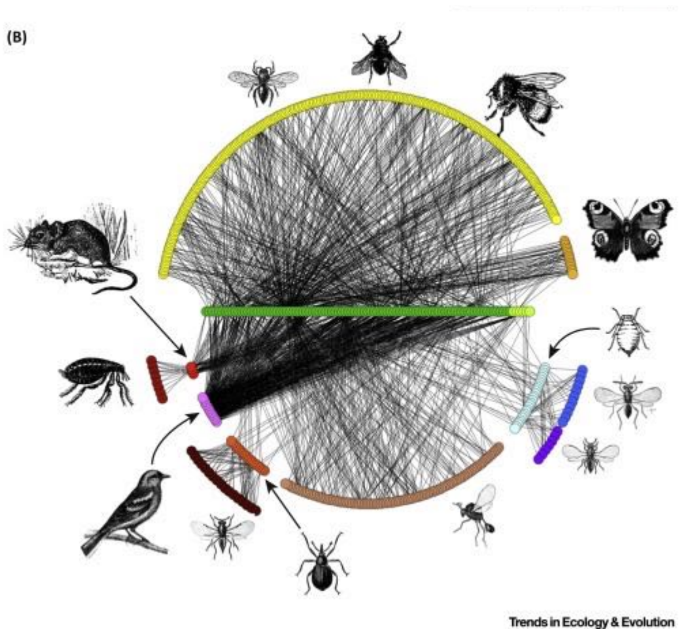
INFERRING HOST REPERTOIRE EVOLUTION

Mariana P Braga

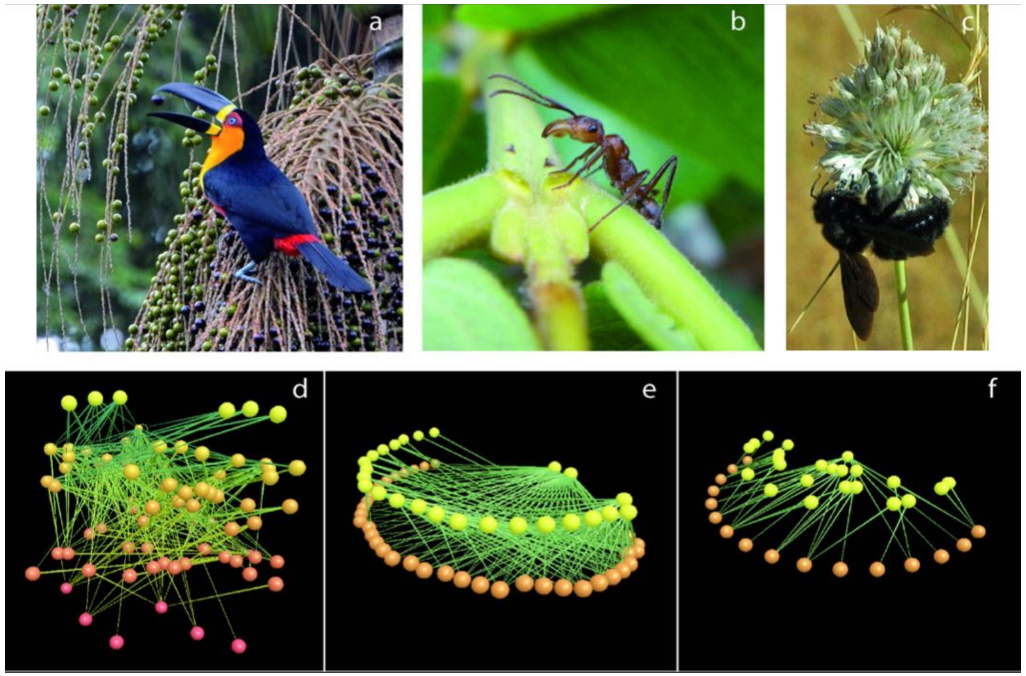
Swedish University of Agricultural Sciences

Assistant professor from January 2025

Biodiversity and species interactions



The QUINTESSENCE Consortium (2016) TREE 31(2)



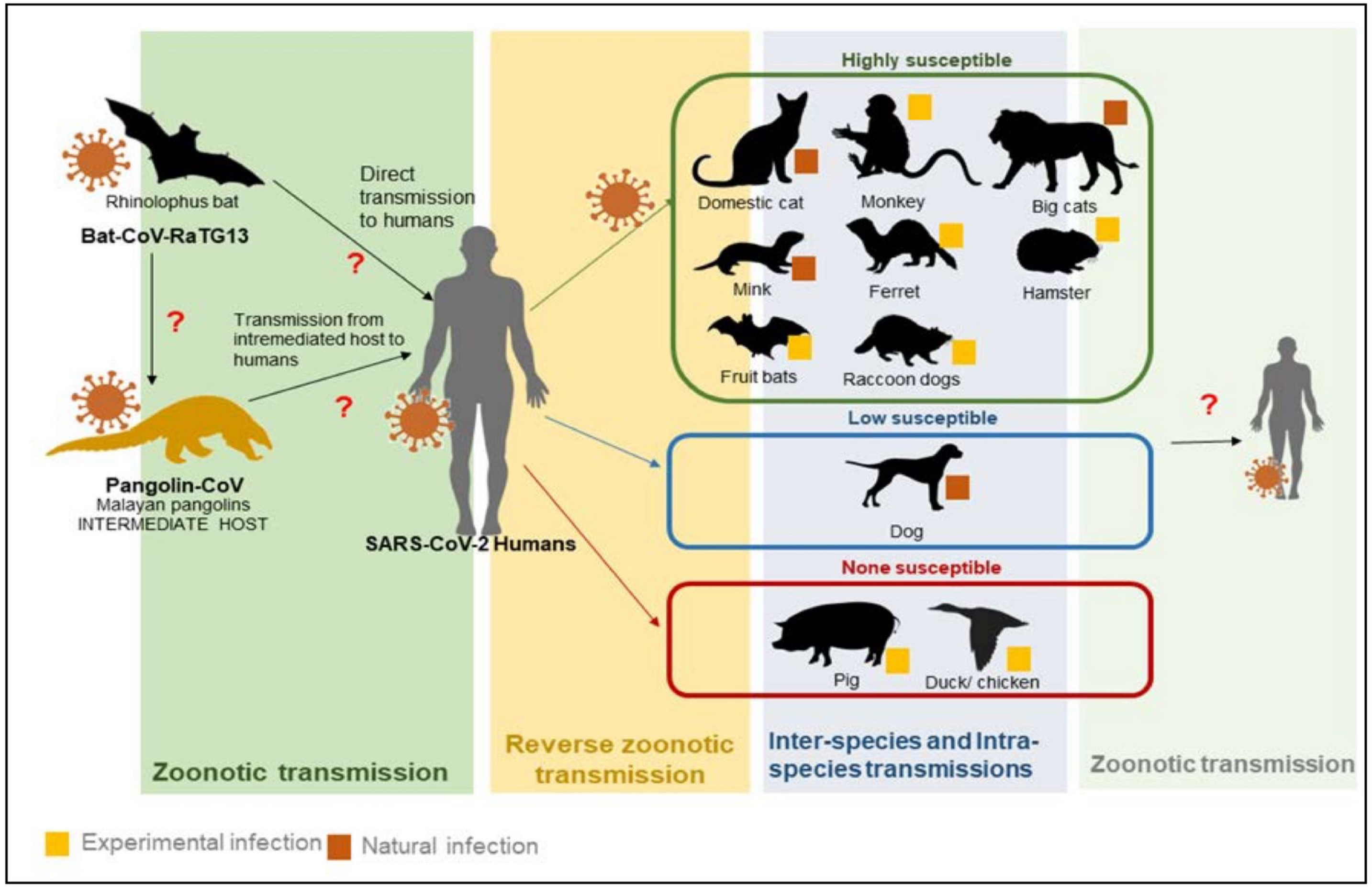
Jordano P (2016) Chasing Ecological Interactions. PLoS Biol 14(9)

Can we predict new interactions?

Can we predict new interactions?

- Biodiversity - species persistence
- Ecosystem functioning
- Rewilding / ecological restoration
- Invasive species
- Emerging diseases

Can we predict new interactions?



Garces et al. (2020) SARS-CoV-2 and animals: what we known. Int J Vet Sci Anim Husbandry 5(6):11-13

Parasitic interactions

Butterfly larvae host plant	Plasmodium insect - bird	Tapeworm fish

(C) (i) (ii) (iii)

Trends in Ecology & Evolution

Figure 1. Examples of Strong Similarities between Ecological and Evolutionary Patterns Observed in Parasite–Host and Insect–Plant Systems.

Nylin et al. (2018)
Embracing colonizations: a new paradigm for species association dynamics.
TREE

How do interactions evolve? - Data

20 possible interactions

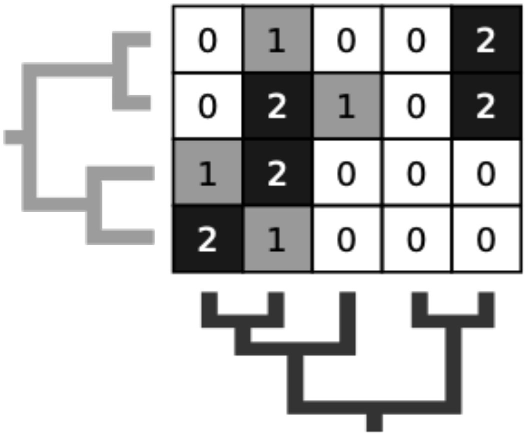
Do these species interact?

4 species of group 1

5 species of group 2

How do interactions evolve? - Data

4 species of group 1



5 species of group 2

20 possible interactions

Do these species interact?

