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Analysis of sampling problems using dispersion models

ABSTRACT - Sampling problems were analysed using random and contagious dispersion models simulated by computer. The models were two-dimensional homogeneous point patterns produced by pseudo-random number generators. Taking different random samples we found that the adequate size of sampling units was largely effected by the type of dispersion. In the case of random dispersion all sizes gave acceptable evaluations of the population size and distribution. When examining contagious models, Morisita's index of dispersion proved to be useful in determining adequate sampling unit sizes, which gave precise estimations of the type of dispersion and of the two major population parameters, the mean and variance. A graphical method was proposed for the determination of the adequate number of sampling units for a given sampling accuracy. Applying it together with the common index of precision enables more accurate evaluation of the population mean and variation. No considerable differences were found in the results given by random and systematic sampling, a fact probably due to the random characteristics of our models. Spatial and temporal changes of dispersion are briefly discussed, providing a possibility for further improvement for our work.

1. Introduction

The dispersion of organisms, ie. the distribution of their representatives in certain ranges of real space and time, is not only a population characteristic. As it is in close connection with community structure it may indicate environmental changes as well. A number of widely used textbooks (eg. GREIG-SMITH 1964; ENGEN 1978) have dealt with the problems of estimating the dispersion of populations and with related sampling questions. The rest of the literature, however, has either used a totally theoretical approach, or tried to model the dispersion of natural populations with fitting theoretical probability distributions to sample data. In such cases the actual type of dispersion and the

characteristic parameters of the population are unknown, making error estimation inaccurate and unreliable.

In order to avoid such difficulties we applied computer simulation to produce a variety of dispersion models based on probability distributions with known parameters. After reviewing the possibilities for computer simulation of various types of dispersion, we analysed sampling problems associated with the dispersion of organisms. The two main questions were the dependence of 1/sampling unit size and 2/ sample size (number of sampling units needed for a given precision) on dispersion, with special regard to the role of distribution inhomogeneities in the accuracy of estimations. Besides, we analyzed the possible differences of sampling results due to systematic or random allocation of sampling points. A theoretical discussion was also made on the state-space changes of dispersion types and the possibilities for tracing these changes by field sampling.

1.1. Definitions

The area of one sampling unit (ie. quadrat-size) divided by the total sampling area gives the total number of possible sampling units. The area (or the volume) covered by one sampling unit will be referred to as sampling unit size. The total number of sampling units is the sample size (N).

2. Main types of distributions with biological significance

2.1. General principles in modelling dispersion

The dispersion of a universe of organisms can be characterized by a certain probability distribution. Only by being aware of the distribution type and its parameters can we determine the optimal sampling strategy for the given universe. In practice, however, the distribution of the universe is hardly ever known, so the first task is to estimate its type and parameters.

Let us assume that in nature there are infinitely many types of dispersion, and with their abstraction we can obtain infinitely many empirical distribution functions. The distribution function defines the distribution unambiguously. Let us further assume that the distribution function of samples taken from the universe does not differ essentially from the actual distribution function of the universe itself. Let $\{F_i\}$ indicate the set of "known" distribution functions. This $\{F_i\}$ set consists of the theoretical distribution functions having practical significance. From this set we must choose the F_i most

similar to the distribution function of the sample. In practice we can simplify this process into testing statistical hypotheses. These statistical tests (eg.chi-square test) analyse the "fit" of theoretical distribution functions in consideration to the empirical ones pair by pair. It is possible, however, that none of the theoretical functions are "fitting" to the empirical distribution function at the given level of significance. On the other hand, we may have several empirical distribution functions fitting, which again is a problematic case.

In modelling dispersion mathematical statistics utilizes another concept. It assumes that in an ideal case,the organisms are distributed according to a known theoretical distribution (F_j where $F_j \in \{F_i\}$ $i \in N$, $i \leq \infty$). Random effects may distort this ideal case and it is further "injured" by the sampling process. Our task is to determine the "ideal" probability distribution. The analysis of fit can be applied to solve this problem.

Here we are going to review briefly the distribution types having biological significance. Their detailed description can be found in statistical textbooks (eg. JOHNSON-KOTZ 1969).

