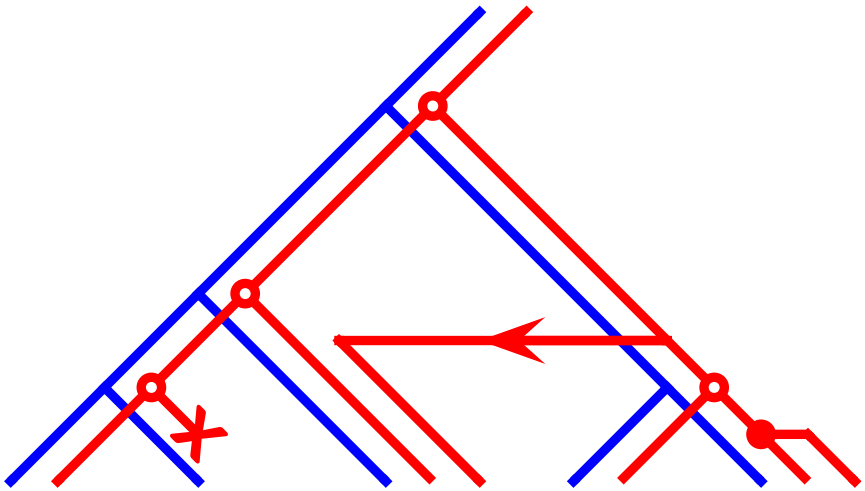
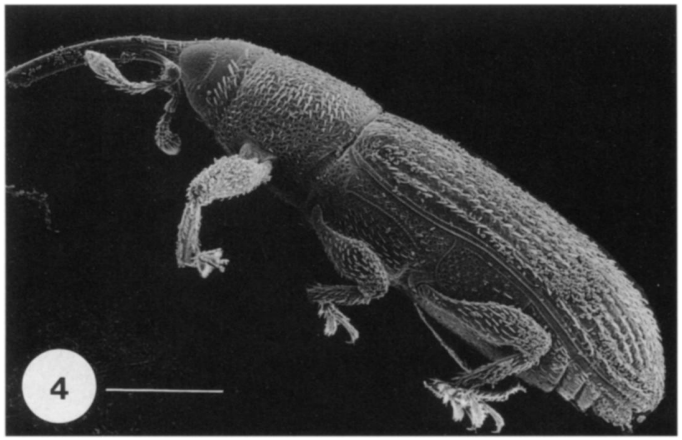
Bayesian Reconstruction of Coevolutionary Histories

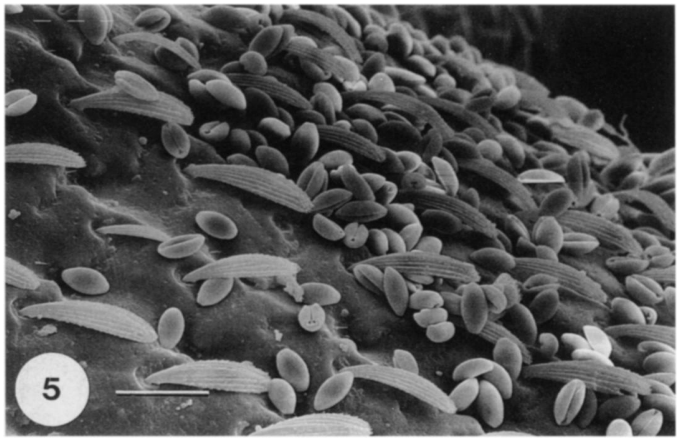
Arman Bilge

March 13, 2013



Phylogenetic Evidence for Cycad–Weevil Coevolution





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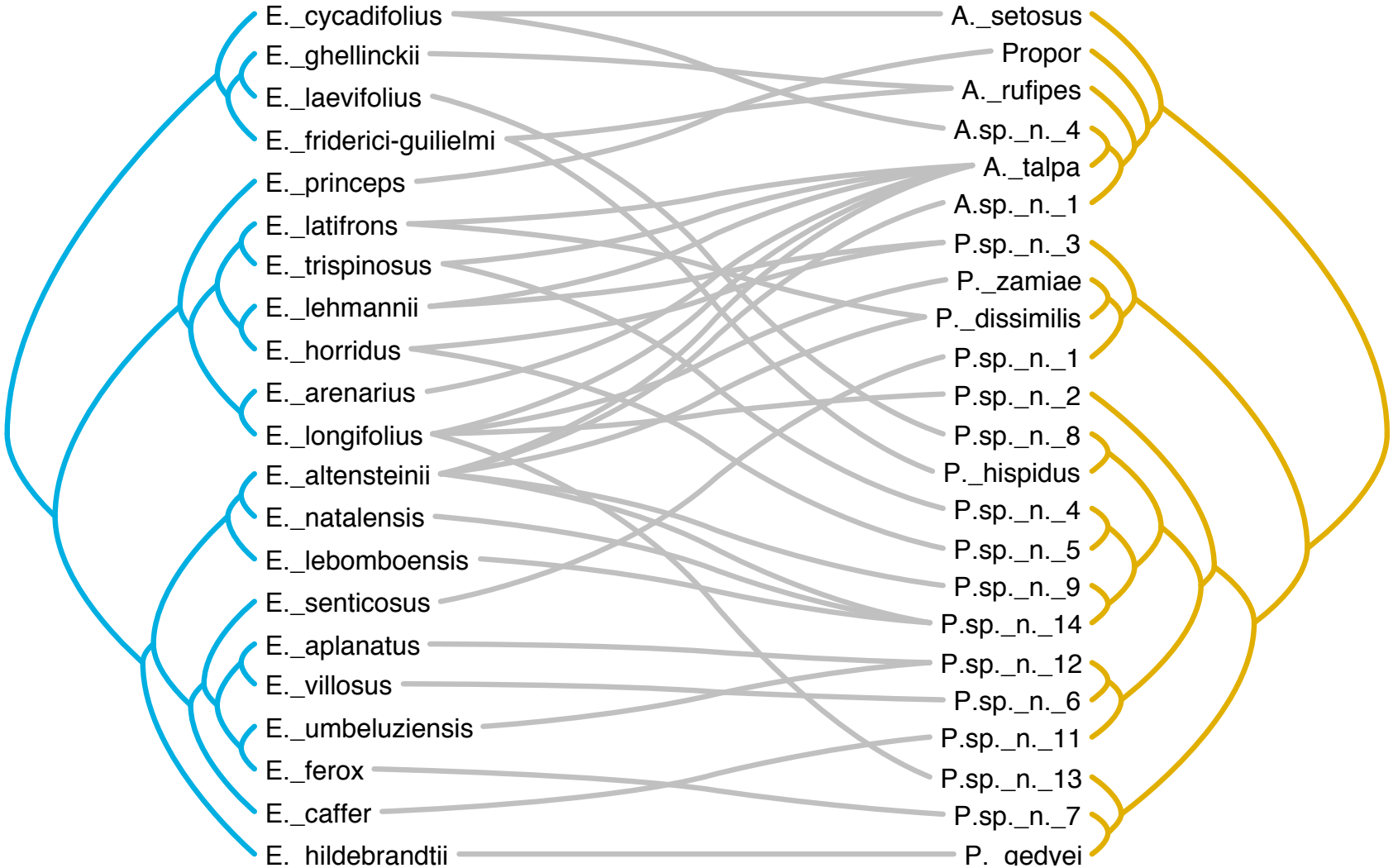

