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Sample-based estimation of "contagion metric" using line intersect sampling method (LIS)

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Abstract Ouantification of landscape pattern is of primary interest in landscape ecological studies. For quantification purposes, a large number of landscape metrics have been developed, with definitions based on measurable patch attributes. Calculation of these metrics is commonly conducted on wall-to-wall maps, whereas a new interest is to use sample data. It is argued that a sample survey takes less time and results are more reliable. The overall objective in this paper was to present the potential of the line interest sampling method for estimating a special contagion metric. The specific objective was to assess statistical properties in terms of root mean square error (RMSE) and bias of the contagion metric estimator. This study was conducted on 50.1 km² already manually delineated land cover maps from the National Inventory of Landscape in Sweden. Monte-Carlo sampling simulation was employed to assess the statistical properties of the estimator. The simulation was conducted for different combinations of two sampling designs, four sample sizes, five lines transect configurations, three lines transect lengths, and two classification systems. The systematic sampling design resulted in lower RMSE and bias compared to a simple random one. Both RMSE and bias of the contagion estimator tended to decrease with increasing sample size and line transect length. We recommend using a combination of systematic sampling design, straight line configuration and long line transect. We conclude that there is no need to use mapped data and thus polygon delineation errors can considerably be reduced or eliminated.

H. Ramezani (⊠) · S. Holm Swedish University of Agricultural Sciences, Umeå, Sweden e-mail: Ramezani.habib@gmail.com **Keywords** Spatial indicators · Landscape metrics · Monte-Carlo simulation · Bias · Root mean square error

Introduction

In landscape ecological surveys, much attention is given to landscape pattern analysis since it is argued that landscape pattern can influence many ecological processes such as biodiversity and population dynamic (Turner 1989; Gustafson 1998). The pattern as a predictor variable should be quantified at the first step, in order to gain a better understanding of the pattern-process relationship (Wiens and Moss 2005). For this purpose, a large number of landscape metrics have been developed (McGarigal and Marks 1995). These metrics are defined in terms of quantities of landscape elements (patches), such as the number, area and edge length of patches. Landscape metrics have various applications; for instance, they have been employed to predict variables such as abundance and distribution of both animal and plant species (McGarigal and Marks 1995; With et al. 1997); landscape metrics are useful tools to describe current status and also to monitor landscape changes over time (O'Neill et al. 1988).

A common approach for quantifying landscape pattern through landscape metrics is to use (raster-based) wall-towall maps. FRAGSTATS (McGarigal and Marks 1995) is a frequently used software for this purpose. In mapping, homogenous areas are first delineated as polygons, either manually or automatically. Manual approaches are usually applied, but some automated and computer-assisted approaches have recently been developed (e.g., Blaschke 2004). A manual approach is time–consuming and can be associated with subjective polygon delineation errors (Corona et al. 2004). The automated approach is sometimes unreliable; for instance, when land cover types that are similar in terms of spectral reflectance should be separated (Wulder et al. 2008). In some cases, monitoring analyses are based on vector based data, i.e., aerial photographs such as Norwegian 3Q (NIJOS 2001) and National inventory of landscape in Sweden (NILS) (Ståhl et al. 2011). In addition, some errors can be introduced by converting vector data to raster; for instance, small patches may disappear (Lunetta et al. 1991; Wade et al. 2003; Jenness 2004).

A new interest, however, is to use sample data where basic sampling methods like point, line intersect sampling (LIS) and plot sampling have been used in remote sensing data for estimating some landscape metrics (Hunsaker et al. 1994; Corona et al. 2004; Ramezani et al. 2010; Hassett et al. 2011; Ramezani and Holm 2011). Kleinn (2000) and Kleinn et al. (2011) also demonstrated the possibility of deriving some metrics from field-based forest inventory. The sample-based approach was found as a promising alternative to the wall-to-wall approach in terms of both cost and data quality. Note that currently used landscape metrics were originally defined for mapped data. Hence, many of them might not be estimated by sampling data (Ramezani et al. 2013), and this issue is considered to be a main disadvantage of sample-based estimation of landscape metrics.

