Supporting Information

Inferring multi-species distributional aggregation level from limited line transect-derived

biodiversity data

Youhua Chen[1], Tsung-Jen Shen[2*], Hoang Van Chung[1], Shengchao Shi[1], Jianping Jiang[1], Richard

Condit[3,4], Stephen P. Hubbell[5,6]

[1]CAS Key Laboratory of Mountain Ecological Restoration and Bioresource Utilization &

Ecological Restoration and Biodiversity Conservation Key Laboratory of Sichuan Province,

Chengdu Institute of Biology, Chinese Academy of Sciences, Chengdu 610041, China

[2]Institute of Statistics & Department of Applied Mathematics, National Chung Hsing University,

250 Kuo Kuang Road, Taichung 40227, Taiwan

[3]Field Museum of Natural History, 1400 S. Lake Shore Dr., Chicago, IL 60605, USA

[4]Morton Arboretum, 4100 Illinois Rte. 53, Lisle, IL 60532, USA

[5]Smithsonian Tropical Research Institute, Apartado 0843-03092, Balboa, Panama

[6]Department of Ecology and Evolutionary Biology, University of California, Los Angeles, CA

90095, USA

*Email for correspondence: tjshen@nchu.edu.tw

Variance estimation of the intraspecific-encounter index (*v*)

For simplification in notation, we define

$$\theta_k = \sum_{i=1}^{S} I(Z_k = i, Z_{k-1} = i), \tag{S1}$$

where $k = 2, 3, ..., m$. Note that, using the notation in Eq. S1, we can show $E(\theta_k) = E(v)$ for all

$k \geq 2$, and the intraspecific-encounter index, *v*, is concisely expressed as:

$$v = \frac{1}{m-1} \sum_{k=2}^{m} \theta_k. \tag{S2}$$

As a result, the variance of *v* is

$$Var(v) = \left(\frac{1}{m-1}\right)^2 \left\{ \sum_{k=2}^{m} Var(\theta_k) + 2 \sum_{k=2}^{m-1} \sum_{j=k+1}^{m} Cov(\theta_k, \theta_j) \right\}. \tag{S3}$$

For deriving an accurate estimator of *Var*(*v*) from Eq. S3, in which we need to derive the

$Var(\theta_k)$ and $Cov(\theta_k, \theta_j)$, for all $2 \leq k < j \leq m$, in detail. First, we have

$$
\begin{aligned}
&Var(\theta_k) \\
&= E(\theta_k^2) - [E(\theta_k)]^2 \\
&= E\left\{ \sum_{i=1}^{S} I^2(Z_k = i, Z_{k-1} = i) + \sum_{i \neq j}^{S} I(Z_k = i, Z_{k-1} = i) I(Z_k = j, Z_{k-1} = j) \right\} - [E(v)]^2, \quad \text{(S4)} \\
&= E\left\{ \sum_{i=1}^{S} I(Z_k = i, Z_{k-1} = i) \right\} - [E(v)]^2 \\
&= E(v) - [E(v)]^2
\end{aligned}
$$

in which the last term can straightforward be estimated by $v(1-v)$, when applying the moment

method. Given $j = k + 1$, we specifically derive the covariance of θ_k and θ_j from

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$$Cov(\theta_k, \theta_{k+1})$$

$$= Cov\left(\sum_{i=1}^{S} I(Z_k = i, Z_{k-1} = i), \sum_{i=1}^{S} I(Z_{k+1} = i, Z_k = i)\right)$$

$$= E\left(\sum_{i=1}^{S} I(Z_{k+1} = Z_k = Z_{k-1} = i)\right) +$$

$$E\left(\sum_{i \neq j}^{S} I(Z_k = i, Z_{k-1} = i)I(Z_{k+1} = j, Z_k = j)\right) - E(\theta_k)E(\theta_{k+1})' \tag{S5}$$

$$= E\left(\sum_{i=1}^{S} I(Z_{k+1} = Z_k = Z_{k-1} = i)\right) - [E(v)]^2$$

$$= \sum_{i=1}^{S} p_i s_i^2 - \left[\sum_{i=1}^{S} p_i s_i\right]^2$$

where we define $s_i = \pi + (1-\pi)p_i$ for convenience in notation.