2.2 Dispersion and types of distribution

While dispersion in space is usually two- or three-dimensional, from sampling data we can conclude only to one-dimensional distribution-types. Nevertheless, fitting theoretical distributions can reveal the major features of dispersion ie. the local point-distribution, which is most simply characterized by the variance to mean ratio ($\sigma^2 : \mu$).

For example, regular dispersion ($\delta^2 < \mu$), which occurs rarely in nature (ASHBY, 1948), may be modelled by the binomial and hypergeometric probability distributions. Random dispersion ($\delta^2 = \mu$), usually approached by Poisson distribution, is also rare (TAYLOR, 1976), but may result when all environmental factors are in optimum (GREIG-SMITH, 1964). The most frequent way of dispersion is aggregation or contagion ($\delta^2 > \mu$). There are different theories to explain the causes of individuals forming clumps, serving as bases for different models of contagion, ie. negative binomial, logarithmic, PÓLYA-AEPPLI, THOMAS and NEYMAN-A-type (NEYMAN, 1939). The models were reviewed by WESTMAN (1976).

3. Computer-simulation of random point-patterns

For modelling sampling procedures we needed two-dimensional (plane) point-patterns, which had distributions of given types and parameters. Expressed by the terms used in the paper, the point-patterns

which had distributions of given types and parameters. Expressed by the terms used in the paper, the point-patterns were simulated into an m x n grid with the units called cells. We usually chose m=100 and n=100 and thus obtained 10 000 cells. The simulation of a given discrete distribution has several possible ways. Here we mention only one of the simplest cases. The events, here meaning the numbers of points falling into one cell, are drawn 10 000 successive times. Drawing essentially means generating of a number on the interval (0,1) by a random number generator of uniform distribution (here using the " "RANDU" function, designed for IBM 360 computers), and examining which event is represented by the partial interval it falls into. (For further reference on random number generators see SREJGYER (1956),BUSZLENKÓ (1972), TARLOS (1977), SZIDAROVSZKY (1974), RACSKÓ (1977)). Since these events can be considered independent, this one-dimensional distribution can be rearranged to become a two-dimensional. The procedure we used was was to divide the subsequent horizontal 10 000 cells into 100 units with 100 cells in each, and to place these cell-rows one under the other in plane. Thus we obtained a 100x100 grid.

The whole simulation process proved to be very successful for the negative binomial and Poisson-distributions, and it could most probably be used for the generation of several other discrete distributions (for the simulation of the so-called aggregate-type random patterns (NEYMAN-distribution) because the cells there are not independent, and so the above described method for the augmentaion of dimensions cannot be applied. When trying to generate aggregate-patterns, this method will not give aggregating points, and cannot be used for sampling studies on contagious distributions. Namely the "pseudo-aggregate" pattern that we would obtain, could show aggregation when using many different sampling unit sizes and taking large enough number of units, while in the case of real aggregate distributions, a representative sample is very much the question of finding a certain sampling unit size corresponding to the average size of aggregates.

With a special method we managed to produce a two-dimensional aggregate-pattern (other methods, eg. adequately chosen two-dimensional stochastic processes, can also be successful). The model has three basic assumptions:

a/ Let the distribution of aggregates be Poisson-type;

b/ Let the distribution of points within the aggregates be Poisson-type;

c/ Let the distribution of points around the aggregate-center be two-dimensional normal distribution.

We must some additional assumptions:

d/ The dimensions of the two-dimensional normal distributions cannot be correlating;

e/ Let the expected value of normal distributions be equal with the coordinates of aggregate-centres;

f/ For the sake of simplicity let the standard deviation of the normal distribution be equal in each aggregate.

The aggregate-pattern was simulated in to a 100x100 grid. The aggregate-centers were determined first, using a Poisson-distribution of λ=0.1 parameter, then the coordinates of each point were determined. Here we used assumption d/, because the first, and later the second coordinate of the point was determined using a random number generator with a one-dimensional normal distribution (with the well-known "NORML" process). The numbers of points falling into each aggregate were determined by a Poisson-generator with λ=10 parameter, and the standard deviation of normal distribution was chosen to be one unit. The point-coordinates obtained were continuous variables, so we had to discretize them, ie. determine to which cell they fell. For example when three points fell to the area of cell C (I,J), then the content of the cell was three points, independently of their interrelated positions.

