Distinguishing Convergence on Two-Taxon and Three-Taxon Networks

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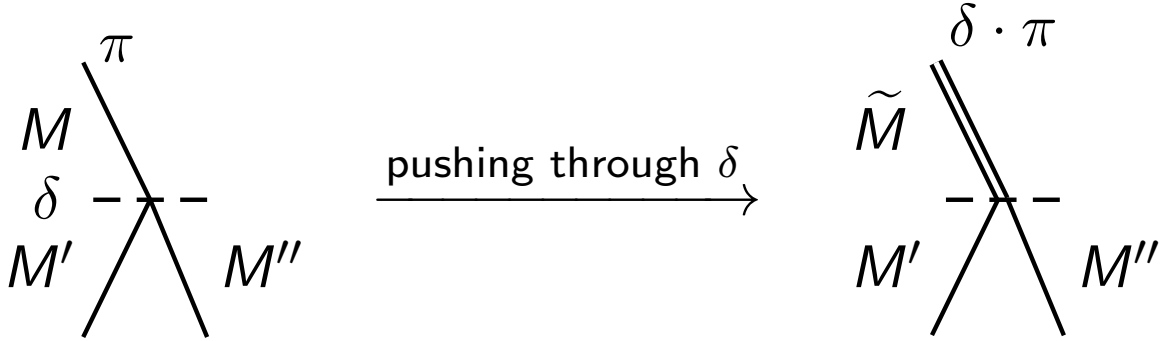
Convergence



Action of the splitting operator on an edge.

- $\widetilde{M}$ plays the role of implementing correlated changes.

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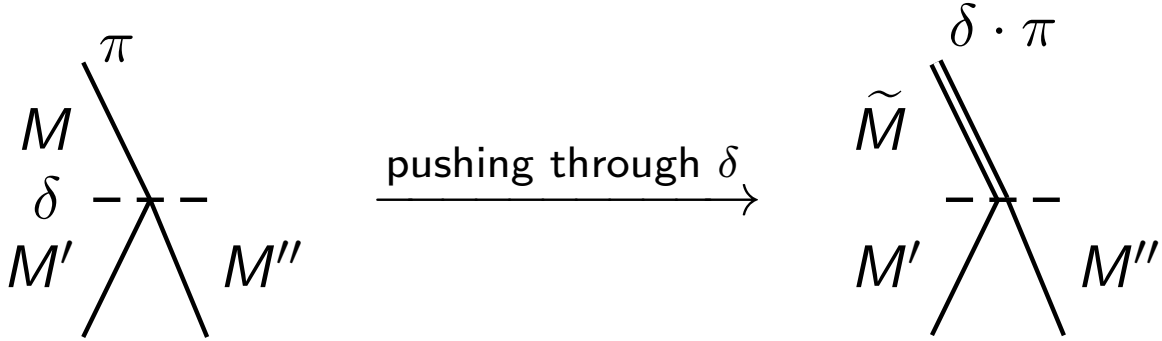

Action of the splitting operator on an edge.

- $\widetilde{M}$ plays the role of implementing correlated changes.
- Sumner et al. [2012] showed that the model can also be used for convergence.

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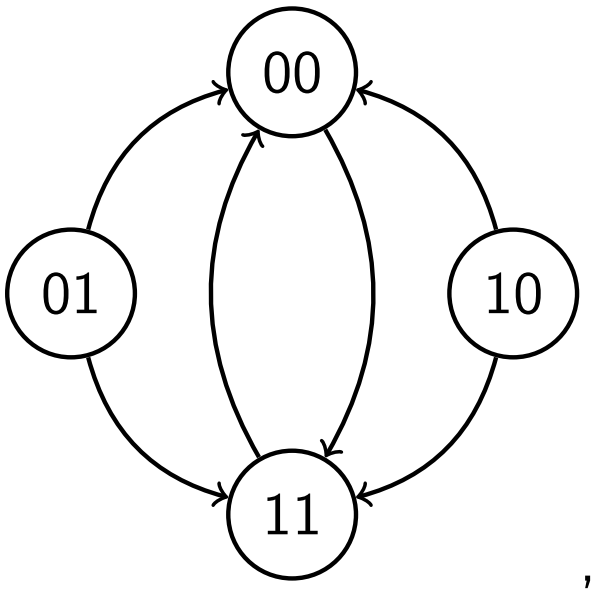
- Compare non-clock-like and clock-like trees to networks with convergence.
- Are our convergence-divergence networks **identifiable**?
- Can our convergence-divergence networks be **distinguished** from simpler trees?

