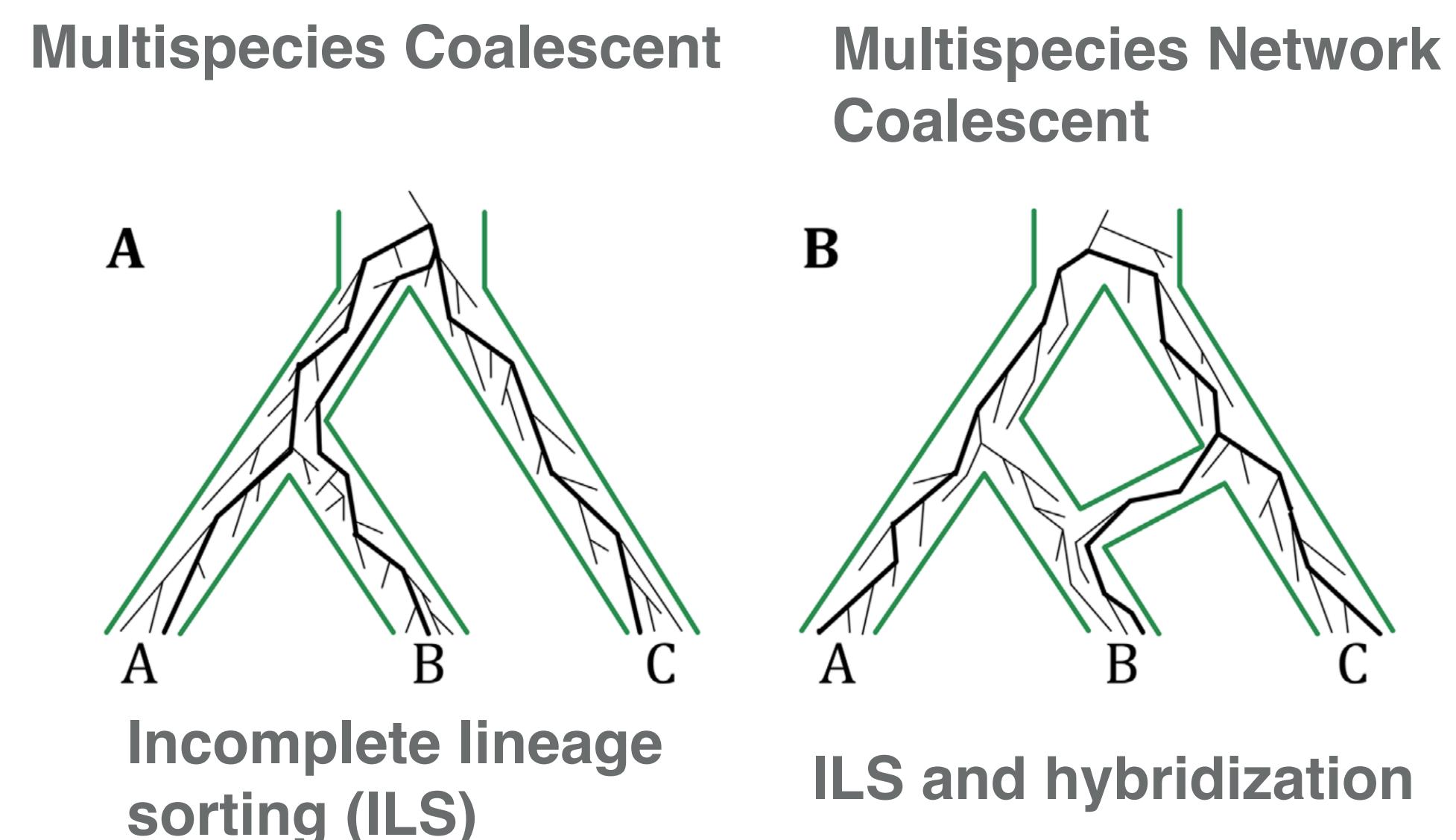


# Analysis of Reticulate Evolutionary Relationships Using PhyloNet

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## Reticulation and ILS



## Input data types

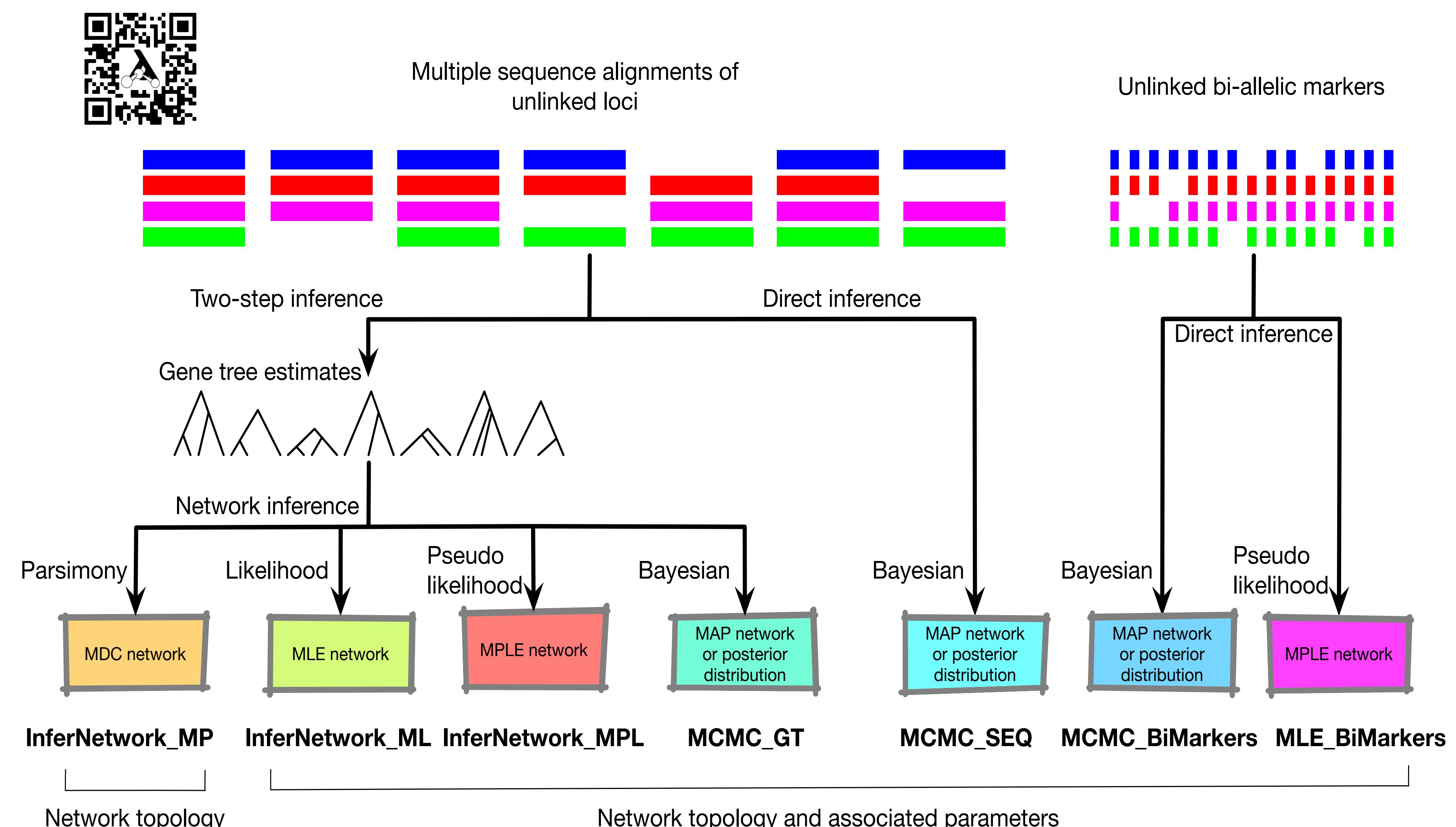
- Bi-allelic markers
  - MCMC\_BiMarkers
  - MLE\_BiMarkers
- Multi-locus sequence alignments
  - MCMC\_SEQ
- Gene trees
  - InferNetwork\_MP
  - InferNetwork\_ML
  - MCMC\_GT
  - InferNetwork\_MPL

