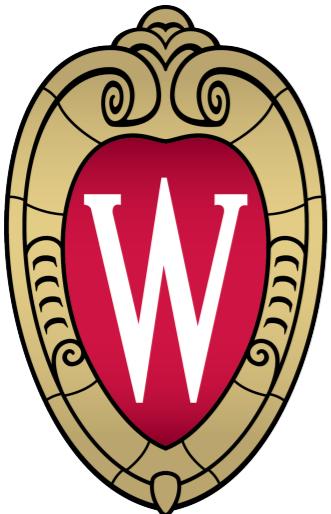


Estimating phylogenetic networks with SnaQ

Claudia Solís-Lemus, PhD

University of Wisconsin-Madison
Wisconsin Institute for Discovery
Department of Plant Pathology



July 23, 2023



<https://solislemuslab.github.io/>



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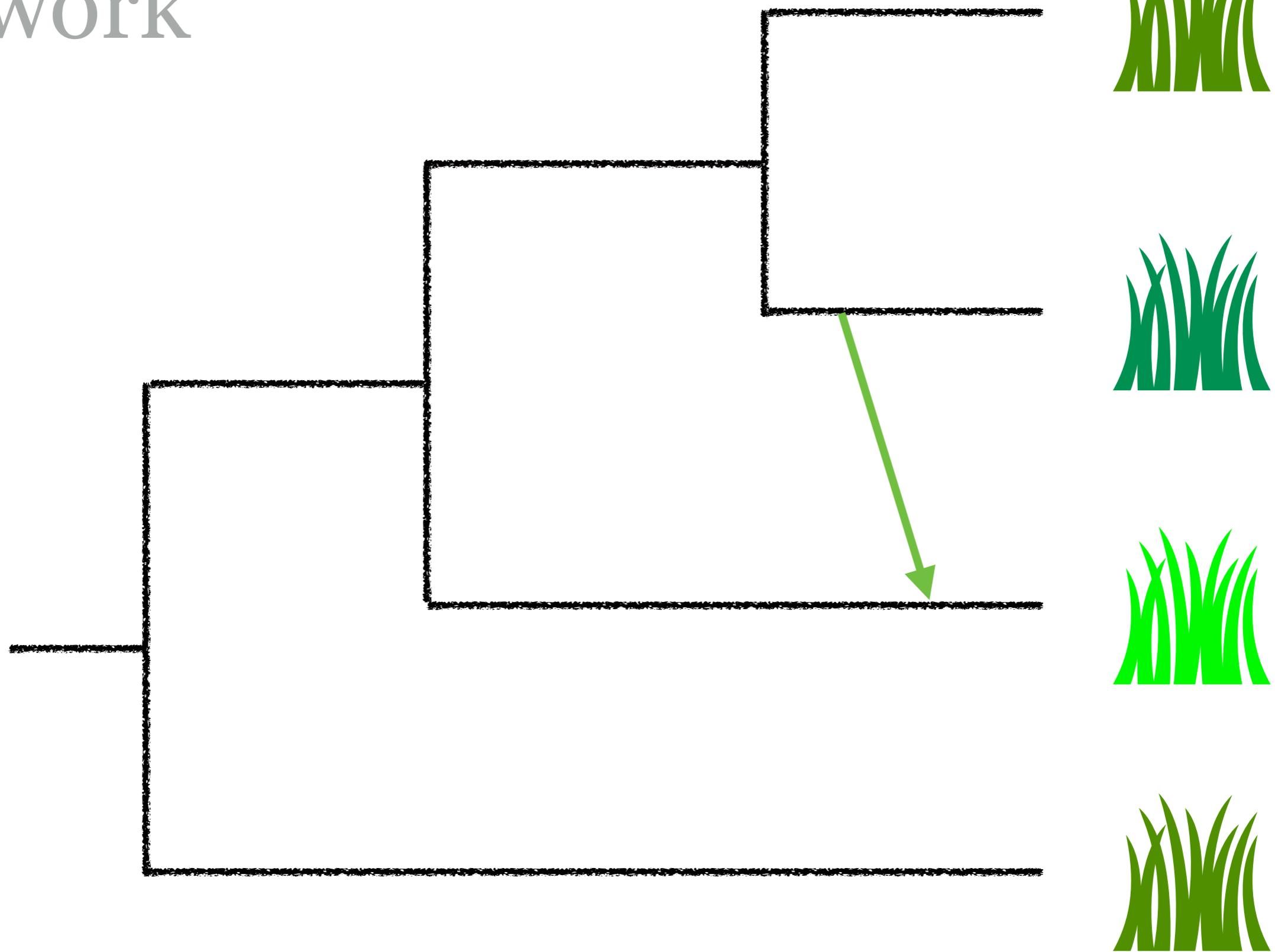


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Phylogenetic network

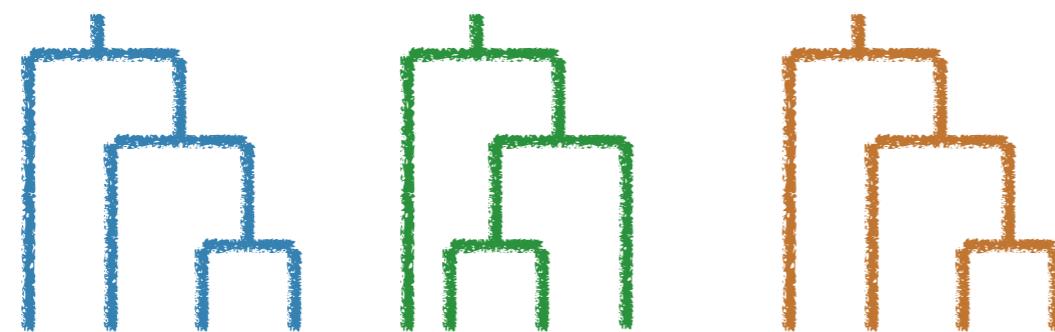


How?

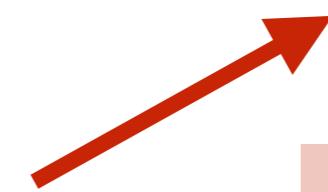
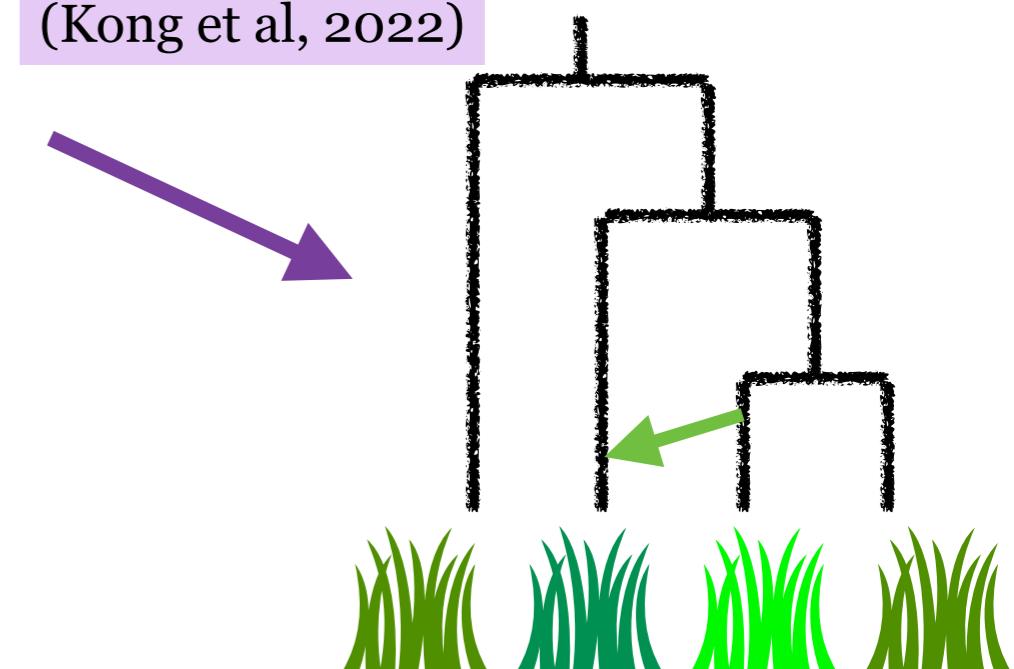
Phylogenetic network



MrBayes
(Huelsenbeck, Ronquist, 2001)
RAxML
(Stamatakis, 2014)
PhyML
(Guindon et al, 2010)
RevBayes
(Hoehna et al, 2016)
IQ-TREE
Nguyen et al. (2015)