Line intersect sampling (LIS) is generally recognized as an efficient and simple method for surveying linear features within landscapes, such as edge lengths, ditches, and roads (Matérn 1964; Eiden et al. 2005). In LIS, assessment is conducted along sampling units (i.e., line transect) and objects are sampled when intersected by the line transect. This sampling method can be carried out both in remote sensing data and in field surveys. In estimating total edge length, LIS is a cost-efficient alternative to the wall-to-wall approach where all the potential polygons are often delineated manually (Corona et al. 2004; Ramezani and Holm 2011).

A contagion metric has been used in many studies for quantifying the configuration aspect of a landscape (e.g., O'Neill et al. 1988; Hunsaker et al. 1994; Ricotta et al. 2003), and there are several definitions of it (see, Riitters et al. 1996; Wickham et al. 1996). Configuration refers to the spatial arrangement of patches within the landscape. Commonly, this metric is calculated on raster-based maps. However, more recently, Ramezani (2010) demonstrated the possibility of estimating this metric through point sample data. A sampling experiment was conducted on a set of vector-based maps made from aerial photographs.

In the sample-based approach, a given metric may be estimated through different sampling methods and the efficiency of a given sampling method depends on the selected metric (Ramezani 2010). For instance, LIS is more efficient for edge-related metrics, whereas point sampling is preferred to metrics involving area proportion of land cover types like Shannon's diversity index. It is thus of interest, from a statistical viewpoint, to explore an efficient sampling method for a given metric (e.g., contagion), in the way Ramezani (2010) previously assessed the statistical performance of the contagion estimator using point sampling method.

The overall objective here was to present the potential of the LIS method for estimating one of the contagion metrics. The specific objective was to assess statistical properties in terms of root mean square error (RMSE) and bias of the contagion metric estimator using LIS. To achieve this, different sampling designs (random and systematic), sample sizes, line transect configurations, and line lengths were tested on real landscape data.

Materials and methods

In this study, the focus was on sampling errors, and the wall-to-wall maps from aerial photographs were used as reference data for the sampling experiment. Both true and estimated values were calculated through a specific program in FORTRAN.

Study area

The study was conducted as a sampling experiment, with line transects selected from already photo-interpreted landscapes in vector format. Interpreted landscapes were obtained from the NILS (Ståhl et al. 2011), which is a major environmental monitoring program run by the Swedish Environmental Protection Agency. A 25 km² quadrate is used in order to capture the broad landscape context. Within a 1-km² centrally located quadrate, a detailed delineation of polygons is made. To obtain a genuine sample of landscapes for our study, we used data from 50 randomly selected NILS quadrates.

The aerial photographs, in which interpretations were made, were infrared in color and had a ground resolution of 0.4 m. Polygon delineation was made using the interpretation program summit evolution from DAT/EM and ArcGIS from ESRI. For the purpose of the present study, the NILS variables were used together with two different classification systems (7 and 20 classes) in order to produce land cover maps. The classification systems are described in Table 1.

Contagion metric (C)

Contagion is a measure of clumping of classes within landscape. This metric was first proposed by O'Neill et al. (1988) and was then improved by Li and Reynolds (1993).

 Table 1
 Classes according to the two different classification systems

 (with seven and 20 classes) (from Ramezani and Holm 2011)

Level 1 (seven classes)	Level 2 (twenty classes)
1-Forest	1-1-Coniferous-dense
	1-2-Coniferous-sparse
	1-3-Deciduous-dense
	1-4-Deciduous-sparse
	1-5-Mixed-forest-dense
	1-6-Mixed-forest-sparse
2-Urban	2-1-Housing-areas
	2-2-Urban-green-areas
	2-3-Urban-forest
3-Cultivated fields	3-1-Crop fields
	3-2-Grassland
4-Wetlands	4-1-Bog
	4-2-Fen
	4-3-Mixed-wetland
5-Water	5-1-Open-water
	5-2-Water-vegetation
6-Pasture	6-1-Open-pasture
	6-2-Pasture-sparse-trees
	6-3-Wooded-pasture
7-Other land	7-1-Other land

