## Occupancy patterns of a small mammal (*Neotoma cinerea*) in the Great Basin through late Quaternary climate changes: assessing the assumption of local adaptation

Angela D. Hornsby and Marjorie D. Matocq

EPSCoR Graduate Fellow

Program in Ecology, Evolution, and Conservation Biology; Department of Natural Resources and Environmental Science; University of Nevada, Reno

It is often assumed that low-vagility montane organisms such as the bushy-tailed woodrat (Neotoma cinerea) underwent demographic declines in the Great Basin following the last glacial maximum due to warming climate and upslope retraction of suitable habitat. A common way to assess this hypothesis is to compare the amounts of suitable habitat using species distribution models projected to paleoclimate reconstructions, which assume temporal niche stability. We may make these models more regionally-specific by using subsets of occurrence data to represent localized clades or ecotypes; however, this introduces the additional assumption of regional adaptation or that localized clades are unable to occupy the full range of the species' realized niche if given the opportunity. Our goal was to assess whether this assumption was fair in *N. cinerea*, an organism known to change phenotype (body size) and thus thermal niche in localized areas over time. We first established *N. cinerea* late Quaternary demographic trends using primary paleomidden data and genetic coalescent and Bayesian skyline analyses, which confirmed the expected demographic declines through the Pleistocene-Holocene transition. We then built both regional and wide-scale distribution models projected to paleoclimate reconstructions for comparison. The wide-scale model agrees with the paleorecord and genetic patterns in suggesting declines of suitable habitat since the last glacial maximum, and the regional model challenges them by suggesting that N. cinerea specific to the Great Basin saw expansion of suitable habitat since the last glacial maximum. In this instance, the model that does not assume regional adaptation was more consistent with the independently inferred demographic trends. Overall, these analyses demonstrate that the biological assumptions behind distribution models must be explicit to avoid misinterpretations when projected to climate models across time.