

Biotic communities are generally expected to be spatially and genetically structured. Phylogeography, biogeography and landscape genetics, among other disciplines, aim to describe these patterns and to reveal the underlying evolutionary processes (e.g. vicariance, dispersion). Among the hypotheses commonly used to explain the spatial genetic structure, the isolation by landscape resistance (IBR) allows to overcome and integrate isolation by barrier (IBB) and isolation by distance (IBD) assumptions.

The assessment of IBR based on least-cost paths analysis has been one of the cornerstone topics in landscape genetics over the last 20 years. Nevertheless, as far as we know, only few studies have tried to integrate past environmental conditions in their analyses, despite the fact that this information might: i) strongly imprints the observed patterns and ii) efficiently explains the current spatial genetic structure. At higher temporal and spatial scales, the relative absence of spatial landscape data of past environmental conditions might explain the quasi-absence of IBR approaches in phylogeographic studies. Fortunately, some recent initiatives (e.g. Land Use Harmonization for IPCC Fifth Assessment Report) have begun to release this kind of data.

Based on a statistical algorithm that optimizes resistance surfaces for least-cost path analysis and historical landuse datasets, we will compare the role of past and present landscapes on the observed spatial genetic structure of some South East Asian rodent populations. First, we will assess the IBR hypothesis for different time-periods. Then, the same analysis will be done using a distance lags approach in order to test a space-time integration hypothesis: the closer are two communities (i.e. geographically), minor will be the impact of ancient landscapes on the IBR. If this hypothesis is acceptable, we expect to show a relation between genetic and geographic distances with the past time since present.