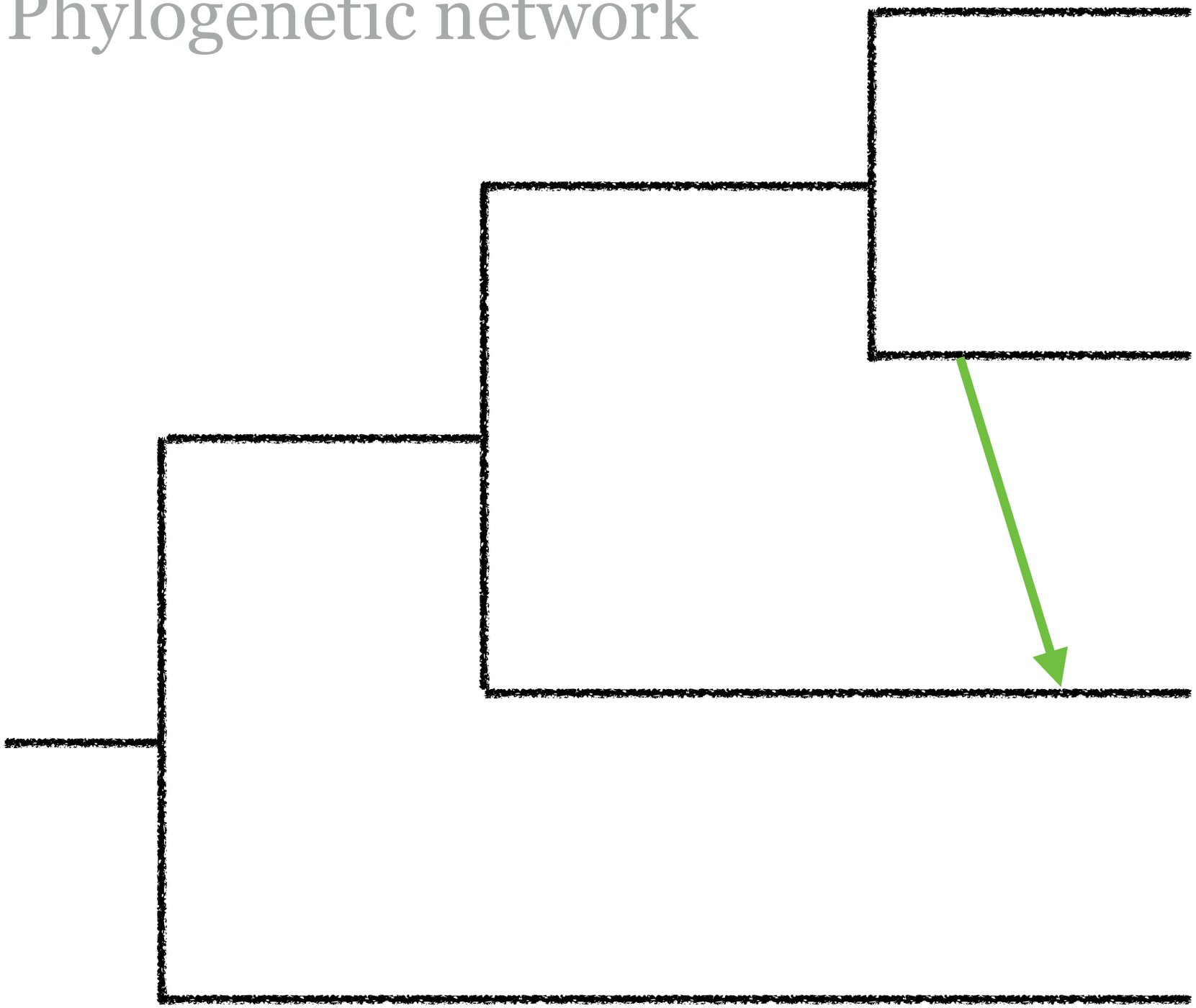
Lecture 14

Coalescent-based methods
Botany/Plant Path 563

- **Previous class check-up:**
    - We studied the coalescent model on a species tree
    - We practiced on ASTRAL and/or BUCKy
- **Learning Objectives:** At the end of today's session, you will be able to
    - Explain the coalescent model on a species network
- **Pre-class work**
    - Read SNaQ book chapter

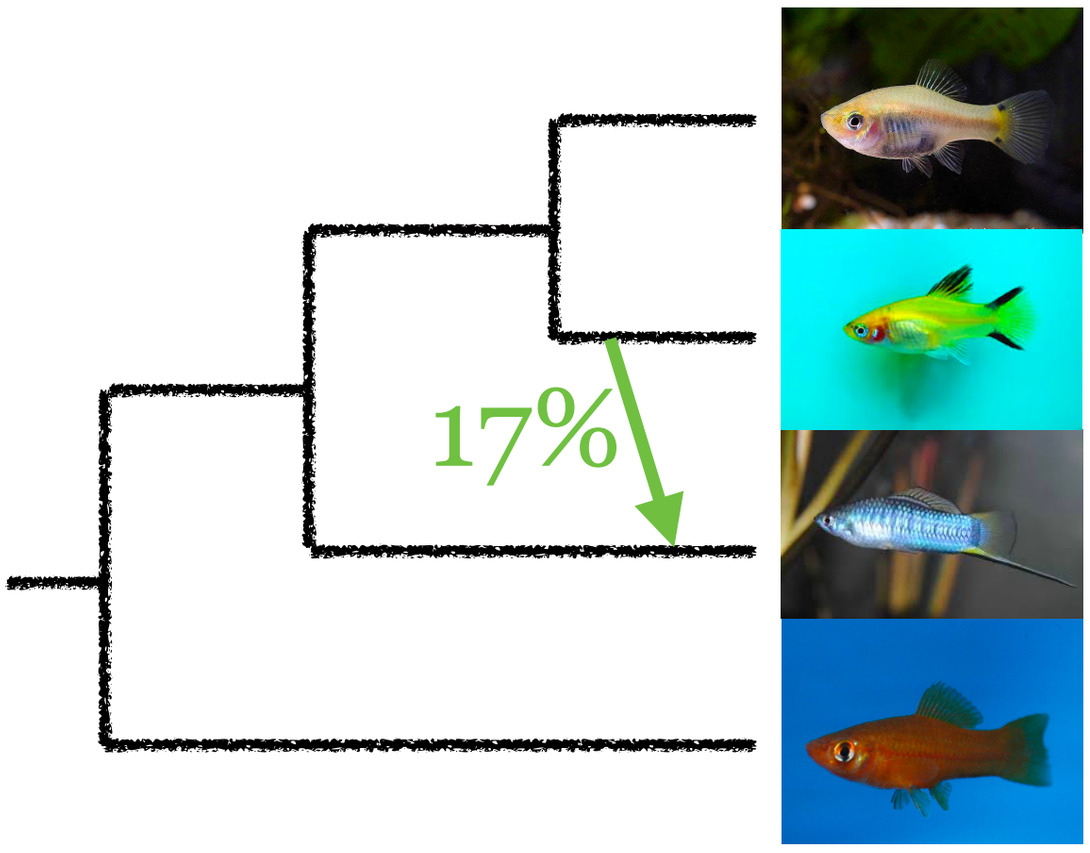
What?

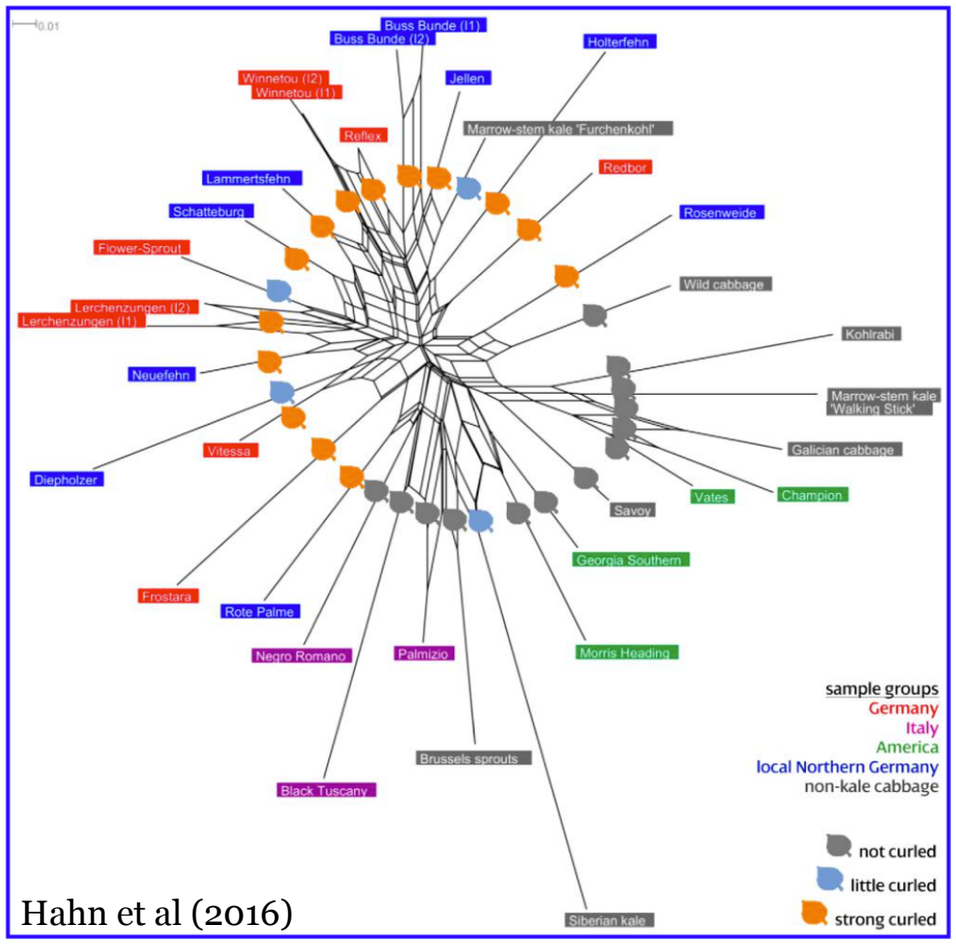
Phylogenetic network



What?

Phylogenetic network





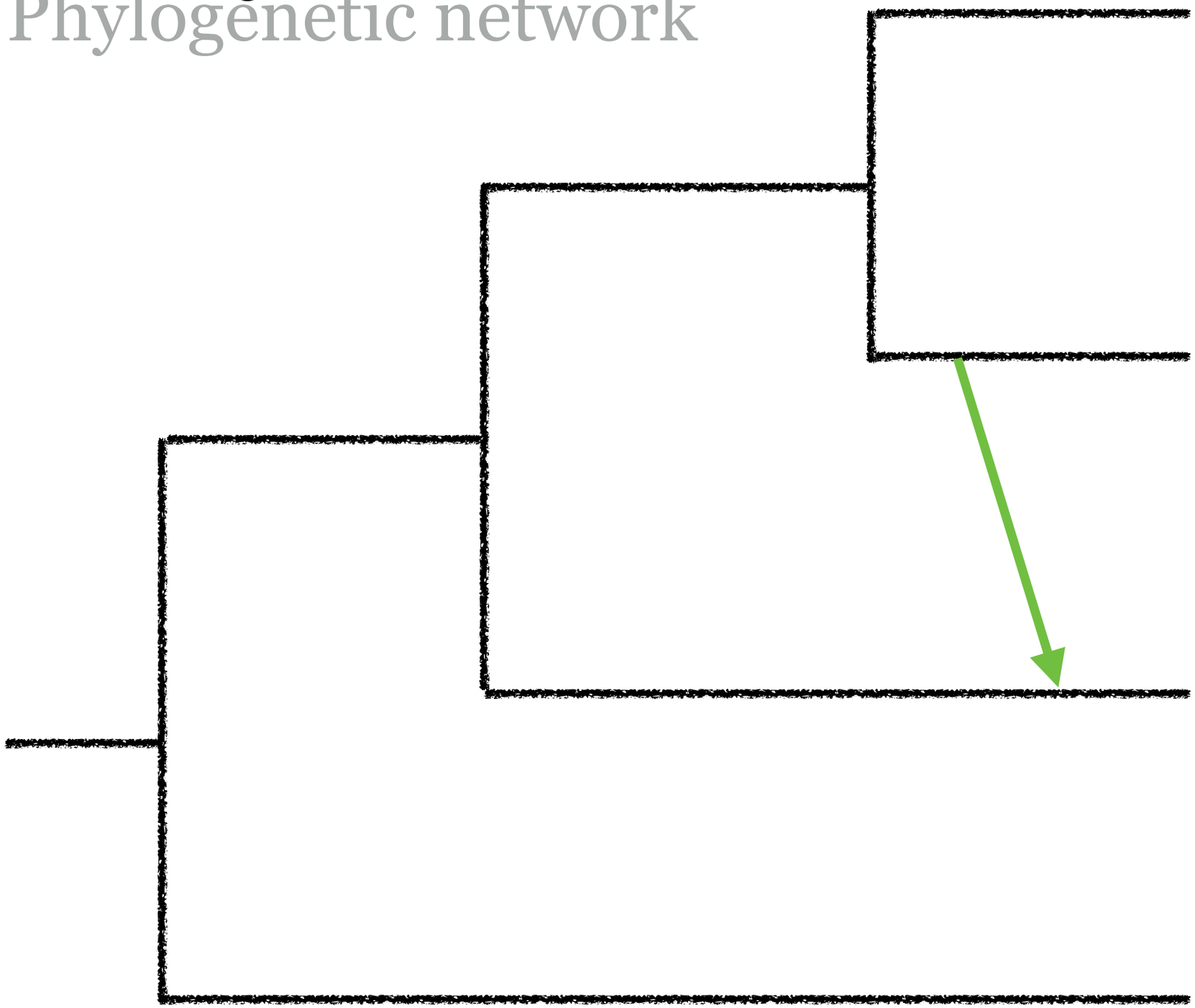
Hahn et al (2016)

Explicit

Implicit

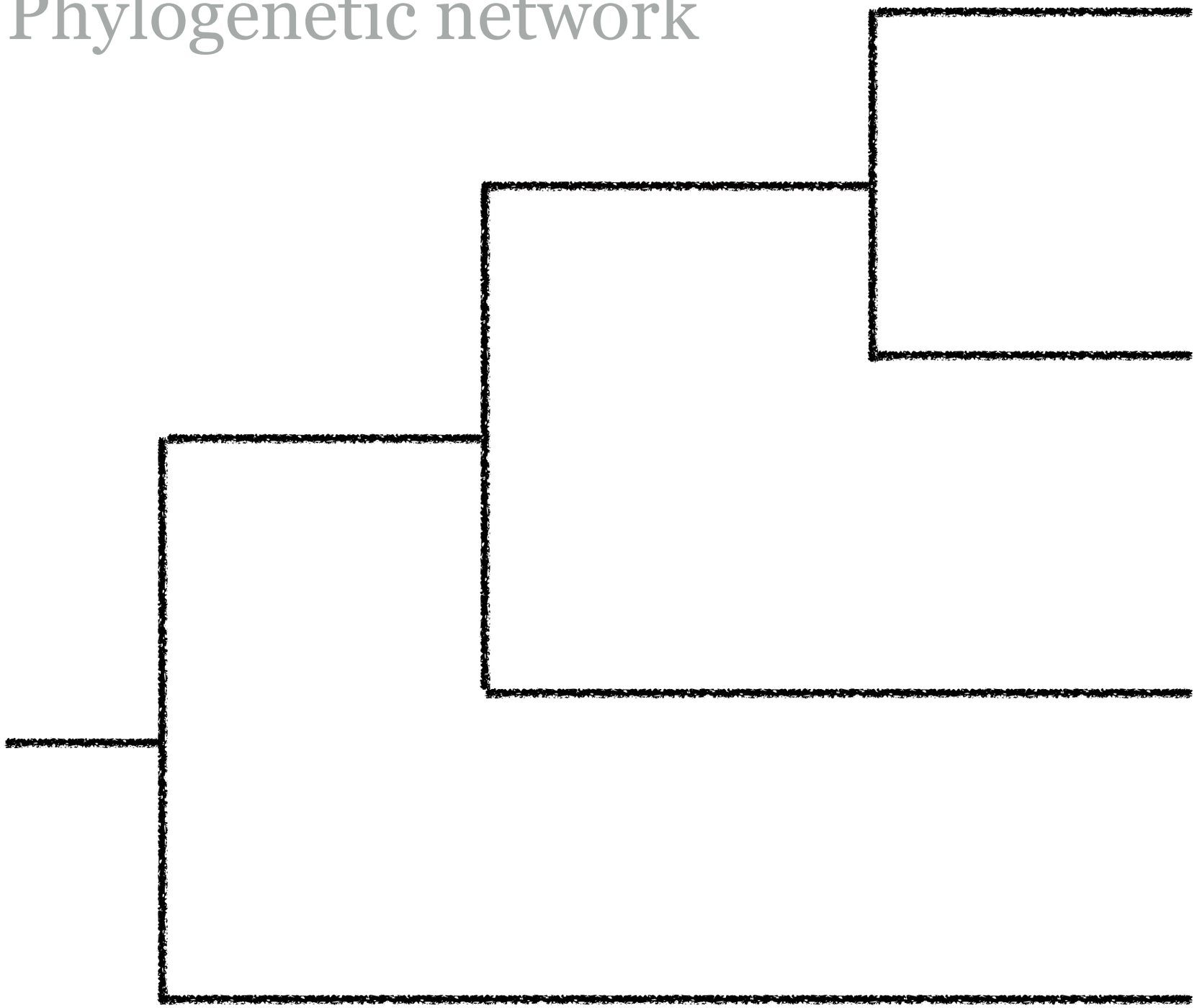
Why?

Phylogenetic network



Why?

