

Testing Ascertainment bias and RNA secondary structure morphometrics as reliable phylogenetic signals

Status: Ongoing

Collaborators:

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Computer based programmes have been developed for the reconstruction of phylogenetic relationships among taxa. However, existing methods are reliable only when the divergence among taxa is moderate. In the extreme cases where divergences are especially deep, they have proved unreliable. This infidelity has misled phylogenetic inferences for many life forms, leading to mismanagement with varying degrees of severity, ranging from taxonomic lumping in biological conservation to misdiagnosis in human medicine. Especially in medicine where human health is concerned and hence accurate phylogenies are essential to understand pathogen lineages and biochemical pathways; accurate algorithms whose fidelity transcends hierarchical levels of genetic divergences are required. This project aims to formulate computational methods that dissipate homoplasy, a common nuisance in phylogenetic inferences among taxa with deep divergences. I am currently testing the diagnostic value of Ascertainment bias, and RNA secondary structure morphometrics as phylogenetic probes. Morphometric variations on RNA secondary structures among taxa is expected to be proportional to their evolutionary distances, while ascertainment bias (absolute allele sizes in focal species being often greater than that found in related species) should reflect the relative phylogenetic distance from the focal taxa.

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