

Key community assembly processes switch between scales in shaping beta diversity in two primary forests, southwest China

Mengesha Asefa¹, Han-Dong Wen¹, Min Cao¹, Yue-Hua Hu^{1*}

Asefa, M. (mengesha@xtbg.ac.cn)¹

Wen, H-D. (wenhandong@xtbg.ac.cn)¹

Cao, M. (caom@xtbg.ac.cn)¹

Hu, Y-H. (corresponding author, huyuehua@xtbg.org.cn)^{1*}

¹CAS Key Laboratory of Tropical Forest Ecology, Xishuangbanna Tropical Botanical Garden, Chinese Academy of Sciences, 666303, Yunnan, China

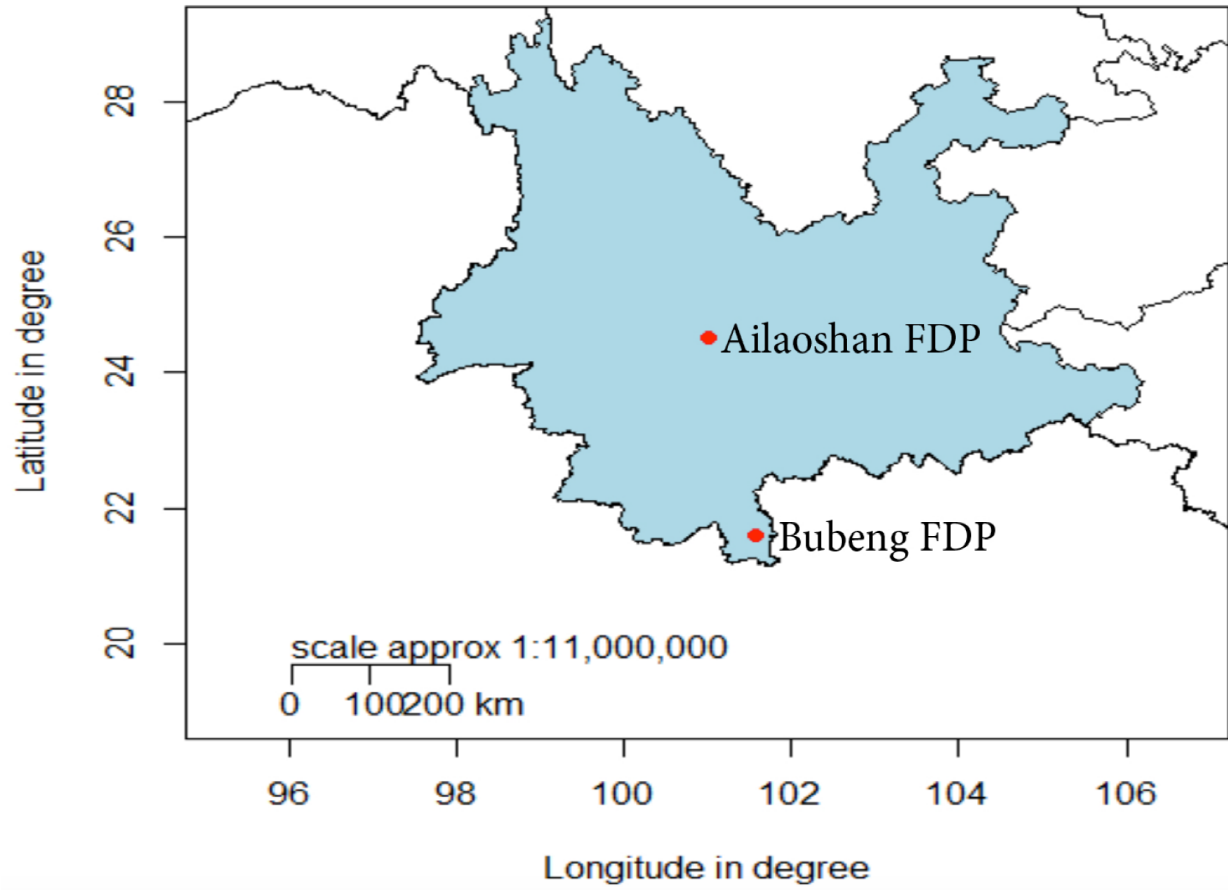


Figure S1: Location of the study sites

Appendix S2: Ecological process models

Random placement hypothesis (HP model)