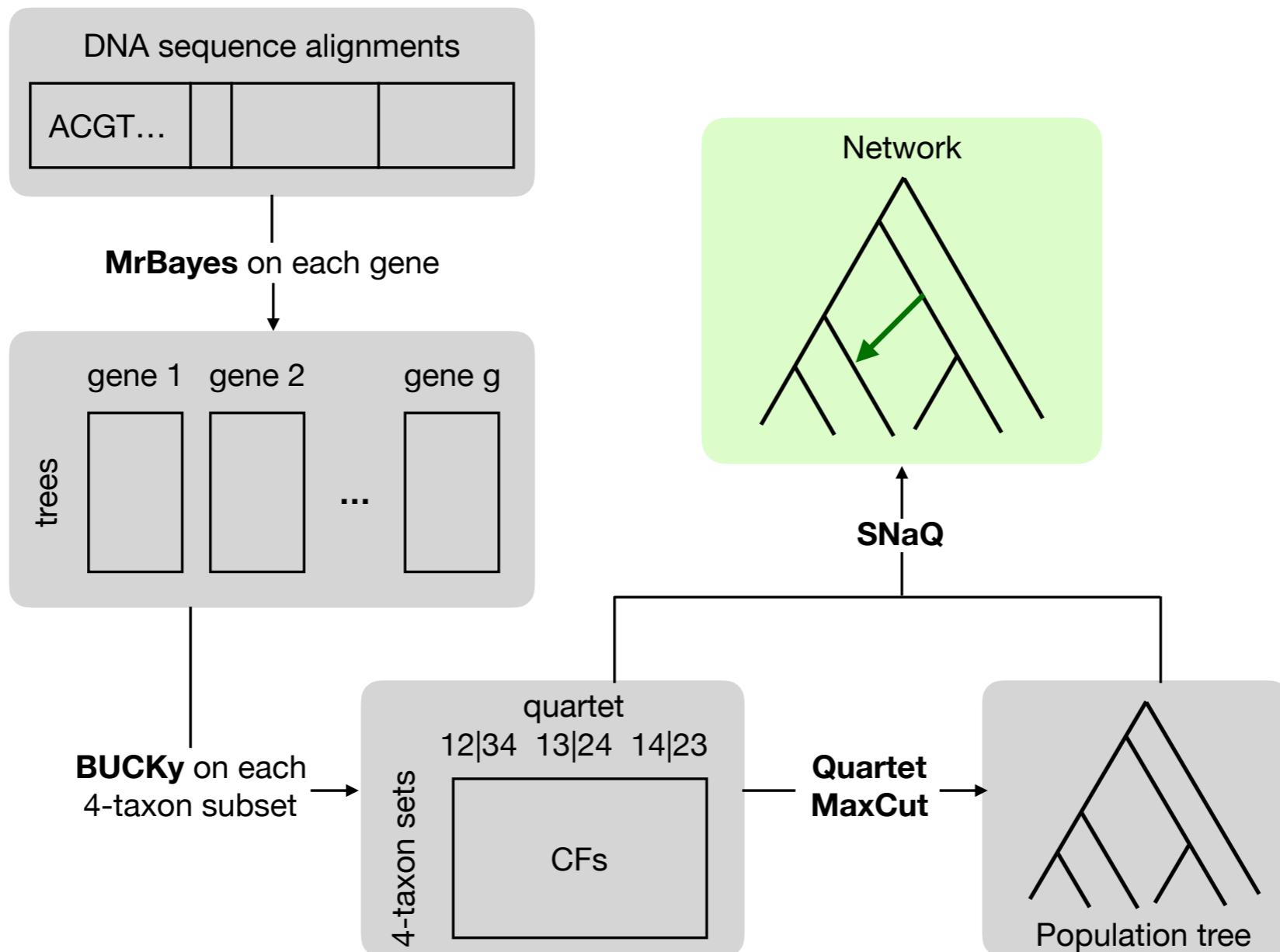
BEAST2
(Zhang et al, 2017)
PhyloNet
(Wen et al, 2016)
PhyNEST
(Kong et al, 2022)



SNaQ
(S.-L., Ane, 2016)
PhyloNet
(Yu et al, 2014)

How?

Phylogenetic network



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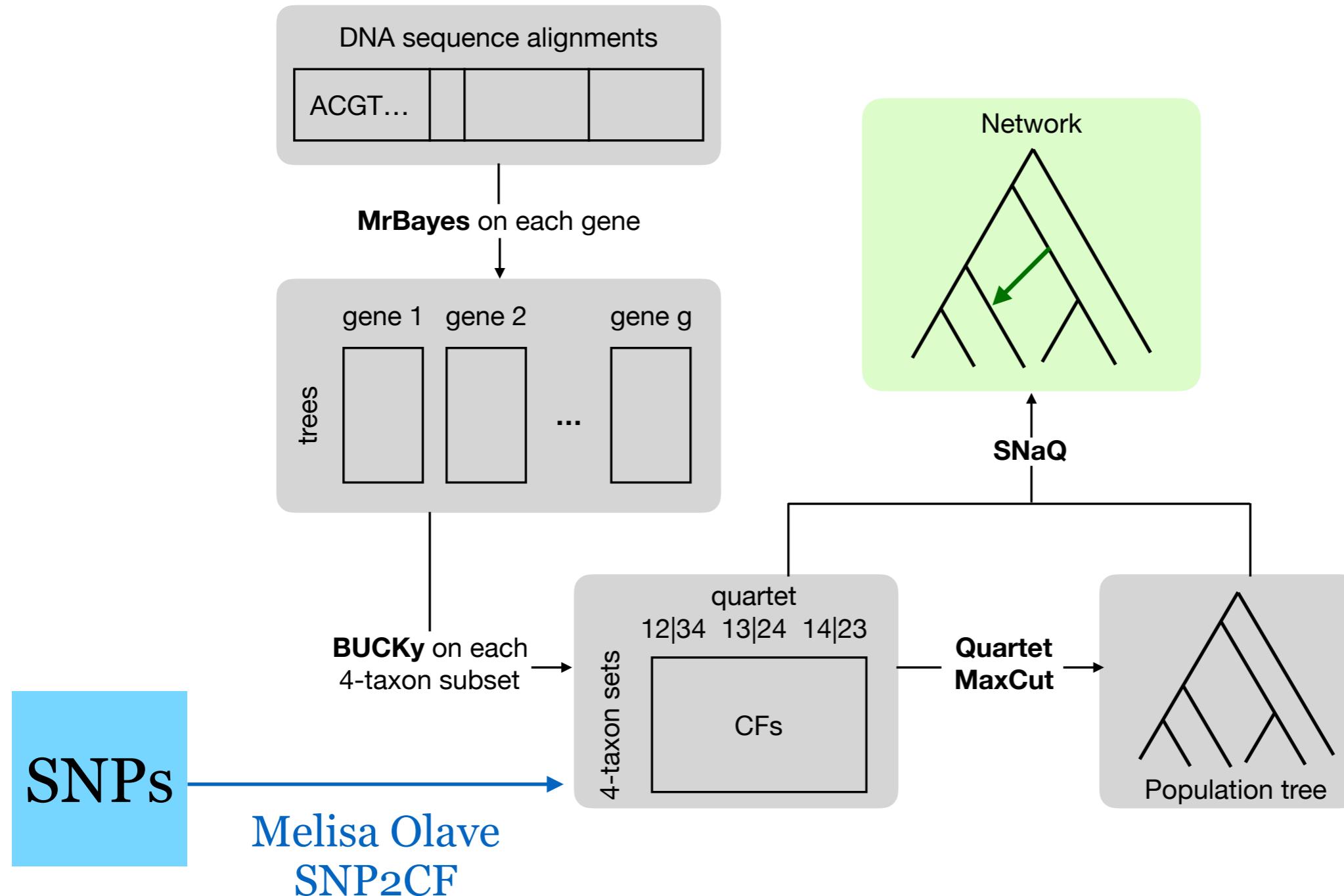
crsl4



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How?

