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 affected 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 variance. 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, i.e. 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 (e.g. GREIG-SMITH 1964; ENGEL 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 (i.e. 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 (e.g. 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 \( F_j \in \mathbb{N} \), \( j = 1 \). 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 (e.g. 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 i.e. the local point-distribution, which is most simply characterized by the variance to mean ratio \((\sigma^2/\mu)\).

For example, regular dispersion \((\sigma^2/\mu)\), which occurs rarely in nature (ASHBY, 1948), may be modelled by the binomial and hypergeometric probability distributions. Random dispersion \((\sigma^2=\mu)\), usually approached by Poisson distribution, is also rare (TAYLOR, 1976). But may result when all environmental factors are in optimum (GREEN-SMITH, 1964). The most frequent way of dispersion is aggregation or contagion \((\sigma^2>\mu)\). There are different theories to explain the causes of individuals forming clumps, serving as bases for different models of contagion, i.e. negative binomial, logarithmic, FÖLIA-KEFFL, THOMAS and NEWMAN-\(a\)-type (NEWMAN, 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 "RAN
DUND", 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 SREJZGER (1956), BUSZLENKÖ
events can be considered independent, this one-dimensional distribution
can be rearranged to become a two-dimensional. The procedure we used 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 augmentation 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, e.g. 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 \( \lambda = 0.1 \) 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 \( \lambda = 10 \) 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, i.e. 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 \( 1q \), i.e.
the area of one cell in the grids, the others were \( 2q, 4q, 8q, 16q, 32q, 64q \times \) larger (denoted by \( 2q, 4q, \ldots \) 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 \( \lambda = 0.2 \), \( \lambda = 0.5 \), and \( \lambda = 28 \) parameters as random models; negative binomial models with \( w = 0.5 \), \( k = 1.0 \) and \( w = 22.0 \), \( k = 7.33 \) parameters as contagious models; the \( \mu = 0.5 \) Poisson-aggregate model, and the \( \mu = 0.9381 \), \( c^2 = 1.5712 \) aggregate model.

The Poisson-aggregate model was made of the \( \lambda = 0.5 \) 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 "goodness of fit" is tested by chi-square \((\chi^2)\) test, though ENGEL (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

\[
\frac{-2}{k} = \lambda s - k
\]

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 64g, and examined the trends of the Morisita-index (ELLICOTT 1971, see 5.3.). Random samples of \( N = 128 \) units were taken from the Poisson model of \( \lambda = 0.5 \) 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 8g.
Table 1.

Fitting Poisson distribution to sample data from random model \( \lambda=0.5 \), \( df=127 \) using \( d = \bar{x}^2 - \frac{\bar{x}}{\bar{x}} \) normal approximation (ELLIOTT 1971)

<table>
<thead>
<tr>
<th>Sampling Unit</th>
<th>( \chi^2 )</th>
<th>( d )</th>
</tr>
</thead>
<tbody>
<tr>
<td>1 q</td>
<td>140.083</td>
<td>0.832</td>
</tr>
<tr>
<td>2 q</td>
<td>133.066</td>
<td>0.406</td>
</tr>
<tr>
<td>4 q</td>
<td>133.894</td>
<td>0.435</td>
</tr>
<tr>
<td>8 q</td>
<td>161.711</td>
<td>2.078</td>
</tr>
<tr>
<td>16 q</td>
<td>132.558</td>
<td>0.376</td>
</tr>
<tr>
<td>32 q</td>
<td>137.884</td>
<td>0.699</td>
</tr>
<tr>
<td>64 q</td>
<td>107.090</td>
<td>1.271</td>
</tr>
</tbody>
</table>

Chi-square values were calculated by:

\[
\chi^2 = \frac{s^2(N-1)}{\bar{x}}
\]

Fit was accepted when \( d < 1.96 \).
Table 1.
Fitting negative binomial and Poisson distributions to sample data from three different contagious models

<table>
<thead>
<tr>
<th>Sampling unit size</th>
<th>Negative binomial distribution</th>
<th>Poisson distribution</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>$x^2$</td>
<td>df</td>
</tr>
<tr>
<td>a) Negative binomial model</td>
<td></td>
<td></td>
</tr>
<tr>
<td>1q</td>
<td>5,875</td>
<td>5</td>
</tr>
<tr>
<td>16q</td>
<td>4,616</td>
<td>11</td>
</tr>
<tr>
<td>b) Aggregate-model</td>
<td></td>
<td></td>
</tr>
<tr>
<td>1q</td>
<td>1,564</td>
<td>6</td>
</tr>
<tr>
<td>2q</td>
<td>12,084</td>
<td>7</td>
</tr>
<tr>
<td>4q</td>
<td>15,070</td>
<td>10</td>
</tr>
<tr>
<td>8q</td>
<td>9,438</td>
<td>11</td>
</tr>
<tr>
<td>16q</td>
<td>25,067</td>
<td>20</td>
</tr>
<tr>
<td>32q</td>
<td>6,745</td>
<td>8</td>
</tr>
<tr>
<td>64q</td>
<td>4,904</td>
<td>7</td>
</tr>
<tr>
<td>c) Poisson-aggregate model</td>
<td></td>
<td></td>
</tr>
<tr>
<td>4q</td>
<td>4,773</td>
<td>7</td>
</tr>
<tr>
<td>8q</td>
<td>cannot be fitted</td>
<td>5,400</td>
</tr>
</tbody>
</table>

*x* ambiguous
Table 1.

