Integrated model of potential biodiversity of the Crimean Peninsula

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Abstract. The study presents a special methodological approach to the construction of the integral model of potential biodiversity on the example of the territory of the Crimean Peninsula. GIS technologies serve the tool for creating this kind of material. The proposed technique allows effectively identifying spatial differences and carrying out multi-criteria analysis of the studied territory. The main stages of the methodology include the construction of vector layers of operational-territorial units, the compilation of a database on biodiversity criteria, the analysis of close relations between the value of biological diversity and the value of habitat diversity, the identification of statistical dependencies, as well as the construction of an integral model based on the results of preparatory stages. The resulting model resembles a raster layer of potential biodiversity for the 1x1 km cell format (potential number of species per 1 km²). The distribution of the potential biodiversity indicator at this cell size smooths certain differences in the overall pattern of the model.

1. Introduction

Biodiversity, as one of the most representative characteristics of the ecosystem, plays an important role in the study and conservation of the natural environment. There are some difficulties in studying the spatial distribution of biodiversity due to high variability of ecosystem conditions. At the same time, it is the conservation of biodiversity at the ecosystem level that is crucial for sustainable development of any territory.

In view of the fact that the direction for the study and conservation of biodiversity has reached the international level [10], it is necessary not only to identify and take into account the stage of ecosystem development at the current moment, but also to form perceptions, accumulate knowledge in the field of modelling of biodiversity change at different time scales in order to solve practical tasks in the field of landscape planning.

Many authors developed excellent biodiversity maps covering natural areas of different scales [1, 5, 9]. The basis for the creation of such graphic materials was the use of GIS technologies. Some examples of the use of GIS technologies for biodiversity mapping are described in [3, 11].

GIS technologies solve the complex task of modelling the spatial changes of biodiversity. There are various methodological approaches to spatial modelling used by foreign [6] and domestic [2] researchers. However, the main principle of all techniques is to work with certain operational-
territorial units, on the basis of which the probabilistic models describing the specificity of the spatial distribution of biodiversity are subsequently applied. The accuracy of the model as a whole depends on the completeness of understanding the structure and functioning of the territory. Biodiversity modelling can be carried out at both regional [7, 8, 12] and local levels [4] based on detailed study possibilities and targets.

The purpose of the study is to obtain the empirical model for mapping the potential biodiversity of the Crimean Peninsula.

2. Methods and materials

The study was carried out at two spatial levels: regional (operational-territorial unit (OTU) – environmental network elements) and local (OTU – Special Protected Natural Areas (SPNA)).

The work included several stages.

The first stage was to construct a mapping model of base locations. The SRTM space snapshot with 30x21 m cell resolution was used (the snapshot was taken from the official website: https://www2.jpl.nasa.gov/srtm/index.html). After the digital relief model was prepared, the geotological parameters were simulated. Raster layers of slope exposure, surface slope, vertical and horizontal surface curvature were built through the dimensional analysis (ArcGIS Spatial Analyst). Next, each raster layer was reclassified according to its features:

- exposition was classified into 8 rhumbs and was divided into 10 classes including flat surfaces and 8 rhumbs (northern exposition was divided into 2 classes (0–22.5°; 337.5–360°)).
- surface slope was reclassified into 6 classes with differentiation intervals of 0–3° (shallow slopes), 3–8° (weak slopes), 8–15° (middle slopes), 15–30° (steep slopes), 30–45° (strong slopes), more than 45° (extremely steep slopes).
- vertical and horizontal curvature of the relief was divided into 2 classes – convex slopes (with positive values of the relief curvature) and concave slopes (with negative values of the relief curvature). Straight slopes were not identified.

Subsequently, on the basis of the obtained rhumbs, a model of basic locations was built with information on all selected geotological parameters embedded in separate cells of the rhumb (cell size – 30x30 m).

The second stage involved identifying base locations within the selected OTU by calculating the following indicators: total OTU area, number of elementary locations (cells), number of base locations within the OTU, area of each base location loop, number of types of unique locations by combination of geotological parameters, area of types of unique locations by combination of geotological parameters.