Phylogenetic network



<https://solislemuslab.github.io/>



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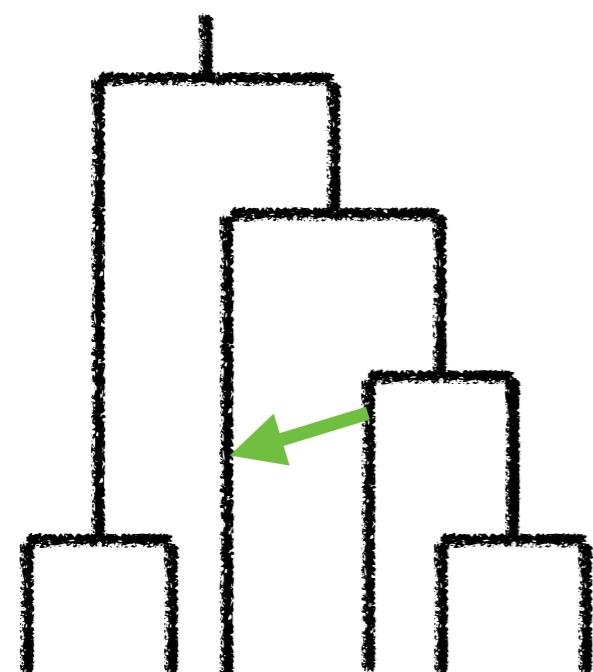
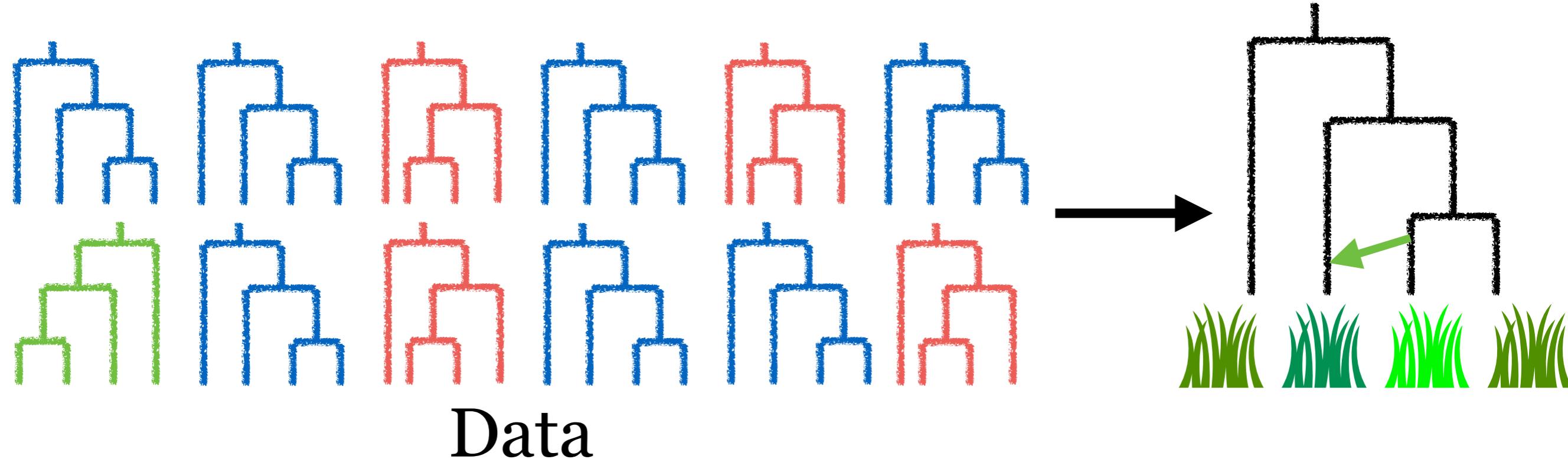


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Maximum pseudolikelihood



Quartet-based inference

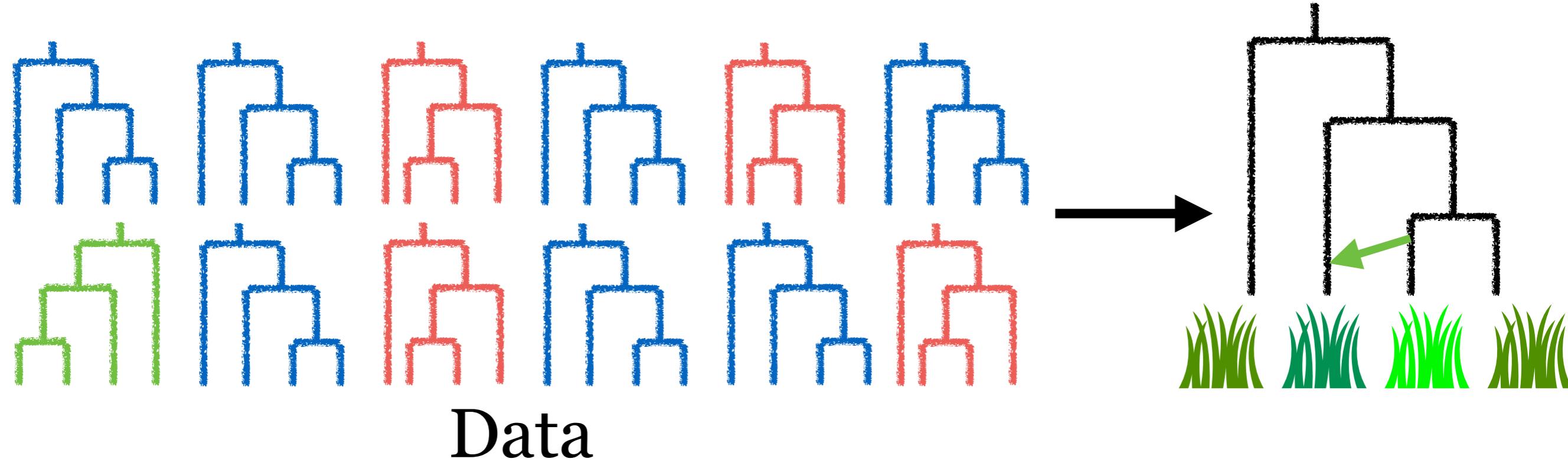
$$\tilde{L}(\textit{network}) = \prod L(\textit{quartet})$$

(S-L, Ané, 2016, PLoS Genetics)

www.github.com/CRSL4/PhyloNetworks

snaQ julia

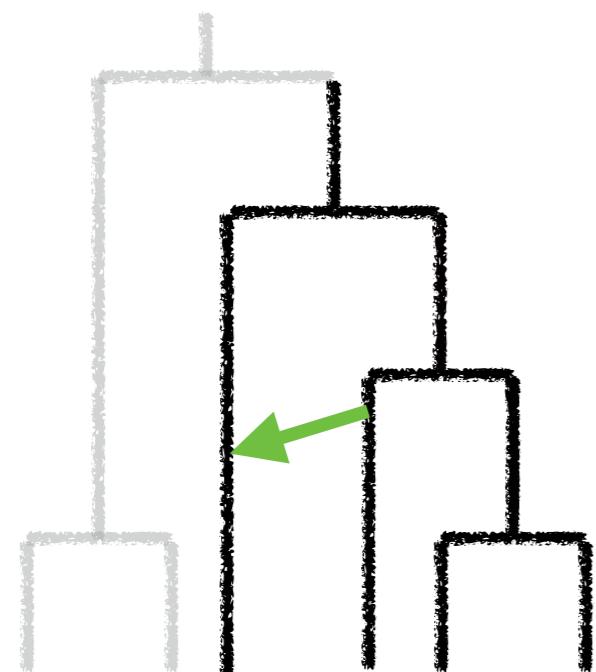
Maximum pseudolikelihood



$$\tilde{L}(\textit{network}) = \prod L(\textit{quartet})$$

(S-L, Ané, 2016, PLoS Genetics)