We have used homogeneous Poisson point process model (HP) to test the random placement hypothesis. Two basic properties characterize homogeneous Poisson process model. The first one is individuals of the species are distributed independently. The location of any point in the pattern is independent of the location of any of the other points in the pattern which means that there is no interaction between individuals. The second property of this model is the intensity λ , of the pattern (i.e. the mean density of the species in a unit area) is constant. The number of individuals in the study plot of area A follows a Poisson distribution with mean λA (i.e. no habitat association). In this case the probability of finding an individual in an infinitesimally small disk of center \mathbf{x} , and area $d\mathbf{x}$ yields $\lambda d\mathbf{x}$ [1]. It doesn't represent any biological processes which brings complete randomness in species spatial distribution. Thus, this point process model has no parameter to be fitted except the number of individuals of a given species which is already determined by the data. Therefore, this point process model generates a completely random pattern (random placement) for each species that does not conserve the observed habitat association, clustering or species interactions [1].

Environmental filtering hypothesis (IP model)

This process explains the patterns of trees associated with environmental resources and assumes that the placement of individuals in a given environment is only influenced by their species-specific habitat suitability. Therefore, the model is used to evaluate the effects of the interaction between tree density and environmental factors [2]. Hence, the intensity of the model depends on location \mathbf{s} (i.e. the probability of finding an individual in an infinitesimally small disk of center \mathbf{s} and area $d\mathbf{s}$ is $\lambda(\mathbf{s})d\mathbf{s}$). The intensity $\lambda(\mathbf{s})$ may be influenced by topographic and edaphic factors. In order to estimate the intensity function $\lambda(\mathbf{s})$ based on environmental covariates (topography, soils, neighboring tree species), the techniques presented by Shen et al. [3] based on log-linear regression models has been applied. Consequently, this inhomogeneous point process (IP) generates for each species a pattern that conserves the observed habitat association, but not the observed clustering or species interactions. Thus, the following function has been used to model the effect of habitat heterogeneity on trees distribution.

$$\lambda(\mathbf{s}) = \alpha \exp \beta^T \chi(\mathbf{s}) \quad (1)$$

where $\alpha > 0$, $\chi(s)$ is a vector of environmental variables and β^T is a vector of regression parameters.

Dispersal limitation hypothesis (HT model)

Homogeneous Thomas process (HT) is a cluster process created by randomly located cluster centers from a Poisson process. It describes the processes of dispersal in which offsprings are limited to aggregate around their parent trees. This model helps to characterize how parent trees disperse their offsprings around themselves. So, it models the impact of dispersal limitation on the spatial distribution of trees [4]. This has produced several clusters which are independently and randomly distributed. The position of the cluster centers follows a homogeneous Poisson process with intensity λ which is the number of clusters in a study area S . The individuals belong to the clusters are then distributed based on two rules. First, the number of individuals that belong to a given cluster follows a Poisson distribution. Second, the actual locations of individuals around the cluster centers follow a bivariate Gaussian distribution with variance δ^2 [5].

The Thomas point process χ is a superposition of mother point's c in a stationary Poisson point process of intensity λ , with associated offspring clumps χ_c

$$\lambda(s) = \alpha \exp(\beta^T \chi(s)) k(\mu - c, \delta) \quad (2)$$

Where $\alpha > 0$, $k(\mu - c, \delta)$ is a probability density function depending on a parameter $\delta > 0$ determining the spread of offspring points around c . $\alpha \exp(\beta^T \chi(s))$ represents the covariance between tree density and environment at point S . k is the density of parent trees per unit area; μ is the expected number of offspring trees per parent tree; δ is the standard deviation for the location distribution of the offspring for a given parent, which is assumed to be independently and isotropically normally distributed for the spatial distances between a parent and its offspring. When $\alpha \exp(\beta^T \chi(s)) = 1$, the function represents a homogeneous Thomas process; otherwise, the function is inhomogeneous Thomas process [3].

