstract: Density dependent population models, such as the logistic model, usually assumes a stationary environment when fitted to simple count data. This assumption can be unrealistic due to anthropogenic effect on the environment or natural catastrophes, and instead require model parameters to vary in time. For instance, a deteriorating habitat can be described by a gradually declining carrying capacity, while an oil spill might abruptly affect the growth rate of a species. Such models can be approximated by diffusion processes with parameters changing through time and illustrate how population fluctuations respond to changes in different parameters. The estimation should be easy to implement and the results capture earlier (abrupt) or ongoing changes. We will present how temporal changes in different parameters can be estimated using maximum likelihood estimation with parametric bootstrap and the Integrated Nested Laplace Approximation (INLA) method. We illustrate how the quality of data and sample size influence the inference of the parameters. We discuss the difference between a trend in density independent populations, which is a trend in population fluctuations, versus gradual change in carrying capacity of a density dependent population, which is a trend in a population parameter. This distinction will also be discussed in terms of prediction.

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Inference for Size Demography from Point Pattern Data using Integral Projection Models

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Keywords: density dependence; hierarchical model; nonhomogeneous Poisson process

Abstract: Population dynamics with regard to evolution of traits has typically been studied using matrix projection models (MPMs). Recently, to work with continuous traits, integral projection models (IPMs) have been proposed. IPMs are handled first with a fitting stage, then with a projection stage. Fitting these models has so far been done only with individual-level transition data. These data are used to estimate the demographic functions that comprise the *kernel* of the IPM specification. Then, the estimated kernel is iterated from an initial trait distribution to project steady state population behavior under this kernel. When trait distributions are observed over time, such an approach fails to align projected distributions with these observed temporal benchmarks.

The contribution here, focusing on size distributions, is to address this issue. We claim the above approach introduces an inherent mismatch in scales. The redistribution kernel in the IPM describes population level redistribution and the kernel should be interpreted at that scale. Fitting at the individual level produces parameter estimates which are at the wrong scale and do not allow this interpretation. Our approach views the observed size distribution at a given time as a point pattern over a bounded interval. We build a three-stage hierarchical model to infer about the dynamic intensities used to explain the observed point patterns. This model is driven by a *latent* deterministic IPM and we introduce uncertainty by having the operating IPM vary around this deterministic specification. Further uncertainty arises in the realization of the point pattern given the operating IPM. Fitted within a Bayesian framework, such modeling enables full inference about all features of the model. Such dynamic modeling, *optimized* by fitting data observed over time, is better suited to projection.

Measuring Distance Between the Compositional Diet Estimates Produced by Quantitative Fatty Acid Signature Analysis

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Keywords: Diet Estimation; Compositional Data; Distance Measures; Essential Zeros; QFASA

Abstract:

In ecological applications involving compositional data, zeros can be problematic and may preclude the use of standard statistical techniques. This is especially true in applications requiring a valid measure of distance. In quantitative fatty acid signature analysis (QFASA), compositional diet estimates containing the proportion of each species of prey potentially in the predator's diet are produced and zeros often arise corresponding to species estimated to be absent from the diet. QFASA diet estimates may then be used to test whether differences in diet exist, for instance, between male and female predators or across different seasons and years, provided an appropriate measure of distance has been established. Traditional distance measures such as Aitchison's distance, however, either cannot be applied directly when zeros are present or do not satisfy fundamental properties of compositional data analysis. In this talk we compare three distance measures that are capable of handling zeros but do not satisfy one of the fundamental properties, namely the principle of subcompositional coherence. Following the ideas of Greenacre (2011), we attempt to measure the subcompositional incoherence of the distance measures in order to determine if the measures may, from a practical point of view, satisfy the principle. Based on the results of a simulation study, we recommend a distance measure that may be useful in compositional data applications involving zeros. We subsequently apply this distance measure to test for differences in the diet of real-life grey seals inhabiting the eastern coast of Canada.

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Validating a data-limited stock assessment method using data-rich stocks

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Keywords: Population dynamics

Abstract: The sustainable harvesting of fish stocks depends on the estimation of their status, i.e. their exploitation level. In practice, stock assessment is often hindered by data limitations. For example, age readings are not always available or of poor quality. Further, time series of data are not always available. Those limitations make commonly used age-based approaches not applicable. As an alternative, a theoretical single-species, size-structured model (Andersen and Beyer, 2013) is used to estimate the stock status, quantified by the ratio (F/F_{MSY}) between the fishing mortality (F) and the fishing mortality leading to the maximum sustainable yield (F_{MSY}). The model describes the growth, mortality and recruitment of the population combining the theory of Beverton-Holt life history invariants with metabolic theory. The parameters of the model are estimated using maximum likelihood. Minimum data requirement of the method is the size distribution of commercial catches. If more information is available, e.g. survey data, or life history parameters, they can be used to improve the estimation. The method is validated using only size-specific data from different stocks of Atlantic cod, *Gadus morhua*, (e.g. North Sea cod, Eastern Baltic cod). The results are compared with the official data-rich age-based assessment.

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Modelling the population dynamics of a native plant: application to sustainable management of the babassu palm tree in Brazil

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Keywords: population dynamics; palm; modelling

Abstract: Largely represented in Brazil, the babassu palm (*Attalea speciosa* Mart. ex Spreng.) is an endemic species of the primary forests in South America. In these forests the progress of the pioneer front has highlighted the babassu in the henceforth man-made open areas: pastures and cultivated fields. Babassu is a part of the "extractive" resources: gathering activity followed by marketing of non-timber products. According to estimates, this activity involves two million people among the most disadvantaged in the country. Despite this fact, the knowledge of sustainable functioning of this species among these anthropic environments are sorely lacking. Our work serves to clarify this functioning and to provide support of local populations to guide them towards a sustainable management of the babassu. This work is organized around the selection and the implementation of a mathematical model of population dynamics. The matrix transition models (integrating only stages) are the most commonly used. However, we have selected a model from those used for modelling Arecaceae which is based on the cohorts (integrates stage and age). We finally confronted these two models. The results obtained in this study have shown that the model we have proposed is more suitable than the currently used matrix transition models. This substitution model can better integrate the concept of annual variability in population caused by both the external and internal factors. We have proved that the concept of age of the individual is essential and inseparable from that of stage. The results obtained from simulations based on our model indicate that the unstationarity and stochasticity can be introduced for both parameters. Currently our team conducts a three years field study in Brazil. The results will allow us to have a clearer outline of the structure of our model. Moreover, these data will serve to feed and calibrate the model.

Zooplankton biodiversity in response to environmental change

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Keywords: community structure and dynamics, monitoring of biodiversity, survey design and analysis.

Abstract: The aim of this work is to explore structural and functional modifications of zooplankton communities in response to environmental change, including eutrophication and acidification. In order to do so, we need to model reference conditions and trends for zooplankton based indicators under different scenarios. The data set will be zooplankton species abundance data from several hundred lakes. To obtain a data set for a lake that is as representative as possible for the community composition a given year, we reduce the effect of sampling and seasonal variation by collecting two samples from the littoral and one from the pelagic zone at least twice each season. The similarity in community composition between samples was evaluated by fitting a bivariate Poisson-lognormal species abundance model. The estimated correlation in this bivariate distribution is used as a measure of similarity since this approach is utilizing all the available abundance information and accounts for the sampling process. Application of the bivariate correlation as a similarity measure offers advantages over traditional measures because it takes account of the complete species abundance distributions. This approach provides an approximately unbiased estimate of similarity despite varying sample sizes and detection/ non-detection of species that are present, but rare. The temporal or spatial change in community structure, quantified by the bivariate correlation, can now be modeled by some environmental covariates.

A shared component hierarchical model to represent how fish assemblages vary as a function of river temperatures and flow regimes

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Keywords: Fish assemblages, Temperature and flow regimes, Hierarchical modelling, Bayesian statistics
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Abstract: Studies on global change have pointed out a fast evolution of temperature and flow regimes over the few last decades. It is therefore of primary importance to understand how these changes influence the aquatic systems functioning. A hierarchical model is developed to understand how juvenile fish assemblage structure answers to interannual variations of temperature and flow regimes. Long-term datasets are necessary to study global change effects. Datasets of water temperatures, flows and electric fishing samples have been collected on the upper River Rhone since 1980. A latent variable of interest is introduced to represent the common source of variation for the environmental and the biological data. This shared component links two sets of variables with different types: on one side, the latent variable can be understood as a factor from the continuous explanatory variables recording the environmental variations while, on the other side, it can be considered as a logistic regressor in a multinomial response model for proportions of various fish species juvenile collected under poorly controlled electro-fishing experiments. The response variable consists in three groups of species determined according to their synchronic reaction to environmental variations. Inference relies on Monte Carlo Markov Chain techniques under the Bayesian paradigm.

Modeling the feeding patterns of marine predators from stomach content data.

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Keywords: Multispecies models; Community structure and dynamics; Feeding behavior; Compound Poisson models; Bayesian inference.

Abstract: Estimating the feeding patterns of marine top predators using stomach contents is challenging, while knowledge about the competition between predatory fish and about the interactions with their prey is important for understanding trophic pathways.

Stomach contents of fish are commonly documented to understand feeding habits, feeding preferences and consumption rates. Prey data are usually expressed in count or in weight. However simple statistical distributions poorly fit these data as they generally are zero-inflated (many empty stomachs) and over-dispersed. Here we tested several statistical hierarchical models that accounts for these two characteristics : a Zero Inflated Negative Binomial Model and other forms of the Compound Poisson models (Tweedie models).

Tweedie moddels allowed us to mimic the feeding behavior of a large pelagic fish predator (such as tuna) when hunting on prey schools: the stomach content is then considered as the sum of the preys caught in each prey school met by the predator. Indeed tunas are caught in surface schools by purse seiners, when tuna seek out schools of favoured prey aggregations. This information can be included in the model, taking benefit that two individuals caught in the same school had encountered the same prey schools. A simulation analysis has been performed to quantify the influence of this information on parameters estimation, and predator size has been included to explain the food quantity consumed in each school.

Different models are compared and applied to investigate feeding patterns of two tuna species in the context of the industrial purse seine fishery in the Indian ocean.

Bias due to autocorrelation where no one expects it: the relationship between community-weighted mean traits and environmental variables

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Keywords: autocorrelation of residuals, functional traits, inflated type I error rate, Monte Carlo permutation test.

Abstract:

Community-weighted mean of species trait values (CWM), one of functional diversity indices, became a standard tool to scale-up functional traits from individual to community or ecosystem level. Common practice is to test the relationship between CWM and environmental variables or ecosystem properties, e.g. using regression or correlation. In this study, I point out the bias inherited in these analyses, including inflated type I error rate and overestimated explained variation, leading to results more optimistic than would be justified by data. To explain the cause of this bias and to seek a potential remedy, I use a surprisingly helpful analogy with an analysis of spatially autocorrelated variables. I demonstrate this property on regression between set of CWM and set of environmental variables, using artificial and real community datasets. I propose using the Monte Carlo permutation test to correct an inflated type I error rate.

Results clearly show that CWM calculated from randomly generated species functional trait values has several times higher probability of being significantly related with environmental variables than would correspond to nominal significance level. Moreover, this inflation of type I error rate increases with increasing effect of environmental variables on species composition. Proposed Monte Carlo permutation test gives unbiased levels of type I error rate. The example with real community data shows that uncorrected and corrected results as well as interpretation can differ dramatically.

This is the first time to report that overly optimistic results may be expected when analysing the relationship between CWM and other variables, derived from or influencing a species composition. In future, this bias needs to be acknowledged and corrected, to avoid excessive reporting of significant relationships between community-aggregated traits and environmental variables or ecosystem properties.

Non deterministic modeling of food web dynamics

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Keywords: community structure and dynamics, multispecies models, mass-balance, trophic interactions.

Abstract: A conventional way to build numerical models of multiple species and their trophic interactions is to assemble a food web topology, where species are nodes and trophic interactions are flows, and subsequently define rules and parameters which characterise individual species dynamics and the flows of mass (or energy) between them. While early models of this kind were build on purely deterministic principles, current models generally incorporate a stochastic component in addition to a deterministic skeleton.

In the present contribution, we show that it is possible to construct such models without need for a deterministic skeleton. Instead, the flows of mass (or energy) between species can be considered to be purely stochastic if they are bounded according to rules pertaining to thermodynamics and physiology.

This model construction based on 'chance and necessity', requires a minimal amount of assumptions and parameters, and is capable of reproducing patterns of population variability while accounting for balance of mass/energy at the food web level. This can serve as a reference against which the performance of deterministic models can be evaluated.

Individual-based simulation of tree line dynamics in the Siberian North

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Keywords: community structure and dynamics, individual-based models, movement ecology.

Abstract: Throughout the last decades, climate change led to a dramatic increase of temperatures in the Arctic. As a consequence, vast tundra areas might be transformed to taiga by immigration of tree species which were released from temperature limitation. The geographical position of the tree line is predicted to shift further north, and, alongside the tundra-taiga transitions the areas' albedo decreases, which additionally increase local temperatures and might positively feedback to global warming. However, major uncertainties prevail in predicting the speed and magnitude of the tree line advance due to complex interactions of intraspecific processes determining tree stand dynamics. For this reason, an individual-based and spatially explicit model was developed and calibrated for the dominant larch tree species forming the tree line in the Siberian North. In order to achieve a most realistic model, the model handles explicitly each life history stage of the larch individuals and the models' processes were adapted to observed patterns of surveyed tree stands. The credibility of simulated results is supported by results of a thorough sensitivity and uncertainty analysis, namely small resulting sensitivity values. Forcing the model with a reconstructed millennial long weather time series for the region realistic tree stands emerged. Furthermore, the model reliably predicted the current tree line position. Additionally, large area simulations were used to compare model results to findings of palaeoecological approaches. After profound calibrations the presented model can be used as a suitable tool for investigations of the tree line position through space and time, including yet uncertain future changes.

Species co-occurrence – Looking at species associations differently

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Keywords: community structure and dynamics, multispecies models

Abstract: Species interact with both biotic and abiotics aspects of their surrounding. Although there has been a broad interest in better understanding how species co-occur, very few approaches have been efficient in modelling species co-occurrence. A reason for the few modelling tools available to estimate species associations is partly due to sparseness of community data combined with the typically large number of species found in an ecological community. We propose an approach that models species co-occurrence by estimating the positive and negative correlations among species within a community. From the estimated matrix of correlations, it becomes possible to make inferences about the association among interacting species. We use a sparse Bayesian factor approach to parameterize the model, which is efficient to accurately estimate high-dimensional correlation matrices and thus makes our technique applicable to species-rich communities. This modelling approach can be included in a broader modelling framework where species characteristics (such as traits and phylogenetic relationships) and habitat structure can be considered to refine our understanding of why species are found in a particular location. The theoretical developments presented here are currently being implemented in an R package, making this new modelling framework available to a broad audience and allowing it to be applicable to a range of data. The application of our new method will be illustrated with simulated and real ecological data.

Discussing problems vs. finding solutions: an operational framework for dealing with imperfect detection in species distribution modelling

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Keywords: abundance, distance sampling, species distribution models

Abstract: Methods for dealing with imperfect detection have gained increasing attention in species distribution models (SDMs), yet there seems to be more discussion of the problems than efficient solutions. Part of the issue is that many historical and current data sets have been collected without multiple-visits to locations, thus conventional models based on multiple visits are not applicable. Another problem is the lack of standardized protocols when combining disparate data sets in order to cover larger geographic areas for SDMs. We show that recently proposed methodologies (single visit based N-mixture models; Sólymos et al. 2012) allow for correcting for detection error without replicate surveys; and that using a subset of the data to develop correction factors based on a combination of removal and distance sampling can be used to correct for imperfect detection while dealing with variation in survey protocols (QPAD approach; Sólymos et al. 2013). The QPAD approach can be used in combination with common modelling techniques including GLMs, GAMs, GLMMs, and regression trees. A common feature of these methods is the use of conditional maximum likelihood estimators that lead to reduced computation when fitting complex models to large data sets. These methods are also cost effective enabling ecologists to cover a larger geographical region than possible when having to return to sites. We use bird point count surveys from the Boreal Avian Modelling Project and the Alberta Biodiversity Monitoring Institute to demonstrate some of the possible applications of these methodologies for conservation and management of species over large spatial scales.

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A community distance sampling model for estimating seabird abundance and distribution

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Keywords: Bayesian p-value, hierarchical model, negative binomial abundance model, sparse data

Abstract: Distance sampling is a widely used framework for studying the abundance of wildlife that can be observed directly. Hierarchical distance sampling allows linking abundance at a sample site to site-specific covariates. Using this framework, we developed a community distance sampling (CDS) model. In this model, information is shared across species by assuming a common underlying distribution for abundance and detection parameters, whose hyperparameters are estimated as part of the model. This enables us to include species with sparse data sets into the community analysis.

We applied the CDS model to shipboard distance sampling data of 15 seabird species, collected in April 2012 off the coast of Maryland, USA, within a project to inform future placement of offshore wind farms. Our model included random species effects of salinity and sea surface temperature on abundance; and a random species effect and a fixed effect of sea state on the scale parameter of the half normal detection function, σ. We fit both Poisson and negative binomial abundance models and assessed model fit using Bayesian p-values. The negative binomial model fit the data adequately while the Poisson model failed to capture the spatial variability in seabird abundance. Sea state had a negative effect on the detectability of seabirds. Species specific scale parameters for detection were consistently between 200 and 300 m. Seabird abundance was negatively correlated with both salinity and water temperature. Salinity had a significantly negative effect on the abundance of six species, while temperature only affected one species significantly negatively. The CDS model allowed us to make inference on the distribution and abundance of 15 seabird species, ten of which did not yield sufficient data to

be modeled individually. Thus, the CDS shows promise for many distance sampling applications to improve estimation of detection and abundance of a suite of species.

Using Spatial Models to Refine Distance Sampling Estimates of Black Bears

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Keywords: abundance, spatial model, density surface model, distance sampling, bear estimation, project impact.

Abstract: The Alaska Department of Fish and Game has used a point independence double-observer distance sampling model (Borchers et al. 2006) with an asymmetric normal detection function to obtain bear population estimates over large geographic areas. We developed a spatially explicit model of black bear abundance over a large area of south-central Alaska using a density surface model (Miller et al. 2013) applied to our distance sampling model. We build maps of abundance (and uncertainty) and relate estimates back to biologically meaningful covariates. The potential impacts of a proposed hydroelectric project on black bear populations can more accurately be calculated with the spatial model.

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General model-based methods for distance sampling

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Keywords: Bayesian model fitting; distance sampling; integrated likelihood; model-based methods.

Abstract: In distance sampling, distances of detected animals from a line or point are used to estimate animal density and abundance. Conventional distance sampling is a hybrid method; probability of detection is estimated from the recorded distances using model-based methods, while encounter rate (number of animals per unit distance for lines, number of animals per visit to a point for points) is estimated using design-based methods. In the last decade, there has been much interest in developing methods that are fully model-based. Such methods allow inference on the relationships between animal density and covariates. By including random effects, spatial and temporal correlations may be accommodated. We explore the potential for full likelihood approaches to distance sampling, using either maximum likelihood or Bayesian methods for fitting. We discuss how key assumptions of standard distance sampling may be relaxed in a model-based framework, and speculate on future developments.

Accounting for Partial Overlap of Observation Zones and Lack of Independence in MRDS, with Application to Abundance Estimation of Hector's Dolphin.

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Keywords: abundance, *Cephalorhynchus hectori hectori*, distance sampling, Hector's dolphin

Abstract: In most double observer mark-recapture distance sampling applications, it is anticipated that each observer will search the same area within a transect. However this is not always possible depending on the resources available, as was the case in a recent fixed-wing aerial line-transect survey for Hector's dolphin (*Cephalorhynchus hectori hectori*) off the north and east coasts of the New Zealand's South Island. There, the rear observer could search the full transect width through a bubble window while the front observer could not search within 70 m of the trackline as a flat window was mounted in that section of the aircraft. In order to make full use of the available data, current methods were extended to account for the partial overlap of the observation zones. Furthermore, a lack of independence between sightings from each observer position can lead to an underestimate of abundance and, following Buckland et al. (2010), we wished to consider different forms of dependence in our analysis, although using an alternative parameterization. This new paramterization is intuitive and amounts to including the sighting record of one observer as a detection covariate for the other. Simulation results suggest that the new approach works well for the scenarios considered and when applied to the 2013 summer and winter surveys for Hector's dolphin, abundance is estimated to be in the order of several thousand dolphins within 20 nm of the north and east coasts of the South Island. There is good agreement between the abundance estimates using the full data and a reduced data set using only sightings from within the common search area.

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Identification uncertainty and probabilistic classification methods: from DNA sequences to bird species identity

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Keywords: survey design and analysis; big data; monitoring of biodiversity.

Abstract: Just as next-generation sequencers have fueled research in bioinformatics, autonomous recording units are stimulating the need for new statistical methods related to bioacoustics, especially in data processing, such as automated species identification tools. When collecting bird vocalization data, *e.g.* for studying Amazon bird communities, the use of numerous autonomous recorders as compared to manual listening by field observers can be compared to the revolution of massive parallel sequencing (MPS) and conventional sequencing methods. MPS produces extensive data sets with a fraction of cost compared to Sanger sequencing, but the analysis of MPS data calls for sophisticated bioinformatics methods. Similarly, autonomous audio recording produces extensive datasets, but there are major challenges to extract relevant information from data in a reliable manner. Species identification through genetic barcoding is based on comparing the similarity of a query sequence to reference sequences obtained from well-identified samples. Similarly, acoustic species identification is based on comparing the similarity of a query vocalization to those present in a reference database. Both approaches have traditionally been based on arbitrary threshold levels of similarity between samples, resulting on a poor description of identification uncertainty. In this talk I will present a Bayesian approach to assess identification uncertainty from DNA barcoding data and illustrate how I am adapting this framework to the automated identification of bird vocalizations. A systematic quantification of identification uncertainty is a crucial component when making reliable biological inferences from acoustic data. Using probability as the measure of uncertainty makes it possible to integrate the information into state-space models of community dynamics, propagating identification uncertainty through the entire analytical pipeline from the raw data to the biological inferences.

Historical data for ecological monitoring and management evaluation, some practical experiences

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Keywords: monitoring of biodiversity; citizen sciences; big data

Abstract: Making use of citizen science and big data has become an important focus for ecological statisticians seeking inferences about the state of the environment. Monitoring change through time presents different problems to broad-scale snapshot and ‘atlas-type’ surveys. The lack of implementation of sensitive and robust monitoring concurrent with management may be redressed in the future, but what of learning from the past? Legacy historical datasets provide unique opportunities for analysts to learn about change and effects of management but analysts cannot change the nature of historical data. Common problems posed by the use of historical data include: observational data that may be subjective and coarse and of little relevance to the process of interest; poor survey design and ‘small data’. In this talk I shall describe real examples using historical data to learn about the effectiveness of ecological management interventions. Within a Bayesian framework and the BUGS/JAGS language some tools we use include the use of latent variables, informative Bayesian priors, double sampling and calibration.

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Estimating Abundance from Large Data Sets of Counts in Irregularly-Spaced Plots

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Keywords: abundance; big data; spatial ecology; species distribution models

Abstract: Monitoring environmental populations is an important goal for both academic research and management of natural resources. Successful management of populations often depends on obtaining estimates of their mean or total over a region. The basic problem considered in this paper is the estimation of the total from count data. The application has counts from thousands of irregularly-spaced aerial photo images. I model counts in images as a realization of an inhomogeneous Poisson process and use a fixed-rank spatial-design-matrix approach to model its spatial intensity surface. The fixed rank approach helps speed computations. The fitted intensity surface is integrated to provide an estimate of all unsampled area, which is added to the observed counts and also provides a finite area correction factor to variance estimation. The intensity surface from an inhomogenous Poisson process tends to be too smooth for locally clustered points, as often happens for animals, so I consider three different overdispersion estimators. I use simulated data to examine estimation bias and to investigate several variance estimators with overdispersion. A real example is given of harbor seal counts from aerial surveys in an Alaskan glacial fjord.

Causes of spatial synchrony in UK aphids

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Keywords: big data; metapopulation dynamics; spatial ecology

Abstract: We examine 35 years of variation in UK climate and aphid data from 11 sites, including counts and phenological data for 20 important species. We apply a Morlet wavelet transform to break down the fluctuations into complex components with different timescales of variability. The mean field of the wavelet components indicates the synchrony of the different sites. Long timescale fluctuations are more spatially synchronous than short timescale fluctuations. We introduce a technique based on spatially synchronous surrogates to determine the significance of the coherence between the aphid and climate transforms. We find statistically significant relationships between the winter NAO, local temperatures, and aphid ecology, particularly at timescales greater than 4 years. Those species showing greatest wavelet coherence with climatic variation have the highest spatial synchrony. We introduce a frequency specific Moran theorem and show that on average approximately 70% of the spatial synchrony of long timescale fluctuations in aphid first flight times can be explained by the influence of winter climate fluctuations.