4. Sampling from patterns produced by simulation

4.1. Establishing the final "sample area"

With the simulation of the different patterns we always obtained grids consisting of 10 000 cells, but to be able to test different sampling strategies we produced a large net of 1 million cells, with the random rotation of grids. These point-patterns were considered as single-species populations, in order to avoid the perturbing effect of the presence of other species.

Sampling was carried out using a table of random numbers in order to avoid statistical bias. The smallest sampling unit size was 1q, ie. the area of one cell in the grids, the others were 2,4,8,16,32,64 times larger (denoted by 2q, 4 q,...etc.). "N" indicated the number of sampling units in the samples.

5. Results

5.1. The analysed models and distributions

The following dispersion models were used in the study:

Poisson-models with λ=0.2, λ=0.5, λ= 28 parameters as random models; negative binomial models with μ=0.5, k=1.0 and μ=22.0, k=7.33 parameters as contagious models; the μ=0.5 Poisson-aggregate model, and the μ=0.9381, δ^2=1.5712 aggregate model.

The Poisson-aggregate model was made of the λ=0.5 Poisson model, in which the values equal and larger than 2 were chosen as aggregate centers, and all the values 1 nearby were gathered around them. The hypotheses that the dispersion is random or contagious can be tested most simply by fitting Poisson and negative binomial distributions, respectively. The "goodeness of fit" is tested by chi-square (χ^2) test, though ENGEN (1978) stated that it could not be adequate in every case. Thus we accepted or regretted fitting, using this test, only when the chi-square values obtained were much higher or much lower than the tabulated values. For the estimation of "k" in the negative binomial we used the simplest method, the expression

$$\hat{k} = \frac{\bar{x}^2}{s^2 - \bar{x}}$$

5.2. The question of sampling unit size

Without testing any sampling strategy it should be obvious that the random distribution of any "per se" environmental factors, eg. food will cause random dispersion of the organisms, while if eg. food is available in forms of aggregates, the dispersion turns into contagious as well. In order to be able to detect the resulting effect of environmental factors, first we must choose the adequate sampling unit size.

We supposed that if choosing a fairly small size, the sample would always reflect random dispersion. Thus we sampled the different models using sampling unit sizes of 1, 2, 4, 8, 16, 32 and 64q, and examined the trends of the Morisita-index (ELLIOTT 1971, see 5.3.). Random samples of N=128 units were taken from the Poisson model of λ=0.5 parameter. Poisson-distributions fitted well to the frequency distributions in every case (Table 1.). The fitting of negative binomial distributions was not tested, because estimation of parameter "k" gave negative or too high values. In the latter case negative binomial distribution approaches Poisson. According to table 1. all sampling unit sizes proved to be adequate, except 8q.

Table 1.

Table 1.

Fitting Poisson distribution to sample data from random model (λ=0.5, df=127) using $d=\sqrt{2\chi^2} - \sqrt{2v-1}$ normal approximation (ELLIOTT 1971)

sampling unit size	χ^2	d
1 q	140,083	0,832
2 q	133,066	0,408
4 q	133,894	0,458
8 q	161,713	2,078
16 q	132,558	0,376
32 q	137,864	0,699
64 q	107,090	1,271

(Chi-square values were calculated by: $\chi^2 = \frac{s^2(N-1)}{\bar{x}}$

Fit was accepted when d< 1,96.)

Table 2.

Fitting negative binomial and Poisson distributions to sample data from three different contagious models

sampling unit size	negative binomial distribution χ^2	df	p	Poisson distribution χ^2	df	p
a/ negative binomial model						
1q	5,875	5	>0,30			<0,001
16q	4,616	11	>0,95	4,588	10	>0,90
b/ aggregate-model						
1q	1,564	6	>0,95	4,897	6	>0,50
2q	12,086	7	>0,05x	31,424	7	<0,001
4q	15,070	10	>0,10	37,279	9	<0,001
8q	9,458	11	>0,50	83,402	11	<0,001
16q	25,067	20	>0,10	120,487	15	<0,001
32q	6,245	8	>0,50	93,805	19	<0,001
64q	4,904	7	>0,50	74,884	7	<0,001
c/ Poisson-aggregate model						
4q	4,773	7	>0,70	44,581	7	<0,001
8q	cannot be fitted (k = -51,90)			5,409	9	>0,70

x ambiguous

Table 1.

