Interrelationships Among SADIE Indices for Characterizing Spatial Patterns of Organisms

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Accepted for publication 30 March 2005.

ABSTRACT

Xu, X.-M., and Madden, L. V. 2005. Interrelationships among SADIE indices for characterizing spatial patterns of organisms. *Phytopathology* 95:874-883.

The SADIE (spatial analysis by distance indices) methodology for data analysis is a useful approach for quantifying the patterns of organisms (in terms of patches and gaps) and testing for randomness of the patterns. We investigated the interrelationship among key SADIE indices: index for distance to regularity for a data set (I_a), a global measure of aggregation or clustering; the local clustering indices (v_i and v_j), scaled distances to regularity for each individual sampling unit; and the averages of v_i and v_j across all sampling units, which are additional global measures of aggregation. We demonstrated that v_i and v_j are mathematically related to I_a and showed conditions when I_a and mean local clustering indices give very

similar results. Overall differences in average v_i and $|v_j|$ values, and between I_a and these averages, decreased with increasing size of the sampling grid in a simulation study. This was because one component of v_i and v_j (Y)—a measure of the distance to regularity under randomness for a given location (not a given count)—was found generally to vary little with location, except for locations near corners of the sampling grid. Nevertheless, because distance to regularity for individual observed counts was location-dependent, and this location effect varied with the observed counts value as well, a new-scaled index for each count $\times$ location combination may be warranted. The implications of these findings on epidemiological research are discussed.

Additional keywords: index to regularity, sampling size.

Recently, a novel and innovative approach called SADIE (spatial analysis by distance indices) was developed to quantify spatial patterns of organisms for either spatially referenced sampling units (7,8) or individuals (7). The methodology has been successfully used in several epidemiological studies (11–13). The basis of SADIE for spatially referenced sampling units, in its most commonly used form, is to quantify pattern by the total distance that individuals (e.g., diseased plants) must be moved between sampling units so that the data are as regular as possible (i.e., there is the same number of individuals in each sampling unit). The degree of nonrandomness is quantified by comparing the distance to regularity for the observed data set with distance to regularity for rearrangements of the observed data. One of the SADIE statistics, I_a , is defined as D/E_a , where D is the distance moved to achieve the regular pattern for the observed data, and E_a is the arithmetic mean distance to regularity for the m randomized samples.

The SADIE methodology was expanded further to define and analyze the spatial pattern of a data set (10). The contribution of each sampling-unit count to the pattern (in terms of “patches” and “gaps”) is quantified by determining a scaled and unitless clustering index for each sampling unit using the observed and randomized data. The clustering indices for sampling units with observed counts greater and less than the mean are indicated by v_i (a positive value) and v_j (a negative value), respectively. The indices v_i and v_j measure the respective degree to which a sampling unit contributes to clustering as a member of a patch and as a member of a gap. Mean v_i ($\bar{v}_i$) and v_j ($\bar{v}_j$) values for a data set are to be used as measures of the degree of nonrandomness in addition to

I_a . Recently, the SADIE method has been extended to assess the spatial association of two species (9,15) by correlating local association indices calculated from the individual sampling-unit clustering indices for each species. The SADIE methodology has evolved into a more graphical analysis of spatial patterns of local clustering and associating indices, rather than focusing solely on single indices of aggregation and association (10).

SADIE methodology has recently been used in several epidemiological investigations (11–13). However, the interpretation of and the interrelationships among the SADIE statistics are not always apparent because SADIE is based explicitly on randomization results for determining all indices and significance tests. For instance, we recently found that I_a has near-perfect linear correlation with $\bar{v}_i$ and $\bar{v}_j$ in a simulation study of plant disease epidemics (17). Indeed, the absolute values of these three indices are nearly equal, suggesting that just one of the indices may be sufficient to represent the pattern. Most importantly, these indices depended critically on initial epidemic conditions: number of initial infected plants and their spatial configuration (17). Although Perry et al. (10) now recommend the use of v_i - and v_j -based statistics for quantifying patterns in addition to the I_a statistic, it is still common for others to simply report I_a (and associated significance level).

In order to fully exploit the value of SADIE in comparing spatial results from different experiments, and hence, inferring biological/ecological differences between experiments, we need to understand the relationships of SADIE statistics with underlying biological and physical processes. Only then may we be able to ascertain to what extent the differences among statistics from different studies reflect biological/ecological differences of interest. SADIE indices previously were shown to be sensitive to absolute (and not just relative) positions of patches (16). Since v_i and v_j have been given paramount importance in graphical representations of the spatial system under investigation and in quantifying

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DOI: 10.1094/PHYTO-95-0874

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species association (9,10,15), it is important to understand how these indices depend on physical properties of the spatial system being studied.

In this study, we aim to investigate the basis of the observed close relationship among the SADIE indices (I_a , $\bar{v}_i$, and $\bar{v}_j$) and the relationship of local clustering indices with physical properties of the system. First, we show the relationship among SADIE indices using results from two recently published experimental investigations. Then, we show the mathematical interrelationships among the three SADIE indices. Finally, we shall use a few artificially generated data sets to illustrate the interrelationships among I_a , $\bar{v}_i$, and $\bar{v}_j$, and the properties of clustering indices in relation to several physical factors often encountered in epidemiological experiments, including sampling sizes, grid index system, and number of randomizations. SADIE statistics were calculated using the software (SADIESHELL) provided by J. N. Perry of Rothamsted Research, England, UK.

SADIE methodology—description of the method. Table 1 provides the notation and definition of important variables used to define SADIE statistics. The number or count of individuals in a sampling unit is given by x , and the mean count for the data set by $\bar{x}$. In SADIE methodology, sampling units with counts larger than the mean are donors, designated with an i subscript, in that individuals are moved out of these units in determining the total moves to regularity. Similarly, sampling units with counts smaller than the mean are receivers, designated with a j subscript, in that individuals moved out of the donor units are eventually placed in these units. For donor unit i , the total outflow of individuals is given by $x_i - \bar{x}$. Likewise, for receiver unit j , total inflow of individuals is given by $\bar{x} - x_j$. There are a total of n_i donor ($i = 1, \dots, n_i$) sampling units and n_j receiver ($j = 1, \dots, n_j$) sampling units. The specific moves to regularity are determined by a transportation algorithm (7,8), a computationally intensive procedure.