Statistical ecology: everything we know isn't wrong

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Keywords: statistical inference; data science; significance vs power

Abstract: Debates over which statistical methods to use and which paradigm to follow have become increasingly polarised in ecology over recent years. But the lack of agreement may be due, at least in part, to fundamental misunderstandings or even forgetting what we already know. The controversy surrounding AIC and the recommendations found in Burnham and Anderson (2002) is a case in point; a simple appeal to asking "What are we modelling *for*?" is sufficient to resolve the situation, taking inspiration from Shmueli (2010). As a second example, concern has been expressed over reproducibility of scientific findings—a technical examination is found in Johnson (2013)—but discussion has focussed on significance rather than power.

Elsewhere in this conference, Ben Bolker will be discussing when novel statistical methods should be used and when not; a related but inverse question is: why am I often criticised for **not using** "fancy statistical methods"? New methodology should augment, but not necessarily supplant older methods; my being told (a) to use mixed models with only five groups, or (b) use GAMs for a set of binary explanatory variables suggests that some have forgotten what we already know. Appropriate methods are not "old school" or "outdated" (both actual criticisms received) simply because they weren't developed in the last ten years.

A brief discussion on the above will also consider the fledgling "data science" and where statistics as a discipline fits in (or should fit in).

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Decomposing correlated occurrence with a hierarchical Joint Species Distribution Model

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Keywords: multivariate probit model; latent variable model; eucalypt distribution, frog distribution.

Abstract: A goal of ecology is to understand the processes underlying species distributions. Two major strands of ecology—habitat modelling and community ecology—approach this problem differently. Habitat modellers often use species distribution models (SDMs) to quantify the relationship between species and their environments without considering potential biotic interactions. Community ecologists, on the other hand, tend to focus on biotic interactions and, in observational studies, use co-occurrence patterns to identify ecological processes. Here, we describe an approach that integrates these branches of ecology by incorporating species co-occurrence data into a SDM. We describe a hierarchical multispecies SDM and use it to decompose species co-occurrence patterns into components of shared environmental response and residual co-occurrence. Environmental filtering is captured by correlations in occurrence due to the environment, whereas residual correlation suggests that other ecological or evolutionary processes may be important. We demonstrate our modelling approach using two case studies: frogs and *Eucalyptus* trees. Overall, shared environmental correlation was stronger than residual correlation for both frogs and eucalypts, but there were cases of strong residual correlation, suggesting that biotic interactions may influence species distributions. Including residual correlations between species in SDMs provides a more refined depiction of the relationship between species distributions and environmental variables and can help clarify the influence of ecological processes (e.g. environmental filtering and species interactions) on species assemblages.

State space modelling of temporal dependence in fisheries data using copulas

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Keywords: population dynamics, multispecies models, Schaefer model, time-varying catchability

Abstract: Fisheries management decisions are often informed by models based on catch per unit effort (CPUE) data, for example, the number of fish caught per hour of fishing. Uncertainty arises from three sources: (1) observation error in the aggregated catch or effort data, (2) the interaction between a fishery and the fish population ("catchability"), and (3) the unobserved population's dynamics. Here, a state space model is used within the context of unknown observation error and catchability to explore whether or not the dynamics of two managed populations display stochastic dependence features. This dependence is modelled with Archimedean copulas previously applied in the domains of hydrology, financial and insurance risk. A positive association between the two populations is suggested, where the choice of copula affects the probability that the populations exceed a management threshold. An alternative hypothesis instead considers a common factor that introduces temporal dependence among the CPUE data independent of the populations' dynamics; this second pathway of dependence is imposed through the catchabilities of the multiple fisheries. Although this hypothesis also receives some support from the data, the inclusion of the common factor has a negligible impact on the probability of the populations exceeding the management threshold, compared to the choice of copula.

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Modelling dependence in ecological community data

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Keywords: community structure and dynamics; multispecies models

Abstract: Species abundance data often occur as a species by sample (n by p) matrix of counts. Such a matrix may be used to provide ordination by multidimensional scaling or by correspondence analysis, with their associated low-dimensional plots. Traditional methods of analysis are mathematical, using distance metrics or matrix decomposition. Alternative likelihood-based methods using finite mixtures yield low-dimensional plots which are usually similar to those from the traditional methods, but have the added advantage of providing model comparisons and statistical decision-making (Pledger and Arnold, 2014). However, a major concern for ecologists is the assumption of independence in the model-based methods. The previous Poisson-based models are now modified to use the negative binomial distribution as the building block. Making the negative binomial dispersion parameter species-specific helps to account for the spatial clustering frequently observed within species. This talk briefly outlines the model-building, then compares the Poisson and negative binomial results using ecological community data. Possible model extensions to allow for dependence in the data caused by competition between species will be suggested, and discussion will be welcomed. All models are wrong, but useful ones are appreciated.

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Optimal study design for multi-season, multi-species avian monitoring programs

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Keywords: community structure and dynamics; multispecies models; occupancy models; survey design and analysis

Abstract: Understanding ecological factors that influence biological diversity is vital for species conservation, and to the success of monitoring programs designed to guide management decisions for these species. Accurate measures of community structure are paramount for understanding ecological factors that influence biological diversity. Species richness can represent community structure during one time period, while community change can be captured via probabilities of local colonization and extinction. Study design guidelines exist for single-species occupancy models, but few recommendations exist for multi-species community occupancy models for either single or multiple seasons. We recently developed study design recommendations for single season, multi-species programs and extend them here to multiple seasons. Statistical advances in Bayesian hierarchical multi-species occupancy models improve our ability to model data from multi-species monitoring programs, but a design trade-off remains between costs of increased effort from spatial and/or temporal replication and accuracy of parameter estimates of occupancy probability, detection probability, species richness, local colonization probability, and local extinction probability. We used simulated data based on two long-term avian data sets from Arizona, USA to explore design and cost trade-offs for avian community monitoring programs over multiple years, while assessing our ability to detect community change. We used study design combinations (number of sites, sampling occasions) and biological conditions (superpopulation size, species assemblage) to explore design tradeoffs. Optimal designs were different based on the parameter of interest, which strengthens the need for clear *a priori* study objectives.

Stochastic models of grassland community dynamics: a winter wind on inter-annual predictions.

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Keywords: community structure and dynamics, multispecies models, population dynamics.

Abstract: Stochastic models of population and community dynamics constitute major tools in modern ecology (Lande et al. 2003). They have been mainly used for the analysis of animal populations, but much less for plant communities, with the notable exception of tree communities (e.g., Hubbell 2001). Recently, a stochastic model of community dynamics has been proposed to analyze some famous grassland experiments using species biomass as a measure of population size (De Mazancourt et al. 2013). This approach consists in analyzing inter-annual variations in plant biomass using an annual time step in the model. However, herbaceous plants face a drastic decrease of biomass during winter in temperate areas, which may alter inter-annual temporal autocorrelations in plant biomass, even for perennial species. We here explore whether increasing the temporal resolution of this stochastic model of plant growth (down to a daily resolution) changes the inference one can make on plant community dynamics, by enabling to take into account the effect of biomass decrease during winter. We compare the two temporal resolutions (annual and daily) based on their predictive accuracy of inter-annual biomass temporal stability as in De Mazancourt et al. (2013), using both simulated data and real data from a biodiversity experiment in Jena (Weigelt et al. 2010). We evidence that our approach with daily resolution outperforms the former approach based on an annual resolution of community dynamics, whereas it is based on the same inter-annual data. We hence point out that not taking into account biomass decrease during winter in analyses of plant community dynamics in temperate areas may substantially limit the inference power and predictive accuracy of process-based approaches, even for inter-annual predictions. We further provide efficient computational routines to calibrate the new model with inter-annual data.

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A multi-method multi-species occupancy study with adaptive sampling of a small mammal assemblage

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Keywords: occupancy models, survey design and analysis, community structure and dynamics, population dynamics, spatial ecology, species distribution models

Abstract: In multi-species occupancy studies one often has a choice of methods to detect the presence of different species at distinct sites. Some methods may be inexpensive in terms of effort, but may not give unambiguous information about what species is being detected. Other methods may require more effort but give precise information about the species. Some methods may yield false positives, while other methods will not. Detection probabilities for given methods may also vary greatly among species.

We here present a multi-method occupancy study with adaptive sampling on an alpine assemblage of small mammals (6 species) that shows large fluctuations in community structure, abundances and distributions among seasons and years. At the first sampling-stage we employed surveys by the use of dogs and tracking slides at all sampling sites. These relatively inexpensive methods have a high detection rate, but seldom yield information about the species being detected. At the second sampling-stage, we used live-traps and camera-traps which usually give unambiguous species information. As these methods are more costly, we prioritized sampling the sites where occupancy was confirmed in the first sampling stage. In addition to gaining efficiency by adaptive sampling, we gain information about the occupancy probability of all species by using several methods, compared to single-method approaches. For example, lemmings, unlike the other small mammals, seldom enter live-traps, but are readily detected by the general methods. Hence, a site where an unspecified mammal has been detected, but no mammals were caught in the live-traps, is likely occupied by lemmings. In addition, our multi-species approach enables us to account for the possibility of false positives by some methods (detections by dogs were classified as either a certain detection of a certain species, a certain detection of a uncertain species, or a uncertain detection of an uncertain species).

A novel application of Bayesian hierarchical models and recurrent event survival analysis to cetacean behavioural response studies

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Keywords: multispecies models

Abstract: Measuring and quantifying the behavioural response of marine mammals to dis-

turbance is required for effective management and conservation. Field research to measure responses to acoustic disturbance is ongoing, but analysis and synthesis of the data remains a challenge. We consider data generated from Behavioral Response Studies (BRS) in the Bahamas (BRS07-08), California (SOCAL-BRS) and Norway (3S/3S2), during which simulated military sonar has been used to investigate behavioral responses of multiple cetacean species. We focus here on two analysis methods that have allowed us quantitatively to investigate exposure-behavioural response and exposure-response intensity relationships. Firstly, we have developed a Bayesian hierarchical model to relate expert-scored behavioural responses of multiple cetacean species to sound exposure level. The model allows for variation between species, between whales and between individual sound exposure sessions within the same whale. This model relies on choosing one response per exposure per individual, and we have focused on avoidance responses. The resulting exposure-response function contrasts sharply with current management approaches, predicting a substantial response probability at levels lower than previously assumed. Secondly, we have fitted a stratified Cox proportional hazards (PH) model to the same dataset. This survival analysis approach is well suited to the data: it accounts for the right-censoring in the data, but more importantly, it allows modelling of several types of recurring events associated with different doses of sound. The Cox PH model thus allows assessment of exposure-response relationships for responses of different intensities in one framework, and has also allowed us to investigate the relationship between social and environmental covariates and response severity.

Accounting for species taxonomy improves distribution models

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Keywords: individual-based models, multispecies models, species distribution models

Abstract: The use of species atlas data and correlational modelling approaches has become common practice in species distribution modelling. However, the effect of spatial extent on the performance of species distribution models remains unclear. We propose using species taxonomy to delineate environmental extent, and assess how this affects the performance of species distribution models. Using atlas data, two taxonomically enhanced datasets were created for 356 terrestrial species of mainland Spain. As well as a species' presence, its absence was recorded. However, an absence was only recorded for localities where another species of the same family or order was known to be present. We then assessed the effects of environmental extent on the predictive performance of five species distribution models, namely on model calibration and discrimination, comparing the results to those obtained with the original atlas dataset. Using family and order datasets significantly improved the calibration of the species distribution models. While the discrimination capacity decreased for several species when using the family dataset, this drop was significant when the models were trained with the order dataset. The species distribution model algorithms differed only slightly in performance. Enhancement of atlas data by excluding irrelevant absences based on species taxonomy significantly improved the calibration of species distribution models and thus their capacity to predict environmental potential. We therefore recommend the inclusion of species taxonomical extent when atlas data are employed in distribution models.

Acquired plant–animal interactions influence population growth rates of the invasive orchid *Spathoglottis plicata* in Puerto Rico

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Keyword: population dynamics, capture-recapture, invasive orchids, plant–animal interactions

Abstract: The Philippine ground orchid (*Spathoglottis plicata*) has invaded different tropical regions of the world, and in Puerto Rico, this species is causing negative ecological impacts. To assess the status of this invasive orchid, and the effects of plant–animal interactions on its population growth rates, we used a combination of field, experimental and modeling approaches. We focused on the interactions between the invasive orchid, the native weevil *Stethobaris polita*, and the invasive red fire ant *Solenopsis invicta*. Stage-structured matrix population models based on field observations gathered for four continuous years showed that the invasive population orchid is growing at a rate of 1.05, despite temporal variation and significant weevil damage to inflorescences. When fecundities are manipulated based on experimental exclusions, absence of weevil damage to flowers and fruits significantly increased λ to 1.22, while absence of ant visitation decreased λ to 1.04, with the latter not being significantly different from that obtained under field conditions. However, when demographic and environmental stochasticity are considered, exclusion of ants reduces the population size compared to the population size under field conditions when projected over time, and the stochastic population growth rate is significantly lower than the other treatments. Elasticity analyses show that survival and size-transitions, especially of larger size-stages, contribute the most to λ, rather than fecundities. Although there is some biotic resistance, weevil damage to inflorescences, alone, does not prevent population growth and expansion of *S. plicata*. When demographic and environmental stochasticity are considered, ants have a positive effect on the invasive orchid's λ, partially supporting the invasional meltdown hypothesis. The results of this study highlight the importance of considering acquired plant–animal interactions and stochasticity when evaluating the population growth rates and dynamics of invasive plants, and suggest that this invasive orchid will continue to spread in Puerto Rico.

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Analyzing effects of nonbreeders on population dynamics.

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Keywords: population dynamics; capture-recapture

Abstract: Many populations, particularly of birds, have large segments of nonbreeding individuals that fail to obtain breeding opportunities in a given year. These individuals often go undetected in population studies, which tend to be focused on the breeding population only. Here we have used a range of different techniques, including stochastic matrix modeling, elasticity analysis and social network analysis, to quantify the potential role of these nonbreeders in stochastic population dynamics. We have also looked at how population parameter estimates could be influenced by a failure to explicitly include nonbreeders in population models. We have examined systems with different types of nonbreeders (e.g. prebreeders vs. adult nonbreeders). A population of the Green-rumped parrotlet (*Forpus passerinus*) in Venezuela is used as a case study. Data on individually marked parrotlets from this population have been collected for more than 25 years, including large numbers of nonbreeders.

Bryozoan occupancy and abundance through the last three million years: extending process and observation models to the fossil record.

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Keywords: occupancy modelling, paleoecology, evolution, community, Plio-Pleistocene

Abstract: Bryozoans are colonial organisms that are not only abundant in the fossil record but also have many living representatives today. We are interested in estimating the changing occupancy and mean abundance of encrusting cheilostome bryozoan taxa over a 3 million year interval in a marine sedimentary basin on the east coast of the North Island of New Zealand. Occupancy and mean abundance of these bryozoans are hypothesized to be driven by some combination of temperature and sea-level change, substrate availability, as well as autecological characters and competitive effects by other fouling organisms. Environmental drivers are also postulated to influence preservation and subsequent sampling of fossil Bryozoa. We sampled hard shell substrates systematically for bryozoans such that there are replicate samples in both time and space. In these preliminary analyses, we estimate occupancy and mean abundance of select species of commonly occurring bryozoans to get a glimpse of variation in abundance among species and how environmental drivers such as the degree of physical disturbance in the habitat and regional temperature might affect sampling rates. This is likely the second study where Mackenzie et al.'s occupancy models (Mackenzie et al. 2006) are applied to fossil data (the first being Liow 2013). It demonstrates the importance of explicitly including sampling in the modelling framework used to investigate ecological parameters especially when working with fossil organisms where sampling probability is guaranteed to be less than one.

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Comparing species distribution model accuracies for various species groups and divergent prevalences

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Keywords: species distribution models.

Abstract: Species distribution models (SDM) relate the occurrence of species to a set of explanatory environmental variables. Many different types of measures have been proposed to indicate the models accuracy (Liu et al., 2011). These measures are known to be dependent of the species prevalence for both the training and validation datasets. Most species datasets don’t have explicit data on species absences. One way to overcome this is to select species absences from locations that have been thoroughly investigated. We investigate how different selection strategies from grid based species datasets influence the model results and accuracy measures. For this study we use a collection of datasets with species presences of five different species groups (butterflies, birds, plants, dragonflies and amphibians) in 1x1km grid cells in Flanders (Belgium). Within each species group, a range of rare and common species are selected. The selection of the data is based on different levels of intensity the grid cells have been investigated. We compared some of the most common accuracy measures (AUC, kappa, TSS and overall accuracy) for several model techniques (GAM, RF and Maxent) for all species in each group. The analysis allows determining the optimal selection for each species group.

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Convenient analysis of numerous distance sampling data sets in R

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Keywords: distance sampling, big data

Abstract: Institutions such as governmental agencies and non-governmental organisations attempt to make greater use of historical data they have accumulated. Statisticians are called upon to analyse data sets of increasing size with greater rapidity. The gulf between data gatherers and data analysts is very broad in these circumstances and challenges the opportunity for interactive data analysis. We are developing reproducible research (Gandrud 2013) tools to couple the convenience of R for data manipulation with the Distance package (Miller 2013).

Our tools perform exploratory analysis of data sets and produce a laboratory notebook style digest of preliminary results. The analyst and client then examine the preliminaries to determine the course of action (that may include merging of datasets, degree of truncation or elimination of problematic datasets) for final analyses.

The Distance R package provides a convenient way of fitting detection functions to sighting data. Models involving double observer protocols or covariates influencing detectability are easily incorporated. The detection function fitting routines provide metrics for model selection. These adaptable tools conveniently fit inside many types of analytical systems, we present a system tailored for reproducible methodology when analysing a large number of data sets.

Tools used for the final analysis include a series of standardised graphics and goodness of fit diagnostics. This provides uniformity across data set and allows analyst and client to have a consistent means of examining findings. This addresses the common concern of distance sampling novices "how do I present the results."

We demonstrate use of these tools with a 30-year dataset for a multi-species survey consisting of $\geq$30 species of sea birds. We also discuss the potential to extend the set of tools in a web-based environment to heighten the collaborative aspects.

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Cost-benefit model of clonal plants spread patterns

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Keywords: spatial ecology; evolutionary ecology

Abstract: Many clonal plants spread by runners, the conducting organs serving as functional connections with their asexual offsprings, often used to support the offspring by resources. These clonal plants have to deal with few optimization problems during the daughter shoot establishment process. One of the key decisions is about the optimal distance where the daughter shoot should be placed to. If a daughter shoot is placed too close to its mother shoot, it suffers from competition with mother shoot, if it is too far, the costs for establishing and maintaining the connection are high.

We constructed a simple cost-benefit model weighting the rhizosphere overlap against the cost of connection organ to predict the optimal distance between mother and daughter shoot. As a parameters for this model we use a shape of rhizosphere, a unit cost of connection organ and a productivity of environment. The model predicts that plants from more productive environment spread further, but that relationship is modified by unit cost of the spreading organ. It also predicts a range of poor habitats in which clonal plants with long-term connections between mother and daughter shoot cannot exist.

We compared predictions of the model with the data on large set of species featuring type of clonal growth and environmental optima of these species. The data show that there is an overall trend of increasing lateral spread with environmental productivity, but the intensity varies among plants that use different types of clonal organs. It seems that growth patterns of stoloniferous plants, whose are likely to have constant unit cost per stolon length and thus well fit the model assumptions, are in the best accordance with the model predictions.

Differentiating divaricating species of *Sophora* by the development of shoot architecture.

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Keywords: multispecies models; evolutionary ecology

Abstract: Morphometric measurements of mature organs have been suggested as a means to classify plants as divaricating or not (Kelly 1994). Carswell and Gould (1998) suggest that such measurements do not effectively distinguish between divaricate and non-divaricate species in the *Sophora* genus (New Zealand kōwhai). Instead, they suggest developmental processes might be used to classify divariacates in this genus. We investigate whether there are significant differences in the development of shoot architecture between the divaricate species *S. prostrata* (the prostrate kōwhai) and the arborescent species *S. tetraptera* (the large-leaved kōwhai).

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Do different fishery surveys data lead to same estimations?

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Keywords: species distribution models; survey design and analysis

Abstract: Habitat and species mapping is essential for conservation programmes because it provides a clear picture of the distribution and extent of marine resources, and thus it facilitates the management of the marine environment. The importance of a spatial management of the marine resources and that fishing contribution should be improved for the sustainable development of the ecosystem are widely recognized facts in fishery ecology. Nevertheless, the amount of objective scientific information is limited and the data may not always be strictly comparable due to variations in environmental conditions between sampling periods. In particular, the information about the status of marine species can be derived from either fishery-independent surveys or fishery-dependent surveys (skipper logbooks and/or observers). Each of these sources could provide different results in terms of spatial and temporal approximations with diverse level of detail, and could be used to identify different distribution of the species of interest. Our study aims to identify sensitive habitats of fish species and develop probabilistic spatial scenarios using different sources of fishery data in order to assess whether they detect similar, complementary or different spatial patterns. Bayesian hierarchical spatial models are used to identify the distribution of the main elasmobranchs species (*S. canicula, G. melastomus and E. spinax*) in the western Mediterranean Sea, with respect to environmental and geological variables, using two diffrent sources, observers on board and MEDITS (Mediteranean International Trawl Survey) survey. Bayesian inference and prediction are made by considering the model as a latent Gaussian model, which allows the use of the integrated nested Laplace approximation (INLA) methodology and software (Rue et al., 2009) as an alternative to Markov chain Monte Carlo (MCMC) methods. Finally, different methods are used for the comparison of the spatial structure of the patterns in order to capture and quantify the similarity and to assess which features are more truly representative of the species habitat.

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Do you need all the moves?

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Keywords: capture-recapture; latent-multinomial model; Markov basis; misidentification

Abstract: The latent-multinomial model of Link et al. (2010) provides a general framework for modeling mark-recapture data with identification errors. Assuming that the vector counts for the observed histories is a linear transformation of the latent vector of counts for the true histories, given by $\boldsymbol{f} = \boldsymbol{A}\boldsymbol{x}$, Link et al. (2010) proposes a Bayesian approach using MCMC to sample from the joint posterior distribution of the model parameters and the latent counts. In particular, use a Metropolis-Hastings algorithm to updates the vector latent counts on each MCMC iteration generating proposals by adding or subtracting elements from a basis for the kernel of $\boldsymbol{A}$ one at a time. This mechanism ensures that the proposals satisfy the linear constraints, but the resulting Markov chain may not be irreducible. As Schofield and Bonner (2013) discuss, an irreducible chain can be constructed by augmenting the basis to produce a Markov basis. However, the algorithms for computing Markov bases are computationally intensive and fail for relatively small problems (e.g, 5 or more capture occasions). We discuss conditions on $\boldsymbol{A}$ which ensure that the chains produced by the original method of Link et al. (2010) are irreducible, negating the need to compute the Markov basis, and provide examples of models which do and do not satisfy these conditions. We also discuss alternative methods to avoid computation of the full Markov basis using tailored bases for particular $\boldsymbol{f}$ (called sub-Markov bases) or adjustments to the underlying MCMC algorithms.

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Effect of Agriculture on Local Biodiversity in the Tropics: A Meta-analysis

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Keywords: abundance; big data; monitoring of biodiversity; multispecies models; spatial ecology.

Abstract: Given the increasing human population trends and resource needs, land-use conversion to meet these needs is a growing concern for biodiversity conservation and policy. The tropics undergo the fastest rate of land conversion despite containing some of the most biodiverse regions in the world. Here I investigated the effects of land use change and intensity, human population density and distance to the nearest settlement on species richness (Chao 1 estimator) in the tropics using linear mixed effects models. In addition, agricultural residency time was estimated and species richness was projected into four different land-use change scenarios developed for the Intergovernmental Panel on Climate Change. Land-use and intensity were found to have the greatest effect on species richness, causing a decline as use intensity increased. The residency time was estimated to be a minimum of 17 years overall, above current estimates. Projection models indicated that scenarios where more primary forest is converted to cropland result in the greatest loss of species richness. Combined, these results offer useful tools to aid in producing conservation policy in the future.