0 = no
1 = potentially
2 = yes

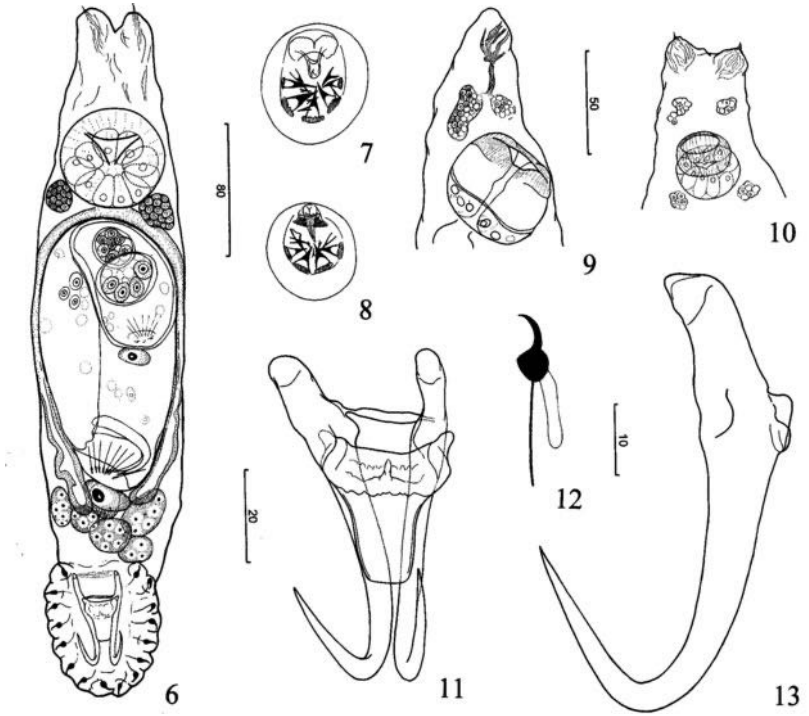
Kinds of available data

Lab rearing – establishment tests

- few studies
- lots of work!
- local population

Source: runwildmychild.com

Kinds of available data



Popazoglo and Boeger (2000) Neotropical Monogenoidea 37. Folia Parasitologica

Species descriptions:

- one host

- one locality

- only available data for many parasite clades

Kinds of available data

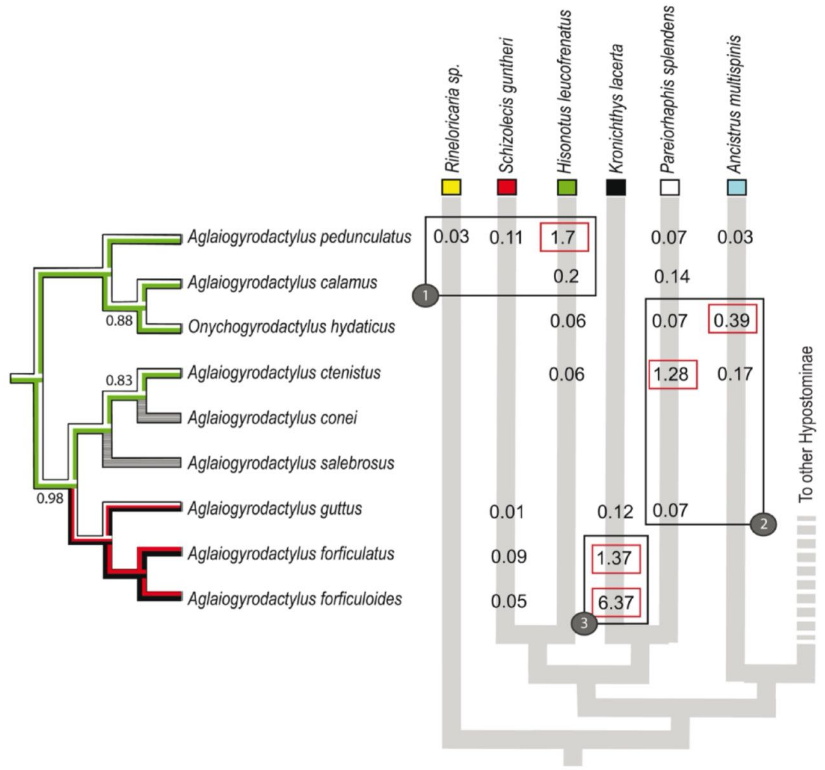


Fig. 1. – Phylogenetic and ecological data for *Aglaiogyrodactylus* spp. and their hosts, loricari-id catfishes, in the Marumbi River, Paraná, Brazil. The phylogenetic relationships of the clade

Patella et al. (2017) Life and Environment

Ecological data:

- many hosts

- one area

- frequency of interaction

Kinds of available data

Compilation of observations:

- mixed quality
- false positives
- regional / global

How do ecological interactions evolve? - Hypotheses

Ecological interactions and diversification

Escape and radiate
Ehrlich and Raven
(1964)

Oscillation hypothesis
Janz and Nylin
(2008)

nature COMMUNICATIONS

ARTICLE

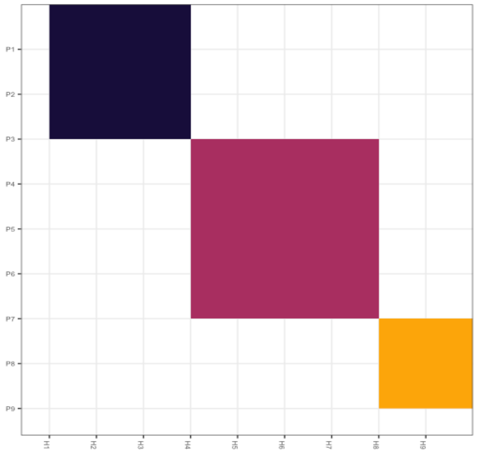
DOI: 10.1038/s41467-018-07677-x OPEN

Unifying host-associated diversification processes using butterfly–plant networks

Mariana P. Braga[1], Paulo R. Guimarães Jr[2], Christopher W. Wheat[1], Sören Nylin[1] & Niklas Janz[1]

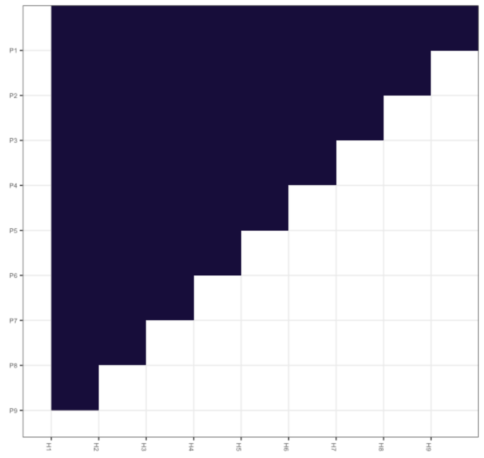
Escape and radiate
Ehrlich and Raven (1964)

Modularity



Oscillation hypothesis
Janz and Nylin (2008)

Nestedness



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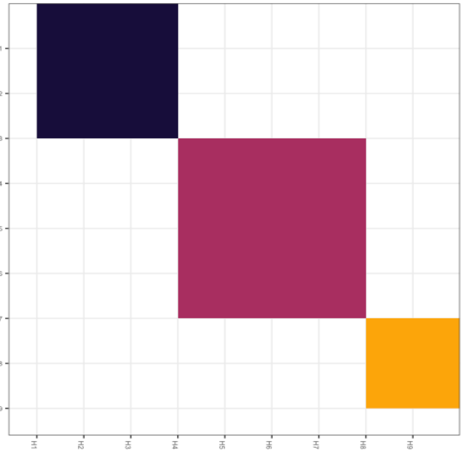
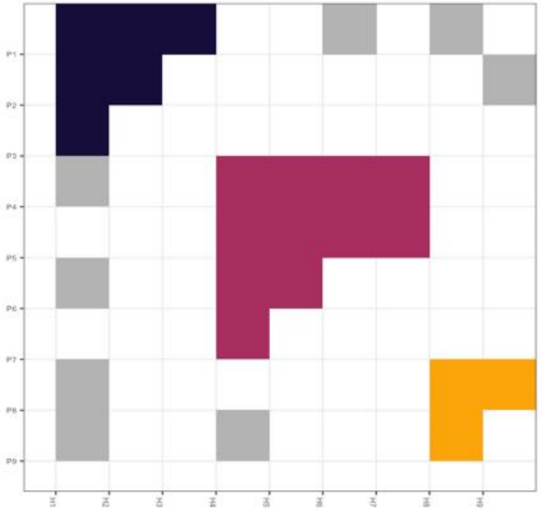
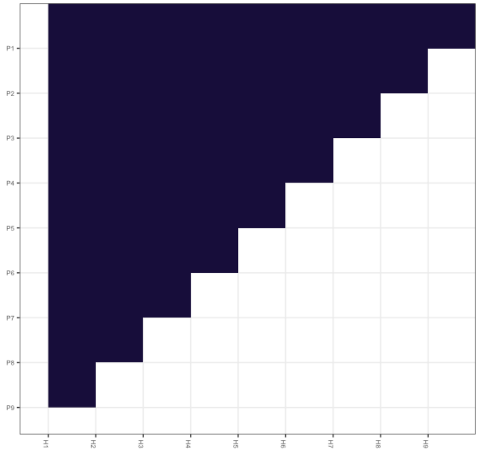




Empirical networks

Oscillation hypothesis
Janz and Nylin (2008)

Nestedness



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Unifying host-associated diversification processes using butterfly–plant networks

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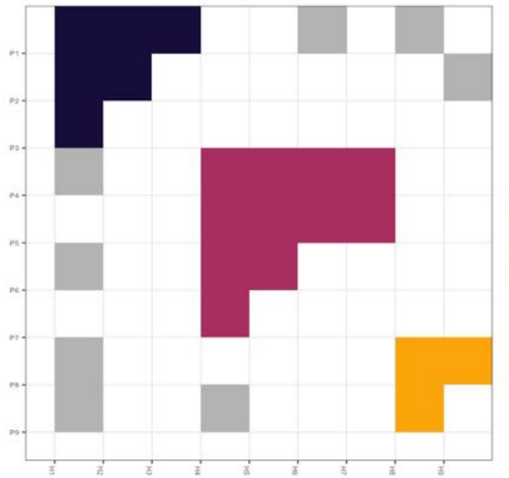
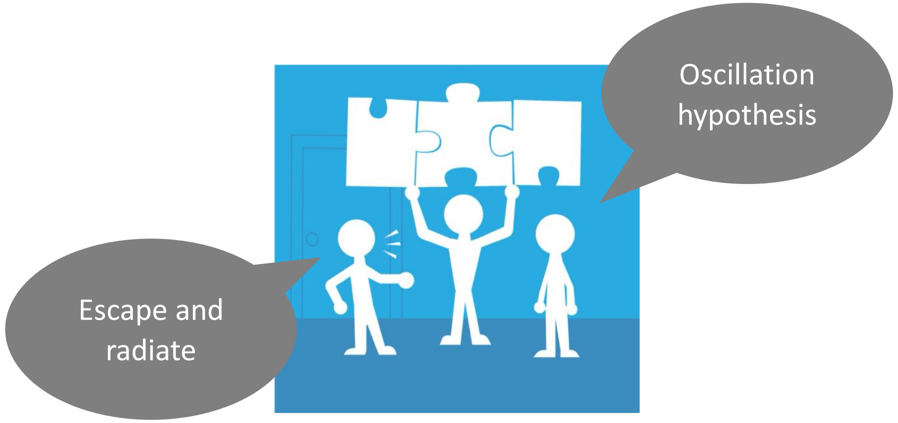
Pattern

present



Process

millions of years



JOURNAL ARTICLE

Bayesian Inference of Ancestral Host–Parasite Interactions under a Phylogenetic Model of Host Repertoire Evolution

Mariana P Braga, Michael J Landis, Sören Nylin, Niklas Janz, Fredrik Ronquist

Systematic Biology, Volume 69, Issue 6, November 2020, Pages 1149–1162,
https://doi.org/10.1093/sysbio/syaa019
Published: 19 March 2020 **Article history** ▾

Decompose the host and symbiont phylogeny into phylogenetic distance matrices to test the extent to which the interactions could have been produced due to chance alone
cophylogenetic signal

