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Comparison of the Three Methods for Creating n-Dimensional Hypervolumes

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Comparison of three methods for creating *n*-dimensional hypervolumes

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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.
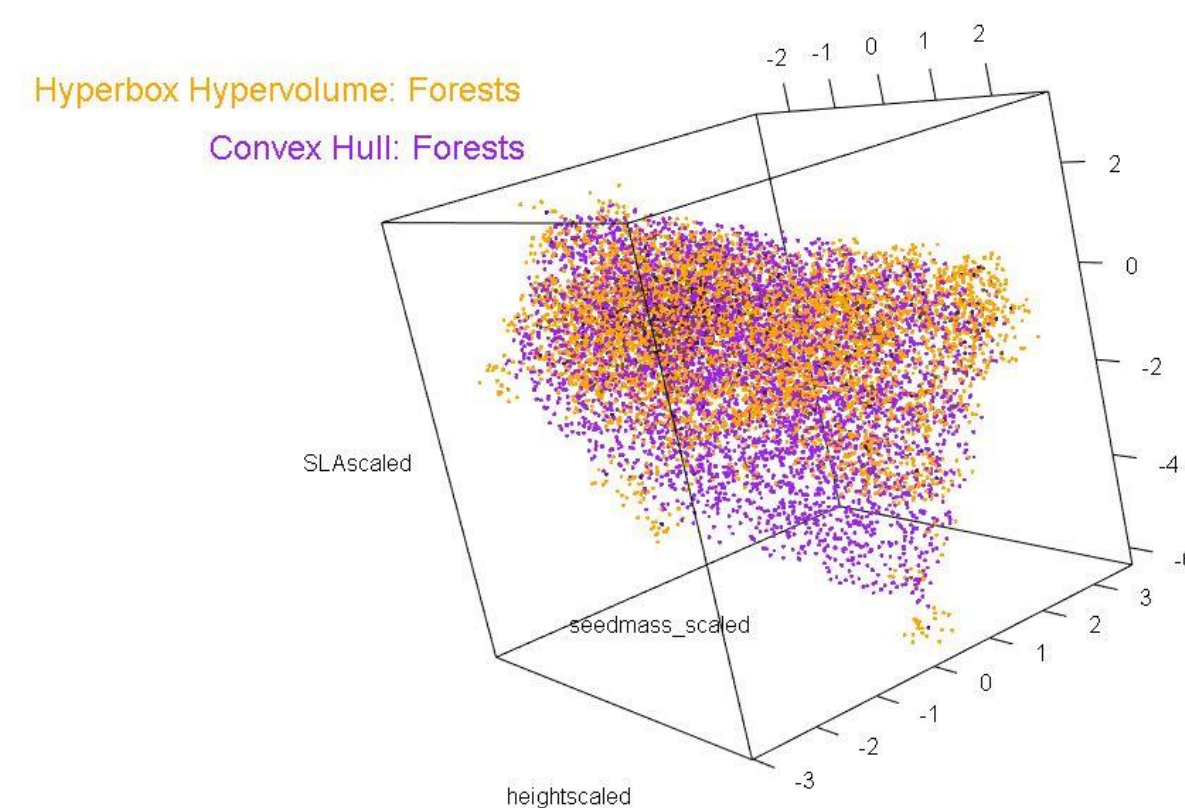
Figure 1. Hypervolume (orange) and convex hull (purple) for New World plants in temperate broadleaf and mixed forests.