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Ensuring successful habitat creation despite ecological experimental design constraints

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Keywords: capture-recapture; disease ecology; movement ecology; population dynamics; survey design and analysis

Abstract: With habitat loss and climate change the greatest threats for endangered species, the restoration or creation of compensatory habitat will be increasingly used for conservation. Achieving successful outcomes requires understanding, prior to implementation, habitat suitability and whether the target species will utilize and survive in the created habitat. Conducting statistically robust surveys and experimental field designs is crucial, with continuous monitoring essential in identifying potential issues. However, due to resource and time limitations, as well as logistical constraints, conducting quality ecological experimental designs is a complex endeavour. This study provides an example of how these complexities can be dealt with through using individual trial sites, long-term monitoring and statistical methodology that account for lack of replication. We used the endangered green and golden bell frog which has been the subject of the largest number of management plans of any amphibian in Australia. However, nearly all have failed to produce a self-sustaining population. A captive breeding and habitat creation project was implemented to improve their persistence and support a sustainable population in the landscape. This study aimed to identify whether past lack of success was due to the inability of created habitats to meet resource requirements or because of other ecological processes. A trial plot consisting of four permanent and six ephemeral waterbodies was constructed, with habitat suitability uncoupled from habitat selection by surrounding half of the site in a frog-proof fence to prevent dispersal and biotic interactions such predation, competition, and disease. Monitoring of the site occurred on a weekly basis for three years and included visual encounter, auditory, dip-netting, and mark-recapture surveys, along with water and weather measurements. The results of the past three years will be presented along with implications of the common limitations on ecological experimental designs.

Estimating plastic and evolutionary change under density-dependence from time series

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Keywords: abundance; evolutionary ecology; population dynamics

Abstract: The selection pressures on natural populations fluctuate, but observed changes in traits are affected not only by selection but by plastic response to environmental change. Further, selection and plasticity may both alter trait distributions, but do not have equivalent effects on demography. In particular, the cost of viability selection is paid through declines in population number. Thus, observed trajectories of trait value and population abundance depend on interactions between plasticity, selection and the environment. Demographic trajectories also contain limited information about the action of selection. For example, it has long been known that density-dependence can dilute the effect of natural selection on population dynamics (Saccheri and Hanski 2006). Specifically, density-dependent compensation can buffer vital rates from the effects of sustained directional selection (Reed *et al.* 2013). Although recent methods decompose observed trait change into contributions due to evolution and plasticity (Crozier *et al.* 2011, Ellner *et al.* 2011) these methods do not account for the effect of density-dependence on population trajectories, or the partial information contained in demographic trajectories concerning the action of selection.

I develop a method for estimating parameters governing change in trait values due to plasticity and due to response to selection, all in the presence of density-dependence. Working in a hierarchical Bayesian framework, I demonstrate how it is possible to infer the action of plasticity and genetic evolution in the presence of density-dependence from time series of trait and abundance data. Using a simulation study, I illustrate the sensitivity of this inference to informativeness of priors on vital rates and the environmental sensitivity of selection. I then apply my framework to a case study of changes in migration timing of Pacific salmon.

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Estimating the Maximum Size of Giant Squid (*Architeuthis* sp.)

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Keywords: evolutionary ecology

Abstract: Giant squid (Mollusca, Cephalopoda, Architeuthidae, *Architeuthis* sp.) are one of the most enigmatic large marine animals on the planet. Given that only approximately c. 450 specimens of giant squid have ever been reported, it is obvious that the probability that the longest individual is among those catalogued is extremely low. Here we generate estimates of the maximum mantle length from known specimens using two extreme value theory methods incorporating uncertainty in estimate of the threshold.

Fitting state-space models to scarse data for seal populations

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Keywords: abundance, population dynamics

Abstract:

Aerial surveys of White Sea harp seal (*pagophilus groenlandicus*) pups during the period 1998-2010 indicate a sudden reduction in pup production after 2003 (ICES 2011). The lack of historical data on fecundity makes the current population model stiff, and unable to capture the dynamics of the pup production estimates. Fecundity rates have been shown to have rapid changes on an annual basis, resulting in significant impact on the population modelling (Sjare and Stenson 2010, Stenson and Wells 2010). A decline in the reproductive status of females may explain the sudden decrease in pup production observed for the White Sea harp seal population after 2003. An age-structured state space model with time dependent fecundity is implemented in AD Model Builder (Fournier et al. 2012). The model is fit to historical catch data and estimates of pup production in order to estimate the current total population size and associated measures of uncertainty.

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Flexible mixed models in ADMB

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Keywords: AD Model Builder (ADMB), random effects, state-space models, spatial statistics.

Abstract:

ADMB is a software package that provides a flexible mixed-model framework, and which is well suited for building R packages. glmmADMB is an example of an R package which does its core computation in ADMB. The term "mixed model" should be interpreted broadly and includes state-space models and models in spatial statistics. This poster gives examples of the use of ADMB and provides a meeting point for people who want to talk to ADMB developers.

Free-ranging marine mammals, the next 'Ships of Opportunity'?

Key words: Survey Design and Analysis, Distance Sampling
Authors: Laurie Baker, Ian D. Jonsen, Joanna Mills Flemming, Sara Iverson

The deployment of two-way coded (transmitting and receiving) acoustic transceivers on marine mammals ("bioprobes") has the potential to provide individual level information about inter- and intra- species interactions from inaccessible marine environments. However, transceivers differ in their detection efficiency due to the time the bioprobe animal spent in sub-optimal environmental conditions for transmitting and receiving data (e.g., complex geomorphology, variation in water properties), as well as influences from the bioprobes' behaviour. These differences in detection efficiency have important implications for drawing biological inferences due to the uncertainty surrounding the number of tagged animals detected. Therefore, to effectively use these data, one must quantify the uncertainty associated with a bioprobe detecting a tagged animal in a given area.

We quantified the detection efficiency of Vemco Mobile Transceivers (VMT) deployed on 38 grey seals (*Halichoerus grypus*) on Sable Island, Canada in 2010 and 2011 in relation to environmental characteristics and aspects of the seals' behavior using generalized linear modeling techniques and Receiver Operator Characteristic curves. We observed the greatest decreases in detection efficiency in areas of high wind stress and as distance increased between seals. We related these findings to metrics of the bioprobe's sampling coverage, exploring the individual's residence time and travel speed across the study area and over time. Using this information, we make recommendations for future surveys of this kind.

Habitat selection and occurrence analysis of "*Scimitar horned Oryx*" according to vegetation cover characteristics in Bouhedma National Park, Southern Tunisia.

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Keywords: Scimitar-horned-Oryx, Occupancy models, vegetation cover, Bouhedma National park.

Abstract: *Scimitar Horned Oryx* is a wild ungulate species disappeared from Tunisian areas since 1902. Some reintroduction projects in national parks has been undertaken since many decades in context of rehabilitation and reconstitution programs of this species.

On the basis of field investigation and statistical models, this study was carried out. It aims to analyze the habitat selection of *Scimitar horned Oryx* population reintroduced in Bouhedma National park located in southern Tunisia during two seasons (winter 2011 and spring 2012) and to identify the phytoecological factors affecting their occurrence. Multivariate analyses of variance (MANOVA) performed by SAS package confirmed the preference of *Scimitar-horned-Oryx* , in terms of vegetation, to the most diversified areas of Bouhedma national park. These analyses reveled also that this species avoids glaze and mountain areas despite the presence of palatable species such as *Stipagrostis tenacissima*. Thus, High affinity to grass species, such as *Digitaria commutata*, *Cenchris ciliaris* and *Stipagrostis ssp* was noted.

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How to predict plant population dynamics out of static information - A case study of Succisa pratensis

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Keywords: integral projection models; ordination; effects of vegetation gradient on population dynamics;

Abstract: Our goal is to outline a prediction model, which would be able to predict for a given plant species and population its demographic fates (growth, survival and reproduction) based on the knowledge of local environmental conditions (as reflected by the surrounding vegetation) and current state of the focal species' population (as measured by a single semiquantitative census). We adopted a two-stage approach. First, we studied detailed demography of our focal plant, *Succisa pratensis*, in 27 populations (and 112 patches as sampling unit) for 2 to 7 years in the whole range of ecological conditions it occurs and summarized it by means of IPM. Second, we attempted to outline possible classifications of population dynamics according to their original state and environmental conditions (both by using clustering and ordination techniques). We validated our predictions on an independent sample of 120 populations. We discuss best possible solutions both from the point of precision of prediction and from the point of applicability in conservation practice (e.g. necessary sampling effort), since our focal plant species is the only host plant of NATURA 2000 protected butterfly, *Euphydryas aurinia*.

Increasing power of using Ellenberg's indicator values for detecting changes in the environment.

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Keywords: Ellenberg's indicator values, environmental indicators, site comparisons

Abstract: Ellenberg's indicator values (EIV, Ellenberg 1992) are frequently used for comparison of environmental conditions at sites where only plant species data are available. These comparisons are done both in space and time.EIVs are per species values of environmental conditions in its habitat, and deal with several factors, e.g. soil moisture and nutrients, temperatures, light availability. Species list includes more than 1000 Central European species. Values are tabulated on the ordinal scale.In a common praxis, EIV for certain factor (e.g. soil moisture) of species present at certain site are viewed as samples from random variable, therefore mean (weighted by species' abundance or not) is calculated and compared across sites (species lists) to asses spatial or temporal trends. We propose to exclude species that occur in bot h units (lists) to be compared from the calculations, hence using "paired" comparisons to increase the chance of detecting trends. Especially when dealing with replications in time, this helps to avoid false similarities that can arise due to plant longevity. On the other hand, it can be argued that such an approach exaggerates the magnitude of change. We think that this argument is invalid, as magnitude of change is not defined on the scale where there is no unit size. Using heterogeneous data that spanned an order of magnitude in size and several decades, we show that this simple adjustment allows to detect changes that went unnoticed previously.

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Modeling the Challenging Impacts of Climate and Fishing on the South Pacific Jack Mackerel

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Predefined Key-words: abundance

`integrated population models, population dynamics, spatial ecology, species distribution models, big data`

For the last 50 years, the South Pacific Jack Mackerel (SPJM, *Trachurus murphyi*) stock has been heavily exploited in the entire South Pacific but no management strategy has yet been developed in national nor in international waters. In addition to a likely multi-national overexploitation, the current precipitous decline of SPJM population could be explained by climate-driven decadal fluctuations as observed for other small pelagic species (anchovies, sardines etc.). Furthermore, previous studies on the stock structure of SPJM suggested a mismatch between an assumed one-stock-population and the biological reality. Since ignoring spatial population structure and dynamics may negatively impact stock assessments and hence management effectiveness, the Spatial Ecosystem And Population Dynamic Model (SEAPODYM) is used to investigate the dramatic changes in SPJM population under the influence of both environment and fishing. The interannual to decadal variability in SPJM population is investigated in relation with Pacific climatic modes (ENSO, PDO). A first optimised parameterisation of the model was achieved in the South Pacific Ocean using environmental fields predicted from a coupled bio-physical model (NEMO-PISCES) forced by an atmospheric reanalysis. A unique multi-national dataset, combining effort-catch data and associated size frequencies, biomass acoustic estimates and eggs-larvae density, was used to optimize the model parameters with a maximum likelihood estimation methodology, allowing robust parameter estimation. A second configuration is used to forecast the future of SPJM populations under an IPCC scenario for the 21th century. Preliminary results are compared to those obtained with the reanalysis for the historical period, and the sources of uncertainty in the projected trends of the population are discussed. These first results enable the use of Seapodym as a predictive and management application tool to test, in future work, various CJM spatial management strategies.

Modelling large scale fluctuations in salmonid abundance in the River Tyne (UK) using local resistivity counter data.

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Keywords: abundance, distance sampling, multispecies models.

Abstract: Migratory species are particularly challenging to monitor and protect. These species move seasonally between breeding grounds and areas where they develop, so monitoring at a single location typically fails to account for a large proportion of their year.

For instance, in the UK, *Salmo salar* and *Salmo trutta* are anadromous salmonids that migrate seasonally between the River Tyne (UK) and the Atlantic Ocean. Both species cover important distances in the open sea for most of the year, but this part of their life cycle if poorly documented.

Since 2004 in the River Tyne, salmonids were recorded as they return to breed; a resistivity fish counter installed in the river is triggered by each fish passage. The counting device produced a time-series of salmonid count (2003-2011), that was investigated using LME models.

Environmental conditions experienced during the unobserved months (November to April, when at sea) were represented by seasonal harmonics and North Atlantic oscillation values (NAO). River temperature, seasonal harmonics, and lagged effect of oceanic conditions (4 years) were important predictors of the salmonid abundance recorded in the River Tyne.

Large scale effects represented the whole migration cycle (harmonics), or represented and/or influenced the unobserved part (NAO); they were combined with a local effect (temperature).

This study supports the argument (Robinson *et al*., 2009 ; Forchhammer *et al*., 2002) that especially in migratory species, large-scale parameters may be relevant even when modelling local fluctuations in abundance.

The aim of this project was to investigate the extent to which it was possible to use statistical modelling to investigate and then predict the return of salmonids to the River Tyne using covariates associated with their migration.

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New methods of model-selection and assessment for complex capture-recapture models

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Keywords: capture-recapture; goodness-of-fit; heterogeneity; hidden Markov models; multi-event models; mixture models; score tests; uncertainty

Abstract: We perform a general review and comparison of different models used for capture-recapture data. The Cormack-Jolly-Seber model makes very strong assumptions, which often do not reflect real-life conditions. Many complex models have since been developed to take into account aspects such as individual heterogeneity for capture and survival probabilities or the different states in which animals can exist. Multievent models, based on hidden Markov models (MacDonald and Zucchini, 1997), allow for uncertainty in the assignment of these states. We consider technical aspects of mixture models (Pledger et al, 2003) and more general multievent models (Pradel, 2005). We explore the use of goodness-of-fit tests and score tests through application to data on Great Cormorants *Phalacrocorax carbo*, extending the work of Cole et al, (2014).

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Occupancy models for characterizing the breeding phenology of Peruvian guano-producing seabirds

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Keywords: occupancy models, breeding seasonality, guano producing seabirds, Humboldt Current System.

Abstract:

In marine ecosystems with seasonal dynamics, seabirds are expected to adjust their breeding period to maximal availability of food. However, detailed information on seabird breeding phenology is often scarce and few studies have attempted to link seabird phenology with physical and prey variability on a seasonal basis. For guano-producing seabirds in the Humboldt Current System (Guanay cormorant *Phalacrocorax bougainvillii*, Peruvian booby *Sula variegata* and Peruvian pelican *Pelecanus thagus*) information on the breeding phenology is scarce and contradictory, varying between no breeding phenology to protracted breeding, and no study investigated the synchrony between environmental conditions and breeding dynamics. Our objectives are i) to describe the species-specific seasonal patterns of breeding; and ii) to identify the main environmental drivers of seabird breeding and quantify their relative contribution. We modelled colonization and extinction probabilities of breeding colonies at nesting sites using occupancy models and the PRESENCE software. Observation data of occupancy of nesting sites came from monthly land-based censuses in 28 islands and headlands during the 2000-2012 period. Environmental variables tested were sea surface temperature, chlorophyll, upwelling index, dissolved oxygen, depth of the 2m l^{-1}oxygen isoline, abundance, gonadosomatic index, body condition and body fat percentage of anchovy. Results showed that pelicans and boobies had a more marked seasonality of colonization and extinction probabilities than cormorants, with higher colonization probabilities for boobies and pelicans in August-September. For the three species colonization probabilities were best correlated with upwelling index and depth of the 2ml.l^{-1}oxygen isoline with a lag of one month. Colonization of nesting sites by boobies and pelicans was also synchronized with anchovy body condition and gonadosomatic index. Our results show a seasonal pattern in the initiation of breeding of three seabird species, which was highly linked to upwelling activity and prey characteristics suggesting that seabirds adjust their timing of breeding according to prey availability and quality.

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On the importance of considering the precision of the measuring instrument in the statistical analyses in ecology

(To be presented as poster)

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Keywords: Monitoring of biodiversity, abundance, repeated observations of continuous random variables, data measured with different precision, unbounded likelihood function, likelihood function for censored data.

Abstract: Many statistical models widely used in ecology such as the three parameter lognormal, Weibull, and Gamma distributions involve a threshold parameter. These distributions have often been used to model waiting times between events of interest, the distribution of tree diameters, species abundance curves, the weight of individuals, and many other types of ecological data. For estimating the parameters of these distributions, the likelihood function, defined as the product of the density functions at the data, is traditionally used but it turns to be unbounded. Consequently, this has been interpreted to mean that no maximum likelihood estimates of the parameters are available (Smith, 1985).

A simple interval censored likelihood function is proposed here that solves the mentioned estimation problems; it is always bounded, incorporates the finite precision of the measuring instrument, and explains the possible occurrence of repeated observations of continuous random variables. All continuous random variables are measured in practice with instruments that have finite precision. When the continuous random variable X is registered as x, in reality this means that X is contained within the interval $(x-\varepsilon, x+\varepsilon)$, where 2ε is the precision of the measuring instrument. This explains why repeated measurements can arise in practice. When there are k observations falling within the interval $(x-\varepsilon, x+\varepsilon)$, they will all be registered as x and, consequently, there will be k repeated observations in the observed sample.

Three practical examples of biology, forestry, and rainfall data are presented where the proposed procedure was used successfully to estimate the parameters of the above mentioned distributions: a) waiting times of mammals to perform certain tasks, b) tree diameter measurements taken to estimate timber yield, and c) rainfall data from the ecological reserve of Chamela, Mexico, where two measuring instruments having different precision were used and where repeated measurements arose.

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Predicting species distribution: complementarity of food webs and hierarchical Bayesian spatial modelling

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Keywords: spatial ecology, species distribution models

Abstract: The spatial prediction of species distributions from survey data has been recognized as a significant component of conservation planning and the ecosystem-based approach to marine resources. A wide variety of statistical and machine-learning methods have been introduced, often in conjunction with geographic information systems (GIS) and remote-sensing. Guisan and Zimmermann (2000) provide an extensive review of these developments, identifying many of the alternative statistical approaches that may be used. Frequently, the purpose of the statistical modelling is to use the information about where a species occurs and the relationship with associated environmental factors to predict how likely the species is to occur in unsampled locations. Spatial prediction of species distributions is thus directly related to the concept of the environmental niche, a specification of a species' response to a suite of environmental factors. But it is known that environmental factors alone may not be sufficient to account for species distribution. Other ecological processes including competition, predation and the dynamics of the population may affect the spatial arrangement of a species, in addition to human activities. Here we compare two novel techniques that use different approaches to estimate species distributions: hierarchical Bayesian spatial models and the Ecospace new habitat capacity food web model. We use both techniques and compare results to assess the distribution of several commercial and non-commercial fish species in the South Catalan Sea, while exploring the complementarity of both approaches. Bayesian models have been used to estimate and predict the distribution of species using mainly environmental factors, and can include biological relationships and human activities, as Ecospace models do. The new Ecospace habitat capacity model combines species distributions with food web model dynamics.

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Predicting the number of new species in a subsequent sample for a finite population

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Keywords: Frequency estimation; Finite population; Good–Turing; Sample coverage

Abstract: Given a sample of abundances (observed data), ecologists or biologists are often interested in the number of species which are undetected in the sample but that would be discovered in a subsequent sample. This quantity is helpful for assessing the value of taking another sample. There are some estimators for such issue in the literature. Nevertheless, existing studies assume sampling with replacement or sampling from an infinite population, which might be inappropriate for many practical applications. In light of this limitation, we present a method to account for finite population sampling.

Quality control of biological indices: a first exercise for an index assessing ecological status of river phytobenthos in Flanders (Belgium)

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Keywords: survey design and analysis, indicators of biodiversity, monitoring of biodiversity

Abstract: The European Water Framework Directive (WFD) requires that every member state assesses the ecological status of its water bodies relative to near-pristine reference conditions. In surface waters, distance to target needs to be measured by Ecological Quality Ratios for a number of relevant biological quality elements. The newly developed PISIAD index assesses phytobenthos for rivers and lakes in Flanders (Belgium) using the proportions (P) in relative abundance of impact-sensitive (IS) and impact-associated (IA) diatoms (D). Compliance to WFD requirements and successful intercalibration at the relevant biogeographical level allow its use in regulatory monitoring by the Flemish Environment Agency. Using initial data from this monitoring programme, we evaluated the properties of PISIAD.

We first investigated the numerical and statistical behaviour of the index, showing that a slight adaptation would increase its stability and robustness near values that are critical to the possible triggering of remediating measures. Simulations provided more insight into the number of diatom valves that need to be counted to obtain reliable outcomes. The quality of species identifications was assessed by independent assessment of documentary records, also allowing recommendations for future improvement.

Next, the general response of the PISIAD index for rivers to measure physical-chemical water quality and its relation to other biotic indices was explored. The metric responded primarily to organic loading and oxygen conditions. It related only weakly to indices for fish, macrophytes or phytoplankton, suggesting significant complementarity. However, data limitations prevented definitive conclusions. Variability of results at water-body level also indicated a need for further scrutiny. Only a more appropriate overall sampling scheme and tailored investigations would allow to elucidate such questions economically.

This first quality control exercise proved fruitful to suggest adjustments as well as future research needs. It is strongly recommended that similar exercises are routinely included in official monitoring programmes.

Quantifying temporal turnover in biodiversity, and how it varies spatially

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Keywords: measures of biodiversity; indicators of biodiversity; big data; abundance; spatial-temporal modelling

Abstract:

Quantifying species compositional change over time plays an important role in measuring biodiversity trends. In the literature, spatial compositional heterogeneity is often referred to as beta diversity (Lande 1996, Jost 2007). Temporal compositional heterogeneity is usually measured by species turnover over time using presence-absence data. However, if available, it is more informative to use species abundance distributions to measure the compositional change over time (Magurran, 2010). We propose several families of indexes to measure the temporal turnover, some of which have been used for measuring compositional similarity between two assemblages, i.e., the beta diversity. Instead of measuring the similarity between two assemblages, we are interested in the compositional change between two different time periods and how it varies spatially.

We use spatial-temporal data analysis to predict the density surface for each species over time, and use the predictions to assess the species compositional change over time in the survey area. To illustrate the method and study how the turnover measures differ from each other, we use the Quarter 1 International Bottom Trawl Survey (IBTS) data (IBTSmanual, 2010). We fit a hierarchical spatial-temporal model to the IBTS data using the stochastic partial differential equation approach (Lindgren et al 2011) implemented in R-INLA package (Rue et al 2009). We then use the predicted density surface to assess the temporal turnover within a 9-year window. We study how the temporal trends in the species turnover vary spatially, which is helpful to identify how climate change is affecting the North Sea fish community.

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Reciprocal sign epistasis and truncation selection: when is recombination favorable?

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Keywords: reciprocal sign epistasis, recombination, truncation selection, bistability

Abstract: In this study we sought to determine conditions in which a genotype of interest could be fixed when truncation selection is applied on an epistatic trait. This type of selection is especially used in varietal breeding; in nature, strict truncation is unlikely, but quasi-truncation may appear in resource-limited species. Previous works have shown that reciprocal sign epistasis with two fitness peaks of unequal height implies the existence of multiple stable stationary solutions. It means that above some critical values, one genotype may be fixed, and above them, another one may. Using a haploid bi-locus model in infinite populations, we could determine how recombination rate affects the evolution of a population selected by truncation for a phenotypic trait subject to reciprocal sign epistasis with unequal peak heights. These results were complemented by stochastic simulations in finite populations. For different initial states, we could determinate which genotype would be fixed, and how quickly, depending on two criteria: the recombination rate and the percentage of selected individuals. The critical parameters at which bistability sets in, were also calculated. Our results confirm that in the case of fitness displaying reciprocal sign epistasis, high recombination rates have a negative effect. Indeed, high rates of recombination induce getting stuck at the local optimum or reaching an equilibrium state between the two peaks. However if linkage disequilibrium is negative at departure, recombination is necessary to create the most favorable genotype. Thus, reciprocal sign epistasis therefore favors non null recombination rates when linkage disequilibrium is negative, in particularly if selection is intense.

Sample size calculations for natural resource surveys assuming zero-inflated beta distributions and AR1 time dependence

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Keywords: monitoring of biodiversity, survey design and analysis.

Abstract:

In order to perform sample size calculations for natural resource surveys, prior estimates of population variance and temporal dependence are needed. Natural resource surveys typically use an areal sampling frame representing the entire land area within a predefined region (e.g. land or continent). These surveys also have multiple objectives such as the estimation of land cover (change) for multiple land cover types.