The original definition was based on raster–based data where the data are assumed to be arrays of pixels with equal side lengths. Contagion values range between 0 and 1. A high value indicates an unfragmented landscape with a few large patches, while a low value indicates a fragmented landscape. This metric is highly correlated with metrics of diversity, dominance, and patches of richness (Riitters et al. 1995; Cain et al. 1997; Frohn 1998).

More recently, a vector-based contagion was developed by Ramezani and Holm (2012), where definition is pointbased and a distance function. However, the vector-based contagion (i.e., Eq. 1) of Wickham et al. (1996) is more adapted to the LIS method. The definition of contagion used by Wickham et al. (1996) is

$$C = 1 + \frac{\sum_{i=1}^{s} \sum_{i\neq j}^{s} p_{ij} \cdot \ln(p_{ij})}{\ln(0.5(s^2 - s))}$$
(1)

where $p_{ij} \left(= L_{ij}/L \right)$ is the proportion of edge length between classes *i* and *j* (L_{ij}) to total edge length (L) within the landscape, and *s* can be either the number of classes in the classification system or the observed number of classes. In this study, *s* refers to the number of classes in the system (here, seven and 20 classes). In order to estimate the contagion value at the first step, its component $p_{ij} \left(= L_{ij}/L \right)$ should be estimated and then inserted into Eq. 1. Both L_{ij} and *L* can unbiasedly be estimated through estimator (2).



Fig. 1 Illustration of systematic distribution and random direction of straight line transect on 1 km \times 1 km land cover map from NILS sample plot

True values of L_{ij} and L were obtained directly from the delineated map.

Line intersect sampling

LIS is a simple and statistically efficient method for the estimation of different types of objects, especially linear shaped objects such as roads, tree rows, and edge lengths. An edge refers to the border between two different classes (land cover types). With LIS, edge length can be estimated without bias by simply counting the number of intersections between a patch border and line transects. The estimators of total and edge length between two adjacent classes (Eq. 2) were based on the method of Matérn (1964). According to Matérn (1964), the edge length estimator \hat{L} (m ha⁻¹), using multiple sampling lines of equal lengths, is given by

$$\hat{L} = \frac{10000 \cdot \pi \cdot t}{2 \cdot l \cdot n} \tag{2}$$

where *t* is the total number of intersections, *l* is the length of the sampling line per configuration (m), and *n* is the sample size (the number of line transect). LIS can be implemented either with single straight lines or multiple-segmented transects such as the L-shape as used in Canada, Y-shape transects as used by the U.S. Forest Service and the National Forest Inventory of Switzerland (Affleck et al. 2005), and square transects as in NILS (Ståhl et al. 2011). Figure 1 shows a systematic distribution of straight line transects with random direction on 1 km \times 1 km land cover map from NILS.

Monte-Carlo sampling simulation

The Monte–Carlo sampling simulation is recognized as a useful approach to study the statistical performance of

estimators in sampling surveys (e.g., Hazard and Pickford 1986; Ståhl 1998). The simulation has also been employed for the assessment of statistical properties of some other landscape metrics (Ramezani et al. 2010; Ramezani and Holm 2011). In this study, sampling simulation was used to estimate bias and RMSE of the contagion estimator. Bias (or systematic error) is the difference between the expected value of the estimator and the true value. RMSE is the square root of the expected squared deviation between the estimator and the true value.

Sampling simulation was conducted for each combination of two sampling designs (random and systematic), four sample sizes (16, 25, 49 and 100), five lines transect configurations (straight line, L, Y, triangle and square shapes), three configuration lengths (37.5, 75 and 150 m), and two classification systems (seven and 20 classes). The direction of line transects was random in both systematic and random sampling designs. The simulations were independently replicated a large number of times.