Fitting negative binomial and Poisson distributions to sample data from a lumbricid population Sikfőkut Project

sampling unit size	negative binomial distribution			Poisson distribution		
	χ^2	df	P	χ^2	df	P
1q	9,438	5	>0,10*	29,809	5	<0,001
4q	7,010	10	>0,70	74,140	9	<0,001
16q	12,666	15	>0,50	140,742	8	<0,001
64q	4,433	10	>0,90	142,579	5	<0,001

* ambiguous

Table 4.

Number of sampling units needed for some models

model		number of sampling units for index of precision		number of sampling units determined by the graphical method	
		D=0,10	D=0,20	10%	20%
λ=0,5	Poisson	183	46	83	76
λ=28	Poisson	4	1	112	87
μ=0,5	negative binomial	279	70	123	123
μ=22	negative binomial	16	4	126	70

Random samples of N=32 were taken from the k=0.5 negative binomial model. Only negative binomial distribution fitted the frequency distribution of the counts of the sample taken with 1q unit size, while in all other cases both the negative binomial and Poisson distributions gave good fit (Table 2.). The reason could be the randomness of aggregates on one hand, and the size of aggregates being equal to one cell on the other, resulting from the characteristics of the basic distribution. Sampling with larger units gives ambiguous results, as the size of the units is greater than that of the aggregates. The same fact is reflected by the result of sampling the aggregate model (N=32) and fitting negative binomial and Poisson distributions (Table 2.). The use of too small sampling unit size (1q) here reflects random dispersion, which is in good agreement with our presumption. The larger the sampling unit size is, the better negative binomial distribution fits the frequency distribution of counts. Samples of N=32 from the Poisson-aggregate model show that both too small, and too large unit sizes give biased estimates of the population dispersion (Table 2.)

The results from our models were compared to data from natural populations. Random samples (N=32) of the lumbricid fauna (Annelida: Lumbricidae) in "Sikfőkut Project" were taken, using different quadrat sizes (Table 3.). Fitting various distributions we established that the worms had contagious distributions, best reflected by sampling unit sizes 4q and 16q.

5.3. The adequate sampling unit size

The index of dispersion I_δ by Morisita (ELLIOTT 1971) can be used for the determination of the adequate quadrat size. The expression is:

$$I_\delta = \frac{\sum_{i=1}^{N} \left[x_i (x_i - 1) \right]}{\sum_{i=1}^{N} x_i \left(\sum_{i=1}^{N} x_i - 1 \right)}$$

The ratio of I_δ for the (i-1)-th quadrat size to I_δ for the i-th quadrat size should be depicted against quadrat size (Fig.2.). The peak of the curve will indicate the size equal to the area of aggregates (GREIG-SMITH, 1964). This will be the adequate sampling unit size.The occurrence of several peaks indicates that there are smaller aggregates within larger clumps. IWAO and KUNO (1961) criticized the use of this index, but their "mean crowding" index has a fairly limited use in real biological situations, even in their opinion.(Here the index was not

Figure 1.: Determination of the adequate sampling unit size using the index of dispersion by Morisita