We consider the case where sampling units contain a mix of land cover classes. Depending on the size of the sampling unit and the detail of the land cover classification, a substantial proportion of sampling units in a sample may be empty for a particular land cover class. This proportion will be determined by the (unknown) proportion of land covered by the particular land cover type and its spatial distribution. In addition, when a particular land cover class is present, it will cover a proportion of the total area of the sampling unit. To estimate the spatial or population variance, we therefore need a distribution that reflects both sources of variability. We show that zero-inflated beta distributions, with the zero-inflated part modelling the absence of a land cover type and the beta part modelling the areal proportion within sampling units when present, fulfil these needs. Land cover classes tend to be persistent features and consequently change in land cover tends to be rare. This can be modelled through a first-order autocorrelated process.

We demonstrate the estimation of realistic spatial variance and temporal dependence using data from five monitoring cycles of the United Kingdom Countryside Survey (UK CS). In turn, these estimates allow us to calculate required sample sizes to detect trends and estimate the area of a land cover class at reasonable quality levels to evaluate similar natural resource surveys at the design stage.

Spatial point process models to determine clustering of American Foulbrood in UK Honeybees

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Keywords: epidemiology; spatial statistics; disease ecology, management, honeybee.

Abstract: American Foulbrood (AFB) caused by *Paenibacillus larvae* is the most damaging bacterial brood disease of the honey bee (*Apis mellifera*) and is usually lethal to the colony if left untreated. AFB has been a persistent problem in the UK for over 70 years, with a fluctuating number of cases discovered annually. Current management measures include destroying infected colonies to reduce pathogen spread. We use complimentary spatial point process models to detect global clustering and characterise local clusters of AFB across England and Wales between 1994 and 2012 with the aim to improve our understanding of the epidemiology of this damaging disease. Our results indicated that AFB exhibits significant spatial aggregation at distances from 10-30 km with aggregations lasting between 1 and 5 year periods. Kernel smoothing indicated areas of elevated relative risk in different years and these were further detailed by spatial scan statistics. We identified disease clusters and successfully estimated their size, location and duration. The majority of clusters did not persist in all years indicating that management measures may lead to localised extinction of the disease. Whilst less common, persistent clusters likely indicate potential endemic or exotic risk points. The application of robust epidemiological approaches to improve the control of AFB are discussed.

Spatially explicit capture-recapture methods in practice; estimating the density of an elusive reedbed Passerine

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Keywords: capture-recapture, abundance, spatial ecology

The Bearded Reedling, *Panurus biarmicus,* is a rare Passerine so dependent on reedbed habitats that individuals may spend their entire life within a single reedbed stand. Despite being widespread throughout Europe, only 800 individuals inhabit the UK making it a specially protected species. Additionally, this species is known for fluctuating population sizes, to which migration, emigration and immigration contribute to a poorly known extent. The Tay Reedbeds, Scotland, are thought to hold the largest population of Bearded Reedlings in the UK. Precise estimates of abundance and density are essential for informed management and monitoring of this vulnerable population, but the difficulties of surveying in inaccessible reedbed habitats, mean number of birds inhabiting this reedbed remains unclear. There is also interest in the effect of harvesting reeds on Reedling distribution and abundance. Mark-recapture data are available from monthly mistnetting with ringing to mark individuals, and data on animal movement is available from telemetry tags attached to a sample of individuals. We use spatially explicit capture-recapture (SECR) methods with non-uniform animal distribution models to estimate the density and distribution of birds throughout the reedbeds; covariates such as distance from managed (cut) reed patches allow inferences to be drawn about the effects of reed cutting on the population.

State-space modelling reveals the multiple drivers of rapid population decline in macaroni penguins

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Abstract: Recent changes in the population trends of Antarctic mega fauna have been extensively linked to parameters of climate change. However, little is known about the relative importance of these drivers in the context of other processes. In order to investigate this, we used a state-space model to disentangle the processes driving a population of macaroni penguins (*Eudyptes chrysolophus*) to rapidly decline between 1985 and 2012. Principally, the population trajectory was most sensitive to regulation of survival rates associated with predation pressure. However, as trends in predation pressure remained stable across the study period, we infer that the observed trajectory was primarily driven by a change in the relationship between fecundity and the El Ni*ñ*o Southern Oscillation. More broadly, this study highlights the importance of considering multiple causal effects across different demographic rates in order to decipher population trends.

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Stock separation based on Fourier analysis of a concave approximation to otolith contours applied to Greenland halibut in Norwegian and Greenland waters

Fourier analysis of otolith contours have been applied successfully in several cases as an efficient technique to discriminate between different fish stocks. Use of elliptical Fourier descriptors (EFDs) is probably the most applied technique in these cases. A recently published Fourier mirror technique transforms the 2D contour to a 1D function with the advantage of reducing the number of coefficients to half the number of EFDs, but with the disadvantage of creating ambiguities in case of non-concave contours. In this paper a concavisation technique is applied to Greenland halibut otolith contours, which are grossly non-concave with a hand-like gross shape with many “fingers” creating a large within-group variance. A classical Fisher discriminant analysis is applied to EFDs as well as to 1D Fourier coefficients of the original contours, smoothed contours and the concave approximation to the original contour, to investigate if one can discriminate between Greenland halibut in Norwegian and Greenland waters, and to compare the different contour modes and the 1D and 2D descriptors. The discrimination score is calculated by the leave one out at a time technique.

Key words:

Community structure and dynamics
Population dynamics
Spatial ecology

taxize: taxonomic search and retrieval in R

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Keywords: big data; ...;

Abstract: Ecologists use data from many sources (e.g. own sampling, governmental monitoring data, data from web-datebases, ...). All these data have a common ground: the taxonomic names of species they contain. For a data analysis a crucial data-cleaning step is to match species identities across different datasets Boyle et al. (2013). Taxonomic data is becoming increasingly available on the web, but scientists need an easy and reproducible way to access it.

We present *taxize* Chamberlain and Szöcs (2013) - an open-source software package for the R language (freely available from `http://cran.r-project.org/web/packages/taxize/index.html`). Taxize is part of the rOpenSci Initiative (`http://ropensci.org/`) and currently under development. It provides simple, programmatic access to taxonomic data for 14 data sources around the web. It simplifies data-cleaning steps, like fixing taxonomic names, aggregating data to a specific taxonomic level and matching tables by species names with different taxonomic resolutions.

We present this taxonomic tool belt in R and outline a suite of use cases for which taxize is ideally suited. The taxize package facilitates open and reproducible science by allowing taxonomic data collection to be done in the open-source R platform. We hope taxize will be taken up by the community and developed collaboratively.

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Temporal changes in parameters of biological community models

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Keywords: community structure and dynamics, population dynamics, species distribution models

Abstract: In order to conserve biological diversity and at the same time allow anthropogenic development, a thorough understanding of how the latter affect the former is a key point. Stochastic community models that jointly consider a large number of species has received increased attention during the past 30 years. Analysis of extinction processes have been developed for so-called homogeneous and neutral community models assuming a stationary environment. Due to anthropogenic effects, we will assume that parameters describing community dynamics can vary in time. Previously, we have studied this concept in models of single species that revealed a time delay in the dynamics of species as a response to the change in a parameter. We now extend this analysis to model changes in communities over time, such as a decrease in available area. We will study such processes for homogeneous as well as heterogeneous models, expressed by the distribution of dynamic parameters across species. We will use simulations and numerical analysis to study change in diversity, extinction processes and community responses to both gradual and abrupt changes in parameters and from a conservation point of view discuss community sustainability in such cases.

Temporal dynamics of orchid communities in Corsica: a study using a Bayesian multispecies site-occupancy model

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Keywords: Bayesian multi-species site-occupancy model, diachronic analysis, long-term dynamics, imperfect detection.

Abstract: Monitoring programs are requested to describe population dynamics in order to evaluate biodiversity changes and elaborate relevant conservation strategies. However, imperfect detection can lead to biased estimates of population abundance. Detectability can be affected by factors, such as species traits (e.g. life-state), observer or environmental context. Using a Bayesian multispecies site-occupancy model, we aimed to (i) test effects of covariates on detection probability of orchids and (ii) describe orchid dynamics in Corsica in evaluating impacts of vegetation cover change on species occurrence. We compared the occurrence of 43 orchid species at 62 locations in Corsica between two periods 1982–1984 and 2009–2011. Data were collected by the same observer during these two sampling periods applying the same protocol of species inventories. Our study showed that detection probability differed between orchid species. Population density affects significantly detectability of orchids. Concerning dynamics, no significant difference in occupancy probability was evidenced at community level between both periods. However, survival probability differed between species, with the highest value found for *Serapias lingua* and the lowest for *Dactylorhiza insularis*. In response to vegetation cover increase, *D. insularis* and *D. saccifera* were significantly and negatively affected. We concluded that the use of site-occupancy models is an appropriate way to analyze temporal dynamics of orchids and to investigate ecological processes underlying these dynamics.

The distribution of the expected numbers of individuals of detectable species as a way of describing species abundance

(To be presented as poster)

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Keywords: Monitoring of biodiversity, abundance, species abundance models, rank abundance distributions.

Abstract:

A different and complementary statistical approach from those previously considered in literature is presented here to describe species abundance data. The data consist of the counts of individuals of each of M different species observed in a random sample taken within a region of interest, where M is also random.

The counts of individuals for a given species are assumed to follow a Poisson distribution and to be independent from the counts of other species. The corresponding Poisson intensity parameter is efficiently estimated by maximum likelihood. It is reasonable to assume for each of the observed species, that its Poisson intensity parameter was not small and that the probability of observing at least one individual in the whole region of interest must have been larger than a value π close to one, since this species was actually observed. The non observed species are consequently assumed here to have small Poisson intensity parameters, all smaller than a given value λ, that depends on π. A Gamma distribution, truncated below at λ, is proposed as the distribution of the expected values (the Poisson intensity parameters) of the counts of the different observed species. A hierarchical statistical model is involved.

The estimated Gamma distribution for a data set is very informative about the behaviour of species abundances in the corresponding region. It can be used to compare two or more locations, or the same location across time. A comparison is made to other approaches such as RAD curves and other types of species abundance distributions as the ones presented in Magurran and Mc Gill (2011). Other distributions such as the lognormal could be considered as well, instead of the Gamma. The above ideas are exemplified with a reptile and tree data sets from the ecological reserve area of Chamela at Mexico.

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The effect of a colonising superpredator on mesopredator survival and reproductive strategies under declining food availability.

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Keywords: capture-recapture, population dynamics, multispecies models, spatial ecology

Abstract: Superpredation can exert 'top down' control on mesopredator population dynamics and the addition of large superpredators into a community can have far reaching effects on the established species. At a time of global change when food resources for many vole eating raptors are declining at a continental scale throughout Europe, understanding how other factors such as superpredation can affect mesopredator survival is important from a conservation management perspective. We used capture mark recapture data from a 30 year raptor monitoring program, to investigate the effect of increasing superpredator (Northern Goshawks *Accipiter gentilis)* abundance on mesopredator (Tawny owls *Strix aluco)* survival. We also investigated whether the distance to the nearest superpredator territory and connectivity to all known superpredator territories affected mesopredator survival. As juvenile Tawny owl survival is lower than adult survival, survival was estimated separately for each age class and adult only analyses were also conducted. To account for annual fluctuations in survival caused by declining food availability, models included field vole abundance as a standardised temporal covariate as they are the main prey species for Tawny owls. Interactions between superpredator covariates and food availability were also examined and all analysis was carried out in ESURGE. Additionally, we investigated how different reproductive strategies affected survival under increasing superpredator abundance. As predicted, our results suggest both connectivity to goshawks and superpredator abundance have an effect on juvenile and adult survival. Survival was highest for individuals that took 'rest years' from breeding and those which spent on average 30% or more of their adult life after becoming reproductively active resting from breeding. This suggests superpredators should be taken into account when formulating mesopredator management programmes as both their abundance and relative spatial distribution is likely to affect both mesopredator survival and could be putting selective pressure on mesopredator reproductive strategies.

The effect of recycled individuals in tag-loss models

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Keywords: capture-recapture; abundance

Abstract: Mark-recapture experiments typically assume that individuals do not lose their tags. This assumption was relaxed by Cowen and Schwarz (Biometrics, 2006) with the development of the Jolly-Seber-Tag-Loss model. However, the number of individuals that lose both tags (recycled individuals) and are captured as “new” are assumed negligible. With high tag-loss rates, high capture rates, and high survival rates; recycled individuals can produce overestimates of population size. Through a simulation-based study, we examine the effect of recycled individuals on parameter estimates and standard errors. We also determine under what conditions recycled individuals have the most impact and offer management advice for study designs.

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The use of spatio-temporal ecological models in predictive policing.

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Keywords: predictive policing, point pattern, log-Gaussian Cox process, spatio-temporal point processes

Abstract:

While most ecological processes take place in in time and space an increasing number of spatio-temporal data are being collected, existing spatio-temporal modelling methods are often lacking the flexibility that is necessary for the use with real data. This poster presents an approach to constructing flexible spatio-temporal point process models based on the stochastic partial differential equation (SPDE) approach introduced by Lindgren et al. 2011. In particular, we will construct a class of spatio-temporal log-Gaussian Cox processes.

The models' flexibility does not only allow us to construct realistically complex models relevant to specific ecological data sets on habitat preference, say, but also to extend their use to the many other data structures, such as those derived from criminology. We will discuss differences and similarities between structures in ecological data and data detailing the locations of crime events. The development of such models will identify environmental, and socio-economic factors that encourage crime, aiding evidenced based policing but will also provide new tools for spatio-temporal modelling in the context of ecological data.

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Using power analysis for monitoring environmental variables: New approaches applied to marine ecology in New Caledonia.

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Keywords: Survey design and analysis - Community structure and dynamics - Spatial ecology

Abstract: Monitoring ecological variables is mandatory to detect abnormal changes in ecosystems. In population ecology, trends in density, abundance and cover are usually monitored. When the studied variables exceed predefined alert thresholds, management actions may be required. Previously, alert thresholds have rather been defined using expert judgments and descriptive statistics. Recently, approaches based on statistical power have also gained momentum. Here, we present a study which defines alert thresholds for seagrass beds diversity in New Caledonia. Seagrass monitoring is a priority given their vulnerability to natural and anthropogenic disturbances. Using 5 years of reference quadrat data (species cover) on 20 stations around a new mining site, we compared a Percentile Based Approach (PBA) and a sensitivity analysis of power (SAP) to define a suitable monitoring strategy and relevant alert thresholds. Both methods defined statistically relevant alert thresholds, but the SAP approach was more robust to spatial and temporal variability of seagrass cover. Moreover, SAP allows defining sensitivity of threshold values to sampling efforts, and helped improving survey design overall. Using SAP, managers can thus better appreciate the reliability of alert thresholds according to the sampling effort involved in a variety of monitoring context.

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Using Vornoi Tesselation to estimate Animal Home Ranges

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Keywords: home range estimation; animal biotelemetry; voronoi tesselation; space use

Abstract: Tracking animals through time and space using telemetry is an important tool to study, movement, behavior and habitat relationships of wild animals. Home range estimation is often employed to analyze such data. Over the last decades, many different methods emerged to estimate home ranges from relocation data. Generally, the problem of estimating a home range can also be regarded as estimating a density surface from a finite sample of relocations. Browne (2012) presented a novel approach using tessellation density estimation to obtain such a surface. In order to overcome some of the difficulties of tessellation density estimation (e.g., discontinuity) Browne (2012) put the density estimation within a bootstrap aggregation algorithm and incorporated model selection with complexity penalization to find the model with most favorable bias/variance compromise. We used Penalized Bootstrap Aggregated Tessellation Density Estimation (PBATDE) to estimate home ranges from simulated and real animal relocation data. We then compare different properties (e.g., accuracy to predict the home range area, volume of intersection between the true and the estimated utilization distribution) from home ranges estimated with PBATDE with home ranges estimated using other frequently employed estimation methods such as kernel density estimation and local convex hulls.

References

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Some solutions to the Behrens-Fisher problem for multivariate ecological data

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Abstract: The Behrens-Fisher problem (BFP) is one of the oldest puzzles in statistics. The essence of this problem is how validly to compare means (or multivariate centroids) between two or more populations when their variances (or multivariate dispersions) differ. This is especially irksome in ecology whenever variables consist of counts of abundances of species, because any differences in means will be accompanied by differences in variances as well. Some solutions to the BFP do exist for the univariate case, but they assume variables are normally distributed, whereas species' counts tend to be long-tailed and overdispersed, with many zeros. This issue is exacerbated for multivariate ecological data (counts of many species in a community), which often also have more variables (species) than samples. This means none of the existing attempts to solve the multivariate BFP (all of which also assume normality) can be used in practice.

In this talk, I will outline, compare and contrast some potential solutions to the multivariate BFP that rely on some rather clever permutation, bootstrap or Monte Carlo (re-)sampling methods. While the permutation approach tends to be mildly liberal, the bootstrap approach, even with reasonable empirical bias-corrections, tends to be overly conservative. But will the Monte Carlo approach come to the rescue with a more exact test? And at what cost in terms of additional underlying assumptions?

Goodness of fit procedures for Integrated Population Models

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Keywords: integrated population modelling; state-space models; capture-recapture; goodness of fit.

Abstract: Integrated population modelling has become an increasingly familiar technique in statistical ecology. However there is currently no formal method for judging how well models fit data. We propose and evaluate a new approach, of calibrated simulation. Here comparative data sets are obtained from simulating data when model parameter values are obtained from asymptotic normal distributions of the maximum-likelihood estimators from the real data. The approach is attractively simple relative to Monte Carlo randomisation techniques, as it limits the additional model-fitting that is required. We discuss issues with respect to, for example, choice of discrepancy measure and lack of asymptotic normality, and illustrate the approach using real avian abundance and demographic data. The potential of the approach in capture-recapture in general is discussed.

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State-space models for incorporating multiple data sources in capture-recapture models

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Keywords: Capture-recapture, telemetry, data integration

Abstract: Capture-mark-recapture (CMR) techniques are used in a wide variety of sampling scenarios, but remain vulnerable to sources of bias such as temporary migration and individual heterogreneity. We show how a state-space framework can be used to jointly analyze traditional CMR in combination with multiple data sources aimed at clarifying such sources of bias. We demonstrate the general modeling framework on a dataset for native fish in the Murray river, Australia. Using a combination of CMR data, roaming telemetry, stationary telemetry and resighting data, we account for individual movement, temporary migration and growth in estimates of mortality rates. We find that using the traditional CMR dataset alone, we have little power to estimate factors relating to individual movement, and that estimates of mortality rates are confounded by low detectability. Augmenting the CMR data with telemetry allowed us to estimate mortality rates more precisely, albeit at the cost of increased model complexity. Conversely, the volunteer resighting data provided little additional benefit, likely due to low recapture rates and variable effort. Overall, the joint analysis of telemetry and CMR data led to an increase in statistical power, suggesting excellent potential for integration of similarly complementary datasets.

Linking breeding outcome to the unknown time of arrival at the breeding site; a study of great tits

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Keywords: capture-recapture; individual-based models; integrated population models; population dynamics

Abstract: Arrival time at a breeding site is likely to reflect the costs of dispersal incurred by individuals during dispersal. It is of interest to determine whether these costs are reflected in subsequent breeding success.

The data set considered in this paper comes from an intensively monitored population of great tits *Parus major* in Wytham Woods, near Oxford, UK. Great tits arrive at the site throughout the non-breeding season and are sampled using both mist nets and automated logging detection systems. During the breeding season, individuals that have established nests are sampled by scanning the nest boxes and/or by physical capture.

We develop models, motivated by this study but generally applicable to other breeding populations, that combine the data sets collected during both the non-breeding and the breeding seasons and allow for different types of sampling and changes in the probabilities of detection after the first encounter. These models estimate the total number of birds present at the breeding site, their arrival pattern at the site, as well as the probability of a bird becoming a breeder and subsequently the probability of that bird successfully fledging chicks. Both these probabilities are allowed to depend on the unknown time of arrival at the site.

Our results suggest that early arrivals have a considerably greater probability of becoming breeders compared to late arrivals but once a bird has become a breeder, the probability of successfully fledging chicks is independent of its arrival time.

These models have a wide range of applications since they can easily be adjusted to different species or sampling techniques and they are a valuable tool for modelling the effects of changes in arrival times at breeding sites on breeding outcome.

An integrated population model for Svalbard reindeer.

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Keywords: capture-recapture; integrated population models; population dynamics

Abstract: An integrated population model for Svalbard reindeer (*Rangifer tarandus platyrhynchus*) will be presented. This model combines individual mark-recapture data with census data and harvesting data within a Bayesian framework. Both demographic and environmental stochasticity are incorporated, as is age structure. The model allows us to estimate age structure from census data that is not age-structured, as well as estimating survival for an age class for which we have no individual survival data, and facilitates the analysis of age structure effects on population growth. Survival and fecundity estimates, as well as estimates of population size and age structure, will be presented and compared to independent population counts from the same study area.

INTEGRATED MODELLING OF BIRD POPULATIONS – THE VALUE OF DIRECT MEASURES OF RECRUITMENT

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ABSTRACT: Integrated Population Models allow optimal inferences about population processes where there are measurements of abundance and one or more demographic rates for the same population. However, in many such models one or more demographic components cannot be estimated directly, and must therefore be estimated by inference from other demographic rates. Such indirect estimates may reflect biases in the data sets included in the model, in addition to information on the parameter of interest.

Many of these problems can be addressed by measuring recruitment into the breeding population directly and we explore two approaches to obtaining such estimates for bird populations. First, where all birds born in the previous breeding season can be separated from older birds using plumage characteristics, it is possible to obtain a direct measure of recruitment (the inventory method). Second, where breeding season mark-recapture data are available, as in the case of Constant Effort Sites, it is possible to estimate recruitment from an analysis of reverse capture histories (the Pradel method). We use both approaches to obtain estimates of annual recruitment for European blackbirds (*Turdusmerula*) breeding in southern Britain.

We construct initial Integrated Population Models for blackbird populations incorporating estimates of relative abundance from large-scale census data (Common Birds Census/Breeding Bird Survey) with data on breeding performance from the Nest Record Scheme and age-specific survival estimates from ring recoveries. Results from these relatively standard models are compared with those from models where recruitment is estimated using either the inventory method or the Pradel method. The models are developed within a state-space framework with parameters and credible intervals being estimated using Bayesian MCMC techniques. Direct recruitment measures are expected to provide improved inferences about population processes and the potential for collecting such data should be taken into account when designing large-scale demographic monitoring schemes.

Behavioral inference and habitat modelling for the conservation of highly mobile animals

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Keywords: spatial ecology, movement ecology, modelling of animal movement, conservation biogeography, species distribution models

Abstract: The design of protected area networks is generally based on the identification of areas of high abundance for species of conservation concern or biodiversity hotspots. The relevance of these criteria for highly mobile animals, which partition their activities (breeding, resting, foraging, travelling) within their extended home-range, is often debated. Advances in electronic tagging techniques and statistical developments have provided the capacity to track animal movements and to infer behavioral states from movement data recorded at fine spatio-temporal scale. As the quantity of energy that an animal is able to extract from its environment directly influences its survival and breeding success, the characterization of foraging areas is essential from a conservation perspective. Hence, habitat models are increasingly used to predict the distribution of foraging zones within an animal home-range and to assess inter-annual persistence.

Based on an extensive GPS tracking dataset collected on 240 Scopoli's shearwaters (*Calonectris diomedea*), a seabird species breeding in the Mediterranean Sea, we inferred foraging behaviour using state-space models adapted from Morales et al. (2004). We then matched estimated foraging locations with 10 remote-sensing oceanographic variables to model foraging habitat using spatially-explicit linear models fitted with INLA (Rue et al 2009). Using an independent dataset for cross-validation, this modeling approach proved to be efficient in predicting foraging zones of this highly mobile species. Model predictions were used to test the adequacy of existing marine protected areas and to propose additional areas of high conservation value at the scale of the Western Mediterranean Sea.

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Handling time varying environmental conditions when analysing acoustic telemetry data

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Keywords: modelling of animal movement, movement ecology, spatial ecology

Abstract: Acoustic telemetry using fixed receiver stations is an increasingly popular method for assessing residency, home range, and habitat utilisation of aquatic animals. Data are collected as presences of individuals instrumented with electronic acoustic transmitters. Because of sound attenuation the probability of detecting a tagged animal depends on the distance to the receiver station. It is furthermore known that temporal changes in local environmental conditions cause the detection probability to also depend on time. Despite acknowledging its existence, the spatio-temporal variation in detection probability is rarely explicitly accounted for in the data analysis. This is unfortunate as ignoring varying detection conditions increases the chance of making erroneous conclusions when interpreting results. Here we present a method for detecting temporal variability in detection conditions and for adjusting the detection probability accordingly. The method utilises the detection efficiency of reference data as a proxy for detection conditions and does therefore not require access to local environmental information such as current speed or water column stratification etc. Using the established framework, we illustrate the benefits of integrating detection condition data into a model for estimating detailed movement and home range. This serves as an example of how analytical methods can be altered to realistically propagate temporal variation in detection efficiency of acoustic telemetry data to temporal variation in the uncertainty of model results.