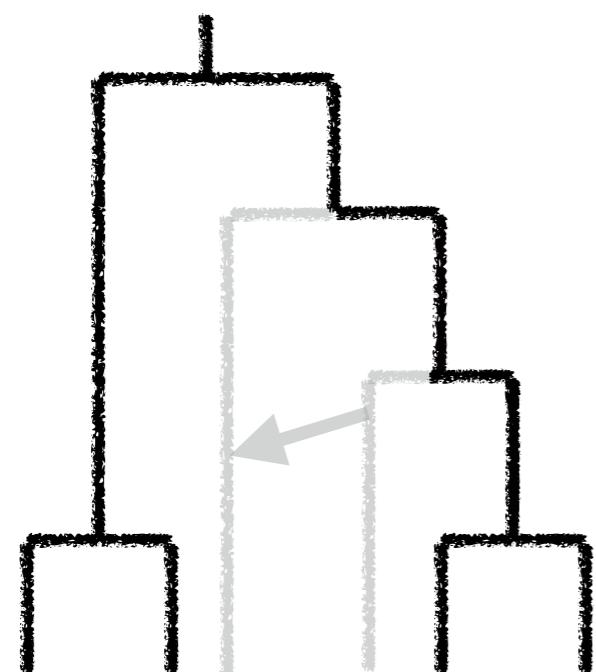
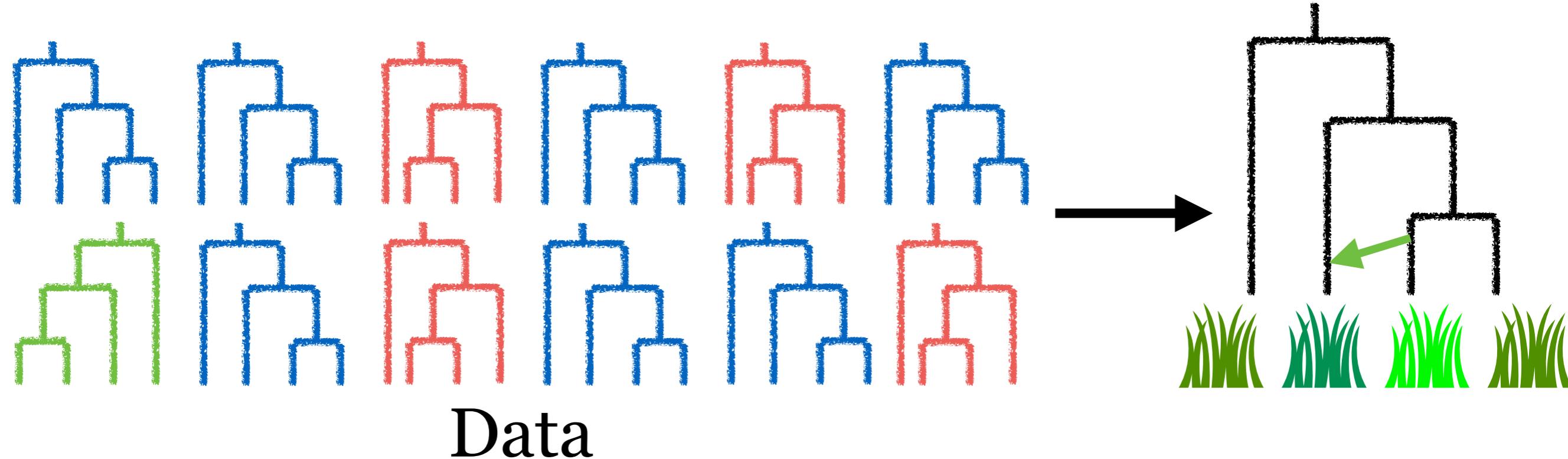
www.github.com/CRSL4/PhyloNetworks



Quartet-based inference

snaQ julia

Maximum pseudolikelihood



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www.github.com/CRSL4/PhyloNetworks

snaQ julia

Maximum pseudolikelihood

Unrooted gene trees

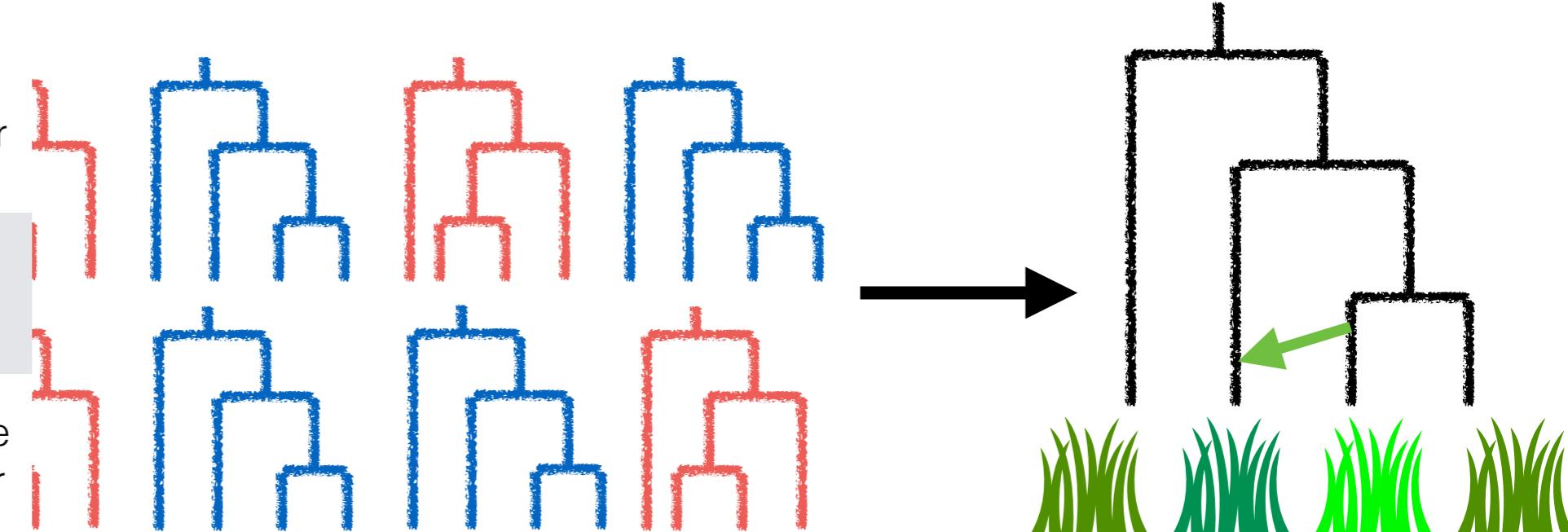
No branch lengths

Concordance factors

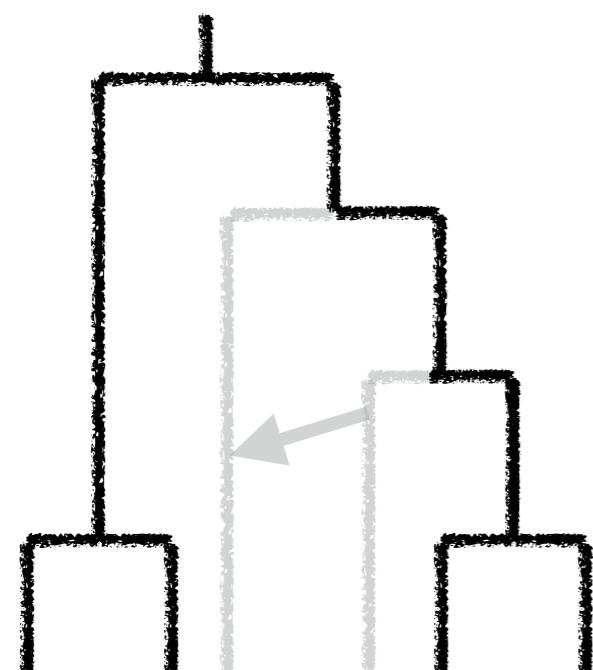
No rooting error

No molecular clock assumption

Account for tree estimation error



Data



Quartet-based inference

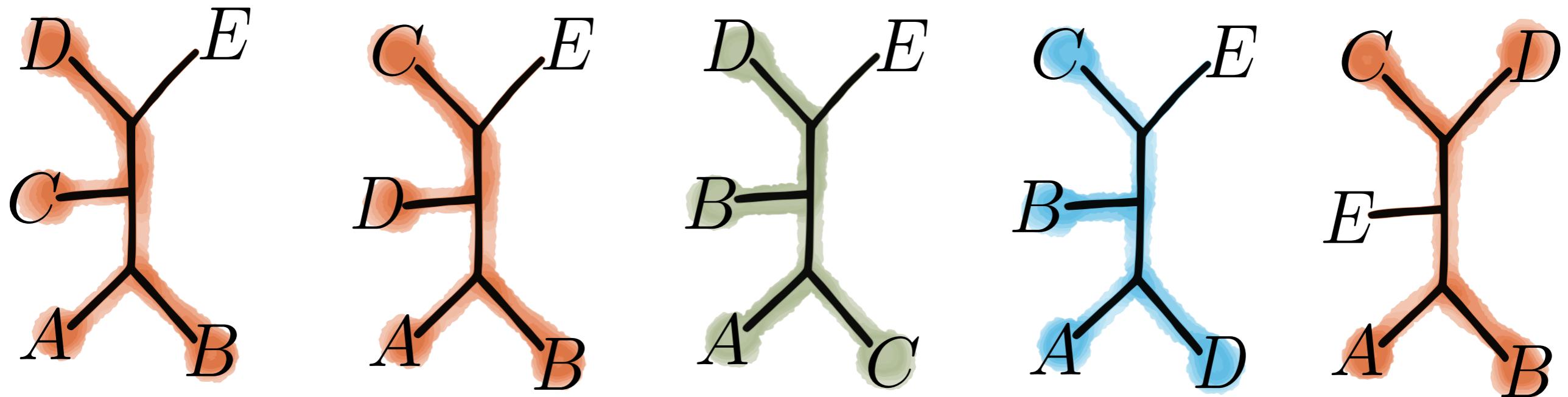
$$\tilde{L}(\textit{network}) = \prod L(\textit{quartet})$$

