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Igor Bychkov  
Victor Voronin *Editors*

# Information Technologies in the Research of Biodiversity

Proceedings of the International  
Conference “Information Technologies in  
the Research of Biodiversity”,  
11–14 September, 2018, Irkutsk, Russia

 Springer

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# Preface

This volume contains the proceedings of the First International Conference “Information Technologies in the Research of Biodiversity” that was held from 11 to 14 September 2018 in Irkutsk, Russia. The conference includes plenary and sectional reports, round tables and master classes on the publication of biodiversity data for use in basic and applied research to provide you with principles for working with existing biodiversity information systems.

Chapters in this book cover areas of interaction of knowledge on biodiversity and information technologies. Integration of modern information technologies and classical methods of biodiversity research enables reaching new levels of knowledge acquisition. New demands on researchers require coordination, standardization and unification of data and methods.

The main topics include methods, models, software systems for the analysis of biodiversity data; global data portals; information and analytical systems on biodiversity; application of remote methods in vegetation mapping; and theoretical fundamentals and organization technologies of the information and telecommunications infrastructures.

The conference was organized by Matrosov Institute for System Dynamics and Control Theory SB RAS in cooperation with Siberian Institute of Plant Physiology and Biochemistry SB RAS, V.B. Sochava Institute of Geography SB RAS, Institute of Mathematical Problems of Biology RAS—the Branch of the Keldysh Institute of Applied Mathematics RAS. The conference was held with the support of the GBIF—Global Biodiversity Information Facility and Department of Nanotechnology and Information Technologies RAS.

The organizers would like to thank all the authors for their participation, Technical Program Committee, Editorial Board and associated reviewers for their good work and important contribution to the conference.

September 2018

Igor Bychkov  
Victor Voronin

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# The Fractal Model of the Microorganism's Frequencies Spectrum for Determining the Diversity of the Biochemical Processes in Soil

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**Abstract.** Modern molecular genetic methods have provided a extended opportunities for studying the frequency taxonomic composition of soil microbial communities, including uncultivated strains of microorganisms. Modern spectrum analysis of operational taxonomic units (OTU) identified by 16Sr RNA gene is limited to the comparison of the nucleotide sequences. We propose to use a fractal model to describe the frequency spectrum of microorganisms. This model necessary to study the network self-organization of microbial communities and the functional diversity of the processes of biological systems. The power series from three frequencies of OTU are the fractal model of frequencies spectrum of OTU (for example: 0.1, 0.01, 0.001). Because there are many OTU's peaks in the original spectrum, peaks grouped with the same or similar amplitudes to form OTU-groups. Fractal topological analysis of the location of OTU-groups on a fractal portrait of the microbial community was been used to search for degenerate triangles with OTU-groups at the vertices, since these OTU-groups correspond to a microbial biosystem and to fractal model for the grouped OTU's frequencies. The functional diversity index ( $I_{FD}$ ) of biochemical processes is been determined by number of OTU-groups in microbial community and by number of OTU-groups in biosystem. The  $I_{FD}$ -dynamics was been calculated with using the daily data of molecular-genetic analysis of soil samples. As a result, we revealed the periodic fluctuations in  $I_{FD}$ -values and the periodic replacing of OTU-groups in a soil microbial biosystems that provide a wide diversity of a biochemical processes in soil microbial communities.

**Keywords:** Fractal model of microorganism's frequency spectrum · Functional diversity of biochemical processes in soil microbial communities · Fractal portrait of microbial community

## 1 The Fractal Model of Frequencies Spectrum of OTU-Groups

As components of biological systems, soil microorganisms with maximum efficiency convert organic substrates into nutrients for plants. To analyze the diversity of biochemical processes in microbial biosystems, it is been proposed to use molecular-genetic data of microbial communities. Since there are many peaks in the original frequency spectrum of the operational taxonomic units (OTU) of microbial communities, the peaks were been first grouped with the same or similar amplitudes to form OTU-groups. To group OTU, the entire range of values of  $\ln(p_i/p_{\max})$  is divided into intervals in steps of 0.1, where  $p_i$ ,  $p_{\max}$  are the OTU-frequencies with the serial number (i) and the highest OTU-frequency. The OTU's frequencies which falling into one interval are been summed to form the common frequency of the OTU-group. As a result, the initial spectrum of the OTU-frequencies can been reduced to 20–40 frequencies of OTU-groups.

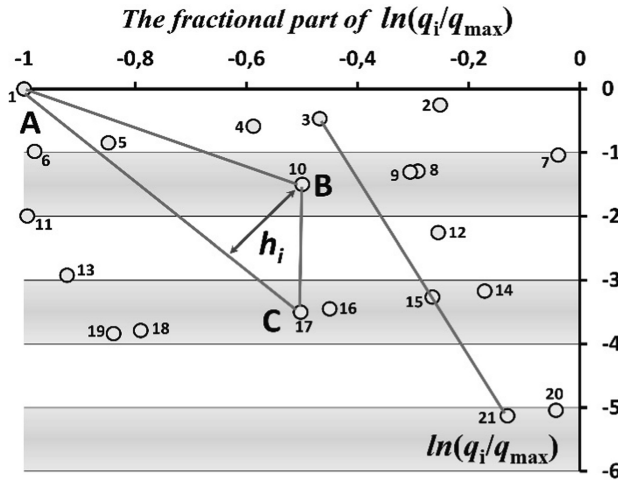
In the frequencies OTU-group spectrum, it is necessary to select three OTU-groups, which frequencies corresponding to a power series as the fractal model [1]. We assume that these three OTUs form a biosystem and perform one biochemical function. The fractal model is a power series of three frequencies of OTU-groups (for example, 0.1, 0.01, 0.001). The logarithms of these frequencies vary linearly (for example,  $-\ln(10)$ ,  $-2\ln(10)$ ,  $-3\ln(10)$ ,...). This property of the fractal model was been used to search for the OTU-groups belonging to biosystems.