For donor unit i , at position (a_i, b_i) , the outflow to the j th of n_j receiver units, $j = 1, \dots, n_j$, at position (a_j, b_j) , is denoted as V_{ij} . The distance of this flow, denoted as d_{ij} , is $\sqrt{(a_i - a_j)^2 + (b_i - b_j)^2}$. The sum of the V_{ij} over all receiver units ($\sum_j V_{ij}$) for this donor unit i is simply $x_i - \bar{x}$. The average distance of outflow from unit i to all receivers, weighted by the magnitude of each individual flow, is denoted as Y_i ,

$$Y_i = \frac{\sum_j d_{ij} V_{ij}}{\sum_j V_{ij}} = \frac{D_i}{x_i - \bar{x}} \quad (1)$$

It should be noted that the global distance to regularity for the entire data set, used in determining I_a , is $D = \sum_i D_i$.

A dimensionless index of clustering, v , was then obtained from Y_i and may be used to compare between different units and between different sets of data. For outflows, a standardized and dimensionless index of clustering, v_i , is given by Perry et al. (10) as

$$v_i = \frac{Y_i {}_oY}{{}_iY {}_cY} \quad (2)$$

where ${}_cY$ and ${}_iY$ are expected values based on the randomizations as described below. The individual (original) counts are kept track of during the randomizations, and their average distance of outflow calculated for each randomization ($Y_{i,k}$; $k = 1, \dots, m$). ${}_cY$ is the average outflow distance for the observed count, x_i , across all the randomizations, i.e.,

$${}_cY = \sum_{k=1}^m Y_{i,k} / m$$

Similarly, instead of following the count through its randomizations to other units, the individual location for the i th unit (a_i, b_i) is kept track of, which will contain any one of the original counts in a given randomization. The absolute value of the average flow distance for each location is determined in each randomization (${}_{k,i}Y$; $k = 1, \dots, m$) and the average for this location across all randomizations for unit i is denoted as ${}_iY$, i.e.,

$${}_iY = \sum_{k=1}^m {}_{k,i}Y / m$$

Hence, ${}_iY$ is the expected value of the average absolute flow distance for the i th unit, under the assumption of a random arrangement of the observed counts among the sample units. Furthermore, the average absolute value of ${}_cY$ for a data set over all donor and receiver units, which is equal to the average value of ${}_iY$ over all the units, is denoted ${}_oY$. The mean clustering index for donor units, averaged across the n_i donor units, is then denoted $\bar{v}_i = (\sum_i v_i) / n_i$.

For inflows, v_j is defined similarly, again with the convention that it is negative in sign. As a general rule, large values of v_i (or $\bar{v}_i$ for the entire data set) $\approx > 1.5$ indicate patchiness; large negative values of v_j (or $\bar{v}_j$) $\approx < -1.5$ indicate membership to a gap; and values close to unity indicate a random placement of that unit in relation to others nearby (10). Note, E_a , ${}_iY$, ${}_cY$, and ${}_oY$ are all defined, theoretically, as expected values for a random pattern (10). More formally, their calculated values are expected values only with an infinite number of randomizations. With the reality of a finite number of randomizations, the calculations give estimates of the true expected values.

Experimental data on the relationship of I_a , $\bar{v}_i$, and $\bar{v}_j$. We have obtained two sets of data on I_a , $\bar{v}_i$, and $\bar{v}_j$ from two recently published studies (11,12) to demonstrate the empirical relationship between these measures of nonrandomness. Although neither paper reported the $\bar{v}_i$ and $\bar{v}_j$ values, we obtained these from the authors and used these with the reported I_a values (with corrections for typesetting errors). Figure 1 shows the pair-wise relationships among the absolute values of I_a , $\bar{v}_i$, and $\bar{v}_j$ for these two data sets. The Pearson product-moment correlation coefficient was > 0.9 ($P < 0.001$) for both data sets.

TABLE 1. Notation and definition of key variables

Symbol	Definition
x_i	Individual donor unit counts ($x_i > \bar{x}$, where $\bar{x}$ is the mean for a data set). Similarly, an index j is used for a receiver unit ($x_j < \bar{x}$). For simplicity, only symbols for donors (index i) are given below
D_i	Overall distance moved to achieve the regular pattern for donor unit i
D	Overall distance moved to achieve the regular pattern for the whole data set = $\sum_i D_i$
E_a	Arithmetic mean distance to regularity for the a number of permutations for a whole data set
I_a	An index to regularity = D/E_a
Y_i	Average distance of outflow from unit i to all receivers = $D_i/(x_i - \bar{x})$
${}_cY$	Average distance of outflow calculated from the randomizations for the observed count in a data set
${}_iY$	Average absolute flow distance calculated from the randomizations for each individual location in a data set
${}_oY$	Average absolute value of ${}_cY$ for a data set over all donor and receiver units, which is equal to the average value of ${}_iY$ over all the units
u_i	A dimensionless index, defined as $u_i = Y_i/{}_cY$
w_i	A dimensionless index, defined as $w_i = {}_oY/{}_iY$
v_i	A dimensionless clustering index for each counts data at a particular location, defined as $v_i = (Y_i {}_oY)/({}_iY {}_cY) = u_i w_i$
$\bar{v}_i$	Average of clustering indices, v_i , over all donor units for a whole data set, equivalent to average of weighted u_i , with weights given by w_i

Mathematical relationship of $\bar{v}_i$ and $\bar{v}_j$ with I_a . Assuming we have m randomizations, then ${}_cY$ can be written as

$${}_cY = \frac{\sum_{k=1}^m Y_{i,k}}{m} = \frac{\sum_{k=1}^m D_{i,k}}{m(x_i - \bar{x})} \quad (3)$$

where $D_{i,k}$ is the total outflow distance for the sampling counts, x_i , in the k th randomization. Combining this with the equation above for Y_i , one obtains

$$v_i = \frac{Y_i {}_oY}{{}_iY {}_cY} = \frac{D_i / (x_i - \bar{x})}{{}_cY} \cdot \frac{{}_oY}{{}_iY} = \frac{D_i}{{}_cY} \cdot \frac{{}_oY}{{}_iY} = \frac{D_i}{\bar{D}_i} \cdot \frac{{}_oY}{{}_iY} \quad (4)$$

where

Fig. 1. Plot of $\bar{v}_i$ against $|\bar{v}_j|$ and $(\bar{v}_i + |\bar{v}_j|)/2$ against I_a from two experimental studies: open circle, Pethybridge and Turecek (11); and filled circle, Scott et al. (12). Table 1 provides notation and symbols.

