

COMPARISON AND STABILITY OF PHYLOGENIC TREES

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Abstract:

Maximum likelihood inferred topologies are commonly used to draw conclusions in evolutionary biology and molecular evolution. These computations are based amongst others upon on the observed nucleotides and as such are subject to sampling error.

In this talk we critically review classical measures of the robustness of the inferred tree. We extend resampling tools to characterize influential sites or species. We also derive bounds for the variations of the computed likelihood around its true value and the probability that a phylogeny has a better likelihood than another one "just by chance".

This is a joint work with Mahendra Mariadassou.

Keywords:

Phylogenetic, genomic data, robustness