Hypervolume Methods

1. Hyperbox
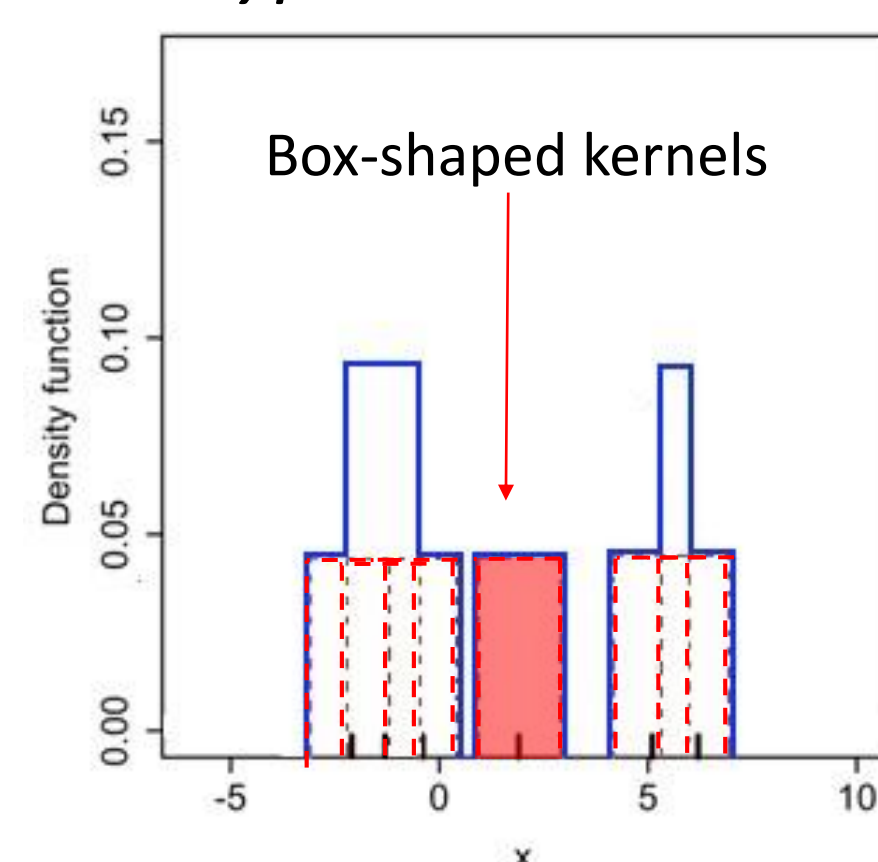
2. Gaussian
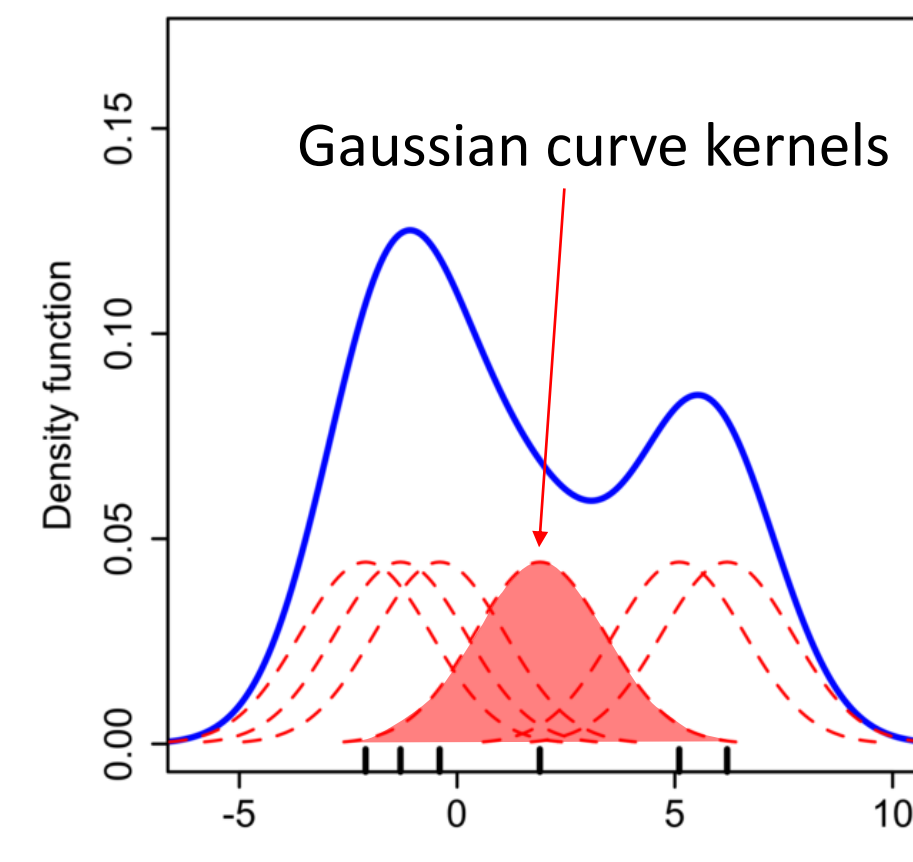
https://en.wikipedia.org/wiki/File:Comparison_of_1D_histogram_and_KDE.png

Both of the above methods create a kernel around each observed data point to create a probability density function. They rely on a bandwidth parameter to specify the width of the kernel.