Phylogenetic network

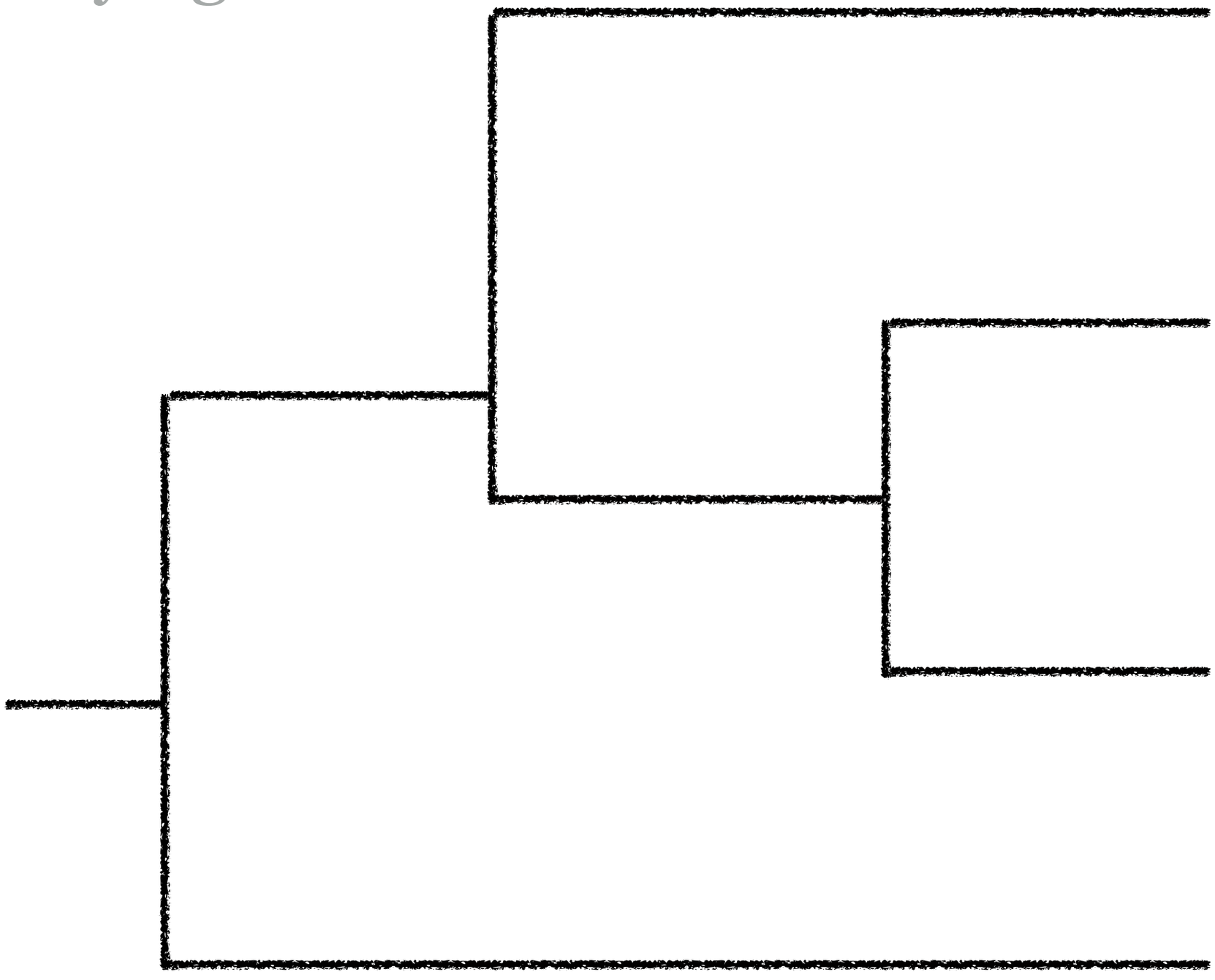


Main tree

Why?

Phylogenetic network

Ignore gene flow
=>Wrong tree!

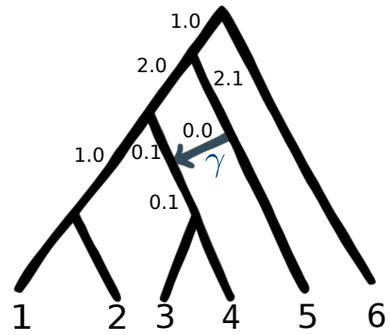


(S.-L., Yang, Ané, 2016, Syst Bio)

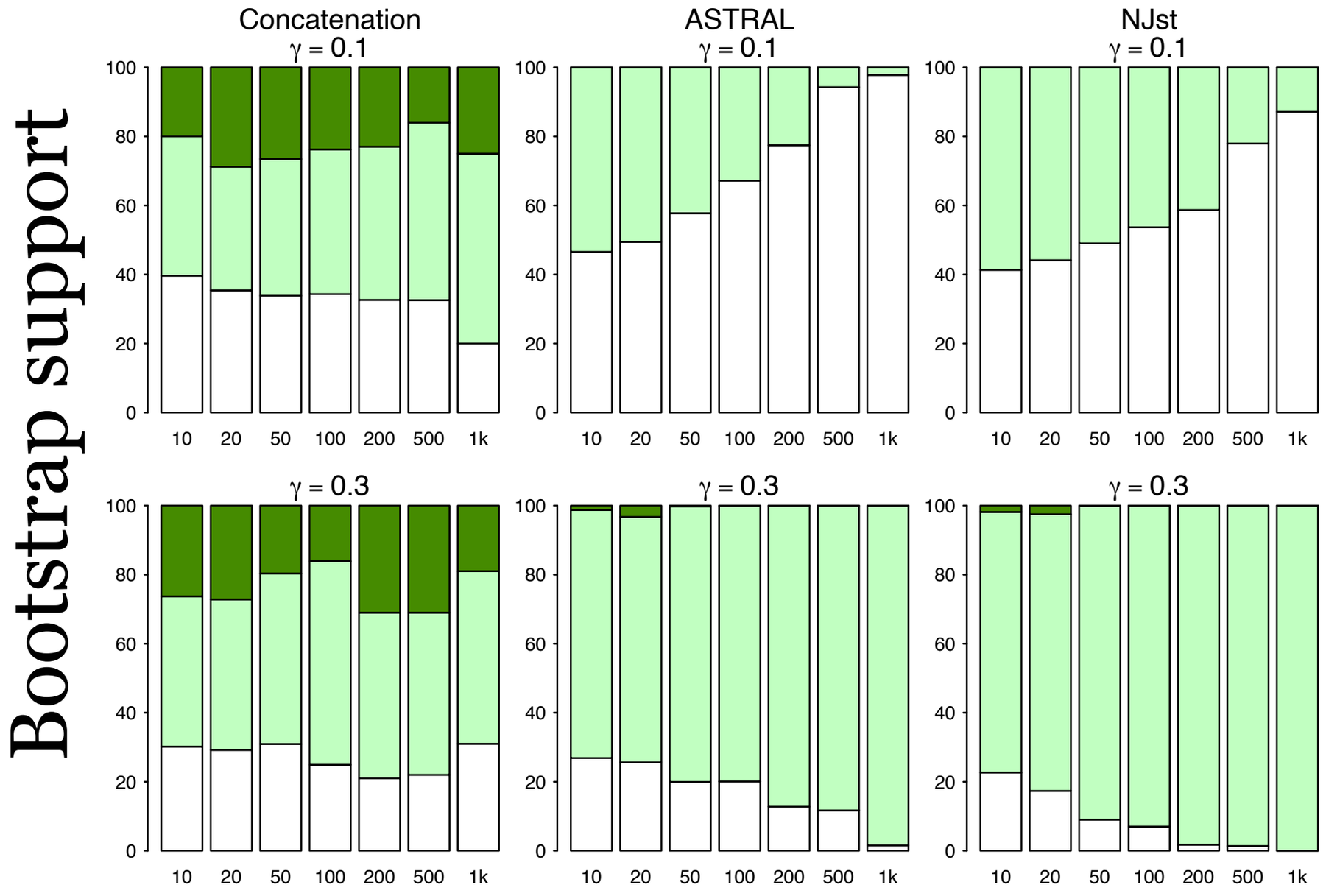
Why?

Phylogenetic network

Coalescent tree methods not robust to gene flow



White: true tree



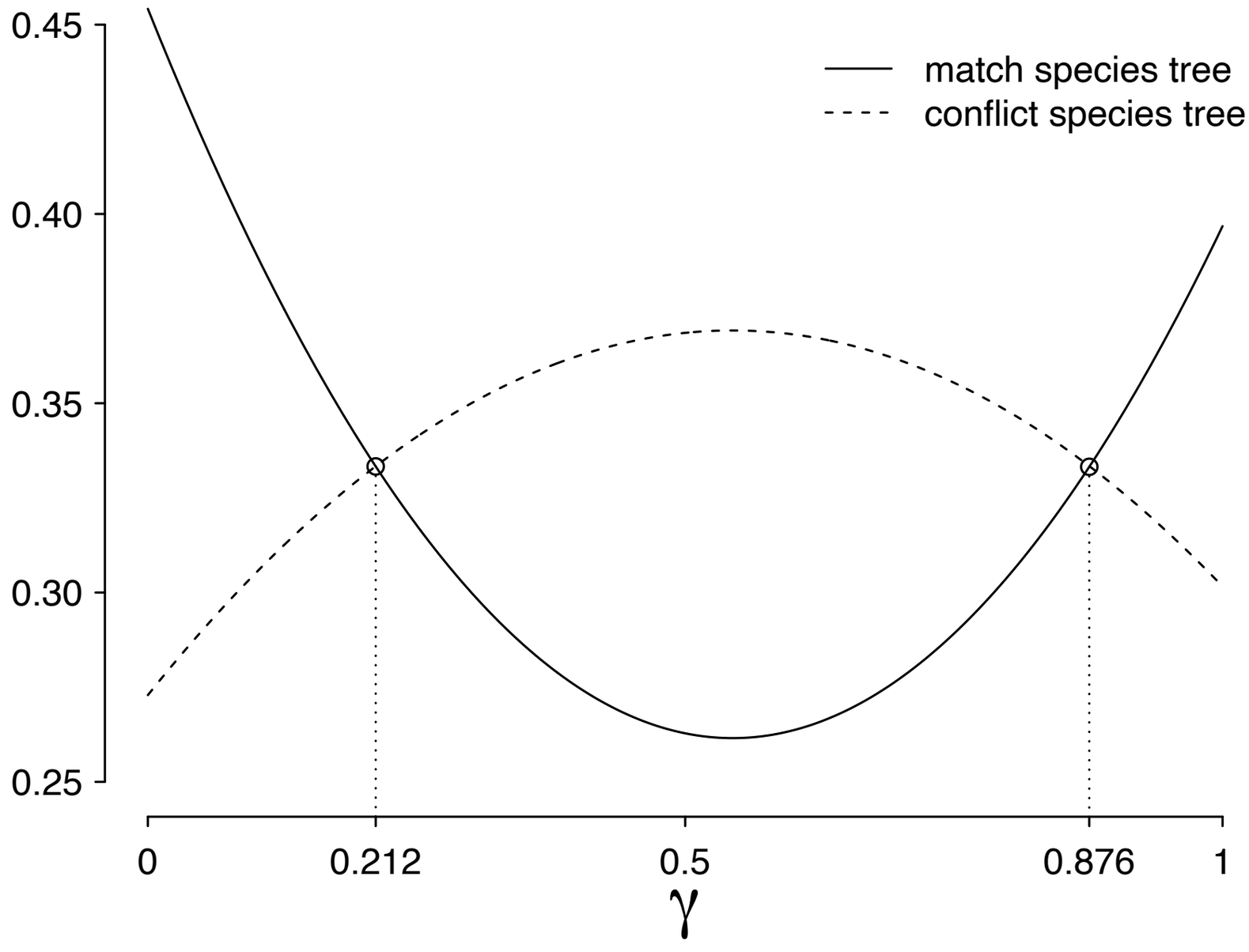
(S.-L., Yang, Ané, 2016, Syst Bio)

ASTRAL (Mirarab et al, 2014)
NJst (Liu&Yu,2011)

Why?

Phylogenetic network

Anomaly zone with gene flow



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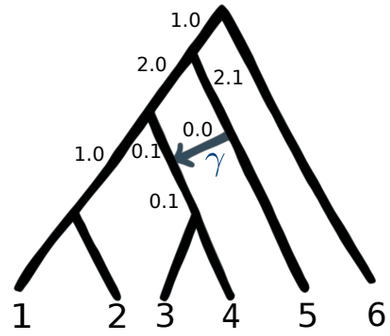
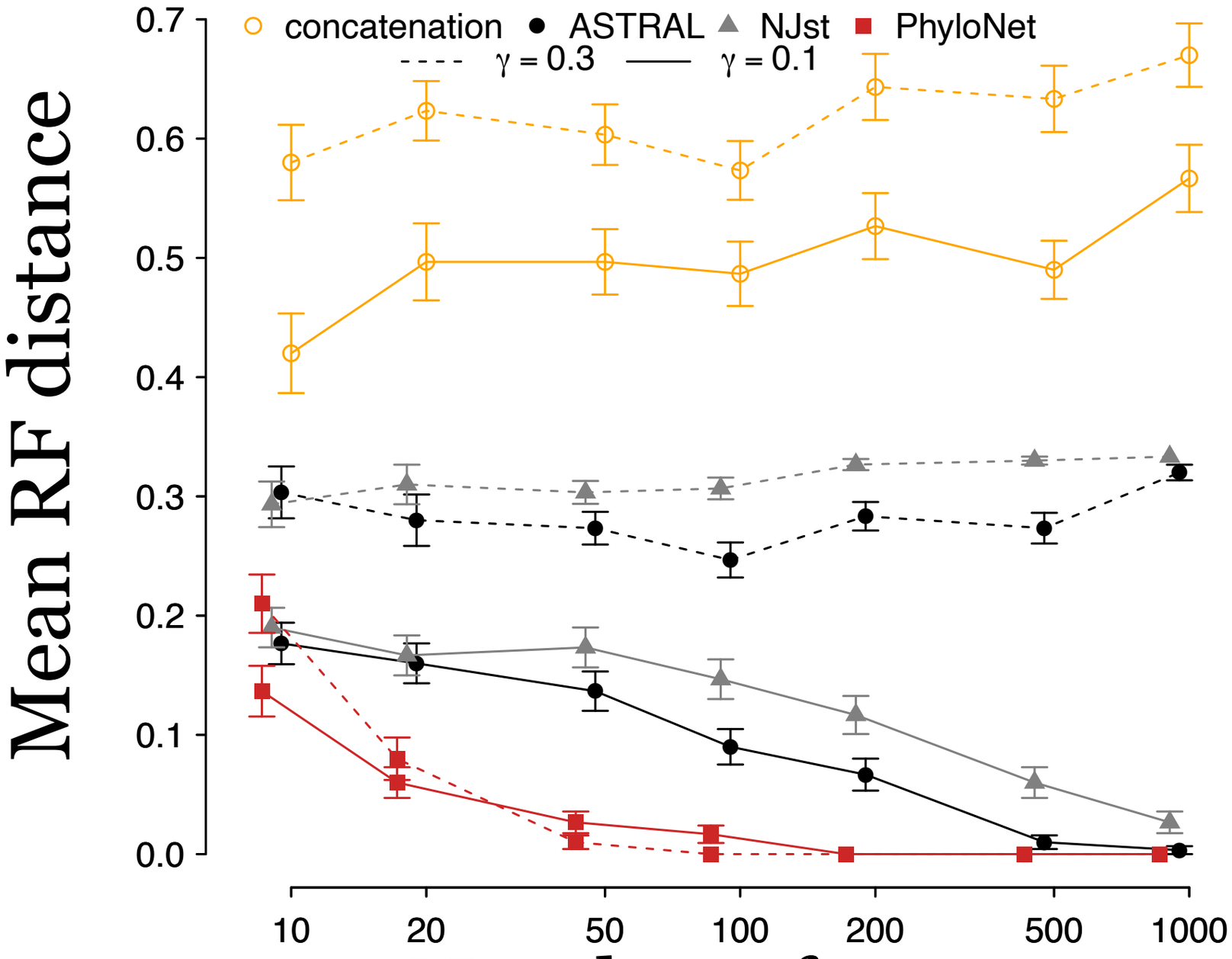
Why?

Phylogenetic network

Coalescent tree methods not robust to gene flow





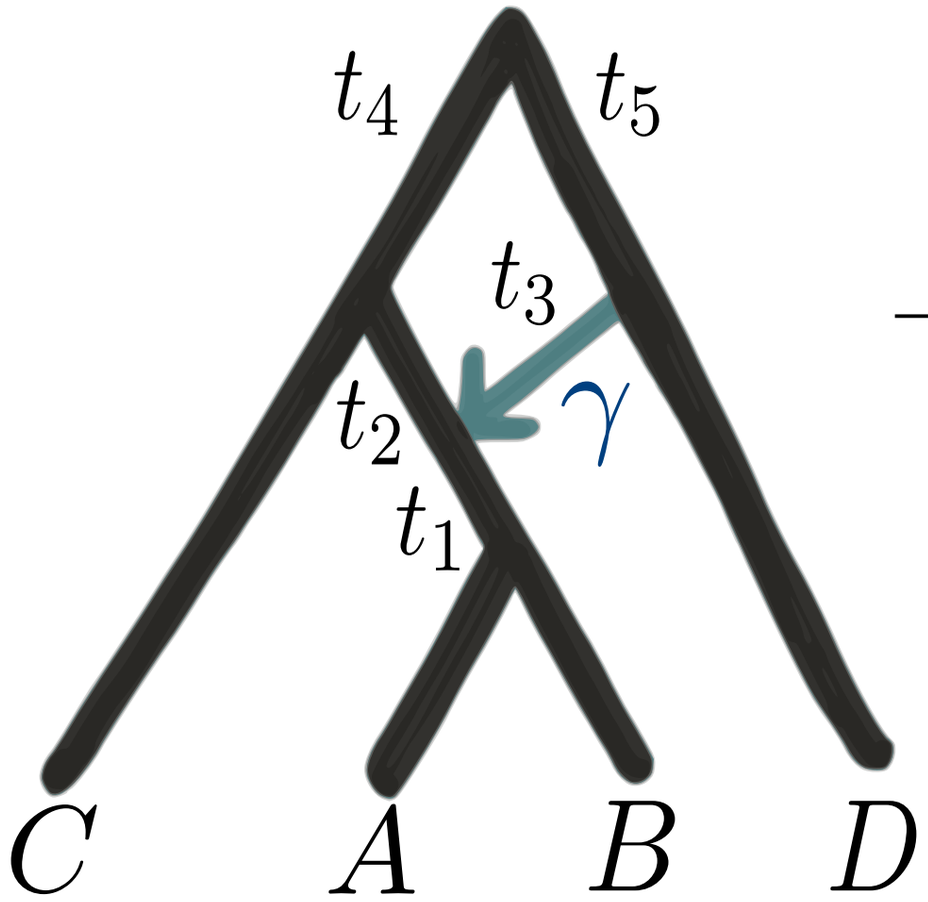
(S.-L., Yang, Ané, 2016, Syst Bio)

ASTRAL (Mirarab et al, 2014)
NJst (Liu&Yu,2011)
PhyloNet (Yu et al 2012, 2014)

Why?

