

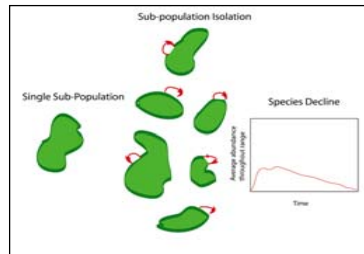
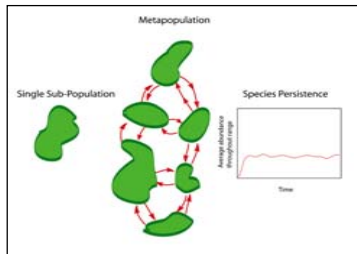


Overview

Habitat loss and fragmentation

are major causes of species decline and extinction. Small populations isolated in habitat fragments are not only vulnerable to edge effects but also to factors such

as demographic instability and the loss of genetic variation through inbreeding and drift. As the distribution of individuals within a species becomes more fragmented these demographic and genetic effects contribute to an “extinction vortex” which may eventually lead to the extinction of the entire species.



Because of the impacts of local dynamics on species at larger scales, there is a connection between the processes that occur within a single population and the persistence of the species on the whole. This connection allows for predictions to be made about species survival based on locally collected data.

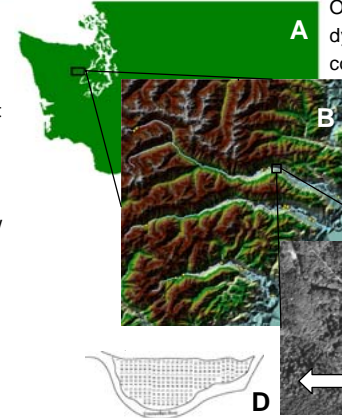


The Pacific jumping mouse is affiliated with habitats (riparian, meadow, and marsh) that are discontinuous throughout its range in the Pacific Northwest. Because of this patchy distribution, semi-isolated groups of animals occur naturally. These

“subpopulations” can be monitored as somewhat distinct units. By understanding how locally collected data relates to larger scale patterns we can better understand how to apply local observations to large scale species risk assessment.

Approach

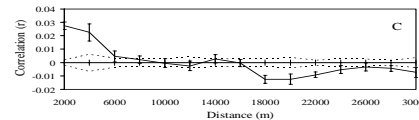
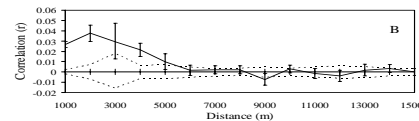
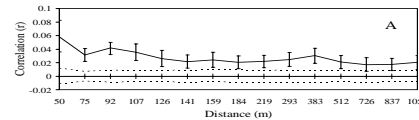
Individuals were sampled from a “metapopulation” within a system of three adjacent river drainages. Each drainage was divided into three subpopulation zones, the mouth, headwaters, and interior. Eight microsatellite loci are being used to investigate patterns of gene-flow and relatedness between the subpopulations. Additionally, within one of the drainages, a single semi-isolated group of individuals was monitored over three years in order to characterize the local breeding structure and the contribution of migrants.



Once we have revealed local migration dynamics and breeding structure we can combine the results with observed patterns of gene-flow and population structure. Through this combination we can begin to reveal how local processes shape long term patterns. The acquisition of results at three hierarchical levels, within a local subpopulation, between subpopulations, and within the metapopulation, allows us to reveal the connection in a stepwise manner and increases our ability to describe the relationship.

A) Study region on the Olympic peninsula of Washington state. B) The three river system (north to south; Dosewallips, Duckabush and Hamma Hamma rivers) and locations of subpopulation samples. C) An aerial photograph of the focal subpopulation site. D) Schematic of the mark-recapture grid covering the local sample area. This trapping grid was used to obtain data regarding home-range, and location of breeders.

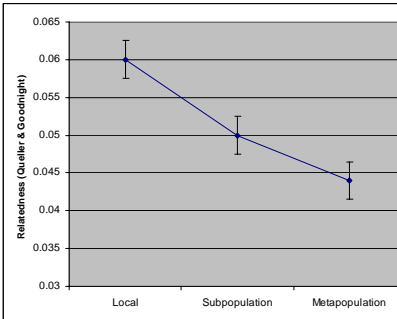
Results...thus far



Spatial autocorrelation correlograms indicating patterns of relatedness between individuals at three scales, local (A), inter-subpopulation (B), and metapopulation (C). A positive correlation at a given distance indicates that individuals within that distance are more closely related than would be expected by chance. A negative correlation indicates a relatedness relationship that is less than expected by chance.

Spatial autocorrelation can reveal the relationship between

the distance between two individuals and their relatedness to each other. The correlograms we obtained across scales reveal limited dispersal at the local scale that creates an isolation by distance pattern at subsequently higher scales. These results reveal the most basic connection between a local process (limited dispersal) and a large scale pattern.



Relatedness values across population

scales indicate a quantifiable trend. The interpolation of this trend will be used as the basis of a predictive model with which we can predict the effect perturbations, such as habitat fragmentation, at the local scale might have at higher scales. The ability to make predictions about large scale impacts based on more easily collected local data will provide us with an important tool for the assessment of risk in anthropogenically impacted species.