3. Support Vector Machine (SVM)
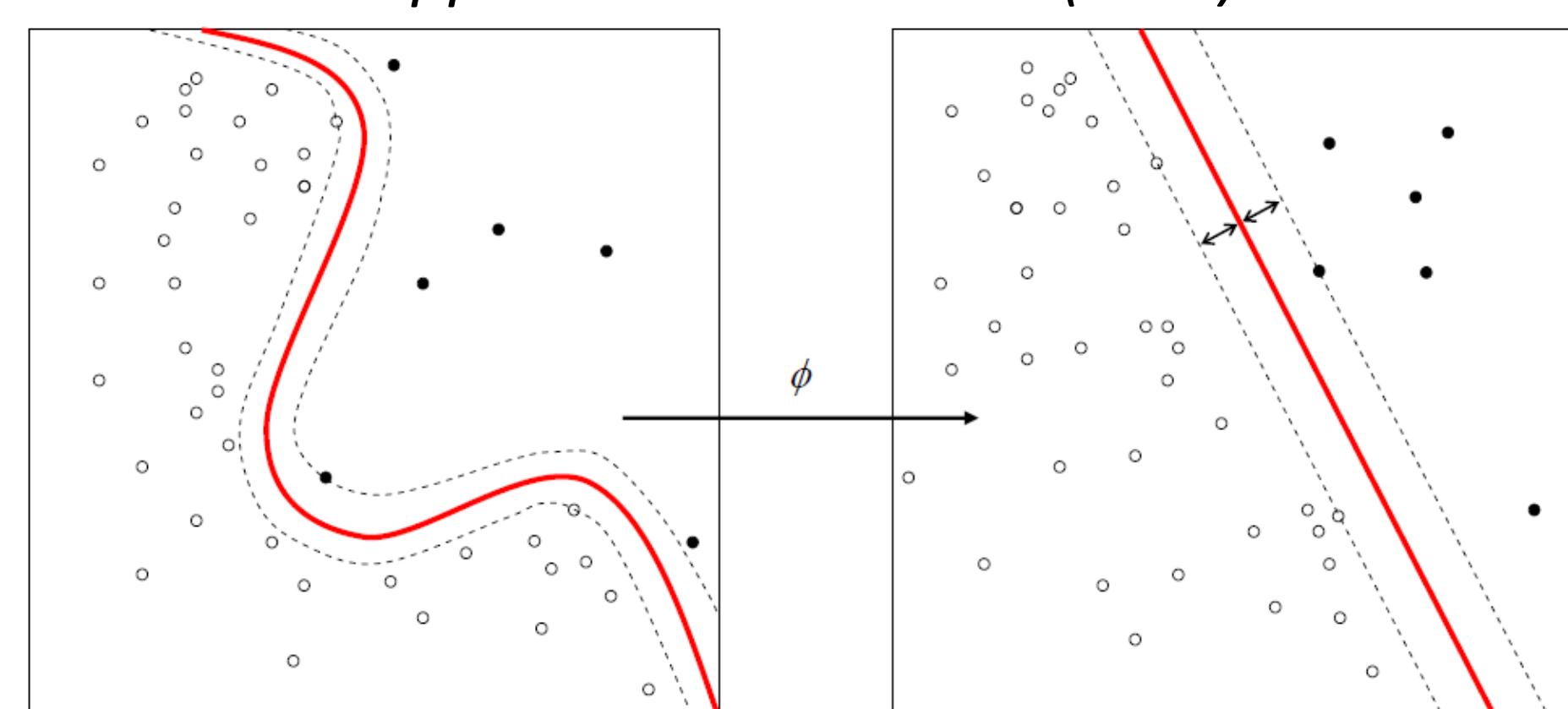
https://commons.wikimedia.org/wiki/File:Kernel_Machine.svg

The SVM method uses machine learning to create a boundary. SVM hypervolumes require one parameter similar to bandwidth (ν) 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) $\dfrac{E}{\alpha} = \dfrac{\text{longevity}}{\text{age of female maturity}}$
  3) $\alpha \cdot b = $ age of female maturity $\cdot$ 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)

α Functional Diversity

α diversity is a measurement of the total diversity of a region.

