

The possibility of constructing species spread models for assessing life sustainability

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Abstract

Zviagintseva A. "The possibility of constructing species spread models for assessing life sustainability" The approaches to model construction of species distribution for assessing life sustainability are presented. The possibility is shown for creating of global biodiversity databases by integrating GIS models of species spread areas with corresponding attribute information as well as characteristics of the environment conditions for those species. Using three distinct examples for three indicator species it is shown that probability dependencies are exist which may reflect the peculiarities of the biodiversity.

Keywords: biodiversity databases, probability dependencies, attributive information, GIS-models, areas of species distribution

Introduction

Biodiversity is a unique feature of nature that connects with the creation of the structural and functional organization of ecological systems. In the last years, the problem of preserving the diversity of organisms reached the level of global concern and poses a number of complex tasks in the field of environmental research studies. Biodiversity monitoring connected with the biosphere monitoring system and the development of species diversity databases as well as with the analysis of development trends and patterns of biological life on Earth. Nowadays different types of human activities have led to the extinction of many species and ecosystems in the biosphere. Here lies one of the major environmental risks associated with the humankind development.

Modern biodiversity problems

Most often, when speaking about the biodiversity it implies species diversity. The number of species according to different sources varies from 5 to 100 million [1 – 3]. At the same time, the taxonomic affiliation in accordance with modern classification is set to only 2 million species: 500 thousands plant species and 1.5 million species of animals [1].

The process of the evolution of life has always been associated with the extinction of biological organisms, populations and species in general. It is believed that average life expectancy of one species is about 5 – 6 million years. The process of the evolution of life has always been associated with the extinction of biological organisms, populations and species in general. It is recognized, that average life expectancy of one

species is 5 – 6 million years. Over the past 200 million years we have lost about 900 thousand species of flora and fauna, or an average of less than one species per year [3]. This means that the extinction of species has always been a natural and necessary process of evolution – more than 99% of species that ever existed have become extinct (Leakey 1996), but it is assumed that species are disappearing today at 100 – 1 000 times faster than before the human existence (Chapin et al. 1998). Experts estimate that over the next 20 – 30 years 25% of the Earth's biodiversity will be under serious threat of extinction, nearly 40 000 species will probably disappear. According to the researchers, biodiversity restores very slowly: in 1000 endangered species appears only one new species (Chapin et al. 1998). This burst of extinction last time was 65 million years ago, since the end of the Cretaceous period, when the dinosaurs disappeared (Meadows et al., 1992, [4]). According to paleontologists, over the past 500 million years on Earth, there were five periods of mass extinction. To restore the biological wealth each time had to be about 10 million years [4]. During our era, there is a real danger of a new period of mass loss of biological diversity. The prediction of the risk of process development requires knowledge of biodiversity patterns.

The first data from studies that examined the biodiversity impact assessment to ecosystem processes have been published only in the early nineties of the XX century. Since then the amount of research in this area has increased significantly. Over a period of 25 – 30 years, since the scientific community expressed the danger of biodiversity loss, it is difficult to assess the evolution processes, which the time of the observation changes in thousands of years.

Back in the 30's of last century, the famous Russian scientist V.A. Kostitsyn conceptually proposed an approach that allows building a model of the species distribution on Earth to assess the sustainability of life [5]. This idea has remained unrealized since at that time it was impossible to implement the information models, covering a huge amount of numerical and graphical data. Models of species are one of the main tools for constructing the life evolution theory on Earth, which in essence would have a theoretical rather than a narrative framework. The basic problem in this area – how to build information resources that would provide data from biological parameters and prevalence of hundreds of thousands species. Obviously, this problem cannot be solved without the usage of information technology.

Today biodiversity assessment is based on a variety of indices, which differ in both ways: in how they are determined, and the methodological principles of their construction. Hypotheses, which are the basis of species distribution models usually are private and cannot serve as a basis for quantitative methods of biodiversity assessment, because ecological systems cannot be assessed at a one, though and complex indicator. In order to construct quantitative models of biodiversity we need to develop scales measuring the prevalence of species that would not have been basically subjective. Nowadays such type of systems in the ecology with a quantitative assessment doesn't exist. Studies show that biodiversity assessment by using different indexes often leads to contradictory conclusions, which are a consequence of subjective perceptions of researchers [7].