Environmental filtering and dispersal limitation hypothesis (IT model)

This hypothesis assumes that the joint effect of dispersal limitation and environmental filtering (IT) is responsible for species assemblage. This hypothesis is represented by inhomogeneous Thomas model. As compared to other models, it is the most complicated model in which habitat heterogeneity and dispersal limitation are simultaneously considered to evaluate their joint effects

on spatial patterns of trees [4]. The above function can also work for Inhomogeneous Thomas process if $\alpha \exp(\beta^T \chi(s))$ is different from one [3]. This model is similar to the homogeneous Thomas process (HT) except that the tree density is associated with the environmental variables, and hence additional parameters are used to model the relationship between the tree density and environmental variables [6]. The simulation was carried out in R version 3.3.1(R Core Team, 2016) using the spatstat package [7].

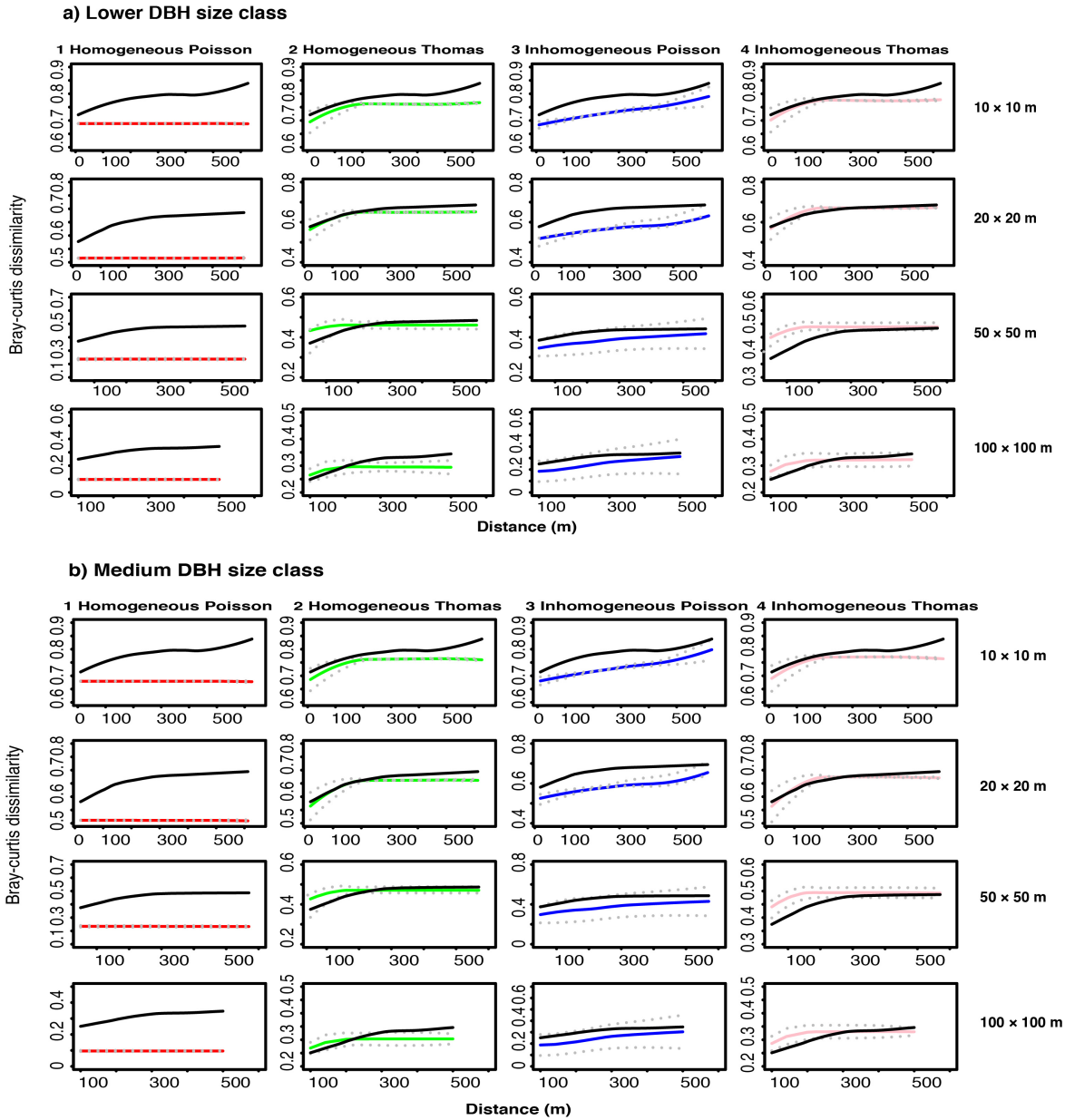


Figure S3: 95% confidence interval of point process models for species beta diversity across spatial scales for lower and Medium DBH-size classes in Bubeng FDP (The black line is the real species beta diversity, the red line is beta diversity predicted by Homogeneous Poisson, the green is beta diversity predicted by Homogeneous Thomas, the blue line is beta diversity predicted by Inhomogeneous Poisson, the pink line is beta diversity predicted by Inhomogeneous Thomas. The dotted lines are confidence intervals).