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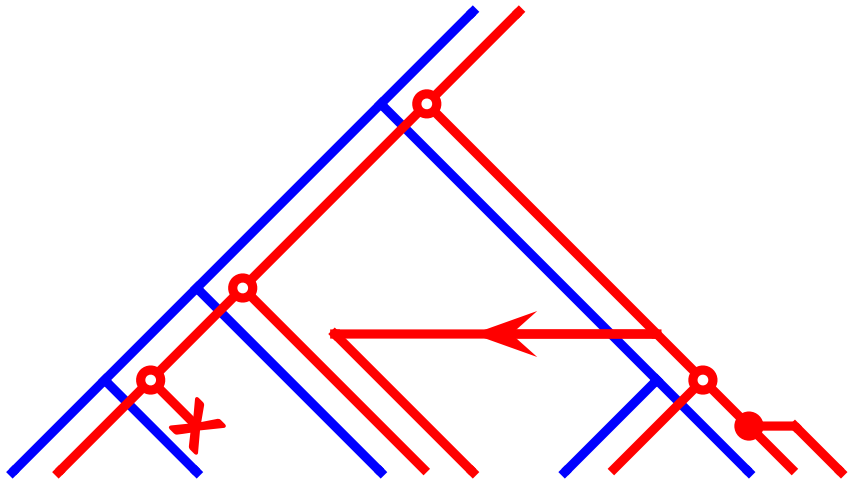
  - Cospeciation, duplication, host-switch, and loss



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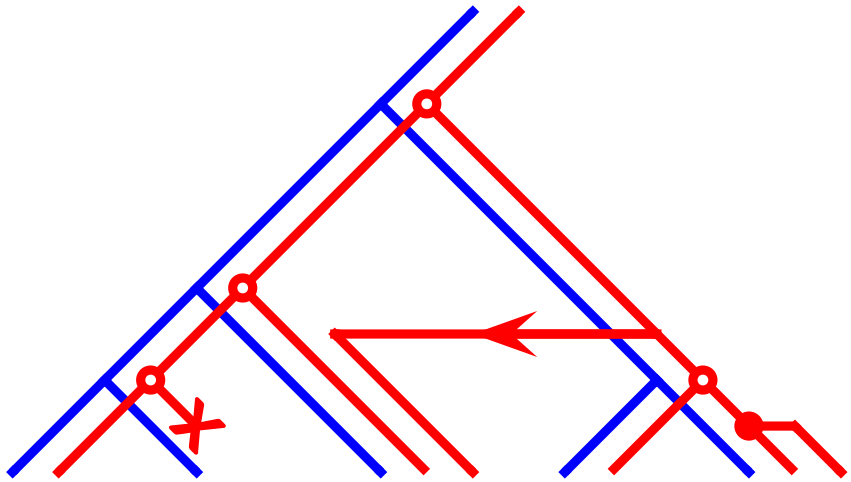
- Also applies to gene tree–species tree reconciliation, particularly involving horizontal transfer events



Existing Work on the Cophylogeny Reconciliation Problem

Parsimony Methods

- Tarzan, CoRe-PA, Jane, TreeMap, AnGST, RANGER-DTL

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- Each relies on various assumptions and simplifications

A Bayesian Interpretation of Cophylogeny

$$\overbrace{P\left(H, S, \mathcal{R} \mid D\right)}^{\text{probability of reconstruction}}$$

H = host tree, S = symbiont tree, $\mathcal{R}$ = reconciliation,
θ = model parameters, $D = (d_H, d_S)$ = sequence data

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Likelihood

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$$\begin{aligned} P\left(d_H, d_S \mid H, S, \mathcal{R}, \theta\right) &= P\left(d_H \mid H, S, \mathcal{R}, \theta\right) P\left(d_S \mid H, S, \mathcal{R}, \theta\right) \\ &= \underbrace{P\left(d_H \mid H\right)}_{\text{tree likelihood}} \underbrace{P\left(d_S \mid S\right)}_{\text{tree likelihood}} \end{aligned}$$

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Computing $P\left(S \mid H, \mathcal{R}, \theta\right)$

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- Symbiont and host must be contemporaneous

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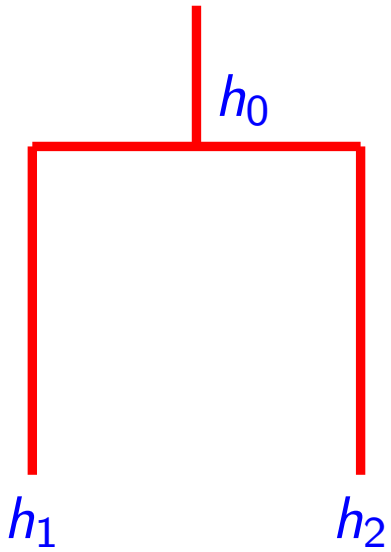

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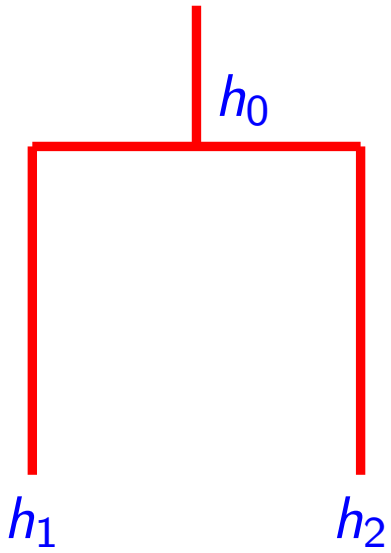

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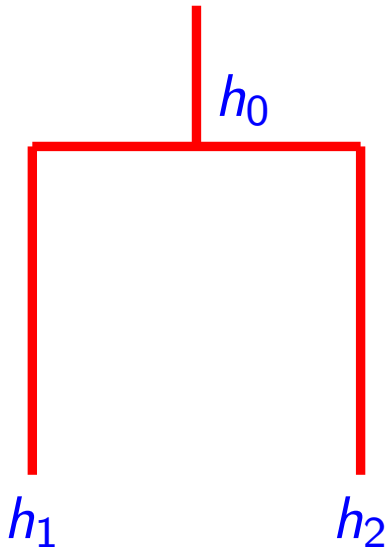