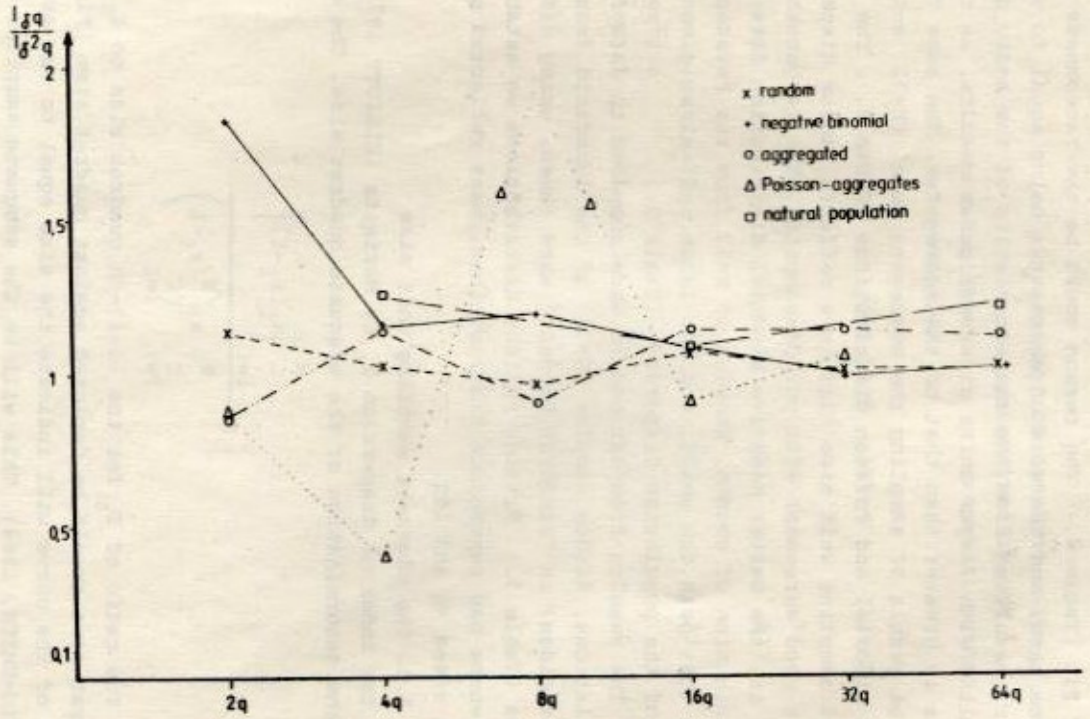
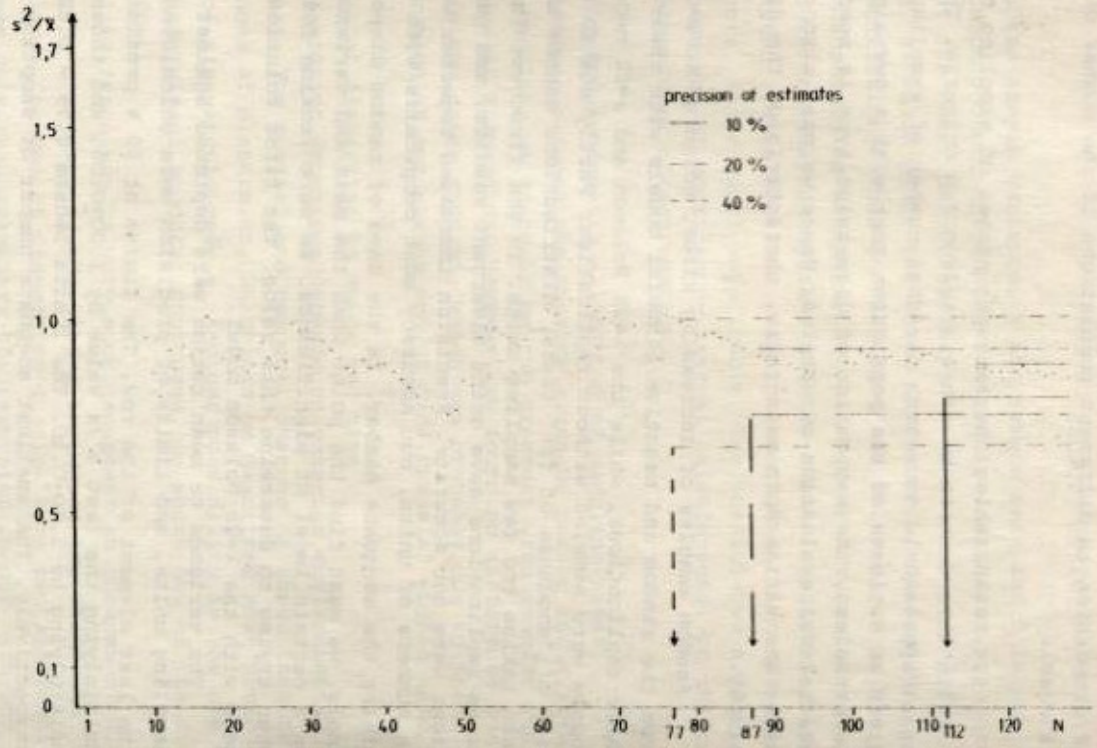