Phylogenetic network

Anomalous unrooted gene trees with gene flow



Frequency among gene trees

Quartet	$\gamma = 0.0$	$\gamma = 0.1$	$\gamma = 0.3$
$AB\|CD$	**0.347**	**0.298**	**0.260**
$CA\|BD$	0.327	0.351	0.370
$CB\|AD$	0.327	0.351	0.370

$$t_1 = t_2 = 0.01, t_3 = t_4 = t_5 = 1$$

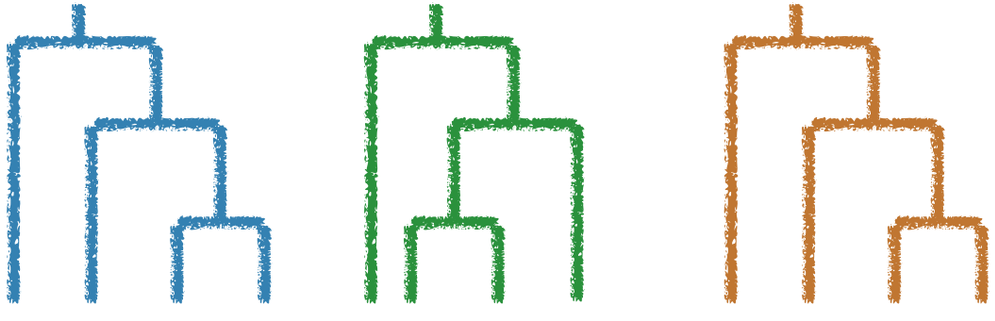
- **ILS**: no AUGT on 4 taxa (Degnan, 2013)
- **ILS**+**HGT**: AUGT on 4 taxa (S.-L., Yang, Ané, 2016, Syst Bio)

See also Long & Kubatko (2018) for AUGT under continuous gene flow between sister species

How?

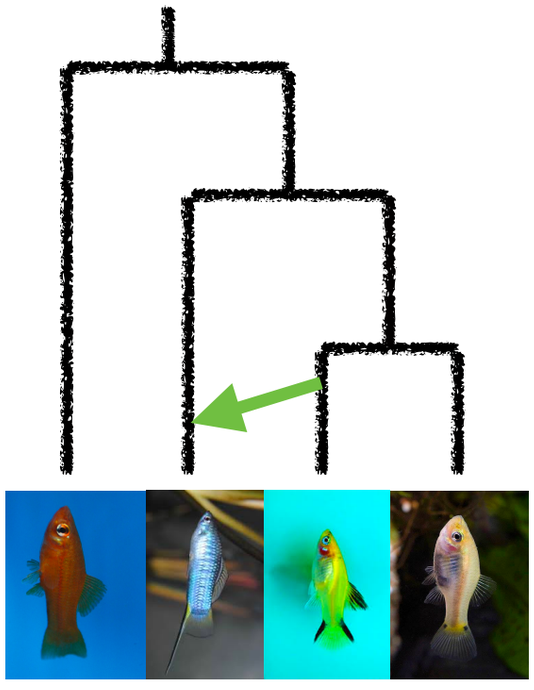
Phylogenetic network

MrBayes
(Huelsenbeck, Ronquist, 2001)
RAxML
(Stamatakis, 2014)
PhyML
(Guindon et al, 2010)



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

BEAST2
(Zhang et al, 2017)
PhyloNet
(Wen et al, 2016)



Multispecies coalescent on a network

(Meng, Kubatko, 2009)
(Yu, Degnan, Nakhleh, 2012)

Multispecies coalescent on a network

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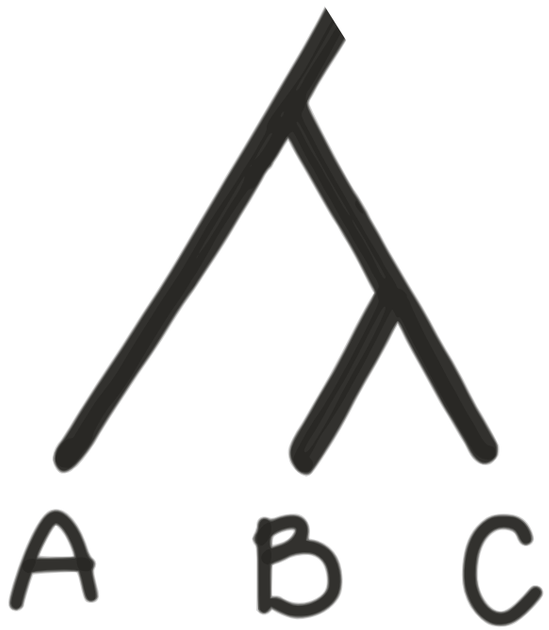
Multispecies coalescent on a network

$$P\left(\quad\right) \mid$$



(Meng, Kubatko, 2009)
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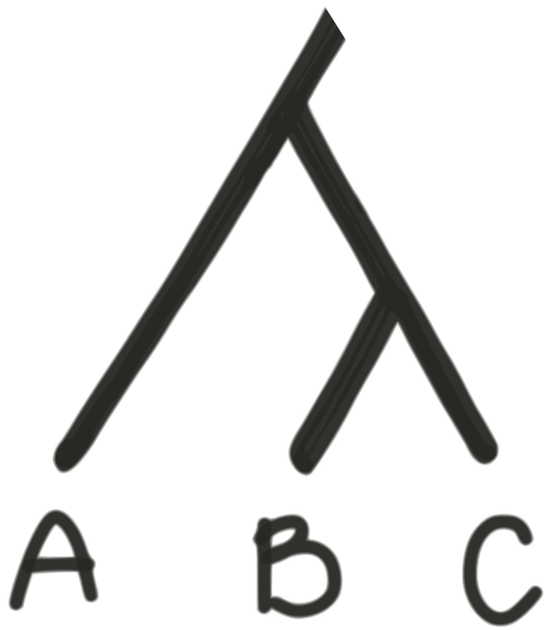
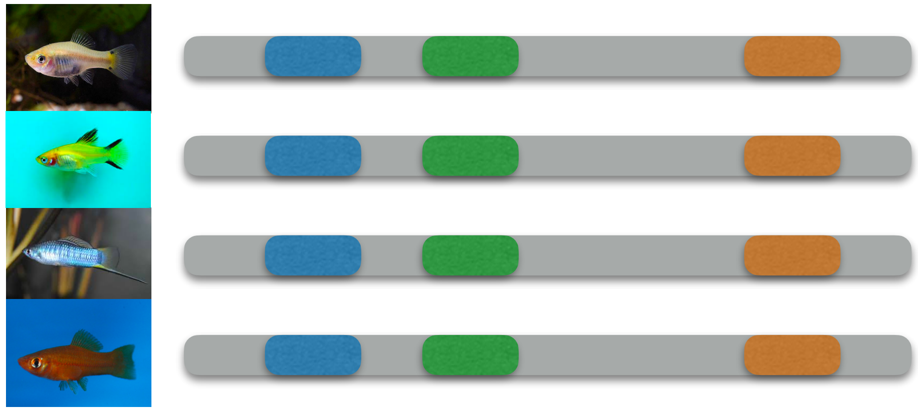
Multispecies coalescent on a network

$P($  $|$  $)$

$$p_{BC|AD}(t, t_2, \gamma) = (1-\gamma)\frac{1}{3}e^{-t} + \gamma(1 - \frac{2}{3}e^{-t_2})$$

(Meng, Kubatko, 2009)
(Yu, Degnan, Nakhleh, 2012)



$$P(N, G, \theta | D) \propto \pi(N)\pi(\theta) \prod_{i=1}^{L} P(D_i|G_i) P(G_i|N)$$

network

gene trees

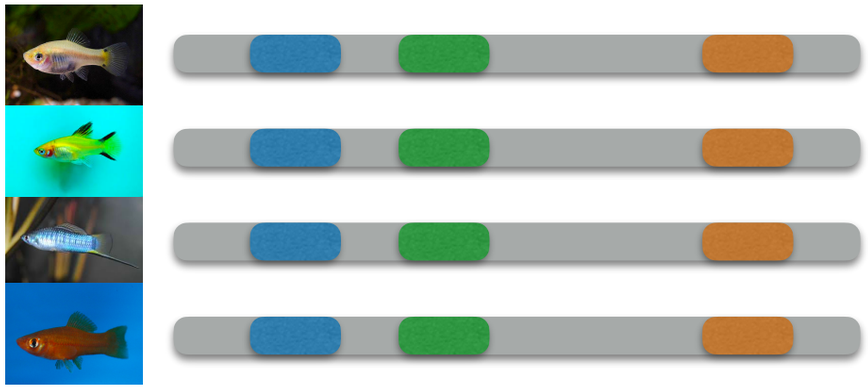
L loci

Prior Network

Substitution Model

Multispecies Coalescent

Birth-hybridization process	BEAST2 (Zhang et al, 2017)
# reticulations, cycle diameter	PhyloNet Bayesian (Wen et al, 2016)



network

$$P(N, G, \theta | D) \propto \pi(N)\pi(\theta) \prod_{i=1}^{L} P(D_i|G_i)P(G_i|N)$$

gene trees | L loci | Prior Network | Substitution Model | Multispecies Coalescent

Birth-hybridization process

reticulations, cycle diameter

BEAST2
(Zhang et al, 2017)

PhyloNet Bayesian
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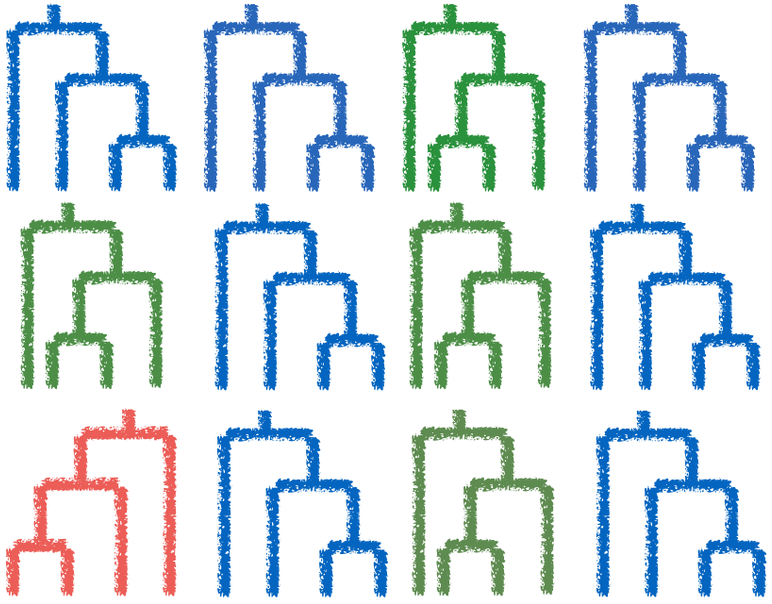
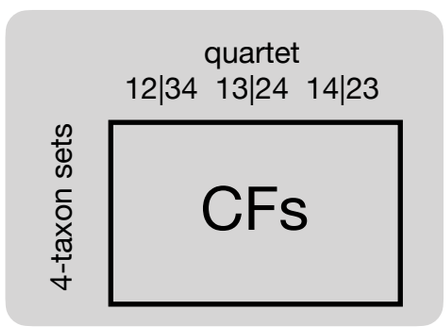


$$P(N, \theta | G) \propto \pi(N)\pi(\theta) \prod_{i=1}^{L} P(G_i|N, \theta)$$

PhyloNet Bayesian
(Wen et al, 2016)

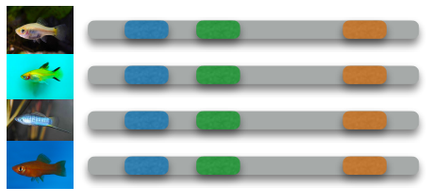
$$L(N, \theta) = \prod_{i=1}^{L} P(G_i|N, \theta)$$

PhyloNet Likelihood
(Yu et al, 2014)



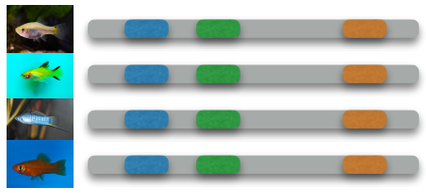
$$\tilde{L}(N, \theta) \propto \prod_{q} L(q|N, \theta)$$

SNaQ
(S.-L., Ane, 2016)



BEAST2
(Zhang et al, 2017)

Birth-hybridization process

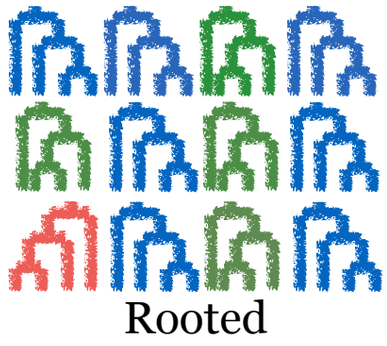


PhyloNet Bayesian
(Wen et al, 2016)

reticulations, cycle diameter

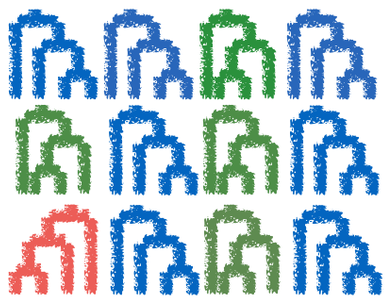
MCMC: Network moves, mixing

Most accurate, not scalable



Rooted

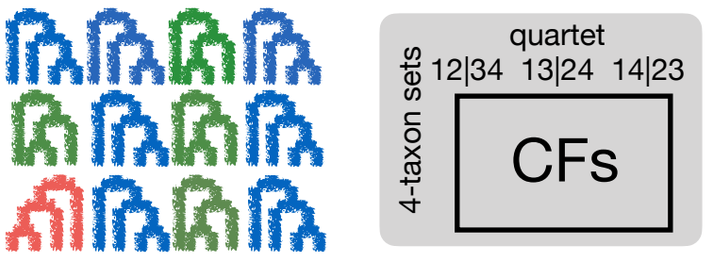
PhyloNet Bayesian
(Wen et al, 2016)



Rooted

PhyloNet Likelihood
(Yu et al, 2014)

Heuristic search: Network moves



Unrooted

SNaQ
(S.-L., Ane, 2016)

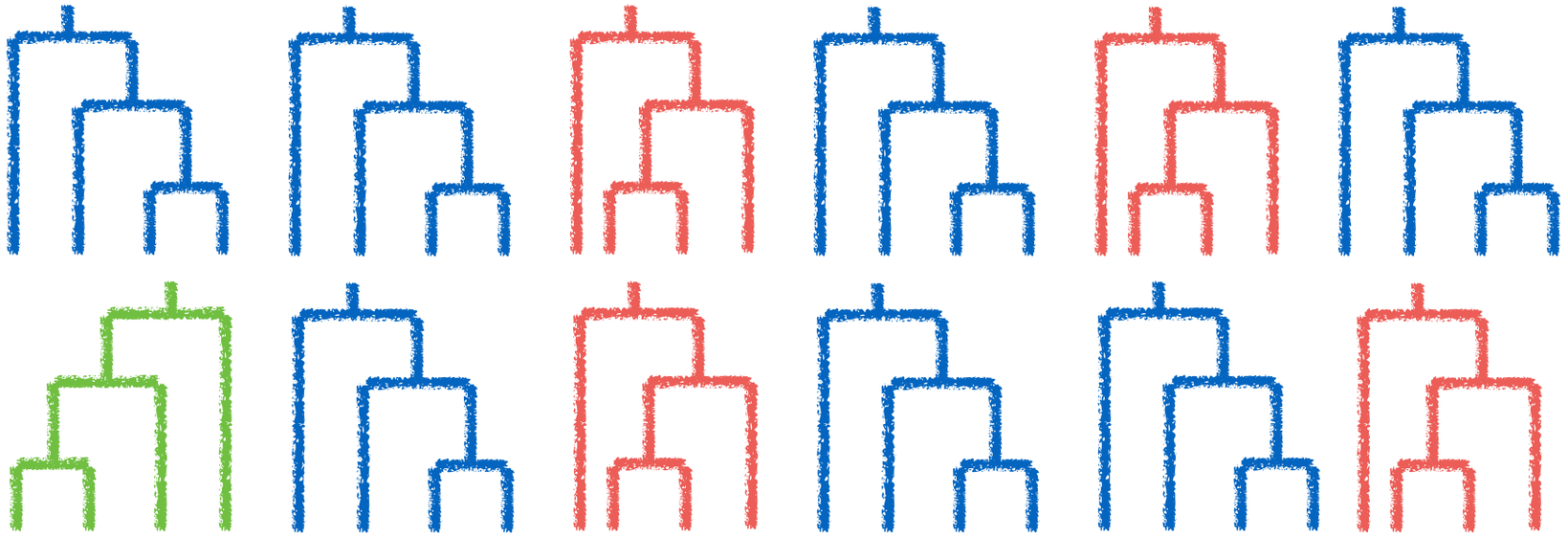
Level-1 networks

More scalable, Robust

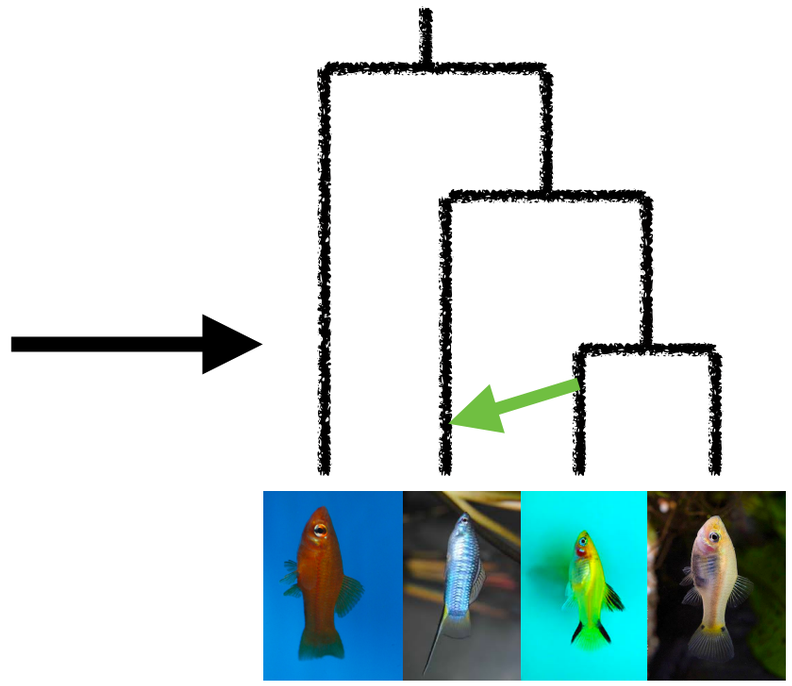
STEM-hy	gene trees rooted, BL	likelihood	hybridization b/w sister lineages
PhyloNet `InferNetwork_ML`	gene trees rooted	likelihood	
PhyloNet `InferNetwork_MPL`	gene trees rooted	triplet likelihood	
PhyloNetworks `SNaQ`	gene trees or quartet CFs	quartet likelihood	level-1 network
PhyloNet `MCMC_GT`	gene trees rooted	Bayesian	compound prior
PhyloNet `MCMC_SEQ`	alignments	Bayesian	compound prior no rate variation
BEAST2 `SpeciesNetwork`	alignments	Bayesian	birth-hyb prior
PhyloNet `MLE_BiMarkers`	biallelic sites	likelihood	compound prior
PhyloNet `MCMC_BiMarkers`	biallelic sites	Bayesian	compound prior
HyDe	sites	invariants	4 taxa, 1 hyb.