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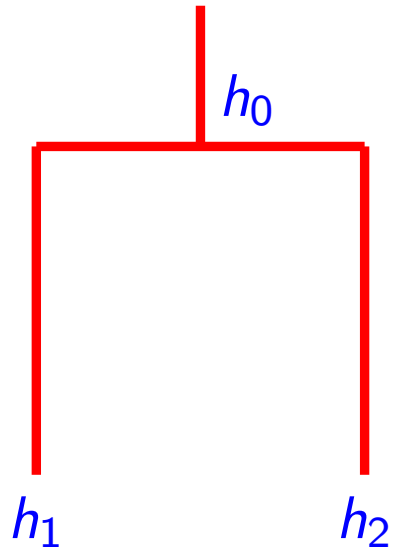

- What is the relationship of h_0 to h_1 and h_2 in the host tree?
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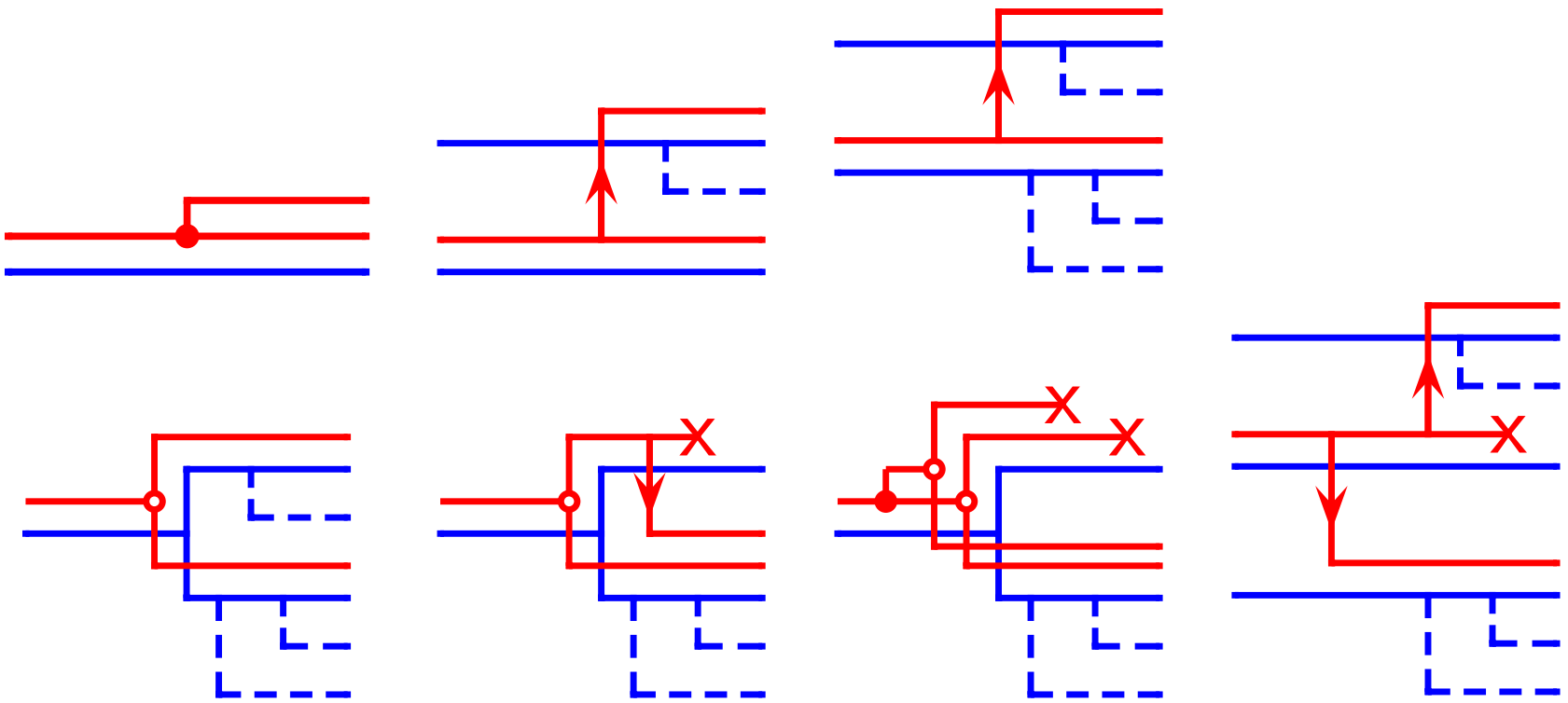
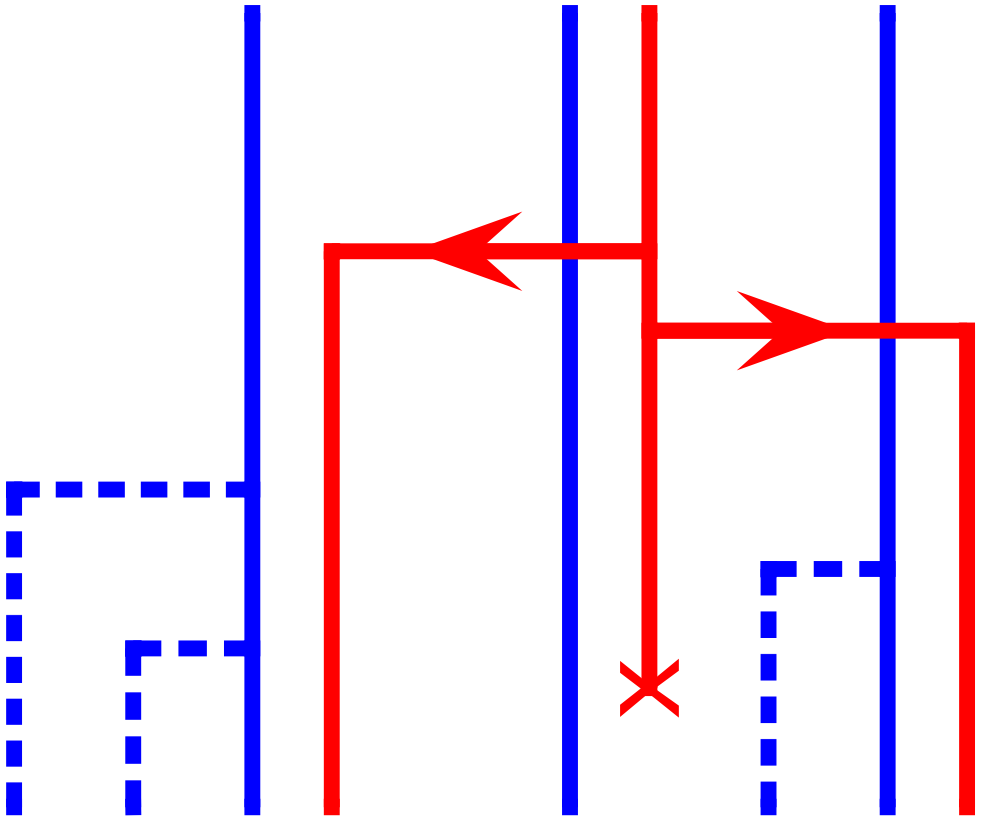
- Permutation of two relationships yields potential scenarios