$$\bar{D}_i = \sum_{k=1}^m D_{i,k} / m$$

is the average total distance to regularity across the randomizations for the observed counts, x_i . Moreover,

$$\sum_{i=1}^{n_i} \bar{D}_i$$

is identical to E_a , the average total distance to regularity for all randomizations. To simplify the following presentations, we can define u_i as

$$u_i = \frac{D_i}{\bar{D}_i} = \frac{Y_i}{{}_cY} \quad (5)$$

for the i th sampling unit. u_j is defined similarly for the sampling units with counts less than the mean. Compared to the I_a definition, u_i is equivalent to the I_a for the individual sampling counts data. Hence, from equation 4, v_i is equivalent to the I_a value for the individual sampling counts data (u_i) weighted by a factor w_i ($w_i = {}_oY / {}_iY$) depending on its spatial location; that is,

$$v_i = \frac{Y_i}{{}_cY} \cdot \frac{{}_oY}{{}_iY} = \frac{Y_i}{{}_cY} \cdot w_i = u_i \cdot w_i \quad (6)$$

Given that there are n_i outflow units in a data set, $\bar{v}_i$, an average of this weighted u_i for each outflow unit is written as

$$\bar{v}_i = \frac{\sum_{i=1}^{n_i} v_i}{n_i} = \frac{\sum_{i=1}^{n_i} (u_i \cdot w_i)}{n_i} = \frac{\sum_{i=1}^{n_i} \left(\frac{D_i}{\bar{D}_i} \cdot w_i \right)}{n_i} \quad (7)$$

Similarly, with n_j inflow units, one can write

$$\bar{v}_j = \frac{\sum_{j=1}^{n_j} v_j}{n_j} = \frac{\sum_{j=1}^{n_j} u_j \cdot w_j}{n_j} = \frac{\sum_{j=1}^{n_j} \left(\frac{D_j}{\bar{D}_j} \cdot w_j \right)}{n_j} \quad (8)$$

For the whole data set, I_a is then

$$I_a = \frac{D}{E_a} = \frac{\sum_{i=1}^{n_i} D_i}{\sum_{i=1}^{n_i} \bar{D}_i} = - \frac{\sum_{j=1}^{n_j} D_j}{\sum_{j=1}^{n_j} \bar{D}_j} \quad (9)$$

where

$$\sum_{i=1}^{n_i} D_i = - \sum_{j=1}^{n_j} D_j = D$$

Therefore, the global I_a is related to the mean clustering index via the distance moved for each individual sampling unit to achieve a regular distribution, whereas the mean clustering index is an average of location-weighted I_a , i.e., u_i or u_j , over all outflow or inflow sampling units.

THEORY AND APPROACHES

The key to understanding the properties of individual clustering indices and the relationships among I_a , $\bar{v}_i$, and $\bar{v}_j$ is to understand the properties of ${}_cY$ and ${}_iY$. In this study, we generated a number of data sets to investigate the properties of ${}_cY$ and ${}_iY$ in relation to nonbiological factors, including sampling grid size, number of randomizations, frequency distribution, and spatial location of a specific count. All statistical analyses were carried out using Genstat (VSN International, Oxford) (6).

Data generation. We generated two data sets for each of three sampling sizes: 5×5 , 10×10 , and 20×20 . One was drawn from a Poisson distribution with a mean (μ) of 50. The other was from a beta-binomial distribution with the parameters of $\alpha = 5$ and $\beta = 5$, and a sample unit size (n_{su}) of 100. This combination of parameters gave a mean the same as the Poisson distribution, $\mu =$

$n_{su}/(\alpha + \beta)$. The heterogeneity parameter of the beta-binomial was $1/(\alpha + \beta) = 0.1$. The exact original spatial location of each count is irrelevant since ${}_cY$ and ${}_iY$ are averages over all randomizations and hence only dependent on the actual counts and the grid system used.

From these initial six data sets, we generated an additional 18 data sets. Six of the eighteen were obtained simply by multiplying the spatial grid indices by five, except the original indices of 1 (i.e., the resulting spatial location indices are (1,1), (1,5), and (1,10) instead of (1,1), (1,2), and (1,3), etc.). This extended the sampling coverage (i.e., physical area) without changing the counts. Another six sets were obtained by modifying original counts data to increase the data range by the following rule:

$$z_i = x_i \left(\frac{x_i}{\bar{x}} \right)^2 \quad (10)$$

where z_i and x_i are the transformed and original counts data, respectively. This transformation is used for two reasons; in addition to the increased data range, the transformation will also generate data that are skewed to the right. Of course, the newly obtained data would not be expected to conform to either a Poisson or a beta-binomial distribution. However, for ease of reference, we still use the distribution name to refer to the origin of the data sets. In the final six data sets, both original data and spatial indices were replaced by the modified data with an increased range and the expanded spatial indices, respectively.

Properties of ${}_cY$ and ${}_iY$. For each of the 24 data sets, we used the SADIE software to calculate the ${}_cY$ and ${}_iY$ values using the 39, 390, and 3,900 randomizations. Through the 24 generated data sets, we were able to investigate the effects of the following factors—data distribution, sampling size and index system, range of counts data, and number of randomizations—on ${}_cY$ and ${}_iY$.

We calculated the coefficient of variation (CV) for each generated set of ${}_cY$ and ${}_iY$. Analysis of variance (ANOVA) was used to determine the magnitude of the effects of the factors on these CVs. Then, we investigated the relationship between ${}_cY$ and count x_i , and between ${}_iY$ and grid position (location; a_i , b_i). By definition, there is no relationship between ${}_cY$ and grid position (since ${}_cY$ is defined only in terms of the count, not location) nor between ${}_iY$ and x_i (since ${}_iY$ is defined only in terms of the location, not the count). In all subsequent analyses, we use x to represent observed counts data when all the data are included in analysis. Regression analysis was used to quantify these relationships. In the analysis of ${}_cY$ and x_i , four different models were used. Model 1 assumed a common relationship for both outflow and inflow units, whereas the other three models assumed a different relationship for outflow and inflow. Namely, model 1 is of the following form:

$$|{}_cY| = a + b|x - \bar{x}| \quad (11)$$

In model 2, a common slope (b) but different intercept (a) were assumed for outflow and inflow; in model 3, a common intercept (a) but different slope (b) were assumed; and in model 4, different slopes as well as intercepts were assumed.