Seabirds foraging within random forests

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Keywords: modelling of animal movement, movementecology, spatial ecology

Abstract:

In the Humboldt Current system, large colonies of boobies and cormorants breed in sympatryand feed on anchovy. Their breeding success depends largely on prey availability around the colonies, which may be compensated to some extent through variation in their foraging effort. Anchovy availabilityin this ecosystem may depend on natural shifts in its distribution triggered by climatic variability and/or on localized depletions generated by the industrial fishery. Deciphering which from the climatic and anthropogenic processes has a more pronounced effect is important for designing pertinent ecosystem-based fishery management options.

To address such question, we use here field data collected in Peru on a breeding colony North of Lima between 2008 and 2013. The foraging effort (time at sea, distances covered, maximum range from the colony, etc.) is documented for >800 trips. The local climatic conditions aregiven by satellite data i.e. sea surface temperature, chlorophyll-a, wind and upwelling intensity. The forage fish abundance and distribution arecharacterized from acoustic scientific surveys. The industrial fishing activity isdescribedby regional landings and the management regime in use. We use random forests (Breiman 2001) of regression trees to assess the relative importance of the covariates on seabird foraging effort because they authorize (i) dealing with 'low n high p' samples possibly concerned by pseudo replication, involving a variety of categorical and continuous variables, relaxing the assumptions of normality or other specific distribution required by classic parametric models (ii) exploring non linear relationships involving complex interactions between predictor variables. We show that the fishing activity has an effect as least as important as the environmental variability and that the two species modulate their foraging effort in different ways. Random forests could be also be used for prediction within the adaptive management currently in use in Peru.

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Drifting Fish Aggregating Device (dFAD) ocean trajectories and their consequences for fisher “foraging strategies” and pelagic ecosystems

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Keywords: discriminative classification methods, movement ecology, spatio-temporal patterns, foraging strategies

Abstract

Since the mid 1990s, drifting Fish Aggregating Devices (dFADs) have become an increasingly important means of catching tropical tunas. These devices consist of bamboo rafts, which tuna schools concentrate under, and attached GPS tracking buoys. The massive use of dFADs has raised serious concerns regarding the potential impacts on tuna ecology and pelagic ecosystems, but relatively little is known on the modalities of dFAD use by fishing vessels. For the first time, the three French fishing companies operating in the Atlantic and Indian Oceans have made accessible to scientists the GPS buoy tracks from their dFADs. After initial processing using discriminative classification methods (e.g. Artificial Neural Networks, Random Forests) to separate the useful ‘at sea’ trajectories from ‘on board’ positions (Maufroy et al. 2013), this data is used to describe the spatial and temporal patterns in dFAD use in the Atlantic and Indian Oceans. ‘at sea’ dFAD trajectories are combined with multiple sources of information: on board observers data, declarative data of the fishery, interviews with fishing masters and trajectories of the French fishing vessels. In particular, we describe the spatio-temporal patterns of the population of floating objects monitored with GPS buoys, develop a method for extrapolating the total number of dFADs based on spatialized raising factors, define the key factors determining dFAD deployment and assess some of the impacts of dFAD use on fisher “foraging strategies” (Bertrand et al. 2007) and pelagic ecosystems. The results we obtain provide a first overview of dFAD use in the Atlantic and Indian Oceans that is key for sustainable exploitation and conservation of pelagic ecosystems.

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Using the Dirichlet distribution to specify a random effect on a transition probability matrix

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Keywords: movement ecology, modelling of animal movement

Abstract: Inter-state transition probability matrices are a common feature of state-space and Markov chain models, which are commonly applied to model animal movements or animal behaviour. In many cases, it may be desirable to include a random effect (of, for example, individual or species) on the transition matrix entries. We propose a simple method for specification of such random effects using the Dirichlet distribution. We detail model specification and maximum likelihood estimation via a case study, in which a Dirichlet random effect accounts for inter-whale variability in a Markov chain model for sperm whale dive-type transitions. The data are time series data on the dive behaviour of 12 sperm whales, where dives have been pre-classified into 11 types by experts. We specify a random effect of individual w on the K-dimensional transition matrix P (for the case study, $K = 11$ and w ranges from 1-12). To do so, we let row i of the individual-specific transition matrix P_w be a draw from a Dirichlet distribution with parameters $\vec{\alpha_i} = (\alpha_{i1}, \alpha_{i2}, ...\alpha_{iK})$. Then the inter-individual variability is measured by $\alpha_{i0} = \sum_{k=1}^{K} \alpha_{ik}$ (with larger α_{i0} indicating less variability), and the population-average transition probability $P(i, j)$ is given by $\frac{\alpha_{ij}}{\alpha_{i0}}$. This formulation results in an analytically tractable likelihood expression, subject to quick, efficient maximisation. The ease of maximum likelihood estimation also facilitates model selection (using, for example, AIC). Application of the method to the case study data provides new biological insight, firstly by quantifying inter-individual variation in sperm whale dive behaviour. Moreover, the dataset includes behaviour data with and without acoustic disturbance, and a random-effect model facilitates more robust measurement of whales' behavioural response to the disturbance. Analogous methods could be used for easy specification of a random effect on any probability mass function.

Reserve selection in a dynamic habitat patch network

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Keywords: indicators of biodiversity, metapopulation dynamics, spatial ecology, species distribution models

Abstract: A noticeable fraction of the World's species inhabit disturbed or early-successional habitats. Reserve selection for these species is challenging due to the temporary nature of their habitats and the resulting lack of a stable habitat patch network. Reserve selection tools have mostly been designed assuming static habitat configuration or a deterministic shift of habitats towards the poles due to climate change.

The false heath fritillary, an endangered Finnish butterfly, inhabits moist *Valeriana sambucifolia* meadows that emerge in disturbed or abandoned sites and have a high destruction rate due to succession and land use changes. We prioritized a set of potential conservation sites for the false heath fritillary with respect to the anticipated temporal instability of the species' habitat patch network. We estimated patch destruction rates based on the present condition of 96 sites that had been delineated as false heath fritillary habitat in the past. Next, we identified areas with high likelihood of patch emergence (right soil type and hydrology) by carrying out habitat suitability modelling based on the present locations of habitat patches. Finally, we run repeated simulations of habitat network change and evaluated relative patch values of the candidate conservation sites to the metapopulation capacities of the resulting networks.

False heath fritillary habitat locations can be predicted with topographic wetness index, distance to rivers and fields, land use intensity and calcareous soil type. The model of habitat network change helped us to identify conservation sites that would remain in spatially valuable locations of the habitat network in the course of time and could thus serve as source patches for a dynamic metapopulation. Our method can be generally used in the reserve selection for species living in dynamic habitats.

Can haphazard sampling still be justified?

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Keywords: monitoring of biodiversity, spatial ecology, survey design and analysis.

Abstract: In field studies, ecologists have historically tended to choose the locations of sampling units haphazardly, rather than randomly. Unfortunately, this approach cannot provide formal statistical inference from the sample to the population without additional, largely untestable, assumptions. I argue that two recent technological advances largely remove the need for haphazard sampling in many situations. Some examples will be shown to demonstrate that even complicated designs can be implemented easily using software widely used among ecologists. More rigorous, randomised sampling designs would strengthen the validity of the conclusions drawn from ecological studies, to the benefit of the discipline as a whole.

Modelling non-negative continuous data with discrete mass at zero with an application to garden bird survey data

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Keywords: community structure and dynamics; population dynamics

Abstract: Models for analysing continuous data with a spike at zero have often received less attention than zero inflated count models. This type of data, however, is commonplace in the life sciences, particularly ecology. In this talk we outline mixed effects Tweedie models (Jørgensen (1987, 1997)) fitted in a Bayesian MCMC framework, which are flexible enough to account for the discrete mass at zero as well as allowing for over- and under-dispersion and apply them to long-term longitudinal data from winter garden bird surveys in the UK. In particular, we look at how an increase in numbers of an avian predator, the Eurasian sparrowhawk, *Accipiter Nisus*, has impacted on the numbers of multiple potential prey species visiting garden feeding stations across the winter, whilst controlling for additional environmental factors.

We will consider two approaches to the modelling process. The first approach models changes in prey numbers as a function of environmental covariates; the second models changes in prey numbers as a function of *change* in environmental covariates. Results will be presented as well as a comparison of the two methods.

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Likelihood-Based Finite Mixture Models for Ecological Ordinal Data

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Keywords: Biclustering; Cluster analysis; Community structure and dynamics; Dimension reduction; EM-algorithm; Finite mixture model; Fuzzy clustering; Likert scale; Multispecies models; Ordinal data; Species distribution models; Stereotype model

Abstract: Many of the methods which deal with the reduction of dimensionality in matrices of data are based on mathematical techniques, such as distance-based algorithms or matrix decomposition and eigenvalues. In general, it is not possible to assess objectively the appropriateness of a model via information criteria with these techniques because there is no underlying probability model. Furthermore, ordinal data are very common in ecological data (e.g. Braun-Blanquet scale). It is advantageous in an analysis to properly treat an ordered categorical variable as ordinal, rather than using the common approach of treating such a variable as nominal or continuous. Recent research has developed a set of likelihood-based finite mixture models for a data matrix of binary or count data (Pledger and Arnold, 2014). We present the extension of this work by formulating likelihood-based multivariate methods for ecological ordinal data. This approach applies fuzzy clustering via finite mixtures to the (ordinal) stereotype model. Fuzzy allocation of rows and columns to corresponding clusters is achieved by performing the expectation-maximization (EM) algorithm, and also by Bayesian model fitting, and their performances are compared. Data from two ecological community data sets are used to illustrate the application of this approach and also to demonstrate new and convenient visualisation tools for ordinal data. Finally, we present the results of a simulation study carried out to determine which information criteria are most appropriate for model selection with these particular mixture models when applied to ordinal data.

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Bayesian mixture modeling to assess year-to-year fluctuations in age structure of Mediterranean anchovy and sardine

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Keywords: small pelagic fish, *Engraulis encrasicolus*, *Sardina pilchardus*, ageing, population dynamics

Abstract:

Since 2009, the Gulf of Lions has shifted to a different regime, characterised by both a lower anchovy (*Engraulis encrasicolus*) and sardine (*Sardina pilchardus*) biomass. To better understand these changes, we investigated the magnitude and the timing of variations in growth, body condition and size and age structure of anchovy and sardine since 1992, using scientific pelagic trawl data. To circumvent usual difficulties in the ageing procedure, mixture models have been applied to decompose size structures into a mixture of Gaussian curves representing age categories. We developed a Bayesian framework that combined the use of size distributions with independent priors, i.e. age-length keys from otolith readings. These finite mixture models were run using the R package 'Rstan' (Stan Development Team 2012). The model provided consistent results, despite the typical absence of multiple distinct peaks in the size structure. For anchovy and sardine a period with per age larger individuals and mostly higher proportions of oldest ages was detected around 2005-2007, in contrast to the most recent years that were characterized by the rarity of old/large fish. The distinguished periods are similar to our findings for growth, condition and size structure. In particular, we conclude that the disappearance of larger individuals since 2011 is due to the combination of both slower growth and the loss of the oldest fish. The analyses of the investigated biological parameters allowed us to obtain a deeper insight into the population structure and dynamics, as well as their current "state of health".

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Statistical inference for complicated models in ecology and evolutionary biology

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Abstract: Monte Carlo simulation has long been a widely used tool in biology, traditionally for predictive modelling, as an adjunct to more analytical approaches, and latterly for statistical inference. The predictive and inferential aspects have typically been considered separately, often by different specialisms. One reason for this is that, while it is generally easy to formulate stochastic data-generating simulations of arbitrary complexity, it may be practically impossible to obtain a likelihood function for the same problem. However, it is now becoming widely appreciated that the predictive and inferential aspects can be viewed, under the Bayesian paradigm, as simply parts of the same whole, depending on which parts of the model are regarded as fixed and which are random. A useful tool that has underpinned this conceptual change in a very practical way is the method of approximate Bayesian computation (ABC). In this talk I will outline the basic ABC approach, and how it has evolved. Using examples in ecology and population genetics I will illustrate how it can be used for Bayesian model choice, posterior predictive modelling, and prior- and posterior-model checking. The known problems of the approach are also discussed. Finally I will end by describing the use of these methods for agent-based models in ecology.

SDR simplex: a framework for evaluating diversity-related structural properties in ecological data

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Keywords: Beta diversity; Community structure; Measures of biodiversity; Nestedness; Simplex; Species replacement.

Abstract: The ecological literature abounds in measures developed for evaluating community data, including diversity, (dis)similarity, and nestedness coefficients. I show that many of these functions fit a common conceptual and methodological framework which produces two-dimensional simplex plots for visual interpretation and percentage contributions for quantification. The essence of the approach is to decompose pairwise site dissimilarity into difference (D) and replacement (R) components and to use similarity (S) as a contrast, based on either presence-absence (Podani and Schmera 211) or abundance (Podani et al. 2013) data matrices with sites as columns and species as rows. The method is invariant to matrix ordering which means that results reflect truly inherent structural properties in the data. The SDR simplex approach can be extended to analyse bipartite ecological networks (Podani et al. submitted) or any other systems that may be described by rectangular data matrices. Further extensions include the comparison of data matrices regardless of their actual dimensions and the visualization of data structures obtained by various null models to enhance interpretation of statistical tests. The approach is illustrated by applications to actual data representing a wide range of ecological communities and biogeographic systems.

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Quantifying spatial patterns of species diversity: integrating methods of spatial and diversity analyses

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Abstract

Spatial pattern of ecological diversity may result from the combine effects of various ecological processes: species migration/colinisation, dispersal of propagules, inter-individual competition/facilitation, habitat preferences, etc. While powerful methods exist for quantifying species diversity on the one hand and spatial patterns on the other hand, current methods do not take full advantage of an integrative approach that could improve robustness of inferences about ecological processes at the origin of observed patterns. We propose here such an integration based on Rao quadratic entropy for a flexible quantification of species diversity accounting for non-uniform between species differences (such as phylogenetic or functional differences) and well established methods of spatial pattern analysis. For the case of fully mapped data (for instance, trees beyond a given threshold in an exhaustively sampled forest plot), a distance-dependent quantification of the spatial variation in alpha diversity is obtained by combining Rao quadratic entropy with Ripley's *K*-function of second-order neighbourhood analysis. For the case of discontinuous spatial samples (for instance, a network of independent forest plots), a distance-dependent quantification of the spatial variation in beta-diversity results from integration of Rao quadratic entropy within the framework of the variogramms. Beyond methodological consistency for quantifying spatial patterns of species diversity, this integration also allows the development of statistical tests of meaningful ecological mechanisms based on reference null hypotheses about either the spatial arrangement of individuals/samples, or the between-species relatedness as introduced in Rao quadratic entropy. Illustrations are provided based on simulated patterns as well as on observed patterns from tropical forest data.

Keywords:

Community structure and dynamics, indicators of biodiversity, measures of biodiversity, monitoring of biodiversity, multispecies models, spatial ecology, survey design and analysis

Invited speaker for the session "Indicators & measures of biodiversity"

Inferring species richness from floras with heterogeneous sampling efforts

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Keywords: indicators of biodiversity; measures of biodiversity; spatial ecology; species distribution models.

Abstract: Species richness of sampling units such as grid cells is frequently calculated by counting species in databases resulting from coordinated sampling schemes (such as the ones of Germany, Britain, Austria or Poland). Unfortunately, not all regions (or grid cells) are equally well sampled. Hence species richness is underestimated in less well sampled grid cells. We propose a method that takes into account sampling preference even if this is correlated with an environmental variable by applying Bayesian Image Restoration (Bierman et al. 2010). Besides environmental covariates, we will consider a spatial neighbourhood component and a model of sampling effort, based on semi-quantitative expert advice. This method allows to restore maps of species richness that come closer to true species richness than methods which do not take sampling effort into account.

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Estimation of dispersal rates with incomplete biodiversity inventories and temporal series of landscape images

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Keywords: Indicators & measures of biodiversity; metapopulation dynamics; monitoring of biodiversity; spatial ecology.

Abstract: A general understanding of the spatial dynamics of natural populations is needed to both predict their response to changing environments and design efficient conservation actions. Most biodiversity data are static and incomplete, which makes difficult the quantification of population dispersal rates for most organisms. We here develop an original approach to improve the estimation of population dispersal rates in fragmented landscapes. This approach is based on the idea to complement incomplete snapshot biodiversity data with a temporal series of landscape images. We develop a pseudo-likelihood method to make use of such data under the framework of metapopulation theory, which builds on the ideas of ter Braak and Etienne (2003) and Verheyen et al. (2004). We test the power and robustness of our method with simulated data and apply it to inventory data of forest understory plants of the Ile-de-France region in France for which landscape images are available since 1700.

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What do we model when we model species distributions?: An ecological and statistical perspective

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The need to understand processes shaping species distributions has resulted in a vast increase in the diversity of spatial wildlife data and statistical models. One may aggregate location data into spatial units (e.g. grid cells) and model the resulting counts or presence–absences as a function of environmental covariates. Alternatively, point data may be modelled directly, by combining the individual observations with a set of random or regular points reflecting habitat availability, a method known as a use-availability, presence – pseudo-absence or case–control design. Although species distribution models fitted to such diverse data are widely used, the ecological literature is not explicit about the statistical and ecological interpretation of their parameter estimates and predictions.

This study's objective is to illustrate that under certain assumptions, models fitted to spatial point, count and presence–absence methods can all be motivated by the same underlying spatial inhomogeneous Poisson point process (IPP) model, in which the intensity function is modelled as a log-linear function of covariates. This result also applies to models fitted using Maxent.

In geographical space, IPP model predictionsare proportional to the expected density of observations, or usage. In environmental space, IPP models are parameterized in terms of the ratio of habitat use over availability. Thus, positive coefficients are assumed to indicate preferential selection for particular environmental conditions. However,when an essential habitat type is already sufficiently abundant to meet an individual's needs, increasing theavailability of this habitat type can lead to negative coefficients, suggesting an apparent avoidance. Such changes in the model coefficients as a function of habitat availabilitycan be captured bygeneralized functional response (GFR) models. Hence, GFRs explicitly estimate the influence of habitat availability on usage, andthus can improve spatial predictions in novel habitats, and may signpost habitats that are critical for the organism's fitness.

Combining Data in Species Distribution Models

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Keywords: big data; citizen sciences; occupancy models; species distribution models

Abstract: The purpose of species distribution models is to use data on observations of species to infer their full distributions, and the drivers of their distributions. But the data itself can come from a variety of sources, from planned surveys to citizen science records and expert range maps. If we are to use this data efficiently, we should be able to combine the different types of data into a single model (Marion *et al.* 2012). A state space approach, modelling the actual distribution as a continuous intensity and developing observation models that are appropriate to the data, will be outlined.
We will use data from the Map of Life project (Jetz *et al.* 2011, www.mappinglife.org) to demonstrate how this approach can be applied to point counts, species lists from nature reserves, and expert range maps.

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New Species Distribution Modelling methods and making them relevant to users.

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Keywords: species distribution models; multispecies models; community structure and dynamics

Abstract: Species Distribution Modelling (SDM) is fascinating. It is a prolific, multi-faceted and often controversial research domain. Controversy arises from a range of sources, including the difficulty of matching the 'hard' topics such as statistics, computation & data, and the challenges in matching that with 'soft' topics such as philosophy, software design practices & SDM culture. In this talk I will talk about published and unpublished work in both areas, based on a variety of multidisciplinary collaborations. Firstly, work we have done in 'hard' topics and describe two methods we developed to address observation and process errors in SDM (Fine-Scale Environmental Variation & Biotic Interactions, two key sources of uncertainty) using MCMC to parameterise the models. And secondly research we carried out in the 'soft' topic of software use and how that contributed development of a new software. I will discuss why these research areas are intimately linked and suggest that adopting a more joined-up approach to these diverse challenges can aid progress in SDM.

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Water, water everywhere? Solutions to modelling the autocorrelated distribution of ubiquitous Amazonian vertebrates

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Keywords: spatial ecology, species distribution models.

Abstract: Making and breaking species distribution models (SDMs) continues to inspire statistical ecologists, however the speed of statistical advances means that the application of SDM methods is often limited by uncertainty regarding model and parameter selection. To compare and evaluate SDM methods (MaxEnt, LASSO penalized point process and Ensemble models) we simulated empirically informed species distributions and ecological sampling patterns. Analysis of simulation results was used to identify the statistical and ecological adequacy of the SDM methods and derive a modelling framework that generates reliable SDMs based on the classification of (i) species distribution and (ii) sample properties. We then challenged this framework by modelling data that violate key SDM assumptions. The presence and absence of 30 species of mid- and large-bodied vertebrates was obtained during 7 years of field surveys in two Amazonian field sites – one terrestrial and one riparian. The “terrestrial” site is a 360 km^2 area located within the Brazilian arc of deforestation. A total of 7904 camera trap days, 4900 track-station nights and 2739 km diurnal line transect census were used to sample forest fragments, corridors, and matrix. The “riparian” site traverses a protected area, and we used 6836 km of boat census to survey 165 km of waterways with a steep gradient in anthropogenic disturbances. We cannot assume that the sampled species are at equilibrium nor that sample locations are spatially independent. The results of the SDM analyses using our framework were compared to Bayesian occupancy model predictions that specifically included spatial autocorrelation and differences in detection probabilities. We found that with certain modifications the SDM framework developed was robust to violations of these key SDM assumptions. It remains to be seen whether this framework can be generalized to different scales or different species groups.

Validation data : keystone to move state-space models for movements to operational models for fisheries and marine ecology

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In line of the recent spread of electronic devices to track animals and of the development of movement ecology, Vessel Monitoring Systems experience a worldwide diffusion allowing tracking fishing boats whose behaviors show similarities with natural top foragers. State-space models are widely used to estimate the states of an unobserved process from tracking data. When tracking data are assumed to be known without error (e.g. GPS position or filtered Argos positions) the unobserved process (also called hidden state process) generally concerns the behavioural states of the tracked individuals. This modelling approach assumes that the characteristics of the movement (speed, turning angle) inform on the behavioural states (fishing/eating, foraging, traveling). In fisheries and in marine ecology, applications concern, up to now, time- and state-discrete versions of these models assuming a Markov or Semi-Markov transition between states and a correlated (or not) random walk to describe movement conditionnaly upon state. Inferences are usually based on maximum likelihood or Bayesian methods. However the selection and validation of state space model lacks of appropriate statistical tools and suffers computational cost. The reliability in model's outputs is therefore questionable and it becomes essential to better control the assumptions introduced in the model (time-correlation, markov/semi-markov) and their consequences. In this communication, we promote the use of validation data sets to design and validate state-space models for movement analyses in fisheries and marine ecology. Three different state-space models were fitted to several tracking data sets with contrasted frequencies of data acquisition associated with validation data sets informing on the true behavioural states. We assess the robustness of state-space models to model hypotheses and derived some recommendations on the formulation of state-space models with respect to time step of observations and behavioural states.

Keywords : vessels' trajectories, behaviour, discrete state-space models, models comparison and validation, modelling of movement

Using stochastic differential equations to model fishing vessels displacement

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Keywords : individual-based models ; movement ecology ; fishermen's dynamics ; stochastic differential equations. *Invited session : Movement*

Abstract : Understanding the dynamics of fishing vessels is essential to characterize spatial distribution of fishing effort on a fine spatial scale and to estimate the impact of fishing pressure on the marine ecosystem. Models that works from the coupling of discrete-time Markov chains for the sequence of hidden behaviours (fishing, steaming . . .) and piecewise linear movement of fishing boats conditioned by these behavioural states have proved their usefulness to describe fishing vessels dynamics. But three major weaknesses of this class of models have been pointed out I) they can hardly cope with irregular data acquisition ; II) switches in the hidden behavioural process are supposed synchronous to the observed positions ; III) they are not spatially explicit.

To fill these gaps we propose a new model for fishing vessel's displacement by coupling a continuous time Hidden Markov process to the observed process derived from a stochastic differential equation which possibly depends on covariates.

The hidden behaviour is supposed to be a Markov process Z_s taking values in $\{1 \dots K\}$ (1 standing for steaming, 2 for fishing, for instance). The observed process X_s is supposed to satisfy a stochastic differential equation which parameters depend on Z_x :

$$dX_s = b_{Z_s}(X_s) + \sigma_{Z_s}(X_s)dW_s$$

where $b_k(\cdot)$ and $\sigma_k(\cdot)$ are respectively the drift and the diffusion functions satisfying regular conditions, and W is the standard Wiener process. In addition to this, an observation process describe the actual position in function of the observed process $Y_s = X_s + \epsilon_s$.

