

**Alexey V. Troitsky**

Department of Evolutionary Biochemistry  
Belozersky Institute of Physico-Chemical Biology  
Lomonosov Moscow State University

**Leonid Yu. Rusin**

Laboratory for Mathematic Methods and Models in Bioinformatics  
Institute for Information Transmission Problems  
Russian Academy of Sciences  
Center of Genetics and Technology  
Faculty of Biology  
Lomonosov Moscow State University

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Knowledge of phylogeny is of fundamental importance in evolutionary studies, from the reconstruction of the Tree of Life to revealing and understanding the laws of body plan formation (the evo-devo realm) and to describing the patterns and processes of microevolution. The discipline of phylogenetics has evolved radically in the new millennium, capitalizing on theoretical and methodological breakthroughs in analysis and algorithms, on the exponential increase in molecular data, and on the availability of vast computing power to enter the phylogenomic era. An integral part of contemporary phylogenetics is the development of mathematical models and effective algorithmic solutions to tackle high-complexity computational problems of building evolutionary scenarios across the levels from genes to species, bioinformatics of next-generation sequencing data, and metagenomic assays. A solid methodological framework of phylogenomic analysis is emerging, applying data derived from whole genomes to problems in deep phylogeny, functional genomics, speciation and divergence, large-scale biodiversity studies, and phylogeography. The mission of the 5th Moscow International Conference “Molecular Phylogenetics and Biodiversity Biobanking” (MolPhy-5) is to provide a stimulating platform for the exchange of ideas and experiences in contemporary phylogenetics, evolutionary genomics and conceptually integrated disciplines. This round the program also places emphasis on genomics of biodiversity and aspects of utilizing molecular data for biodiversity research. The acknowledged focus is to bridge new fundamental knowledge with various applications of phylogenetics in metagenomics, barcoding of biological objects, molecular ecology, and epidemiology.

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