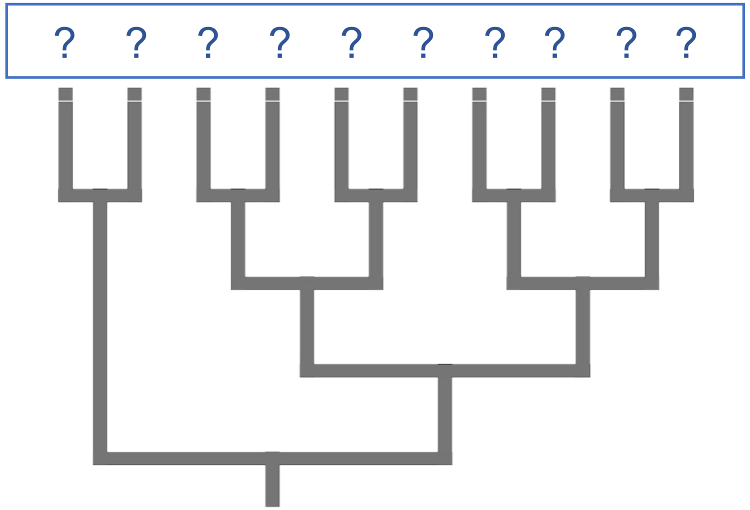
Map a symbiont phylogeny onto a host phylogeny using the classic cophylogenetic events. Each of these events is assigned a cost to determine the lowest cost mapping
cospeciation X host-switch speciation

Use probabilistic models to describe the processes that produce observed cophylogenetic patterns
probability of ancestral states and events

Method	System	Phylogeny	Interactions
PATTERN-BASED STATISTICS			
Mantel test[1]	S	B,D	1
Wilcoxon test[2]	S	B,D	1
Parafit[3]	S	B,D	M
MRCAlink[4]	S	B,D	M
PACo[5]	D,S	B,D	M
Random TaPas[6]	D,S	B	M
EVENT-SCORING METHODS			
BPA[7]	D	T	1,M
TreeMap[8]	D	T	1
Jane[9]	D	B,D	M
Tarzan[10]	D	D	M
COALA[11]	D	B,D	M
Jungles[12]	D	B,D	1
eMPRess[13]	D	B,D	M
DIVA[14]	D	T	M
CoRe-PA[15]	D	D	M
GENERATIVE MODEL–BASED METHODS			
Bayesian host switching[16]	D	D	1
DEC[17]	D	D	M
ALE[18]	D	D	1
Host repertoire evolution[19]	D	D	M

Dismukes et al. 2022 Cophylogenetic Methods to Untangle the Evolutionary History of Ecological Interactions. AREES

Modeling the evolution of interactions



- One host → No, multiple
- One at a time → Independence
- Number of hosts (host range) → Which hosts?

Modeling the evolution of interactions

HOST REPERTOIRE

HOW MANY HOSTS (RANGE) + WHICH HOSTS

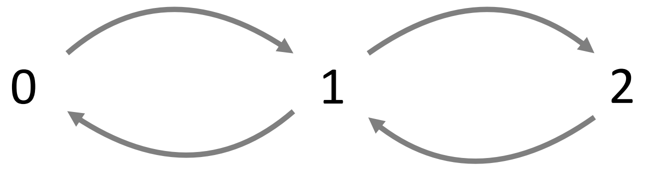
$[\, h_1 \;\; h_2 \;\; h_3 \;\; h_4 \;\; \cdots \;\; h_n \,]$

$h_i = \{0,1,2\}$

0 non-host

1 potential host (e.g. larvae is able to feed)

2 actual host (used in nature)



Modeling the evolution of interactions

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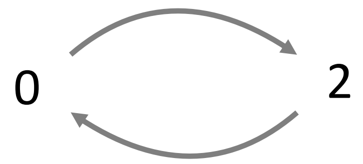
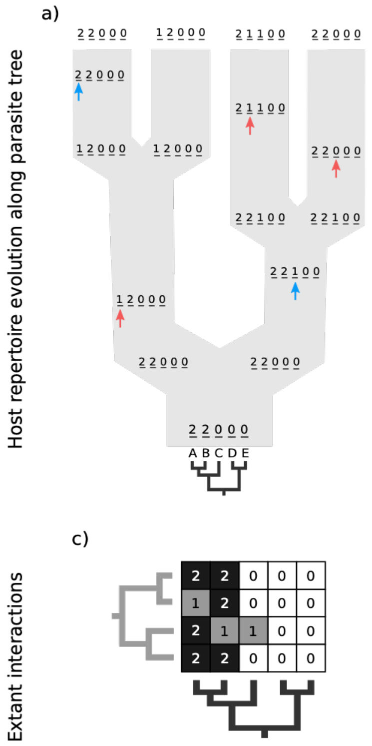


Syst. Biol. 0(0):1–14, 2020

DOI:10.1093/sysbio/syaa019

Bayesian Inference of Ancestral Host–Parasite Interactions under a Phylogenetic Model of Host Repertoire Evolution

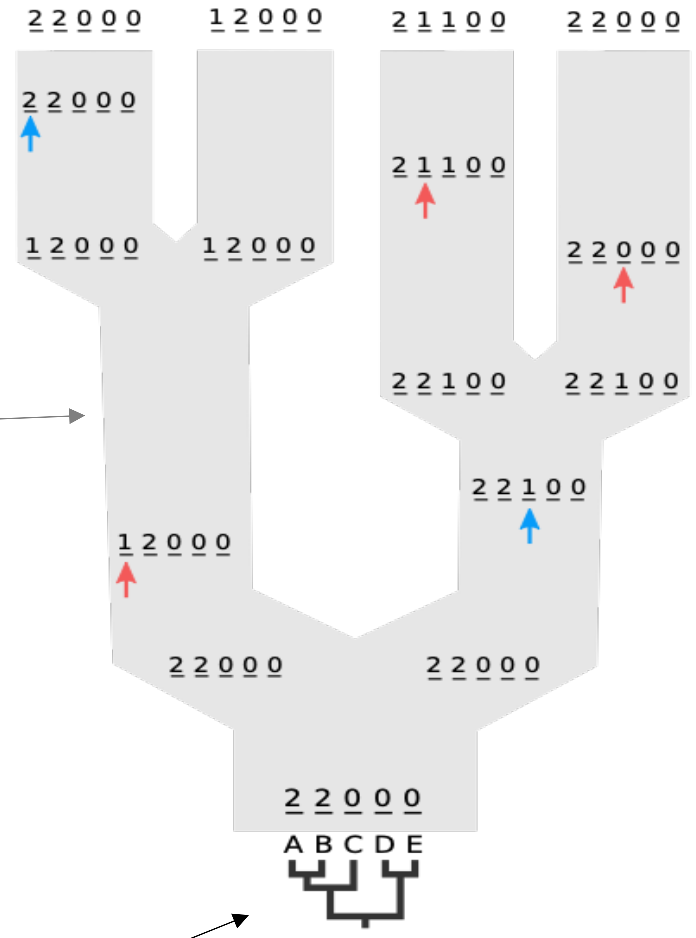
Mariana P. Braga[1,2,*], Michael J. Landis[2,3], Sören Nylin[1], Niklas Janz[1] and Fredrik Ronquist[4]



- Implemented in RevBayes
- **Species can use multiple hosts at any given time**
- **Can include potential hosts**
- **Phylogenetic proximity between hosts**