Statistical techniques based on MCMC algorithms or EM algorithms (and their stochastics variations MCEM, SAEM, ...) are presented to estimate parameters of this model. An application to a set of trajectories of French fishing vessels performing in the Eastern Channel is shown to highlight the potentiality of the method and how it may outperform more classical models.

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When to be discrete: the importance of time formulation in understanding animal movement

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Keywords: modelling of animal movement; movement ecology

Abstract: Animal movement is essential to our understanding of population dynamics, animal behavior, and the impacts of global change. Coupled with high-resolution biotelemetry data, exciting new inferences about animal movement have been facilitated by various specifications of contemporary models that are appearing in the recent literature with great regularity. These models differ, but most share common themes. One key distinction between these approaches seems to be whether the underlying dynamic process is assumed to be discrete or continuous. In our experience, this is the greatest source of confusion among practitioners, both in terms of implementation and biological interpretation. In general, animal movement occurs in continuous time but we observe it at fixed discrete-time intervals. Thus, continuous time is conceptually and theoretically appealing, but in practice it is perhaps more intuitive to interpret movement in discrete intervals. This may in part explain why the methodological development and application of discrete-time formulations has thus far exceeded those in continuous time. We explore the differences and similarities between continuous and discrete versions of mechanistic movement models, establish some common terminology, and indicate under which circumstances one form may be preferred over another. Counter to the overly simplistic view that discrete- and continuous-time conceptualizations are merely different means to the same end, we present novel mathematical results revealing hitherto unappreciated consequences of time formulation on inferences about animal movement. We demonstrate these properties using northern fur seal (*Callorhinus ursinus*) biotelemetry data and conclude with a roadmap for future developments.

Fringe Benefits: The hidden utility of movement constraints in telemetry studies

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Abstract: Advances in animal telemetry data collection techniques has been a catalyst for the creation of statistical methodology for analyzing animal movement data. Such data and methodology has provided a wealth of information about animal space use and the investigation of animal-animal and animal-environment relationships. While the technology for data collection is improving dramatically over time, we are left with massive archives of animal telemetry data that are fraught with issues. One common issue pertains to measurement error, that is, in the telemetry setting uncertainty pertaining to an individual's true location. This form of error arises as a combination of factors due to accuracy of the telemetry device and system, animal behavior, atmospheric interference, and landscape features. Furthermore, the measurement error varies with both location and time and the information available about the accuracy is not easily incorporated into statistical models and is often in flux due to ongoing manufacturer findings. Thus, there is a need for 1.) approaches to better estimate the telemetry error distribution and 2.) improved methods to incorporate it into animal movement models. Using both simulations and real data, we describe how certain forms of auxiliary information (hard constraints to movement) can be surprisingly useful for learning about telemetry error which can then incorporated into statistical models for animal space use.

Statistical analysis of routine behaviour in animal movement

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Keywords: movement ecology

Abstract:

Memory plays an important role in driving animal movement that still remains largely to be understood. When dealing with predictable resources, individuals can develop routine movement behaviour, by regularly revisiting known resource sites such as feeding patches, drinking holes or shelters. It has been acknowledged for a long time for foraging movement of nectarivorous insects and frugivorous primates, but an extensive number of species should rely on some degree of routine behaviour.

Fourier and wavelet analyses can be used to detect periodic revisits and thus to detect some sort of routine behaviour in time. However, we still lack methods and adequate metrics to better characterize the degree of routine spatial behaviour, to detect the repetition of movement sequences and determine which specific sequences are repeated, particularly when data are noisy and thus sequences are not *exactly* repeated.

Here we compare existing methods, developed in other fields, to detect repeated sequences. In particular, we consider a method developed for the detection of repetitions of behavioural sequences that iteratively pairs events when they follow each other within a time window significantly more often than expected by chance. Other methods considered include Markov models of transition matrices, recurrence plots, and algorithms used for the detection of repeated DNA sequences.

After conceptually comparing these methods we adapt the most appropriate for use on movement data, and we estimate the extent to which some animals rely on routine movement sequences to prospect their environment. We assess the degree of routine behaviour of several bird and mammal species. We look for the repetition of sequences of visits to specific feeding sites or water points, and investigate possible links with individual and environmental characteristics.

Integrating movement ecology with popuation dynamics: Approximate Bayesian computation approach

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Keywords: movement ecology; population dynamics; spatial ecology; approximate bayesian computation

Abstract: Statistical approaches for modeling animal movement and (spatial) population dynamics are developed largely independently from each other, even though fundamentally these two phenomena are tightly linked to each other and interact with each other. Population dynamics are ultimately caused by indivdidual-level phenomena (births, deaths, and movement), and individual-level phenomena are in terms influenced by the state of the population (e.g. density-dependence in births, deaths and movements).

We introduce a computational framework based on Approximate Bayesian computation (ABC) for analysing models combining movement ecology and population dynamics. ABC algorithms offer flexibility in formulating the model as they are based on simulating the model and likelihood evaluations are not needed. This is especially advantageous with many complex models in movement ecology, for which likelihood computation is not possible or would require costly numerical techniques. An important aspect of the framework is also the capability to utilize efficiently different types of data that contain complimentary information about the underlying biological processes. We illustrate the framework with simulated and real data.

N-mixture models to estimate abundance and distribution of bird communityat multiple forest sites in the Albertine Rift, Uganda

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Keywords: abundance, measures of biodiversity, multispecies models, species distribution models

Abstract:Uganda's Albertine Rift is a mountainous region in the western part of the country that extends from the northern tip of Lake Albert to the southern end of Lake Tanganyika.This region contains the highest diversity of vertebrates on the African continent, with more than 52% of Africa's birds and nearly 40% of the continent's mammals.In 10 years of bird point count surveysat41 semi-protected forests, >125,000 individual count records were accumulated for >700 species with the aim to investigate factors governing species distribution and community composition.Due to logistical constraints and the relative inaccessibility of several forests, many survey routes were unable to be surveyed >1 during a season (period of assumed population closure), and some were surveyed only once during the entire study period. This lack of temporal replicates generally precludes our ability to account for imperfect detection without additional information (e.g. distance sampling).Here, we build a hierarchical N-mixture modelthat allows sharing of information on detectability across space and species to obtain estimates of bird abundance, including the effects of spatial covariates governing abundance.We investigateoverdispersion in abundance by modeling counts underPoisson, zero-inflated Poisson, and negative binomialdistributions, evaluating model fit using Bayesian p-values. We explore several covariate effects on abundance, including elevation, forest type and anthropogenic disturbance.Our results will provide valuable information for management of bird biodiversity in Uganda, including trends in abundance for rare and endemic species and estimates of the impacts of energy exploitation and other development activities on avian communities.

A new N-mixture model for estimating population sizes of interacting species

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Keywords: Detectability; hierarchical model; invasive species; N-mixture model.

Abstract: Among the factors involved in the decline of endangered species, competition with alien species was rarely studied in natural environments, probably because investigating co-occurrence patterns of species is difficult. Potential problems of empirical approaches include the reliance on population estimates at a single time point, the difficulty to properly account for imperfect detection and for habitat changes over time. Recently, however, some authors proposed promising methods to study species occurrence and co-occurrence patterns based on site-occupancy models using presence-absence data (Miller et al. 2012, Cayuela et al. 2013). In our study, we took those methods one step further by including population counts of interacting species. Based on N-mixture models, we developed an approach to estimate true population sizes of interacting species. In our model, the population size of one species is assumed to depend on the true population of a second species, but the population size of the second species is not assumed to depend on the population size of the first species. In contrast, detection probabilities for both species are assumed to depend on the true population size of the other species. We demonstrate the performance of our method using simulated data and applied it to data from a long-term monitoring program on amphibians from Switzerland.

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Accounting for imperfect detection when evaluating the effectiveness of invasive species control

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Keywords: abundance, movement ecology, spatial ecology, monitoring of biodiversity

Abstract: Many invasive plant species are sparsely distributed across large areas. Management of these species is often undertaken using a search and destroy approach where people search the landscape and treat (destroy) any individuals found. However, detection is imperfect and so these searches need to be undertaken on multiple occasions. Given limited resources, an explicit objective is to optimize efforts by targeting those areas for follow up visits that have the highest predicted abundance. In order to simultaneously estimate both abundances and detection rates from data on search & destroy efforts, it is necessary to have a good model of the detection process itself. Using a case study of invasive willow control across a 120 km^2 region in alpine Australia, we used intensively monitored sample plots to characterise how detection rates depend on perceived abundance for three groups of willow control contractors. We used Bayesian models to fit an exponential detection function where the detection rate varied with plant size, between contractors, with the total number of willows treated, and on features of the contractors' movements. We found that detection rates decreased with increasing abundance but areas with high abundance were subject to greater search effort. We combined these models with GPS tracking data representing six weeks of search and destroy missions to predict the remaining abundance of willows across the landscape and hence identified areas that are priorities for follow up control.

Estimating wildlife population trends from incomplete census data

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Keywords: abundance, monitoring of biodiversity, population dynamics,

Abstract: Understanding the dynamics of wildlife populations is fundamental to managing them. A wide range of methods to assess population trends are available nowadays, to suit many budgets and purposes. A common budget is small, and a common purpose is to assess rare species, which are characteristically difficult to get data on. Classical survey designs may not be applicable due to lack of observations, or lack of marks (natural or strategically added). Known aggregations provide the easy opportunity ability to count individuals, but such 'censuses' rarely fall into robust analytic frameworks or are true 'censuses' of the target population, i.e, they do not count every individual in the population of interest. Notwithstanding, aggregations may be the best or only way to estimate population trends in some cases. Using repeated census data at multiple sites, we developed simple methods to estimate population size and trend using a Bayesian framework. These methods consist of basic population models parameterized by MCMC estimation. . We demonstrate these methods with four critically endangered birds: white-shouldered ibises *Pseudibis davisoni* on roosts, and three species of vultures at carcasses (*Sarcogyps calvus, Gyps tenuirostris, G. bengalensis*). The methods have wider applicability and the potential to support decision making for other roosting, carcass-feasting, or otherwise predictably-aggregating species.

Analysing plant cover class data quantitatively: customized cumulative beta distributions show promising results

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Keywords: abundance, indicators of biodiversity

Abstract: Plant abundance data (such as Braun-Blanquet cover classes) are more often analyzed with ordination techniques than with parametric ones, even if the latter allow for a more interpretable quantification and a better comparison between studies than the former. Among parametric techniques, only the cumulative logit model takes into account all the peculiarities of these abundance data: bounded between 0 and 100%, asymmetric classes, high proportion of zeroes. However, the results that the cumulative logit model provides are difficult to interpret. Here we propose twelve Bayesian models based on a zero-inflated cumulative beta probability distribution which is bounded, can assume various shapes and accounts for zeroes, therefore taking into account the peculiarities of abundance data. Moreover, results of those models are easy to interpret since the user can directly estimate the mean and variance of data underlying abundance class observations, much as in generalized linear models (GLMs). We applied our new models and the cumulative logit model to real data: Braun-Blanquet abundance of 17 understory species in response to two dendrometric biodiversity indicators (tree cover and specific richness). We compared the performance of the models using the Deviance Information Criterion and sampled posterior p-values. Four of the Bayesian beta models consistently outperformed the cumulative logit model and showed an ease of interpretation similar to that of GLMs. They therefore provide promising alternatives to existing parametric methods for modeling plant abundance.

Assessing changes in biodiversity over space and time

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Keywords: abundance; measures of biodiversity; spatial ecology; species distribution models.

Abstract: Partitioning biodiversity change both spatially and temporally is required for effective management at regional and local scales. As biodiversity is a multifaceted concept, comparative analyses of different indices, focussing on different components of biodiversity change (evenness versus abundance), give better information than a single headline index. We model changes in the spatial and temporal distribution of British breeding birds using species-specific generalized additive models (GAMs) applied to count data collected between 1994 and 2011. Combining the results across species we assess temporal trends in biodiversity, and change points in those trends, at different spatial scales. The geometric mean of relative abundance, a headline indicator of biodiversity change, is assessed together with a goodness-of-fit evenness measure focussing separately on the rare and common species. As a complement to the biodiversity indices we also assess temporal turnover in species composition and how that varies spatially based on the results from the above GAMs. Modelling spatio-temporal changes in biodiversity and attributing those changes to potential drivers, such as climate, is a difficult problem. The 'standard' approach for including climate information intospatio-temporal models of this kind – including each weather variable as a linear covariate with a single regression coefficient – confounds thespatial and temporal effects of the covariates. I will end the talk with an example of hierarchical centring methods that enable one to disentangle the spatial and temporal effects of such covariates.

A host's breadth from extinction:
Identifying co-extinction risk of pollinators in a threatened plant community.

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Keywords: abundance, measures of biodiversity, statistical ecology, conservation ecology

Coextinction, the loss of a dependent species with its host, is regarded as one of the most important drivers of biodiversity loss. Biodiversity hotspots feature many threatened and endemic plants and a high potential for coextinction of dependent species, such as pollinators or herbivores. To evaluate a dependent's risk of coextinction, it is crucial to know its host-breadth, i.e. the number of hosts used by a dependent. In this study, we assessed the host-breadth of flower-visitors to a community of threatened plants in a biodiversity hotspot in the southwest Australia. We used a Bayesian, zero-inflated Poisson regression model with a hierarchical structure to estimate the host-breadth conditional upon the presence of the flower-visitors on the plants. While accounting for uncertainty, the model allowed us to identify two flower-visitors with narrow host breadths, a native bee and a yet undescribed click-beetle. These species are cothreatened and have a high potential of being at risk of coextinction. In the future, managers should conserve these flower-visitors in combination with the plant species, especially when *ex situ* actions such as translocation are considered.

Integrated population modeling of American black bears: An application of robust-design spatial capture-recapture combined with mark-recovery and recruitment

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Keywords: integrated population model; robust design; spatial capture-recapture

Abstract: Since 1975, a monitoring program for American black bears (*Ursus americanus*) in Maine, USA, has closely followed several local populations with summer live trapping and winter den visits of radio-collared females. The various field efforts, in conjunction with tag returns from hunter harvest, produce data that can be used to jointly estimate demographic parameters and population dynamics with an integrated modeling approach. We present an integrated population model that combines robust-design spatial capture-recapture and mark-recovery data with individual offspring production and survival to take full advantage of the information available from the bear monitoring program. Our model takes a Bayesian approach to parameter estimation and uses data augmentation to facilitate incorporation of individual covariates such as sex and age. We use data simulations to explore model limitations under realistic sample sizes. We discuss challenges associated with a sampling rotation between study locations for some surveys and the handling of orphaned young in the estimation of population recruitment.

Hierarchical modelling of population growth rate from individual capture-recapture data

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Keywords: Bayesian analysis; temporal symmetry model; climate-driven population dynamics.

Abstract: Different approaches exist to estimate and model population growth and associated vital rates using capture-recapture data from open populations. Among them the temporal symmetry approach (Pradel 1996) has the unique characteristic of combining in the same likelihood the standard-time and the reverse-time approach, simultaneously incorporating survival and recruitment parameters and thus allowing inference on population growth rate. We present a Bayesian formulation of the Pradel's temporal symmetry method in which parameter estimates are derived by the posterior sampling of distributions generated by MCMC methods. The Bayesian formulation permits a hierarchical modelling of the biological and sampling processes, allowing the extension of the original fixed time effects structure to random time effects, an option which is still impractical in a frequentist framework. We illustrated the model by using individual capture histories of a long-lived seabird, the Scopoli's shearwater *Calonectris diomedea*, and assessed the influence of climatic variables on annual survival and population growth rate simultaneously.

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Estimating variability from capture-recapture data using the SAEM algorithm

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Keywords: Capture-recapture, fitness components, heterogeneity, latent process, maximum likelihood estimation, population dynamics.

Abstract: Hidden Markov models are now well spread in capture-recapture analysis, as an appropriate tool to managed correlation between states for two consecutive dates. However, some individual differences or different kind of autocorrelation may remain unaccounted in such models while being present in the data. Mixed hidden Markov models (MHMM) were proposed by Altmann (2007) by introducing random effects to capture differences in the observation and the state processes. The additional variability included in the model may have some biological meaning and may improve the precision of estimators. However fitting such models remains challenging inside a frequentist framework. We applied the SAEM algorithm used by Delattre et Lavielle (2012) to a MHMM with several individual random effects. In addition, we propose a variant of this algorithm to fit a model with a time random effect. We test the algorithms thought 1) capture-recapture simulated data sets and 2) a real case study.

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Use of multi-events framework to explore breeding strategies in a long-breeding-cycle species

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Keywords: capture-recapture, heterogeneity, breeding strategies, fitness components, multi-event model, population dynamics.

Abstract: According to life-history theory, individuals are expected to maximize their number of offspring while minimizing costs on their survival. In long-lived species, breeding season usually occurs once a year and mature individuals can therefore breed every year. However, several strategies are found among these species, breeding attempts regularly occurring every year or irregularly depending on external condition.

In seabirds, the king penguin *Aptenodytes patagonicus* is a singular species with its unusual breeding cycle. A successful breeding cycle lasts more than a year in this species, and the laying period extends from November to March. Depending on the onset of a reproductive event, the breeding cycle can therefore last from couples of month (breeding failure) to up to 14 months (success to fledge a chick).

We used a 10-year dataset of king penguins breeding in a colony at Possession Island, on Crozet Archipelago. Individuals implanted with a passive transponder tag are identified by underground antennas buried on usual pathways used by the birds to leave or enter their colony, allowing continuous and automatic data collection.

We investigated survival and breeding propensity according to the previous breeding status and schedule of the breeding attempt using several multi-events models. In a first step, we explored involved mechanisms using seasonal (3 phases covering the entire 14-month breeding cycle) and annual models. Breeding initiation date and previous breeding status, for the previous breeding cycle and for each phase of the current breeding cycle, strongly affect survival and breeding performance. In a second step, we investigated potential patterns by including heterogeneity or memory in our models. Our results suggest that both heterogeneity and memory may shape breeding strategies in king penguins.

The multi-event framework is a powerful and useful tool to have new insights on demographic parameters and life-history strategies.

Exploring the consequences of reducing survey effort for detecting individual and temporal variability in survival

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Keywords: data thinning; hidden parameters; individual covariates; integrated population models; juvenile survival; long-term monitoring; mark-recapture-recovery; population dynamics; survey design and analysis.

Abstract: Long-term monitoring programmes often involve substantial input of skilled staff time. In mark-recapture studies, considerable effort is usually devoted to both marking and recapturing/resighting individuals. Given increasing budgetary constraints, it is essential to streamline field protocols to minimize data redundancy while still achieving targets such as detecting trends or ecological effects. In our study (Lahoz-Monfort *et al.* 2014) we evaluated different levels of field effort investment in marking and resighting individuals by thinning existing mark-recapture-recovery data to construct plausible scenarios of changes in field protocols. We demonstrate the method with 26 years data from a common guillemot *Uria aalge* monitoring programme at a major North Sea colony, the Isle of May. We also assessed the impact of stopping the ringing of chicks on our ability to study population demography using integrated population models, by artificially removing different data sets to explore the ability to compensate for missing data. When effort reduction is necessary, both post-study evaluation approaches provide decision-support tools for adjusting field protocols to collect demographic data in long-term environmental monitoring programmes.

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Measuring non-Euclidean movement patterns in structured habitat networks using spatial capture-recapture models

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Keywords:capture-recapture; modelling of animal movement; movement ecology; spatial ecology.

Abstract: Movement underpins much of evolutionary and ecological theory, and is often the result of complex relationships between organisms and their environments. Unless studied in isolation, however, animal movements are typically assumed to be symmetric irrespective of landscape heterogeneity (the Euclidean assumption), or asymmetry is incorporated using resistance surfaces that are defined *a priori*. Recently developed spatial capture-recapture (SCR) methods offer the flexibility to relax the Euclidean assumption and specify realistic models of animal movement while simultaneously estimating population density. Here we describe how observations of individuals' movements can be used to estimate landscape resistance using a least cost path approach. The method is developed using simulations that resemble a species with movement associated with, but not restricted to, a stream network. We then apply our model to SCR data collected from a population of American mink *Neovisonvison* - a riparian habitat specialist. Our results suggest that, encouragingly, density estimates are insensitive to mis-specification of the movement model (Euclidean vs. ecological distance), yet the Euclidean assumption does result in biased inference about movement, specifically estimates of home-range shape and size. While primarily developed for inference about density, estimating ecological distance using SCR models provides an important and powerful tool for understanding how movement patterns are influenced by highly structured habitat networks, and thus provide a more realistic understanding of movement ecology, resource selection and landscape connectivity.

Determining individual variation in growth and its implication for life history and population processes using the Empirical Bayes method

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Keywords: Empirical Bayes; random-effects model; body growth.

Abstract: A better understanding of growth will always be an important problem in biology. Variation in growth can have substantial consequences for both ecological and evolutionary dynamics as well as affect the estimation of vital rates and demographic traits, which may translate to incorrect model predictions. However, the implications of including individual differences in growth in the study of population processes are largely unexplored, in part because of the challenges of estimating the determinants and the extent of shared (i.e. among homogeneous groups) and individual (i.e. after accounting for shared component) variation. Our understanding of growth dynamics and of its consequence on population and evolutionary dynamics can greatly benefit from the use of novel and powerful statistical approaches that are able to tease apart the sources of growth variation.

We use an Empirical Bayes (EB) approach to estimate individual and shared variation in somatic growth with a random-effects model. We implemented the EB approach in the module ADMB-RE of the software ADMB and applied the EB approach to the joint estimation of shared and individual variation in growth from longitudinal data using a parameter-rich von Bertalanffy growth (vB) function.

As a case study, we consider two populations of marble trout *Salmo marmoratus* living in Slovenian streams, where individually-tagged fish have been sampled for more than 15 years. We introduce cohort and density during the first year of life as potential predictors of the vB function's parameters k and L_∞ in addition to the individual random effects. We show that our EB approach predicts future growth of organism with substantially greater accuracy than using historical information on growth at the population level, and help us identify year-class effects probably associated with climatic vagaries as the most important determinant of variation in growth.

Exact Bayesian inference for continuous-time modelling of animal movement

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Keywords: modelling of animal movement; movement ecology

Abstract: In this talk I will describe and illustrate some recent progress in Bayesian inference for continuous-time models of movement. The models used will include many of those described in Harris & Blackwell (2013), which incorporate switching between behavioral states and heterogeneity in space and time, and also models for interactions between multiple animals, building on the work of Langrock et al (in press). The inference uses a Markov chain Monte Carlo approach, exploiting an exact simulation technique to avoid any approximation or time-discretization error, despite the complex relationship between location, behaviour and movement. These ideas will be illustrated using real data on individual fishers *Martes pennanti* (courtesy of Scott LaPoint, Max Planck Institute for Ornithology, Konstanz) and on a group of simultaneouslytracked reindeer *Rangifer tarandus* (courtesy of Anna Skarin, Swedish University of Agricultural Sciences, Uppsala).

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The correlated velocity continuous time animal movement model: theory, estimation and applications

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Keywords: correlated velocity movement, CVM, CRW, continuous-time, continuous-space, Ornstein-Uehlenbeck process, parameter estimation

Abstract: Most animal movement models are discrete, despite the fact that animal movements take place in continuous space and time, and data on animal movements is often collected irregularly. Continuous movement models resolve many of the problems with scaling, sampling, and interpretation that affect discrete movement models. For example, the correlated velocity movement (CVM) is a continuous-time analogue to the widely used correlated random walk (CRW) defined in terms of two parameters that have direct biological relevance in terms of energetics at small scales and dispersal at the large scales. Compared to the CRW, however, continuous movement parameters are challenging to estimate and not widely used. We present several methods to estimate CVM parameters - from direct calculation to a complete likelihood of the parameters given movement data. Cases cover a range of resolutions, from very high, as in videography, to low, as in much telemetry, and for data that are regularly sampled or irregularly sampled. We illustrate the application of these methods for several terrestrial and aquatic animal movement datasets, introducing an R package (cvm) for obtaining estimates and confidence intervals. Finally, we discuss ways in which the basic model can be extended to incorporate behaviorally structured movements.