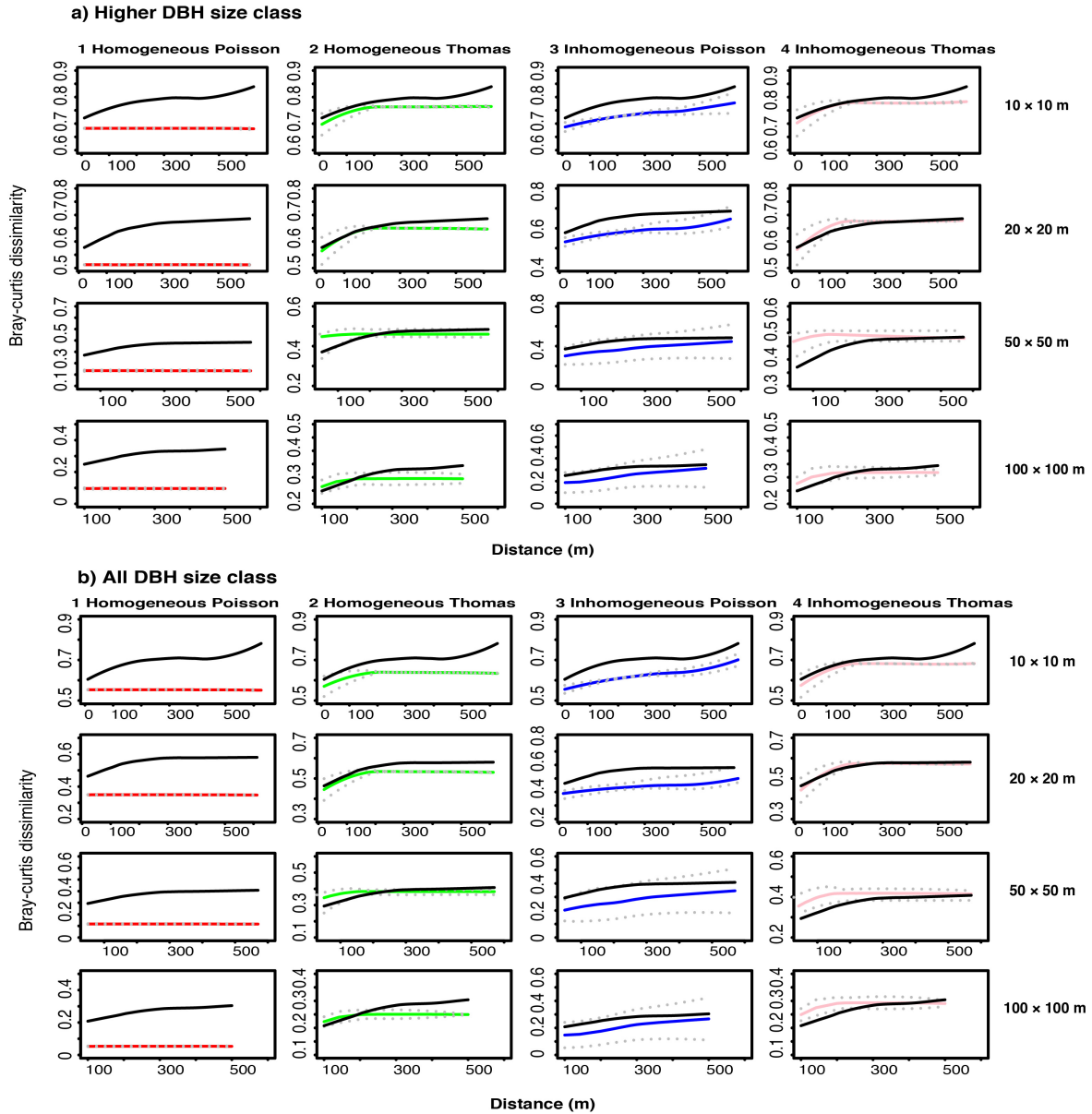


Figure S4: 95% confidence interval of point process models for species beta diversity across spatial scales for Higher & All DBH-size classes in Bubeng FDP (The black line is the real species beta diversity, the red line is beta diversity predicted by Homogeneous Poisson, the green is beta diversity predicted by Homogeneous Thomas, the blue line is beta diversity predicted by Inhomogeneous Poisson, the pink line is beta diversity predicted by Inhomogeneous Thomas. The dotted lines are confidence intervals).

