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Project: Intra-specific Variation in Environmental Niche Modeling

**Effects of Incorporating Genetic Differentiation on Species Distribution Models Under Climate Change**

Habitat range shifts for a variety of species are predicted to occur in response to climate change. Environmental niche models (ENM) are commonly used to model habitat suitability or probability of occurrence. However, most species distribution models do not consider intraspecific genetic variation. Previous research suggests that including population differentiation may increase the accuracy of ENMs. In this study, we used published presence locations for *Aphaenogaster rudis*, a common New England forest ant and seed disperser, to explore the effects of including local adaptation on ENMs. Studies have found that rising minimum temperatures allow *A. rudis’* expansion into northern and higher elevation habitats*.* Although our conventional ENM agrees with this “upward” trend, it does not consider intraspecific genetic variation. Using *kmeans* clustering methods to produce genetic clusters, which simulate maximal local adaptation to minimum daily temperature, we ran an environmental niche model for each cluster for three years. We show that when intraspecific variation is included and dispersal is unlimited, habitat suitability expansion is greater than when compared to our conventional ENM. Although, our “genetically” informed ENMs assume unlimited dispersal, optimal local adaptation, and no panmixis, our simulations suggest that including population differentiation could result in more optimistic ENMs. As genetic information becomes more accurate, available, and cheaper, it is beneficial to include genetic information in species distribution models.

Research Category: Population Genetics; Climate change, Environmental Niche Modeling, Population Ecology