

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.