## 2 The Topological Analysis of OTU-Groups Location on the Fractal Portrait of the Microbial Community

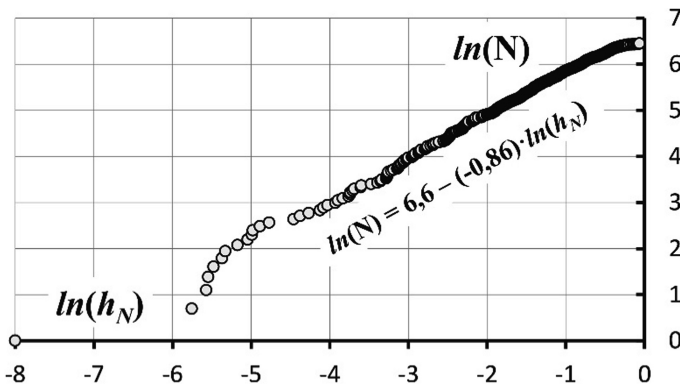
The fractal portrait of a microbial community is the two-dimensional field with points representing the OTU-groups (See Fig. 1) [2]. The Y-coordinate of the OTU-group determines by  $\ln(q_i/q_{\max})$ . The X-coordinate of the OTU-group determines by the fractional part of  $\ln(q_i/q_{\max})$ , where  $q_i$ ,  $q_{\max}$  are the OTU-group's frequency with the serial number (i) and the highest OTU-group's frequency.

The fractal measure of topological analysis is a triangle with three OTU-groups at the vertices. The smallest height ( $h_i$ , see Fig. 1) of the triangle is a scale of the fractal measure. At the vertices of the triangles, there must be OTU-groups for which the integral parts of  $\ln(q_i/q_{\max})$  are not equal. For example, the integral parts of  $\ln(q_1/q_{\max})$ ,  $\ln(q_{10}/q_{\max})$ ,  $\ln(q_{17}/q_{\max})$  are equal respectively 0, -1, -3 (see the points A, B, C in Fig. 1). All triangles that constructed on the fractal portrait can been arranged in ascending order of the smallest height of the triangles ( $h_N$ , see Fig. 2), where N is the serial number of the triangle in this series.

The logarithmic dependence (see Fig. 2) is a quasilinear dependence and it is equivalent to the classical fractal logarithmic dependence [3]. An unusual way of covering by triangles the points on the fractal portrait has led to the fact that the coefficient of fractal dimension has acquired a negative value ( $-0.86$ , see Fig. 2).



**Fig. 1.** The topological analysis of OTU-groups location on fractal portrait of the microbial community. Notes: The OTU-group's frequency determines Y and X coordinates corresponding point on the portrait. The ABC-triangle with OTU-groups No. 1, 10, 17 at the vertices is a fractal measure of topological analysis. The smallest height of the triangle ( $h_i$ ) is a scale of the fractal measure. Since the OTU-groups No. 3, 15, 21 are located on the same straight line and corresponding to a degenerate triangle, we assume that these OTU-groups form a biosystem and perform one biochemical function.



**Fig. 2.** The logarithmic dependence of the serial number (N) of triangles constructed on a fractal portrait and arranged in ascending order of the smallest height of the triangles ( $h_N$ ).

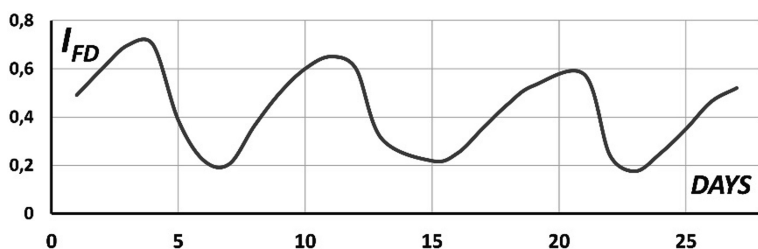
Among all triangles that were constructed on the fractal portrait we choose degenerate triangles for which  $\ln(h_N) < -5$ . We believe that the OTU-groups of these triangles form a biosystem and perform one biochemical transformative function. For example, the OTU-groups No. 3, 15, 21 (see Fig. 1) correspond to a degenerate triangle and to a biosystem performing one biochemical function.

### 3 The Functional Diversity Index of Biochemical Processes in Soil Microbial Biosystem

The number of degenerate triangles found on a fractal portrait determines the number of different processes of biochemical transformation performed by the soil microbial community. The number of OTU-groups ( $M_B$ ) corresponding to degenerate triangles divided by the total number of OTU-groups in the microbial community ( $M_C$ ) is the functional diversity index of a biochemical processes in microbial communities ( $I_{FD}$ , see Formula (1)).

$$I_{FD} = M_B/M_C. \quad (1)$$

In accordance with the proposed computational method, the daily dynamics of  $I_{FD}$  (1) was been calculated with using the molecular-genetic data of soil samples obtained in September 2006 in Moscow Region [4] (see Fig. 3).



**Fig. 3.** The computational daily dynamics of the functional diversity index ( $I_{FD}$ ) of biochemical processes in microbial communities from the Moscow Region soils [4].

The observed  $I_{FD}$  fluctuations (see Fig. 3) mean that in the soil there are constant changes in the structure of microbial biosystems and changes in the direction of biochemical processes. The periodic rearrangement of microbial biosystems with the replacement of OTU-groups and the change in the number of different biochemical transformations points to a wide range of biochemical processes which can supported by the soil microbial community.

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