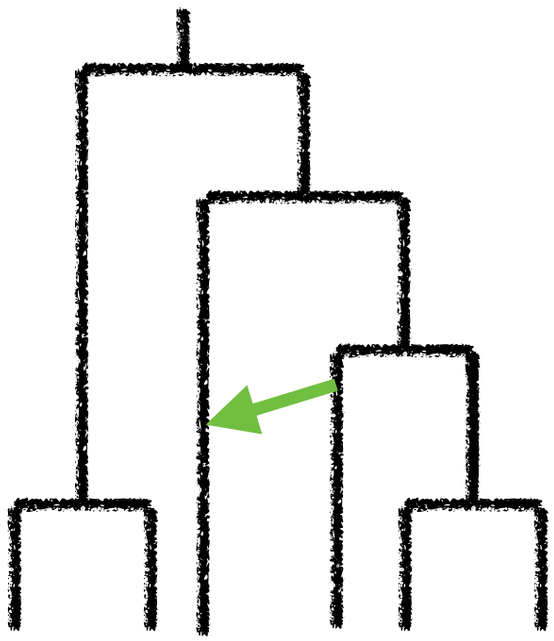
Slide by Cecile Ane

Maximum **pseudo**likelihood



Data





Quartet-based inference

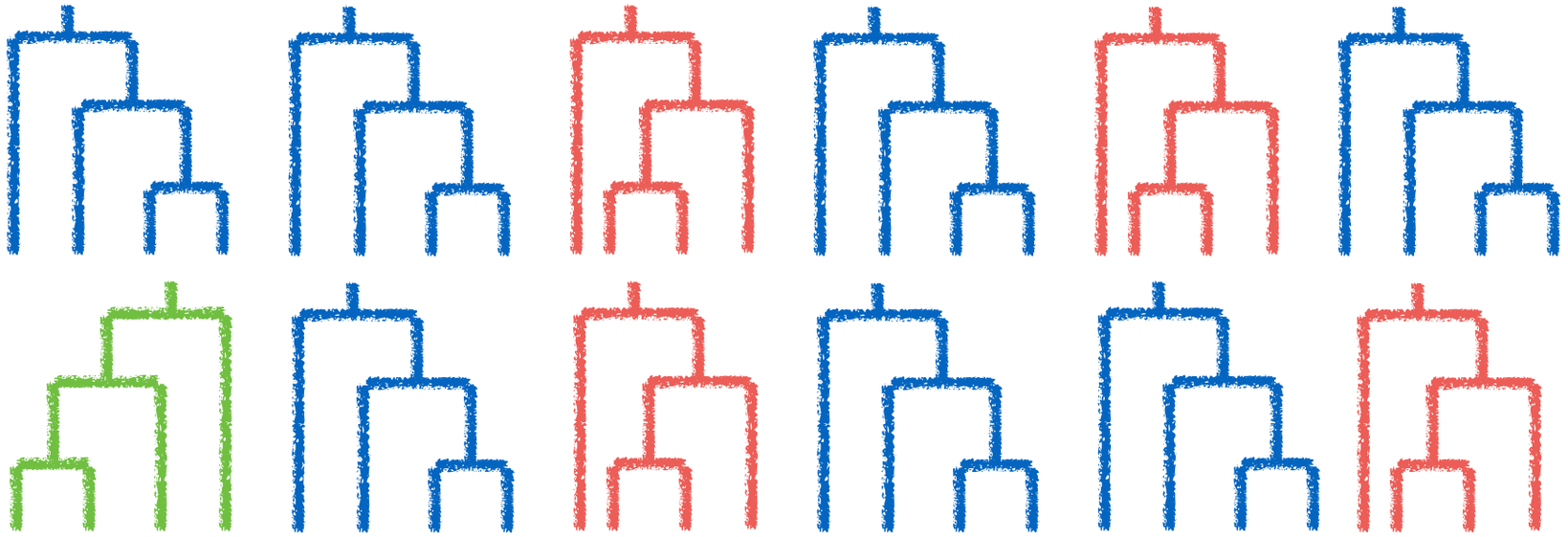
$$\tilde{L}(network) = \prod L(quartet)$$

(S-L, Ané, 2016, PLoS Genetics)

`www.github.com/CRSL4/PhyloNetworks`

https://solislemuslab.github.io/ @solislemuslab crsl4

Maximum **pseudo**likelihood



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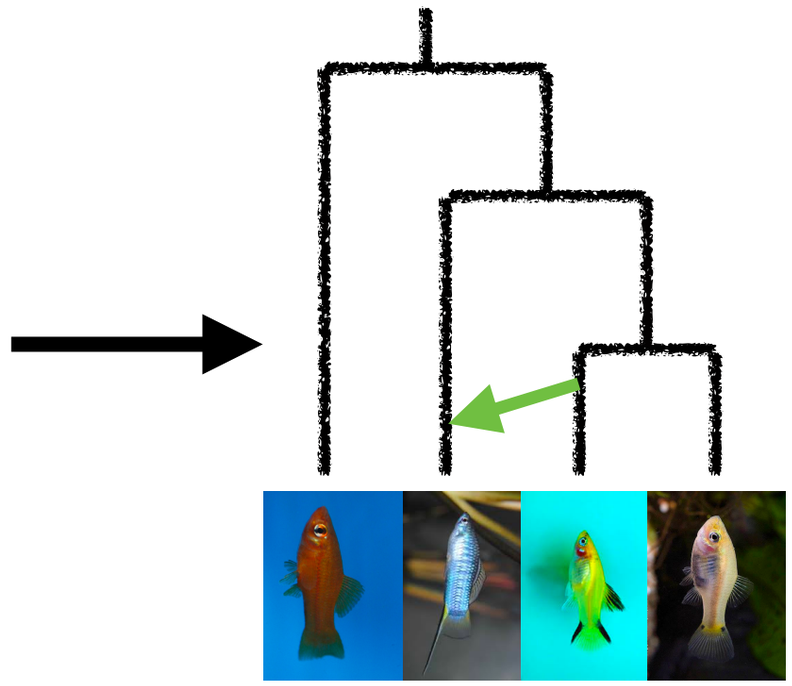

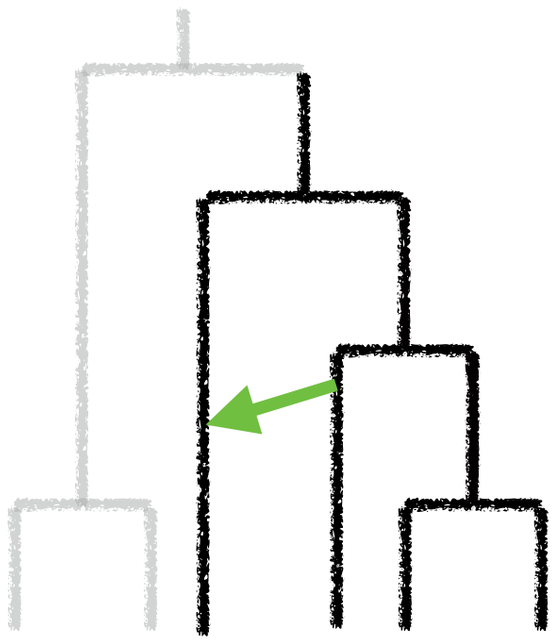

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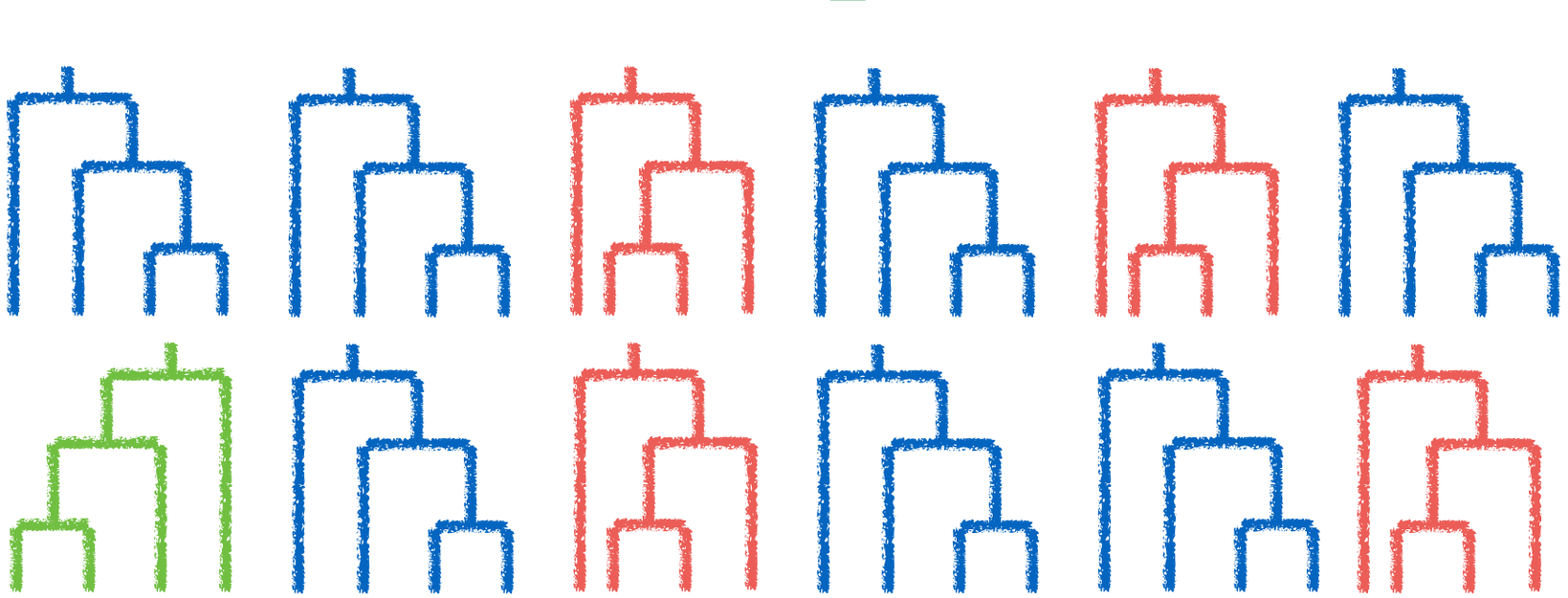
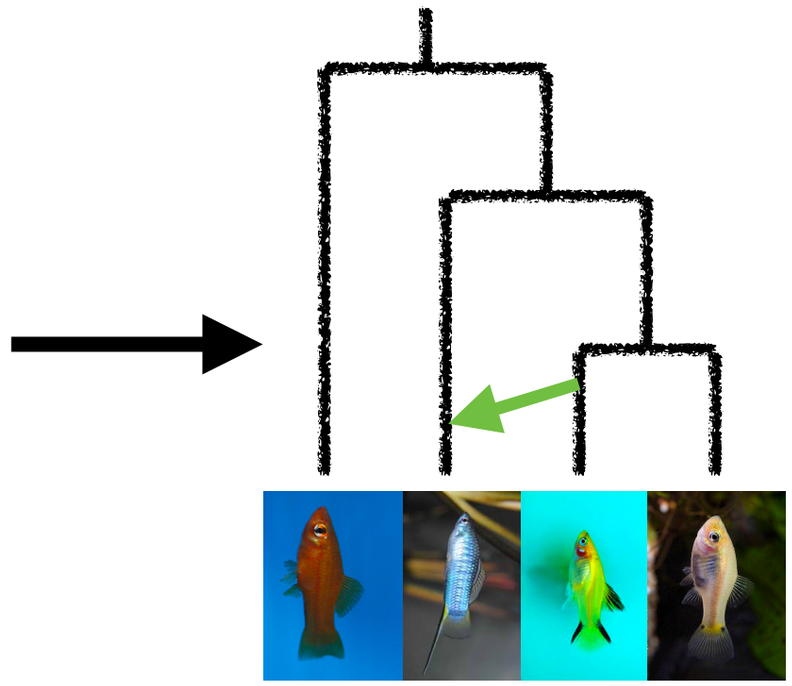
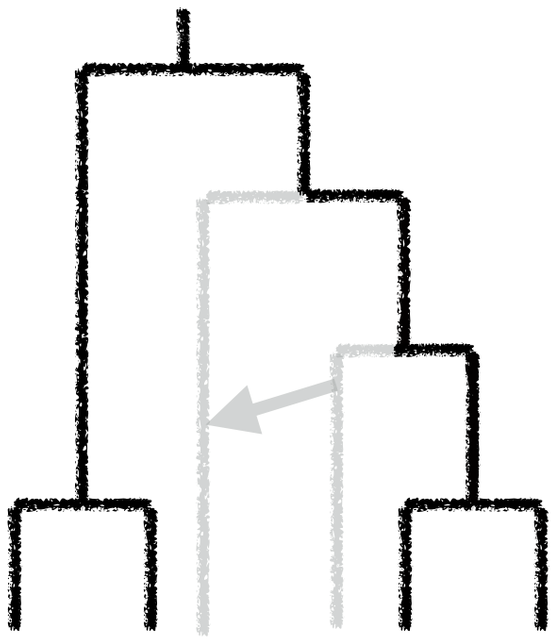


Data





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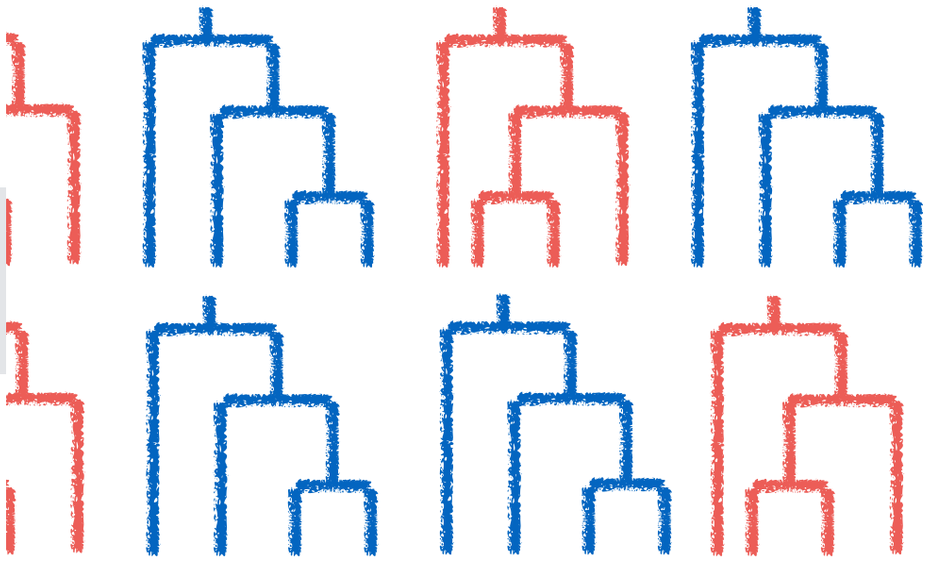
`www.github.com/CRSL4/PhyloNetworks`

SNAQ julia

https://solislemuslab.github.io/ @solislemuslab crsl4

Maximum **pseudo**likelihood

Unrooted gene trees	No rooting error
No branch lengths	No molecular clock assumption
Concordance factors	Account for tree estimation error



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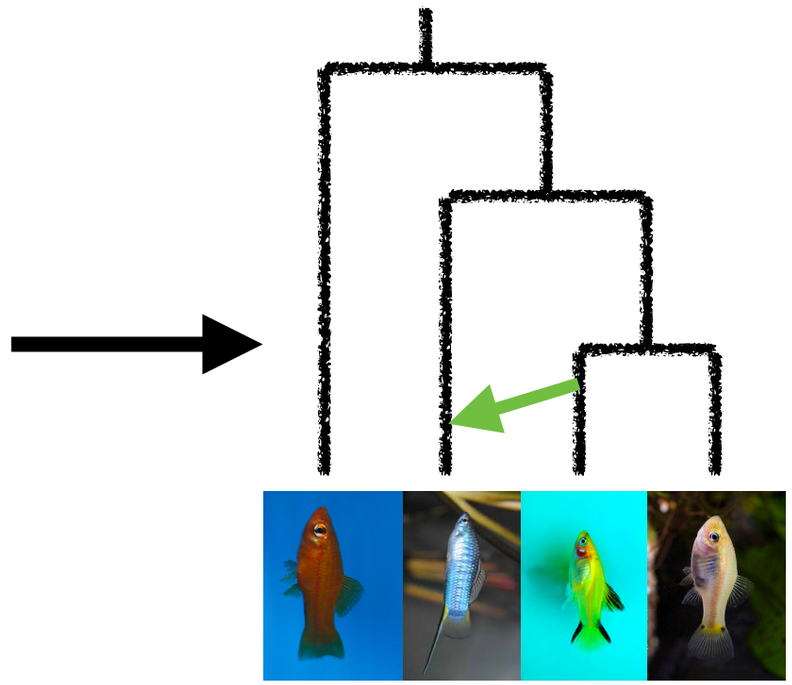