In order to assess the ecosystems biodiversity it requires a certain criterion (or set of criteria), which is likely to have a probabilistic base. Several authors believe that the most important characteristic is the diversity index of evenness of the abundance of species, reflecting the structure of an ecological community and showing the absence of the dominant species. It is believed that the ecological system is a high quality system in terms of biodiversity, only if it differs from others by the abundance of species and the highest rate of equalization. Ecological system, that has rich species diversity, must satisfy the following criteria:

- has a high indicator of species abundance;
- differ with uniform probability distribution for the number of individuals of each species;
- has similar levels of probability density function for each type of species.

The question of whether such environmental system is optimal from the point of view of biological evolution is debatable. However, it can be accepted as a basic model to compare different ecosystems in relation to this system by the criteria of biodiversity. This idea can form the basis of a

criterion that takes into account the probabilistic nature of biodiversity. However, this is possible only if probabilistic models of biological diversity will be built for taxonomic groups – orders, families, etc.

Statement of the problem

The study of biodiversity issues related to necessity of studying the habitats of species, their ecological and morphological characteristics, patterns of distribution according to various indicators of the dynamics of evolution. Priority way is to study the structural features of communities in specific environmental conditions with taking into account their species composition, abundance, life expectancy and other parameters. Without generalizing the data set describing biodiversity, it is impossible to establish the rules of biological evolution of life on Earth.

The aim of this work is to develop GIS models of biodiversity and establish trends and evolution of species, as well as obtaining the probability rules of species distributions.

The object of study is the most common suborders of Muridae and Sciuromorpha of the most numerous groups of mammals - rodents, and also the primates. For these groups, there is a wealth of information in the form of the World database (DB).

Suborder Muridae of order Rodentia is one of the major taxonomic groups of units among mammals, it includes more than 1,000 species of 10 existing families and three extinct. The representatives of the suborder Muridae have been introduced worldwide. Life rodent populations are indicators of the environment.

The term Sciuromorpha has referred to numerous groups of rodents, but the only family common to all variations is the Sciuridae, the squirrels. Most definitions also include the Mountain Beaver. Well-adapting to different conditions of life, the group also has mastered almost all climatic zones of the Earth.

Members of the order Primates – prosimians and simians form a diverse group with complex forms of social organization. Most primate species live in tropical rain forests. The group includes 356 species of 11 families [2]. Suborder of primates is the highest form of animal in the evolutionary chain. The human is also the unit of it.

Patterns of biodiversity for the studied biological groups

Based on collected data a structured information system was built which includes a variety of numerical indicators and contains GIS models of species distribution Muridae, Sciuromorpha and Primates, as well as photographs of individuals of the studied species. Quantitative

indicators include information to indicate the average life expectancy, body temperature, weight, and size of the animals, the number of litters, the interval between litters, length of pregnancy, lactation, metabolic rate, etc. – about 30 indicators for each of the approximately 1 500 species. The total number of entry in the DB is about 50 000. During the data collection there was released the search of mapping information with images of studied habitats species, and also was made the digitizes of this areas. The method used for processing graphic data is a step by step process of digitizing raster images and process them: defining the boundaries of regions and areas of polygons.

To create a database, statistical and graphical data processing was used system MapInfo, which combines the advantages of processing information held by the database (including the query language SQL), and clarity of maps, lists, and charts. Established GIS is presented in Figure 1.

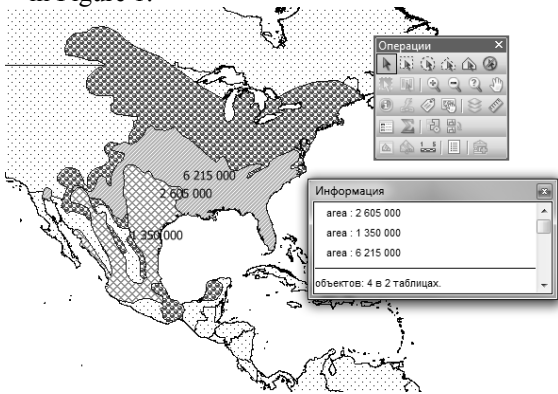


Figure 1. – Example representation of a habitat distribution of species

Over 2 000 maps were processed in total that contain the information on the spread of Muridae, Sciuromorpha and Primates on Earth.