Computing $P\left(S \mid H, \mathcal{R}, \theta\right)$: The Scenarios



Host / **Symbiont**

Computing $P\left(S \mid H, \mathcal{R}, \theta\right)$: An Example Scenario



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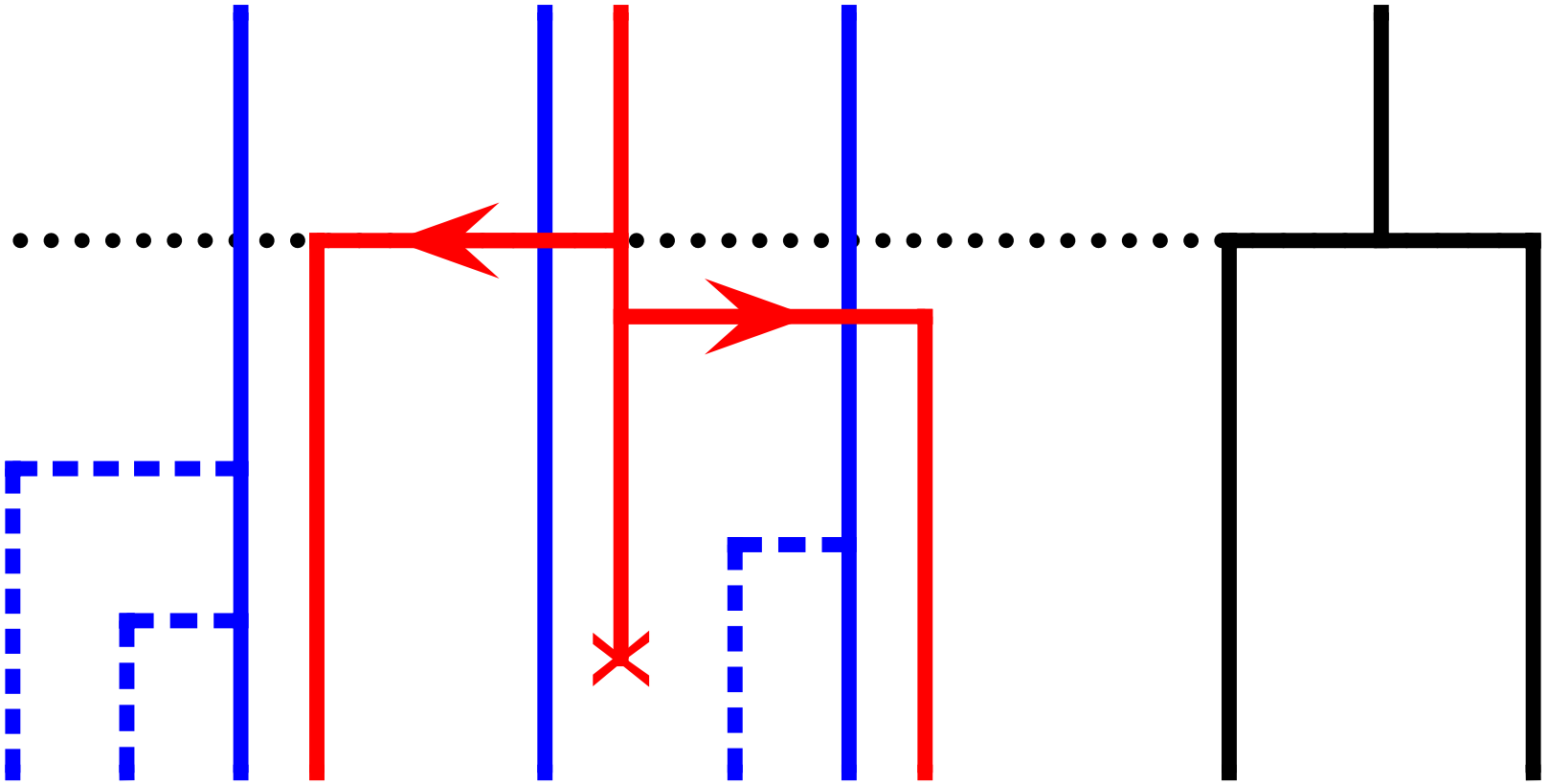

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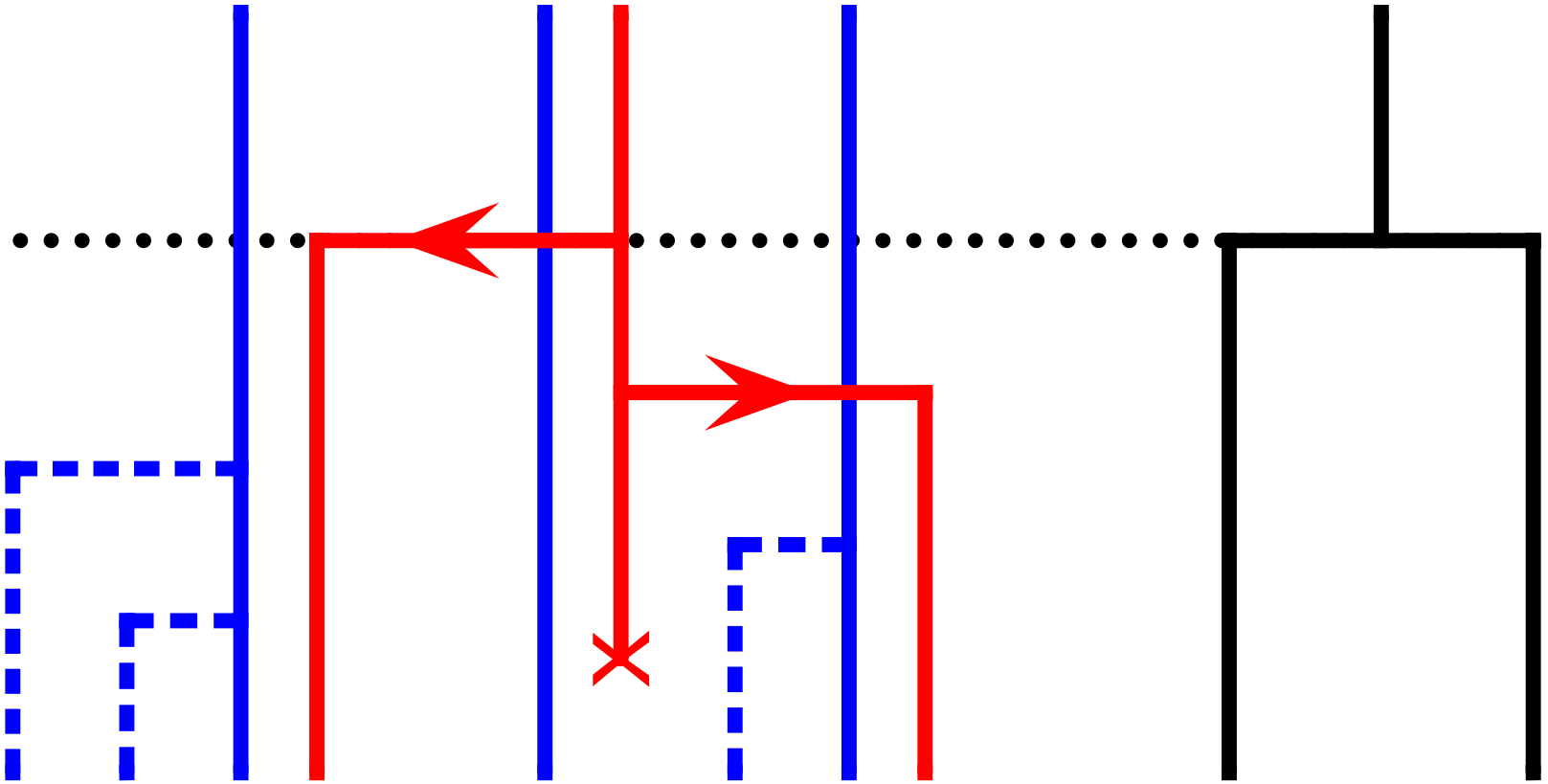