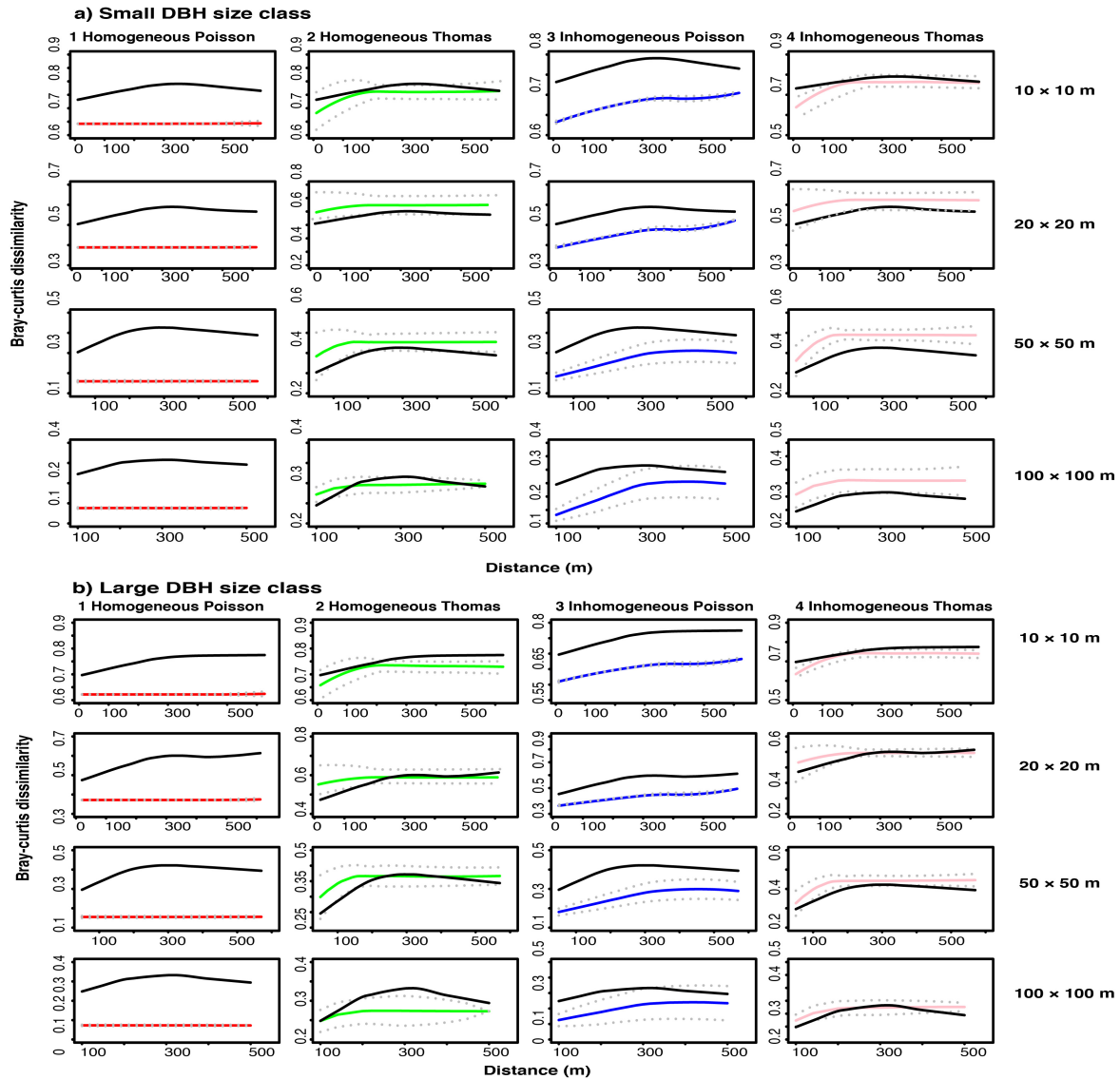


Figure S5: 95% confidence interval of point process models for species beta diversity across spatial scales for small & Large DBH-size classes in Ailaoshan FDP (The black line is the real species beta diversity, the red line is beta diversity predicted by Homogeneous Poisson, the green is beta diversity predicted by Homogeneous Thomas, the blue line is beta diversity predicted by Inhomogeneous Poisson, the pink line is beta diversity predicted by Inhomogeneous Thomas. The dotted lines are confidence intervals).