According to the collected data, we can estimate the probability distribution of the species studied. To do this, we have to use geometric probability, which is the ratio area habitat of each species to the area of the land of the earth's surface. Next, the rules of probability are sought as dependencies between geometric probabilities and various biological parameters of each group or climatic indicators of the environment. For this purpose we used a typical method of estimating the probability of events, which is widely used in biological sciences. This methodology based on the methods of probit analysis was developed in the twentieth century by the famous entomologist Chester Bliss [6]. Numerous experimental data obtained in toxicology, entomology, microbiology, ecology, etc. show that the relationship between the proportion of individuals who are observed with some of the effects, for example the negative, and the amount of exposure, such as dose, expressed in

a probability curve that has an S-shape. Usually, the transformation of the curve to a straight line includes next: on the abscissa axis there are logarithms doses, and the ordinate axis – the probabilistic one, the so-called probits. In the biological sciences, and security systems, probit is determined according to the equation:

$$\Pr = \alpha_0 + \alpha_1 \cdot \ln z_1 + \alpha_2 \cdot \ln z_2 + \dots + \alpha_n \cdot \ln z_n;$$

$$w = \frac{1}{\sqrt{2\pi}} \int_{-\infty}^{\Pr} e^{-\frac{t^2}{2}} dt, \quad (1)$$

where α_i – const, z_i – biological parameters or characteristics of the environment; w – statistical or geometric probability.

Data processing technique involves finding connections between the probability distribution of the species and the most important parameters (weight, life expectancy, body temperature, etc.) in the form of equations (1).

As a non-dimensional characteristics associated with biological parameters during the links search was selected geometric probability distribution of these parameters. It is known that for one-dimensional geometric random variable the probability is finding according to the equation:

$$\rho_i = \frac{z_i - z_{\min}}{z_{\max} - z_{\min}}, \quad (2)$$

where z_i – some biological parameter or characteristic of the environment; z_{\max} , z_{\min} – accordingly the maximum and minimum value for this parameter in the group of all the studied order.

From the collected data we can estimate the probability of distribution of each species W_s . For this goal we can use, as previously mentioned, the ratio of the habitat area of each species to the land area of the earth's surface.

The statistical probability of the species existence W with a certain biological parameters (e.g., life expectancy and body weight) can be found from:

$$W = i/m, \quad (3)$$

where i – the number of species in which there is a certain biological parameters less than specified values; m – total number of all species from studied order (suborder).

Consider the more detail the results of experiments established for the suborder Muridae, which were obtained on the basis of the above methodology.

For example, in Figure 2, the number of species characterized by the number of points in the highlighted area in the figure, and the total number of species characterized by the number of observed data points.

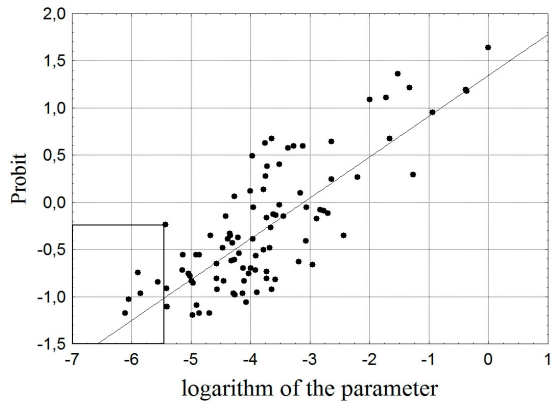


Figure 2. – Dependence probability of species existence from a parameter

When analyzing the data with the most significant relationships of statistical probability of the existence was set with intensity of metabolism, as well as with life expectancy in captivity and an average weight of an individual. The analysis of dependencies for Muridae are presented in Figures 3 and 4.

