

# Handling discordance in phylogenetic inferences

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What are reasons that a 'gene tree' may not show the same relationships as the species tree?

- ▶ incomplete lineage sorting
- ▶ hybridization
- ▶ horizontal gene transfer
- ▶ gene tree error

How do you estimate relationships in the face of these processes?

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It depends what question you are trying to answer!

## Concatenation

Combine all genes or regions for each sample or taxon.

Advantages:

- ▶ Relatively fast
- ▶ Provides single answer (interpretable!)
- ▶ May result in similar or same inferences as more complex methods, especially when gene tree incongruence is rare. Tonini et al. (2015)

Disadvantages:

- ▶ Final tree often doesn't match any of the individual gene trees, and can be the wrong spp tree Kubatko and Degnan (2007)
- ▶ Incorporating coalescent models can improve accuracy Edwards et al. (2016)
- ▶ Potentially interesting conflicting signals are lost Hahn and Nakhleh (2016)

## Gene tree methods

Infer individual gene trees, and combine.

Advantages:

- ▶ Captures gene tree variation
- ▶ Can focus on loci of interest (e.g. Hahn and Nakhleh (2016))
- ▶ Can model variation across gene trees in multiple ways - ILS, HGT, hybridization, and assess model fit.

Disadvantages:

- ▶ Shorter sequences result in higher error
- ▶ Loci from many approaches for generating genomic data are too short to estimate individual trees (SNPs or short loci)

## Gene tree methods

Infer individual gene trees, and combine.

Coalescent analyses

- ▶ Astral: <https://github.com/smirarab/ASTRAL/blob/master/astral-tutorial.md>
- ▶ MP-EST: <https://github.com/lliu1871/mp-est>
- ▶ BUCKY: <http://pages.stat.wisc.edu/~ane/bucky/index.html>

Network/hybridization inference

- ▶ PhyloNet: <https://wiki.rice.edu/confluence/pages/viewpage.action?pageId=39500205>
- ▶ SNaQ: <https://github.com/crsl4/PhyloNetworks.jl/wiki>

## Full data methods

Joint inference of gene trees, model and species tree.

Advantages:

- ▶ Model describes the processes generating the data
- ▶ Full joint likelihood calculation

Disadvantages:

- ▶ Complex models, often very slow to infer for large numbers of taxa (months!)



## Full data methods

### Gene sequences

- ▶ \*BEAST, starBEAST2: <https://taming-the-beast.org/tutorials/StarBeast-Tutorial/>
- ▶ BPP: *Can jointly estimate coalescence and introgression*  
<https://hal.archives-ouvertes.fr/hal-02536475/document>

### SNPs or short loci from across the genome

- ▶ SVDQuartets: *fast, quartet based, so handles missing data well*  
<http://www.phylosolutions.com/tutorials/ssb2018/svdquartets-tutorial.html>
- ▶ SNAPP: <http://evomics.org/wpengine.netdna-cdn.com/wp-content/uploads/2018/01/BFD-tutorial-1.pdf>

## Conclusions:

- ▶ The importance of gene tree discordance, as well as how to address it, depends on both your data and your question!

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