Convergence-Divergence Network

Convergence of two taxa is as follows:

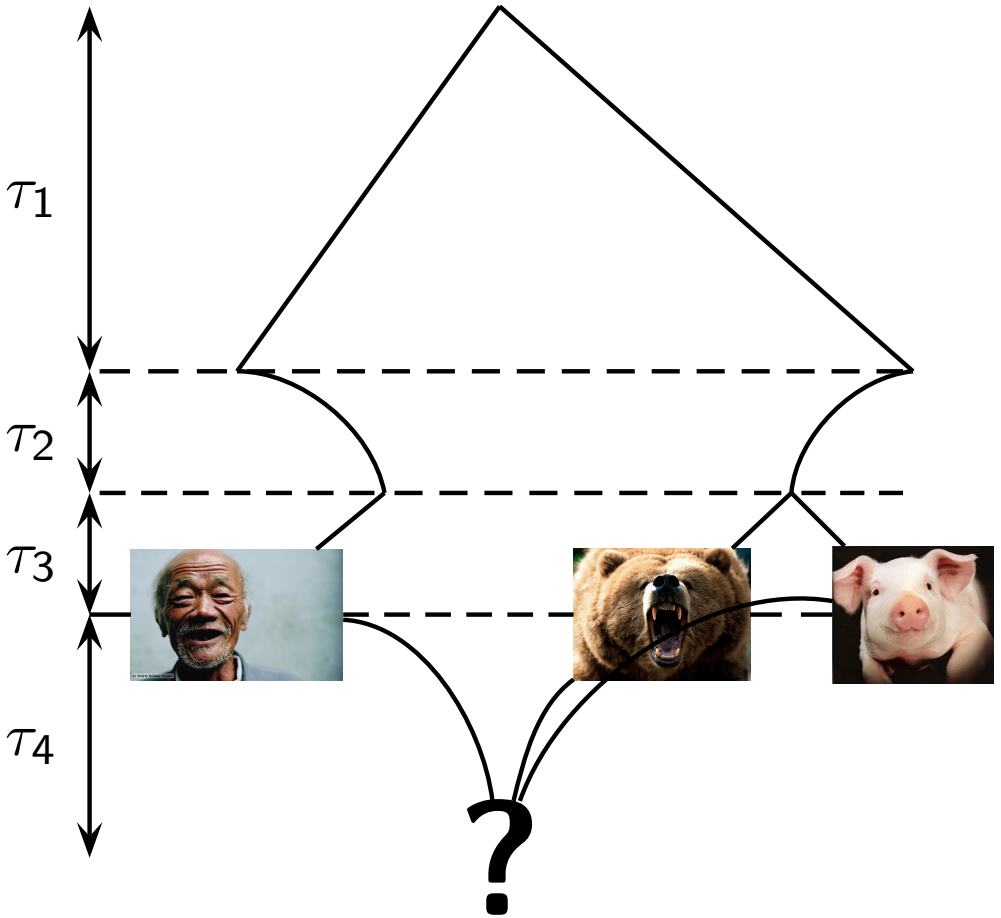


,

Q on two taxa.

