### o19428

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# Appendix A1

Loadings of each environment factors to the first four principal components						
Habitat variables	Principal	Principal	Principal	Principal		
	components 1	components	components 3	components		
		2		4		
Mean elevation	0.9978	0.0624	-0.0048	0.0198		
Convexity	0.0326	-0.2204	0.5009	-0.8339		
Slope	-0.0157	0.3674	-0.7508	-0.5486		
cos(aspect)	0.0008	0.0001	0.0034	-0.0077		
sin(aspect)	-0.0002	-0.0034	-0.0074	0.0014		
Fe	0.0002	-0.0001	0.0051	-0.0060		
Mn	-0.0001	-0.0059	-0.0200	0.0252		
Zn	-0.0001	0.0066	0.0000	0.0076		
Cu	0.0003	0.0004	-0.0014	0.0039		
Κ	-0.0009	0.0052	-0.0071	0.0097		
Р	-0.0045	0.0232	-0.0083	0.0254		
Ca	-0.0001	0.0093	-0.0124	0.0297		
Mg	-0.0005	0.0082	-0.0086	0.0201		
Na	0.0012	-0.0004	-0.0051	0.0044		
В	0.0005	-0.0008	0.0018	-0.0016		
Si	0.0016	-0.0123	-0.0026	-0.0082		
Al	0.0000	0.0034	-0.0007	-0.0021		
Ν	-0.0006	0.0042	-0.0032	0.0062		
pH	0.0000	0.0008	-0.0001	0.0012		
N mineralization rate	-0.0017	0.0114	0.0020	0.0073		
Bulk density	0.0545	-0.9006	-0.4294	-0.0169		
Soil moisture	-0.0014	0.0161	0.0042	0.0088		
Standard deviation	56.5427	7.9814	6.4891	5.8465		
Proportion of variance	0.9575	0.0191	0.0126	0.0102		
Cumulative proportion	0.9575	0.9766	0.9892	0.9994		

The bar plot of observed and predicted species–abundance distribution (SAD) at different scales  $(10 \times 10 - 200 \times 200 \text{ m})$  in Gutian plot. The vertical bars are 95% confidential intervals. Different colors represent different SADs predicted by different processes: black histogram is the mean value of observed SADs from 100 samples in Gutian plot at corresponding scale, blue histogram by homogeneous Poisson process, pink histogram by heterogeneous Poisson process at corresponding scale, red histogram by homogeneous Thomas process, green histogram by heterogeneous Thomas process at corresponding scale. The SADs are plotted using Preston's binning method. The numbers on the *x* axis represent Preston's octave classes, and octave 1 represents1, 2, 3–4, 5–8, 9–16, and so on (Hubbell 2001).





95% confidence intervals of the four processes at scales of  $10 \times 10 - 200 \times 200$  m. Solid line represents mean value of observed species abundance distribution (SADs) of 100 samples in Gutian plot at corresponding scale; Points are the mean values of simulated SADs from 1000 (10 of each simulated communities) samples at corresponding scale. Different symbols represent different SADs predicted by different processes: : homogeneous Poisson process,  $\Box$ : heterogeneous Poisson process,  $\circ$ : homogeneous Thomas process, : heterogeneous Thomas process.







Rank–abundance curves simulated from the four models at different scales: Observed curves of species–abundance distribution (SADs) are shown as black line. Blue dotted-lines are the mean value of SADs from 1000 (10 of each simulated communities) samples simulated by homogeneous Poisson process, pink dotted-lines by heterogeneous Poisson process, red dotted lines by homogeneous Thomas process, and green dotted-lines by heterogeneous Thomas process.



Algorithms for the four spatial point models and model parameterization used in inference mechanisms structuring species abundance distributions (SADs) Calculations of AIC are also detailed. Møller and Waagepetersen (Møller and Waagepetersen 2004) and Shen et al. (2009) carefully described the algorithms of four models used in this study, and Waagepetersen and Guan (2009) and Waagepetersen (2007) clearly exemplified the steps of model parameterization. Here we outline the framework of four models and steps of parameterization. For more details, please refer to three above-mentioned literatures.