The OTU vector layers of different levels were arranged with a raster layer of base locations. The ArcGIS Spatial Analyst was used to determine the variety of base locations within each loop, the area of base locations and OTU loops, and the number of elementary cells. In turn, the raster layer of the locations was reclassified according to unique classes of combinations of geotological parameters and vectorized using ArcGIS conversion module. As a result of combining the obtained vector layers of base locations and the considered OTU contours, a vector file with a database of the number, area and geotological characteristics of base locations within each considered OTU was obtained. The database itself was processed in MS Excel, where the number and area of the contours of each base location were determined.

The third stage of the study was the process of compiling a database on biodiversity criteria (number of species of higher vascular plants, number of endemic and number of rare species) and spatial parameters of territorial units of different spatial levels (regional and local).

The following indicators were chosen for habitat diversity: total number of base locations, total variety of base locations, density of locations per 1 ha, density of locations per 1 km², indices of location diversity based on the Margalef and Menhinik index.

For biological diversity, the following indicators were determined: total number of species of higher vascular plants, density of species per 1 ha, species density per 1 km², Margalef and Menhinik species diversity indices, total species diversity as the ratio of area to the number of species, total
number of plant species listed, total number of species classified as endemic, density of plant species listed as endemic, density of plant species classified as endemic.

At the fourth stage, the degree of spatial relations between biological diversity and habitat diversity (locations) was determined. For this purpose, two spatial relation coefficients were calculated:
- linear regression coefficient (base coefficient to determine the relations between parameters);
- Spearman’s rank correlation coefficient (special coefficient to find the spatial relations of quantitative parameters).

The use of these coefficients is quite effective in such works, as confirmed by the results of many studies. The linear regression coefficient and the Spearman’s rank correlation coefficient were calculated automatically using the statistical tools of ArcGIS and MS Excel. They make it possible to make calculations on the basis of the general consolidated database of parameters, to obtain the assessment of validity of the output dependencies and to build formalized models.

At the fifth stage, an integral model of biological diversity of Crimea was built on the basis of geoinformation modeling and the construction of statistical dependencies. From the methodological point of view, the stage is based on the possibilities of statistical data processing using ArcGIS and MS Excel.

The simulation is based on the results of the analysis of close relations between the value of biological diversity and the value of diversity of habitats derived from the simulation of base locations.

The dependency data was found to be somewhat closer for the local level than for the regional level. Taking this into account, the model was built on the basis of the database of biodiversity and habitat diversity values within the elements of the Crimea SPNA network.

Based on the obtained database, a linear correlation equation for a pair of parameters was built in MS Excel: number of varieties of base locations per unit area (1 km$^2$) / species variety per unit area (specified) (species density per 1 km$^2$) as the simplest and most “open” in terms of experiment reproduction.

The calculation was made for 58 SPNA objects, with reliable follow-up though autocorrelation at 95%.

The mapping model was then built on the basis of standard ArcGIS software, which also included several stages.

The first stage was the creation of a vector polygon layer as part of integral layers of the entire research project, which divided the territory of Crimea into a grid of squares with the sides of 1x1 km, which corresponds to the adopted specific territorial unit in terms of defining the biological diversity.

The second stage was to determine the size of the base location diversity for each grid cell. This procedure is implemented using the ArcGIS spatial analysis module. As a result, we obtained a raster layer of variety of base locations for the 1x1 km grid, as part of the entire mapping project of the study.

The third stage was to calculate the magnitude of potential biodiversity for each grid cell based on the magnitude of the diversity of locations. The algorithm is implemented by constructing the most representative linear regression equation for the considered parameters in the ArcGIS raster calculator.

As a result, a raster layer of potential biodiversity was obtained for the 1x1 km cell layer (potential number of species per 1 km$^2$). This layer represents an integral model of potential biological diversity for the territory of Crimea.

Given that the actual number of species in the model may exceed the actual composition of the flora of higher vascular plants when calculating the magnitude of potential biological diversity, it is necessary to introduce an adjustment for the diversity of species per 1 ha. To this end, the local spatial level of the corresponding indices was calculated in the database. Further, the potential value of diversity was interpolated over the entire cell area of 1 km$^2$.