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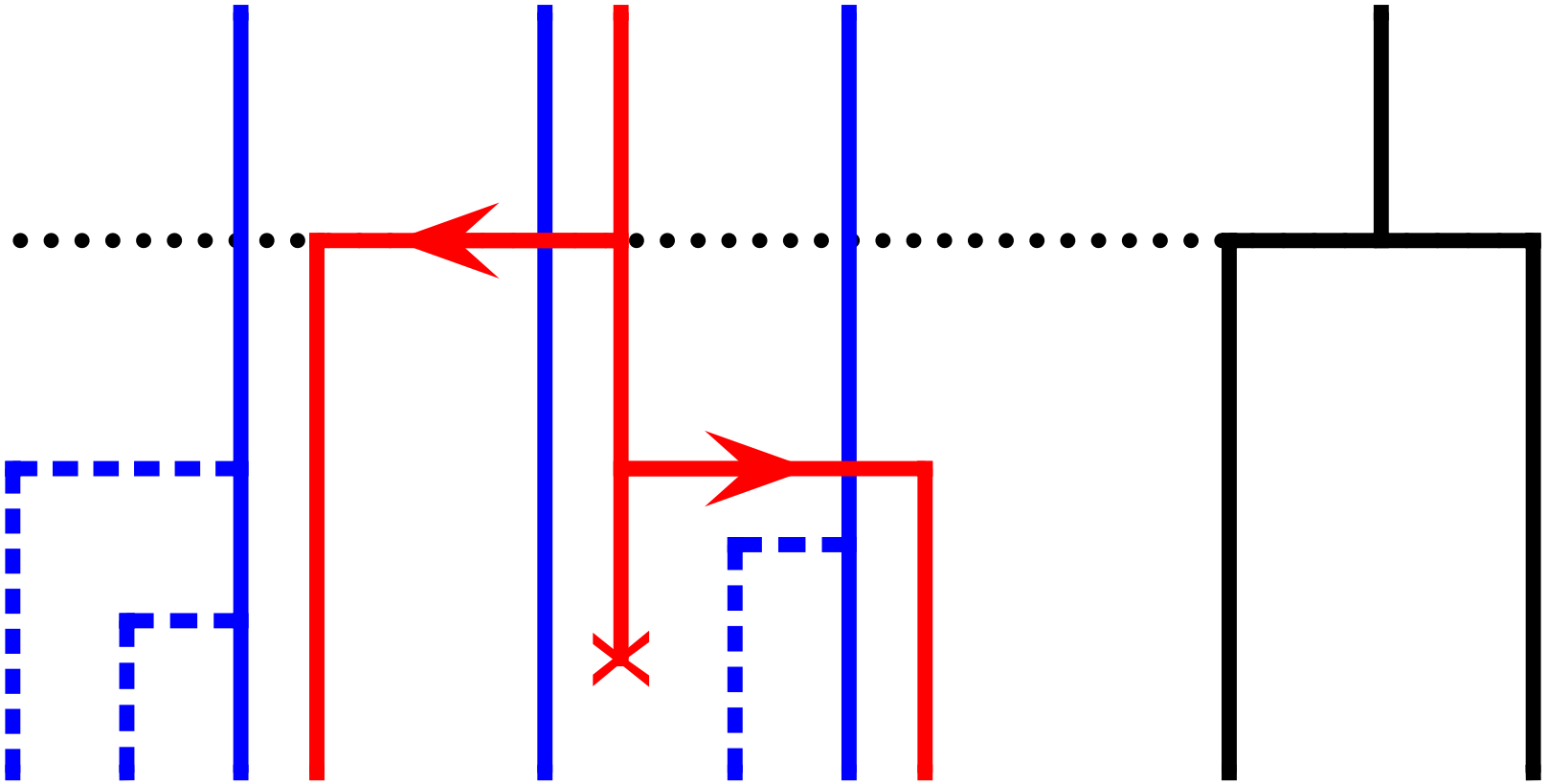

