

Title: Phylogenetic network reconstructions

Thematic axis: Evolutionary Biology, Phylogenetics

Summary: With the advent of next-generation-sequencing technologies, empirical studies based on a huge number of different taxa continue to identify more cases in which interspecific hybridization has left insights along their genomes, and even promoted speciation in many cases. As a basic knowledge and first requirement for understanding diversification dynamics and speciation, the phylogenetic field has been challenged by the extensive impact of hybridization in species evolution. Methodological advances are now revolutionizing the phylogenetic field, as it is now possible to infer phylogenetic networks, which accommodate incomplete lineage sorting (coalescence) and interspecific gene flow. In this workshop, we will learn the basics of phylogenetic trees to phylogenetic networks, starting with a theoretical introduction, and hands on with computational implementation in the Julia package PhyloNetworks. Starting from a genomic dataset (either gene trees or SNPs), we will conduct a step-by-step tutorial to infer phylogenetic networks, calculate bootstrap support, generate plots and interpret results. We will show methods for model selection tools. Finally, we will study the evolution of traits on the network using phylogenetic comparative methods.

Course responsible: Dr. Melisa Olave, CONICET CCT Mendoza, Argentina.

Course assistants: Dr. Mariana Morando, CENPAT-CONICET, Argentina.

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Program:

First steps: Introduction to Phylogenetic trees (3.5 hours)

1. Theoretical introduction I: Phylogenetic trees: gene trees and species trees (1 hour).
2. Practical workshop I: inferring gene trees using RAxML (1 hour).
3. Practical workshop II: inferring species trees using ASTRAL (gene trees) and SVDquartets (SNPs) (1 hour).
4. Biological interpretation of results and discussion (30 min).

Advanced steps: Introduction to Phylogenetic networks (4.5 hours)

5. Theoretical introduction II: The era of Phylogenetic networks (1 hour).
6. Practical workshop III: Introduction to PhyloNetworks: installing packages, preparing datasets (30 min).
7. Practical workshop IV: inferring phylogenetic networks, calculating bootstrap support. Plotting (1 hour).
8. Theoretical introduction III: Trait evolution on a network (30 min).
9. Practical workshop V: Phylogenetic regression, ancestral state reconstructions and transgressive evolution of traits (1 hour).
10. Biological interpretation of results and discussion (30 min).

Requirements:

1. Participants will need their own laptop with Julia and R already installed.
2. Previous knowledge about phylogenetic trees or networks, julia or R is not needed.

Language: English or Spanish, depending on participants preference.