Thus, each raster layer cell contains information on potential biological diversity per 1 ha (number of species per 1 ha).

3. Results
As a result, at the first and second stages of the study, a cartographic model of base locations of the territory of the Crimean Peninsula was built thus giving a serial number to each location. Based on this the habitat diversity was estimated by calculating the density and the number of unique base location types and the Shannon’s diversity index with further visualization in mapping models. Thus, the number of unique locations varies in the range of 18–220 units. The maximum values (150–220) are typical for landscape contours of mountain Crimea, central Prysyvashshia, the Kerch Peninsula and coast of the Tarkhankut Peninsula, minimum (18–70) – central part of lowland Crimea. The density of unique locations varies within 0.18–195.6 units of unique base locations per 1 km$^2$ and is directly dependent on the area of the landscape contour. On average, the density of unique base locations is 22 units per 1 km$^2$. The oscillation range of the Shannon’s index makes 0.11–5.28. The minimum values of the index 0.11–0.36 correspond to landscapes of lowland Crimea with increase of this value within the limits of unique natural objects. In piedmont Crimea the index values increase to 0.37–1.63, in mountain they reach the maximum from 1.64 to 5.28. Within the South Coast of the Crimea the index makes 2.63–3.65.

In the third and fourth stages, the number of species of higher vascular plants, endemic and rare species within the operating territorial units of regional and local level was estimated with further determination of indicators of habitat diversity and biodiversity. The mapping models of the diversity of base locations within operational-territorial units at different levels of ecosystem organization, as well as spatial distribution of indicators of their biological diversity, were compiled.

At the regional level, the maximum values of species density were recorded in the South-West maritime eco-center, high values – in Tarkhankut and Karadag, low values – in East Sivash and Baidar, low values – in mountain Crimea and minimum values – in all other eco-centers. Spatial differences in the distribution of rare and endemic species are rather weak. With regard to the Margalef and Menhinik biodiversity indices, the former, according to the authors, does not fully reflect the spatial distribution of biodiversity at the regional level, while the latter, in turn, is more reliable. The maximum values of the Menhinik index are typical for the West-South Bank and Karadag eco-center, high – to Central Prysyvashshia, medium – to Belogorsk and Sasyk, minimum – to Tarkhankut. The total number of base locations made 5440040 elementary units combined in 1048576 base locations. The coefficients of linear and spatial relations between biodiversity and diversity of locations were 0.17–0.79 and 0.16–0.85, respectively, indicating a lack of sustainability between indicators.

At the local level, 28370301 elementary locations forming 40587 contours were identified within the considered SPNA. The analysis of habitat diversity indicators determined that one of the key factors influencing the change in its values was the SPNA area: feedback between the density of unique locations and the area was identified; this value causes a wide range of Margalef index values (0.003–159); the relations between the number of locations and the area is correctly determined for territories greater than 10 hectares. However, it is not possible to create a clear classification of “area – number of locations since many SPNA are characterized by a great influence of geotological factors.

If the calculation of the Margalef index took into account the OTU area and the number of unique locations, the calculation of the Menhinik index (0.1–182) took into account the number of locations. The spatial distribution of both indices is similar, as they are close in their formalized form. With regard to biodiversity, the relations with the area is rather weak and the conditions for both the number of species of higher vascular plants and their density per 1 km$^2$ or 1 ha come to the fore. The average values of the number of species are typical for SPNA of both large and small areas, dependence is evident only at extreme points of range. The analysis of species density revealed a significant role of habitat diversity in its spatial distribution. The Margalef and Menhinik species diversity indices with ranges 0.1–5.32 and 0.0141–1.211 respectively divided the studied objects into almost two identical intervals. It was not possible to establish clear spatial trends in the density of protected and endemic species.