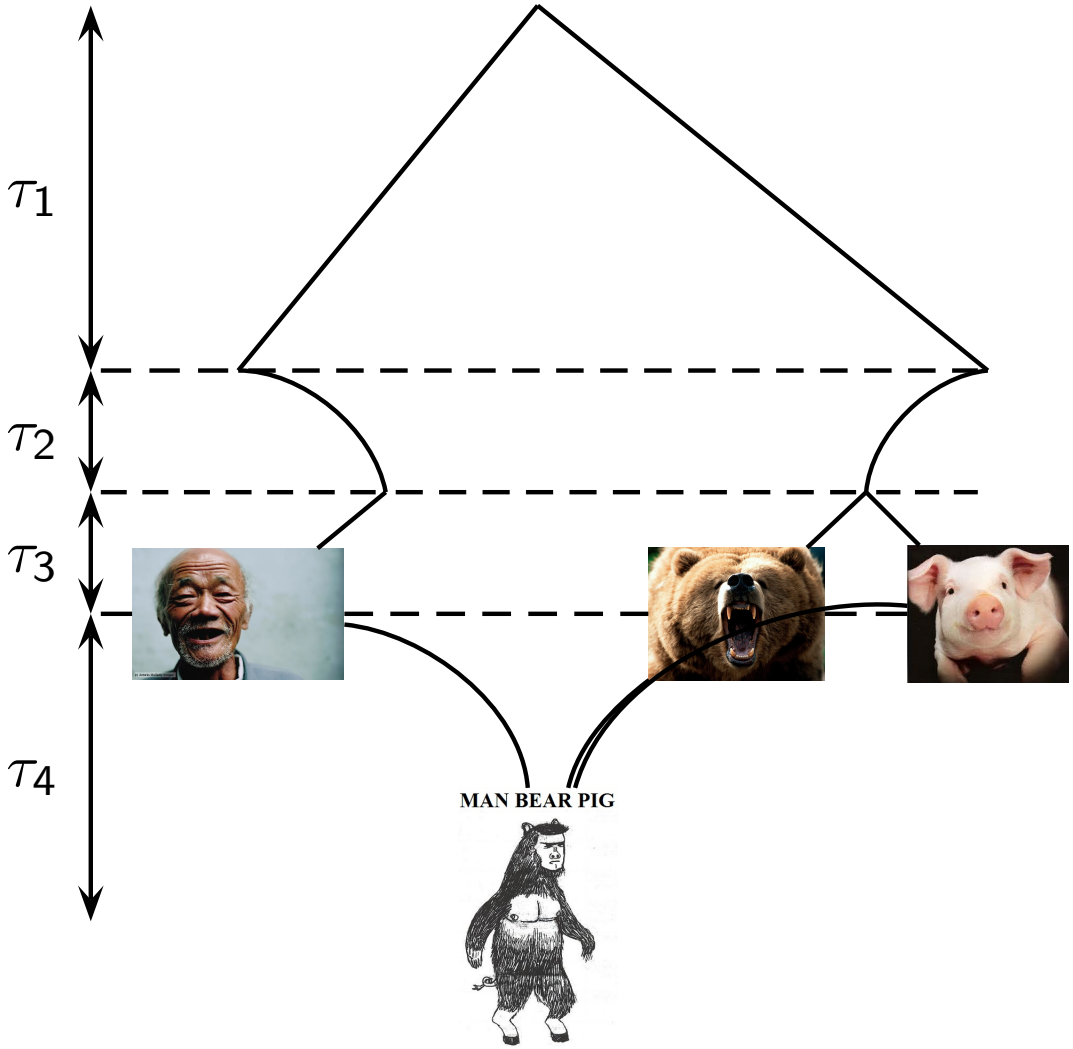
with each character state transition having the same rate, λ, from the binary symmetrical model.

Convergence-Divergence Network



A three-taxon convergence-divergence network.

Convergence-Divergence Network



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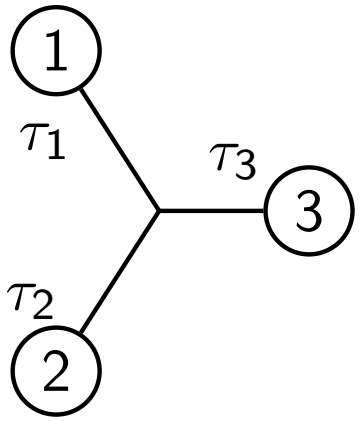
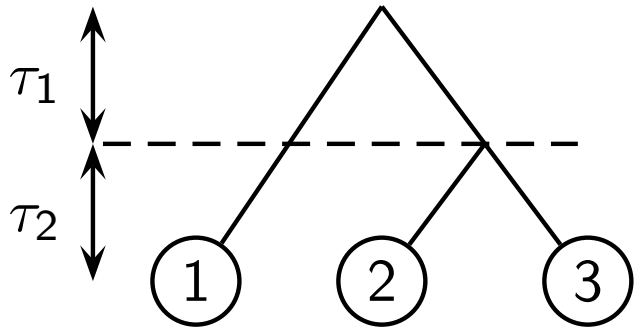
- From here we can compare the probability spaces of competing trees and networks.
- If two trees or networks have the same probability space they are said to not be **distinguishable**.