## Comparing and summarizing networks

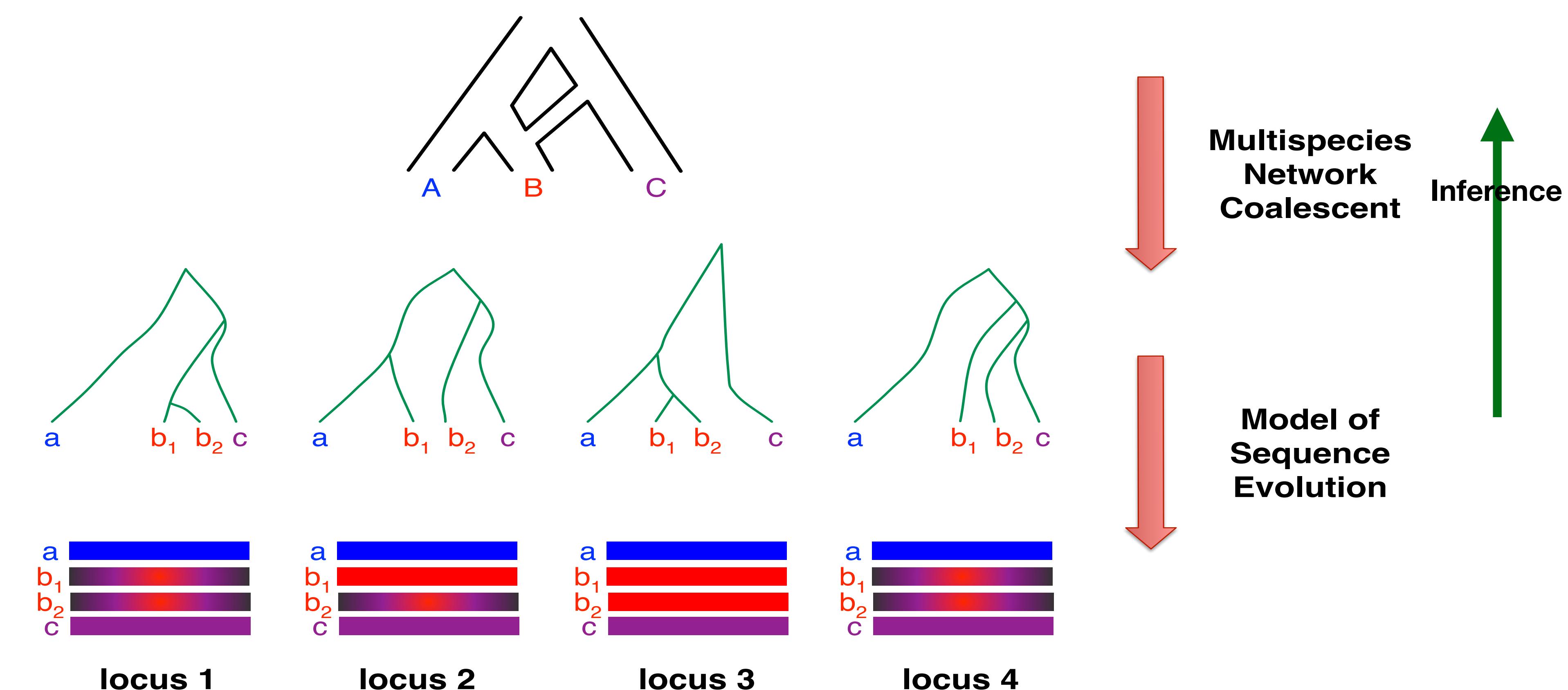
- Displayed Trees
- Backbone Networks
- Tree Decompositions
- Tripartitions
- Major Trees

## PhyloNet

## bioinfocs.rice.edu/phylonet



## Network inference: generative model



## Future development

- Adding gene duplication & loss
- Scalability improvement

## Scalability

To handle large dataset, PhyloNet implements the following methods:

- Maximum pseudo-likelihood  
*(Approximation of likelihood)*
  - InferNetwork\_MPL
- Tree-based augmentation:  
*(Fixing a starting tree topology and augmenting it to a network)*
  - InferNetwork\_MP -fs
  - InferNetwork\_MPL -fs
- Divide-and-conquer  
*(Inferring subnetworks, and merging them together )*
  - NetMerger

## References

- Advances in Computational Methods for Phylogenetic Networks in the Presence of Hybridization. RA Elworth, Huw Ogilvie, Jiafan Zhu, and Luay Nakhleh.
- Practical Aspects of Phylogenetic Network Analysis Using PhyloNet. Zhen Cao, Xinhao Liu, Huw Ogilvie, Zhi Yan, and Luay Nakhleh.

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