Inference of historical interactions

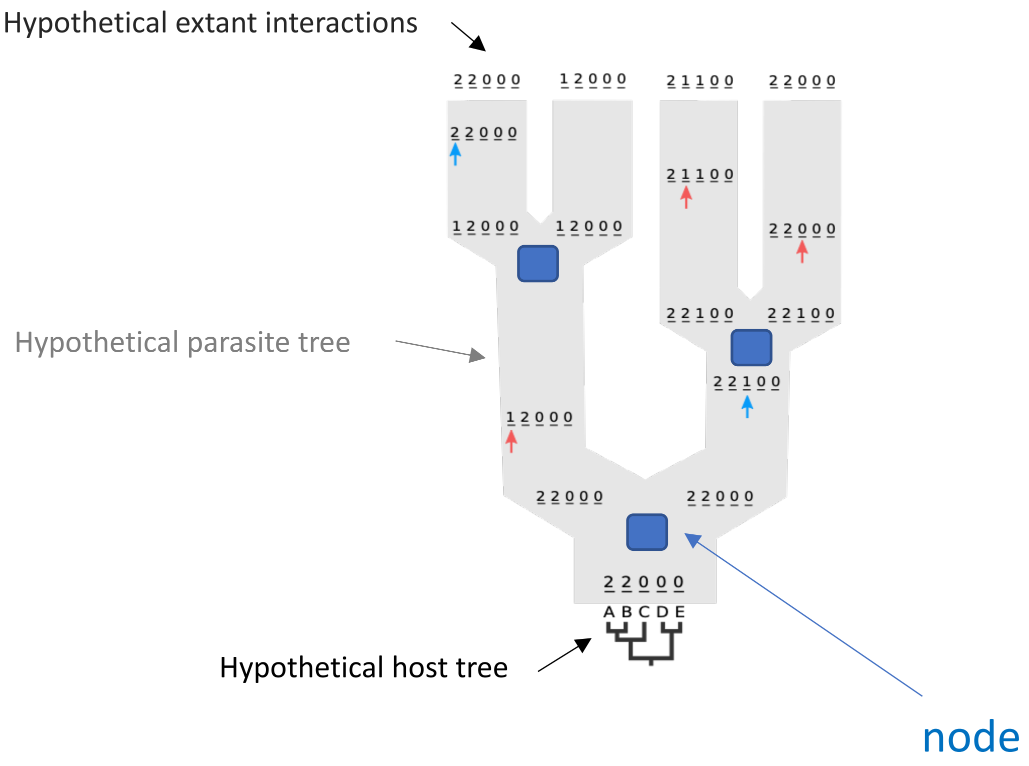
Hypothetical extant interactions

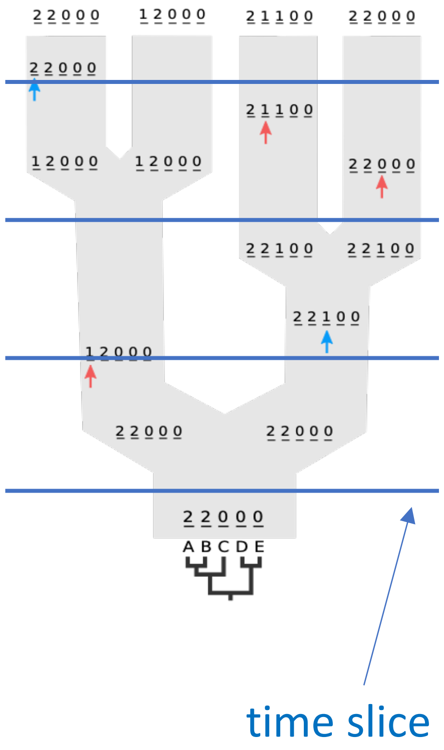


Hypothetical parasite tree

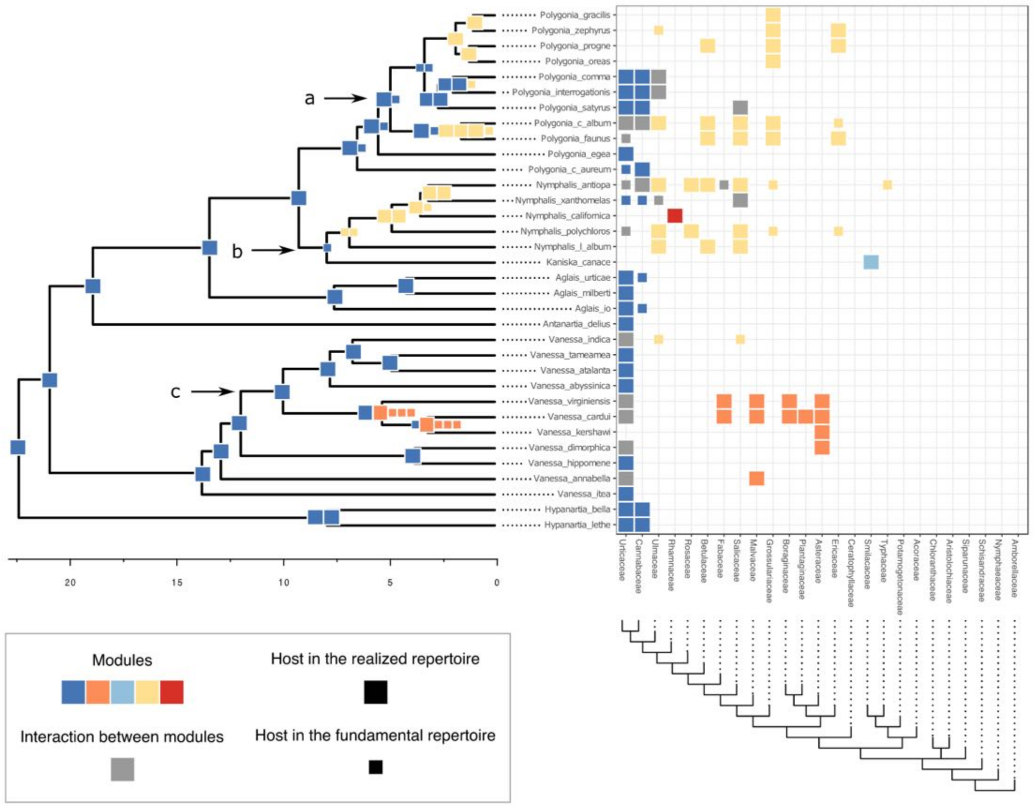
Hypothetical host tree

Inference of historical interactions





Modeling the evolution of interactions



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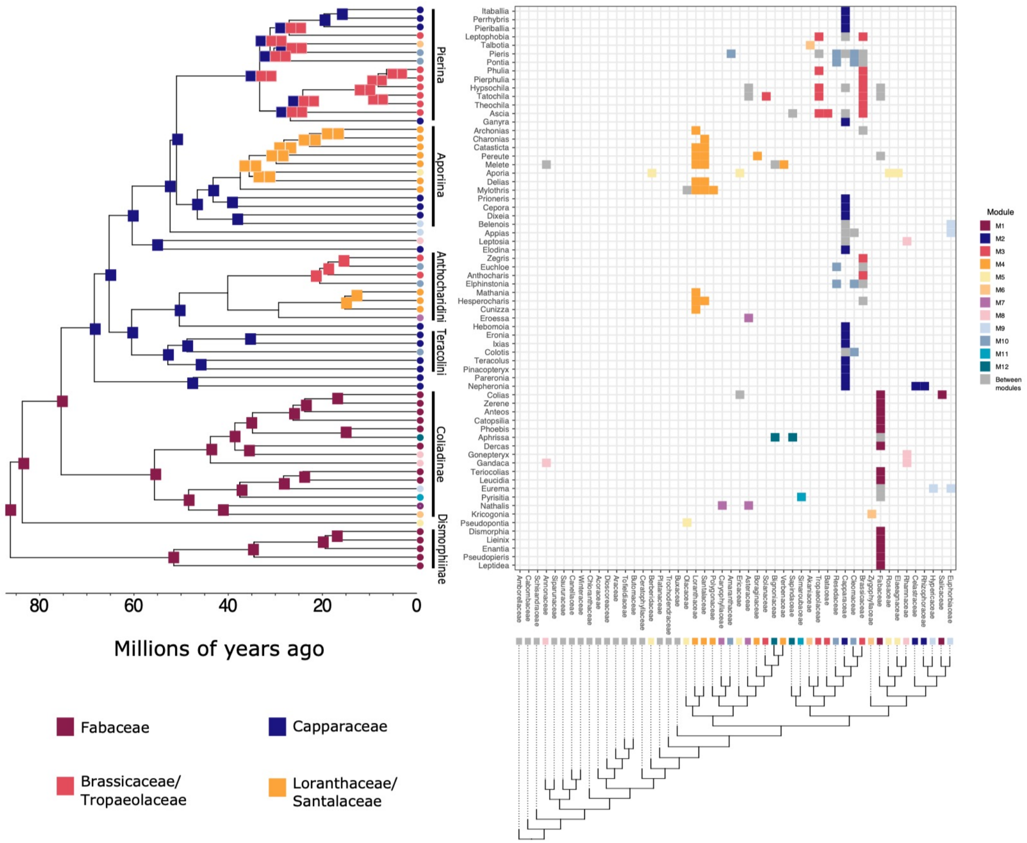
MARIANA P. BRAGA[1,2,*], MICHAEL J. LANDIS[2,3], SÖREN NYLIN[1], NIKLAS JANZ[1] AND FREDRIK RONQUIST[4]

RevBayes

Network evolution



DOI: 10.1111/ele.13842

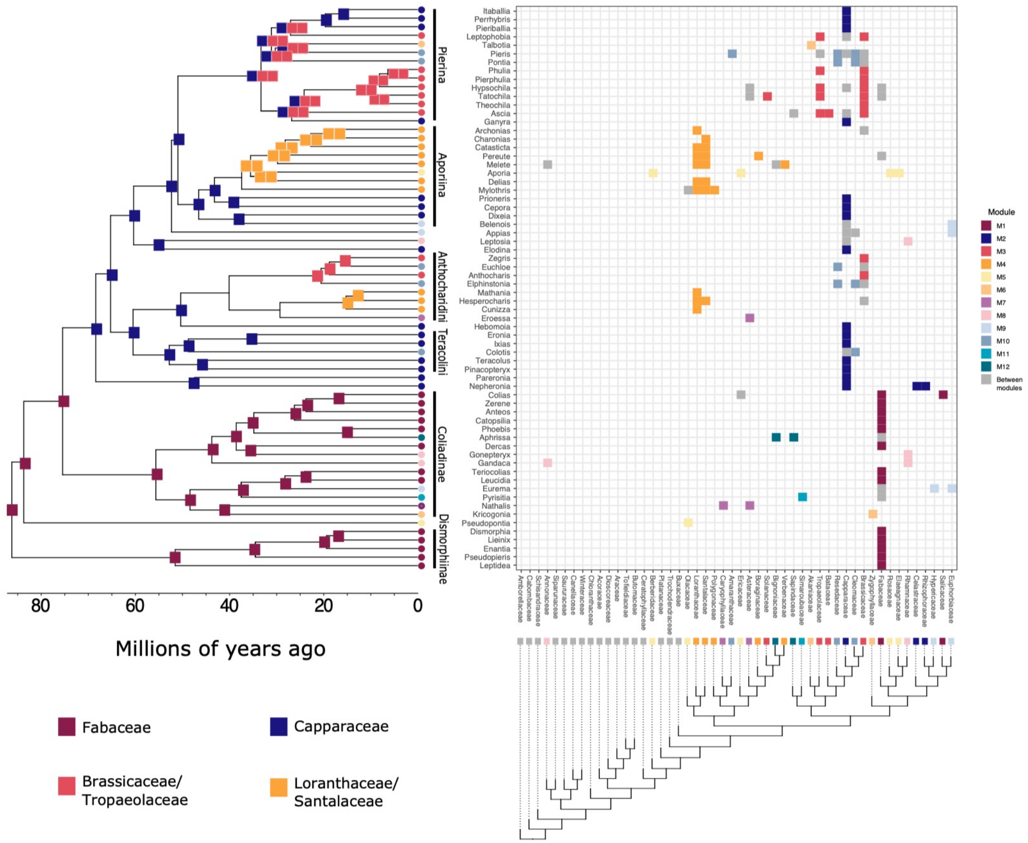
ECOLOGY LETTERS cnrs WILEY

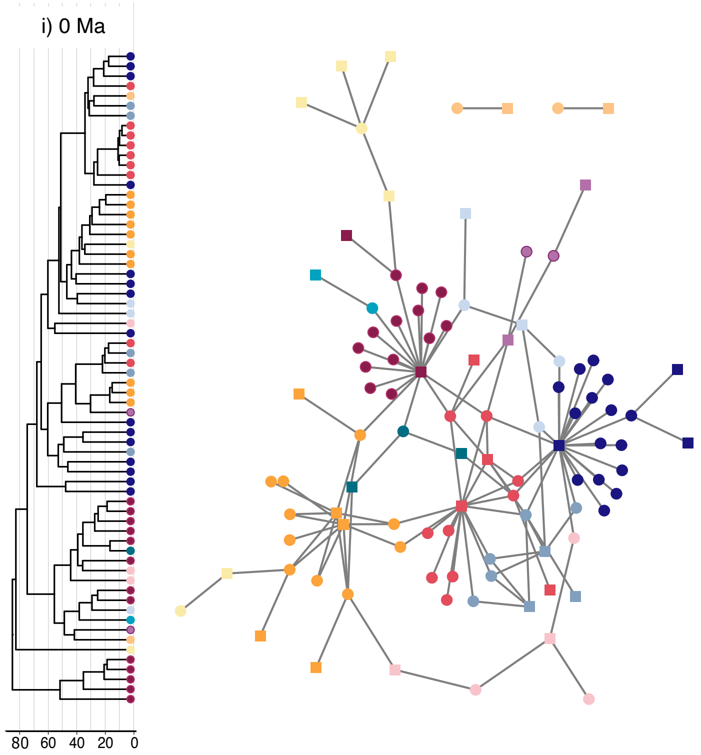
LETTER

Phylogenetic reconstruction of ancestral ecological networks through time for pierid butterflies and their host plants

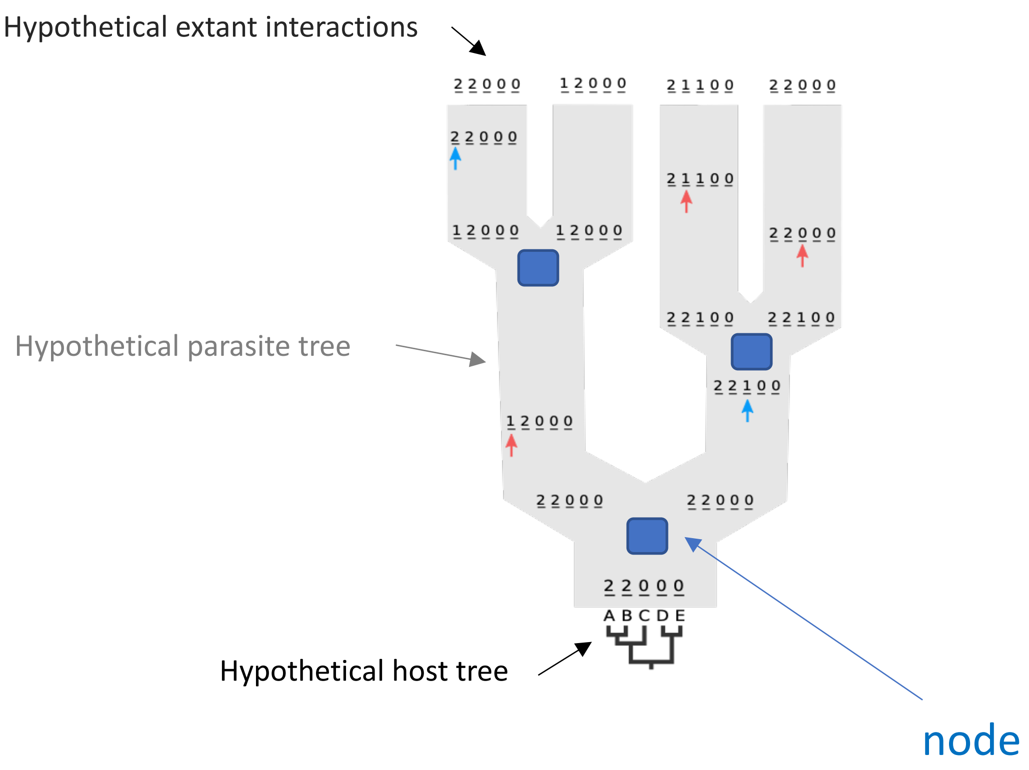
Mariana P. Braga[1,2] | Niklas Janz[1] | Sören Nylin[1] | Fredrik Ronquist[3] | Michael J. Landis[2]