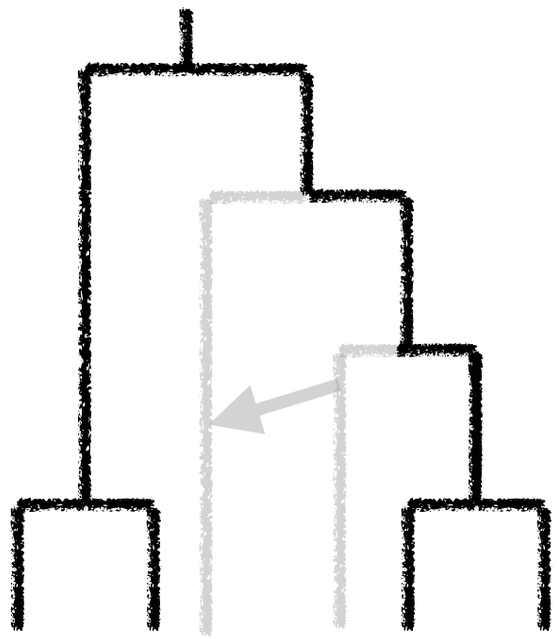

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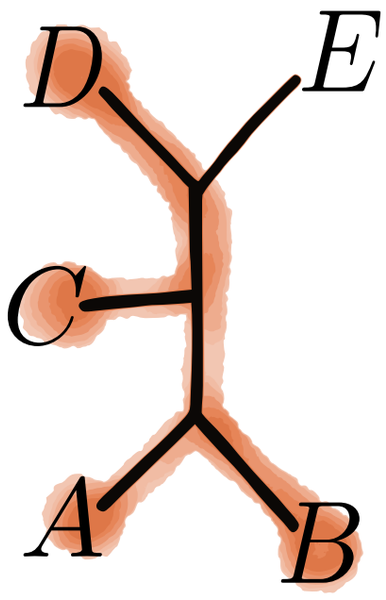
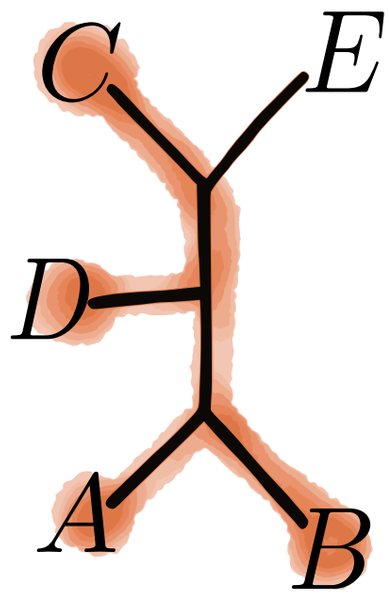
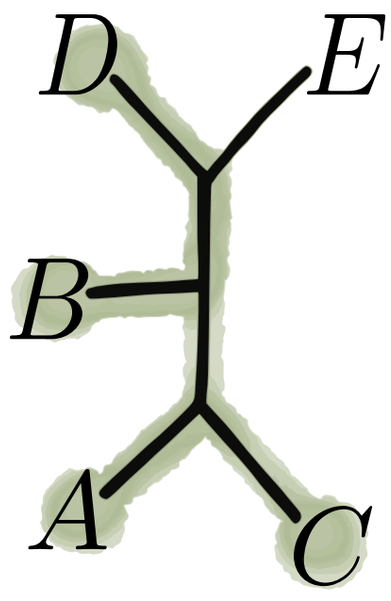
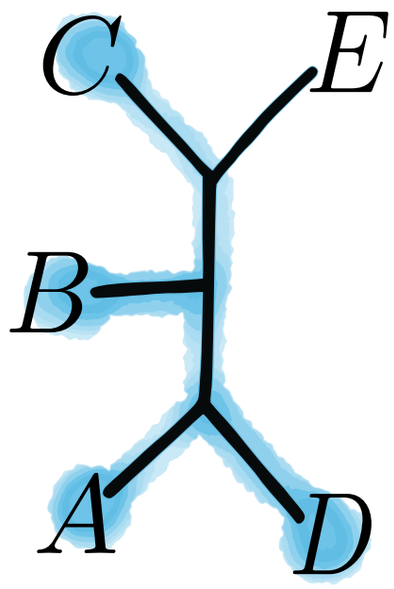
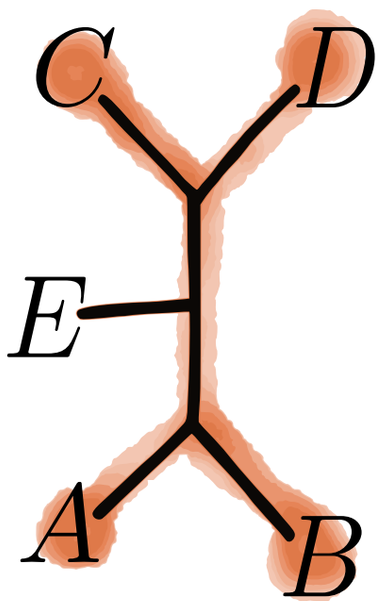


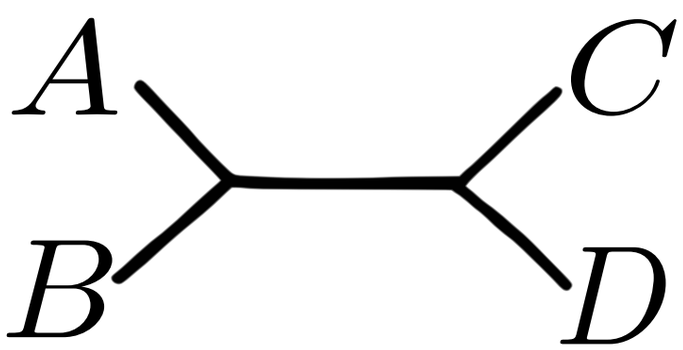




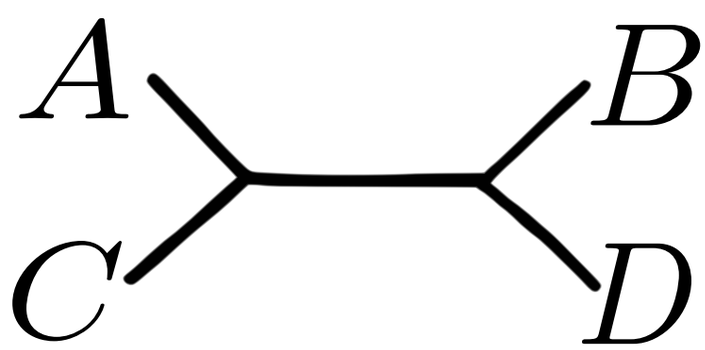




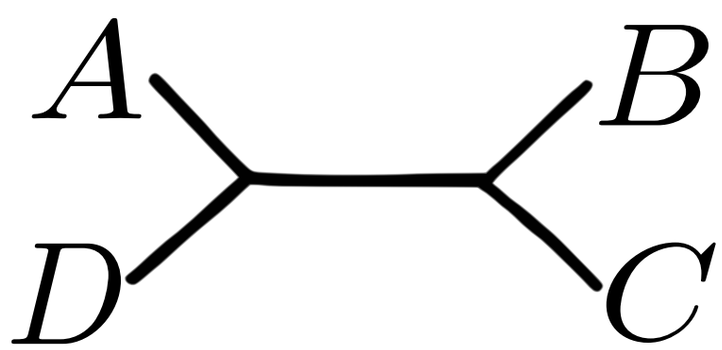
Concordance factors (CF):
% of genes having the quartet in their tree



3/5



1/5



1/5

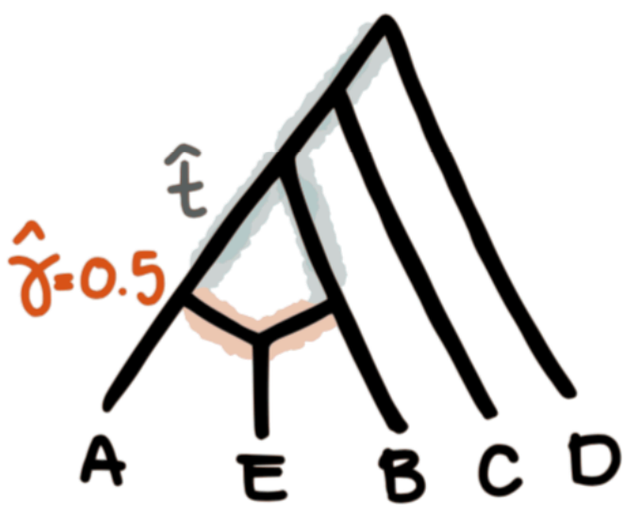
Quartet-based inference

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

$\longrightarrow$

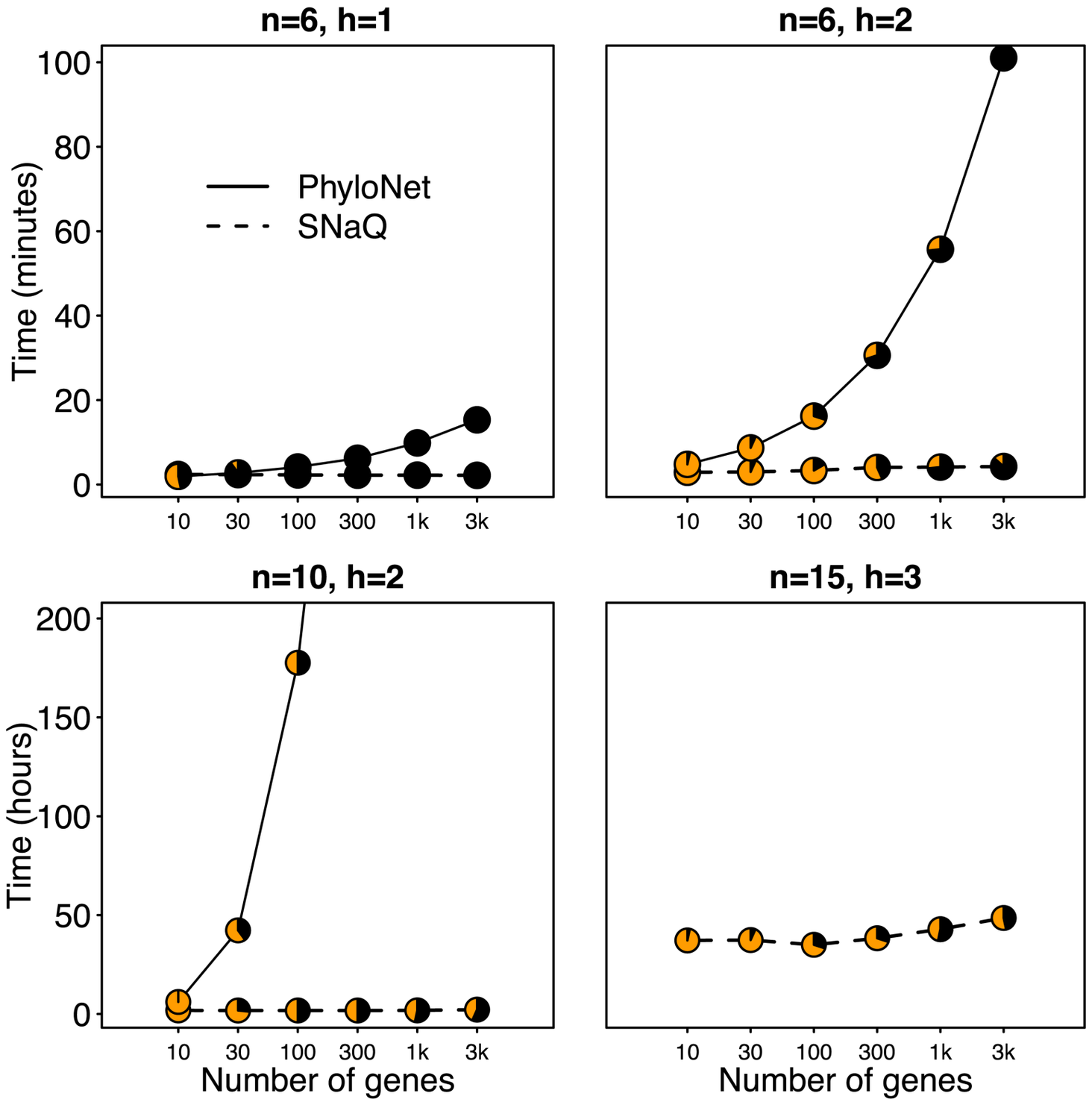
inferred network:



Maximum Pseudo-Likelihood:

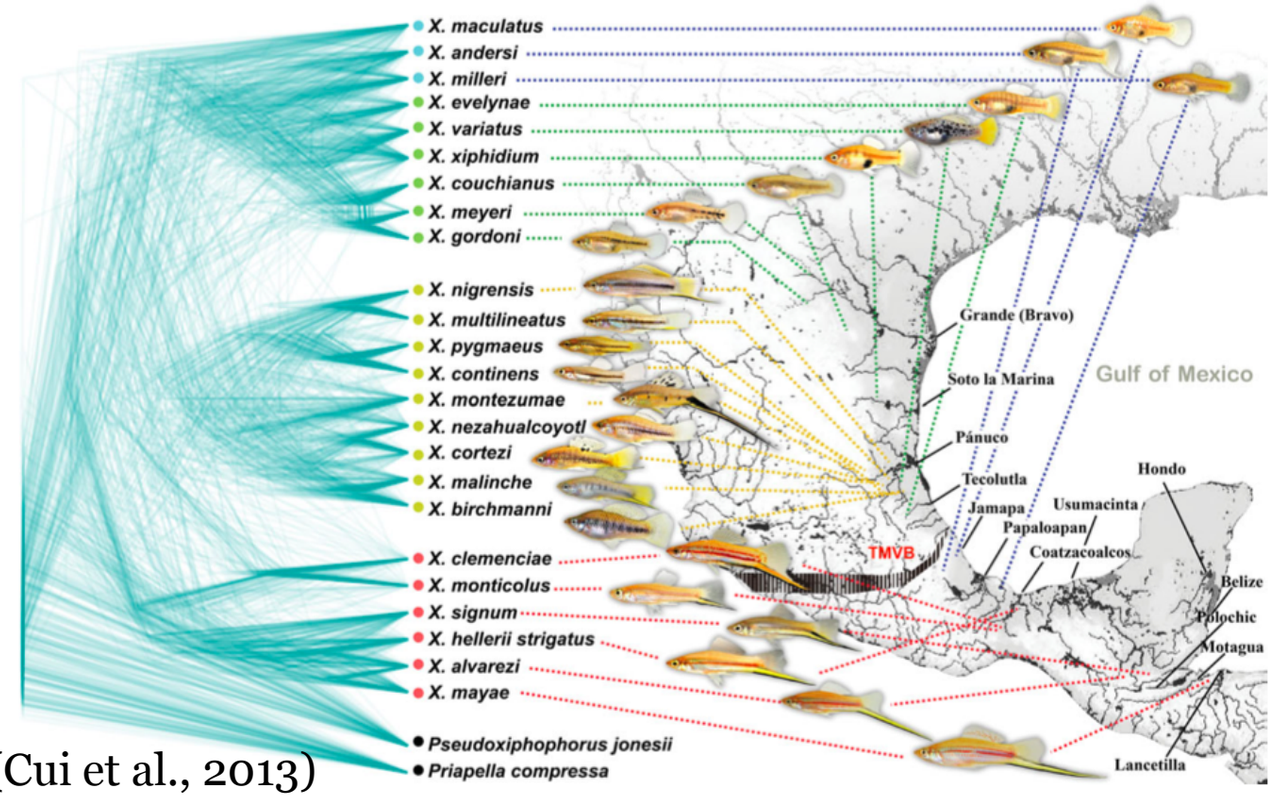
$$\log \tilde{L} = \sum_{q \in Q(N)} \mathrm{CF}_{in,1} \log(\mathrm{CF}_{net,1}) + \mathrm{CF}_{in,2} \log(\mathrm{CF}_{net,2}) + \mathrm{CF}_{in,3} \log(\mathrm{CF}_{net,3})$$

Scalability gains



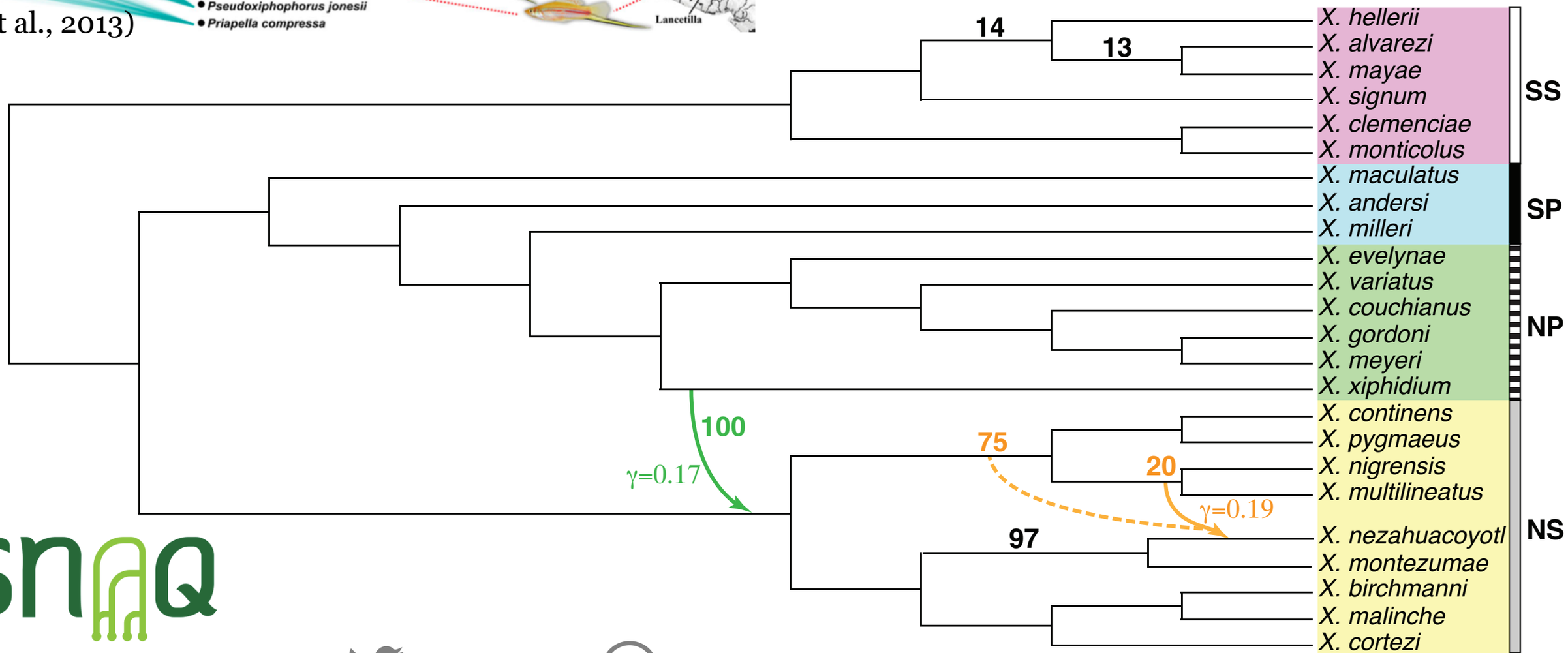
(Solís-Lemus, Ané, 2016, PLoS Genetics)