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

Figure 2. Ratio of the volume of each biome's hypervolume to the volume of the corresponding convex. Filled boxplots are for plant data and shaded boxplots are for mammals.

β Functional Diversity

β diversity measures the overlap in diversity between two regions.

We represented β diversity as the volume of the intersection of the two hypervolumes divided by the total volume of both hypervolumes.
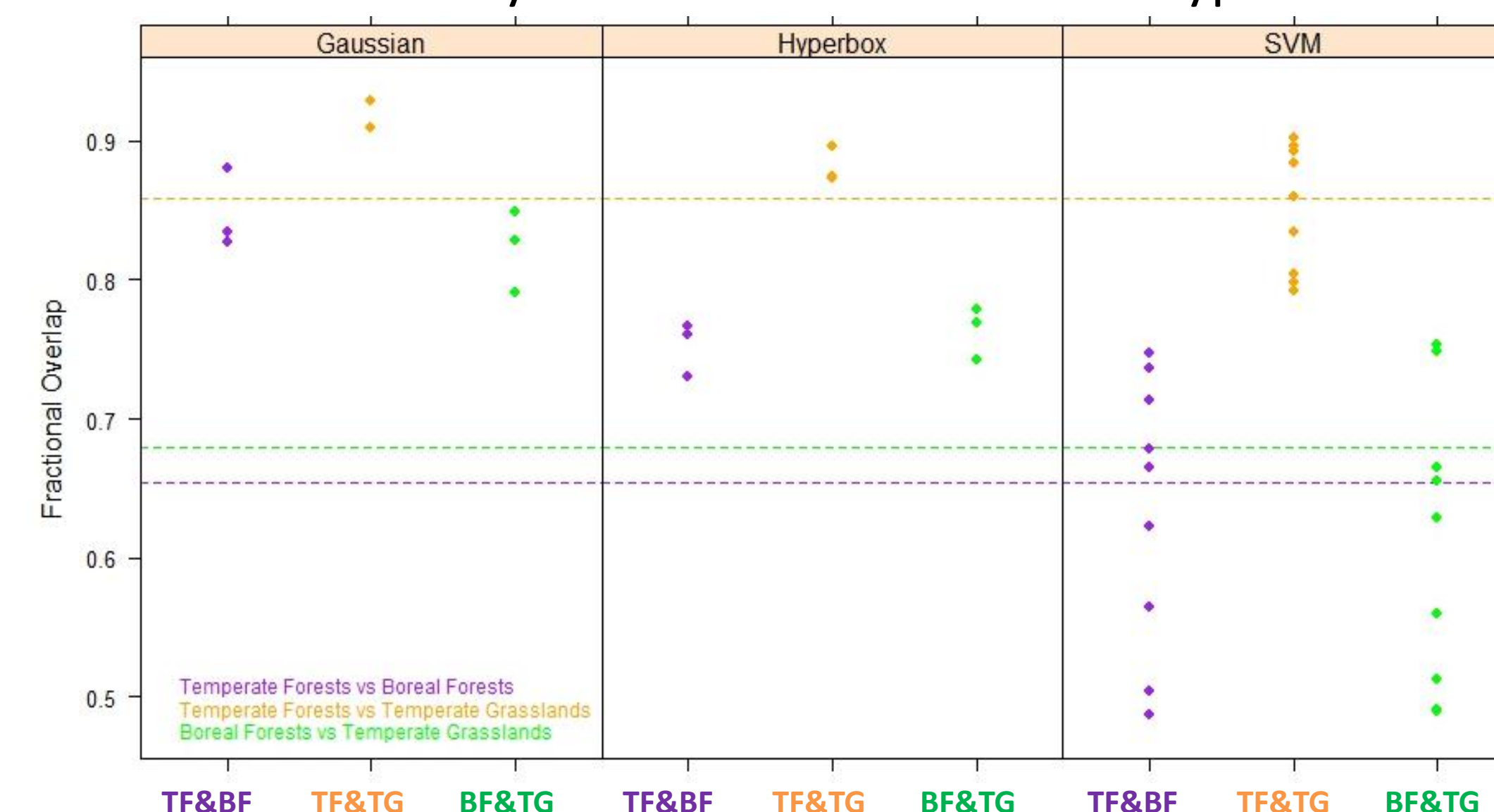
Figure 3. Fractional overlap of hypervolumes between temperate broadleaf and mixed forests (TF), boreal forests and taiga (BF), and temperate grasslands and savannas (TG) for the plant data. Reference lines are for the fractional overlap of the convex hulls for those biomes.