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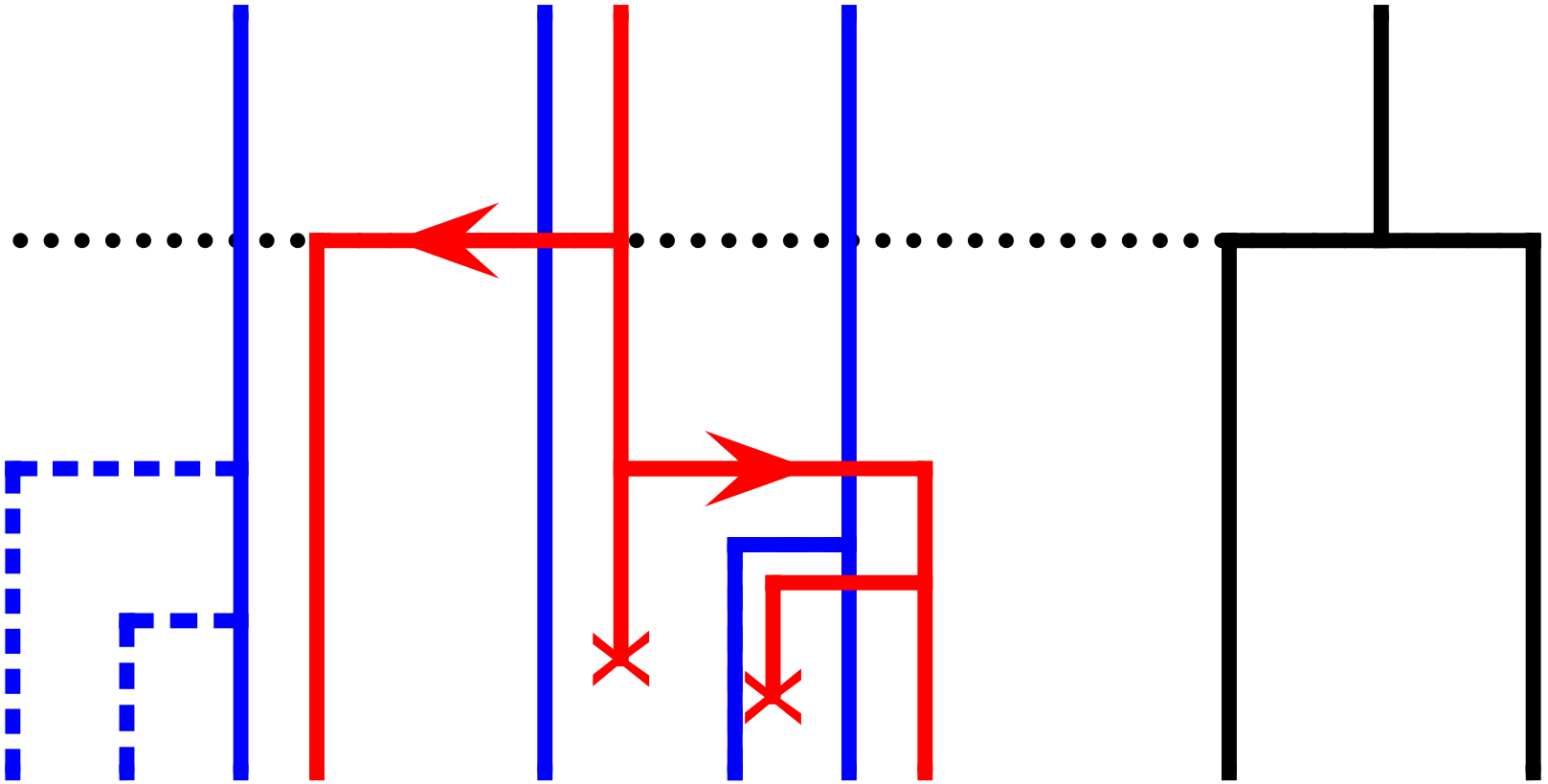

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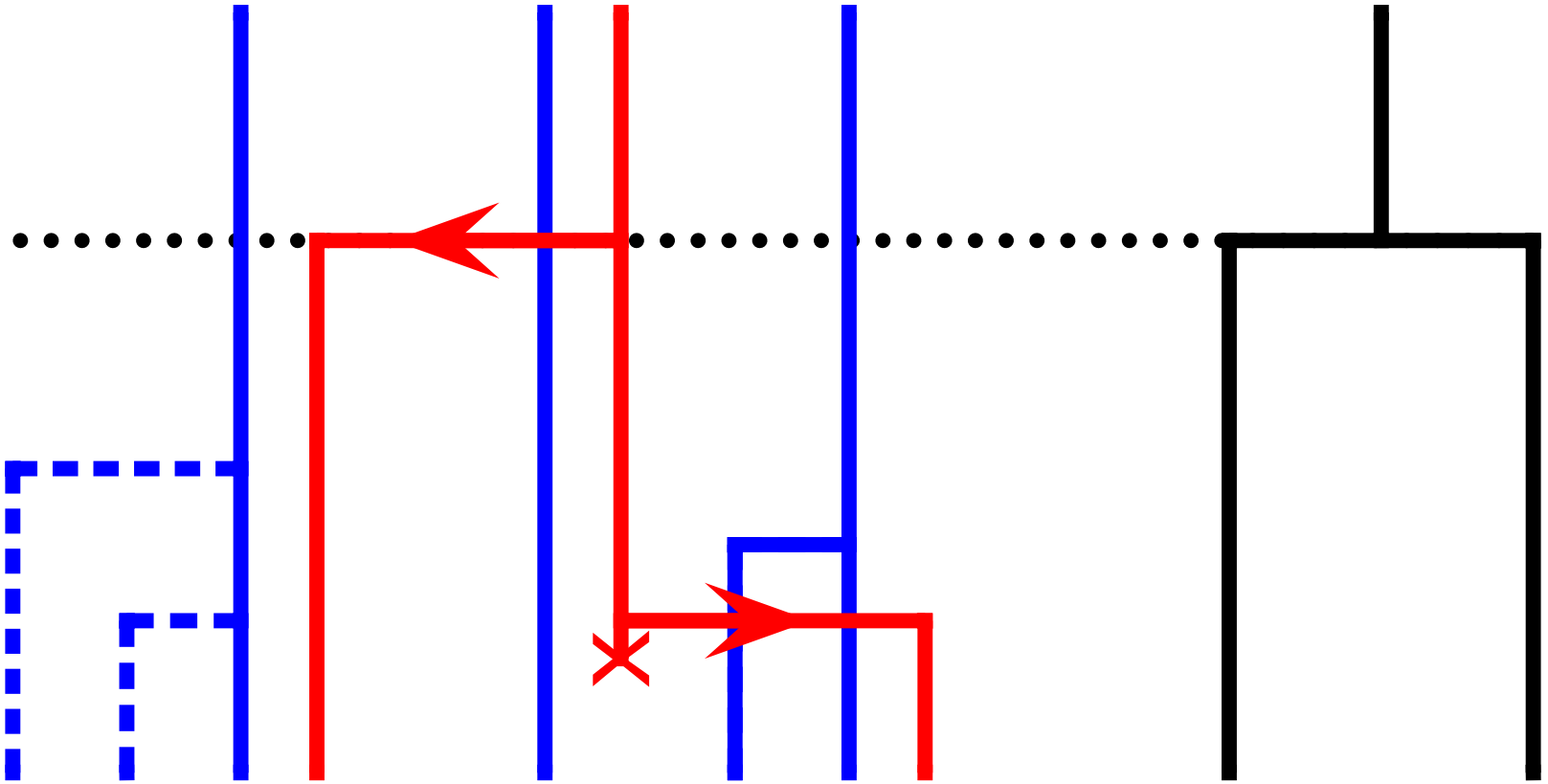