References

Supervised vs. non-supervised hidden semi-Markov modeling for inferring behavioral modes from movement paths

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Keywords: movement ecology; modelling of animal movement; Markov models; machine learning; trajectories; Vessel Monitoring System; fishermen; *Engraulis ringens*

Abstract: In movement ecology, the inference of behavioral modes of individuals from their trajectories is commonly addressed using hidden Markov models (HMMs). Recently, hidden semi-Markov models (HSMMs), extensions of HMMs, have been applied to animal and human movement, showing better fit and better inference of behavioral modes, respectively, than HMMs. HSMMs are usually fitted within a non-supervised framework, using an EM algorithm. Availability of tracking data for which the true behavioral modes are known, i.e. ground-truthed data, would allow for model validation, as well as for a supervised setting for HSMMs fitting. One of the few predators for whom we can have access to true foraging behavioral modes in a natural environment is the fisherman. Here, using ground-truthed data collected on fishermen in the Humboldt Current System, we are able to fit HSMMs within a supervised setting and perform an independent validation of the model. For testing whether if a supervised setting improves inference accuracy, we compare the performance of supervised and non-supervised HSMMs. Results support the use of supervised setting therefore highlighting the importance of ground-truthed data for model validation and higher inference accuracy. Further perspectives are presented, including the use of supervised and semi-supervised approaches for other animals' movement and the estimation of the resources (i.e. number of observations) to be allocated for gathering an optimal ground-truthed dataset.

Preferred habitat of juvenile southern bluefin tuna in the Great Australian Bight

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Keywords: species distribution models, archival tags, sea surface temperature, chlorophyll a, seasonal forecast

Abstract: Large numbers of juvenile southern bluefin tuna (SBT) are found, and caught by commercial purse-seine vessels, in the Great Australian Bight (GAB) during the austral summer. We used data from a large-scale archival tagging experiment conducted on juvenile SBT in the mid to late 2000s to investigate habitat preferences in the GAB. This involved a number of steps: first, estimating the most probable track of each fish from the light and temperature records on the returned archival tags (done using an in-house geolocation method); second, using a state-space model to estimate periods of residency versus migration; third, matching up remote-sensing data for candidate environmental variables (sea surface temperature (SST) and chlorophyll a (chl a)) with estimated fish locations when in a resident state; and fourth, comparing environmental observations for the entire GAB to observations where fish were resident to see if fish were concentrated within given ranges (indicating preferred habitat) or randomly distributed (no habitat preference). Both SST and chl a were found to influence the distribution of SBT. Once habitat preferences were established, we produced maps of the GAB showing regions of preferred SBT habitat for specified time periods. In addition, seasonal forecasts of environmental variables (produced by the Bureau of Meteorology (BoM)) were used to predict regions of preferred SBT habitat in the GAB up to two months in future. Because the BoM seasonal forecasting model is strictly a physical model and does not simulate chla a levels, only SST data could be included in the habitat forecasts. These habitat forecasts are being used by members of the Australian SBT fishing industry to help plan their fishing operations. As the fishery is managed under a quota system, this application does not lead to more fish being captured, but should improve the economic efficiency of the catching operations.

Interpreting the movement behaviour of the flapper skate across the water column by Markov switching autoregressive models

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Keywords: modelling of animal movement; movement ecology.

Abstract: The flapper skate (*Dipturus intermedia*) is an apex predator that used to be widely distributed in the North East Atlantic. Due to its size and non-selective distribution, all age classes of the flapper skate have constantly been part of the by-catch of ground trawling fisheries throughout the years causing a 90% decline of the population. To test appropriate conservation measures to help the species recolonize its former range, Data Storage Tags (DSTs) were applied on 18 individuals in the Sound of Jura (Scotland). Four tagged individuals were recovered after different time spans ranging from two weeks to twelve months. DSTs collected pressure levels every two minutes. Pressure data were then converted into depth values, showing skates' behaviour across the water column. The four series of depth exhibit high autocorrelations at the higher lags, with a slow decay, and asymmetric cycles. Both issues suggest to handle the series as realizations of a stochastic regime switching process. Hence, Markov switching autoregressive models have been applied. Covariates were also incorporated into the model through the Markov chain: the transition probabilities are time-varying and dependent on dynamic categorical variables, such as daylight duration and lunar cycles (a proxy for the tidal cycle). Only the shortest series has been analysed at the moment. A two-state hidden Markov chain was selected, representing different regimes of animal movement, i.e., state 1 for resting or horizontal swimming or slow ascending and descending; state 2 for fast ascending and descending. Daylight duration is the environmental covariate that better explains the hidden state dynamics: higher activity during the night is often related to foraging activity for predators of crustaceans and fish. The flapper skate uses the whole water column throughout the year suggesting that areas of high densities should be closed to fisheries at all depths to conserve this species.

Learning about colonization under an adaptive management framework

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Key words: spatial ecology, population dynamics, modelling of animal movement

Abstract: Adaptive management is a framework for resolving key uncertainties while managing complex ecological systems. Its use has been prominent in fisheries research and wildlife harvesting; however, its application to other areas of environmental management remains somewhat limited. Indeed, despite the considerable uncertainty surrounding metapopulation restoration, adaptive management has not been used to guide and inform such restoration actions. In this study, we determined how best to learn about the colonization rate when managing metapopulations under an adaptive management framework. We developed a mainland-island metapopulation model based on the threatened bay checkerspot butterfly (*Euphydryas editha bayensis*) and assessed three management approaches: adding new patches, adding area to existing patches and doing nothing. Using stochastic dynamic programming, we found the optimal passive and active adaptive management strategy by monitoring colonization of vacant patches. Under a passive adaptive strategy, increasing patch area was best when the expected colonization rate was below a threshold; otherwise, adding new patches was optimal. Under an active adaptive strategy, it was best to add patches only when the colonization rate was certain to be high. This research provides a framework for managing mainland-island metapopulations in the face of uncertainty while learning about of the dynamics of these complex systems.

Including drift in analyses of observation data reveals environmental effects on copepod biomass in the Barents Sea

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Abstract: The advective nature of marine systems presents a challenge in zooplankton studies. Knowledge about the role of advection is needed to (1) assess the relative importance of advection versus other environmental variables in shaping zooplankton dynamics, and to (2) reveal the actual habitat of zooplankton to more accurately study the role of local environmental variables. In highly advective areas such as the Barents Sea, zooplankton might drift vast distances during the growth season, but these trajectories are not detected by traditional sampling methods.

We analysed spatially resolved *Calanus finmarchicus* biomass data collected bi-annually in the Barents Sea between 1959 and 1993 (Nesterova 1990). Generalized additive models were used to assess the effects of environmental variables in spring, and advection from spring to summer, on the spatiotemporal variation in summer biomass. Particles representing *C. finmarchicus* were released in spring based on observed spring distribution, using a particle tracking model with input from the Regional Ocean Modelling System (ROMS). After drifting, the particles were sampled at the time and positions of summer observations, and the density of particles was used as explanatory variable in the statistical model. Temperature and mixed-layer depth at back-tracked locations in spring were used as proxies for zooplankton growth conditions.

Significant positive relationships were detected between *C. finmarchicus* summer biomass and particle density, spring temperature and mixed-layer depth. The simulation was thus able to reproduce some of the variation in the observation data. This study demonstrates how combining hydrodynamic modelling and statistical analyses of observation data can shed light on the importance of advection and local environmental variation on zooplankton dynamics.

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Statistical machismo vs common sense: when are new methods worthwhile?

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Abstract: Statisticians' bread and butter, the work that excites us and brings academic rewards, is developing novel methods. Applying existing methods to new problems and new data sets, no matter how exciting the scientific results or useful the management conclusions, doesn't have the same intellectual thrill. A recent blog post by Brian McGill accused ecologists of "statistical machismo", using unwarrantedly fancy statistical methods for swank; I will explore the costs and benefits of new, complex statistics from the statistician's point of view. When are new methods really useful, and when do they just enable statistical machismo? What are the tradeoffs between robustness, ease of use, transparency, and correctness? Is providing easy-to-use software doing users a favour? How often do our new methods solve problems that ecologists really need solved?

The Problem with Parameter Redundancy

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Keywords: capture-recapture, survey design and analysis, identifiability, simulation

Abstract: Consider the time-dependent Cormack Jolly Seber model, which is based on capture-recapture data. This has the last survival and last capture probabilities only ever appearing as a product and therefore they cannot be independently estimated. This is an example of parameter redundancy or non-identifiability of the parameters. In more complex models, it is not always as obvious that the model is parameter redundant (see for example Cole *et al*, 2010).

There are several characteristics of a parameter redundant model. Such a model does not have a unique maximum likelihood estimate as there will be a flat ridge in the likelihood surface (Catchpole and Morgan, 1997). In addition, the expected information matrix will be singular (Rothenberg, 1971) so that it is not possible to find standard errors. To use a parameter redundant model some form of constraints or a robust design is needed.

In practise, most ecology models are fitted using numerical methods so the flat ridge might not be obvious and therefore missed, or the approximate expected information matrix may not be singular. When fitting a model if standard errors are defined it is assumed that the model is not parameter redundant. However, this is not always the case. It is possible for parameter redundancy to be missed in a naive fit of a model. Using simulation, we demonstrate that up to half of models that are fitted naively are not obviously parameter redundant, and any estimates derived from these models can be biased.

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Hidden Markov and related models as powerful and versatile devices for modelling ecological time series

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Keywords: latent-state model; maximum likelihood; state-space model; Viterbi algorithm

Abstract: The class of hidden Markov models (HMMs) is fairly easily accessible, yet it constitutes an extremely powerful toolbox for conducting statistical inference in surprisingly many ecological scenarios. In this talk, I will briefly review some of the key inferential tools available for HMMs, including maximum likelihood estimation, state decoding and pseudo-residuals for model checking. I will also give a short overview of some extensions of the basic HMM framework that I believe to be particularly relevant in ecology. I will attempt to illustrate the usefulness of these models by sketching various areas of ecological applications, including animal movement, capture-recapture, abundance estimation and population modelling.

Title:
A multi-event capture-recapture model to account for mark loss: comparison of monitoring protocols in the southern elephant seal as a case study.

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Abstract:

Monitoring of wild populations has generated a large number of studies investigating ecological processes, as well as conservation and management issues. In this approach, the monitoring protocol is a central element, balancing the information collected against the effort needed in the field. The quality and quantity of the data can set some limits to the analysis and lead to severe biases in conclusions about ecological systems if overlooked. However, the performance of population monitoring protocol has rarely been assessed in the long term. In individual-based capture-mark-recapture monitoring programs, data analysis relies on the assumptions that marks are not lost. However, this assumption is rarely met for a range of taxa. Although post hoc correction of demographic parameters for mark loss has been used to account for surviving animals that are not recognized, this approach has some limitations. Accurate mark loss rate may be difficult to estimate in the wild without additional experimental support. Also, it does not account for a potential influence of mark type or localization on observation parameters.

At Marion Island, southern elephant seals are individually marked with two tags that can be lost. A change in the monitoring protocol took place ten years ago to improve detection probability and reduce fieldwork effort. This offers a unique opportunity to compare different marking localization on a single wild population and to assess monitoring design in the long-term. Here we propose a multi-event capture-mark-recapture model to estimate the impact of the marking protocol on both state (mark loss) and observation (detection, uncertainty and error) parameters, while accounting for imperfect source of information (transience, imperfect detection and state uncertainty). We discuss our results to alert researchers and managers to the importance of choosing an appropriate protocol, depending on ecological constraints and monitoring objectives, in this and other populations.

Keywords:
capture-recapture, survey design and analysis

Misidentification in mark-recapture: have you got the moves?

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Keywords: Misidentification; Null basis; Markov basis

Abstract: Misidentification in mark-recapture studies can lead to biased estimation and inaccurate decision making. Link et al. (2010) proposed a solution when the observed data can be expressed as a linear function of known configuration matrix $\boldsymbol{A}$ and latent (correctly identified) data $\boldsymbol{x}$ with corresponding model $f(\boldsymbol{x}|\theta)$. Fitting the model via MCMC is challenging since $\boldsymbol{x}$ must satisfy the linear constraint. Link et al. overcame this difficulty by (i) finding a set of vectors (called moves) that form a basis for the null space of $\boldsymbol{A}$, and (ii) using these moves one-at-a-time to go between legitimate values of $\boldsymbol{x}$. However, we give examples that show that the approach of Link et al. may not be sufficient to produce an irreducible Markov chain; there may be (at least) two data vectors $\boldsymbol{x}_1$ and $\boldsymbol{x}_2$ that we cannot transition between when applying the moves one-at-a-time, yet both satisfy the linear constraint. To solve this problem, we consider the notion of a Markov basis; a larger set of vectors (moves) that form a spanning set for the null space of $\boldsymbol{A}$ that ensure irreducibility of the Markov chain when using one-at-a-time to update $\boldsymbol{x}$. We illustrate the use of a Markov basis for the examples considered earlier.

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Efficient and flexible MCMC algorithms for capture-recapture using the NIMBLE software package

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Keywords: capture-recapture, population dynamics

Abstract: Capture-recapture analyses have a long history in the field of ecological statistics, providing inference for a variety of population parameters. In the absence of individual random effects, a closed-form likelihood function for capture-recapture models is often available, providing a direct means for likelihood-based calculations. However, the inclusion of random effects for individuals, sites, or sampling occasions often leads the analyst to rely upon MCMC algorithms. The use of mainstream MCMC software (e.g. WinBUGS) requires specifying a binomial response for each sampling occasion, along with latent states when individuals are not detected, rather than directly evaluating the capture-recapture likelihood. MCMC sampling of the population parameters of interest is thereafter hampered by the inefficient calculation of capture history likelihoods and the interlaced sampling of latent states, which may lead to poor mixing and slow convergence. Using the new NIMBLE software package, we show how capture-recapture likelihoods can be built directly into a BUGS model specification to greatly improve algorithmic performance. This native specification also allows the unrestricted use of other numerical algorithms, in addition to MCMC. In models with individual state uncertainty, such as multi-state capture-recapture, we show how a hybrid ”MCMC-filtering” algorithm can be implemented, in which MCMC sampling is used for some parameters, but individual capture history likelihoods are calculated via direct filtering. This MCMC-filtering algorithm is applied to the well-known European dippers dataset (Lebreton et al., 1992), and results are compared to those using WinBUGS.

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Measuring Lack-of-Fit of a Bayesian Model

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Keywords: Bayesian model, lack-of-fit, overdispersion, posterior predictive p-value

Abstract: When using the Bayesian framework to fit a model, it is common practice to use posterior predictive checking as a means of assessing lack-of-fit. In particular, the posterior predictive p-value is often used to help decide whether the model needs to be improved. We propose a new type of posterior predictive check that quantifies the amount of lack-of-fit of the model. We use examples to illustrate the benefits of this new tool, and compare it with the posterior predictive p-value.

A hidden Markov model framework for occupancy modeling.

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Keywords: hidden-Markov model; dynamic occupancy models; E-SURGE.

Abstract: Occupancy – the proportion of area occupied by a species – is a key notion for addressing important questions in ecology, biogeography and conservation biology. Occupancy models allow estimating and inferring about species occurrence while accounting for false absences (or imperfect species detection). We show that most occupancy models can be formulated as hidden Markov models (HMM) in which the state process captures the Markovian dynamic of the actual but latent states while the observation process consists of observations that are made from these underlying states. The HMM framework provides a powerful alternative to the Bayesian state-space implementation of occupancy models. In particular, we show how occupancy models can be implemented in program E-SURGE, which was initially developed to analyse capture-recapture data in the HMM framework. Replacing individuals by sites provides the user with access to several appealing features of E-SURGE like, e.g., i) user-friendly model specification through a SAS/R-like syntax without having to write custom code, ii) decomposition of the observation and state processes in several steps to provide flexible parameterisation, iii) up-to-date diagnostics of model identifiability and iv) advanced numerical algorithms to produce fast and reliable results (including site random effects). Examples are provided, and gathered in a wiki platform http://occupancyinesurge.wikidot.com/.

Inferring on innate locust behavior with individual based models and an information criteria

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Keywords: individual-based models; multi-model inference; animal behaviour.

Abstract: Locusts are grasshopper species that change behaviour, physiology, morphology and life history in response to crowding. This extreme form of phenotypic plasticity is called phase polyphenism. Two extremes are characteristics of phase polyphenism: a solitarious cryptic phase and an aggregating colourful gregarious phase that confers to locusts the capacity to create large destructive hopper bands and adult swarms. Desert locust, *Schistocerca gregaria*, is one of the most infamous locust species, transmitting epigenetically phase characteristics to its progenies. However, recent laboratory works argued on an identical aggregating behaviour at hatching time among progenies of solitarious and gregarious mothers.

We conducted 17 laboratory experiments to test the effect of different mother histories on innate locust behaviour. Eggs from grouped or isolated mothers were placed in an arena with climbing sticks for the new born. We measured aggregation and activity on these sticks from photo recording. These laboratory experiments were coupled with an individual-based modelling approach. The model was built to mimic the experiments and the data collection through individual history and behaviour. The objective was to compare three competing model versions of locust behaviour. Multiple criteria of laboratory data (aggregation and activity) were used to adjust and sample parameters related to locusts' behaviour with Metropolis sampling for each model version and each experiment. The POMIC approach (Piou et al. 2009) was used to compare the different model versions. Both origins of eggs were showing aggregating behaviour in some experiments, but in some other, random movement was enough to explain aggregation and activity measures. The modelling approach is promising but further laboratory data are necessary to be more conclusive.

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Vertical migrations of Bigeye tuna:
A time series analysis based on dynamic optimal foraging

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Keywords: Bigeye tuna, vertical migrations, dynamic optimal foraging, time series analysis, gray box modeling.

Abstract: Bigeye tuna is known for remarkable vertical migrations between deep layers, where food is abundant but the water is too cold to maintain high swimming speeds, and the surface, where water is warm but food is scarce. In a modeling study, we have investigated if these dive patterns can be explained by dynamic optimal foraging theory, where the individual tuna aims to maximize its average energy gain rate. Using a state-space approach, where the tuna is characterized by its mean body temperature and its vertical position, we solve this dynamic optimization problem numerically using dynamic programming. Unknown parameters are estimated statistically based on time series of depth, ambient water temperature, and body temperature, measured at the individual. The time series analysis follows the gray box paradigm and employs a predictive filter based on stochastic differential equations to evaluate the likelihood function. The study reveals lack of robustness of the maximum likelihood estimator, which can be attributed to fast sampling in combination with unmodeled fast dynamics, and which can be remedied by extending the prediction horizon of the filter, thus departing from the maximum likelihood framework. The final model, being conceptually simple while technically sophisticated, is able to explain the main patterns in the data, although not all features, which we discuss. We find that the optimal strategies bifurcate from constant-depth strategies to vertical migrations, when the tuna is sufficiently large or the food is at sufficiently cold water layers. The study demonstrates the feasibility of combining dynamic optimization models with time series analysis, all in a consistent state-space framework. The analysis supports the hypothesis that the tuna behaves such as to maximize its net energy gains, and allows to predict foraging behavior in unobserved environments, for example in future scenarios.

Modelling movement and activity patterns in black eagles *Aquila verreauxii*

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Keywords: individual-based models; modelling of animal movement; movement ecology; spatial ecology

Abstract: Tracking data from black eagles were collected to investigate their movement and activity patterns, as part of the first dedicated study of their breeding ecology and conservation status in the Western Cape, South Africa. Telemetry tags were deployed on five adult birds in 2012 and 2013, in two areas. Two tags were deployed on birds in the relatively pristine Cederberg mountains, and three in the heavily agricultural Sandveld region. The Cederberg has low prey diversity and a high variability in temperature, compared to the Sandveld where there is higher prey diversity, but less suitable nesting habitat, and a milder climate. These factors, among others, are likely to result in different movement and activity patterns of eagles living in the two areas. The movement data include high temporal resolution GPS location data, altitude, and three-axis acceleration data. Speed is problematic for inferring movement in soaring birds, since they can appear stationary in terms of speed relative to the ground while soaring. In addition, the steep relief of the cliffs they nest on and the outcrops they perch on, regularly results in poor quality GPS locations while they are stationary. Acceleration measurements are comparatively noise-free and can be used to infer activity patterns and posture. We develop

a two-state Bayesian mechanistic model, using minimum specific acceleration to estimate the behavioural state associated with each GPS location. We use a simple distinction between "flying" and "perched". This approach allows for an early comparison of activity patterns in the two regions where birds were tagged, and provides a starting point for the development of more complex models of bird movement e.g., including environmental covariates.

Dealing with incomplete data in survival analysis: A model based on probabilistic prior information on time of occurrence

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Keywords: individual-based models, survey design and analysis, proportional hazards, left-truncation

Abstract:

Efficient methods have been described to deal with incomplete data when modelling survival through lifetime analysis. However, some cases of left-truncated data may still be a source of bias in parameter estimation of these models. This is especially true in plant survival studies where the time of occurrence (i.e. establishment) t_i of an observed individual i is unknown. In the present work we propose a method to cope with this shortcoming based on prior probabilistic information on t_i. In order to illustrate it, a dataset of *Pinus pinea* seedling survival in Central Spain was used. The data consisted on interval- and right-censored observations. Left-truncation was also present because seedlings did not enter the experiment at germination time (t_i), which was also undefined. A proportional hazards model was fitted to these data, the likelihood function being defined accordingly as to consider all forms of data incompleteness. However, the likelihood for seedling i cannot be referred to a specific time of emergence, since there are as many values of t_i as days where germination was possible. Therefore, the likelihood for all possible values of t_i needed to be calculated, the resulting outputs being weighted by the corresponding germination probability obtained from a predicted germination probability mass function (pmf_i), and eventually summed over. In our case, pmf_i was derived from an existing germination model for the species but whatever sensitive prior probability mass function could have been used. Provided that the exact information on t_i is not available in most datasets based on field experiments, the proposed methodology may be of great interest for ecologists, overcoming the current limitations of survival analysis.

From integrated population models to integral projection models

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Keywords: continuous states; individual-based models; integrated population models; population dynamics.

Abstract: Multiple types of data have been collected on a single population and analysed separately as each type of data provide information on parameters of interest, for example productivity counts provide information on fecundity and recapture data provide information on survival. However, developments of integrated population models (Besbeas et al, 2002) broke this trend, when it was shown that multiple data sets with parameters in common could be coherently modelled in order to provide the best estimates for demographic parameters.

It has been shown that many capture-recapture models can be fitted using a state-space framework (Gimenez et al, 2007). State-space models require the assignment of individuals to a set of discrete states. For some applications this may be trivial, such as age-stage assignment, or classification by sex, however as more individual time-varying data is being collected it may be of use to consider a model which includes the potential to incorporate continuous states. Integral projection models, first proposed for ecological application in Easterling et al, (2000), provide the means to incorporate continuous states.

Currently, approaches are piecemeal in nature, and parameter estimates are obtained separately from component data sets; see for example Coulson et al, 2010. This talk will present current research on the simultaneous estimation of parameters of interest within the integral projection model.

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Animal migration modelling: an analytical description of the two-dimensional time-integrated Brownian bridge

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Keywords: modelling of animal movement, spatial ecology, movement ecology, individual-based models

Abstract: Both monitoring and modelling help to gain insight into the dynamics of animal migration. The delineation of important regions for the studied species is one possible goal of a monitoring campaign. This can be achieved by determining the probability distribution function (PDF) or the probability density that an animal is located at a certain location at an arbitrary point in time. In order to account for the relative amounts of time the animal has spent in various regions and for the chronological order of the data points, continuous trajectories should be used instead of discrete measured locations. The construction of such trajectories can be achieved by assuming random movement between the data points. The process of random movement restricted by a starting and ending location is called a Brownian bridge (BB) and is used in the Brownian Bridge Movement Model [1, 2]. More specifically, the latter constructs the PDFs of the BBs at several time instances between every two consecutive observations. The resulting PDFs are then integrated over time in order to determine the PDF of the time-integrated BB. This PDF describes the probability density that an animal is located at a certain location at an arbitrary time instant in the considered time interval and thus delineates important regions. To the best of our knowledge, the integral is always computed numerically. Therefore, an analytical description is derived since this would be more accurate and speed up the calculations.

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Calibrating process-based models using several data sources and Approximate Bayesian Computation: illustration with a forest simulation model

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Keywords: individual-based models; multispecies models; forest dynamics; Approximate Bayesian Computation

Abstract: Ecological research increasingly relies on model-based inference. Often, models are too complex, or available data too coarse, so that standard likelihood-based methods cannot be used to estimate the model parameters. In those cases, a number of likelihood-free methods have been proposed. However, these methods rely on intensive model simulations, so that most applications have been restricted to relatively simple models with few parameters. In this study, we were interested in the use of such methods with more complex models involving a large number of parameters. Our case study was the calibration of the individual-based forest model Samsara2. The initial model calibration, carried out with detailed data, was used to estimate prior knowledge. Low-informative data coming from historical management were then used to test the limitations of current Approximate Bayesian Computation (ABC) approaches. We addressed three questions: (1) Is it possible to reach a reasonable posterior approximation of model parameters with a drastically limited number of simulations and relatively coarse data? (2) How many model parameters can be estimated with this approach and is this number limited by the number of simulations? (3) How much estimated parameters uncertainty is increased when propagating other model parameters uncertainties? With a relative small number of simulations and an appropriate choice of the model parameters, we demonstrated the relevance of the ABC technique to calibrate a complex model such as Samsara2. Our approach illustrates how detailed knowledge on ecological processes drawn from the literature or from detailed field studies can be combined with more widely available coarse data to calibrate complex mechanistic models. This approach potentially enables to perform the calibration of complex models to a large number of field sites, for which coarse data are available, instead of being restricted to the few sites were detailed studies have been conducted.