(S-L, Ané, 2016, PLoS Genetics)

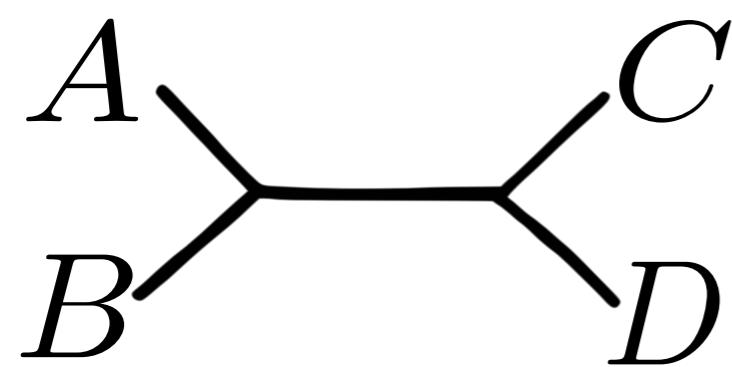
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snaQ julia

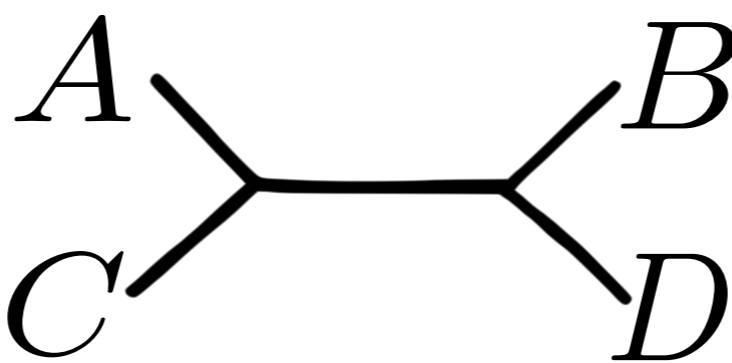
Quartet-based inference



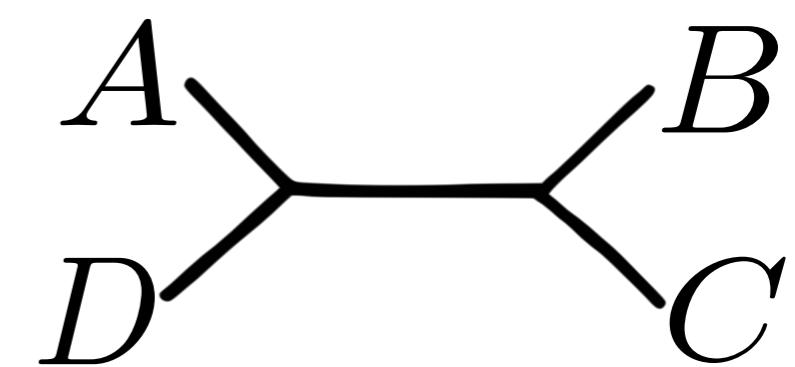
Concordance factors (CF):
% of genes having the quartet in their tree



3/5



1/5



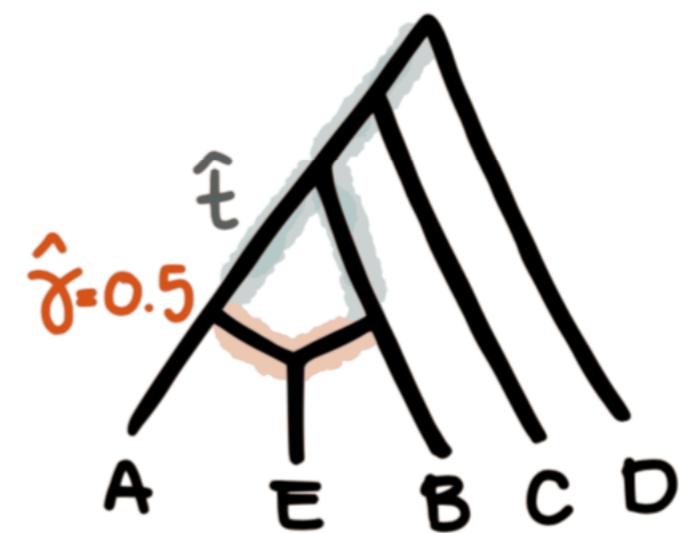
1/5

Quartet-based inference

Observed **quartet** CFs:

4 taxon set	CF_1	CF_2	CF_3
A B C D	.80	.10	.10
A B C E	.40	.40	.20
A B D E	.40	.40	.20
A C D E	.84	.08	.08
B C D E	.82	.10	.08

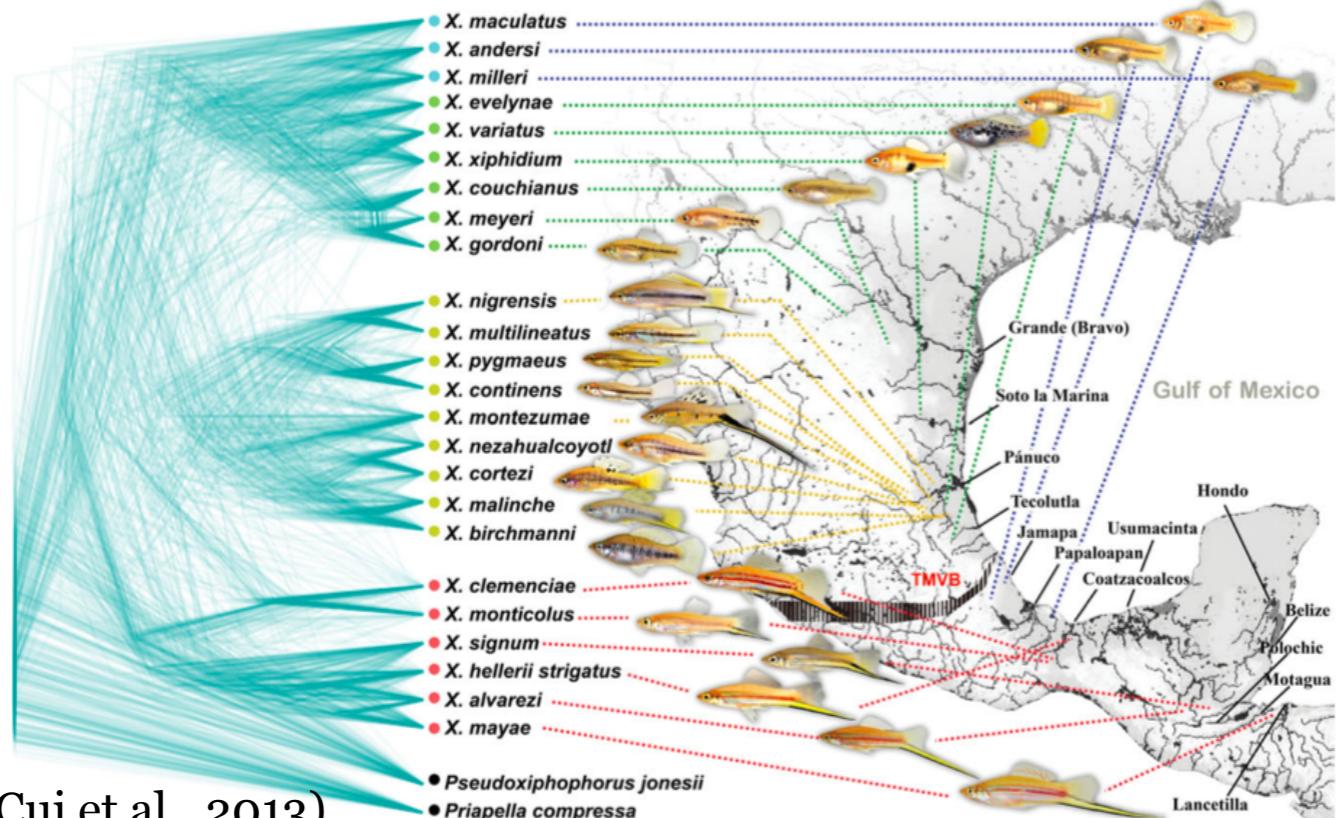
inferred network:



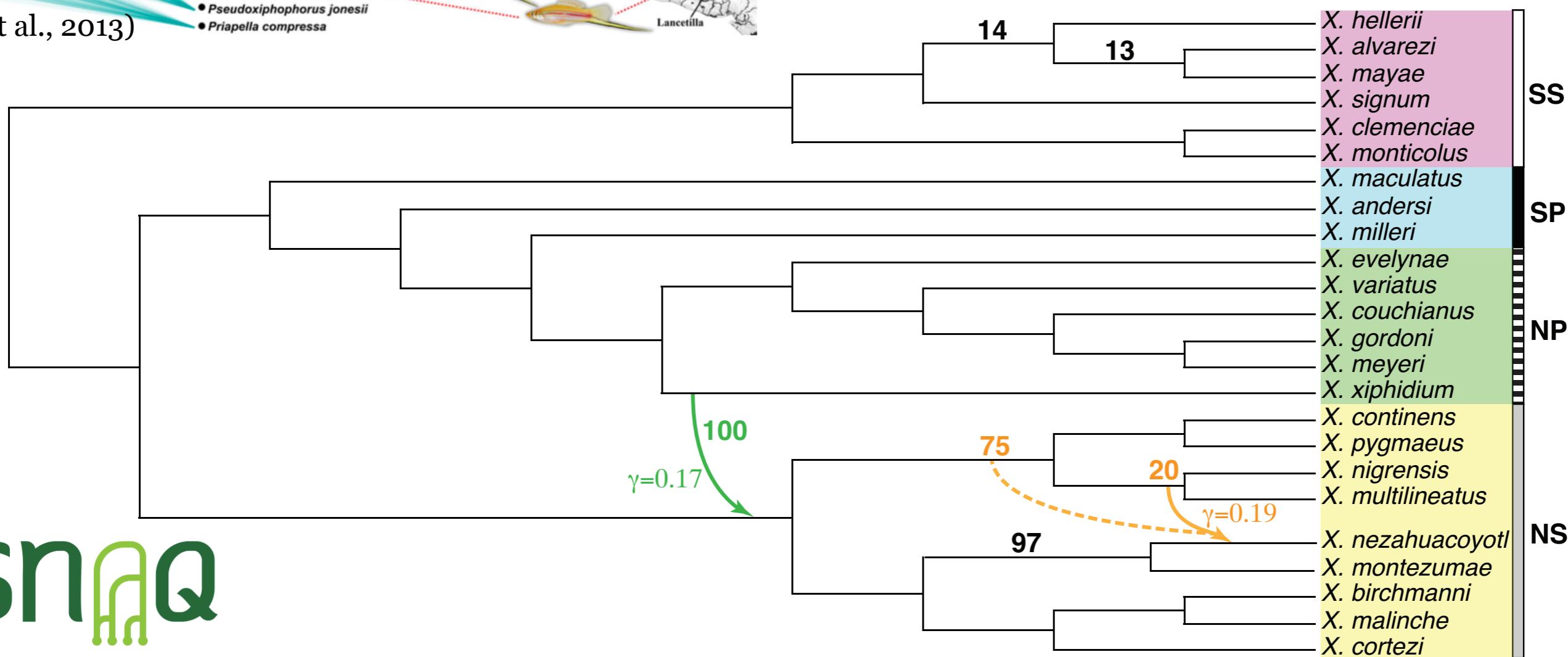
Maximum Pseudo-Likelihood:

$$\log \tilde{L} = \sum_{q \in Q(N)} CF_{in,1} \log(CF_{net,1}) + CF_{in,2} \log(CF_{net,2}) + CF_{in,3} \log(CF_{net,3})$$