Figure 2.: Determining the number of sampling units needed (N) on the basis of variance to mean ratio for the λ=28 random model



tested). The index of dispersion by Morisita, however, can be sussessfully used for working out sampling strategies, and for the comparison of dispersion in different populations if the number of sampling units is equal.

5.4 Establishing the adequate number of sampling units

In this section we can start from two criteria. The basis of usual approach is to search for that number of sampling units which given an estimate of the population mean with a certain accuracy. Nevertheless, the estimation of dispersion type is needed for the statistical evaluation of samples. Hence we must also consider at least the variance to mean ratio, characterizing the dispersion most simply.

Random samples of increasing sizes, going up to N=128 were taken from the random and negative binomial models with their mean = 0.5, three replications, while the λ=28 Poisson and μ=22 negative binomial models were sampled without replication. Partly due to the characteristics of "goodness of fit" tests, distributions cannot be fitted well when taking too few sampling units. In the first two (N=4 and N=8) cases replications gave quite divergent results, and parameter estimations were not accurate. Precision increased together with the increase in numbers of units, but accuracy must compromize with cost when determining the adequate number. In the case of random dispersion, for example, we must find the point when the mean and variance do not differ on a certain level of significance. We were looking for a new method when trying to determine this value. The first solution is demonstrated here with the λ=28 Poisson model.

The variance to mean ratios were depicted against the number of sampling units, and limits of precision were calculated on the basis of the last element of the row. The limits of 10 % precision we got with multiplying the last s^2/x value by 1.00 ± 0.05, and those of 20 % with multiplying by 1.00 ± 0.10. The limits became 0.79 - 0.88 and 0.75 -0.92, respectively. The smallest adequate number of sampling units is the one where the ratio curve remains between these limits. They are: N=112 for 10% precision, and N=87 for 20 % precision (Fig.3.).

For the determination of the number of sampling units needed, for a specified precision the following term is generally used:

$$N = \frac{s^2}{D^2 \bar{x}^2}$$ (ELLIOTT 1971).

where s^2 means the sample variance, x the sample mean and D is the index of precision chosen, originally the required standard error as a proportion of the mean. Using this term in our case gave N=4 for 10 % precision, at which point the curve in figure 3 still shows significant oscillations. Thus in this case the value given by the graphical method should be accepted, but as a general rule the two methods should be considered together and the resulting higher value should be accepted (Table 4.). The graphical method still needs a lot more improvements, to be easily applicable. The possible ways for that could be the use of confidence-interval calculations, or the use of a more precise index of aggregation.

5.5. Random and systematic allocation of sampling sites

The differences between the results given by random and systematic allocation of sampling units could be the greatest with regular and contagious types of dispersion. However, we found no difference between the two in the cases studied, which was probably due to the random distribution of aggregates and of "individuals" within them.

6. Changes of dispersion in space and time

The dispersion of organisms depends on exterior environmental and interior factors. The spatial and temporal changes of these factors cause the changes of dispersion, which can be described most obviously by by series of time-static models. Another possibility is the use of such a multi-dimensional stochastic process, in which one of the dimensions is time.

The sampling frequency is very much dependent on changes of dispersion, thus the analyisis of the latter has great importance in sampling problems. Changes of dispersion in time have two alternatives. In a simpler case only the parameters of dispersion change with the type remaining unaltered, while in other cases the type of dispersion may change as well (HAIRSTON, HILL, RITTE 1976). A good example of the latter can be based on NEYMAN's distribution. It was constructed to describe the dispersion of insect larvae recently hatched from randomly distributed clumps of eggs. Then larvae have contagious dispersion for

a certain period of time, but eg. a decrease of abundance due to emergence could result in a shift towards random dispersion. Regular distribution can also follow, due to ethological reasons, eg. territorial behaviour. Here dispersion problems are closely related to density-dependent and density-independent population dynamic processes (such as mortality. see IWAO, JUNO 1976). Consequently, the frequency of sampling should always be determined on the basis of the species and dispersion area characteristics.