Relationships among SADIE statistics. Six data sets were used to explore the relationship of u_i (i.e., individual sampling-unit I_a) with v_i and v_j , and of I_a with $\bar{v}_i$ and $\bar{v}_j$: original 5×5 , 10×10 , and 20×20 beta-binomial data sets and their corresponding data sets with larger range. In addition, a set of 3×3 counts data was generated from a beta-binomial distribution ($\alpha = \beta = 5$ and $n_{su} = 100$) to further investigate the effect of small sampling sizes on the relationships among SADIE indices.

For each of the above seven data sets, we conducted 500 random permutations to generate 500 different spatial data sets but with the same counts data. For each permutation, the total distance to regularity (D) was obtained. Theoretically, the E_a , ${}_cY$, and ${}_iY$ values obtained from the SADIE randomizations for these 500 permuted data sets of each of the seven original data sets should be the same since these are functions of the frequency distribution

of the original counts and not of the spatial locations of the counts. However, the *estimated* values of E_a , ${}_cY$, and ${}_iY$ obtained from the SADIE software vary between the 500 permuted data sets, because the number of randomizations (even when m is $>3,000$) typically is not large enough to capture all the possible arrangements of the counts. So, in order to eliminate the effects of variation in estimates of E_a , ${}_cY$, and ${}_iY$ among the permutations on the estimates of I_a , u_i , v_i , and v_j , only one common set of E_a , ${}_cY$, and ${}_iY$ was used for each of the seven original data sets. In addition, ${}_cY$ values should be the same for all sampling units with the same counts data within a data set. However, as currently implemented in the SADIE software, this is not the case because the ${}_cY$ values are not averaged over all sampling units with same counts within a data set. As demonstrated herein, ${}_cY$ can be accurately estimated for a given data set with a regression model (model 2 where a common slope (b) but different intercept (a) were assumed for outflow and inflow in equation 11). Thus for the above two reasons, instead of using the ${}_cY$ value directly from randomizations, this regression model was used to estimate ${}_cY$ using the one common set of ${}_cY$ values, as described previously, for each of these seven data sets. For all permuted data sets, 3,900 randomizations were used to calculate SADIE statistics. For each of the seven original data sets, we used regression analysis to determine the relationships between 500 pairs of $\bar{v}_i$ and $|\bar{v}_j|$, and $(\bar{v}_i + |\bar{v}_j|)/2$ and I_a , i.e., one pair from each permutation.

Effects of spatial location on v_i and v_j . Because of the intensive computation required, we only used the original 5×5 data set generated with a beta-binomial distribution to investigate the effect of spatial locations of individual counts data on Y_i , hence v_i and v_j . We generated a further 1,000 permutations for each of four situations where the maximum count [$\max(x_i)=78$] was forced to be placed in a specified location (but the other counts were randomly placed, as before, for each permutation). The maximum count was placed at either (1,1), i.e., at the corner; (1,3), i.e., on the edge, half-way from the corners; (3,3), i.e., in the center; and randomly (the nominal approach). For each of the above permutations, we calculated Y_i for the count $x_i = 78$ using the SADIE software. The cumulative frequency distribution of this Y_i across the 1,000 permutations was then compared between the four locations. This procedure was repeated for two more counts: $x_j = 15$ (minimum) and $x_j = 52$ (close to the mean count) in the same 5×5 data set. In calculating v_i and v_j for all permutations at all positions for the three selected counts, ${}_cY$ and ${}_iY$ values from the 3,900 randomizations of the corresponding original data set, as described above, were used.

RESULTS

Properties of ${}_cY$ and ${}_iY$. Table 2 shows a partial summary of the effects of physical factors on variation of ${}_iY$ and ${}_cY$. ANOVA of the CV values showed the importance of the number of randomizations to the resulting indices. For the CVs, more than 75% of the variation was due to the main effects of the number of randomizations and its interaction with other factors. As expected, the greater the number of randomizations, the smaller the CV.

In all the following analyses, only results from 3,900 randomizations were used. Overall, the CV of ${}_iY$ was about half of that of ${}_cY$. Average CV for ${}_iY$ was about 3.6%. ${}_iY$ was significantly related to spatial location (Fig. 2). In particular, those units near (but not at) the corners had much smaller ${}_iY$ values than other units. Interestingly, the corner units had much greater ${}_iY$ values than those nearby units (Fig. 2). On the other hand, units on the edges but not near the corners had greater ${}_iY$ values for sampling sizes of 10×10 and 20×20 . For the sampling size of 5×5 , the corner units had the greatest ${}_iY$ values, whereas those units on edges but not at the corner had the lowest ${}_iY$. If those units at or near the corners were excluded, the CV was reduced to about 2.5%. A quadratic model of the spatial locations accounted for about 60%

of the variation in iY . As expected, iY was not related to the actual counts (data not shown). The CV of iY did not vary much with sampling size, range of counts data, and grid indices, although it appears that larger sampling size led to a smaller CV (Table 2).

Regression analysis showed that $|cY|$ was almost perfectly linearly related to $|x - \bar{x}|$ (Fig. 3). Increasing the numbers of randomizations led to a significant increase in the accuracy of this regression model, as seen from the percent variance accounted for (R_a^2 ; Table 2), particularly for the large sampling sizes. The precise form of this linear relationship could, however, differ between inflow and outflow units; this was particularly so for the data set with large range and large sampling size (Table 2). That is, model 1 (which specifies a common relationship for outflow and inflow) was often inferior to the other models (in terms of percent variance accounted for) for the 10×10 and 20×20 grids with large data range. Interestingly, results for the 5×5 sampling size differed from those for 10×10 and 20×20 sizes for the Poisson-generated data. For the cases in which there were significant differences in the linear relationship between inflow and outflow units, the differences appeared to result mainly from the differences in the intercept rather than the slope (Table 2). Namely, where significant differences existed in model fits, model 2 often resulted in a better fit than model 3 and accounted for a similar amount of variance as model 4.

Relationships among SADIE statistics. The Pearson product-moment correlation of u_i (or $|u_i|$) with v_i (or $|v_i|$) was very high and, on average, increased with increasing sampling size. For the 3×3 sampling size, there were a considerable number (22 of 500) of permutations where the correlation was <0.85 , although for most cases (342 of 500) it was >0.95 . For the 5×5 sampling size, all correlations were >0.95 , whereas for the 10×10 and 20×20 , all correlations were >0.99 . There were no discernible differences in the correlation between different data sets of the same sampling size with different data ranges.