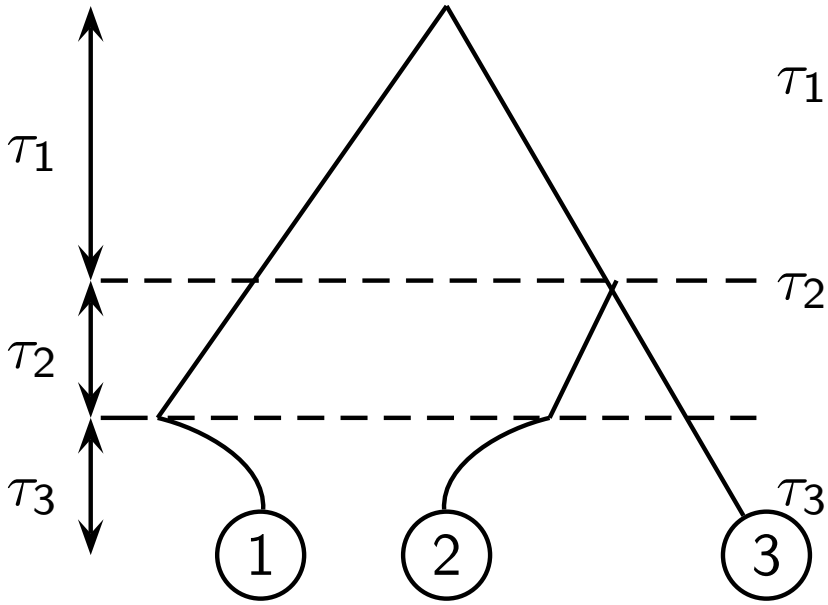
Three-Taxon Networks



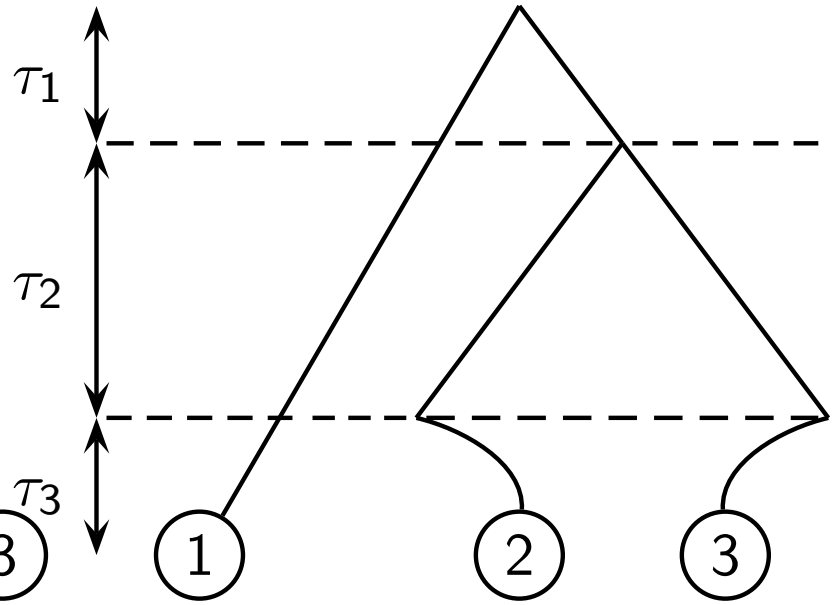
Network 1



Network 2

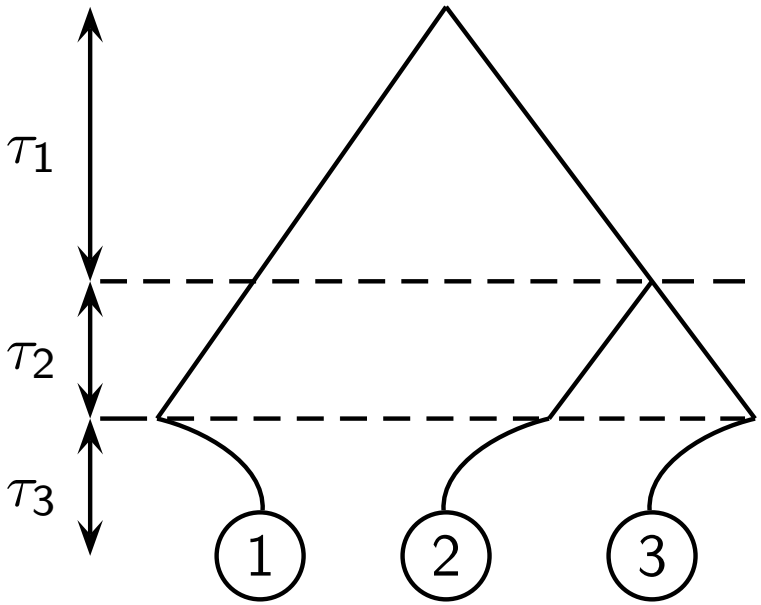


Network 3

