

1041-60-237

**Elchanan Mossel**, University of California, Berkeley, and **Sebastien Roch\***, Microsoft Research. *Reconstructing Phylogenetic Mixtures*.

Phylogenies are used to model the stochastic evolution of genetic data on the ancestral tree relating a group of species. Their reconstruction from DNA or protein sequences is one of the major tasks of evolutionary biology. Various ‘misleading’ phenomena, notably the variation in mutation rates across the genome as well as incongruent gene lineage histories, often make it necessary to model molecular data as coming from a ‘mixture’ of different phylogenies. Such mixed models play an increasingly important role in practice. In this talk, I will discuss new rigorous techniques to efficiently reconstruct large-scale phylogenetic mixtures. (Received August 12, 2008)