Parameter Variation

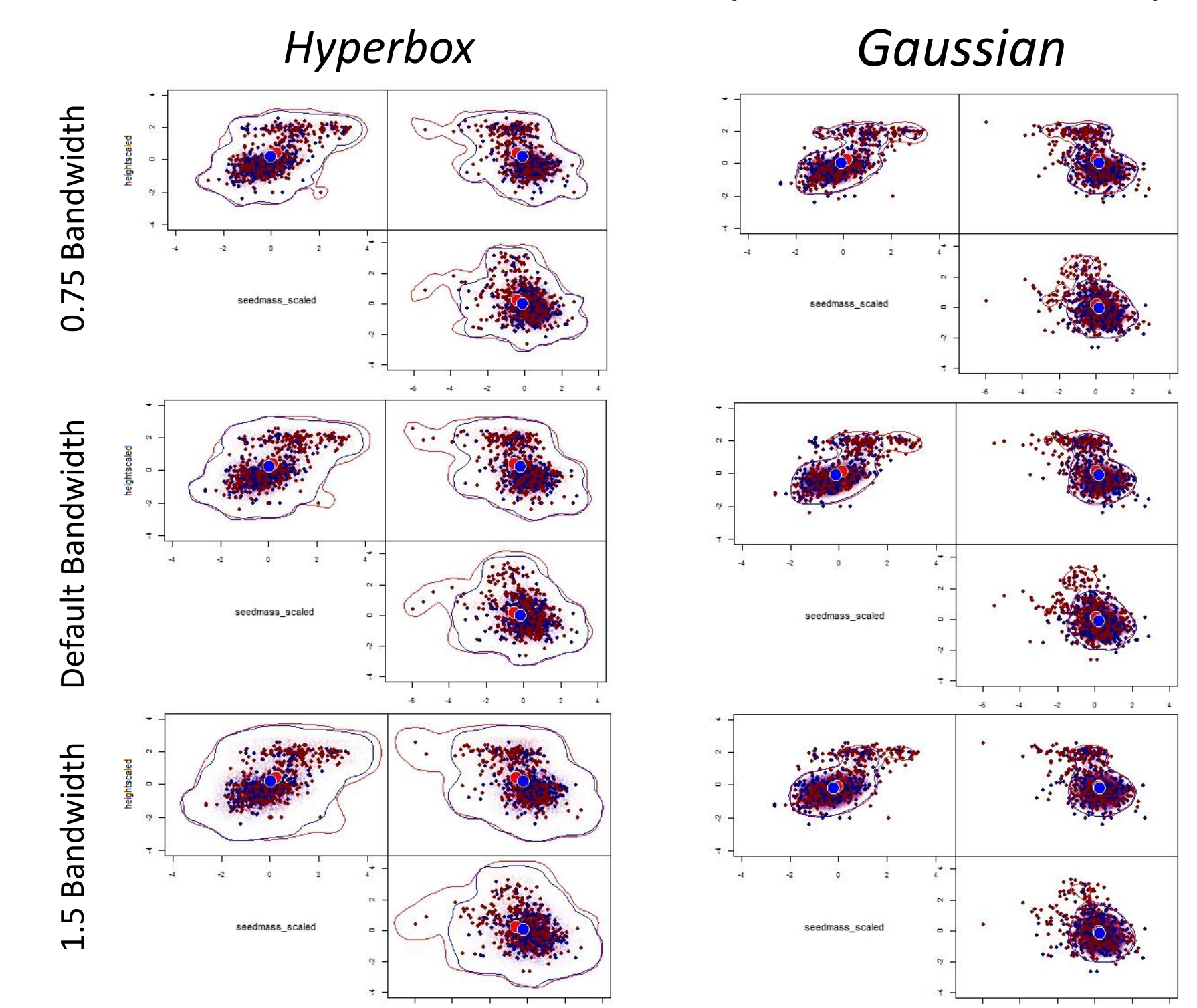The hyperbox and Gaussian methods require a bandwidth parameter.