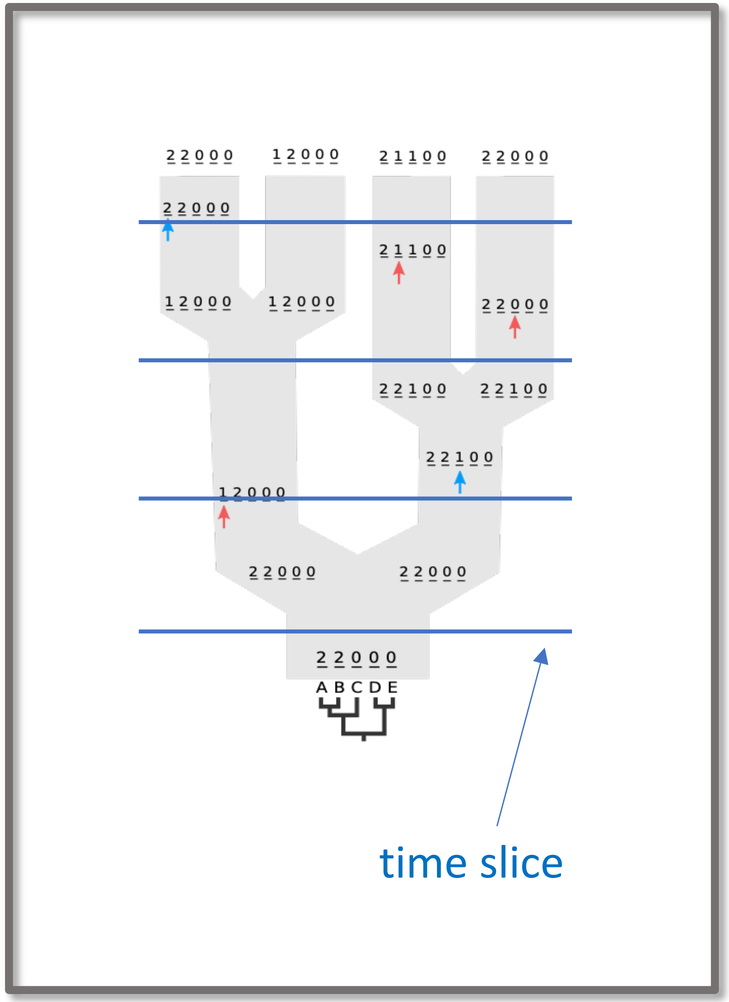
Network evolution

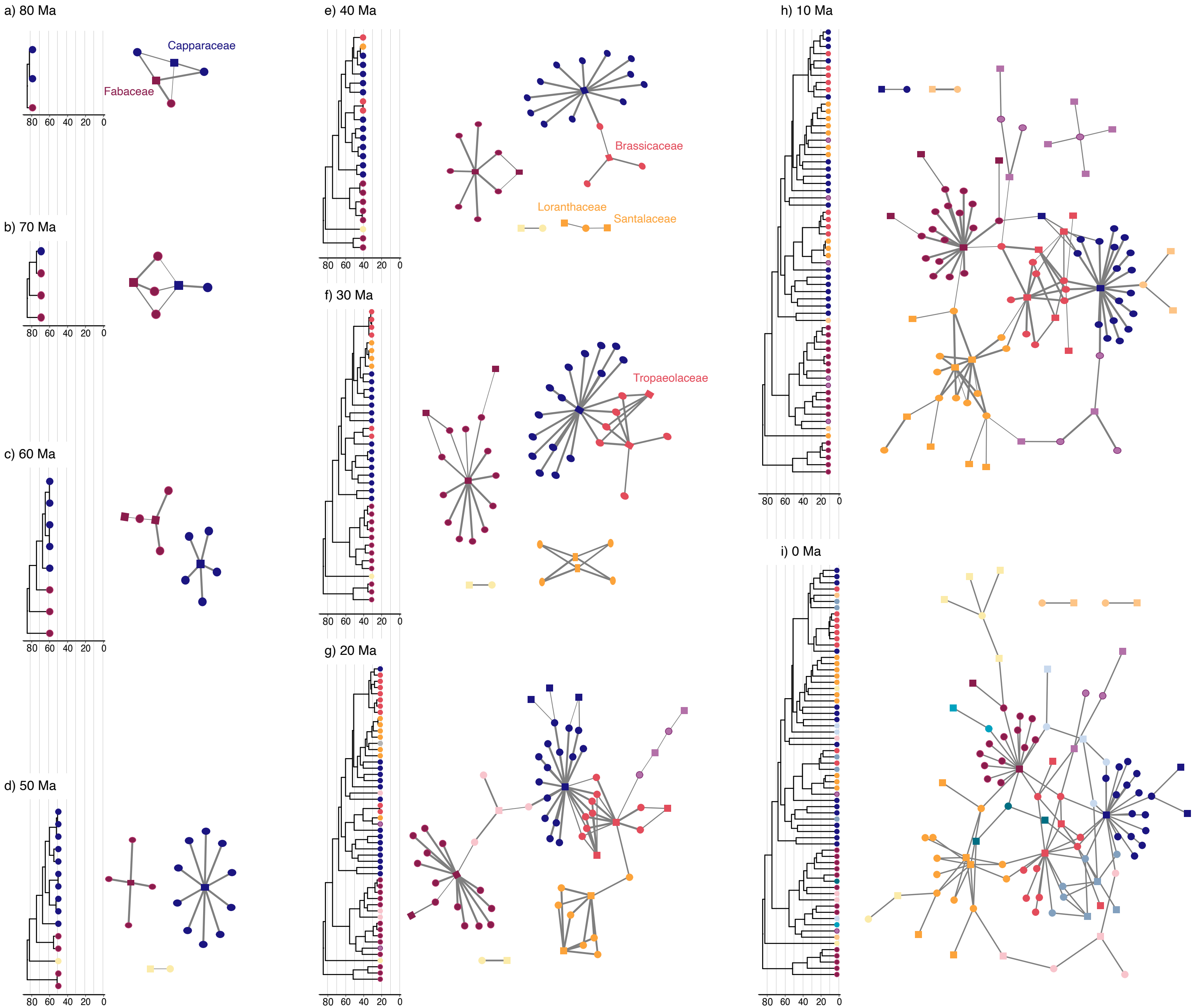




Inference of historical interactions

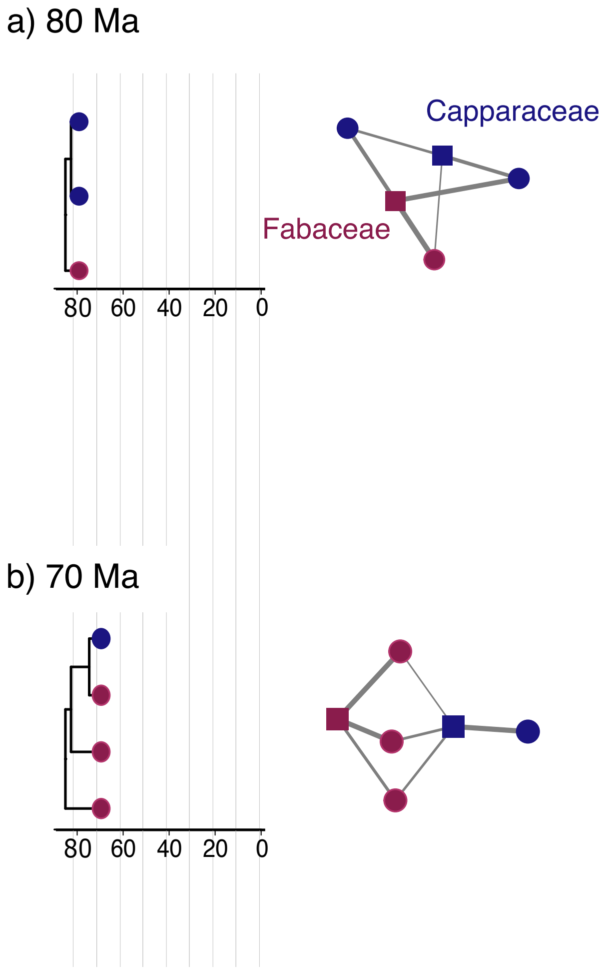




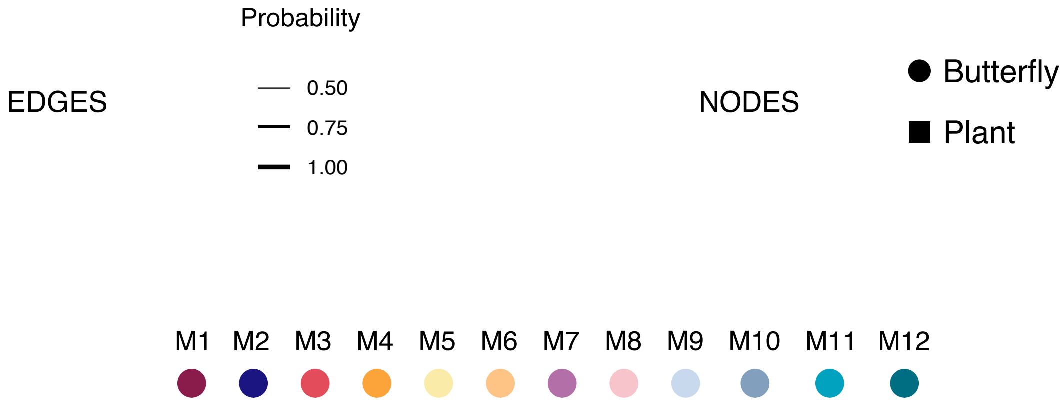


a) 80 Ma
Capparaceae
Fabaceae
80 60 40 20 0
b) 70 Ma
80 60 40 20 0
c) 60 Ma
80 60 40 20 0
d) 50 Ma
80 60 40 20 0
e) 40 Ma
Brassicaceae
Loranthaceae
Santalaceae
80 60 40 20 0
f) 30 Ma
Tropaeolaceae
80 60 40 20 0
g) 20 Ma
80 60 40 20 0
h) 10 Ma
80 60 40 20 0
i) 0 Ma
80 60 40 20 0