For the case $j = k + 2$, we can show that the covariance of θ_k and θ_j is

$$Cov(\theta_k, \theta_{k+2})$$

$$= Cov\left(\sum_{i=1}^{S} I(Z_k = i, Z_{k-1} = i), \sum_{i=1}^{S} I(Z_{k+2} = i, Z_{k+1} = i)\right)$$

$$= E\left(\sum_{i=1}^{S} I(Z_{k+2} = Z_{k+1} = Z_k = Z_{k-1} = i)\right) + \qquad .$$

$$E\left(\sum_{i \neq j}^{S} I(Z_k = i, Z_{k-1} = i)I(Z_{k+2} = j, Z_{k+1} = j)\right) - E(\theta_k)E(\theta_{k+2})$$

$$= \pi\left\{\sum_{i=1}^{S} p_i s_i^2 - \left[\sum_{i=1}^{S} p_i s_i\right]^2\right\}$$

As a result, we have the general result for the covariance of θ_k and θ_j with the form of

$$Cov(\theta_k, \theta_j) = \pi^{|k-j|-1}\left\{\sum_{i=1}^{S} p_i s_i^2 - \left[\sum_{i=1}^{S} p_i s_i\right]^2\right\}. \tag{S6}$$

Note that, in Eq. S6, the parameter π can be simply estimated by v, and the term within curly

braces stands for $Cov(\theta_k, \theta_{k+1})$ as shown in Eq. S5 and is estimated by

$$C\hat{o}v(\theta_k, \theta_{k+1}) = (t - v^2)I(t > v^2), \tag{S7}$$

where $t = \dfrac{1}{m-2}\sum\limits_{k=2}^{m-1}\sum\limits_{i=1}^{S} I(Z_{k+1} = Z_k = Z_{k-1} = i)$ as defined in the main text; additionally, the

indicator variable, $I(t > v^2)$, is used to account for theoretically $Cov(\theta_k, \theta_j) \geq 0$ for $j \neq k$,

which is proven by using the Cauchy-Schwarz inequality of the form as

$$\left\{\sum_{i=1}^{S} p_i s_i\right\}^2 \leq \left(\sum_{i=1}^{S}\left(\sqrt{p_i}\right)^2\right)\left(\sum_{i=1}^{S}\left\{\sqrt{p_i}s_i\right\}^2\right)$$
$$= \sum_{i=1}^{S} p_i s_i^2$$

(S8)

Applying the results in Eqs. S4 and S7 to the Eq. S3 leads to the variance estimator of the

conspecific-encounter index which is

$$V\hat{a}r(v) = \left(\frac{1}{m-1}\right)^2\left\{\sum_{k=2}^{m} v(1-v) + 2\sum_{k=2}^{m-1}\sum_{j=k+1}^{m} v^{|k-j|-1}(t-v^2)I\left(t \geq v^2\right)\right\}$$
$$\approx \frac{1}{m-1}\left\{v(1-v) + \frac{2}{1-v}(t-v^2)I(t \geq v^2)\right\}$$

(S9)

Note that, to further elucidate the approximate derivation in Eq. S9, we reshape the double

summation in the curly brackets of Eq. S9 as

$$2\sum_{k=2}^{m-1}\sum_{j=k+1}^{m} v^{|k-j|-1} = \mathbf{1}'\,\mathbf{\Psi 1},$$

(S10)

where $\mathbf{1}'$ is the transpose of a column vector or a $1 \times (m-1)$ matrix composed of all entries

equal to one (i.e., $\mathbf{1}' = (1,1,\dots,1)$), and $\mathbf{\Psi}$ is a $(m-1) \times (m-1)$ symmetric matrix having all

diagonal entries equal to zeros and explicitly given below

$$\begin{bmatrix} 0 & 1 & v & & \cdots & v^{m-5} & v^{m-4} & v^{m-3} \\ 1 & 0 & 1 & & & v^{m-6} & v^{m-5} & v^{m-4} \\ & \vdots & & \ddots & & & \vdots & \\ v^{m-4} & v^{m-5} & v^{m-6} & & \cdots & 1 & 0 & 1 \\ v^{m-3} & v^{m-4} & v^{m-5} & & & v & 1 & 0 \end{bmatrix}.$$

