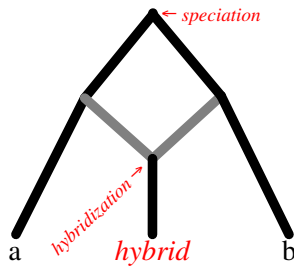


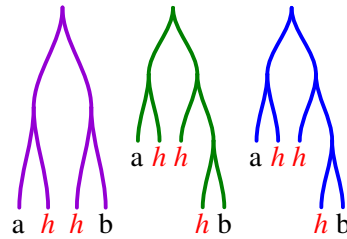
UNIFYING MACRO-EVOLUTIONARY MODELS AND PHYLOGENETIC NETWORKS

Popular Scientific Abstract

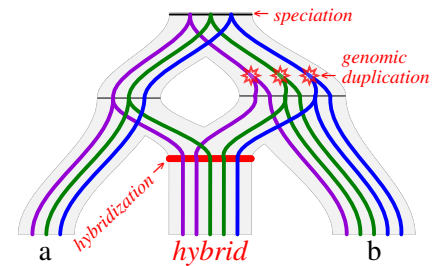
Biology is full of captivating relationships, where genetically distant organisms forge intricate connections. The exploration of these relationships has become increasingly feasible due to a deeper understanding of biological processes, spanning not only the molecular level but also encompassing the evolutionary events that sculpted the histories of corresponding genomes. These relationships are frequently portrayed as networks, providing a natural and intuitive means of visualization. In this proposal, we plan to investigate complex biological models with several macro-evolutionary events: speciation, hybridizations and genomic duplications.



A phylogenetic network of three species *a*, *b*, and their hybrid with macro-evolutionary events: speciation and hybridization.



Gene family trees with sequences from genomes of species *a*, *b*, and the hybrid (*h*) with each leaf representing individual gene.



Gene trees jointly embedded into their network with three gene duplications (stars) forming a macro-evolutionary event: a genomic duplication.

A *hybridization* event occurs when two species have offspring together, known as a *hybrid*. These hybrids inherit traits, or genes, from both parents. In plants, animals, and microorganisms, hybridization can create new species, providing an alternative to classical *speciation*, which occurs when new, distinct species evolve from a common ancestor.

On the other hand, a *genomic duplication* event involves the duplication of large DNA regions, resulting in extra copies of specific genes or even entire sections of the genome. Genomic duplication is a natural process in the evolutionary history of organisms, similar to hybridization, and it plays a significant role in enhancing genetic diversity.

One of the main goals of this project is to investigate novel advanced biological models and efficient algorithms to identify and study phylogenetic networks under hybridization and genomic duplication events. To successfully address this multidisciplinary endeavor, we have assembled an international team of experts in biology, medicine, mathematics, and computer science.

Our algorithmic solutions will draw partially upon our prior experience, utilizing a wide range of modern mathematics and computer science techniques. We will develop phylogenetic and simulation pipelines to facilitate data processing and validate results.

The presented challenges offer an opportunity to investigate macro-evolutionary events beyond conventional tree-like structures. They present a gateway for practitioners to access innovative tools that facilitate the exploration of complex evolutionary relationships among sequences, genes, genomes, and species, integrating biological models that account for genomic duplication events, and species-level reticulate events like species hybridization, viral reassortment, or recombination.