1183 genes, 24 swordtails and platyfish



(Cui et al., 2013)

Xiphophorus fish data



snaq

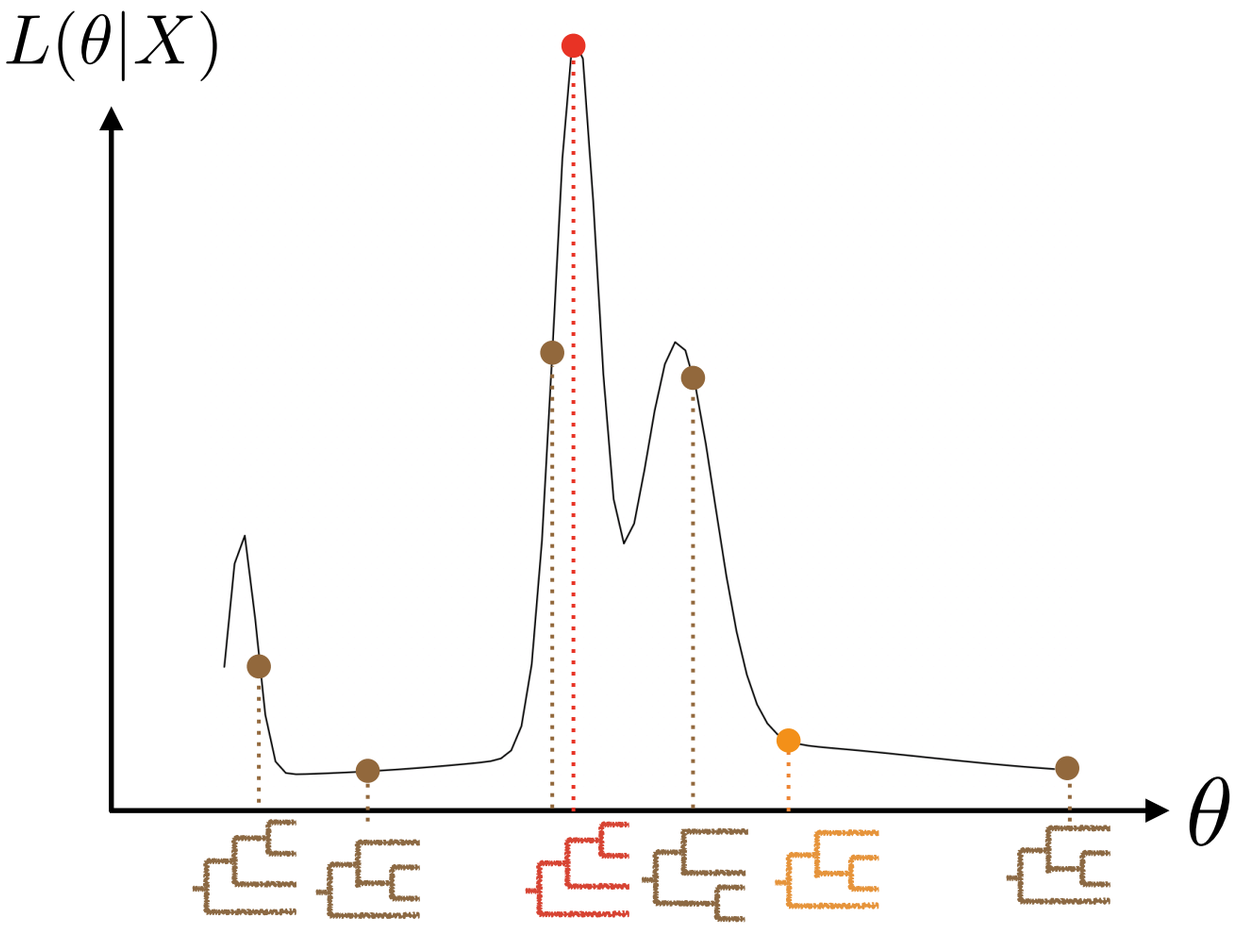
http://solislemuslab.github.io/ @solislemuslab crsl4

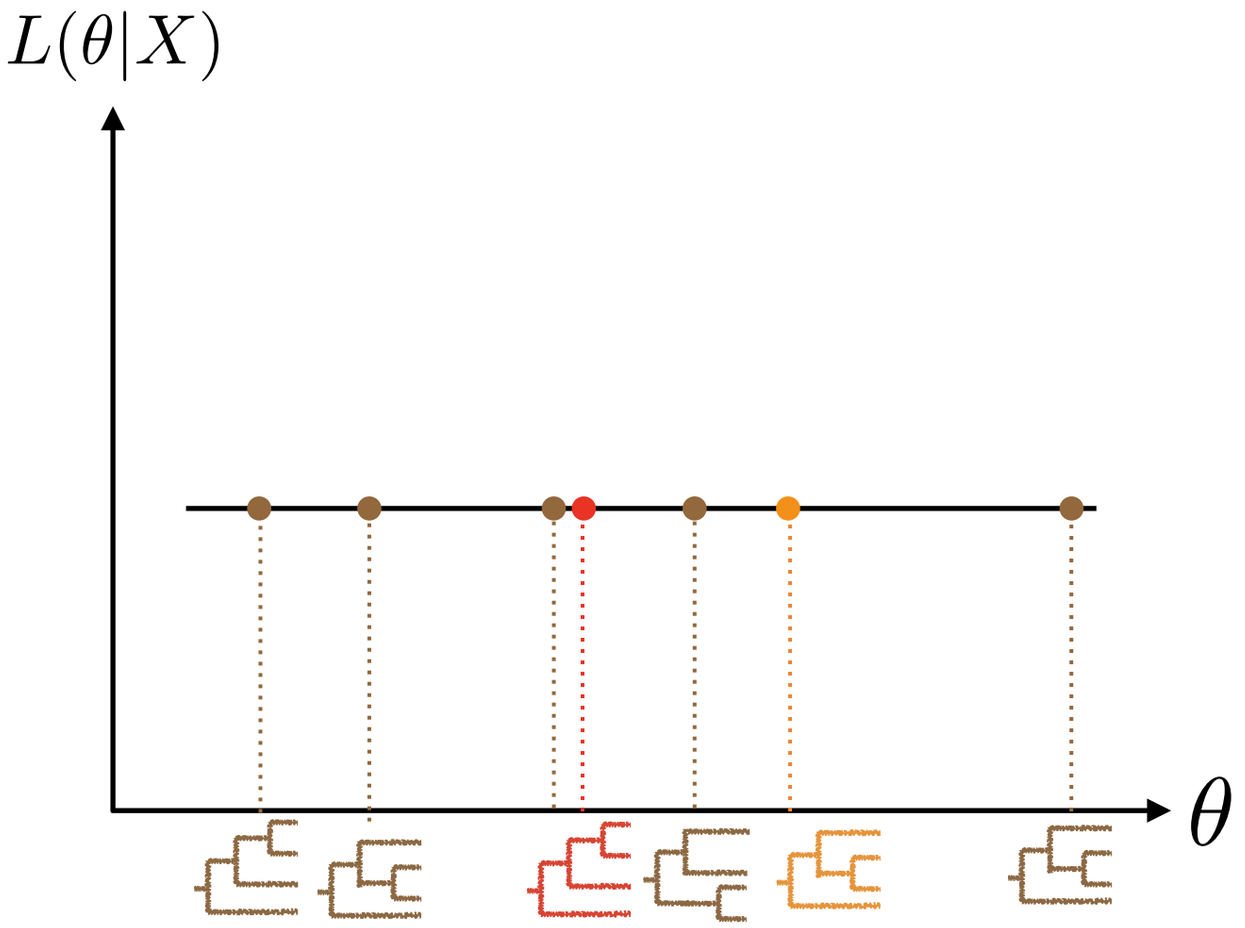
(Solís-Lemus, Ané, 2016, PLoS Genetics)

Challenges

- Network space
- Identifiability
- Network comparison

Identifiability





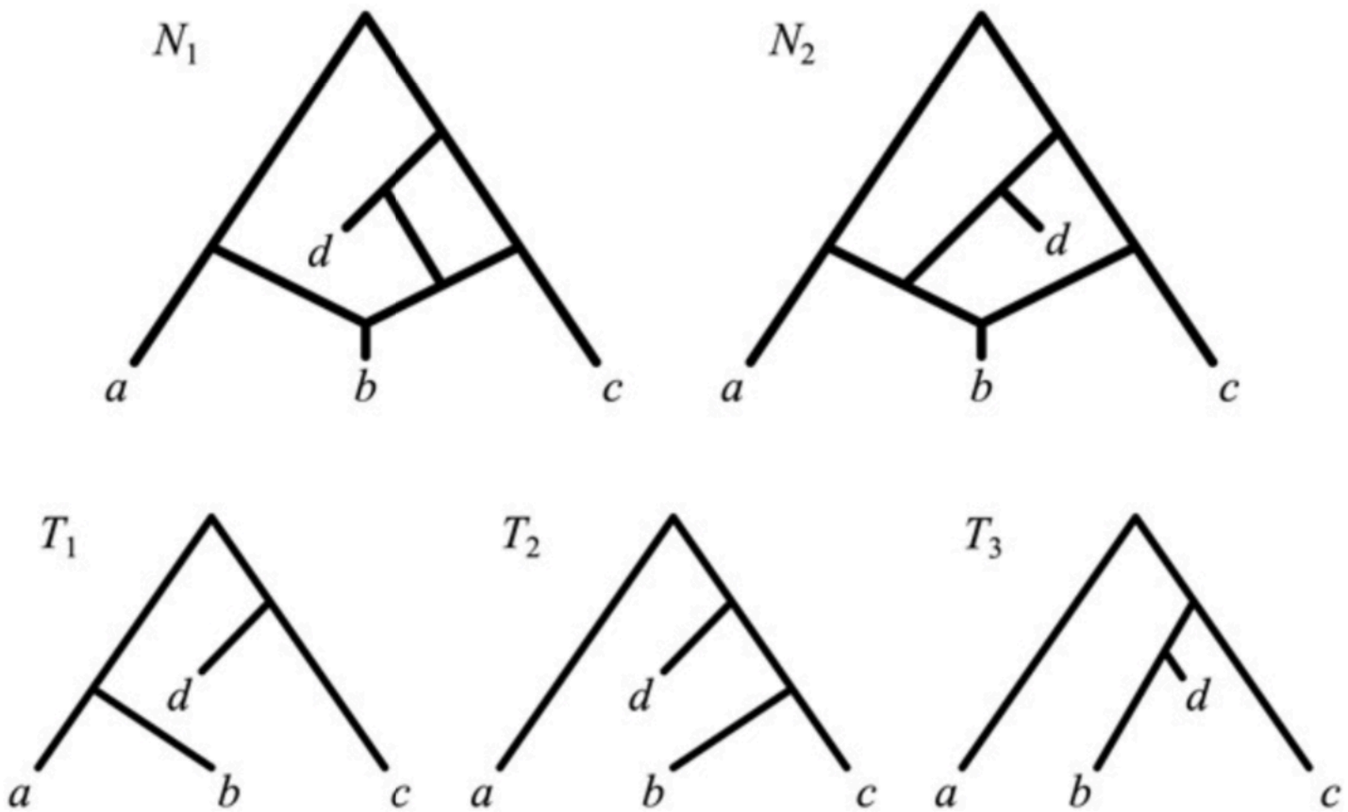
PLOS | COMPUTATIONAL BIOLOGY

RESEARCH ARTICLE

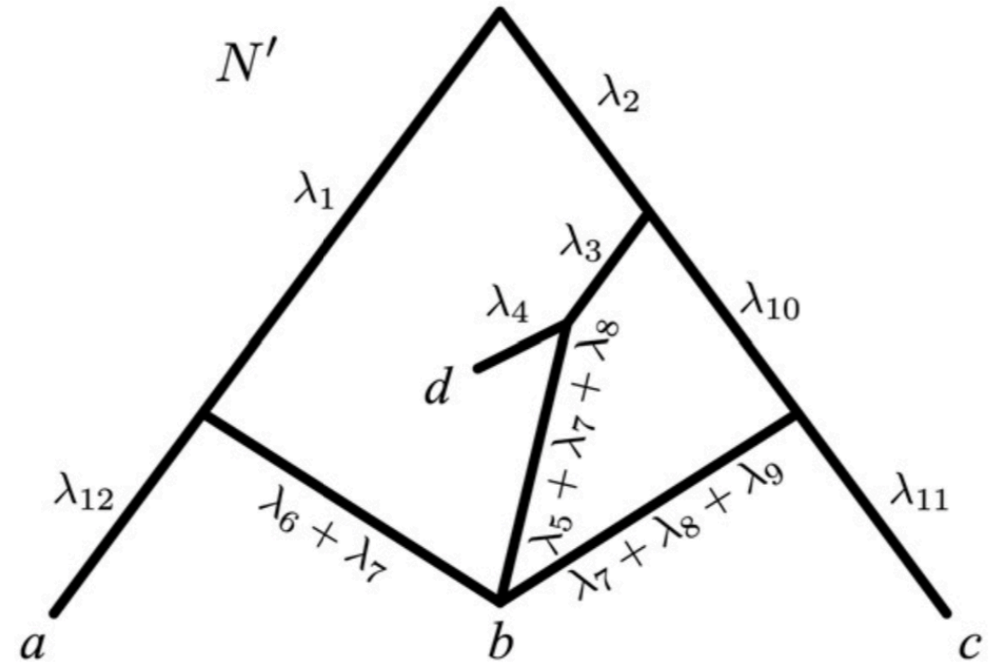
Reconstructible Phylogenetic Networks: Do Not Distinguish the Indistinguishable

Fabio Pardi[1,3]*, **Celine Scornavacca**[2,3]

1 Laboratoire d'Informatique, de Robotique et de Microélectronique de Montpellier (LIRMM, UMR 5506) CNRS, Université de Montpellier, France, **2** Institut des Sciences de l'Evolution de Montpellier (ISE-M, UMR 5554) CNRS, IRD, Université de Montpellier, France, **3** Institut de Biologie Computationnelle, Montpellier, France



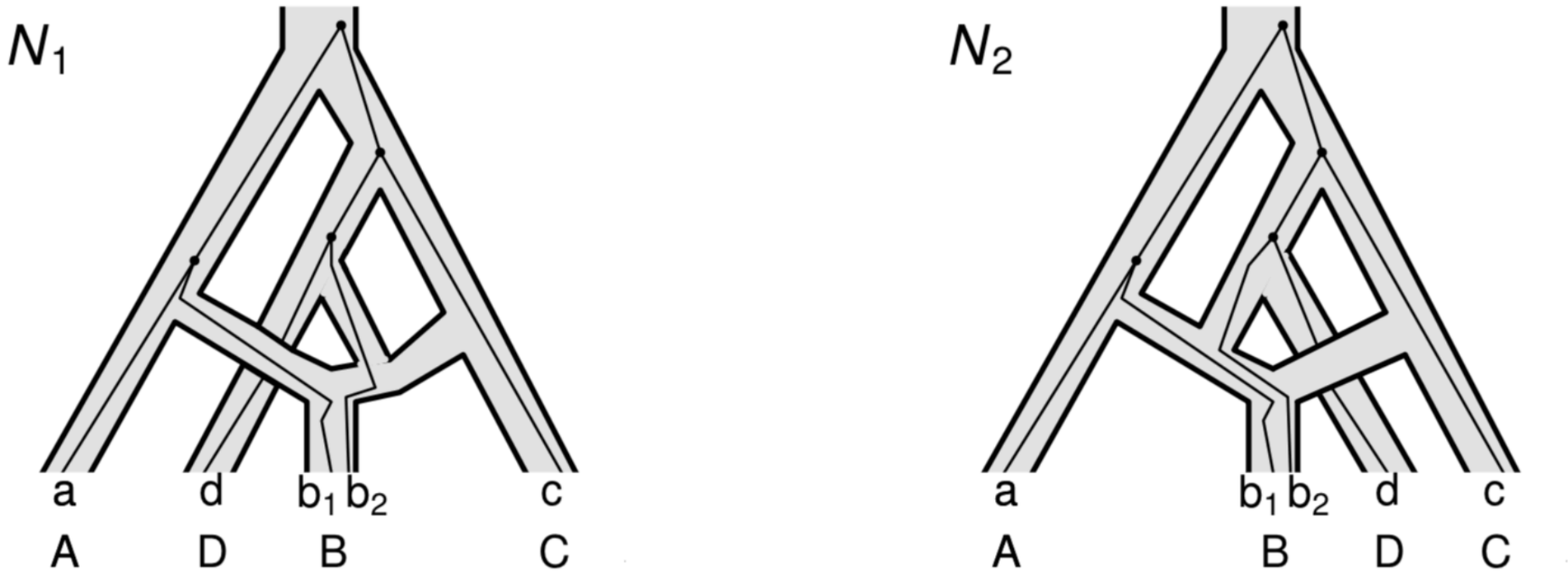
Undistinguishable with the "displayed trees" criterion



Solution: Canonical network ("unzipped")

Displayed Trees Do Not Determine Distinguishability Under the Network Multispecies Coalescent

