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Hierarchical Bayesian analysis and habitat analysis using spatial data for conservation of biodiversity

Kaori Murase

*Graduate School of Natural Sciences, and Research Center for Biological Diversity,
Nagoya City University, 1 Yamanohata, Mizuho-cho, Mizuho-ku, Nagoya, Aichi
467-8501, Japan*

Abstract

Although many publications describe how to measure biodiversity, not much attention has been given to the use of rare species information, except in making a species list. To conserve biodiversity, it is important to use all species information, including that of the many rare species. Many species in the samples, however, cannot be consistently collected, in biological hot spots. Moreover, many scientists mention that sample number is always important. Ants can be considered an appropriate insect group to investigate the problem because there are many species, including many rare species in single environments within national parks in the countries that have biological hotspots. I propose some bioinformatics methods to use all ant species in a single environment.

Moreover, I want to show how to apply the sampling location data for the conservation of biodiversity. I chose several Japanese ant species in several prefectures in central Japan, where the captured area has been decreasing over the last few decades. To explore the significantly effective environmental factors in the habitat preference of Japanese ant species, I performed Generalized Linear Model (GLM) analyses with the model selection using Akaike's Information Criterion (AIC). I used logistic as a link function when analyzing the GLM model. I also show how to make biodiversity conservation maps generated from sampling location data.

Key words: ant species, GLM, habitat preference, Japan

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