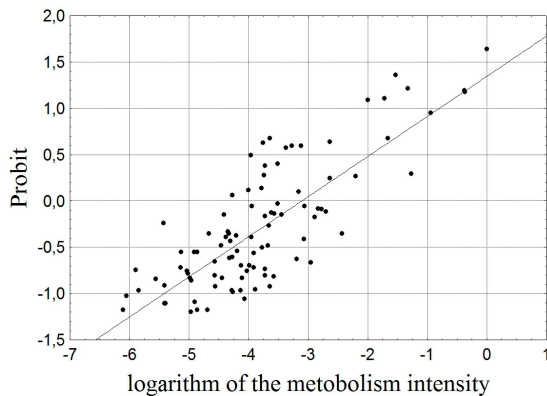


Figure 3. – Dependence probability of species existence from the metabolism intensity

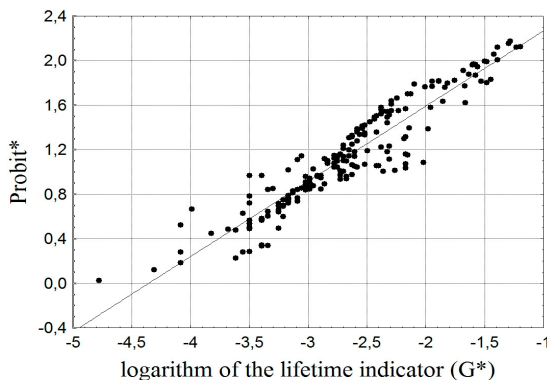


Figure 4. – Dependence probability of species existence from life expectancy in captivity:
 $Probit^* = Probit - 0,211 \cdot \ln \rho_v$; $G^* = \ln(\rho_\tau)$

It was found that dependence probability of species existence from the metabolism intensity for Muridae has the next form:

$$Probit = 1,1602 + 0,04 \cdot \ln \rho_M, \quad (4)$$

where $\rho_M = \frac{Metab - Metab_{min}}{Metab_{max} - Metab_{min}}$; $Metab$ – metabolism intensity (W).

The correlation coefficient was based 0,78.

On the other hand the statistical probability dependence of species existence of Muridae from life expectancy in captivity and the average weight of an individual is:

$$Probit = 2,713 + 0,593 \cdot \ln \rho_\tau + 0,211 \cdot \ln \rho_v, \quad (5)$$

where $\rho_\tau = \frac{\tau - \tau_{min}}{\tau_{max} - \tau_{min}}$, $\rho_v = \frac{v - v_{min}}{v_{max} - v_{min}}$, τ – life expectancy in captivity (years); v – average weight of an individual (kg). The correlation coefficient was based 0,94.

Based on the value of the habitats area of species were found geometric probabilities by dividing the space areas to the area of the earth's land surface, which is equal to 148940000 km². When analyzing the data most significant relationships of probability species distribution were established with a body temperature of a species (fig. 5).

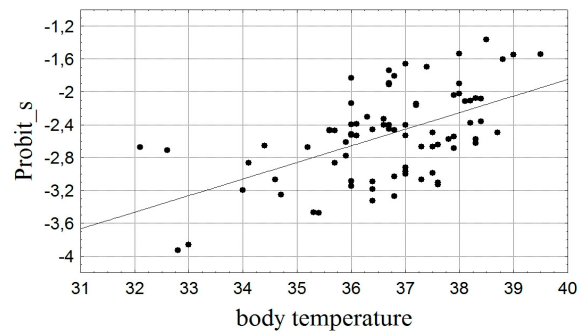


Figure 5. – Dependence probability of species existence from a body temperature

The probability dependence of species distribution Muridae from body temperature has the form:

$$Probit_s = -9,326 + 0,1840 \cdot \ln t_T \quad (6)$$

where t_T – body temperature; $Probit_s$ – probit of the probability dependence of species distribution.

This dependence is significant since the correlation coefficient was based 0,5.

From these results it can be concluded that the habitats area distribution is greater in area for those species which body temperature of individuals is higher.

In the similar way, we obtained the dependencies for suborder Sciuromorpha and for Primates.