As a result, the right-hand side of Eq. S10 is equal to summing up all entries of the matrix Ψ or to summing up the entries of the upper triangular part of Ψ and doubling the resulting sum, because Ψ is symmetric. With the latter case, we can compute

$$
\begin{aligned}
\frac{\mathbf{1}'\,\Psi\mathbf{1}}{2} &= \sum_{k=1}^{m-2} \frac{1-v^k}{1-v} \\
&= \frac{m-2}{1-v} - \sum_{k=1}^{m-2} \frac{v^k}{1-v} \\
&= \frac{m-2}{1-v} - \frac{v(1-v^{m-2})}{(1-v)^2} \\
&= \frac{(m-2)(1-v) - v(1-v^{m-2})}{(1-v)^2} \\
&= \frac{(m-1)(1-v) + v^{m-1} - 1}{(1-v)^2} \\
&\approx \frac{(m-1)}{(1-v)},
\end{aligned}
\tag{S11}
$$

where the approximation in the rightmost term of Eq. S11 is from ignoring $v^{m-1}-1$ in the numerator of its previous equality when the sample size m is not very small. Actually, the absolute value of this term is not small, which tends to -1 when m gets large. But comparing to the first term $(m-1)(1-v)$, it is small, which is usually one or two orders smaller. Accordingly, the approximate formula of Eq. S9 is the desired result given in Eq. 4 of the main text.

Modeling of alternative spatial distribution patterns of species using different spatial point models

We utilize R package *spatstat* (Baddeley & Turner, 2005; Baddeley, Rubak, & Turner, 2015) to construct different spatial point processes to model alternative spatial distributional patterns of

species. In detail, we use homogeneous Poisson process as the reference model to generate totally random distribution of species (Baddeley & Turner, 2005; Baddeley et al., 2015). Homogeneous Poisson process contains a single parameter, which describes density per unit area of a single species.

To model aggregate distribution, in addition to the modified Thomas cluster process mentioned in the main text, two cluster processes were implemented: Matern cluster process and Cauchy cluster process (Thomas, 1949; Matern, 1986; Waagepetersen, 2007; Ghorbani, 2013). The Matern cluster process assumes uniform distribution of offsprings around a disc of each cluster. Therefore, the radius of the disc is used to quantify the strength of aggregation. When the radius is small, the aggregation effect is expected to be high. For the Cauchy cluster process, offspring individuals are randomly placed around each cluster point following a Cauchy kernel characterized by a scale parameter. Higher scale parameter implies that the random replacement of individuals around parental points will become wide (less aggregate). Detailed parameter settings were presented in Table S1.

To model regular distribution, we utilize Strauss and Strauss hard processes (Strauss, 1975). In these processes, the key parameter controlling distribution regularity is the interaction parameter, which is a number between 0 and 1. When the interaction parameter is lower, the inhibition of neighboring points is higher, and thus stronger regularity of distribution is expected. Detailed parameter settings in these numerical simulations were presented in Table S1.

Robustness evaluation of the conspecific-encounter index and its variance estimator

Because the conspecific-encounter index was developed on the basis of a first-order Markov transition model, it would be informative to test its performance and robustness when the sampled biodiversity data do not rigorously follow the first-order Markov transition model. To do so, we conducted a numerical simulation by letting π vary when simulating data from the Markov model using Eqs. 2 and 3 in the main text.

Because the value of π has a range between 0 and 1, we consider letting π become a random variate and follow a beta distribution which should be one of the most popular probability distributions with range between 0 and 1. According to the magnitude of $E(\pi)$ (i.e., the expectation of π), we consider five beta distributions (denoted by beta (a, b) with two positive parameters a and b): $a = 1, b = 9$ with $E(\pi) = 0.1$; $a = 1, b = 3$ with $E(\pi) = 0.25$; $a = 2, b = 3$ with $E(\pi) = 0.4$; $a = 11, b = 9$ with $E(\pi) = 0.55$; $a = 7, b = 3$ with $E(\pi) = 0.7$.

Assume that the distribution of species relative abundances is composed of $p_i = cq_i, i = 1,2, \dots, S$, where S represents the number of species, q_is are positive numbers, and $c = \left(\sum_{i=1}^{S} q_i\right)^{-1}$ as a normalizing factor such that $\sum_{i=1}^{S} p_i = 1$. Four distributions of species relative abundances are considered and briefly summarized below.

