Abstract

Multidimensional hypervolumes enable ecologists to visualize the functional trait space occupied by an ecological community. Previously, hypervolumes have been measured using a minimum convex hull, but convex hulls are exclusively determined by extreme points and they cannot account for possible holes in the trait space. A multivariate kernel density estimation method with hyperbox kernels was proposed to deal with high-dimensional or holey datasets, but this method produces unrealistically blocky hypervolumes. We examined two alternatives: a Gaussian kernel density estimation method and a support vector machine method. We tested these two new methods and the hyperbox method by creating hypervolumes for three New World biomes using trait data from plants and mammals. We varied the parameters for each method in order to determine sensitivity to parameter variation. The resulting hypervolumes were compared with respect to their total volume, shape, and overlap. The hyperbox hypervolumes consistently had the largest volume of the three methods. The Gaussian method proved least sensitive to variation in bandwidth, while the support vector machine is the most customizable in terms of its two parameters, but may be susceptible to overfitting.

What is a hypervolume?

A hypervolume is a multidimensional representation of functional diversity (Blonder et al. 2015). Each species in the community is represented as a point corresponding to the values for a common set of functional traits. Hypervolumes are an alternative to convex hulls.

Hypervolume Methods

1. Hyperbox
   - Box-shaped kernels
2. Gaussian
   - Gaussian curve kernels
3. Support Vector Machine (SVM)
   - The SVM method uses machine learning to create a boundary. SVM hypervolumes require one parameter similar to bandwidth (v) and one parameter to regulate the influence of each data point (γ).

Data

Plants:
- Trait data from the Botanical Information and Ecology Network (BIEN) (Enquist et al. 2009)
  1) Specific leaf area (SLA)
  2) Height
  3) Seed mass

Mammals:
- Trait data from amniote trait database (Myhrvold et al. 2015)
  1) Body mass

Since body mass is correlated with many mammal functional traits, we also used two "invariant" traits (Charnov et al. 2001, Charnov 2002).
  2) \( \alpha = \frac{\text{age of female maturity}}{\text{longevity}} \)
  3) \( \alpha \cdot b = \text{age of female maturity} \cdot \text{number of daughters/year} \)

3 New World biomes for particular analysis:
- Temperate Broadleaf and Mixed Forests (red)
- Boreal Forests/Taiga (blue)
- Temperate grasslands, savannas (yellow)

\( \alpha \) Functional Diversity

\( \alpha \) diversity is a measurement of the total diversity of a region.

In the case of hypervolumes, \( \alpha \) diversity is measured by the total volume occupied by the hypervolume in multi-dimensional space.

\( \beta \) Functional Diversity

\( \beta \) diversity measures the overlap in diversity between two regions.

We represented \( \beta \) diversity as the volume of the intersection of the two hypervolumes divided by the total volume of both hypervolumes.

Parameter Variation

The hyperbox and Gaussian methods require a bandwidth parameter.

Conclusions

The methods differ quite a bit from each other and from the convex hull in their implications for \( \alpha \) and \( \beta \) diversity.

Increasing bandwidth increases the volume of hyperbox and Gaussian hypervolumes while maintaining overall shape. Varying the SVM parameters changes hypervolume size and shape.

These methods may allow for a more ecologically realistic picture of functional diversity. More work must be done to determine when each method and parameter(s) is most suitable.

References


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