

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

Etienne KLEIN<sup>a</sup>, Aurore BONTEMPS<sup>b</sup>, and Sylvie ODDOU-MURATORIO<sup>b</sup>

<sup>a</sup> UR546 Biostatistiques et Processus Spatiaux (BioSP), F-84914 Avignon, France

<sup>b</sup> UR629 Ecologie des Forêts Méditerranéennes (URFM), F-84914 Avignon, France

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**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.