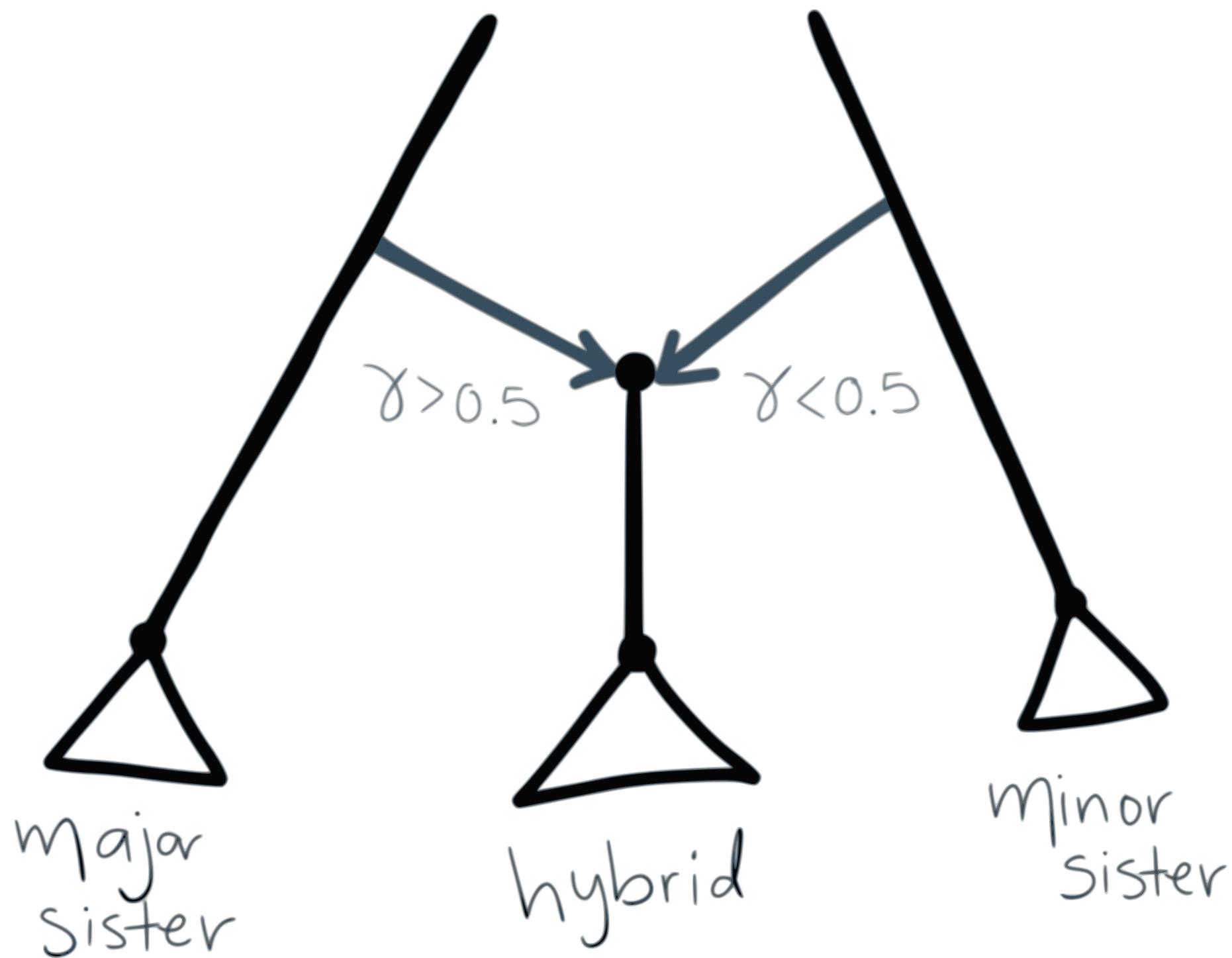
1183 genes, 24 swordtails and platyfish



Xiphophorus fish data

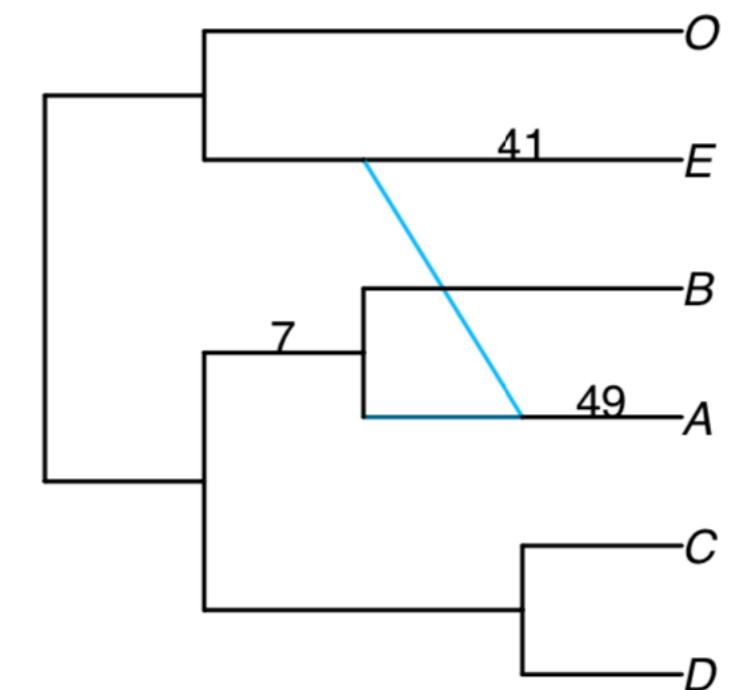
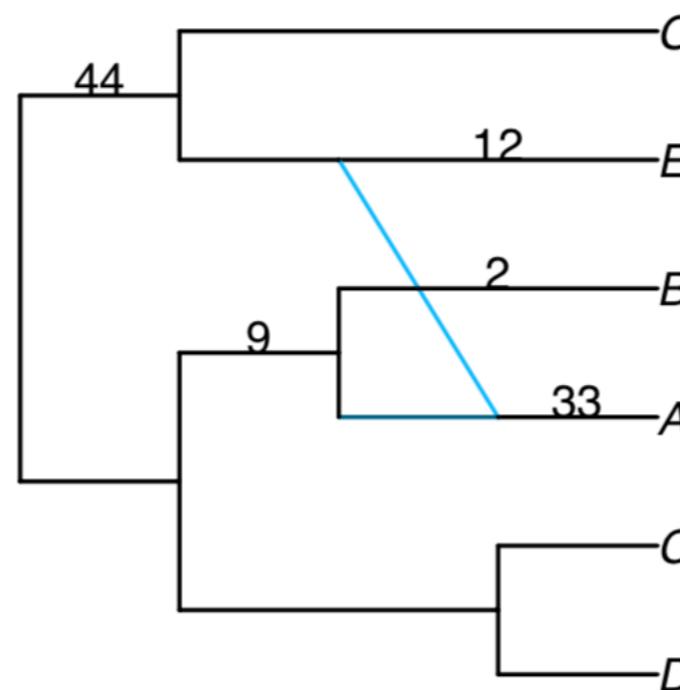
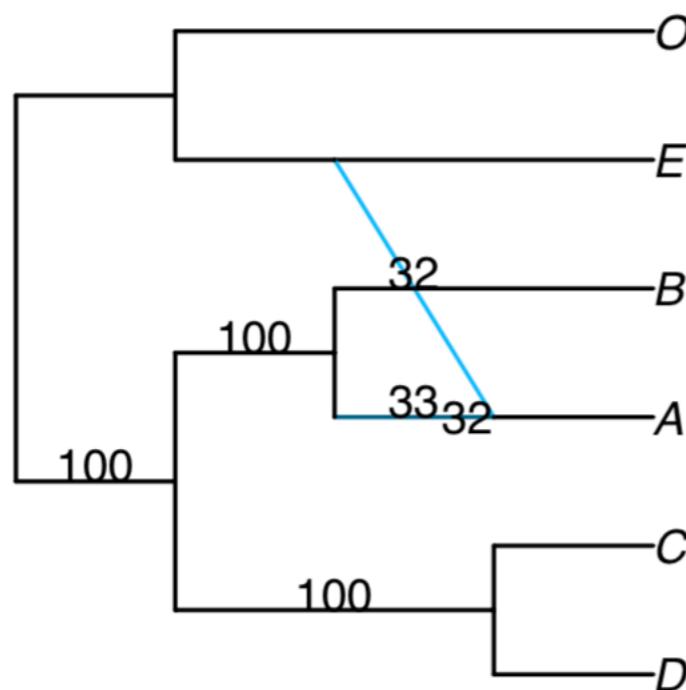


Network Comparison



(S.-L. et al, 2017, MBE)

Uncertainty in the hybridization events

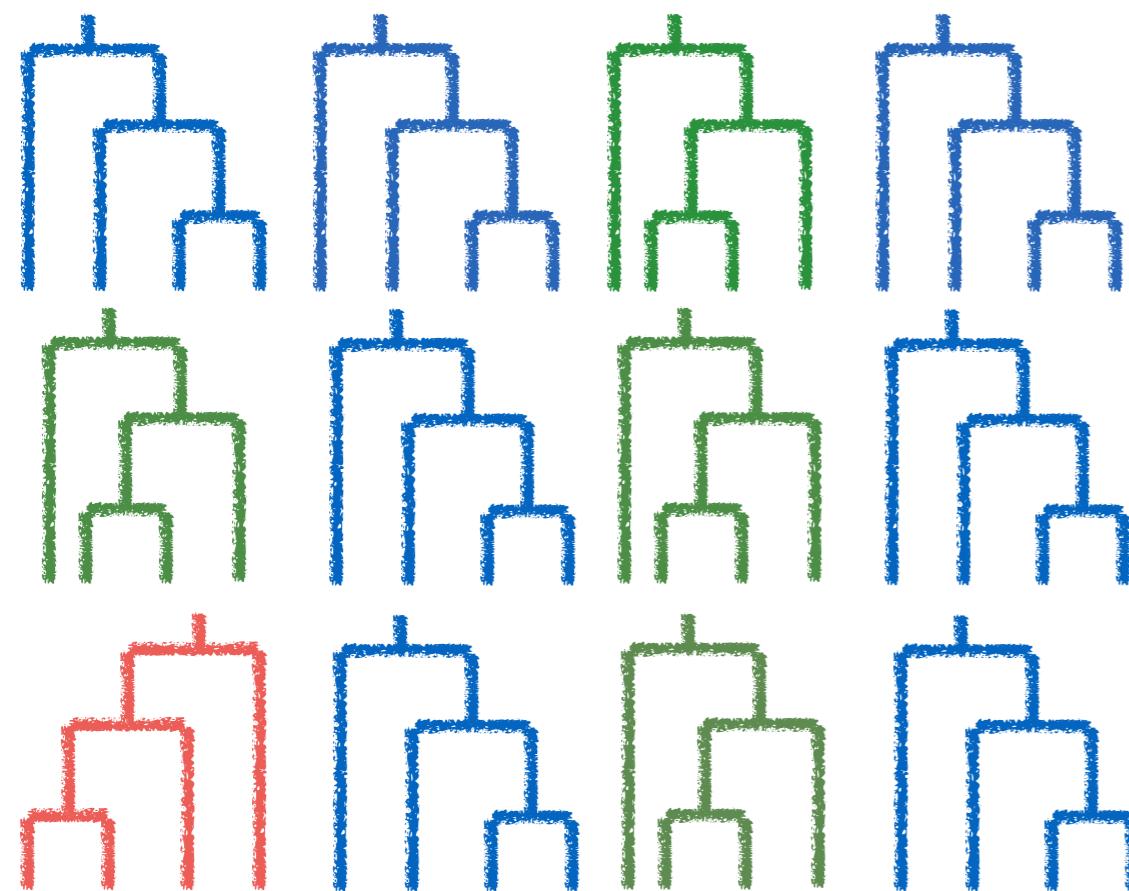
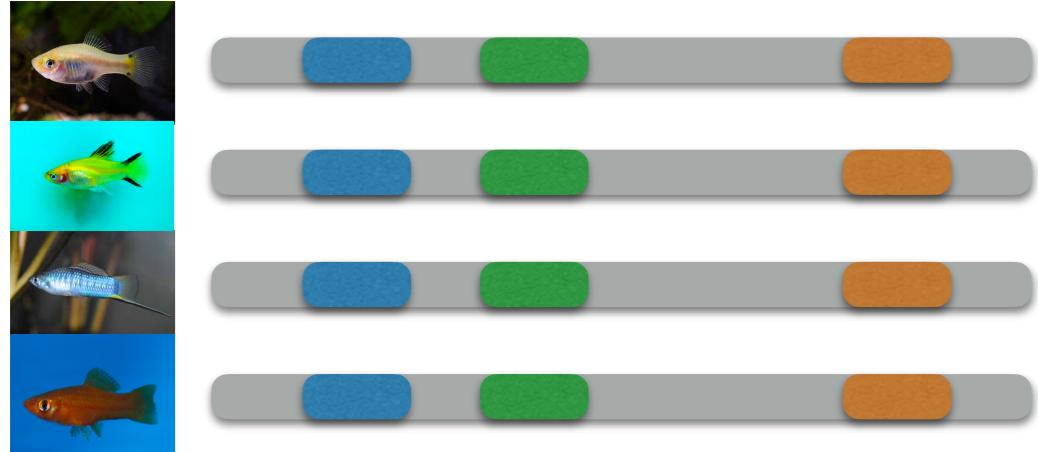