To avoid map border effects, the external buffer zone method was employed (Gregoire and Valentine 2008) where the center of a line configuration was allowed to fall within a buffer outside the map. Only intersections and line lengths within the map were included. Samples in which total numbers of intersections were less than five were excluded.

Efficiency evaluation

Properties of the contagion estimator were derived through a large number of simulated samples, taken independently for all combinations of designs, length, configuration, and classification systems. For an estimator, for example, \hat{C} the expected value was estimated by the mean over the simulations

$$\hat{E}(\hat{C}) = \frac{1}{m} \sum_{i=1}^{m} \hat{C}_i \tag{3}$$

where \hat{C}_i is the estimated value of the *i*th simulation and *m* is the number of simulations. The estimated bias is $\hat{E}(\hat{C}) - C$, where *C* is the true value. The variance was estimated analogously by the sampling variance. The RMSE was estimated by

$$R\hat{M}SE = \sqrt{\sum_{i=1}^{m} (\hat{C}_i - C)^2 / m}$$
 (4)

In the case of an unbiased estimator, RMSE is the same as the obtained standard deviation of the estimator. Finally, the mean value of the estimated bias and RMSE over the 50 squares was calculated.

Table 2 Estimated RMSE and bias of contagion estimator for combinations of four sample sizes, five transect configurations, three transect lengths, two sampling designs (random design is provided in parenthesis) and for a system with seven classes

Sampling design ^a	Sample Con size		Length (m)	RMSE (%)	Bias (%)	
1 (2)	16	1	37.5	35 (38)	29 (31)	
1 (2)	16	1	75	30 (33)	23 (26)	
1 (2)	16	1	150	20 (25)	14 (18)	
1 (2)	25	1	37.5	31 (33)	24 (27)	
1 (2)	25	1	75	23 (26)	17 (20)	
1 (2)	25	1	150	14 (19)	9 (13)	
1 (2)	49	1	37.5	22 (25)	16 (18)	
1 (2)	49	1	75	14 (18)	9 (12)	
1 (2)	49	1	150	8 (12)	4 (7)	
1 (2)	100	1	37.5	13 (16)	8 (10)	
1 (2)	100	1	75	7 (11)	4 (6)	
1 (2)	100	1	150	4 (8)	2 (3)	
1 (2)	16	2	37.5	38 (41)	33 (35)	
1 (2)	16	2	75	32 (36)	26 (29)	
1 (2)	16	2	150	22 (27)	16 (20)	
1 (2)	25	2	37.5	34 (36)	28 (30)	
1 (2)	25	2	75	25 (29)	19 (22)	
1 (2)	25	2	150	16 (21)	10 (14)	
1 (2)	49	2	37.5	25 (27)	19 (21)	
1 (2)	49	2	75	16 (19)	10 (13)	
1 (2)	49	2	150	9 (13)	5 (8)	
1 (2)	100	2	37.5	15 (18)	10 (12)	
1 (2)	100	2	75	9 (12)	4 (7)	
1 (2)	100	2	150	5 (8)	2 (4)	
1 (2)	16	3	37.5	39 (41)	33 (35)	
1 (2)	16	3	75	32 (35)	26 (28)	
1 (2)	16	3	150	23 (27)	17 (21)	
1 (2)	25	3	37.5	34 (37)	28 (30)	
1 (2)	25	3	75	26 (29)	20 (22)	
1 (2)	25	3	150	16 (21)	10 (14)	
1 (2)	49	3	37.5	25 (27)	19 (21)	
1 (2)	49	3	75	16 (19)	11 (13)	
1 (2)	49	3	150	9 (13)	5 (8)	
1 (2)	100	3	37.5	15 (18)	10 (12)	
1 (2)	100	3	75	8 (12)	4 (7)	
1 (2)	100	3	150	4 (8)	2 (4)	
1 (2)	16	4	37.5	45 (47)	39 (41)	
1 (2)	16	4	75	40 (42)	34 (35)	
1 (2)	16	4	150	29 (33)	23 (26)	
1 (2)	25	4	37.5	41 (43)	35 (37)	
1 (2)	25	4	75	33 (36)	27 (29)	
1 (2)	25	4	150	22 (26)	16 (19)	
1 (2)	49	4	37.5	33 (35)	26 (28)	
1 (2)	49	4	75	22 (25)	16 (18)	
1 (2)	49	4	150	13 (17)	7 (11)	