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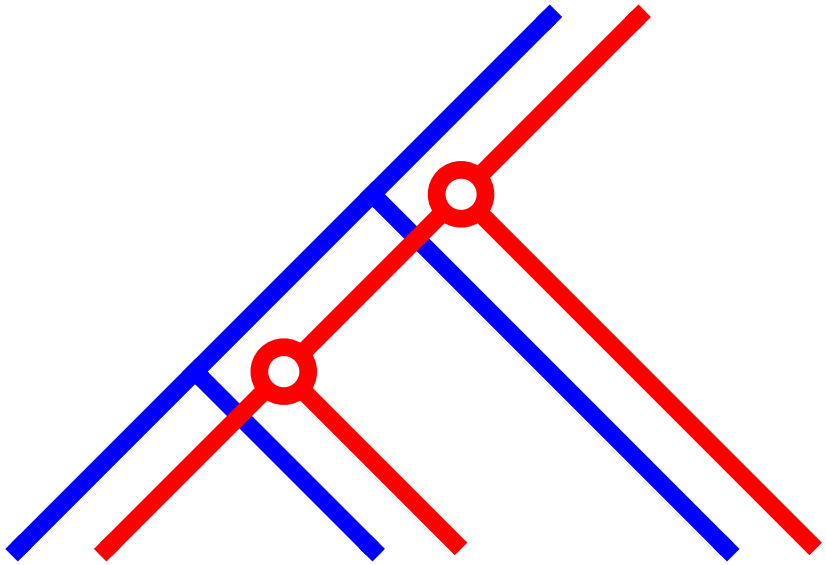

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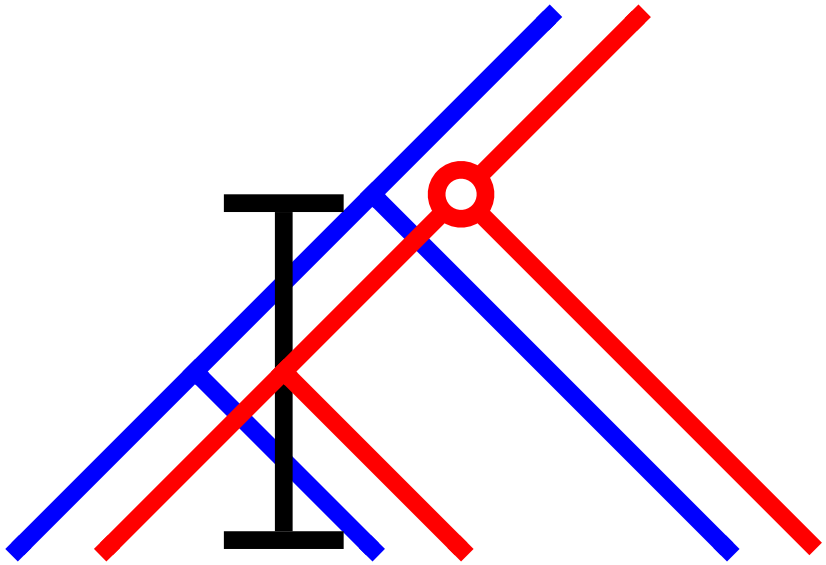

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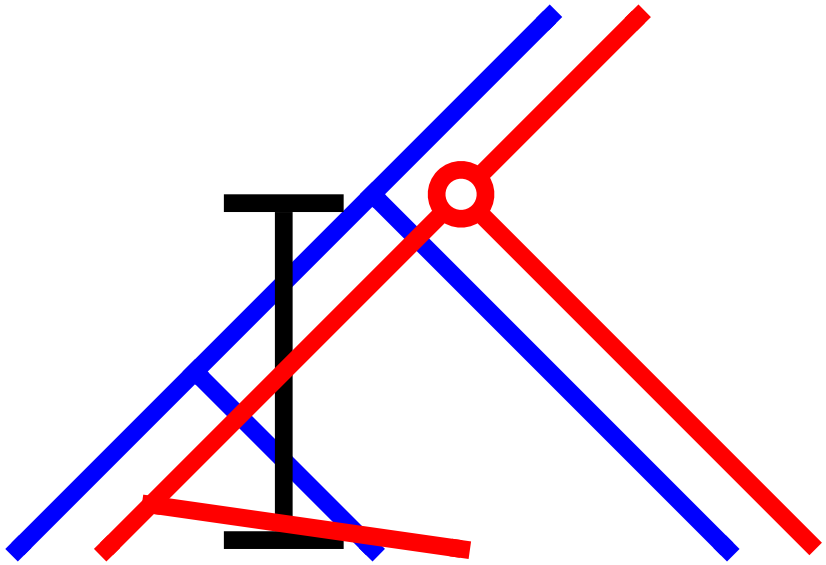

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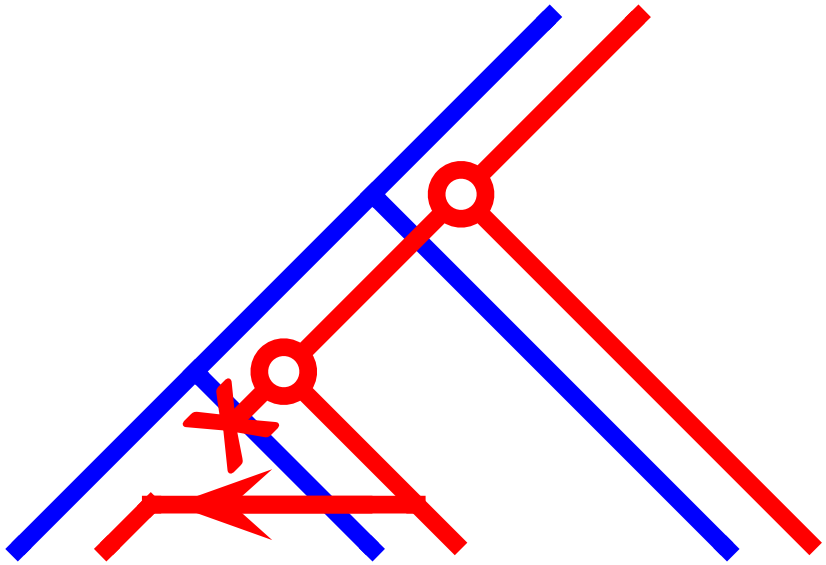

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- Implemented as plugin for BEAST1