Population 1. $(q_1, q_2, \dots, q_S)$ is a random sample from an exponential distribution with mean 1. Note that it is equivalent to that the resulting $(p_1, p_2, \dots, p_S)$ follows a Dirichlet

distribution with parameter 1.

Population 2. $(q_1, q_2, \ldots, q_S)$ is a random sample from a uniform distribution over (0, 1).

Population 3. $(q_1, q_2, \ldots, q_S)$ is species abundance data from the Pasoh plot (Manokaran et al., 1992; Adhul Rahim et al., 2004), in which 814 species are identified from 335240 trees.

Population 4. $(q_1, q_2, \ldots, q_S)$ is tree species abundance data collected from the interior and edge areas of Brazilian forests (Magnago et al., 2014), in which 443 species are found from 4140 trees.

Note that species richness is fixed at $S = 200$ for the first two hypothetical communities.

Given each combination of π's beta distribution and the sample size m, we simulate 1000 replicates using the Markov model (Eqs. 1 and 2 in the main text), in which π follows the given beta distribution and consistently varies in the consecutive simulation of subsequent individuals. As a result, the averaged v, the sample standard error (SE) and the estimated SE based on these 1000 replicates are calculated to evaluate the robustness of the proposed index v along with its variance estimator (Eq. 4 of the main text). Note that, in Tables S2-S5, "Sample SE" represents the sample SE of 1000 v's, while "Estimated SE" is to average 1000 estimated SEs using Eq. 4. If the estimated and sample SEs are comparable, it means that the proposed method (Eq. 4) is applicable to estimating the SE of the new index (v).

The results showed that, the proposed estimator in Eq. 4 is valid for estimating the variance of

v and robust when the assumption of the first Markov model used is violated, because most results

in Tables S2-S5 do not show sizable differences between the "Sample SE" and the "Estimated SE".

The key factor contributing to the high robustness of the proposed conspecific-encounter index

and its variance estimator is that the corresponding calculation formulae (Eqs. 3-4) are simply

composed of indicator functions (or binary random variates).

Impacts of combined line transects on the estimation of the conspecific-encounter index

Following the procedure that we manipulated the amphibian datasets sampled from different

field locations in China and Vietnam (Fig. S1), we tested whether the combination of sampled

biodiversity data derived from multiple line transects can have impacts on the estimation of the

conspecific-encounter index.

To be specific, we simulated hypothetical ecological communities with 100 species using the

modified Thomas process. The distributional aggregation level of each species is solely

determined by the dispersion parameter σ^2 (≤ 50 or ≥ 500). We then conducted the line transect

sampling with a fixed width (0.5 m). 1000 replicates were conducted in the numerical simulation.

For each replicate, the number of line transects was set to 3, 5, 10 and 20, respectively. After line-

transect sampling, we then compared the calculated value of the conspecific-encounter index

using the combined dataset derived from the multiple line transects (e.g., 5) versus the average of

the values, each of which was computed from the data collected from a single line transect only.

The simulation results showed that, when the number of line-transect varied (Figs. S4-S5), the combination of multiple line transects had similar results as the average value over the resulting v values, each of which was calculated from a single line transect. Regardless of how the distributional aggregation level of the simulated communities varied (highly aggregate or less aggregate), the calculated values for the proposed index using the combined or single line-transect datasets were consistently laid around the one-to-one ratio red line (Figs. S4-S5).

All these results supported the validity and appropriateness of using combined line-transect datasets when assessing the multi-species distributional aggregation level of amphibian assemblages in China and Vietnam in the main text.

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Additional figures and tables

Fig. S1. Sampling line-transect locations in southwest China and central-south Vietnam. Different