Figure 4A plots the differences between $\bar{v}_i$ and $|\bar{v}_j|$ for four selected data sets. Clearly, the difference between $\bar{v}_i$ and $|\bar{v}_j|$ decreased with increasing sampling size. The average differences between $\bar{v}_i$ and $|\bar{v}_j|$ were 8.6, 7.5, 4.1, and 2.7% of their averages for sampling sizes of 3×3 , 5×5 , 10×10 , and 20×20 , respectively. The average $\bar{v}_i$ and $|\bar{v}_j|$ values were close to 1, as expected. Furthermore, there were similar numbers of permutations with $\bar{v}_i > |\bar{v}_j|$, as those with $\bar{v}_i < |\bar{v}_j|$ (Fig. 4A). The effect of sampling size on the relationship between $\bar{v}_i$ and $|\bar{v}_j|$ is further demonstrated in the regression analysis (Table 3). The smaller the sampling size, the smaller the percentage of variance accounted for by the linear model. Similarly, the smaller the sampling size, the greater the intercept and the greater the slope deviated from 1.0.

TABLE 2. Summary of the effects of simulation conditions^a on the coefficient of variation (CV) of iY and cY indices, and the percentage of variance accounted for (R_a^2 , the adjusted coefficient of determination) by four models relating cY to counts per quadrat^b

Sampling size	Data range	Grid index	Randomizations	Poisson distribution						Beta-binomial distribution					
				CV		R_a^2 for each model				CV		R_a^2 for each model			
				cY	iY	1	2	3	4	cY	iY	1	2	3	4
5×5	1	1	39	9.5	7.6	0.65	0.73	0.70	0.73	8.3	6.6	0.58	0.70	0.62	0.72
			390	9.2	4.5	0.86	0.96	0.92	0.96	9.1	4.2	0.85	0.95	0.92	0.95
			3,900	8.8	4.1	0.87	0.97	0.93	0.97	8.3	3.7	0.87	0.99	0.94	0.99
		2	39	11.7	5.5	0.71	0.76	0.76	0.77	9.2	6.2	0.46	0.65	0.49	0.71
			390	9.3	4.8	0.83	0.91	0.89	0.91	9.1	4.9	0.86	0.95	0.93	0.95
			3,900	8.9	4.2	0.87	0.96	0.93	0.96	8.5	3.9	0.88	0.99	0.95	0.99
	2	1	39	8.9	6.4	0.81	0.81	0.81	0.81	9.3	7.6	0.56	0.72	0.66	0.72
			390	8.1	3.4	0.96	0.96	0.96	0.96	9.0	4.4	0.77	0.96	0.91	0.96
			3,900	8.2	3.5	0.98	0.98	0.98	0.98	8.3	3.2	0.80	0.99	0.95	1.00
		2	39	10.1	5.3	0.66	0.66	0.66	0.67	10.7	6.7	0.65	0.73	0.77	0.77
			390	8.6	3.7	0.96	0.96	0.96	0.96	8.2	3.7	0.75	0.94	0.89	0.94
			3,900	8.3	3.6	0.98	0.99	0.98	0.99	8.2	3.2	0.78	1.00	0.93	1.00
10×10	1	1	39	10.3	6.8	0.50	0.50	0.50	0.50	11.1	7.7	0.54	0.55	0.54	0.55
			390	7.6	3.4	0.90	0.90	0.90	0.90	7.8	3.5	0.91	0.92	0.92	0.92
			3,900	7.2	3.0	0.99	0.99	0.99	0.99	7.0	2.7	0.97	0.99	0.98	0.99
		2	39	9.5	7.0	0.43	0.43	0.43	0.45	9.6	7.7	0.52	0.53	0.52	0.53
			390	7.4	3.8	0.92	0.92	0.92	0.93	7.2	3.4	0.90	0.91	0.90	0.92
			3,900	7.3	3.1	0.99	0.99	0.99	0.99	6.9	3.0	0.97	0.99	0.98	0.99
	2	1	39	9.3	8.0	0.47	0.58	0.52	0.58	9.2	6.4	0.30	0.44	0.40	0.44
			390	7.2	3.5	0.76	0.89	0.84	0.89	7.2	3.5	0.56	0.90	0.76	0.91
			3,900	7.1	3.1	0.84	0.99	0.93	0.99	6.5	2.7	0.60	0.98	0.81	0.98
		2	39	9.1	6.8	0.41	0.51	0.45	0.51	9.8	6.8	0.26	0.41	0.35	0.41
			390	7.5	3.3	0.80	0.93	0.89	0.93	6.8	3.3	0.55	0.90	0.74	0.90
			3,900	7.0	2.9	0.85	0.99	0.94	0.99	6.6	2.8	0.61	0.98	0.82	0.98
20×20	1	1	39	10.5	8.6	0.49	0.50	0.50	0.50	13.0	9.7	0.42	0.42	0.42	0.42
			390	7.9	4.3	0.86	0.88	0.88	0.88	7.6	4.6	0.86	0.86	0.86	0.87
			3,900	7.4	3.7	0.97	0.99	0.98	0.99	7.3	3.8	0.98	0.98	0.98	0.99
		2	39	11.9	9.0	0.47	0.49	0.48	0.49	11.6	9.6	0.40	0.41	0.40	0.41
			390	7.8	4.8	0.88	0.89	0.89	0.89	7.9	5.1	0.88	0.89	0.88	0.89
			3,900	7.4	3.7	0.97	0.99	0.98	0.99	7.3	3.7	0.98	0.98	0.98	0.99
	2	1	39	10.8	10.5	0.25	0.36	0.32	0.36	12.7	9.7	0.27	0.45	0.40	0.45
			390	8.0	5.2	0.63	0.88	0.81	0.88	9.2	4.3	0.55	0.90	0.82	0.90
			3,900	7.4	4.3	0.70	0.98	0.90	0.98	8.6	3.7	0.59	0.98	0.88	0.98
		2	39	11.1	10.2	0.28	0.39	0.37	0.39	12.9	10.1	0.26	0.45	0.38	0.45
			390	7.8	5.0	0.62	0.88	0.80	0.88	9.3	4.8	0.54	0.89	0.82	0.90
			3,900	7.4	4.2	0.70	0.98	0.90	0.98	8.6	3.5	0.59	0.98	0.88	0.98

^a Number of quadrats (sampling size); data range (original data generated as a binomial or beta-binomial distribution, [coded as 1], or increased range based on equation 10 in text [coded as 2]); grid index (original distances between quadrats [coded as 1], or distances increased by a factor of 5 [coded as 2]); and number of randomizations in the simulations.

