

Molecular Phylogenetics

Contributions to the 4th Moscow
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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, inferring patterns of coevolution of molecules, pathways, regulation systems, and species, assembling of sequence and tree data, etc. 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, barcoding, and phylogeography. The mission of the IV Moscow International Conference “Molecular Phylogenetics” (MolPhy-4) is to provide a stimulating platform for the exchange of ideas in such top areas of evolutionary research as evolutionary genomics, molecular phylogenetics and systematics, studies of complex traits of coevolution of different genomic and proteomic elements and their ancestral reconstruction, modeling evolution in a contemporary framework of algorithmic and computer science. The acknowledged focus is to bridge new fundamental knowledge with various applications like biodiversity studies, barcoding of biological objects, molecular ecology, epidemiology and anthropology, and other actively developing fields.

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PREFACE

Since its inception about 50 years ago, phylogenetics has permeated nearly every branch of biology. Initially developed to classify objects based on a set of cladistic rules, it has now become the central paradigm of evolutionary biology and a key framework for making sense of a wide range of disciplines such as genomics, community ecology, epidemiology, conservation biology, population dynamics, to name just a few. It is a testament to the power of phylogenetic methods that its application has expanded far beyond its original inception, now including the study of human culture, such as language and cultural memes.

Phylogenetic principles are used to reconstruct complex ancestral traits of morphological characters, genome structures and their properties, and evolutionary events (like gene duplications, losses, transfers, or chromosomal rearrangements). Phylogeny is also essential to infer gene and protein families, uncover complex population histories in epidemiological and other studies, understand viral and cell genealogies in medicine and developmental biology. New concepts are developing that tackle various aspects of coevolution, including approaches to define and algorithmically construct complex evolutionary scenarios for genetic systems, their regulations, epigenetic and intrinsic factors, noncoding genome elements, sequence primary and secondary structures, speciation process, etc.

The growth of phylogenetics is not just in breadth of disciplines but also in the sheer volume of published phylogenetic results. Some 20 years ago, near-exponential growth in phylogenetic publications had already been noticed, a growth that was probably attributable to the advent of powerful computers, Polymerase Chain Reaction, and Sanger sequencing. An update on the assessment of phylogenetic growth shows that not only is the growth in phylogenetic papers exponential, but more important the growth in the percentage of papers that report phylogenetic results is also exponential, indicating its increasing share in scientific research. Journals and databases have worked hard to keep pace with this growth, with the development of data repositories to archive and share data (e. g., TreeBASE, <http://treebase.org> and Dryad, <http://datadryad.org>) that would otherwise be inefficient to distribute as supplementary addenda.

In the last 10 years, the rate of growth of phylogenetic publications has waned somewhat, but with the recent advent of next-generation sequencing (NGS), we anticipate a new flood of phylogenetic results that is commensurate with this explosion of NGS data. In addition to the phylogenetic results themselves, we also anticipate the need for new methodological advances to improve efficiencies in sequence assembly, multiple alignment, genome annotation, and pipelining of massive analyses.

The Moscow Conference on Molecular Phylogenetics (MolPhy) strives to attract contributors in the broad area of molecular evolution and its applications. It is organized jointly by M. V. Lomonosov Moscow State University (A. N. Belozersky Institute for Physicochemical Biology, Faculty of Biology, Faculty of Bioengineering and Bioinformatics) and the Russian Academy of Sciences (Institute for Information Transmission Problems), with the support by leading academic organizations and scientific funds.

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