Simulation Methodology

- Simple simulation pipeline
  1. Host tree generated under constant size coalescent
  2. DNA simulated on host tree under JC69 model
  3. Symbiont tree generated on host tree under described model (three Poisson processes)
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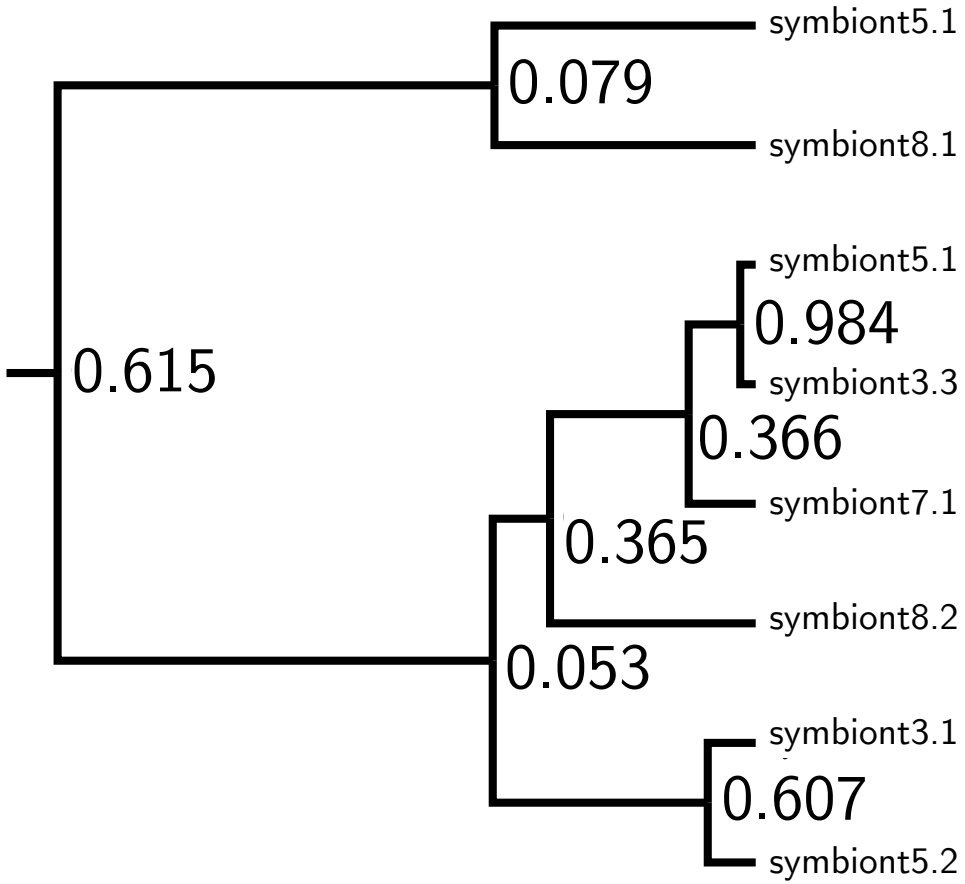
- 2nd simulation: 8 host taxa, all event rates 1.0, 8 symbionts
  - Trees reconstructed accurately, reconciliation questionable...

Results from Second Simulation

	median	**95% HPD**
λ	1.42	$[0.10, 4.63]$
τ	2.48	$[0.20, 9.18]$
μ	1.60	$[0.11, 7.24]$



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- Implemented the algorithm in an MCMC framework

Open Questions and Problems

Detecting Cospeciation

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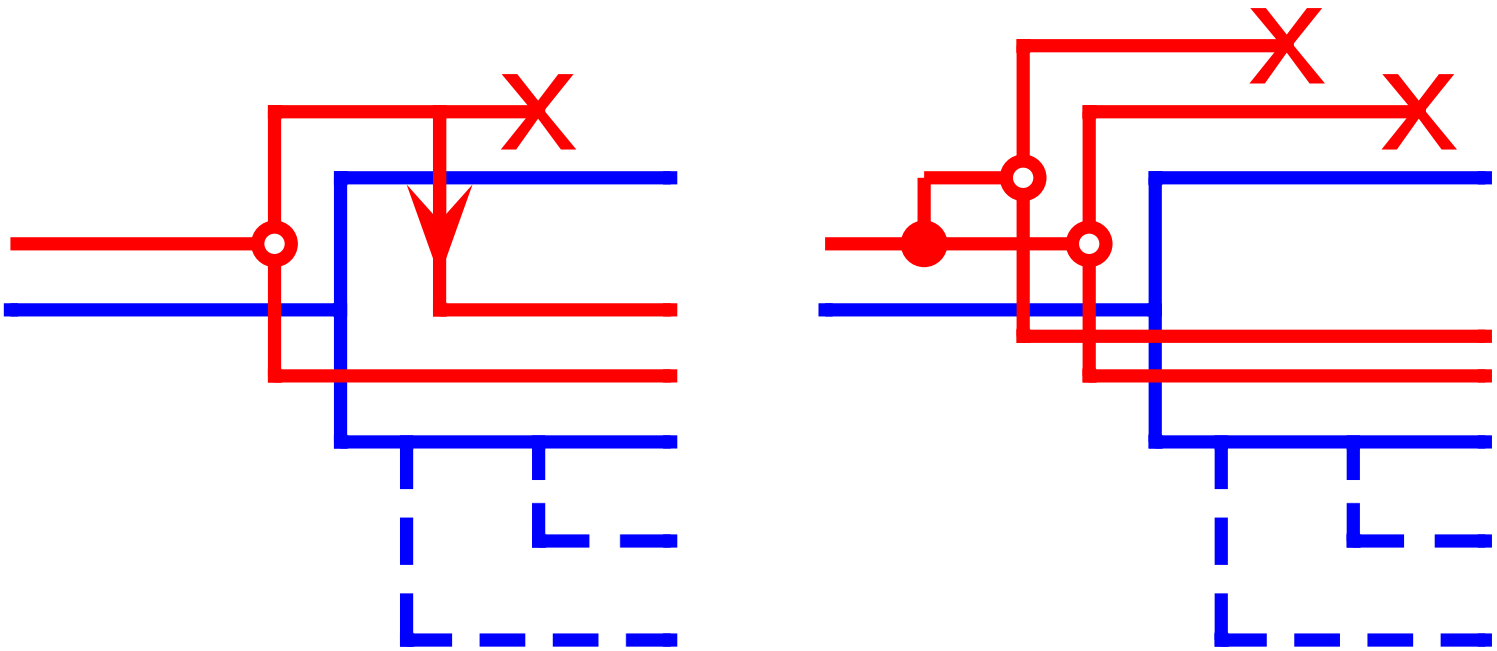
- Important for identifying between some scenarios



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- What is the effect of the operator on mixing?
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- How best can we evaluate the model performance via simulation studies?

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- Can we test coevolutionary theories, e.g. GMTC or escape-and-radiate?

Acknowledgements

- My mentors, Dr. Yi-Chieh Jessica Wu, Rachel Sealfon, and Prof. Mukul Bansal
- Andrew Brownjohn, Jon Sanders, Prof. Ran Libeskind-Hadas, Hayden Metsky, and Prof. Manolis Kellis, for helpful discussions
- Dr. Susan Offner, for inspiring me