Table 2 continued

Sampling design ^a	Sample size	Conf. ^b	Length (m)	RMSE (%)	Bias (%)	
1 (2)	100	4	37.5	21 (23)	15 (17)	
1 (2)	100	4	75	12 (15)	7 (10)	
1 (2)	100	4	150	6 (10)	3 (5)	
1 (2)	16	5	37.5	45 (47)	39 (41)	
1 (2)	16	5	75	39 (41)	33 (35)	
1 (2)	16	5	150	29 (32)	22 (25)	
1 (2)	25	5	37.5	41 (43)	35 (37)	
1 (2)	25	5	75	32 (35)	26 (29)	
1 (2)	25	5	150	21 (25)	15 (18)	
1 (2)	49	5	37.5	33 (35)	26 (28)	
1 (2)	49	5	75	21 (24)	15 (18)	
1 (2)	49	5	150	12 (16)	7 (10)	
1 (2)	100	5	37.5	21 (23)	15 (17)	
1 (2)	100	5	75	12 (15)	7 (10)	
1 (2)	100	5	150	6 (10)	2 (5)	

^a Sampling design; systematic 1, random 2

^b Configuration; straight line 1, L shape 2, Y shape 3, triangle 4, square 5

Results

The statistical properties (RMSE and bias) of the contagion estimator were investigated for different sampling designs and combinations. As expected, in all cases, a simple random sampling design resulted in larger RMSE and bias compared to systematic design. Estimated RMSE and bias of contagion estimator for all combinations are provided in Tables 2 and 3.

Figure 2 shows the relationship between RMSE and bias of the contagion estimator and different sampling line lengths. Both RMSE and bias of the estimator decreases with increasing sample size and line length per configuration. Straight line transect resulted in smaller RMSE and bias than did the other four configurations, and for a given sample size, a longer line transects resulted in smaller RMSE and bias compared to a shorter one.

The contagion estimator generally showed the same behavior in both seven and 20 classification systems. A comparison in terms of RMSE of the contagion estimator was also made between two classification systems (seven and 20 classes). The system with 20 classes showed a larger RMSE than the system with seven classes, in particular with a small sample size (16). This holds true for all five line transect configurations. Figure 3 shows an example the RMSE of the contagion estimator in seven and 20 classification systems with two lines transect configurations (straight line and square shape).

Table 3 Estimated RMSE and bias of contagion estimator for combinations of four sample sizes, five transect configurations, three transect lengths, two sampling designs (random design is provided in parenthesis) and a system with 20 classes