On the basis of the obtained quantitative indicators of diversity of locations and biological diversity, the coefficients of linear and spatial relations were calculated. Their values range between
0.48–0.78 and 0.71–0.83, respectively, indicating a relationship between the two values. This relationship is statistically significant, sustainable and supports the hypothesis of the study on the relations of the considered indicators. Besides, the correlation dependencies are quite high, which makes it possible to conclude that the diversity of locations mainly determines the diversity of habitats. In turn, in the conditions of the Crimean Peninsula, such dependence determines the diversity of ecotopic conditions of ecosystems and, as a result, defines the level of biological diversity at regional and local spatial levels. However, it is the local level that shows a closer relation in differentiating the magnitude of biological diversity and the diversity of habitats (locations).

The calculations and analysis made during the first four stages of the study show the possibility of finding integral dependencies in the relations between the magnitude of diversity of habitat types and the magnitude of biological diversity.

Due to the fact that the closest statistical dependencies were identified for the local level, the construction of an integral model of the peninsula’s biological diversity was done using correlation dependencies derived for a given spatial level.

The database compiled in the framework of the study can be used to build the model of integral biodiversity using different models and correlation dependencies. In order to prevent congestion of the actual material and ensure certain “transparency” of simulation, we decided to use the simplest coefficient of linear correlation and to build formalized models on the basis of linear dependencies as the most objective and easy tools to understand and unambiguous results.

Among the total number of pairs of coefficients for which the model was constructed, the simplest pair of indicators was also chosen to obtain the linear regression equation: the linear correlation coefficient for the pair of the number of varieties of base locations per unit area (1 km\(^2\)) / species variety per unit area (refined) (species density per 1 km\(^2\)).

Let us consider the results of linear regression models. In the formula below, \(Y\) – sought value of potential biodiversity, \(X\) – value of habitat diversity. For the equation, the whole necessary complex of calculation of regression statistics, multiple criteria, normalized criterion, standard error, standard quadratic deviation was made. The Student’s criterion was accepted at the level of 0.05. The validity of all models makes 95 %.

The calculation takes into account all 58 SPNA objects, and the results are checked on the basis of autocorrelation.

Thus, the following relations were obtained:

\[
Y = 69.72 \cdot X - 143.43
\]

The degree of autocorrelation when comparing the obtained values and values determined on the basis of the actual data within a specific SPNA, when comparing the actual biological diversity data of the model and the simulated value for each object are within the permissible error, which is logical given the autocorrelation system.

Figure 1 and 2 show the mapping models of the diversity of locations within a kilometer grid, and the mapping model of the potential biodiversity in specific values per 1 ha.

When considering the map-diagrams, the transition of mapping detail with change of cell value from 21x30 m to 1000x1000 is noted. This is caused by both the logic and program of the study, as well as the actual possibilities of processing the mapping model and the convenience of its use. We used quite powerful and modern computers, but even they process information when building a model for 5–6 hours, which makes it difficult to work. Besides, with a fine granularity of the cell, a computer with a powerful video memory will be needed to work with the resulting raster layer, which in some cases also complicates the work with the resulting materials. When working with a bitmap image with a cell size of 1000x1000 m, the output file size is significantly smaller, making it easier and faster to work with.

It shall be noted that despite changing the level of detail, the model constructed is rather fractional, has high degree of spatial differentiation and clearly identifies differences in the value of habitat diversity and the magnitude of biological diversity. Let us take a brief look at the distribution of these values.
The range of variation in the number of unique habitats is within the range of up to 168 per 1 km$^2$. The range is quite spatially differentiated within the territory of the peninsula.

The maximum values are typical for the territory of Mountain Crimea with the presence of local pronounced spatial maxima in the range of 129–168 units. Besides, the South Coast of Crimea is separated with a range of 65–128 units, while the South-East, Central, South-West parts of this territory are slightly different in the value of this indicator.

The territory of the Kerch Peninsula has strong spatial differentiation of the location number per 1 km$^2$. Local maxima are present here, increasing the number of locations to 130, with a total relatively low value in 50–65 unique locations per 1 km$^2$. There are also local minimums with a reduction of the indicator to 15 locations.

**Figure 1.** Number of habitats in 1x1 km cell

In terms of the number of locations the average position is held by the piedmont Crimea, where the values of the number of unique locations are in the range of 58–88, at the same time the river valleys are quite clearly distinguished in the form of peculiar intrazonal maxima, the impact of which on the overall picture of the distribution of the indicator also affects the plain Crimea.

