

Genome-wide Molecular Dating

Abstract

The recent sequencing of genomes of closely related species and of many individuals from the same species enables the study of speciation and the inference of the history of populations. Standard phylogenetic methods reduce entire populations to single points in genotypic space by modelling evolution as a process in which a single sequence mutates along the branches of a phylogeny. In reality, each population consists of many individuals related by trees of genetic ancestry known as genealogies. We have recently developed an allele-frequency based approach called Polymorphism-Aware Phylogenetic Models (PoMo). Standard models treat substitutions as instantaneous events but PoMo describes them as a process: substitutions start as mutations to new, low-frequency alleles, then experience a series of changes in allele frequency. Our innovation solves a major problem in classical phylogenetics, namely incomplete lineage sorting, which causes the tree topology to vary along the genome. This project also addresses a number of important problems in mathematical phylogenetics. We will (i) provide a proof that species tree inference with PoMo is statistically consistent, (ii) tackle the molecular dating problem using modern genomic data rather than the small datasets used by other methods and (iii) integrate the PoMo approach in a Bayesian framework that allows gene duplication, transfer and loss. We will implement all three approaches in free and user friendly software and apply the new methods to data from mammals.

Scientific disciplines:

101004 Biomathematics (50%) | 106012 Evolutionary research (25%) | 106005 Bioinformatics (25%)

Keywords:

Stochastic processes, coalescent theory, diffusion processes, phylogeny, population genetics

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Further links about the involved persons and regarding the project you can find at

<https://archiv.wwtf.at/programmes/mathematics/MA16-061>