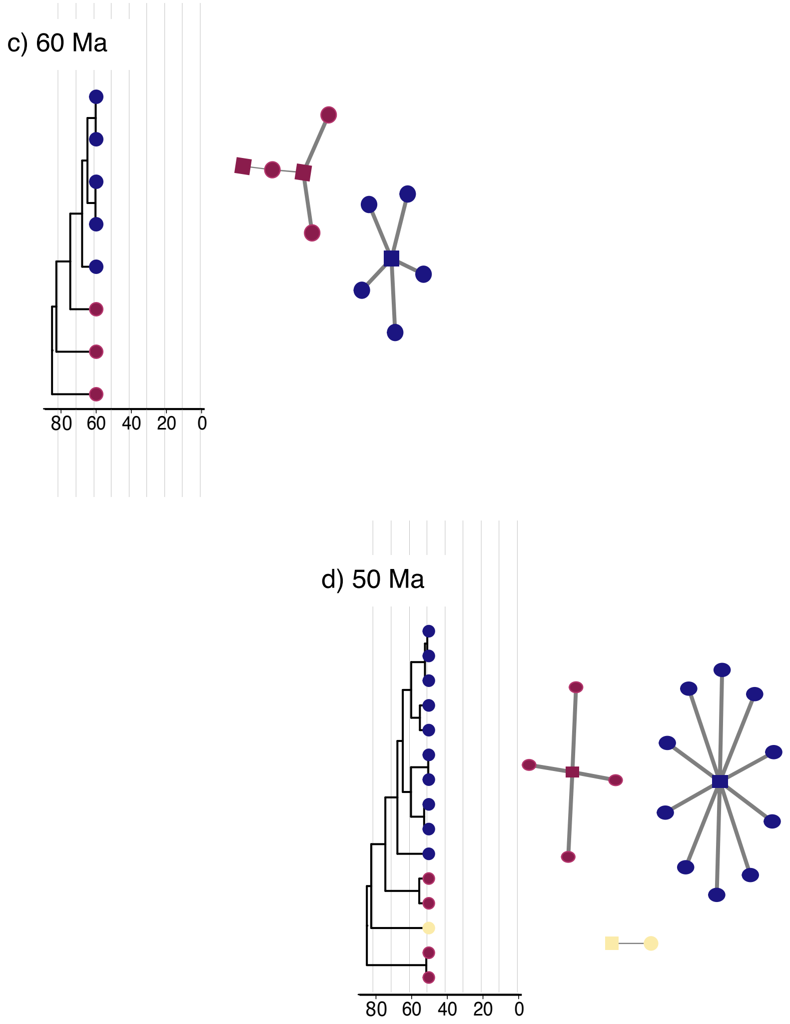
Ancestral networks



- Fabaceae is the most likely ancestral host
- Capparaceae is less likely

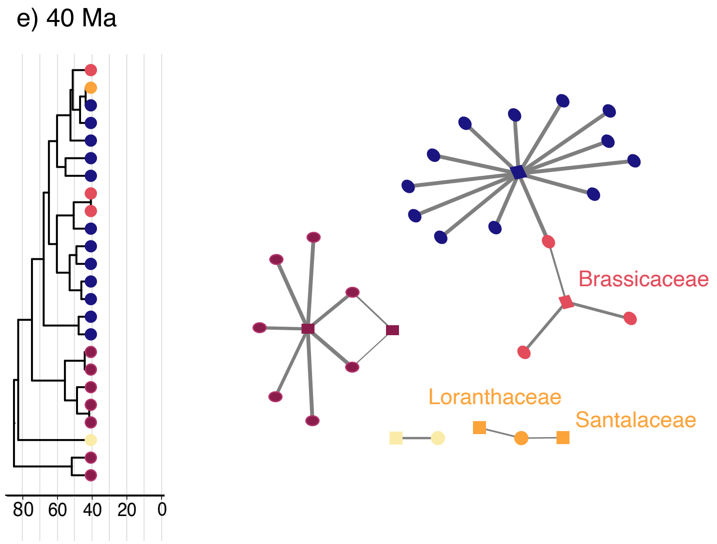


Module separation



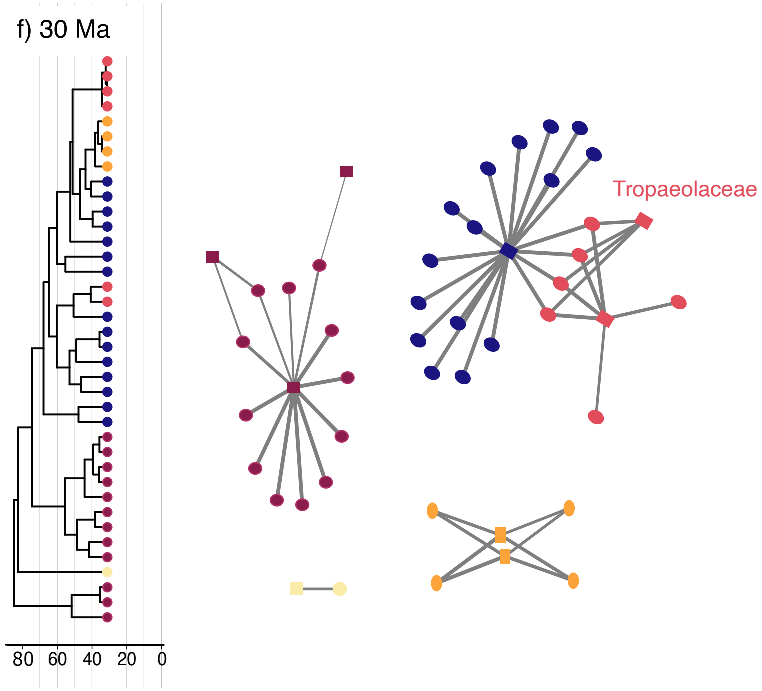
- Two distinct modules
- Fabaceae – basal pierids
- Capparaceae – Pierinae
  - diversification

Two new modules



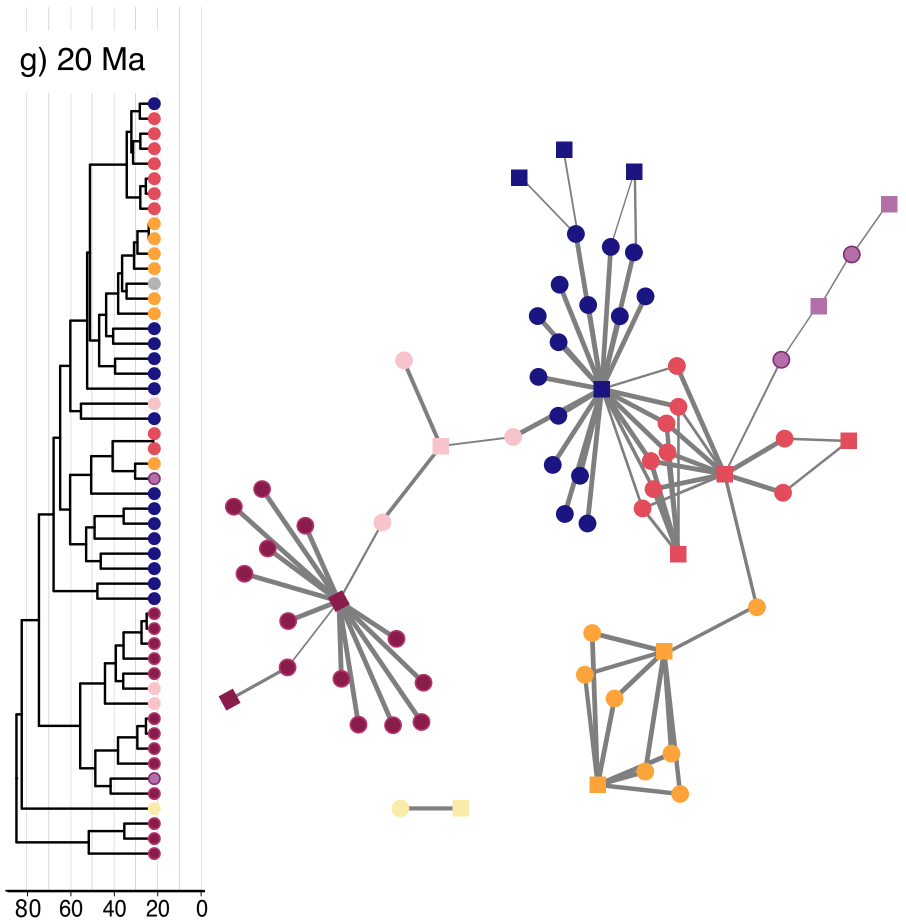
- Brassicaceae is colonized by a host range expansion and a host shift

- Loranthaceae and Santalaceae are colonized by a host shift



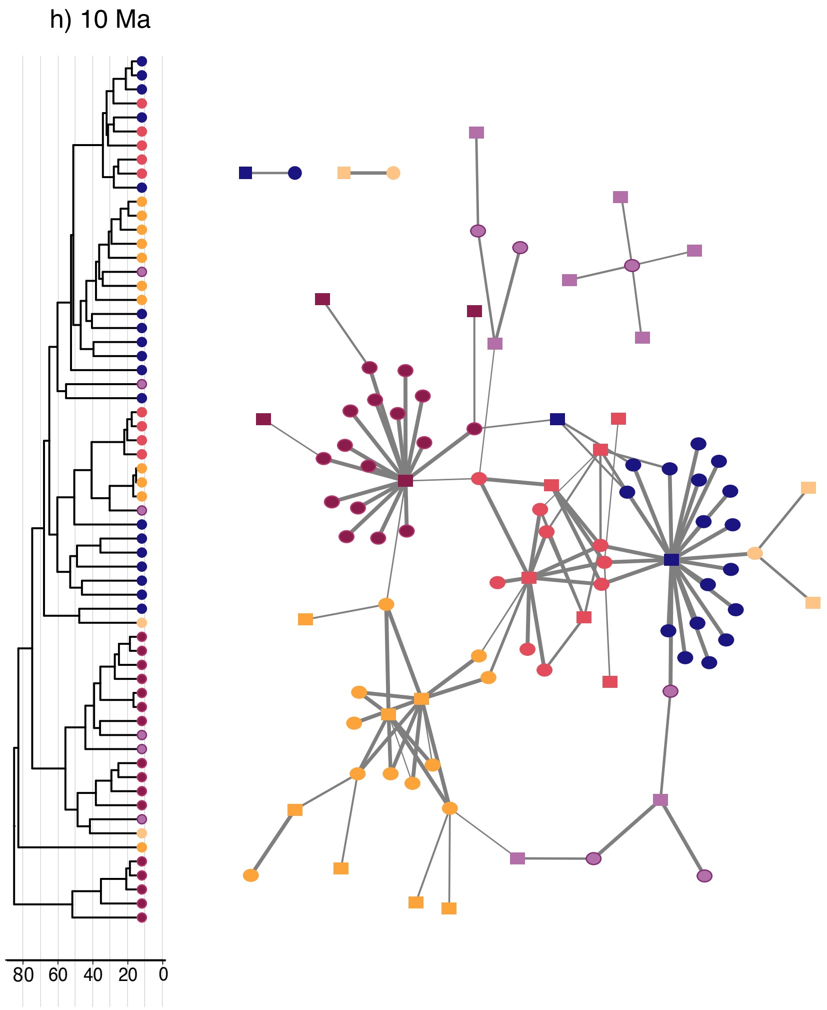
- Modules M3 and M2 are connected

All big modules are connected



- Network increases with butterfly diversification and colonization of new hosts
- Recolonizations connect new modules to older modules