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

<table>
<thead>
<tr>
<th>Sampling Unit Size</th>
<th>Negative Binomial Distribution</th>
<th>Poisson Distribution</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>df</td>
<td>p</td>
</tr>
<tr>
<td>1q</td>
<td>3</td>
<td>0.10</td>
</tr>
<tr>
<td>4q</td>
<td>10</td>
<td>0.70</td>
</tr>
<tr>
<td>16q</td>
<td>15</td>
<td>0.30</td>
</tr>
<tr>
<td>64q</td>
<td>10</td>
<td>0.90</td>
</tr>
</tbody>
</table>

*ambiguous*
<table>
<thead>
<tr>
<th>model</th>
<th>number of sampling units determined by the term for index of precision</th>
<th>graphical method</th>
</tr>
</thead>
<tbody>
<tr>
<td>λ=0.5 Poisson</td>
<td>D=0.10: 183  D=0.20: 46  10%: 83  20%: 76</td>
<td></td>
</tr>
<tr>
<td>λ=28 Poisson</td>
<td>D=0.10: 4  D=0.20: 1  10%: 112  20%: 87</td>
<td></td>
</tr>
<tr>
<td>µ=0.5 negative binomial</td>
<td>D=0.10: 279  D=0.20: 70  10%: 123  20%: 123</td>
<td></td>
</tr>
<tr>
<td>µ=22 negative binomial</td>
<td>D=0.10: 16  D=0.20: 4  10%: 126  20%: 70</td>
<td></td>
</tr>
</tbody>
</table>
Random samples of N=32 were taken from the \( \lambda = 0.5 \) 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 2.1). 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 "Sik фон Project" were taken, using different quadrat sizes (Table 1.). Fitting various distributions we established that the worms had contagious distributions, best reflected by sampling unit sizes 4q and 16q.

2.3. The adequate sampling unit size

The index of dispersion \( I_0 \) by Morisita (ELLIOTT 1971) can be used for the determination of the adequate quadrat size. The expression is:

\[
I_0 = \frac{\sum_{i=1}^{N} x_i (x_i - 1)}{\sum_{i=1}^{N} x_i (\sum_{i=1}^{N} x_i - 1)}
\]

The ratio of \( I_0 \) for the (i-1)-th quadrat size to \( I_0 \) 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. INAO 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 2.1: 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 successfully 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 \( \lambda=28 \) Poisson and \( \mu=22 \) 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 compromise 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 \( \lambda=28 \) 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 \( \sigma^2/x \) value by 1.00\( \pm \)0.05, and those of 20 % with multiplying by 1.00\( \pm \)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.1.).

For the determination of the number of sampling units needed, for a specified precision the following term is generally used:
\[
N = \frac{s^2}{D^2}
\]

(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 be-
tween 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 di-
mensions is time.

The sampling frequency is very much dependent on changes of dis-
persion, thus the analysis 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, MITTE 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 emer-
genesis could result in a shift towards random dispersion. Regular dis-
tribution 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 simplifying 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 ci-
neres populations, nestling along a mountain creek.

If our sampling area is not homogeneous, 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 sam-
pling (GREUG.SNUTS 1964; ELLIOTT 1971). If the dispersion all over the
sample area is the same, but the parameters within larger 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 BMDF 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 pro-
duced 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 dis-
"persion, 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

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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 deserves more attention.

Acknowledgement

The authors thank Dr. István Précsényi (ELTE) and Dr. Pál Juhász-Nagy (ELTE) for their comments, helpful advice and review of the manuscript, and Hanan J. McIntosh (Queen’s Univ.) for the stylistical corrections.

MOLDOVÁN JUDIT – MOSKÁT CSABA – NAGY SANDOR

Mintavételi problémák vizsgálata diszpergáltságú modelléken

ÖSSZEFoglalás – Mintavételi problémákat vizsgáltunk számítógépes szimulációval előállított diszpergáltságú modelléken. Pszeudo-véletlenszám generátorok segítségével súlyos homogén pontmintaizatokat hoztunk létre, s az ezekből vett minták segítségével megállapítottuk, hogy a diszpergáltság típus nagyban befolyásolja a mintavételi eredmények alakulmazatának mértéket. Randomizált diszpergáltság esetén minden területnyag segítségével az eredeti populáció jó becsülését kapott, míg a kontagion típus esetén a Morisita-index segítségével meghatározhatók voltek olyan kitudott, az aggregáció területétől függő területnyagságok, melyek alkalmaznak a diszpergáltság típus felderítésére. A többi nagságú történő mintavétel a paraméterek becsülését történt, így lehetetlenné teszi a diszpergáltság típus felismerését. A megfelelő pontoságú becsüléshez szükséges mintaképesség megállapítására kidolgoztuk egy grafikus módszert, amely a szokványos pontosságú indexével való számítással együtt alkalmazva biztosabb becsülést tesz lehetővé. Valószínűleg az elemzett modellének véletlenszerű jellegé miatt az általunk alkalmazott szimuláciom és randomiszt mintavétel eredményei között nem találunk jelentős különbséget. A számítógépes modellékek sajátosságából következően nem állott módunkban megvizsgálni a mintavételi eredmények alakjának hatását a mintavételi eredményességére. A további történő felismerési esetekben a diszpergáltság térának és időbeli változásának kapcsán. A továbbiakban pontosnak tartjuk még megvizsgálni nagysorozatú mintavétel esetén a becslőt paraméterek állandómodját. Eredményeink felhasználásával lehetővé válik egy-egy terület ökológiai felmérésének pontosabb megtervezése, az adatok pontosabb becsülése.
REFERENCES


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