Figure 3. Hyperbox and Gaussian hypervolumes for plants in temperate broadleaf/mixed forests (red) and boreal forests/taiga (blue) for varying bandwidth values.

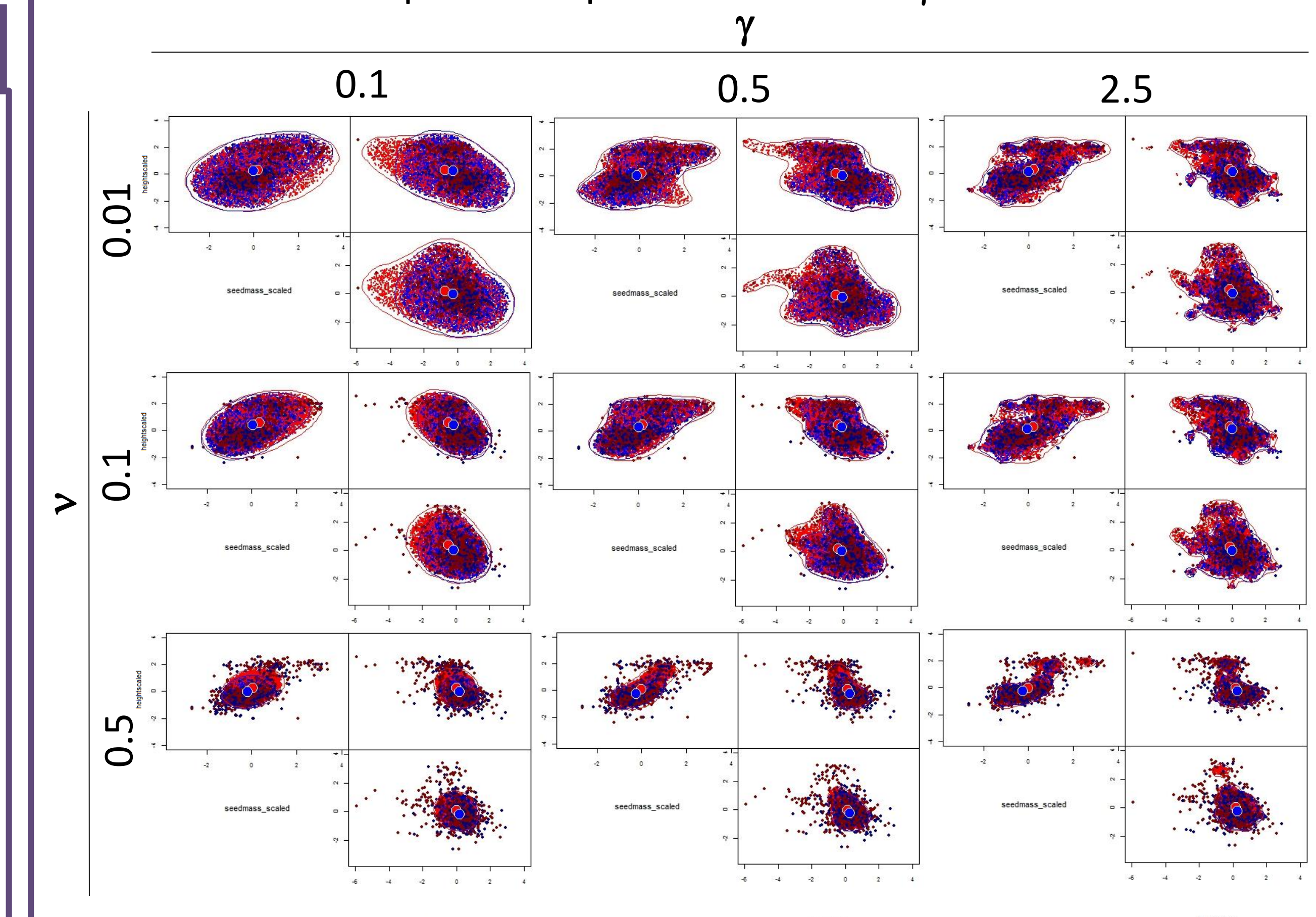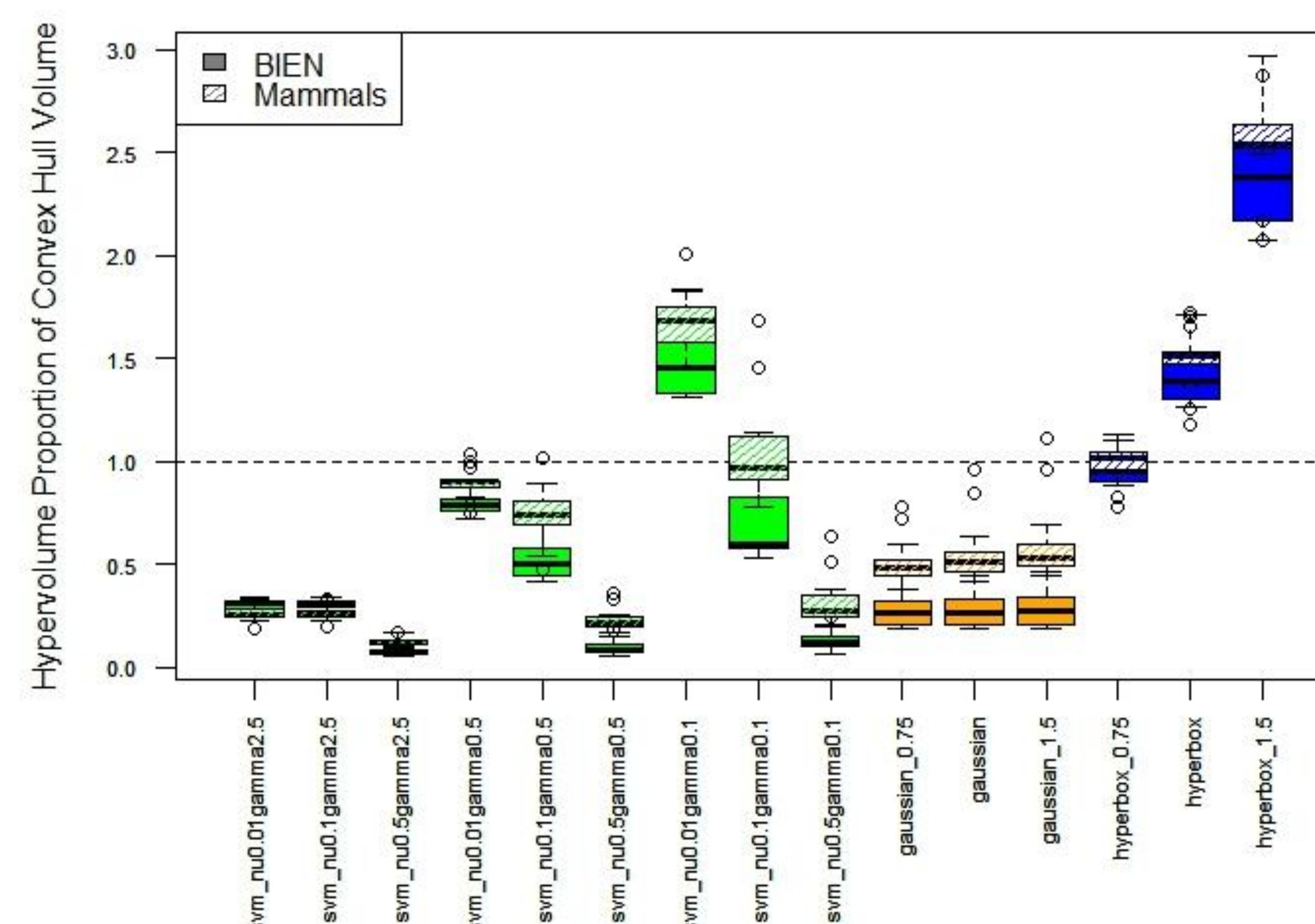The SVM method requires two parameters: ν and γ.

Figure 4. SVM hypervolumes for plants in temperate broadleaf/mixed forests (red) and boreal forests/taiga (blue) for varying values of ν and γ.

Conclusions

The methods differ quite a bit from each other and from the convex hull in their implications for α and β 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.

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Acknowledgments