Network grows with the same structure



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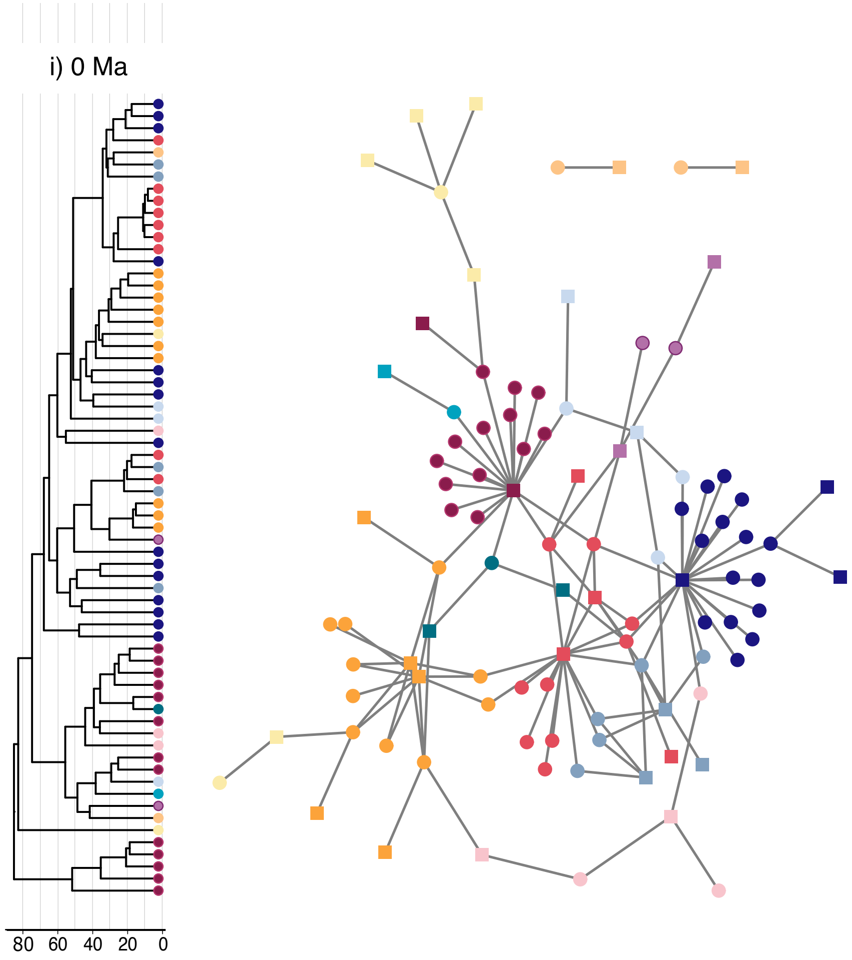

- Network increases with butterfly diversification and colonization of new hosts
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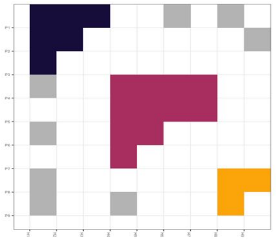
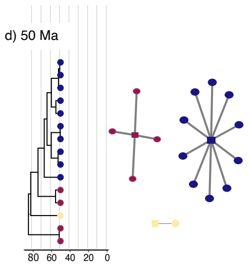
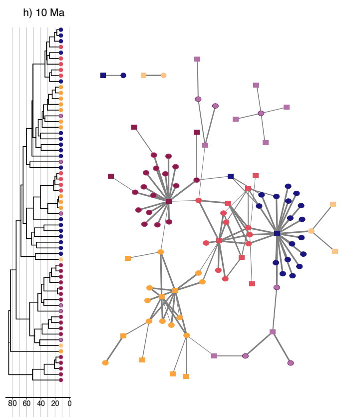
Conclusions from this study

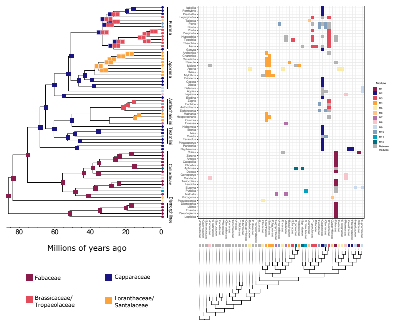


- Means to test ideas about evolution of ecological networks



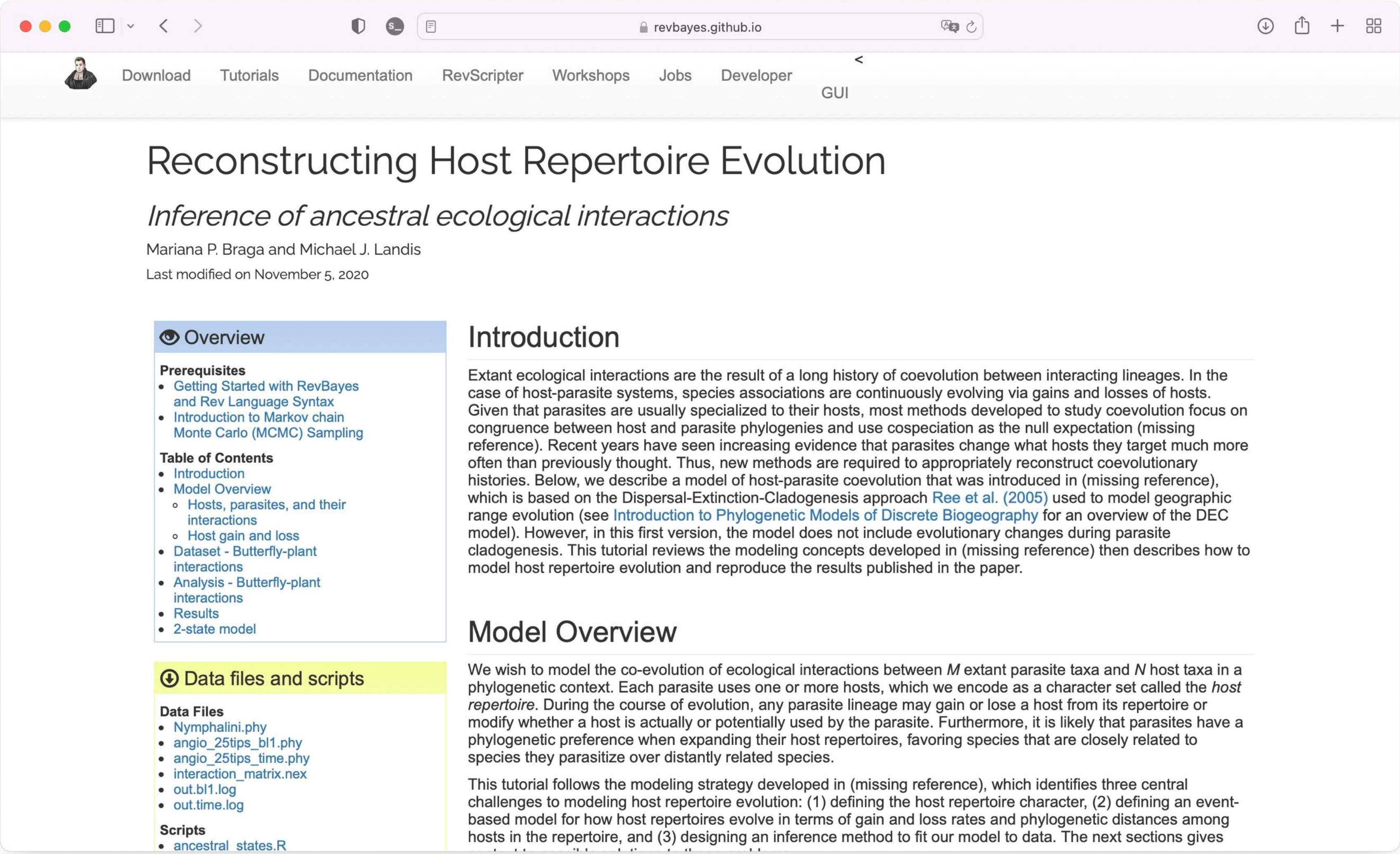


- New probabilistic representation that makes fuller use of the posterior distribution of ancestral states



- Reconstruct specific host shifts, host-range expansions, and recolonizations that have shaped the Pieridae-angiosperm network

Analysis tutorial


revbayes.github.io

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Reconstructing Host Repertoire Evolution

Inference of ancestral ecological interactions

Mariana P. Braga and Michael J. Landis

Last modified on November 5, 2020

Overview

Prerequisites
- Getting Started with RevBayes and Rev Language Syntax
- Introduction to Markov chain Monte Carlo (MCMC) Sampling

Table of Contents

Data files and scripts

Data Files
- Nymphalini.phy
- angio_25tips_bl1.phy
- angio_25tips_time.phy
- interaction_matrix.nex
- out.bl1.log
- out.time.log