^b Table 1 provides explanation of notation and text for description of the four models.

Since the correlation of u_i (and $|u_i|$) with v_i (and $|v_i|$) was generally very high, especially for large sampling sizes, the linear relationship of $\bar{v}_i$ and $|\bar{v}_i|$ with I_a was nearly identical to that of $\bar{u}_i$ with I_a . The pattern in the differences between I_a and $\bar{u}_i$ is very similar to that between $\bar{v}_i$ and $|\bar{v}_i|$ (Fig. 4A versus Fig. 4B).

Fig. 2. Plot of spatial analysis by distance indices (SADIE) $|Y$ and $|Y|$ against spatial locations for the original beta-binomial data set of **A**, 5×5 , **B**, 10×10 , and **C**, 20×20 sampling units, obtained from 3,900 randomizations. Table 1 provides notation and symbols.

Fig. 3. Plot of spatial analysis by distance indices (SADIE) $|cY|$ against x_i for the original beta-binomial data set of **A**, 5×5 , **B**, 10×10 , and **C**, 20×20 sampling units, obtained from 3,900 randomizations. Table 1 provides notation and symbols.

The correlation between $\bar{u}_i$ and I_a increased with increasing sampling size: it was 0.90, 0.92, 0.98, and 0.99 for sampling sizes of 3×3 , 5×5 , 10×10 , and 20×20 , respectively, which was equal to the correlation between $(\bar{v}_i + |\bar{v}_j|)/2$ and I_a (up to two significant numbers) for the same data sets. The effects of sam-

pling size on the relationship among these indices were further confirmed by regression analyses (Table 3). The larger the sampling size, the closer the intercept was to zero and the slope was to 1.0. Indeed, for a sampling size of 20×20 , the intercept and slope estimates were not significantly different from 0 and 1.0, respectively.

Effects of spatial locations on v_i and v_j . Figure 5 shows the cumulative frequency distribution of Y_i (or Y_j) corresponding to the three individual counts ($x_i = 78$ [maximum], 52 [~mean], and 15 [minimum]) for four sets of permutations. There were considerable differences among the four distributions for x_i values of either 78 or 15. When $x_i = 78$, there was the greatest number of large Y_i values when this count was at the corner, whereas there was the smallest number of large Y_i values when this count was at the center of the grid. The average Y_i values were 1.96, 1.62, 1.56, and 1.66 for the locations of (1,1), (1,3), (3,3), and random position, respectively (Table 4); based on pair-wise t tests, all differences were significant except between 1.62 and 1.66. Placing the maximum count at the corner also resulted in greatest variation in Y_i (CV = 39%), whereas placing it at the center resulted in least variation (CV = 28%). Similarly, for $x_i = 15$, the average $|Y_j|$ values were 2.00, 1.68, 1.58, and 1.71 for the locations of (1,1), (1,3), (3,3), and random position, respectively (Table 4). In contrast, for $x_i = 52$, differences in Y_i between the four placement conditions were far less apparent compared with those found for extreme counts of 78 and 15 (Fig. 5). Because $x_i = 52$ is close to the average of this data set, there are only a few moves to regularity (since $x_i - \bar{x}$ is close to 0). Thus, Y_i can only take a few possible values, and there is a corresponding zig-zag shape (pronounced step-function) to the cumulative distribution. For this count, the average Y_i values were 1.38, 1.30, 1.42, and 1.35 for the locations of (1,1), (1,3), (3,3), and random position, respectively (Table 4). As expected from the definition of cY , the average value of Y_i for the final location treatment (i.e., random location) over the 1,000 permutations was very close to the estimated cY from the 3,900 randomizations for all three counts (Table 4).

Table 4 shows the summary results of u_i and u_j and the clustering indices (v_i and v_j) calculated from the Y_i (Y_j) values presented in Figure 5. The u_i (u_j) value (hence v_i and v_j) was influenced by both counts and spatial location. Because the 1,000 Y_i (or Y_j) in Figure 5, as well as v_i (or v_j) values were from randomly permuted data sets (with one value being fixed), these permutations can be considered a random sample of the population of spatial patterns where the specific count was held at the specific location in relation to all possible combinations of all other counts in the remaining locations. The specific spatial patterns for each permutation range from regular to highly aggregated, but will be expected to be random on average. The principle of the SADIE methodology is that a value of an index (v_i , $|v_j|$, $\bar{v}_i$ and $|\bar{v}_j|$, I_a) close to unity indicates a random pattern, because the index is a ratio between an observed (local or global) distance value (or its scaled version) and an average value across randomizations. It follows that for each count the average v_i and v_j over the 1,000 random permutations should be close to 1.0 over the 1,000

Fig. 4. Boxplots of the differences **A**, between $\bar{v}_i$ and $|\bar{v}_j|$, and **B**, between I_a and $\bar{u}_i$. Table 1 provides notation and symbols. The upper and lower limits of the box indicate the upper and lower quartiles of the distribution and the horizontal line through the box indicates the median. The ‘whiskers’ extending beyond the box indicate the range of 10th and 90th percentiles; ‘outlying’ points are shown individually as open circles.

TABLE 3. Summary of regression analyses of $\bar{v}_i$ on $|\bar{v}_j|$, and of I_a on $(\bar{v}_i + |\bar{v}_j|)/2^a$

Sampling size	$\bar{v}_i$ on $ \bar{v}_j $ ^b			I_a on $(\bar{v}_i + \bar{v}_j)/2^b$		
	Intercept	Slope	R_a^2	Intercept	Slope	R_a^2
3×3	0.278 (0.037)	0.698 (0.036)	0.42	-0.147 (0.026)	1.158 (0.026)	0.80
5×5	0.214 (0.027)	0.782 (0.027)	0.63	-0.042 (0.020)	1.039 (0.020)	0.85
10×10	0.074 (0.016)	0.923 (0.016)	0.87	-0.037 (0.010)	1.039 (0.010)	0.95
20×20	0.028 (0.011)	0.970 (0.011)	0.94	... ^c	0.999 (0.001)	0.97

^a The data used for the analysis are shown in Figures 4 and 5 and generated using the original beta-binomial distribution data sets. Table 1 provides explanation of notation.

^b Linear regression model. Numbers in parentheses are standard errors of intercepts and slopes. The percentage of variance accounted for by the model is summarized as R_a^2 (the coefficient of determination adjusted for degrees of freedom).