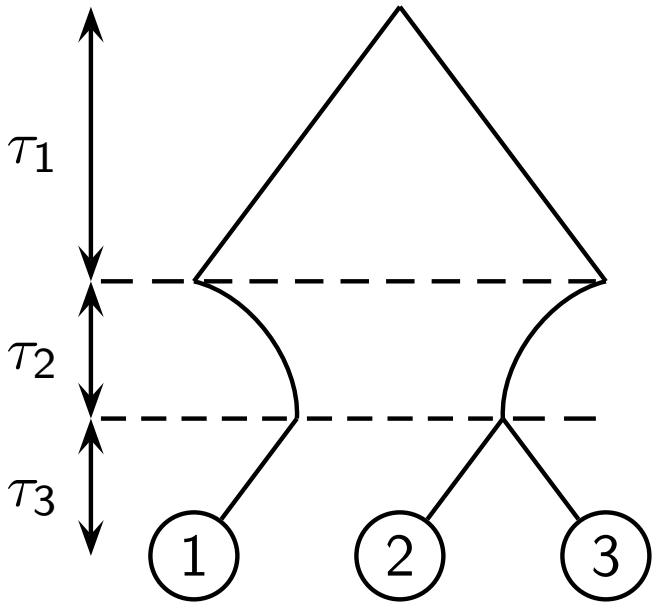


Network 4

Three-Taxon Networks



Network 5



Network 6

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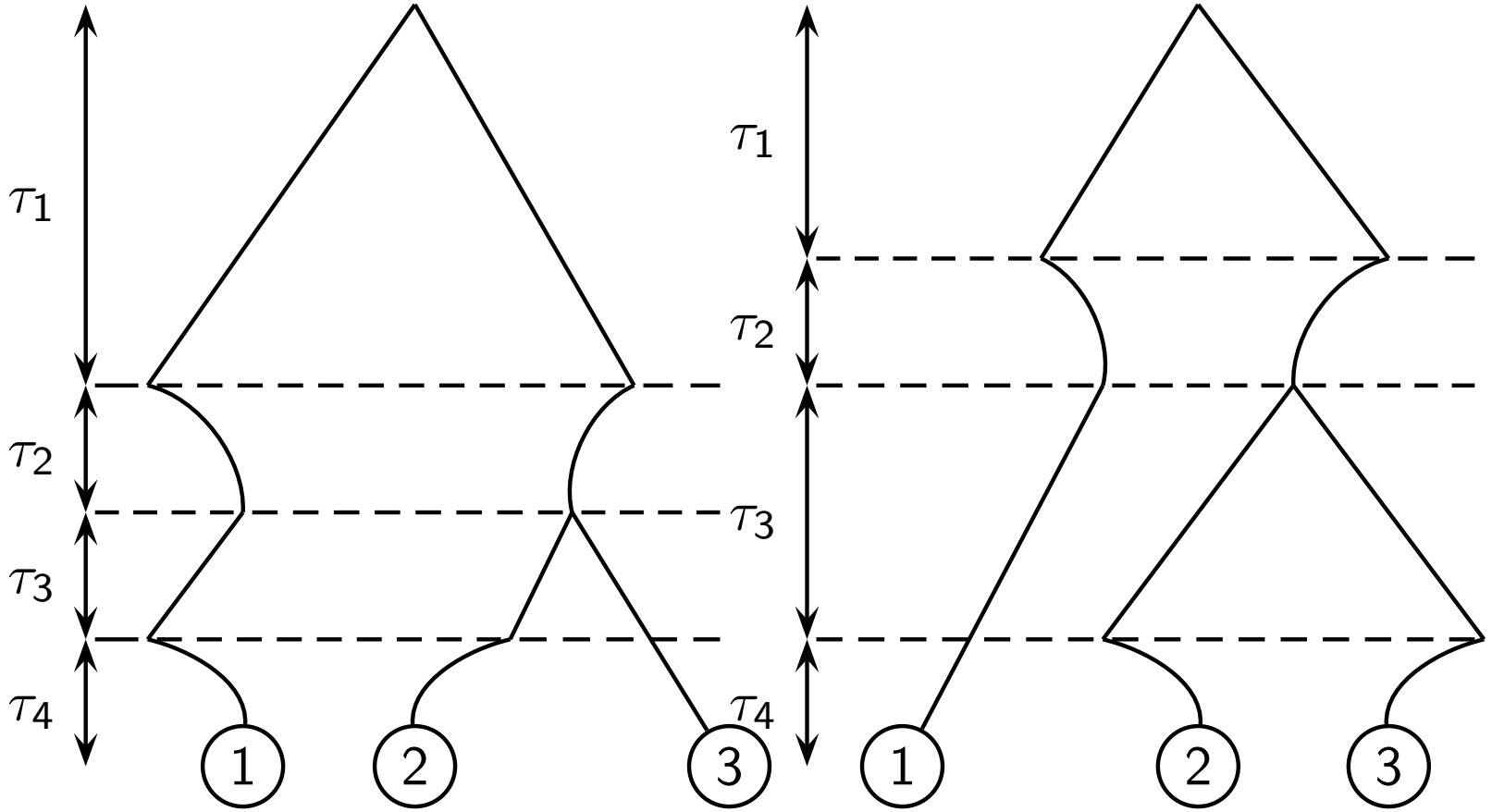