In our study we examined only two dimensional types of dispersion, thus considerably simplifiyng the real three-dimensional problem. In nature, however, one-dimensional dispersion can also occur with good approximation, for example in nests and territories of Motacilla cinerea populations, nestling along a mountain creek.

If our sampling area is not homogeneuos, it should be divided into relatively uniform areas, and different sampling strategies should be worked out for each of them. This process is called stratified sampling (GREUG.SNUTG 1964; ELLIOTT 1971). If the dispersion all over the sample area is the same, but the parameters within large units are different, the deviation cannot be revealed by simple sampling. In order to study this question we sampled a "mixed population", taking a sample with 16 units from the λ=0.2 and 16 from the λ=0.5 Poisson models and taking a N=32 sample from each model separately. Analysis of variance was carried out with all samples, using a BMDP program. In two replications out of the three was no significant difference among the three samples (P>0,05). Greater differences in parameters, however, can be revealed by well organized sampling.

Summary

Dispersion models made by computer simulation were used for the analysis of sampling problems. Homogeneous plane point-patterns produced by random number generator were sampled, and the effect of the type of dispersion on the adequate sampling unit size and on the number of sampling unit size and on the number of sampling units was examined. The use of all sampling unit sizes gave good results with random dispersion, while in the case of contagious populations the index of dispersion by Morisita proved to be useful in determining the size of sampling units adequately revealing the type of dispersion. The area of the unit depends on the size of aggregates. For a certain level of precision the number of sampling units needed can be determined, when applying the common expression together with a graphical method worked

out here. No difference was found between the results of random and systematic sampling, probably due to the random character of the models studied. One further aspect of the problem was described shortly with the spatial and temporal changes of dispersion. The stability of parameter estimates in time-series sampling also desires more attention.

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MOLDOVÁN JUDIT - MOSKÁT CSABA - NAGY SÁNDOR
Mintavételi problémák vizsgálata diszpergáltsági modelleken

ÖSSZEFOGLALÁS - Mintavételi problémákat vizsgáltunk számítógépes szimulációval előállított diszpergáltsági modelleken. Pszeudo-véletlenszám generátorok segítségével síkbeli homogén pontmintázatokat hoztunk létre, s az ezekből vett minták segítségével megállapítottuk, hogy a diszpergáltsági tipus nagyban befolyásolja a mintavételi egység alakalmazható méretét. Randomizált diszpergáltság esetén minden területnagysággal az eredeti populáció jó becslését kaptuk, míg a kontagion tipus esetén a Morisita-index segítségével meghatározhatók voltak olyan kitüntetett, az aggregátumok területétől függő területnagyságok, melyek alkalmasak a diszpergáltsági tipus felderítésére. A többi nagysággal történő mintavétel a paraméterek becslését torzítja, így lehetetlenné teszi a diszpergáltsági tipus felismerését. A megfelelő pontosságú becsléshez szükséges mintaelemszám megállapítására kidolgoztunk egy grafikus módszert, amely a szokványos pontossági indexxel való számítással együtt alkalmazva biztosabb becslést tesz lehetővé. Valószínüleg az elemzett modellek véletlen jellege miatt az általunk alkalmazott szisztematikus és randomizált mintavétel eredményei között nem találunk jelentős különbséget. A számítógépes modellek sajátosságaiból következően nem állott módunkban megvizsgálni a mintavételi egységek alakjának hatását a mintavétel eredményességére. A továbblépés lehetőségeiről szóltunk a diszpergáltság tér- és időbeli változásának kapcsán. A továbbiakban fontosnak tartjuk még megvizsgálni nagysorozatú mintavételek esetén a becsült paraméterek állandóságát. Eredményeink felhasználásával lehetővé válhat egy-egy terület ökológiai felmérésének pontosabb megtervezése, az adatok pontosabb becslése.

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