^c The intercept is not significantly different from zero and hence set to zero when fitting the model.

permutations. For all three counts, the average values of v_i and v_j were close to this expected value of 1.0 only when the point was held at the middle of an edge, but for the other two positions they deviated considerably from 1.0 (Table 4). This deviation appeared to increase as the count concerned was further away from the mean.

DISCUSSION

SADIE methodology has been widely and successfully used recently in describing and quantifying spatial count data in several disciplines, including plant pathology (1–5,11,12,14,15). Although Perry et al. (10) now recommend the use of v_i - and v_j -based statistics for quantifying patterns in addition to the I_a statistic, it is still common for others to simply report I_a (and associated significance level). In assessing the results from several experimental data sets (11,12) and from a spatial analysis of predictions from a stochastic epidemic simulation model (17), a close correlation between $\bar{v}_i$, $|\bar{v}_j|$, and I_a was observed. Here we have shown that $\bar{v}_i$ and $|\bar{v}_j|$ are mathematically related to I_a . Both $\bar{v}_i$ and $|\bar{v}_j|$ are weighted averages of individual I_a values (i.e., u_i ; equations 4 and 5), with the weight proportional to $1/iY$, and I_a is the ratio of the unweighted mean numerator and denominator of the u_i values, which will approximately equal the mean of u_i , depending on the exact configuration of average distance moved for each counts. This is indeed shown to be the case in several artificially generated data sets. This relationship improved as sampling size increased. Thus, both types of statistics are essentially sums or averages of the distance moved by individuals for each sampling unit to achieve a regular distribution, but measured at two different scales: I_a on the whole sampling grid, whereas $\bar{v}_i$ and $|\bar{v}_j|$ (or u_i) on individual sampling units.

We have shown that ${}_cY$ (a component of v_i and v_j ; equation 4) had a near-perfect linear relationship with x (the original counts) using a limited number of data sets, although this relationship for outflow units may be different from inflow units. A common relationship may exist between ${}_cY$ and x for both inflow and outflow units if counts data are approximately symmetrical, i.e., for those data sets generated with either a Poisson or a beta-binomial distribution about the mean irrespective of their spatial locations. Further studies are needed to investigate the applicability of this linear relationship. Theoretically, ${}_cY$ is strictly a function of x for a given data set (i.e., for a given frequency distribution). Thus, identical counts within a given data set should result in identical ${}_cY$ values. However, due to insufficient randomizations (for instance, even with a 3×3 lattice, there are $9! = 362,880$ possible arrangements of nine unique counts), we found that calculated ${}_cY$ values for identical counts (within a single data set) were usually different, albeit the differences were often very small with the SADIE algorithm. This anomaly could be removed by using ${}_cY$ values estimated from its relationship with x , which is derived from the ${}_cY$ values from randomizations. This is the main justification for estimating ${}_cY$ from the counts rather than using ${}_cY$ values directly from the randomizations in some of this study.

Perry et al. (10) made a highly significant advance in the SADIE approach to spatial analysis by quantifying the contribution of *each* sampling unit to the pattern through the average distance index, Y_i (or Y_j). The collection of these indices for a data set can be used directly to determine the pattern to the organism under investigation (Figs. 4 and 5 in Perry et al. [10]). However, Perry et al. (10) pointed out the value of obtaining standardized and unitless indices for each sampling unit (v_i or v_j). Equation 2 is one way of obtaining this standardized index, based on the global averages ${}_iY$ and ${}_cY$. Using several artificially generated data sets, we have shown that the variation of the location-dependent weight (${}_cY$) used to calculate v_i and v_j was generally small (its CV was generally <4%). Particularly, the units near the corners and on the

Fig. 5. Empirical cumulative distributions of Y_i or $|Y_j|$, where the count **A**, $x_i = 78$ (maximum in data set), **B**, $x_i = 52$ (close to the mean), and **C**, $x_i = 15$ (minimum) of the original beta-binomial 5×5 data set was either fixed at one of three positions, corner, edge, and center, or allowed to move in all randomizations (the latter being the standard approach). For each case, 1,000 randomizations were done. Table 1 provides notation and symbols.

edge appeared to have lower and higher iY values, respectively, especially for large sampling sizes. Hence, in calculating v_i or v_j , more weight is given to the sampling units near the corners (but not necessarily exactly at the corner) and less to other units on the edge.

On the basis of the results obtained here, we suggest that use of iY in determining a location-specific clustering index such as v_i (or v_j) may be unnecessary or undesirable. First, nonweighted clustering indices (i.e., u_i) were highly correlated with weighted indices (i.e., v_i or v_j) even for a sampling size as small as 5×5 . These two types of indices were virtually identical for sampling sizes of 10×10 and 20×20 (correlation coefficient >0.99). This is because sampling units at or near the corners and edges were the only locations that had a discernible (or consistent) effect on iY , and these locations comprise only a small-to-moderate percentage of the total for large sampling areas. However, there were considerable differences between the weighted and unweighted statistics in some permutations for the sampling size of 3×3 . This is because the edges and corners comprised a large proportion of the total for such a small sampling size; eight out of the total nine sampling units are on the edges and corners. However, it is very unlikely that in practice we would use a sampling size as small as 3×3 . Furthermore, at all sampling sizes, even for 3×3 , I_a was highly correlated with $\bar{v}_i$ and $|\bar{v}_j|$, as well as with $\bar{u}_i$. Second, average CV of iY was about 3.6%. Assuming a normal distribution for iY , 95% of the values are within 7.2% of the mean. Therefore, for most sampling units, $1.08 > w_i = ({}_oY/iY) > 0.93$, close to 1. Therefore for larger sampling sizes, u_i is nearly identical to v_i (v_j). If standardization was done without reliance on iY , such as the use of u_i (equation 5) for the location-specific index, the relationship of I_a with the location-specific indices would be easier to interpret. Namely, the indices all measure generally the same phenomenon, relative distance to regularity, but at different scales. I_a measures the relative distance to regularity for the whole sampling grid (a global index), whereas u_i values measure relative distance to regularity for each individual sampling unit.