Since there is a relationship between the probability distribution of the species and its temperature for Muridae, suborder Sciuromorpha and for Primates, it is natural to assume the existence of the probability species distribution due to climate indices. Therefore the possible direction for future research could be the development of models aimed to the search for patterns species distribution for studied groups (suborders), that are depending on the climatic parameters of each type of habitat. This can be done with the usage of climatic database, which is time series for each cell of a regular latitude-longitude grid with sets of climatic parameters, which could be available from the system Climate Wikience [8] developed by DonNTU. This becomes possible with a combination of established in this paper DB of Muridae, Sciuromorpha and Primates with the DB of the World Climate Center [9], which holds the archives of climate data analysis and which are represented in Climate Wikience.

Archive data from the World Climate Center allows you to build in time averaged field of climatic parameters for the planet. Such averaging can be carried out for 15 years on latitude and longitude grid of the world with a cell of the 1x1 degree. The archive information is stored in a few terabytes with 80 climatic parameters, such as temperature, relative humidity, wind speed and direction of wind, light, rainfall, altitude, etc. With the use of regression analysis we can identify the most important climatic parameters that affect the habitats species distribution. As a result of a species habitat GIS model can be put in correspondence with the attribute information of the 80 averaged climate indicators. Besides from the database can be taken attribute information quantitatively characterizing each type. That is, the union of created DB with the averaged World Climate Centre DB, that will help to create models of species distribution in the world. It is assumed that future researches will be done in this area.

Summary

Therefore, the developed GIS model of species distribution and created DB with mapping and attribute data allow to establish the rules of probability species distribution. The majority of the information about the existing species of flora and fauna in the world will be processed using the same technique, it would be possible to build a global model of the planet's biodiversity for the life sustainability assess, similar to the ideas of V.A. Kostitsyn.

Therefore, the basis of the modeling methodology of species distribution for assessing

life sustainability must be formed by the following approaches:

- **zonal approach**, which allows to select main climatic zones on the planet and inherent ecosystems to them. In the first phase here it is possible to build models at the zonal and continental levels, what will cover living environment of large scales;

- **global approach**, that differs mass accounting of species in diverse selected zones and ecosystems connected to different zonal characteristics of territories;

- **indicator approach**, which allows for each selected ecosystem to identify key species of flora and fauna, which are the basis of biological life of these ecosystems;

- **hierarchical approach**, which allows to highlight the most important tiers in the structure of ecosystems as well as key species that determine the life of the ecosystems;

- **probability approach**, enabling to tie the probabilities of species distribution with their biological parameters, as well as characteristics of the environment and peculiarities of ecosystems functioning;

The complexity of this problem is connected with the necessity of selecting a number of key (indicator) species, building a significant amount of probability models and evaluation of the relationship of parameters of species with climatic factors. The only way to solve this problem – is the use of global modeling techniques that use the latest information technology.

References

1. <http://base.safework.ru/iloenc?doc&nd=857100187&nh=0&ssect=0> (14.10.2012).
2. Животные. – М.: Астрель, АСТ, 2008. – 624 с.
3. <http://bibliofond.ru/view.aspx?id=432952>.
4. <http://www.ecolife.ru/e-lib/UR.pdf> (17.09.2012).
5. В.А. Костицын. Эволюция атмосферы, биосферы и климата. – М.: Наука, 1984. – 96 с.
6. А.Г. Платонов, М.Я. Ахалая. Применение метода пробит-анализа в радиобиологии. Расчет полулетальной дозы ЛД50. Уч.-метод. пос. – М.: НИИЯУ МИФИ, 2010. – 36 с.
7. В.К. Шитиков, Г.С. Розенберг. Оценка биоразнообразия: попытка формального обобщения / Jahrbuch fur EcoAnalytic und EcoPatologic. 2004. – 39 с.
8. Climate Wikience <http://wikience.donntu.edu.ua/> (07.10.2012).
9. Climatic indicators of the environment http://data-portal.ecmwf.int/data/d/interim_full_moda/; <http://nomads.ncdc.noaa.gov/data.php?name=access#CFSR-data> (20.10.2012).