The plain Crimea has the minimum values in the average range of 25–50 units with quite extensive local maxima present with an increase in the indicator to 70 units.
Slightly higher values are observed in the Tarkhankut Peninsula and the Donuzlav Lake, where it is possible to reduce the value to 15 unique locations per 1 km² in local minimums and to significantly increase it to 100 or more units.

The overall picture of the indicator distribution at a given cell size as a whole somewhat amplifies the model of base locations and smooths out certain narrow differences.

Next, let us consider the diversity of local ecosystems by habitat type and the mapping model of the biological diversity potential (number of species / 1 ha).

The total amount of variation of potential biological diversity within the territory of Crimea is the range of 15–116 species per 1 ha, and this range is sufficiently clearly divided into natural intervals, which are clearly confined to certain zone ecosystems. Let us look at specific examples.

The range of potential number of species within 90–116 units per 1 ha acts as a certain local maximum and is present in various parts of mountain Crimea, piedmont and the South Coast of the Crimea.

The most spatially common value of potential biodiversity per 1 ha within mountain Crimea is the range of 71–81 species per 1 ha.

It is interesting to consider the river valleys of the northern macro slope of the Crimean Mountains. They are presented in the form of intrazonal corridors of increased potential biological diversity, which is generally confirmed by already established ideas on the role of rivers in differentiation of landscapes, ecosystems, elements of ecological network. This fact is confirmed by the developed model.

For example, when rivers “exit” into the lowland part of Crimea here the value of potential biological diversity lies within the limits of 51–60 species per 1 ha, with possible local increase to 80 species with total background value of adjacent lowland areas making 30–40 species per 1 ha. The same picture is observed in the piedmont Crimea.
It is interesting to study the local minimums of potential diversity within the lower portions of the slopes of the cuesta arrays of the Inner and Outer Range, where the value of potential biological diversity per 1 ha is reduced to 35–45 units with the total diversity in the swale features and river valleys making 70–80 units per 1 ha.

A similar pattern is observed on the shallow plateau of the Main Range of the Crimean Mountains in their eastern part, with only the difference that the local minimum will be less contrasting, and the decrease in diversity will make up to 50–60 units with a general background on the Main Row making 70–90 units of species per 1 ha.

The territory of the Kerch Peninsula is quite contrasting in comparison with the whole plain Crimea. Here, the range of variation of potential biological diversity is extremely high. Within the southern and central part of the peninsula, the values are minimal and amount to not more than 40 species per 1 ha. In the north-western part and along the coast along the boundaries of the peninsula there are local peaks of potential biodiversity with increase of values to 69–79 species per 1 ha and possible local peaks with values of 90 units.

The territory of the Tarkhankut Peninsula is interesting from the point of view of spatial differentiation of the potential biological diversity. Thus, in its southern part near the coast of the Kalamitskiy Bay there is a large local minimum of diversity with potential diversity making 15–30 species per 1 ha. In turn, within the tip of the peninsula in the northern part there are local maxima with values up to 50–80 species per 1 ha, which is comparable to the piedmont Crimea. Similar maxima are also present within the central part of the peninsula, for which in general there are peculiar alternating “waves” of increase from 30-40 to 40-50 species per 1 ha.

The total distribution of the value of potential “restored” biological diversity for plain Crimea within the expanded territories can be differentiated into two intervals: the first and the most common – 35–45 species per 1 ha, and the second – 45–50 species per 1 ha in the form of peculiar zones with increased diversity. It shall be noted that within Prysyvashshia these zones are larger, as well as their area. Here, the prevailing value of potential “restored” biological diversity can be up to 55 species per 1 ha.

4. Conclusion
The presented model for the first time reveals a spatial picture of biodiversity differentiation derived from a new approach to modelling the potential biodiversity based on its relations to habitat diversity. The model shows high efficiency in assessing spatial aspects of biological diversity for the territory of the Crimean Peninsula, allows effectively detecting spatial differences and carrying out the multi-criteria analysis. Another field of interest is the possibility of testing the model for other regions of Russia both with similar zone features of ecosystems and fundamentally different.

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