Hybrid
clades

Minor
sister
clades

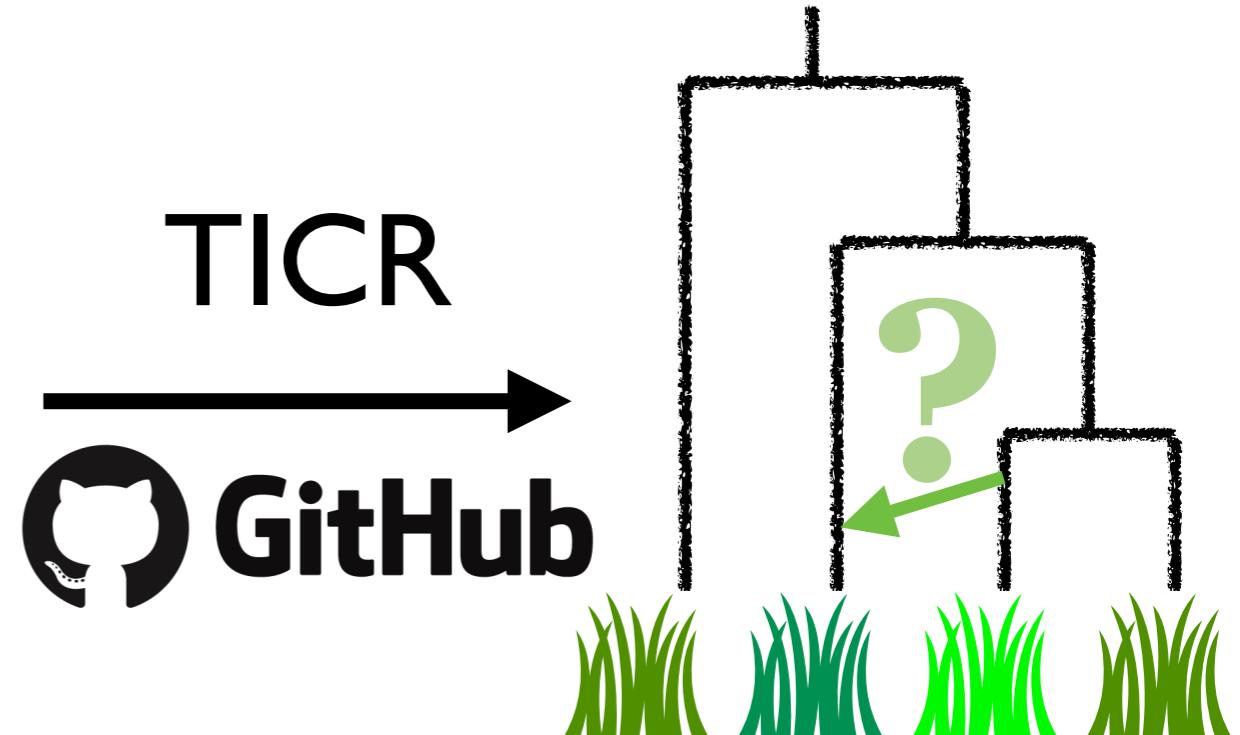
When?

Phylogenetic network



Data

Goodness-of-fit test
Hypothesis test:
Is a tree a good fit?



<https://github.com/nstenz/TICR>
(Stenz et al, 2015, Syst Bio)

PhyloNetworks: analysis for phylogenetic networks

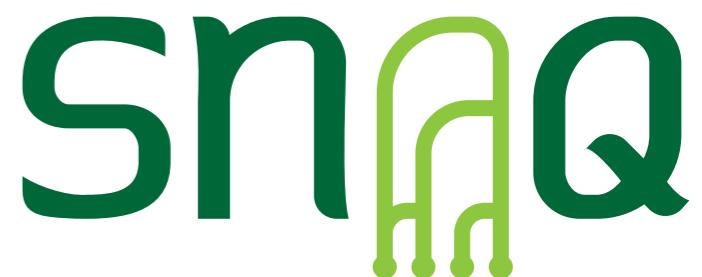
build passing docs stable docs dev codecov 81% coverage 67%



Overview

PhyloNetworks is a [Julia](#) package with utilities to:

- read / write phylogenetic trees and networks, in (extended) Newick format. Networks are considered explicit: nodes represent ancestral species. They can be rooted or unrooted.
- manipulate networks: re-root, prune taxa, remove hybrid edges, extract the major tree from a network, extract displayed networks / trees
- compare networks / trees with dissimilarity measures (Robinson-Foulds distance on trees)
- summarize samples of bootstrap networks (or trees) with edge and node support
- estimate species networks from multilocus data (see below)
- phylogenetic comparative methods for continuous trait evolution on species networks / trees



- Step-by-step tutorial
- Online documentation
- Google user group



(Solis-Lemus & Ane, 2016; Solis-Lemus. et al, 2017)



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PhyloNetworks: analysis for phylogenetic networks

build passing docs stable docs dev codecov 81% coverage 67%

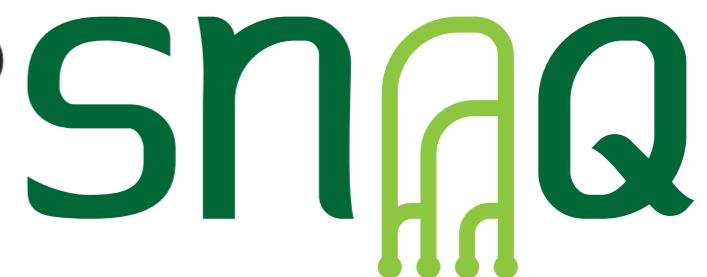
Overview

Get your stickers!



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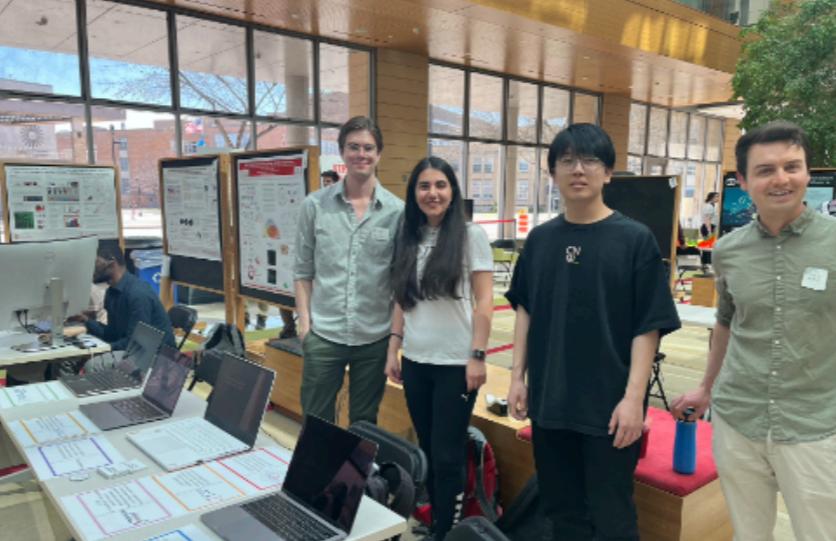


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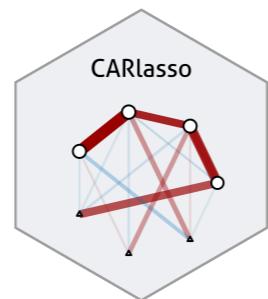
WISCONSIN
UNIVERSITY OF WISCONSIN-MADISON



Thank you!



Bayesian
NetworkRegression.jl



snaQ

phylo
networks



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Questions?