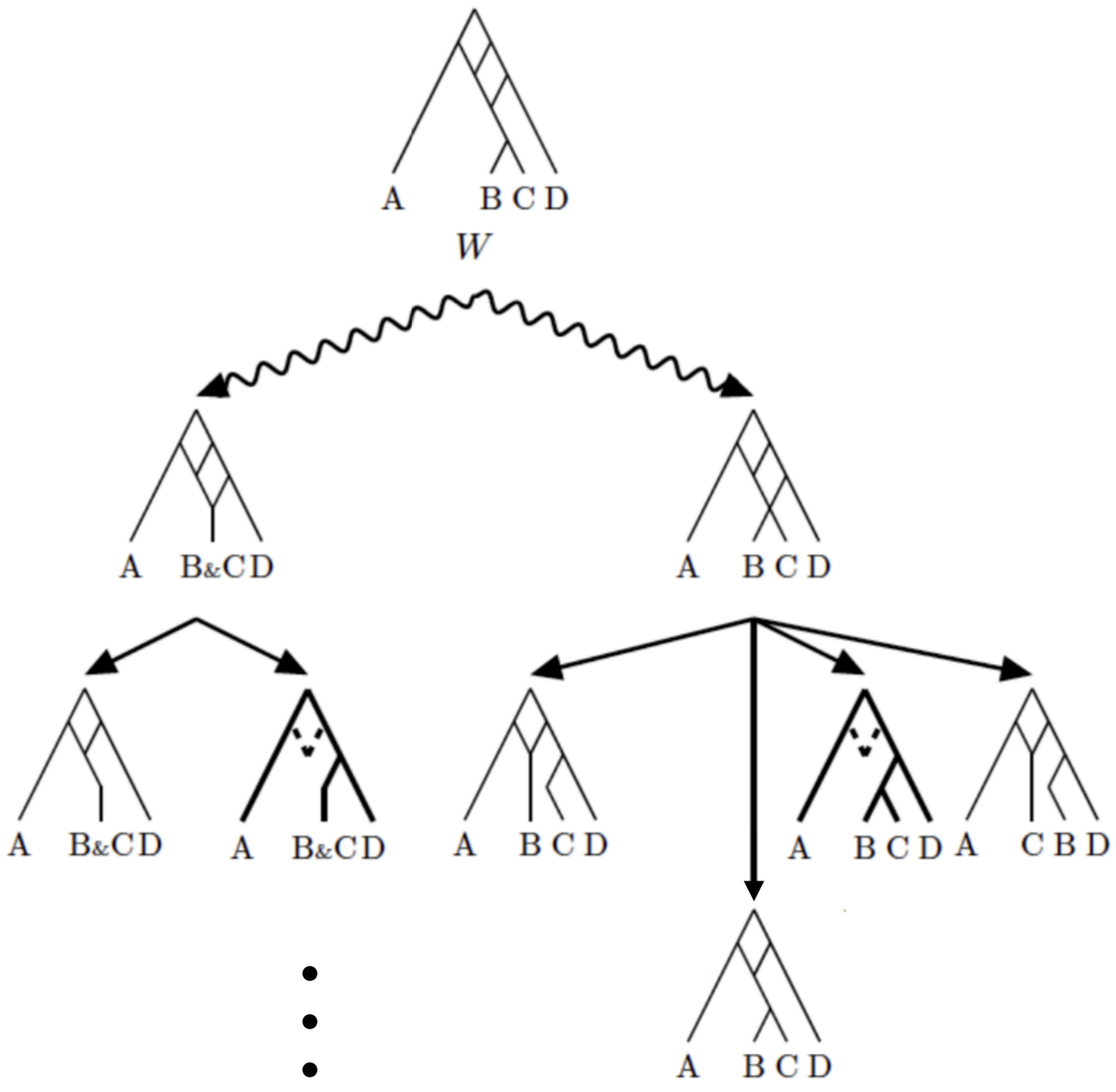
Sha Zhu[1], James H. Degnan[2]



Distinguishable under the MSC

Displayed Trees Do Not Determine Distinguishability Under the Network Multispecies Coalescent

Sha Zhu[1], James H. Degnan[2]



Decomposing network in **parental** trees

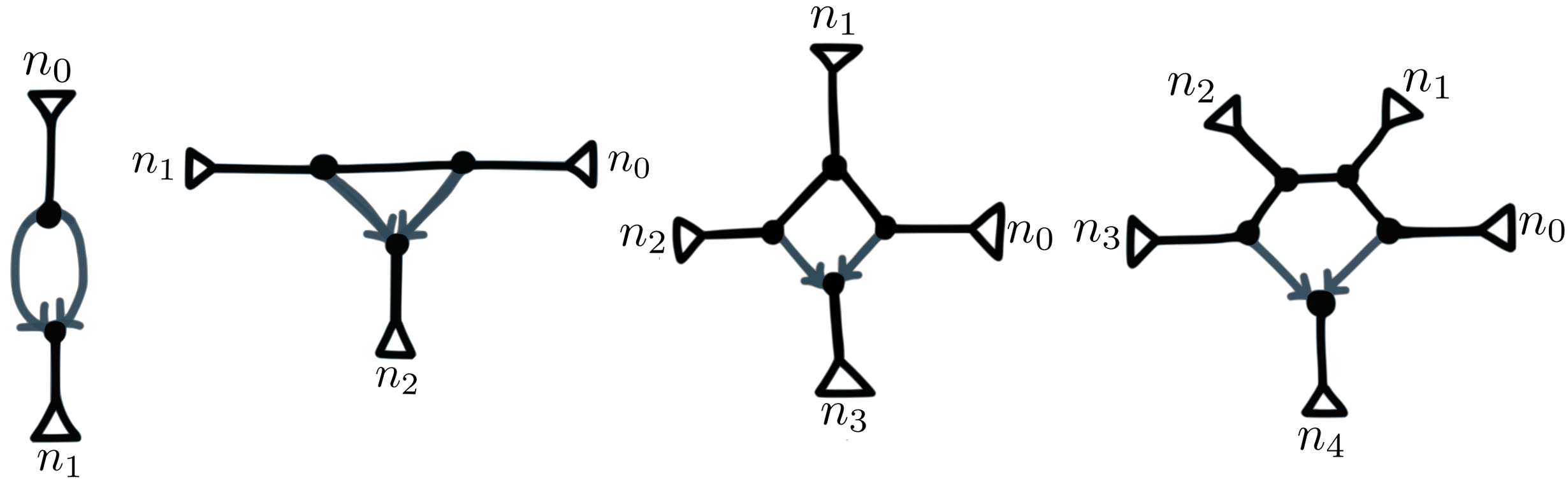
PLOS | GENETICS

RESEARCH ARTICLE

Inferring Phylogenetic Networks with Maximum Pseudolikelihood under Incomplete Lineage Sorting

Claudia Solís-Lemus[1]*, Cécile Ané[1,2]

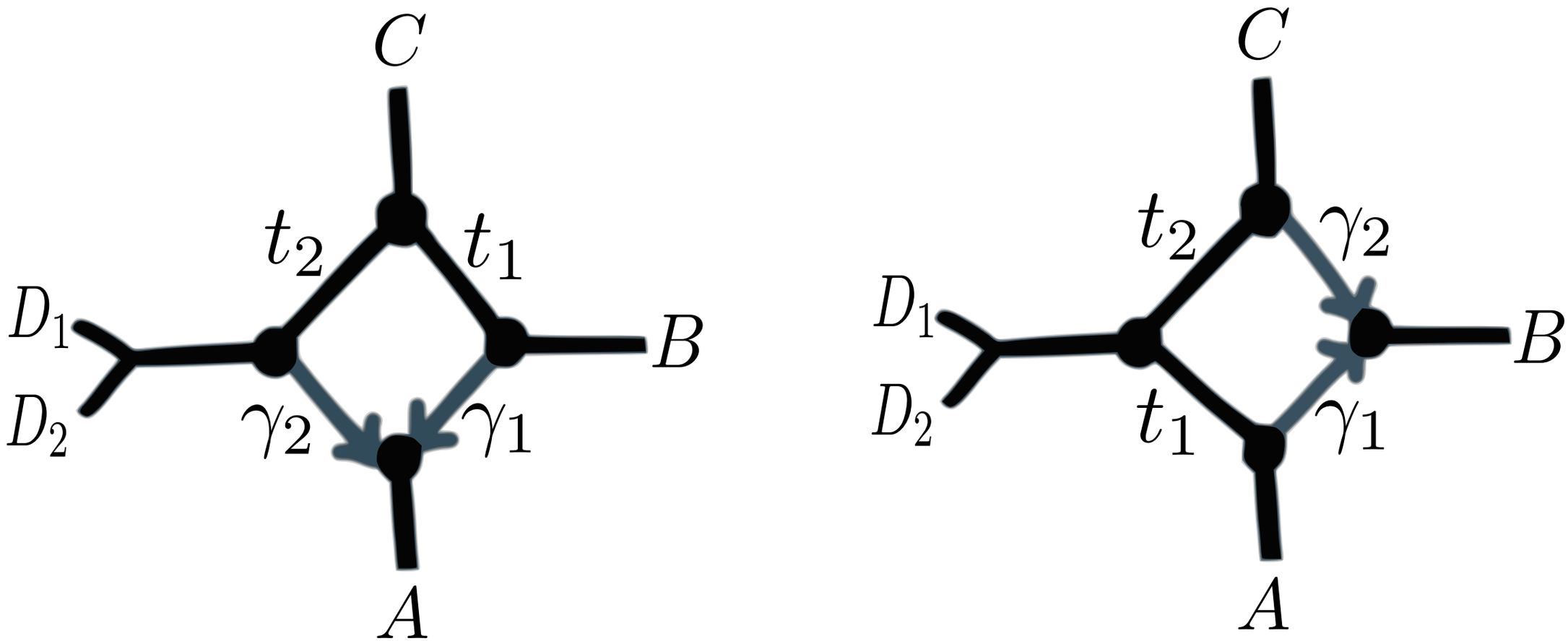
Can we detect the presence of hybridization in level-1 networks?



No **Yes** $(n_i, n_j \geq 2)$ **Yes** $(n_i \geq 2)$ **Yes**

Generic Identifiability $t_i \in (0, \infty), \gamma \in (0, 1)$

In practice: flat pseudolikelihood



(S.-L., Ané, 2016, PLoS Genetics)

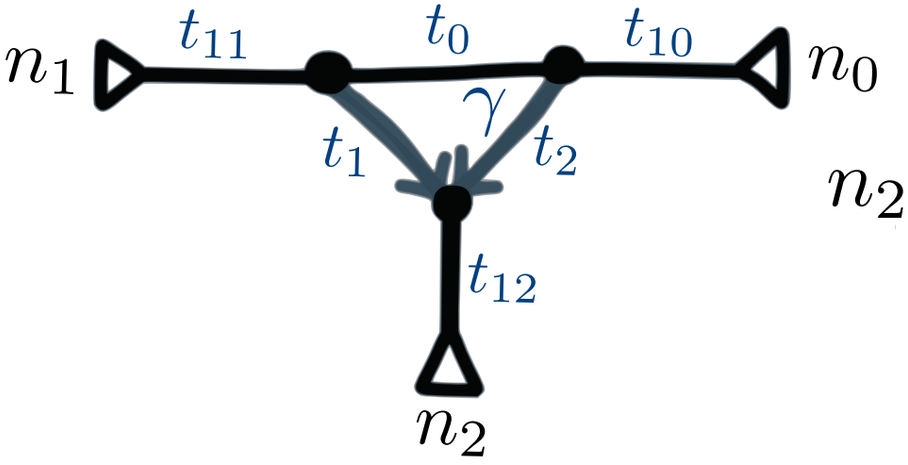
PLOS | GENETICS

RESEARCH ARTICLE

Inferring Phylogenetic Networks with Maximum Pseudolikelihood under Incomplete Lineage Sorting

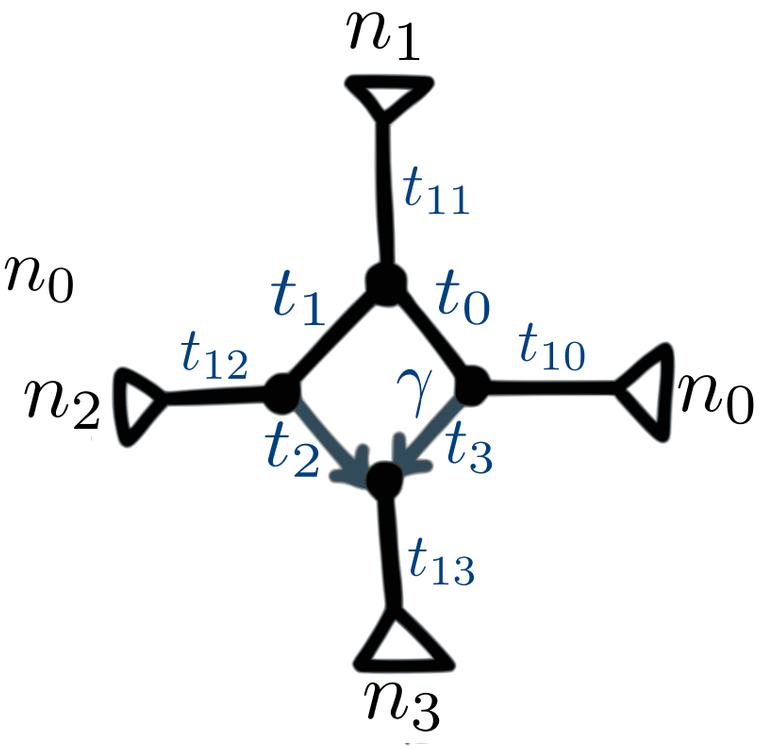
Claudia Solís-Lemus[1]*, Cécile Ané[1,2]

Can we estimate numerical parameters?



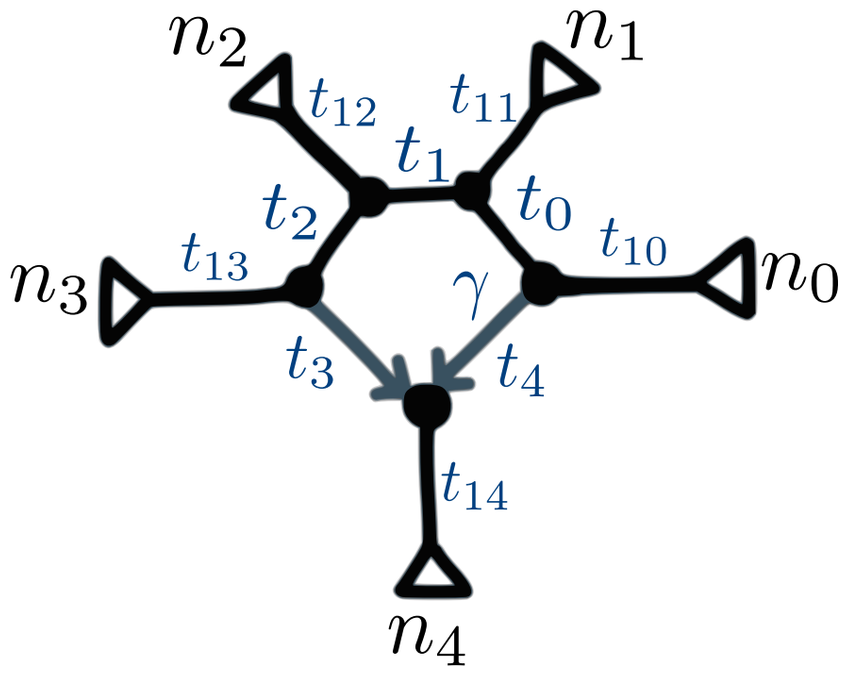
No

Good triangle
$(t_{12} = 0)$



Yes

Good diamond
$(n_0, n_2 \geq 2)$

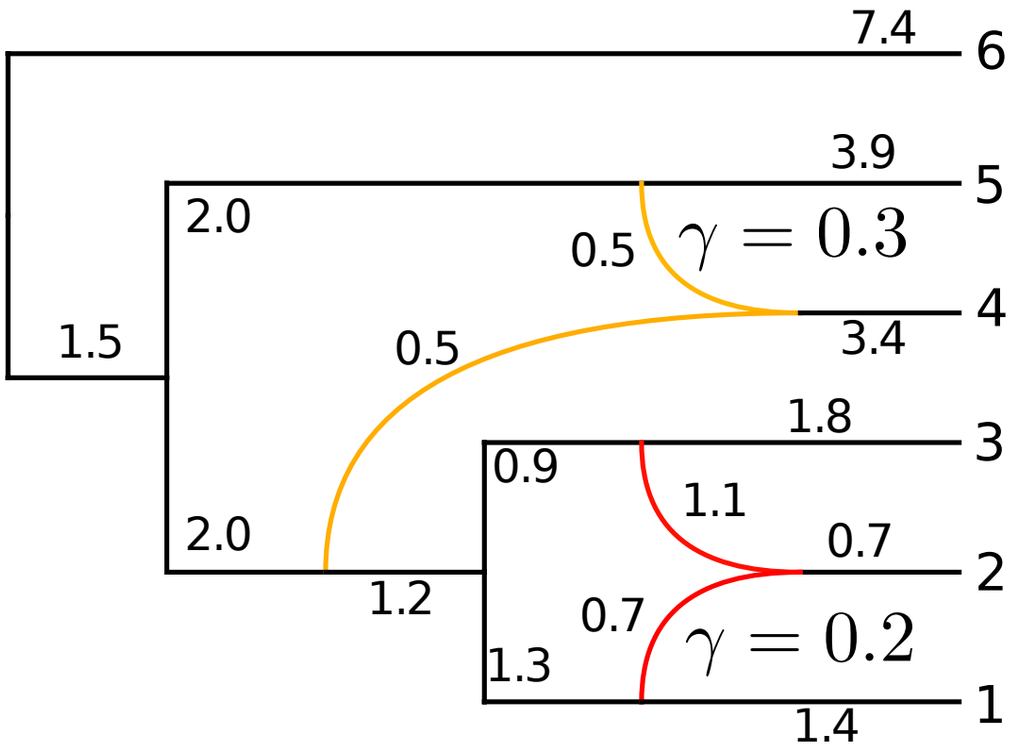


Yes

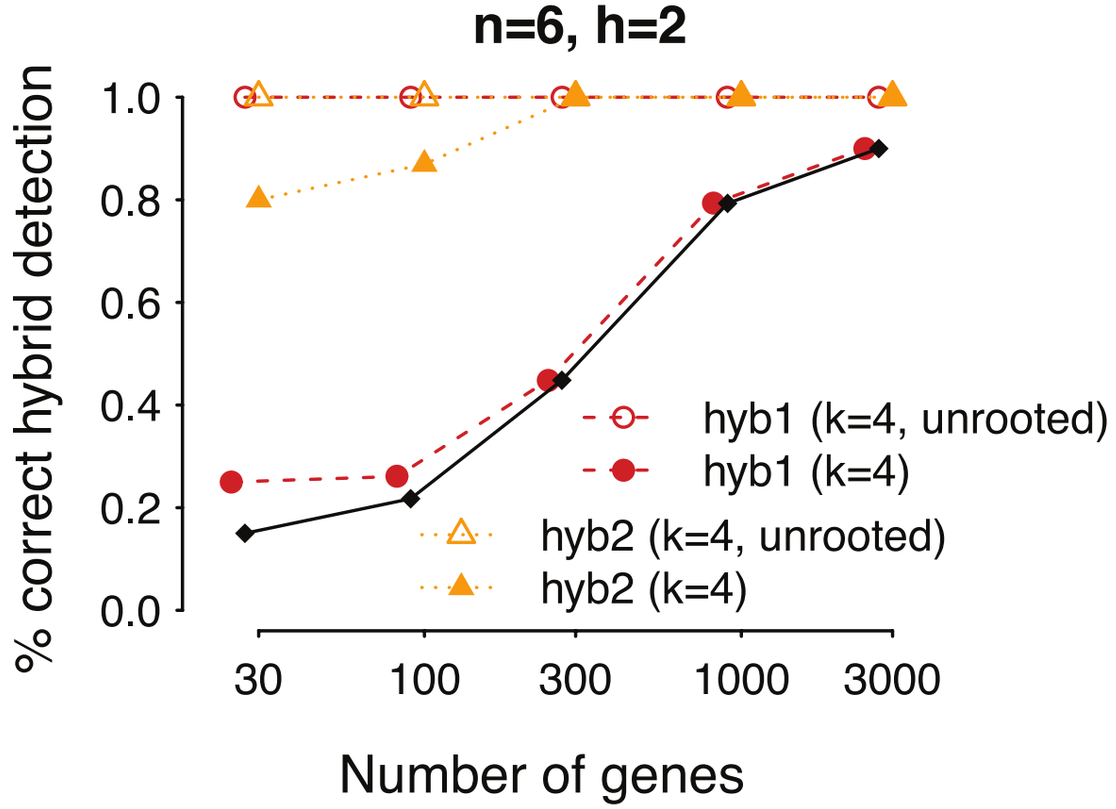
Generic Identifiability $t_i \in (0, \infty), \gamma \in (0, 1)$