colors represent different line transects sampled from different counties of China or different
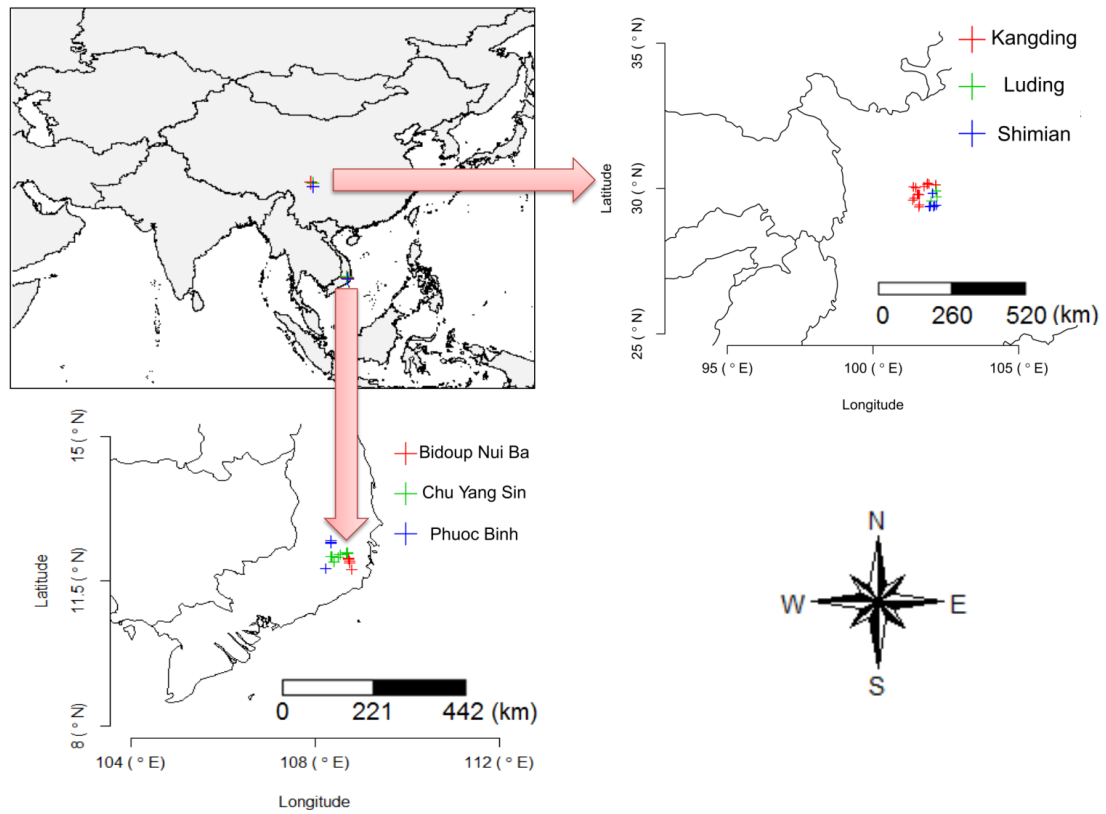
national parks of Vietnam.

Fig. S2. On the relationship between conspecific-encounter index and scale parameter in the simulated data using Cauchy and Matern cluster processes, respectively. Scale parameter in both cluster processes implies the relative concentration of random placement of offsprings around parental clusters (higher scale parameter implies low concentration, thus being less aggregate).
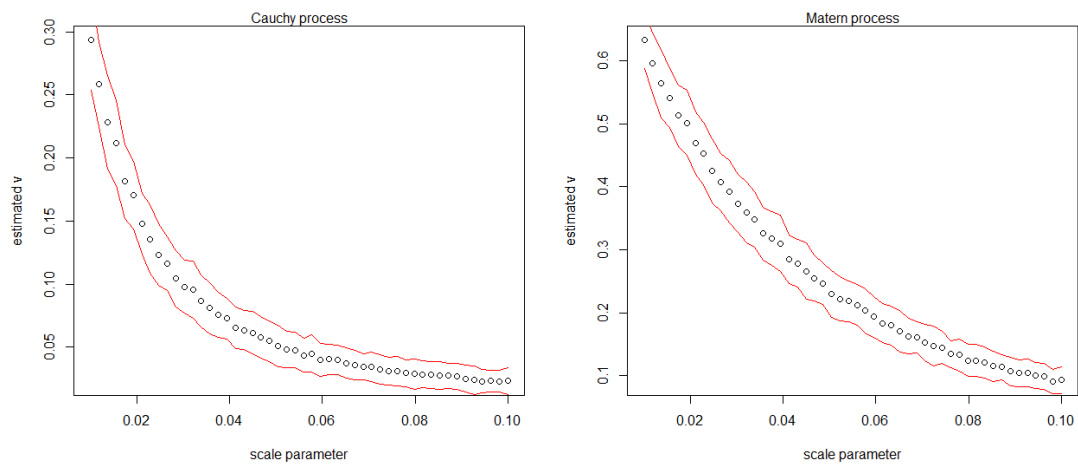
Fig. S3. On the relationship between conspecific-encounter index and inhibition strength gamma

parameter in the simulated data using Strauss and Strauss hard processes, respectively. Low

gamma value implies that conspecifics are strongly inhibited to occur around each individual point,

resulting in strong regular distribution.