Sampling design ^a	Sample size	Conf. ^b	Length (m)	RMSE (%)	Bias (%)
1 (2)	16	1	37.5	44 (45)	42 (44)
1 (2)	16	1	75	33 (36)	31 (34)
1 (2)	16	1	150	21 (25)	19 (23)
1 (2)	25	1	37.5	36 (38)	34 (36)
1 (2)	25	1	75	24 (27)	22 (25)
1 (2)	25	1	150	14 (18)	12 (16)
1 (2)	49	1	37.5	23 (26)	21 (24)
1 (2)	49	1	75	13 (17)	12 (15)
1 (2)	49	1	150	7 (11)	6 (9)
1 (2)	100	1	37.5	13 (15)	11 (14)
1 (2)	100	1	75	7 (10)	5 (8)
1 (2)	100	1	150	4 (6)	3 (5)
1 (2)	16	2	37.5	47 (49)	46 (47)
1 (2)	16	2	75	35 (39)	34 (36)
1 (2)	16	2	150	22 (26)	21 (24)
1 (2)	25	2	37.5	39 (41)	38 (39)
1 (2)	25	2	75	26 (29)	25 (27)
1 (2)	25	2	150	15 (19)	14 (17)
1 (2)	49	2	37.5	26 (28)	24 (26)
1 (2)	49	2	75	25 (18)	14 (17)
1 (2)	49	2	150	8 (12)	7 (10)
1 (2)	100	2	37.5	15 (17)	13 (16)
1 (2)	100	2	75	8 (11)	7 (9)
1 (2)	100	2	150	4 (7)	3 (5)
1 (2)	16	3	37.5	47 (49)	46 (47)
1 (2)	16	3	75	36 (38)	34 (36)
1 (2)	16	3	150	23 (27)	21 (25)
1 (2)	25	3	37.5	39 (41)	38 (39)
1 (2)	25	3	75	27 (29)	25 (27)
1 (2)	25	3	150	16 (20)	14 (18)
1 (2)	49	3	37.5	26 (28)	24 (27)
1 (2)	49	3	75	15 (19)	14 (17)
1 (2)	49	3	150	8 (12)	7 (10)
1 (2)	100	3	37.5	15 (17)	13 (16)
1 (2)	100	3	75	8 (11)	7 (9)
1 (2)	100	3	150	3 (7)	3 (5)
1 (2)	16	4	37.5	56 (58)	55 (56)
1 (2)	16	4	75	45 (47)	43 (44)
1 (2)	16	4	150	29 (33)	28 (30)
1 (2)	25	4	37.5	50 (51)	48 (49)
1 (2)	25	4	75	35 (37)	33 (35)
1 (2)	25	4	150	21 (24)	19 (22)
1 (2)	49	4	37.5	35 (37)	33 (35)
1 (2)	49	4	75	21 (24)	20 (22)
1 (2)	49	4	150	11 (15)	10 (13)

Table 3 continued

Sampling design ^a	Sample size	Conf. ^b	Length (m)	RMSE (%)	Bias (%)	
1 (2)	100	4	37.5	21 (23)	20 (21)	
1 (2)	100	4	75	12 (14)	10 (13)	
1 (2)	100	4	150	5 (9)	4 (7)	
1 (2)	16	5	37.5	56 (57)	54 (56)	
1 (2)	16	5	75	44 (46)	42 (44)	
1 (2)	16	5	150	29 (32)	27 (29)	
1 (2)	25	5	37.5	49 (50)	47 (48)	
1 (2)	25	5	75	34 (37)	32 (35)	
1 (2)	25	5	150	20 (23)	18 (21)	
1 (2)	49	5	37.5	35 (37)	33 (35)	
1 (2)	49	5	75	21 (24)	19 (22)	
1 (2)	49	5	150	11 (14)	9 (13)	
1 (2)	100	5	37.5	21 (23)	19 (21)	
1 (2)	100	5	75	11 (14)	10 (12)	
1 (2)	100	5	150	5 (8)	4 (7)	

^a Sampling design; systematic 1, random 2

^b Configuration; straight line 1, L shape 2, Y shape 3, triangle 4, square 5

Discussion

Sample-based assessment of landscape metrics is a new trend in landscape pattern analysis. It is considered as a cost-efficient alternative to the wall-to-wall mapping approach (Ramezani et al. 2010). This study shows the potential of LIS for estimating a contagion metric. The main advantage is that the method can readily be implemented

Fig. 2 Relationship between relative RMSE (*left*) and bias (*right*) of the contagion estimator and different sampling line lengths, for seven classes (*top*) and 20 classes (*bottom*), sample size 49 and systematic design



Straight line

L shape

where there is no need to delineate patch borders (i.e., mapping), since the survey is only conducted along line transects. In such a procedure, the result is more reliable, in terms of time needed, than the traditional wall-to-wall mapping approach, as demonstrated by Corona et al. (2004) and Ramezani and Holm (2011). LIS also has potential for estimating other landscape metrics like Shannon's diversity and edge density (Ramezani and Holm 2011). Thus, in sample-based landscape pattern analysis where a set of metrics is often needed, LIS is a potential sampling method in estimating several metrics simultaneously.