Identifiability matters: SNaQ performance

Good diamond



Bad diamond



(S.-L., Ané, 2016, PLoS Genetics)

Challenges

- Network space
- Identifiability

Displayed vs Parental trees
Level-1 semi-directed networks
Hybridizations: case by case
Missing: likelihood, level-k semi-directed

- Network comparison

Challenges

- Network space

K. Huber, V. Moulton, C. Scornavacca,…
Missing: path through tree space, semi-directed

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- Network space

K. Huber, V. Moulton, C. Scornavacca,…
Missing: path through tree space, semi-directed

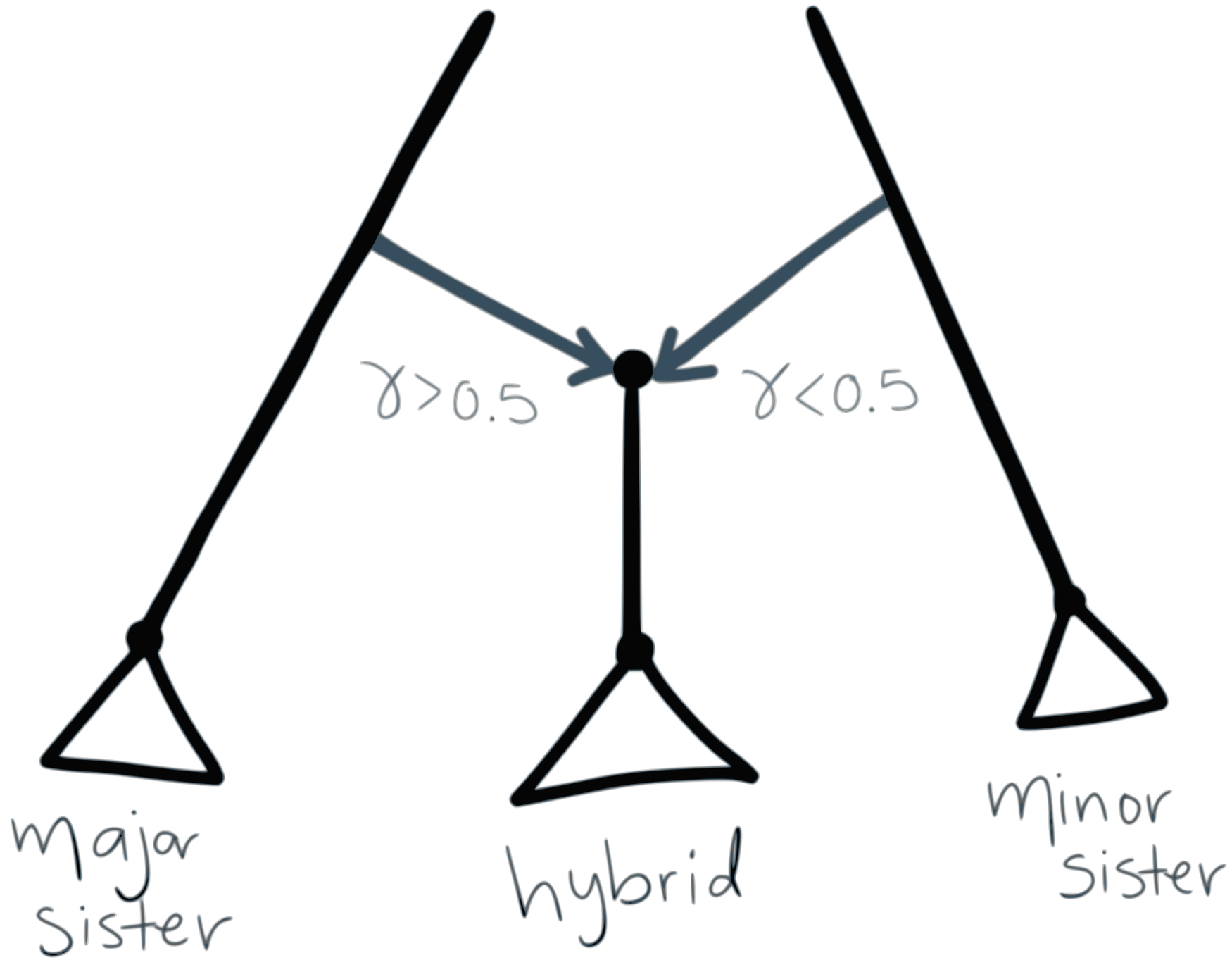
- Identifiability

Displayed vs Parental trees
Level-1 semi-directed networks
Hybridizations: case by case
Missing: likelihood, level-k semi-directed

- Network comparison

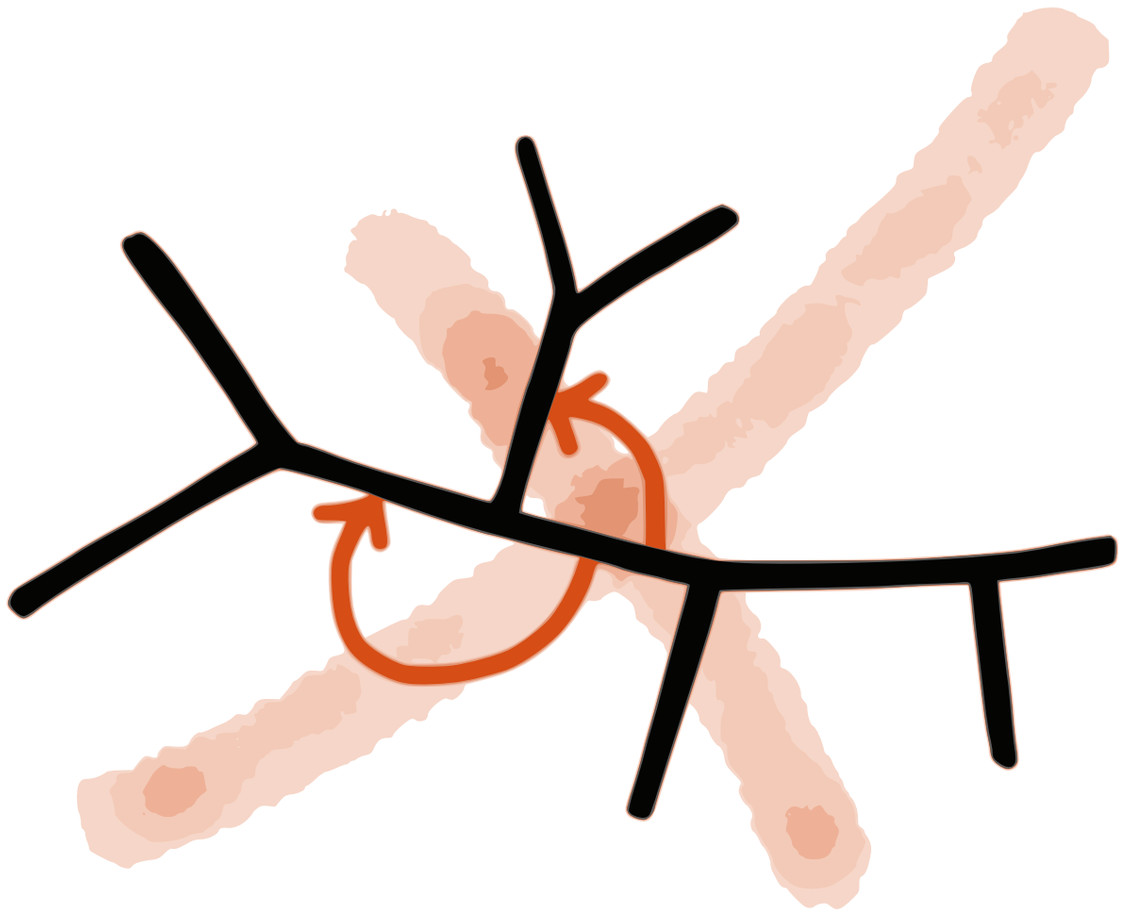
Missing: distance function
Hardwired-cluster distance only for rooted networks
Summary of networks: clades!

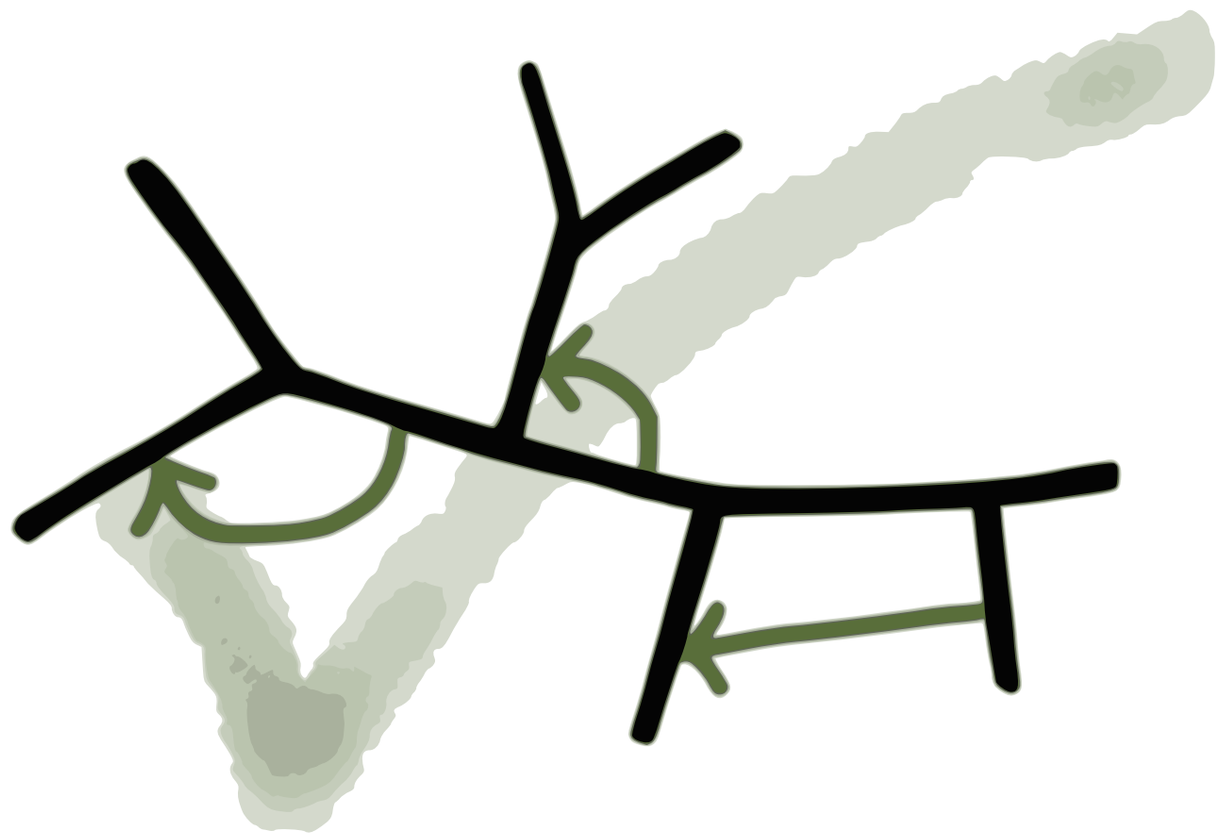
Network summary



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

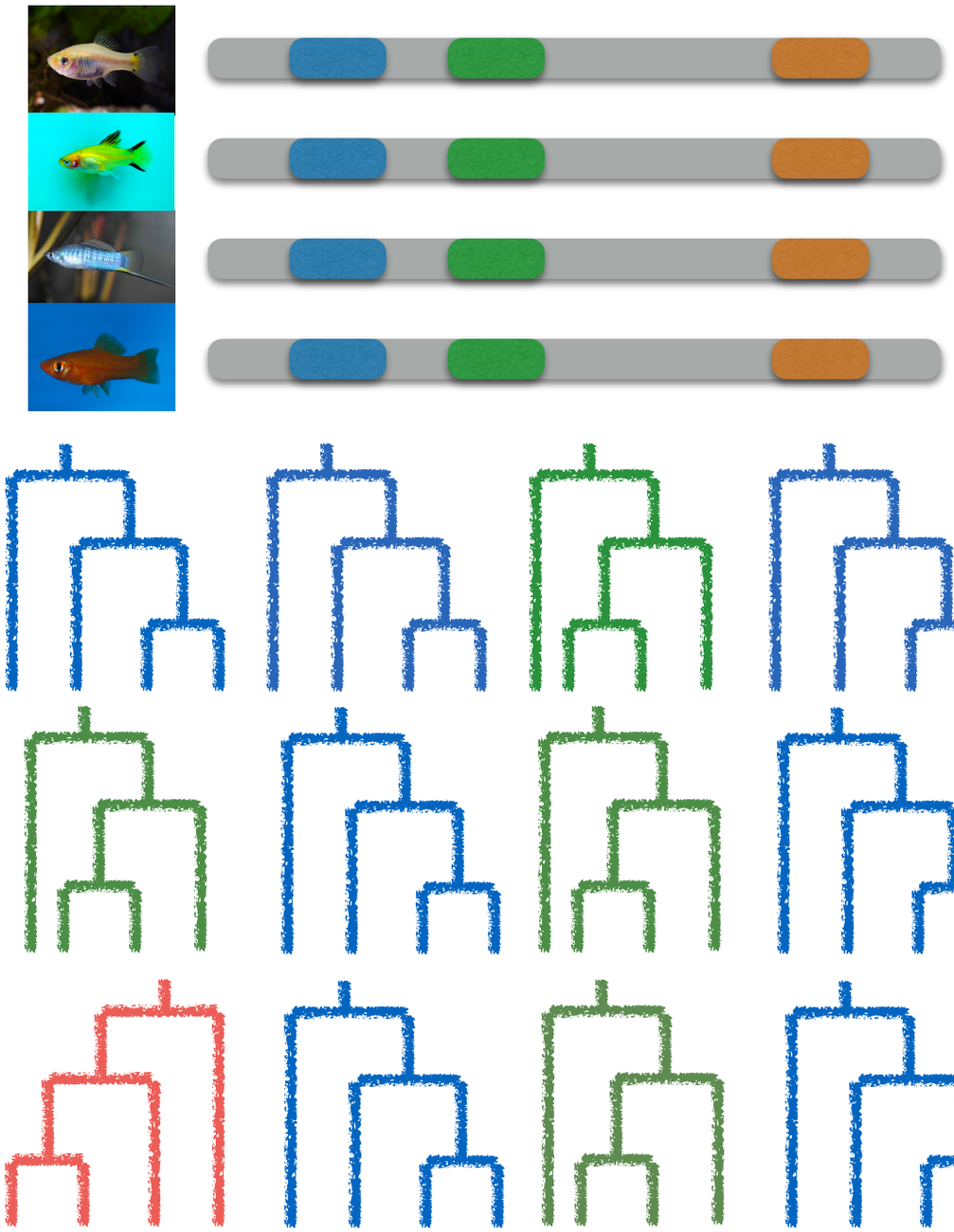
snaQ limitation: Level-1 networks





When?

Phylogenetic network



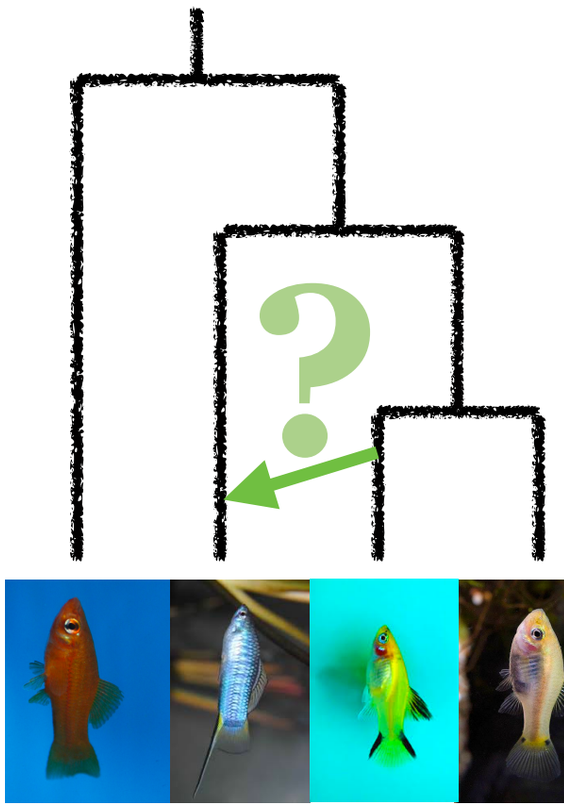
Data

TICR

GitHub

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

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

 https://solislemuslab.github.io/  @solislemuslab  crsl4

Practical advice

- Do multiple runs
- Do bootstrap
- Check the .networks output file (especially if hybridization conflicts with outgroup)
- What is the quality of my input data (gene trees/CFs)?
- Run SNaQ sequentially: h=0, h=1, h=2,…

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When to stop?
(Cai and Ané, 2020)