Network 7 Network 8

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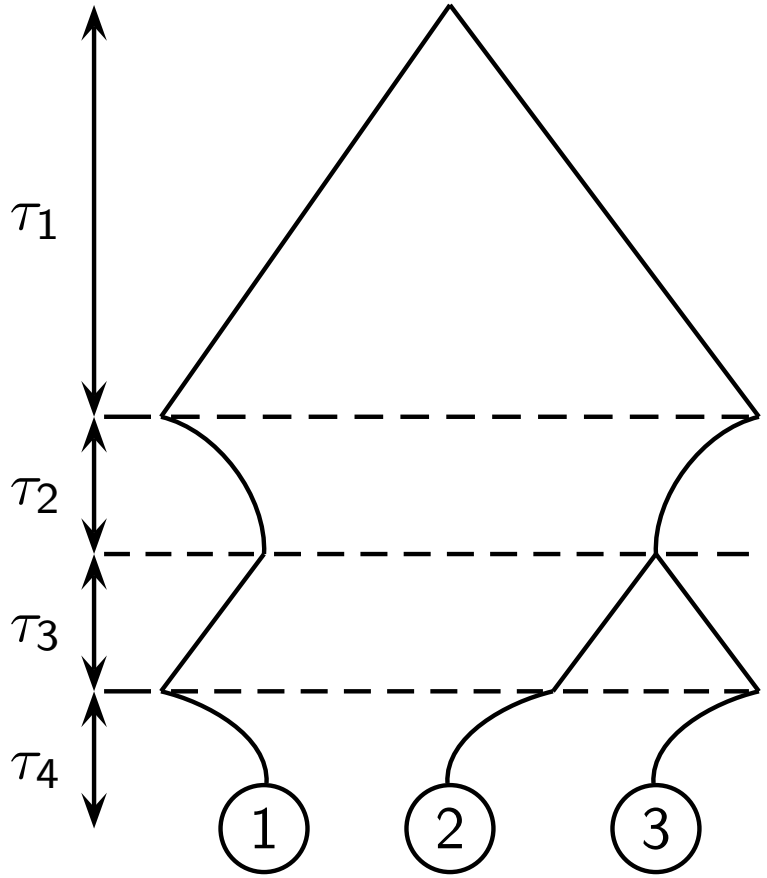
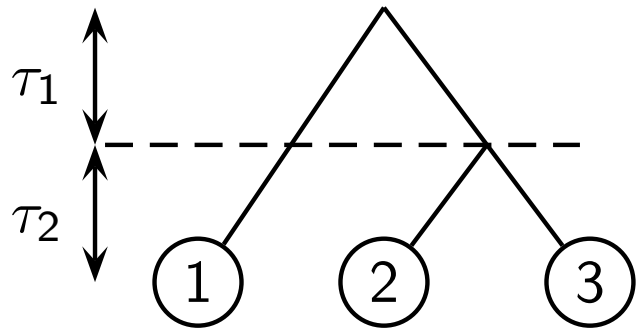


Network 9

An Example: Three-Taxon Clock-Like Tree



Three-taxon clock-like tree.

- In the regular basis, P, and the Hadamard basis, $\widehat{P}$, the probability distribution is

$$P = \begin{bmatrix} p_{000} \\ p_{001} \\ p_{010} \\ p_{011} \\ p_{100} \\ p_{101} \\ p_{110} \\ p_{111} \end{bmatrix}, \quad \widehat{P} = \begin{bmatrix} q_{000} \\ q_{001} \\ q_{010} \\ q_{011} \\ q_{100} \\ q_{101} \\ q_{110} \\ q_{111} \end{bmatrix} = \begin{bmatrix} 1 \\ 0 \\ 0 \\ e^{-2\tau_2} \\ 0 \\ e^{-2(\tau_1+\tau_2)} \\ e^{-2(\tau_1+\tau_2)} \\ 0 \end{bmatrix}.$$

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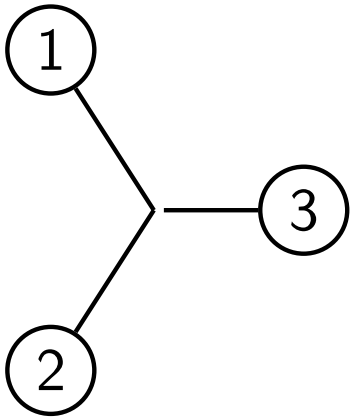
- Constraints are, $\{q_{101} = q_{110}, \quad q_{011} \geq q_{101}\}$.