Scripts
- ancestral_states.R

Introduction

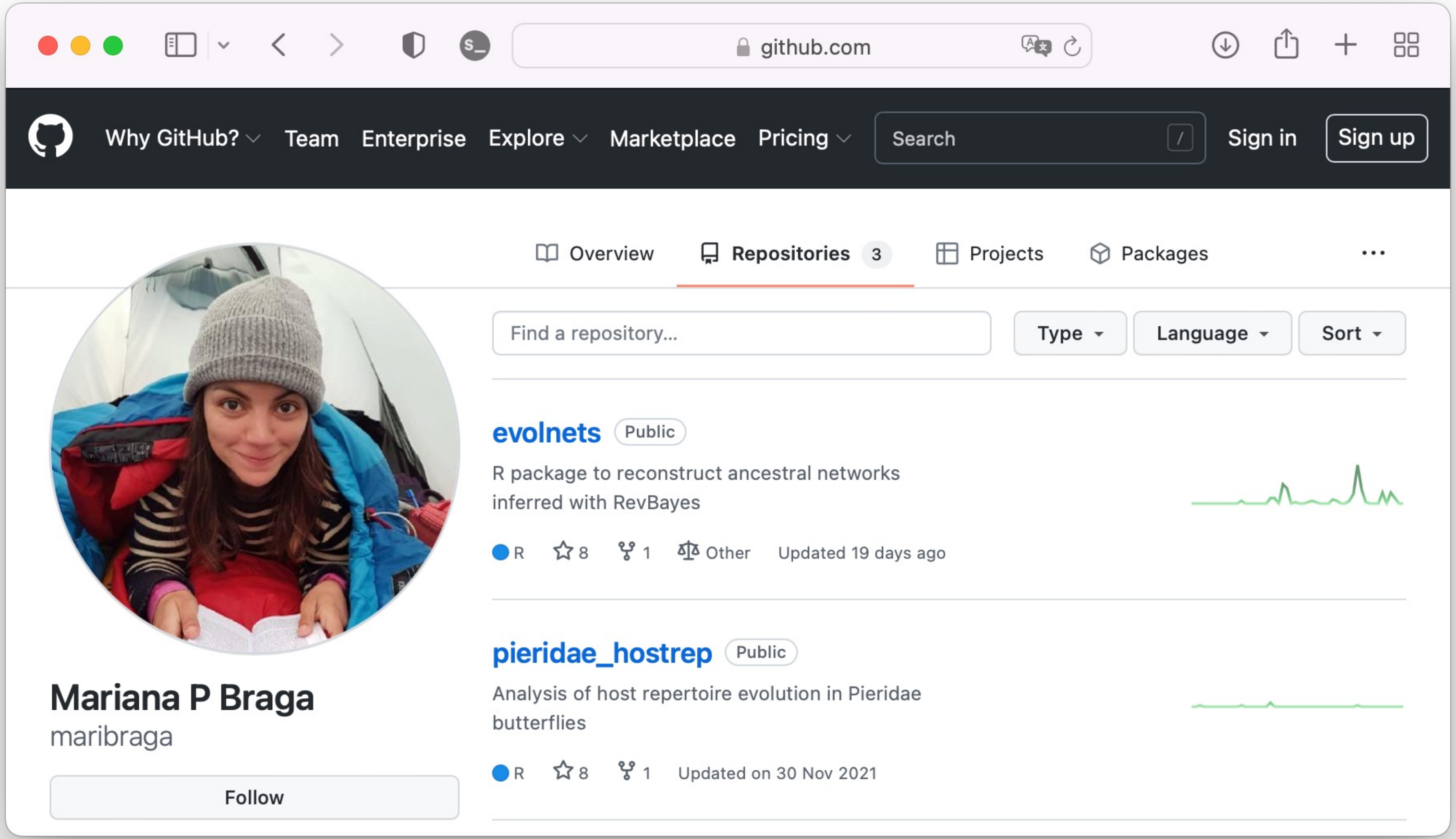
Extant ecological interactions are the result of a long history of coevolution between interacting lineages. In the case of host-parasite systems, species associations are continuously evolving via gains and losses of hosts. Given that parasites are usually specialized to their hosts, most methods developed to study coevolution focus on congruence between host and parasite phylogenies and use cospeciation as the null expectation (missing reference). Recent years have seen increasing evidence that parasites change what hosts they target much more often than previously thought. Thus, new methods are required to appropriately reconstruct coevolutionary histories. Below, we describe a model of host-parasite coevolution that was introduced in (missing reference), which is based on the Dispersal-Extinction-Cladogenesis approach Ree et al. (2005) used to model geographic range evolution (see Introduction to Phylogenetic Models of Discrete Biogeography for an overview of the DEC model). However, in this first version, the model does not include evolutionary changes during parasite cladogenesis. This tutorial reviews the modeling concepts developed in (missing reference) then describes how to model host repertoire evolution and reproduce the results published in the paper.

Model Overview

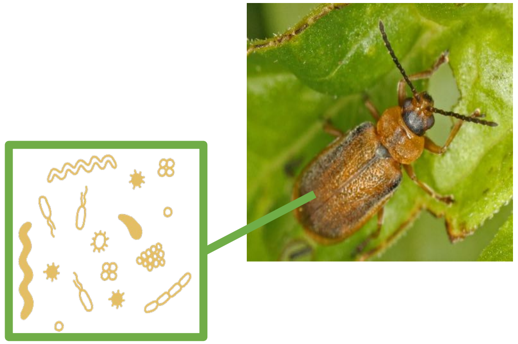
We wish to model the co-evolution of ecological interactions between *M* extant parasite taxa and *N* host taxa in a phylogenetic context. Each parasite uses one or more hosts, which we encode as a character set called the *host repertoire*. During the course of evolution, any parasite lineage may gain or lose a host from its repertoire or modify whether a host is actually or potentially used by the parasite. Furthermore, it is likely that parasites have a phylogenetic preference when expanding their host repertoires, favoring species that are closely related to species they parasitize over distantly related species.

This tutorial follows the modeling strategy developed in (missing reference), which identifies three central challenges to modeling host repertoire evolution: (1) defining the host repertoire character, (2) defining an event-based model for how host repertoires evolve in terms of gain and loss rates and phylogenetic distances among hosts in the repertoire, and (3) designing an inference method to fit our model to data. The next sections gives

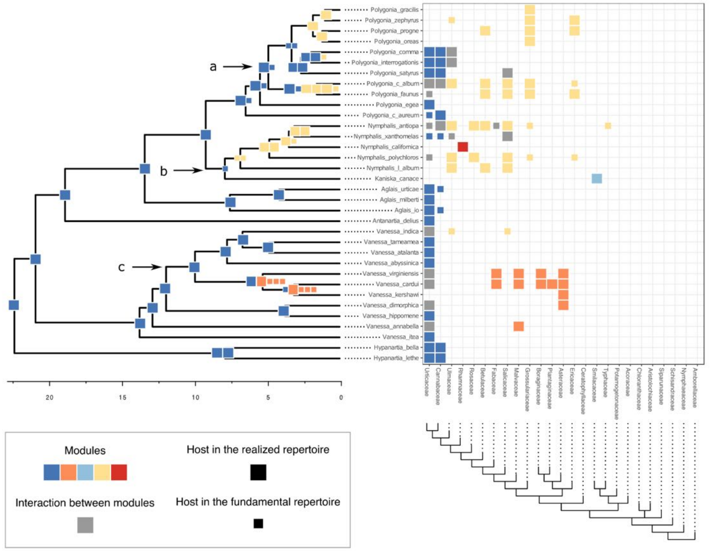
Network evolution: R package *evolnets*

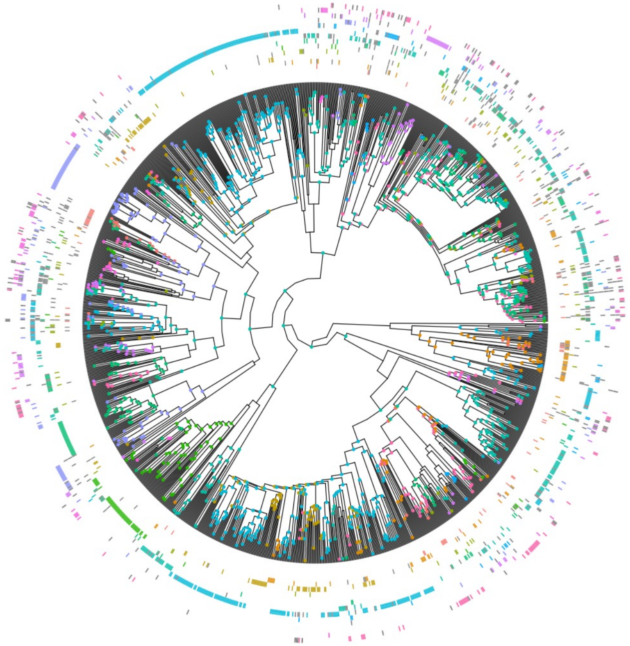


Studies using the host repertoire model



- Ancestral hosts of all butterflies
- Color patterns (mimicry)
- Beetles and microbiome
- Fish and parasitic mussels
- Beetles – host plant

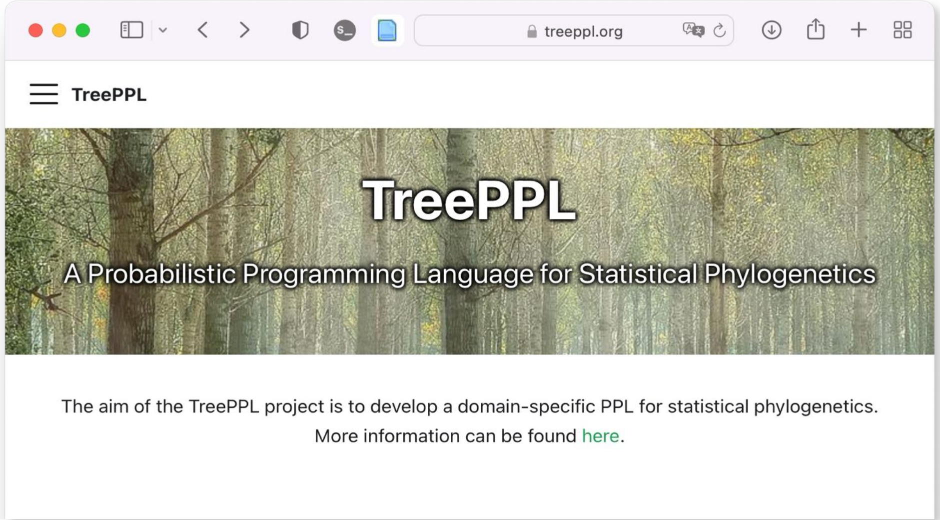




Can we predict new interactions?

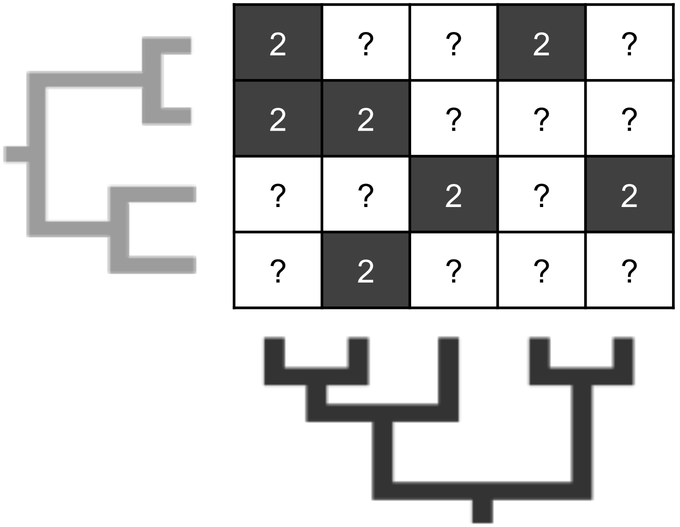
- Biodiversity - species persistence
- Ecosystem functioning
- Rewilding / ecological restoration
- Invasive species
- Emerging diseases

New model implementation

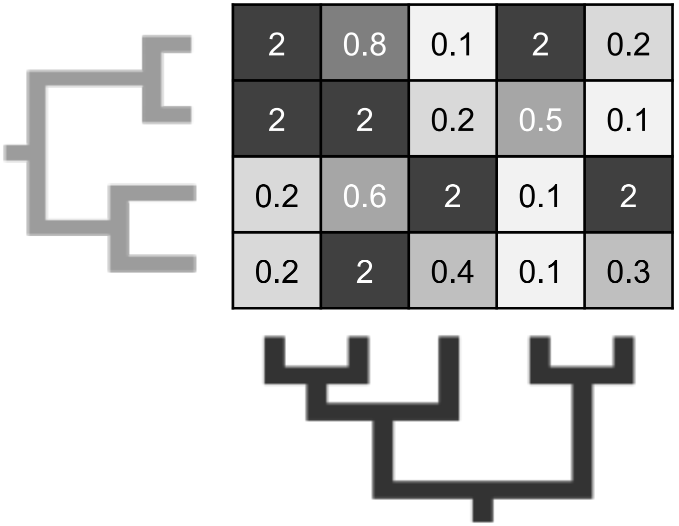


treeppl.org

Input



Output



Thank you!

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