Our results show that, in all cases, the systematic sampling design is more precise than simple random sampling. The efficiency of systematic design has also been demonstrated by Ramezani and Holm (2011) for estimating Shannon's diversity. The reason is that the systematic sample is spread more evenly over the study area, and thus there may be less variability among sampling units (line transects). The results also show that, for a given sampling design and given transect line length, straight line transects are more efficient than the other four configurations. The reason is that with straight line transect, data can be captured from father away.

The efficiency of the contagion estimator, in terms of RMSE and bias, is related to the degree of landscape fragmentation. In the classification system with seven classes and with a given sample size, the estimator is more efficient than in the system with 20 classes. This is because with the 20 classification system, a large class is broken into small classes and thus the landscape seems more fragmented. Hence, a larger sample size is needed in order to achieve an acceptable precision. As our results show, L and Y shapes



75

Sampling line length per configuration (m)

125

175

0

25











Sampling line length per configuration (m)

Fig. 4 Example of two landscapes (A and B) in the seven classification system with minimum (*left*) and maximum (*right*) absolute RMSE



show the same behavior, whereas triangle and square shapes show the same behavior. Gregoire and Valentine (2008) classified the line transects into three categories: (1) straight line; (2) radial transects (L and Y shapes); and (3) polygon transects (triangle and square shapes).

In related studies, statistical properties of the contagion estimator were assessed using (hexagon) plot (Hunsaker et al. 1994) and point sampling methods (Ramezani and Holm 2013), but a direct comparison of results is difficult, because different definitions of the contagion metric were used. A common finding was that the contagion estimator wass biased, regardless of the sampling method. In this study, although both L_{ij} and L can be unbiasedly estimated, the contagion estimator shows bias. This bias can be **Table 4** Absolute maximum and minimum RMSE of the contagion

 estimator and corresponding total edge length within a landscape

Landscape	Absolute RMSE	Total edge withir landscape (m)	
А	0.064 (0.772)	67	
В	0.287 (0.270)	160	

True contagion value is given in parenthesis

explained by the ratio estimator p_{ij} and the non-linear expression in the numerator function of contagion definition. The latter source of bias is independent of sampling procedure, and has also been found in point sampling



Fig. 5 An example of a landscape with two classes. Both true and estimated values of contagion are possible maximum (i.e., 1) whereas the landscape is fragmented with several small patches

(Ramezani and Holm 2013) and plot sampling (Hunsaker et al. 1994) methods.

The results presented here have been the average of relative RMSEs and bias of 48 (for the seven class system) and 50 (for the 20 class system) landscapes. However, extreme RMSE of the contagion estimator is related to the degree of landscape fragmentation in terms of total amount of edge within the landscape. A minimum RMSE has been found in landscapes with a small amount of edge, whereas a maximum RMSE was found in landscapes with a large amount of edge. The maximum extreme case can be explained by a large variation between sampling line transects in terms of the number of intersections. Examples of landscapes with extreme RMSEs and their corresponding total edge lengths and true contagion are provided in Fig. 4 and Table 4.

The method proposed in this study break downs in landscapes with two classes (see Fig. 5). In such landscapes, both true and estimated values are the maximum possible value (i.e., 1) since $L_{ii} = L$.

Finally, in practice, it is recommended to use a combination of systematic sampling design, straight line transects and long transects. Furthermore, in order to achieve an acceptable level of accuracy, the sample size has to be adjusted correspondingly. The method is applicable in fieldbased inventory such as ongoing national forest inventories (NFI), where a virtual line between plots or sub-plots (in cluster design) can be treated as a line transect.