Three-Taxon Networks



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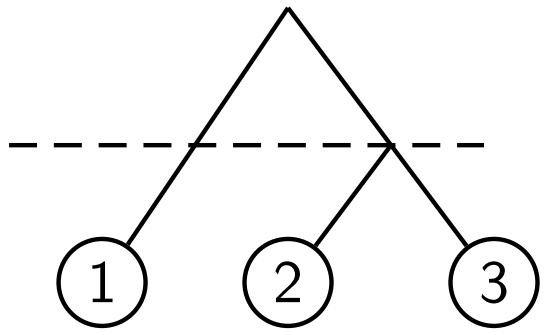
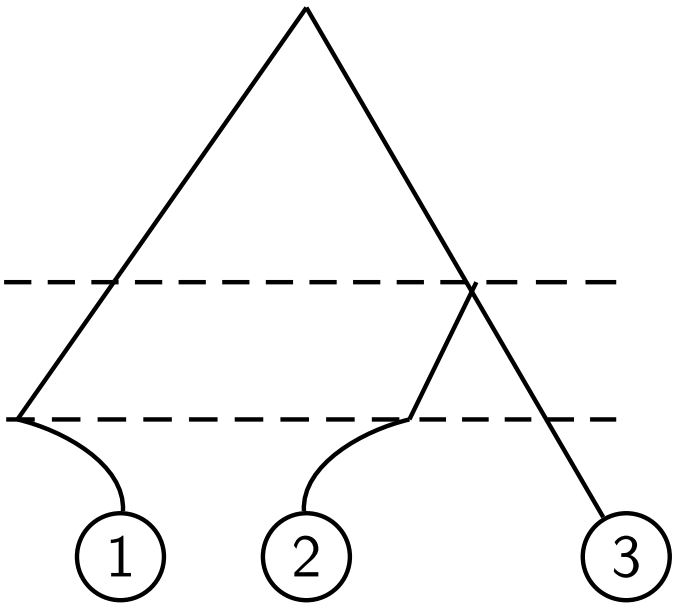


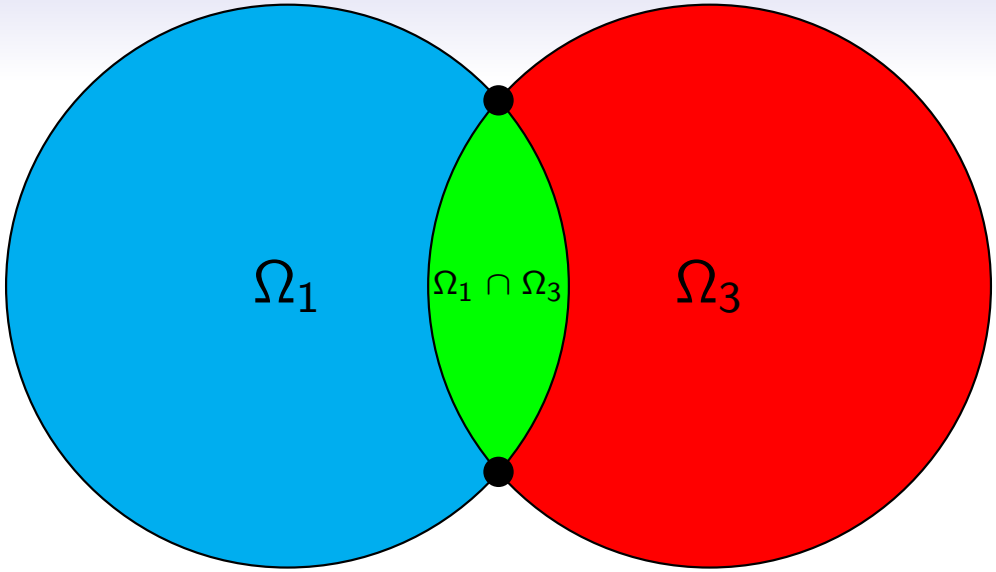
Network 2



Network 3

Network(s)	$q_{101} = q_{110}$ (Y/N)	$q_{110} \geq q_{101}$ (Y/N)	$q_{011} \geq q_{101}$ (Y/N)	$q_{011}(1-q_{110})^2 \geq (q_{011}-q_{101})^2$ (Y/N)
1	N	N	N	N
2, 4, 5, 6, 8, 9	Y	N	Y	N
3, 7	N	Y	Y	Y

In addition, the non-clock-like tree (Network 1) must meet the constraints $\{q_{011} \geq q_{101}q_{110}, \quad q_{101} \geq q_{011}q_{110}, \quad q_{110} \geq q_{011}q_{101}\}$.