Point process model solutions to presence-only data problems

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Keywords: species distribution models

Abstract: Often, the best available data for species distribution modelling is so-called "presence-only" data, which consists of a list of observed species locations with no corresponding information about species absences. A number of methods have been developed to create species distribution models using presence-only data, in particular MAXENT and pseudo-absence logistic regression. Most of these methods face challenges in implementation, interpretation and checking model assumptions.

These challenges can be addressed by instead using Poisson point process models, which have been shown to be equivalent to pseudo-absence logistic regression (Warton and Shepherd 2010) and MAXENT (Renner and Warton 2013). In particular, I will show how the point process model framework offers to solutions to the questions of how to choose pseudo-absences, how to account for sampling bias (Warton, Renner and Ramp 2013), how to interpret model output, how to assess model assumptions, and how to choose the LASSO penalty to regularise model coefficients.

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Towards AIC-like model weights and model averaging of black-box models

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Keywords: AIC, degrees of freedom, non-parametric model, machine learning

Abstract: Machine-learning methods such as neural networks or boosted and bagged approaches are currently combined with more parametric methods in a typically unweighted fashion. The reason is that no AIC (or equivalent) can be computed for them, as the number of parameters in a model fit cannot be readily quantified. We here present an approach based on Generalised (or Effective) Degrees of Freedom and illustrate its application with a species distribution analysis. This approach offers some potential, but also has some computational drawbacks. We shall therefore also present an alternative based on cross-validation.

Fast forward selection for correlated clustered data with a large number of predictor variables

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Keywords: Generalized Estimating Equations; Model Selection; Multivariate Analysis; Negative Binomial Regression; Score Statistics; Trait/Environment Relationship.

Abstract: We propose a new variable selection criterion designed for use with forward selection algorithms; the score information criterion (SIC). The proposed criterion is based on generalized estimating equations (GEE) and score statistics which incorporate correlated response data. The main advantages of SIC, as compared to competing GEE information criteria, are: (1) it is much faster to compute than existing model selection criteria when the number of predictor variables added to a model is large; (2) it incorporates the correlation between variables into its quasi-likelihood. Our motivating example arises in ecology, and involves selecting from a large number of interaction terms in order to explain environmental-trait association in an arthropod community. In addition to applying SIC to the arthropod data, we also show by theory and simulation that SIC has a number of desirable properties, such as model selection consistency and efficiency.

Model selection for spatially adaptive two dimensional smoothers using a spatially adaptive smoothing algorithm (SALSA2D)

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Keywords: species distribution models, spatially adaptive smoothers,

Abstract: The distribution of animals in a surveyed area can often be highly uneven and thus frequently benefit from modelling methods which permit some areas of the surface to be (markedly) more flexible than others. Recently developed spatially adaptive smoothing methods allow for differential amounts of flexibility across the surface (e.g. Scott-Hayward et al, 2013) however this can add to the model selection task. The spatially adaptive smoothing algorithm (SALSA) developed for one dimensional smoothers (Walker et al, 2011) has been extended for two dimensional applications to meet this model selection task (SALSA2D) and target model flexibility across the surface. The performance of SALSA2D is compared with other spatially adaptive methods with good results. Results are presented for simulated data and illustrated using an environmental impact assessment (EIA) example.

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hSDM, an R package for hierarchical species distribution models taking into account imperfect detection and spatial correlation of the observations.

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Keywords: biodiversity; Bayesian approach; conditional autoregressive model; site-occupancy model; N-mixture model;

Abstract:

Imperfect detection of individuals (Iknayan et al., *in press*) and spatial correlation of the observations (Lichstein et al., 2002) must be taken into account to obtain unbiased estimates of species distribution from presence and count data.
To do so, hierarchical Bayesian models that incorporate multiple hierarchical processes (detection process, suitability process and spatial correlation process) provide a promising way forward (Latimer et al., 2006). These hierarchical models are relatively complex and beyond the experience of many potential users (Iknayan et al., *in press*). Classical softwares used for hierarchical models (such as WinBUGS) usually fail at estimating the parameters of such complex models for large data-sets (number of spatial cells superior to tens of thousands).
Here we present the hSDM R package to estimate the parameters of site-occupancy (MacKenzie et al., 2002) and N-mixture models (Royle, 2004) for large data-sets. Models take into account the spatial correlation of the observations. Functions from the hSDM R package provide user-friendly and fast implementations of these models that would facilitate their use and acceptance by the scientific community in ecology.

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Incorporating spatial autocorrelation into species distribution models alters forecasts of climate mediated range shifts

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Keywords:species distribution models, spatial autocorrelation, mangrove, sea level rise, climate change, Boosted Regression Tree (BRT) models, Generalized Boosting Models (GBM).

Abstract: Species distribution models (SDMs) are widely used to forecast changes in the spatial distributions of species and communities in response to climate change. However, spatial autocorrelation (SA) is rarely accounted for in these models, despite its ubiquity in broad-scale ecological data. While spatial autocorrelation in model residuals is known to result in biased parameter estimates and the inflation of Type I errors, the influence of unmodeled SA on species' range forecasts is poorly understood. Here we quantify how accounting for SA in SDMs influences the magnitude of range shift forecasts produced by SDMs for multiple climate change scenarios. SDMs were fitted to simulated data with a known autocorrelation structure, and to field observations of three highly spatially autocorrelated mangrove communities from northern Australia. Three modelling approaches were implemented: environment-only models (most frequently applied in species' range forecasts), and two approaches that incorporate SA;autologistic models and residuals autocovariate (RAC) models. Differences in forecasts among modelling approaches and climate scenarios were quantified. While all model predictions at the current time closely matched that of the actual current distribution of the simulated organism and the mangrove communities, under the climate change scenarios environment-only models forecast substantially greater range shifts than models incorporating SA. Furthermore, the magnitude of these differences intensified with increasing increments of climate change across the scenarios. When models do not account for SA, forecasts of species' range shifts indicate more extreme impacts of climate change, compared to models that explicitly account for SA. Therefore, where biological or population processes induce substantial autocorrelation in the distribution of organisms, and this is not modelled, model predictions will be inaccurate. These results have global importance for conservation efforts as inaccurate forecasts lead to ineffective prioritization of conservation activities and potentially to avoidable species extinctions.

Using Dempster-Shafer's evidence theory for species distribution modelling

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Keywords: citizen sciences, spatial ecology, species distribution models

Abstract: Conservation managers rely on the knowledge of experts where information describing species distribution is scarce or unobtainable. However, experts' knowledge is always subject to uncertainty and accounting for this uncertainty into a modelling procedure poses a challenge. We propose using the Dempster-Shafer Theory of Evidence (DST) to accommodate knowledge uncertainty, and assess how this affects the performance of species distribution models. We applied DST to model the distribution of a well-known, and a poorly-studied raptor species in Spain. We invited experts to form a knowledge domain, and asked them through online questionnaires to express their knowledge on the habitat of the target species by assigning a probability value for a given environmental variable. Experts were also asked to acknowledge their confidence level on the assigned probability values. Then we calculated evidential belief functions and combined them using Dempster's rules of combination. We evaluated and compared the calibration and discrimination capacity of the DST models with two other conventional inductive models. The DST models yields similar results to conventional inductive methods for both species. Although the habitat of the well-known species was well-discriminated, DST models were generally underestimating the habitat favourability. In contrast, the models for the poorly-studied species were well-calibrated though the discrimination capacity remained low. Our proposed approach offers a practical alternative where knowledge of a species' geographic distribution is needed, and the distribution data is not sufficient. The particular strength of the developed approach is that it explicitly accommodates knowledge uncertainty. It also provides a framework to propagate and aggregate uncertainty, and it capitalizes on the range of data sources usually considered by an expert.

Bayesians, frequentists, and pragmatists: the interaction of methods and software.

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Abstract: Ecologists take pride in statistical pragmatism, doing "whatever works." I will attempt to unpack this sense of pragmatism specifically for hierarchical statistical models and look at how it involves a swirl of principles and practices. Moreover, one's sense of pragmatism depends on available software, yet the statistical literature abounds with ideas for numerical methods for hierarchical model estimation, prediction, and diagnostics that are not readily available in software. On simple goal in principle would be to critically evaluate Bayesian results from a frequentist perspective, but this is rarely done because it is not practical. Some complex algorithms for some hierarchical models are available, while some simple algorithms are not. Therefore, the future of pragmatism is tied to the future of software. I will present progress on a new software package that allows flexible programming of algorithms that operate on shared model structures. This means that rather than tying specification of a model structure to a particular algorithm, such as one flavor of MCMC provided as a "black box", one can specify a model structure and run a variety of algorithms on it. Since algorithms can be concisely programmed, the system is naturally extensible and provides a way to disseminate new methods.

Hierarchical Bayesian model for a strip-transect survey employing intense search units

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Keywords: population dynamics; survey design and analysis;species distribution models

Abstract: Sea otters (*Enhydra lutris*) were reintroduced to southeast Alaska in the 1970s. Aerial strip-transect surveys were conducted in northern southeast Alaska in 2002 and 2010 and southern southeast Alaska in 2003 and 2011 to monitor the population size and range expansion. Intense search units (ISUs) were conducted during the surveys prior to 2011 to estimate detection probabilities. An ISU is searched by flying five concentric circles around a group of otters sighted on the transect. The ISU data will be explicitly incorporated into a hierarchical Bayesian model and used to estimate sighting probabilities and sea otter density. The Bayesian model partitions the survey data into a process model that describes the population density and an observation model that describes the sampling error. The hierarchical Bayesian approach provides a flexible framework to quantify the observer-specific observation error for each survey, and a hierarchical approach can be used to describe variation in observer error between different habitat types or survey sub-regions. The results of this analysis will allow for estimates of local density and growth rates in specific habitats, as well as associated uncertainty. The Bayesian model will be used to estimate a detection probability and sea otter density from the 2011 survey, which did not conduct ISUs. The population estimates and sighting probabilities from the Bayesian analysis will be compared to results estimated using a maximum likelihood approach.

Inferring habitat use, population distribution and total population size by combining individual-level and population-level data

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Keywords: abundance; population dynamics; spatial ecology

Abstract: Winter track counting is a non-invasive population survey method developed for terrestrial mammals. We represent a spatio-temporal Bayesian smoothing model extending the classical result to convert transect crossing counts of animals to population density. The model combines population-level counts with individual-level movement activity and habitat use from GPS tracking information. We infer the movement activity from individual traits and biotic and abiotic factors, with a correction for straight-line distance bias, and the habitat use with a step selection function approach. Furthermore, we adjust the results to match with the population using removal statistics. We demonstrate use of the model with a survey of large temporal and spatial scale and verify population size estimates with assessments from independent sources.

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Population trends and density: a spatial modeling approach applied to the exploited giant clam *Tridacna maxima* in French Polynesia

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Key-words: Population dynamics - Metapopulation dynamics – Spatial ecology – Abundance – Capture-recapture

Abstract: The giant clam *Tridacna maxima* has been largely overexploited in many tropical regions over the past decades and is listed in appendix II of the Convention of International Trade in Endangered Species (CITES) since 1985. In French Polynesia, several atolls and islands harbor the world's highest densities of giant clams in very shallow and accessible areas. These stocks are vulnerable to fishing pressure and massive (but natural) mortality events, and management actions are required to sustain resource uses on the long term.

Here, we report on the use of a spatially-explicit population dynamics model applied to 1/ the clam population of Tubuai Island (Austral archipelago) affected by high fishing pressure (deterministic approach) and 2/ the population of Tatakoto (Tuamotu archipelago) affected by both fishing pressure and observed natural mortality events (stochastic approach). Giant clam abundances were estimated *in situ* in 2004/2010 and in 2004/2012/2013 in Tubuai and Tatakoto respectively. Growth, mortality, and recruitment were also estimated *in situ* in 2007 and alimented the model. When compared to field data, the model successfully predicted stock evolution from 2004 to 2010 and from 2004 to 2013 for Tubuai and Tatakoto respectively. The size-based population model also predicted future *T. maxima* abundances when populations were submitted to different management strategies (quotas, closure, rotational closure, size limits). For Tubuai, where abundances were primarily dependent on recruitment processes, spatial modelling suggested that reducing fishing effort (through fixed quotas) and banning fishing below the 12 cm size limit (as currently implemented) were the most effective management actions. By contrast, in Tatakoto where abundances were a trade-off between recruitment and random high mortalities, spatial modelling suggested that fishing effort had low impact on giant clam abundance. Management effects could be of secondary order for this atoll to maintain population when compared to natural stochastic processes.

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New models for reptile and amphibian removal data

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Keywords: abundance; population dynamics; survey design and analysis

Abstract: Removal experiments involve successively sampling a closed area for particular animal species and each time removing those individuals found. The objective is to estimate the number of animals in the area, and probability models date from Moran (1951) and Zippin (1956).These removal models result in geometric declines of expected numbers of individuals in the area as time progresses and the removals take place. When removals are conducted on cryptic species, such as reptiles and amphibians, the animals removed on one sampling occasion may be replaced by other individuals which might have previously remained undetected below ground. In these cases more complex models are needed to account for the apparent appearance of new animals in the study area.

We are motivated by removal data on slow worms, *Anguis fragilis*, common lizards, *Zootoca vivipara*, and Great crested newts, *Triturus cristatus*. These protected species are frequently removed from the path of development. In some cases there are known reductions to the site area available following removals. In others such information is not available, and stop-over models are instead employed; see Matechou et al (2013). In all illustrations it is possible to undertake model selection, and much improved descriptions of data are obtained, with associated estimates of population size. The use of both classical and Bayesian methods of inference will be illustrated, in the latter case using RJMCMC.

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Covariate measurement error and species distribution models: an important source of bias?

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Keywords: species distribution models, logistic regression, interpolation, prediction

Abstract: As is well known for linear and nonlinear regression models, covariate measurement error in species distributions models (SDMs) may lead to biased regression coefficient estimates and biased predictions (e.g., Carroll et al. 2006). However, understanding the direction and level of bias requires that the structure of measurement error is well known (e.g., Reeves et al. 1998). In particular, measurement error rarely has a simple structure: it often has a systematic component, is not additive and does not have a constant variance. Taking the example of climatic data from the Alps and northern Norway, we first describe the structure of measurement error for temperature and precipitation. We then show that bias in SDMs is likely to be much more severe for precipitation than for temperature, due to the difficulty in interpolating precipitation in mountainous areas. We finally evaluate if different methods (e.g., Reeves et al. 1998, Carroll et al. 2006) correct the observed biases of regression coefficients and predictions.

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Imperfect detection impacts on the performance of species distribution models

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Keywords: species distribution models.

Abstract: Species often remain undetected at sites where they are present. However, the impact of imperfect detection on species distribution models (SDMs) is not fully appreciated. We evaluate the influence of imperfect detection on the calibration and predictive discrimination of SDMs. We compare the performance of three types of SDMs: (1) a technique based on presence–absence data, (2) a technique based on presence–background data, and (3) a technique based on detection/ non-detection data that accounts for imperfect detection. We use simulations to evaluate the impacts of imperfect detection in SDMs in terms of how well they characterise the true spatial distribution. We study a range of occupancy and detection scenarios based on ecologically plausible environmental relationships and identify the circumstances in which imperfect detection affects model calibration and discrimination. We show that imperfect detection can substantially reduce the inferential and predictive accuracy of presence–absence and presence–background methods that do not account for detectability. While calibration is always affected, the influence on discrimination depends on the relationship of detectability and environmental variables.
The performance of a model should be assessed with respect to its objectives. Comparative studies that assess the performance of an SDM by evaluating its ability to predict detections (e.g. Rota et al. 2011; Compte & Grenouillet 2013) rather than presences fail to reveal the benefits of accounting for detectability. We find that disregarding imperfect detection can have severe consequences for SDM performance, and hence for the estimation of species distributions. To date, this issue has been largely ignored in the SDM literature. Simultaneously modelling occupancy and detection does not necessarily require a greater sampling effort, but rather that data are collected and recorded so that they are informative about detectability. We recommend that consideration of imperfect detection become standard practice for species distribution modelling.

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Criteria for selecting species distribution models for management decisions

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Keywords: occupancy models; spatial ecology; species distribution models; survey design and analysis.

Abstract: Selection of species distribution models is often based on information criteria (e.g., AIC) or discrimination ability (e.g., area under ROC curves). However, when species distribution models are developed for particular management purposes, the model from a set of candidates that best supports management decisions should be selected. Determining this *a priori* is difficult. Species distribution models can assist searches for rare or invasive species (Hauser and McCarthy 2008). In this case, the probability of detecting a species at site *i*, given it is present, increases with search effort at that site (x_i). For a random encounter model, this probability of detection is $1 - \exp(-bx_i)$, where *b* is the detection rate when the species is present. The probability the species is present at each site (p_i) is predicted by a species distribution model. When a budget of search effort *B* is available, the allocation to each of *k* sites that minimizes the expected number of sites where the species is present but remains undetected is

$$x_i^* = \frac{B}{k} + \frac{\ln p_i}{b} - \frac{\ln \bar{p}}{b},$$

where $\bar{p}$ is the geometric mean of the values of p_i. The expected number of sites with missed detections is

$$L_{\min} = \exp(-b\frac{B}{k})\bar{p}k.$$

However, this will be a biased estimate of performance if the predicted probabilities of presence are imprecise. The expected bias in performance can be estimated depending on uncertainty in the values of p_i. Assuming beta distributions for the uncertainty (with parameters a_i and b_i for each site), the proportional bias is expected to be:

$$\text{Bias}_{\text{beta}} = \bar{f}\sum_{i=1}^{k} a_i(a_i + b_i - 1)/[(a_i - 1)(a_i + b_i).$$

where $\bar{f}$ is the geometric mean of the estimated probabilities of presence. An approximate estimate of the proportional bias for any assumed distribution is

$$\text{Bias} = \bar{f}\sum_{i=1}^{k}(1 + c_i^2),$$

where c_i is the coefficient of variation of the prediction at each site *i*. This helps consider trade-offs between species distribution models with smaller geometric mean predictions ($\bar{f}$) and those with less uncertainty in those predictions (c_i).

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Accounting for species detectability is not a waste!

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Keywords: detectability, imperfect detection, occupancy estimation

Abstract: It has long been recognized that detection is often imperfect in wildlife surveys, and that this can bias the estimators of ecologically relevant state variables. As a response to this problem, a suite of statistical methods have been developed that account for detectability, aiming to provide more reliable estimates. "Detectability-aware" methods are generally considered a step forward with respect to approaches that naïvely ignore detection issues. However, recent published work (Welsh et al. 2013) strongly questions the usefulness of models that estimate species occupancy while accounting for detectability. Claims include that these models are difficult to fit and that disregarding detectability can be better than trying to adjust for it, with authors concluding that adjusting for non-detection "is simply not worthwhile". In this talk I will explain why we think that these conclusions and related recommendation are not well founded and may have a negative impact on the quality of statistical inference in ecology. In particular, I will show how it is the choice of specific scenarios used to support these negative claims that provides a distorted picture of the actual value of accounting for detectability (Guillera-Arroita et al., in review).

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Analysing opportunist data in Citizen Sciences: statistical modelling for loose protocols

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Keywords: citizen sciences, bigdata, species distributions, spatial hierarchical model, INLA.

Abstract: Volunteers networks involved in citizen science (SC) programs provide a real opportunity to address conservation and species distributions questions on broad temporal and spatial scales. In the last ten years development of new technologies – smart-phones, friendly user websites – has dramatically increased the volume of collected data and the number of SC programs, but in most cases, with weakly defined and heterogeneous data collection protocols. Opportunist data in our case are data collected by a large number of different observers, whose spatial and temporal distribution is greatly heterogeneous, the effort is usually unknown, zeros are generally unreported, and finally positive count may be reported differently or even censured according to species. To analyse such data we propose a multivariate hierarchical model with latent spatial – spatiotemporal – fields for relative abundances of each considered species. Its specificity is to account for different types of observation and for observer characteristics in distribution or behaviour. First results show that it seems possible to correct several main biases, to model count positive-only data and to infer fairly well relative density maps in a multi-species context, using a Bayesian framework and INLA R-package tools. We analysed a case study data set of several thousand observations from the French Ligue pour la Protection des Oiseaux (LPO, Birdlife France) to show the feasibility of such approaches and we checked the inference quality and limits on smaller simulated examples.

Quantifying the impact of human activity on seabird behaviour: a statistical perspective

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Keywords: Seabirds, foraging, hidden Markov model, GPS tag.

Abstract: Seabirds are a familiar but elusive part of our natural environment, and a vital part of the marine ecosystem. We need to be able to understand the key aspects of their behaviour - such as breeding and foraging - in order to assess the impacts of offshore wind farms, fishing, and other human activities upon their populations.

In this talk we will illustrate an approach by which empirical data from GPS tags and mechanistic stochastic models can together be used to evaluate the impact of human activities upon seabird foraging - and thereby upon breeding success and survival.

A key step in such assessments is the estimation of the spatial distribution of foraging birds, and we will begin by outlining some of the ways in which statistical models - including hidden Markov models and generalized linear mixed models – can be used to address this problem.

A stochastic mechanistic model of seabird behaviour has then been used to explore the consequences of modifications to the environment (such as the construction of a wind farm) upon the energy budgets and daily time expenditure of adult seabirds during chick rearing: and thereby upon adult and chick survival. We will discuss the ways in which this model can be used to evaluate the impacts of potential developments in a way that properly accounts for uncertainty, and will demonstrate some of the results that are obtained by applying this approach to real data.

Building robust abundance indices combining commercial data and scientific survey

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Keywords: abundance; big data; spatial ecology

Abstract: The quality of a stock assessment strongly depends on the quality of the underlying fitted population dynamic model used to investigate the consequence of different harvest rules. The estimation and even the selection of the appropriate model is mainly driven by the abundance indices considered.

Those indices are derived either from marine scientific surveys or obtained with ad-hoc normalisation of the commercial catch, called Catch Per Unit of Effort (CPUE). Data sampled during marine scientific surveys and CPUE often present a high proportion of zeros with, possibly skewed, positive continuous values. In addition for commercial fisheries, the sampling process and the latent biomass process are stochastically dependent since professionals - conversely to scientists - use to concentrate in areas that are thought likely to yield high fish abundance. The spatial locations of the commercial catch provide information on the spatial biomass repartition. Furthermore, because of the spatial structure of the population and of the sampling process, a naive abundance index produces biased estimates of the trends. The spatial aspect of the sampling process has to be accounted for. But zero inflated continuous data and preferential sampling prevent from using standard geostatistical methods. In addition, the fishermen data are cheap but massive and require to use model that can accommodate big datasets.

We develop a model that addresses the two limiting specific features, give a general expression for the likelihood function, and discuss how inference can be performed, at least approximately, using advanced Monte Carlo methods. We finally describe a possible application of such a model to bottom fish data from the continental shelf of the coast of British Columbia, Canada collected both by marine scientists (Ocean and Fisheries, Canada) and by fishermen.

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Multiple Method Inference reveals instability of indexcalibration experiments: counting tigers at macroecological scales

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Keywords: macroecology, abundance estimation, large scale, indices, double-sampling, occupancy.

Abstract: Progress in macroecology has relied heavily on synthesis of multiple studies in the form of “meta-analyses”. Meta-analyses can yield poor inferences because they are usually oblivious to methodological uncertainties arising because multiple studies rarely use similar methods. We propose and demonstrate the power of the Multiple Method Inference (MPMI) approach of “meta-analyses” and resolve a long-standing debate about the value of index-calibration experiments based on linear regression in macroecology. The index-calibration experiment involves rigorous estimation of animal abundance at a small scale to calibrate a, less rigorously derived, “index" of abundance using the R^2 statistic. The calibrated index is then used to draw inferences about animal abundance at a large scale using the index. In this paper, we first derive the constituent elements of the R^2 statistic of such index-calibration experiments, and discuss the stability of such R^2 statistics. We then confront these theoretical derivations with an empirical study using the MPMI approach to ‘link’ results of some recent, large-scale, assessments of tiger *Panthera tigris* distribution and abundance across India. These results have overarching implications on similar macroecological, resource-intensive, studies that attempt to derive explanatory patterns in phenomena such as biological diversity, speciation, and disease ecology.

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