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Appendix

See Tables 5 and 6.

Table 5Estimated range andmean of RMSE for thecontagion estimator over 48.1-km² NILS plots for some	Parameter set				Sample replication	Range	Mean
	Sampling design ^a	Sample size	Conf. ^b	Length (m) ^c			
	1	16	1	1	1000	0.063-0.337	0.188
a system with seven classes	1	16	5	2	800	0.069-0.309	0.212
a system whit seven enastes	1	16	3	2	800	0.071-0.328	0.204
	1	25	1	2	800	0.053-0.351	0.166
	1	25	3	1	1000	0.040-0.303	0.174
	1	25	5	3	600	0.047-0.433	0.179
	1	49	1	3	300	0.026-0.602	0.120
	1	49	5	2	600	0.044-0.403	0.185
	1	49	3	1	800	0.040-0.459	0.166
	1	100	1	3	300	0.013-0.478	0.069
	1	100	3	2	300	0.032-0.540	0.124
	1	100	5	1	600	0.074-0.406	0.192
	2	16	1	1	1000	0.035-0.292	0.178
	2	16	5	2	800	0.048-0.324	0.214
	2	16	3	2	800	0.062-0.337	0.198
	2	25	1	2	800	0.066-0.363	0.178
	2	25	3	1	1000	0.057-0.335	0.172
	2	25	5	3	600	0.083-0.413	0.210
	2	49	1	3	300	0.055-0.414	0.188
^a Sampling design: systematic 1	2	49	5	2	600	0.071-0.426	0.201
random 2	2	49	3	1	800	0.069-0.364	0.172
^b Configuration; straight line 1, Y	2	100	5	1	600	0.026-0.376	0.139
shape 3, square 5	2	100	3	3	300	0.032-0.517	0.133
^c Transect length; $37.5 = 1$, 75 = 2, $150 = 3$	2	100	1	2	300	0.037-0.563	0.171

75 = 2, 150 = 3

Table 6 Estimated range and mean of RMSE for the contagion estimator over Contagion estimator over Contagion estimator over	Parameter set		Sample replication	Range	Mean		
	Sampling design ^a	Sample size	Conf. ^b	Length (m) ^c			
sampling combinations and for	1	16	1	1	1000	0.061-0.286	0.125
a system with 20 classes	1	16	5	2	800	0.065-0.338	0.143
	1	16	3	2	800	0.048-0.320	0.122
	1	25	1	2	800	0.027-0.280	0.095
	1	25	3	1	1000	0.032-0.184	0.105
	1	25	5	3	600	0.041-0.408	0.107
	1	49	1	3	300	0.029-0.294	0.085
	1	49	5	2	600	0.040-0.410	0.107
	1	49	3	1	800	0.043-0.404	0.101
	1	100	1	3	300	0.016-0.217	0.054
	1	100	3	2	300	0.029 -0.306	0.082
	1	100	5	1	600	0.016-0.515	0.075
	2	16	1	1	1000	0.049-0.292	0.123
	2	16	5	2	800	0.049-0.255	0.123
	2	16	3	2	800	0.042-0.309	0.111
	2	25	1	2	800	0.034-0.380	0.090
	2	25	3	1	1000	0.040-0.243	0.103
	2	25	5	3	600	0.035-0.380	0.096
	2	49	1	3	300	0.023-0.304	0.057
^a Sampling design; systematic	2	49	5	2	600	0.023-0.357	0.085
1, random 2	2	49	3	1	800	0.018-0.446	0.080
^b Configuration; straight line 1,	2	100	5	1	300	0.044-0.376	0.098
Y shape 3, square 5	2	100	3	3	300	0.011-0.135	0.032
^c Transect length; $37.5 = 1$, 75 = 2, $150 = 3$	2	100	1	2	600	0.013-0.277	0.048

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