Metadata for data associated to paper

Individual-level trait variation and negative density dependence affects growth in tropical tree seedlings, Umana, Maria Natalia, Zipkin, Elise, Zhang, Caicai, Cao, Min, Lin, Luxiang, Swenson, Nathan

Seedling growth and trait data from 171 plots and 61 species from a tropical forest in Xishuangbanna.

**Variables description**

**species.code =** species codes, three first letters correspond to first three letters of genus and three last letters correspond to three first letters of specific epithet

**plot =** seedling plot ID

**rgr.h =** relative growth rate calculated from changes in seedling height.

**hetspecific.mean.trait.distance.allpca =** Mean trait dissimilarity calculated between the focal individual and the heterospecific neighbouring seedlings in the same plot. This trait distance is based in the combination of all 3 PC axes.

**conspecific.mean.trait.distance.allpca=** Mean trait dissimilarity calculated between the focal individual and the conspecific neighbouring seedlings in the same plot. This trait distance is based in the combination of all 3 PC axes.

**hetspecific.mean.trait.distance.pca1 =** Mean trait dissimilarity calculated between the focal individual and the heterospecific neighbouring seedlings in the same plot. This trait distance is based on PC1.

**conspecific.mean.trait.distance.pca1 =** Mean trait dissimilarity calculated between the focal individual and the conspecific neighbouring seedlings in the same plot. This trait distance is based on PC1.

**hetspecific.mean.trait.distance.pca2 =** Mean trait dissimilarity calculated between the focal individual and the heterospecific neighbouring seedlings in the same plot. This trait distance is based on PC2.

**conspecific.mean.trait.distance.pca2 =** Mean trait dissimilarity calculated between the focal individual and the conspecific neighbouring seedlings in the same plot. This trait distance is based on PC2.

**hetspecific.mean.trait.distance.pca3=** Mean trait dissimilarity calculated between the focal individual and the heterospecific neighbouring seedlings in the same plot. This trait distance is based on PC3.

**conspecific.mean.trait.distance.pca3 =** Mean trait dissimilarity calculated between the focal individual and the conspecific neighbouring seedlings in the same plot. This trait distance is based on PC3.

**Initial.Height.cm =** Seedling height measured at the tagging moment in cm.

**PCA.1 =** loadings from PC1 obtained from a principal component analysis on all traits, using individual-level data.

**PCA.2 =** loadings from PC2 obtained from a principal component analysis on all traits, using individual-level data.

**PCA.3 =** loadings from PC3 obtained from a principal component analysis on all traits, using individual-level data.

**PCA1.sp =** loadings from PC1 obtained from a principal component analysis on all traits, using species-level data.

**PCA2.sp =** loadings from PC2 obtained from a principal component analysis on all traits, using species-level data.

**PCA3.sp =** loadings from PC3 obtained from a principal component analysis on all traits, using species-level data.

**density.co.sp** = initial density of conspecific seedlings

**density.het.sp** = initial density of heterospecific seedlings

**chge.cosp.neigh** = change in the number of conspecific seedlings

**chge.hetsp.neigh** = change in the number of heterospecific seedlings