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**Molecular Phylogenetics 2014**

# CALL FOR PAPERS

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, and so forth. 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.

Potential topics include, but are not limited to:

- ▶ Evolutionary genomics
- ▶ Molecular phylogenetics and systematics
- ▶ Molecular dating, inferring complex scenarios of coevolution, and reconstruction of complex ancestral traits and events in genome evolution
- ▶ Development and phylogeny (evo-devo)
- ▶ Models and algorithms for molecular evolution
- ▶ Applied phylogenetics: genotyping and barcoding of biological objects, molecular anthropology, molecular epidemiology, and forensic science
- ▶ Molecular ecology, biodiversity, and biogeography

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