When there is a large difference between $\bar{v}_i$ and $|\bar{v}_j|$ in an observed data set, it is important to know the biological, ecological, and/or physical reasons for such a difference. Our investigation indicated the large difference in $\bar{v}_i$ and $|\bar{v}_j|$ can result from sampling sizes: the difference increases with decreasing sizes. This may result from a high number of sampling units in corners and on edges relative to those in interior units for small sampling sizes based on simple geometric principles. Hence, it is more probable to have a situation where most inflow or outflow units are in the interior region, or on the edges, or near/on the corner for a given

small data set. Of course, such an extreme spatial arrangement may be due to some biological/ecological factors. This may lead to a large difference in $\bar{v}_i$ and $|\bar{v}_j|$ due to differences in iY and Y_j . For larger sampling sizes, the number of sampling units at or near corners and on edges relative to those interior units is small and, hence, their effects may be expected to be relatively less important. Hence, we suggest that a large difference in $\bar{v}_i$ and $|\bar{v}_j|$ is less likely due to biological or ecological factors for small sampling sizes than for large sampling sizes where edge/corner effects are not dominating the results.

The individual clustering indices of SADIE are defined and calculated as standardized Y_i values in an attempt to take into account independently the potential effects of the spatial location of counts, in the form of iY , and the actual count itself, in the form of ${}_oY$. However, results from a few selected examples indicated that the effects of the spatial location and the count itself on Y_i are not independent. iY did not adequately account for the location effects since the average v_i and v_j values for the three selected points deviated considerably from the expected value of 1.0 for the corner and center positions. Moreover, the effect of spatial location of the count on Y_i varied with the count itself. This tendency of overestimating clustering indices might partially explain the observation that the test based on the clustering indices can be much more powerful at detecting nonrandomness than the overall index I_a , especially for situations with large counts around the boundaries of the sampled area (10). It may also partially explain the finding that mean clustering indices are sensitive to absolute patch positions (16). We conclude that v_i (or v_j) and u_i (or u_j), as currently defined, do not fully account for spatial-location effects on clustering because of the interaction of spatial location and count values on the iY statistic. Further research is needed to explore possible alternative standardization methods for the local clustering index. Because of the nature of the SADIE approach, any alternative will require intensive computation.

In summary, we have arrived at several conclusions regarding the interrelationships between I_a , $\bar{v}_i$, and $|\bar{v}_j|$, as well as between the indices for the individual sampling units (u_i , v_i , and v_j), based on artificially generated data sets and demonstrated mathematical relationships in the current study and the interpretation of results from our previous investigations (16,17). First, we have suggested that it may not be necessary to use iY when calculating a scaled index for each sampling unit such as v_i and v_j . Second, we conclude that differences in $\bar{v}_i$ and $|\bar{v}_j|$, if any, are critically affected by sampling sizes. Third, except for very small sampling grids, there is little difference in results based on I_a , and $\bar{v}_i$ (or $|\bar{v}_j|$).

TABLE 4. Summary of Y_i (or $|Y_j|$) and v_i (or $|v_j|$) for counts of 78, 52, and 15 either fixed at three different positions, or allowed to vary randomly over 1,000 permutations of the original 5×5 data set generated from a beta-binomial distribution^a

Counts	Position	$\bar{Y}_i$	$u_i = Y_i/{}_oY$			iY^b	$v_i = w_i u_i = ({}_oY/iY)u_i$		
			Minimum	Mean	Maximum		Minimum	Mean	Maximum
78 (${}_oY = 1.656$) ^c	Corner	1.957	0.604	1.182	2.693	1.574	0.555	1.087	2.476
	Edge	1.623	0.604	0.980	2.460	1.423	0.614	0.997	2.502
	Center	1.563	0.604	0.944	1.708	1.471	0.594	0.929	1.680
	Random	1.658	0.604	1.001	2.616	...	...	...	...
52 (${}_oY = 1.335$)	Corner	1.375	0.749	1.030	3.178	1.574	0.689	0.947	2.922
	Edge	1.296	0.749	0.971	2.724	1.423	0.762	0.987	2.770
	Center	1.419	0.749	1.063	2.118	1.471	0.737	1.046	2.083
	Random	1.347	0.749	1.009	3.088	...	...	...	...
15 (${}_oY = 1.714$)	Corner	2.002	0.583	1.168	2.571	1.574	0.536	1.074	2.364
	Edge	1.682	0.583	0.981	2.122	1.423	0.593	0.998	2.158
	Center	1.578	0.583	0.921	1.535	1.471	0.574	0.906	1.510
	Random	1.712	0.583	0.999	2.223	...	...	...	...

^a Table 1 provides notation and full explanation of symbols.

^b iY is defined strictly in terms of specific position, so is not defined for random position of count. ${}_oY$ ($=1.447$) and iY values were determined from the 3,900 randomizations of the original data set as described in the text.

^c ${}_oY$ values in parentheses were determined from normal run of spatial analysis by distance indices (SADIE) (3,900 randomizations); mean Y_i value for random position of count was based on the 1,000 randomizations and is equivalent to the ${}_oY$ in parentheses.

Finally, in interpreting SADIE indices and comparing them between different studies, investigators must keep in mind that the magnitudes of I_a , and $\bar{v}_i$ (or $|\bar{v}_j|$), are more influenced by the absolute sampling position and initial epidemic conditions (number of initial infected plants and their spatial configuration) than with spore dispersal gradients (i.e., length scale over which disease spread occurs) or other ecological/biological processes occurring during the epidemics (16,17). We have shown here that the current method for calculating clustering indices does not completely adjust for the effects of the actual counts and their sampling positions. Thus, we can conclude that differences in the calculated SADIE indices, as currently defined, between different data sets are probably mostly due to nonbiological factors or processes, such as sampling scheme used, and initial conditions. Direct quantitative comparison of the magnitude of indices should be restricted to data sets with similar sampling schemes and initial conditions (e.g., physical position of the original patches of disease). We agree with Perry et al. (10) regarding the value of a local clustering index for characterizing patterns of organisms, including diseased plants. The v_i (or v_j) index, however, is not the only possible scaled metric for representing clustering at a particular location. We thus believe, as discussed above, that alternative definitions of a unitless local clustering index, taking into account the effects of the interactions between the spatial location and the counts itself on the distance to regularity, are warranted. Research on alternative local clustering indices in comparison to the current one would ultimately indicate the degree of statistical bias that may exist in the current approach to quantifying the clustering at each location, as well as the conditions that lead to low or high bias. It should be noted, however, that bias is not by itself a problem in analysis, if the magnitude of the bias is known or can be estimated.

ACKNOWLEDGMENTS

We thank J. B. Scott and S. J. Pethybridge for sharing their results for I_a , $\bar{v}_i$, and $|\bar{v}_j|$ with us.

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