#### 1) Description and model parameterization of Poisson process

A Poisson process X in a two-dimensional region  $S \subset \Re^2$  is characterized by two fundamental properties (1) the number of point N in any boundary subregion B has a Poisson distribution with mean intensity measure  $\mu(B)$  ( $\mu > 0$ ); (2) given that  $N(X \cap B) = n$ , the n points are independent and identically distributed, with intensity function  $\rho(u)$ :

$$\rho(u) = \alpha \exp(Z_{1:k}(u)\beta_{1:k}^T) \tag{1}$$

where  $u \subset B$ , and  $\alpha > 0$ ,  $Z_{1:k}(u)$  is the 1× k vector of non-constant environmental variables,  $\beta_{1:k}$  is the 1× k vector of corresponding regression parameters.

If  $\rho(u)$  is constant for all  $u \in S$ , the Poisson process is homogeneous or stationary, that is, a completely spatial random process. If  $\rho(u)$  is a function of environmental variables  $Z_{1:k}(u)$ on location  $u \in S$ , the Poisson process is heterogeneous. The points of heterogeneous Poisson process have no interaction, but intensity changes with environmental variables. Waagepetersen (2007) suggested to extract the regression parameters  $\beta = (\beta_0, \beta_{1:k})$ , where  $\beta_0 = \log(\alpha)$ using maximum likelihood method based on the following equation to obtain  $\hat{\beta}$ :

$$l(\beta) = \sum_{u \in X \cap S} Z(u)\beta^T - \int_S (\exp(Z(u)\beta^T)du$$
(2)

where  $Z(u) = (1, Z_{1:k}(u))$ , and  $l(\beta)$  is the likelihood function.

#### (2) Description and model parameterization of Thomas process

In Thomas processe X, the clusters  $X_c$  of the offspring points are symmetrically and normally distributed around the parent points c in a homogeneous Poisson process of intensity  $\kappa$ . Given c, the clusters  $X_c$  are independent Poisson process with intensity functions:

$$\rho_c(u) = \exp(Z_{1k}(u)\beta_{1k}^T)\alpha k(u-c,\delta)$$
(3)

where  $\alpha > 0$ ,  $k(u - c, \delta)$  is a probability density depending on  $\delta > 0$  determining the spread of offspring points around c. Similar to Eq. 1,  $\exp(Z_{1:k}(u)\beta_{1:k}^{T})$  still represents the covariance between point density and environmental variables  $Z_{1:k}(u)$  at location u. X is a homogeneous Thomas process when  $\exp(Z_{1:k}(u)\beta_{1:k}^{T}) = 1$ . Otherwise X is a heterogeneous Thomas process.

Assume that  $\exp(Z_{1:k}(u)\beta_{1:k}^T)$  is bounded by some constant M, and a cluster  $X_c$  may then be considered as independent thinning of a cluster  $X_c$  with intensity function  $M \partial k(\cdot - c, \delta)$  where the spatially varying thinning probability is  $\exp(Z_{1:k}(u)\beta_{1:k}^T)/M$ . Using this thinning perspective, the intensity function of Thomas process X is:

$$\rho(u) = \alpha \kappa \exp(Z_{1:k}(u)\beta_{1:k}^T)$$
(4)

The parameters of heterogeneous Thomas process  $\hat{\beta}$  can be estimated using maximum likelihood method as Eq. 2. Other parameters  $\hat{\kappa}$  and  $\hat{\delta}$  can be estimated by minimum contrast methods:

$$m(\kappa, \delta) = \int_{0}^{r} (\hat{K}(t)^{1/4} - K(t; \kappa, \delta)^{1/4})^{2} dt$$

where r is user-specific constants, and K is heterogeneous K-function of X which is defined as:

$$\hat{K} = \sum_{u,\eta \in X \cap S} \frac{1[0 < ||u - \eta|| < t]}{\exp((Z(u) - Z(\eta))\hat{\beta}^T)} e_{u,\eta}$$

where  $e_{u,\eta}$  is edge correction. Considering the bias of *K* increases with r, we set r = 100 m. The expected number of offspring points around each parent point can be calculated as:  $\hat{\mu} = M / \hat{\kappa}$ , and  $\hat{\alpha} = \exp(\beta_0) / \hat{\kappa}$  for Thomas process.

