

Using movement models to define metapopulation patch structure based on interaction probabilities

Metapopulation models assume that organisms live and interact within well-mixed patches. Interactions between individuals that affect demographic rates are assumed to only occur within patches, and populations in different patches are connected via dispersal. However, what constitutes a patch for a model of a given landscape is generally based on what researchers perceived as contiguous habitat regions in a landscape, rather than any formal measure of local interaction strength. This ignores the fact that animals moving through that landscape may not perceive patches in the same way as researchers. In the last decade, substantial strides have been made in developing statistical models of how animals choose to move across landscapes. However, these models have not been applied to the problem of how to segment landscapes into patches. In part, this is because quantifying what “well mixed” means when viewed through the lens of movement behaviour.

We propose a new criterion to determine if two locations are part of the same patch: they are part of the same patch if there is a high probability of finding an individual in both locations, and if individuals starting from the two locations have a high probability of encountering one another in a demographically relevant period of time somewhere on the landscape; this interaction probability is the “kinetic distance” between the two points. This metric can account for complex movement patterns such as advection and boundary effects.

We propose a new method based on this metric, “eigenpatch”, for clustering landscapes into patches based on random walk models of movement across the landscape. The eigenpatch method defines patches by translating a movement model of fine-scale rates of movements between locations on a landscape into a dispersal matrix, then using an eigen-decomposition of this matrix to calculate average occupancy rates and kinetic distances between locations, and applying clustering algorithms to the kinetic distance to group regions into patches. We test this method on a range of simulated landscapes and to a movement model of Northern Shrimp populations on the Labrador Shelf to demonstrate the effectiveness of this approach for quantifying metapopulation structure in complex landscapes.