Fig. S4. A comparison on the conspecific-encounter index calculated using the combined dataset

collected from multiple line transects versus the separate datasets collected from single line

transects. $v_{combined}$ denotes the value calculated using the combined dataset, while v_{single}

denotes the average value calculated from single line-transect datasets. 1000 replicates of line-

transect sampling are conducted here and the hypothetical ecological community is simulated to
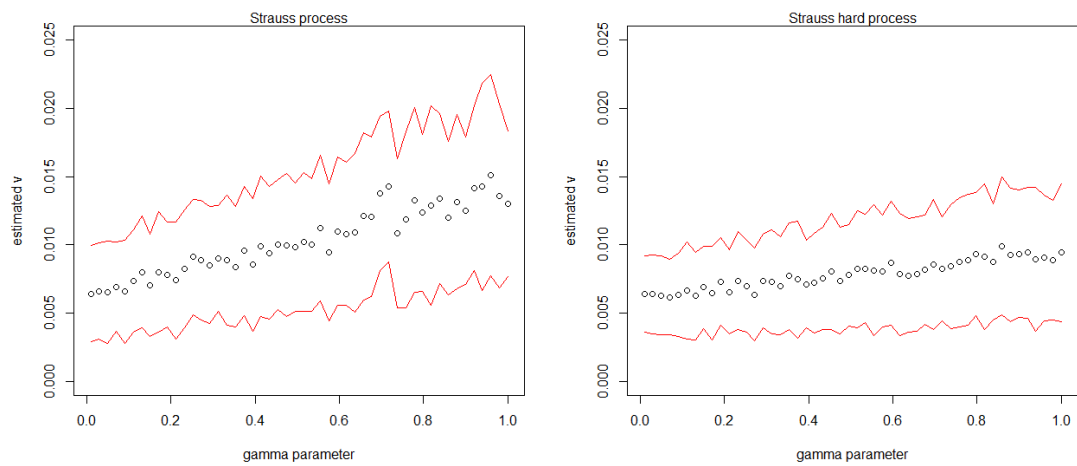
be highly aggregate.