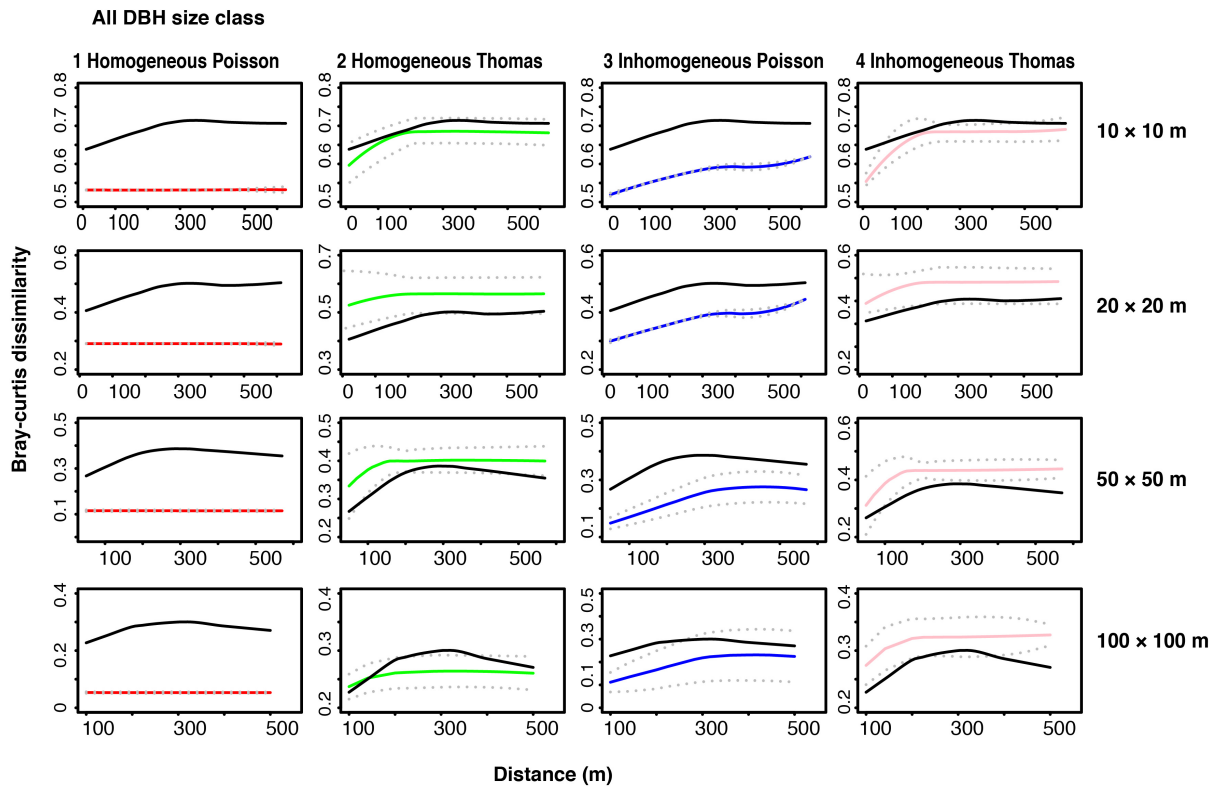


Figure S6: 95% confidence interval of point process models for species beta diversity across spatial scales for all DBH-size class in Ailaoshan FDP (The black line is the real species beta diversity, the red line is beta diversity predicted by Homogeneous Poisson, the green is beta diversity predicted by Homogeneous Thomas, the blue line is