### 2. Akaike's information criterion

The Akaike information criterion (AIC) is a way of selecting a model that has a good fit to the truth but few parameters from a set of models. In general case, AIC is defined as:

$$AIC = -2\ln(L) + 2k$$

where likelihood is the maximized value of the likelihood function for the estimated model and K is the number of free parameters in the model. A problem in the application of this criterion in our study is that estimation of our model parameters is not totally based on maximum likelihood method. However, we can use the following estimation  $\hat{A}$  in our current modeling framework (Webster and McBratney 1989):

$$\hat{A} = \left\{ n \ln \left[ \frac{2\pi}{n} \right] + n + 2 \right\} + n \ln R + 2k$$

where n is the number of ranks or octaves classes, k is the number of parameters in a model and R is the sum of squared deviations in species abundance at each species rank or octave class. The quantity in the curly brackets is constant for a given set of data and so models can be compared by computing: AIC ~  $n\ln R + 2k$  and BIC~ $n\ln R + k\ln n$  (Webster and McBratney 1989). However, one of implicit assumption of this approximation is normally distributed deviations. We transformed the abundance-rank type SADs using  $\ln(A_i + c)$ , where  $A_i$  is the abundance of the *i*th species and c is a constant around 0.5. The deviations of transformed abundance-rank type SADs and Preston-like SADs are close to normal distribution. Thus, it makes sense to assume that the

deviations of SADs are normally distribution (Hilborn and Mangel, 1997), and we use  $n \ln R + 2k$ and  $n \ln R + k \ln n$  to approximate AIC and BIC.

To test the robustness of approximated AIC and BIC, we also use adjusted mean sum of squared residual ( $MR_a$ ) to compare the performance of the four models.  $MR_a$  can be calculated as following (Efron and Tibshirani 1993, Hilborn and Mangel 1997):  $MR_a = R/(n-2k)$  for abundance-rank type SAD, and  $MR_a = R/(n-k)$  for Preston-like SAD, where n, R and k is as above-described.  $MR_a$  (R/(n-2k)) is approximate the same as Mallows Cp which is special case of AIC for general models (Efron and Tibshirani 1993, Hilborn and Mangel 1997), and  $MR_a$  does not assume normally distributed deviations. Using  $MR_a$  as criterion of model selection, we find the similar result as approximated AIC and BIC (except at scales of 20 × 20 and 20 × 20 m for homogeneous Thomas process and heterogeneous Thomas process model, Table 1, Appendix A6 Table A1, A2). These similar results from AIC, BIC and  $MR_a$  indicate that approximated AIC and BIC are robust for our data.

## References

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Adjusted mean sum of squared residual (MR<sub>a</sub>) and approximated Akaike's information criterion (AIC) values of four spatial point pattern models

Table A1. Adjusted mean sum of squared residual (MR<sub>a</sub>) of four spatial point pattern models for species abundance distributions (SADs) of Preston-like and rank-abundance type

SAD type	Scale $(m^2)$	Homogeneous	Heterogeneous	Homogenous	Heterogeneous
		Poisson	Poisson	Thomas	Thomas
		(purely	(niche)	(dispersal)	(niche +
		random)			dispersal)
Preston-like	10×10	4.6901	3.1390	0.3823	0.5387
	20×20	6.0563	4.2647	1.2469	0.5807
	40×40	4.8618	1.9616	1.9869	0.3348
	80×80	9.6176	4.5474	4.4849	3.3380
	100×100	6.4288	3.4251	4.0809	2.9873
	200×200	10.9165	5.4832	6.3714	4.8850
Rank-	10×10	0.8247	0.5743	0.2162	0.7291
abundance	20×20	10.3879	6.7116	0.4141	0.8034
type	40×40	50.97835	26.3659	4.8685	4.7146
	80×80	289.3106	154.8750	19.0198	5.7320
	100×100	823.8921	461.0679	36.4542	62.7459
	200×200	2833.289	662.8333	275.7352	89.7644

The lowest MR<sub>a</sub> in the four spatial process models in bold.

Table A2. Approximated Akaike's information criterion (AIC) values of four spatial point pattern models for species abundance distributions (SADs) of rank-abundance type with original abundance data.

SAD type	Scale $(m^2)$	Homogeneous	Heterogeneous	Homogenous	Heterogeneous
		Poisson	Poisson	Thomas	Thomas
		(purely	(niche)	(dispersal)	(niche +
		random)			dispersal)
Rank-	10×10	130.8519	111.4253	58.31158	76.73214
abundance	20×20	378.638	351.944	147.0958	176.6004
type	40×40	674.3688	611.6455	421.6162	420.0009
	80×80	1027.247	868.7732	636.1655	531.5328
	100×100	1144.225	1038.147	728.4186	795.224
	200×200	1282.545	1133.868	1033.505	929.0566

The lowest AIC value in the four spatial process models in bold.