Fig. S5. A comparison on the conspecific-encounter index calculated using the combined dataset collected from multiple line transects versus the separate datasets collected from single line transects. $v_{combined}$ denotes the value calculated using the combined dataset, while v_{single} denotes the average value calculated from single line-transect datasets. 1000 replicates of line-transect sampling are conducted here and the hypothetical ecological community is simulated to be less aggregate.
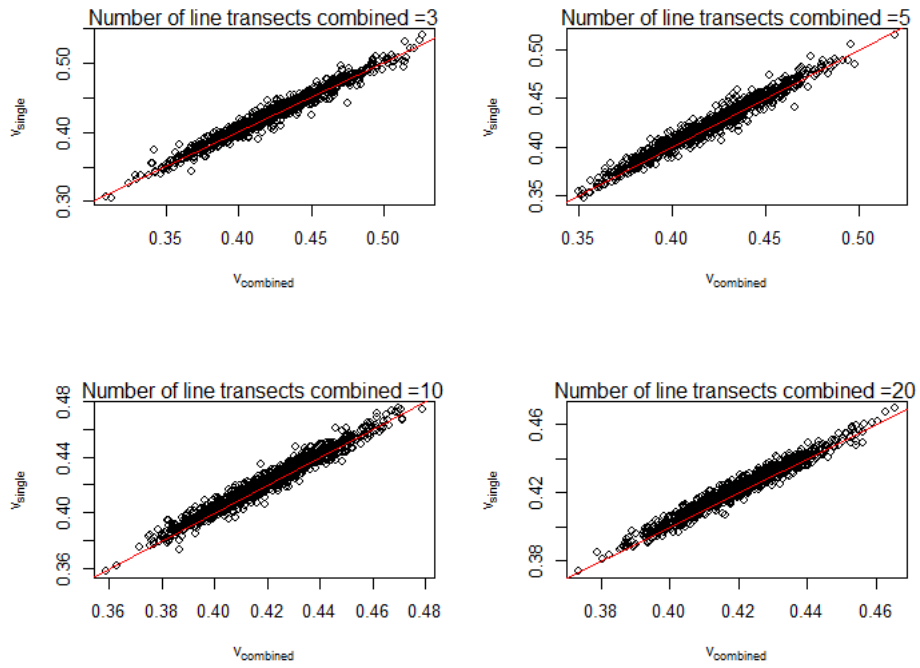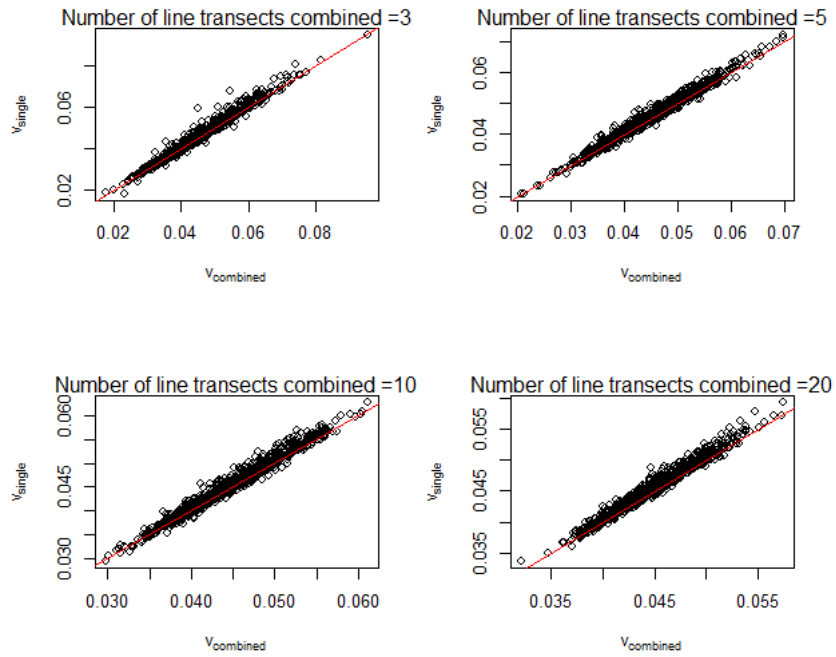
Table S1. Parameter settings in numerical simulations for different spatial point models.

Spatial point models	Parameter setting
Cauchy cluster process	Intensity of the Poisson process of cluster centres kappa=3; Mean number of points per cluster mu=5; Scale parameter for cluster kernel is allowed to vary from 0.01 to 0.1; Simulation window in R: [0,5]×[0,5]; line transect sampling width=0.05
Matern cluster process	Intensity of the Poisson process of cluster centres kappa=3; Mean number of points per cluster mu=5; Scale parameter for describing the radius of offsprings around the clusters is allowed to vary from 0.01 to 0.1; Simulation window in R: [0,5]×[0,5]; line transect sampling width=0.05
Strauss inhibition process	Interaction radius=0.1; Interaction parameter gamma is allowed to vary from 0.01 to 1; Simulation window in R: [0,5]×[0,5]; line transect sampling width=0.05
Strauss hard inhibition process	Interaction radius=0.1; Hard core distance=0.05; Interaction parameter gamma is allowed to vary from 0.01 to 1; Simulation window in R: [0,5]×[0,5]; line transect sampling width=0.05

Table S2. A sensitivity analysis of the proposed index v along with its variance estimator (Eq. 4 of the main text). In the numerical simulation, 1000 replicates are conducted and generated from the relative species abundance distribution set as Population 1 while the used probability model violates the first order Markov model.