Probability spaces of the networks. The probability space for Network 2 is the two black dots where the probability spaces for networks 1 and 3 intersect. Not to scale.

Colour	Probability Space	Constraints
Blue	Ω_1	$\{q_{011} \geq q_{101}q_{110}, \quad q_{101} \geq q_{011}q_{110}, \quad q_{110} \geq q_{011}q_{101}\}$
Red	Ω_3	$\{q_{011} \geq q_{101}, \quad q_{110} \geq q_{101}, \quad q_{011}(1-q_{110})^2 \geq (q_{011}-q_{101})^2\}$
Green	$\Omega_1 \cap \Omega_3$	$\{q_{011} \geq q_{101}, \quad q_{110} \geq q_{101}, \quad q_{101} \geq q_{011}q_{110}\}$
Black	$\Omega_1 \cap \Omega_2 \cap \Omega_3$	$\{q_{101} = q_{110}, \quad q_{011} \geq q_{110}\}$

Summary of network constraints which must be met in the region of the probability space.

- As an example, the constraints for the black region in regular basis are $\{p_{010} + p_{101} = p_{001} + p_{110}, \quad p_{011} + p_{100} \geq p_{001} + p_{110}\}$.

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- Analysed all sets of triplets.

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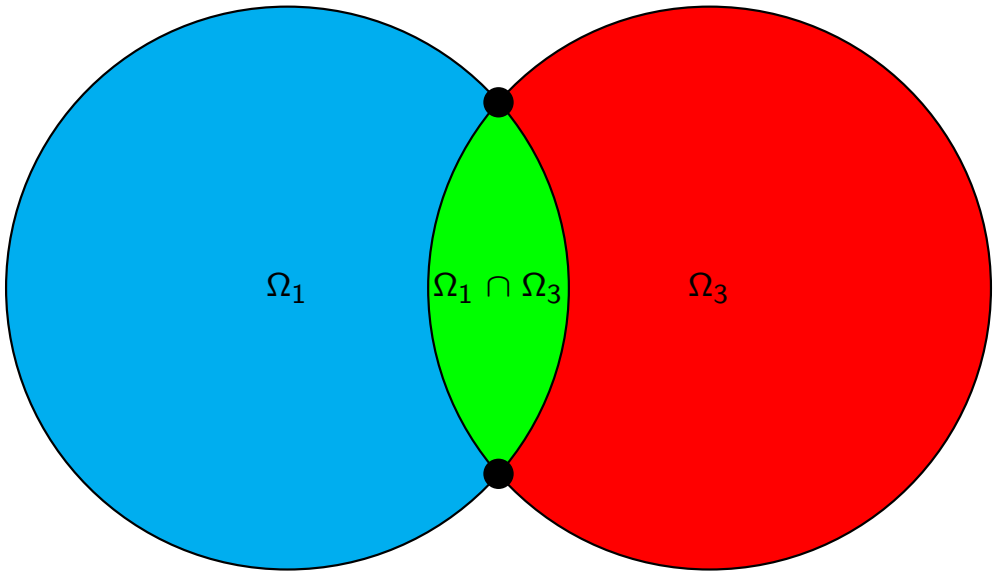

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BIC_{nc}	BIC_{cl}	BIC_{cd0+}	BIC_{cd2+}	BIC_{cd6+}	BIC_{cd10+}
0.0367	0.8547	0.1451	0.03153	0.009113	0.007635

Summary statistics.

Note: $BIC_{nc} + BIC_{cl} + BIC_{cd0+} = 0.0367 + 0.8547 + 0.1451 = 1.0365 > 1$. For some triplets the BIC values tied between two or more of the trees and networks. In these circumstances each tree or network was counted as having the lowest BIC value.

Future Work

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- Analyse four-taxon case and extend beyond binary symmetric model.
- For more than three taxa we can use methods from alegbraic geometry (Gröbner bases).

References

B. R. Holland, H. G. Spencer, T. H. Worthy, and M. Kennedy. Identifying cliques of convergent characters: Concerted evolution in the cormorants and shags. *Systematic Biology*, 59(4): 433–445, 2010.

D. Siegel-Causey. Phylogeny of the phalacrocoracidae. *Condor*, pages 885–905, 1988.

J. G. Sumner, B. R. Holland, and P. D. Jarvis. The algebra of the general markov model on phylogenetic trees and networks. *Bulletin of Mathematical Biology*, 74:858–880, 2012.