beta diversity predicted by Inhomogeneous Poisson, the pink line is beta diversity predicted by Inhomogeneous Thomas. The dotted lines are confidence intervals).

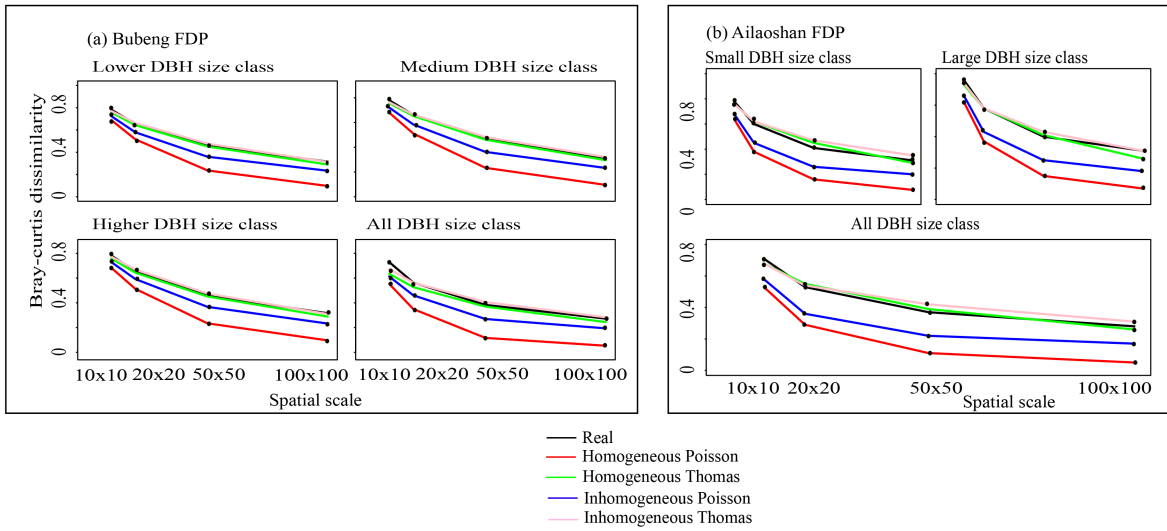


Figure S7: Effect of spatial scale on the observed and predicted beta diversity values for each DBH-size class in the three plots.

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