Sample Size		π follows a beta distribution with parameters (a, b)				
		(1,9)	(1,3)	(2,3)	(11,9)	(7,3)
$m = 50$						
	Average v	0.111	0.256	0.405	0.551	0.705
	Sample SE	0.044	0.064	0.068	0.071	0.064
	Estimated SE	0.046	0.065	0.074	0.077	0.073
$m = 75$						
	Average v	0.109	0.256	0.406	0.553	0.703
	Sample SE	0.038	0.050	0.058	0.056	0.054
	Estimated SE	0.037	0.053	0.060	0.062	0.059
$m = 100$						
	Average v	0.108	0.259	0.408	0.555	0.705
	Sample SE	0.032	0.044	0.050	0.053	0.048
	Estimated SE	0.032	0.046	0.052	0.053	0.051
$m = 125$						
	Average v	0.107	0.258	0.407	0.556	0.705
	Sample SE	0.028	0.039	0.044	0.044	0.041
	Estimated SE	0.028	0.041	0.046	0.048	0.045

Table S3. A sensitivity analysis of the proposed index v along with its variance estimator (Eq. 4 of the main text). In the numerical simulation, 1000 replicates are conducted and generated from the relative species abundance distribution set as Population 2 while the used probability model violates the first order Markov model.

Sample Size		π follows a beta distribution with parameters (a, b)				
		(1,9)	(1,3)	(2,3)	(11,9)	(7,3)
$m = 50$						
	Average v	0.106	0.260	0.405	0.553	0.703
	Sample SE	0.045	0.064	0.071	0.071	0.064
	Estimated SE	0.044	0.066	0.074	0.077	0.073
$m = 75$						
	Average v	0.106	0.253	0.403	0.558	0.706
	Sample SE	0.036	0.050	0.058	0.058	0.052
	Estimated SE	0.037	0.053	0.060	0.062	0.059
$m = 100$						
	Average v	0.107	0.257	0.404	0.554	0.704
	Sample SE	0.032	0.046	0.051	0.049	0.044
	Estimated SE	0.032	0.046	0.052	0.053	0.050
$m = 125$						
	Average v	0.106	0.254	0.403	0.553	0.702
	Sample SE	0.028	0.039	0.045	0.043	0.040
	Estimated SE	0.028	0.040	0.046	0.047	0.045

Table S4. A sensitivity analysis of the proposed index v along with its variance estimator (Eq. 4 of the main text). In the numerical simulation, 1000 replicates are conducted and generated from the relative species abundance distribution set as Population 3 while the used probability model violates the first order Markov model.

Sample Size		π follows a beta distribution with parameters (a, b)				
		(1,9)	(1,3)	(2,3)	(11,9)	(7,3)
$m = 50$						
	Average v	0.108	0.257	0.401	0.552	0.704
	Sample SE	0.044	0.062	0.070	0.072	0.063
	Estimated SE	0.045	0.065	0.075	0.077	0.074
$m = 75$						
	Average v	0.103	0.253	0.406	0.554	0.703
	Sample SE	0.034	0.051	0.056	0.059	0.051
	Estimated SE	0.036	0.052	0.060	0.062	0.059
$m = 100$						
	Average v	0.106	0.255	0.403	0.550	0.701
	Sample SE	0.030	0.044	0.050	0.051	0.045
	Estimated SE	0.032	0.045	0.052	0.053	0.051
$m = 125$						
	Average v	0.106	0.254	0.403	0.554	0.702
	Sample SE	0.028	0.039	0.044	0.044	0.042
	Estimated SE	0.028	0.040	0.046	0.047	0.045

Table S5. A sensitivity analysis of the proposed index v along with its variance estimator (Eq. 4 of the main text). In the numerical simulation, 1000 replicates are conducted and generated from the relative species abundance distribution set as Population 4 while the used probability model violates the first order Markov model.

Sample Size		π follows a beta distribution with parameters (a, b)				
		(1,9)	(1,3)	(2,3)	(11,9)	(7,3)
$m = 50$						
	Average v	0.108	0.257	0.408	0.555	0.701
	Sample SE	0.044	0.064	0.071	0.071	0.065
	Estimated SE	0.045	0.065	0.074	0.077	0.074
$m = 75$						
	Average v	0.109	0.260	0.406	0.552	0.701
	Sample SE	0.035	0.051	0.056	0.055	0.054
	Estimated SE	0.037	0.053	0.061	0.062	0.059
$m = 100$						
	Average v	0.110	0.257	0.404	0.554	0.700
	Sample SE	0.031	0.043	0.048	0.051	0.046
	Estimated SE	0.032	0.045	0.052	0.053	0.050
$m = 125$						
	Average v	0.108	0.257	0.405	0.556	0.702
	Sample SE	0.028	0.039	0.045	0.044	0.041
	Estimated SE	0.028	0.040	0.046	0.047	0.045