

A Friendly Reminder that AToL Is Really ANoL



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Main Points

- **Reticulation (hybrid speciation and horizontal gene transfer/introgression) is so common in some groups that the AToL project should incorporate it from the outset.**
- **Detection and reconstruction of reticulation is in its infancy.**
- **Combined data analyses will require explicitly ruling out reticulation.**
- **Systematics will need to become more intimate with population genetics.**

Unruly Nature

Whatever is not forbidden will occur.

**-- Gerald Myers
(ca 1980)**

In Other Words

- **If a set of genes can be brought together in a cell, survival and reproduction will be determined by the phenotype produced in the environment of the organism.**
- **If the organism can survive and reproduce as well as or better than its competitors, it “works” no matter the mating/process that produced it**

Evidence of HGT in Bacteria

- Relatively large proportions of bacterial genomes appear to be subject to horizontal gene transfer.
- Recent evidence indicates there is probably a “core” set of genes that are unlikely to be involved in HGT (Daubin et al. 2003. Science 301:829).
- Can these low transfer genes be routinely identified and used for reconstruction?
 - Need to look in order to know

Hybrid Speciation in Eukaryotes

- **Primarily found in plants, but also some fish and amphibians**
 - Also in some reptiles but these are usually sterile asexual lineages.
 - What's up with fungi?
- **Most recent estimates suggest that about 7% of new fern lineages have arisen by hybrid speciation and 3-4% of angiosperm lineages (Otto and Whitten. 2000. Annu. Rev. Genet. 34:40)**

Current Methods for Detecting and Reconstructing Hybrid Speciation are in their Infancy



Phylogenetic Trees: Models, Methods, and Results

- Models of speciation: **YES**
- Models of sequence evolution: **YES**
- Tree distances and accuracy measures:
YES
- Methods and optimization problems for
tree inference: **YES**

Phylogenetic Networks: Models, Methods, and Results

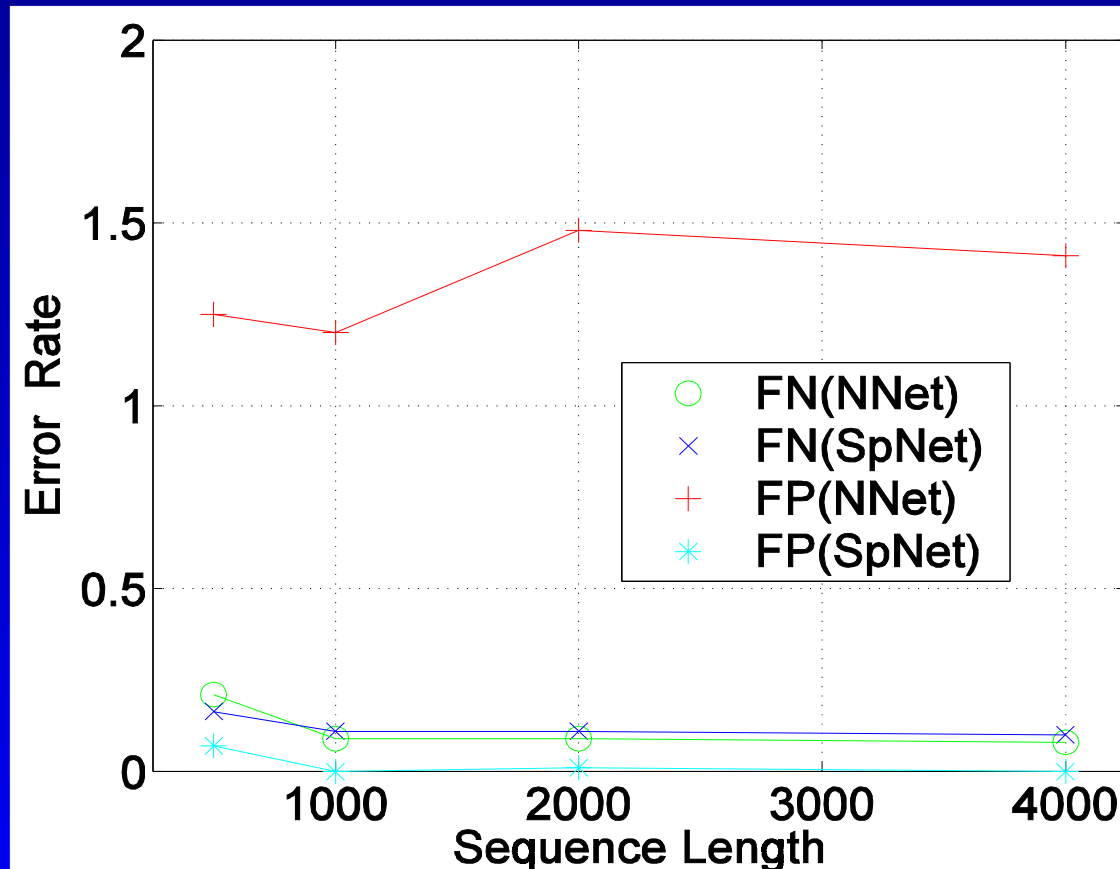
- **Just two years ago:**
 - Models of speciation: **NO**
 - Models of sequence evolution: **NO**
 - Network distances and accuracy measures: **NO**
 - Methods and optimization problems for network inference: **YES/NO**

Where We Are Today

- Models of speciation: **yes**
- Models of sequence evolution: **yes**
- Network distances and accuracy measures: **yes**
- Methods and optimization problems for network inference: **yes**

Reconstruction Quality Model

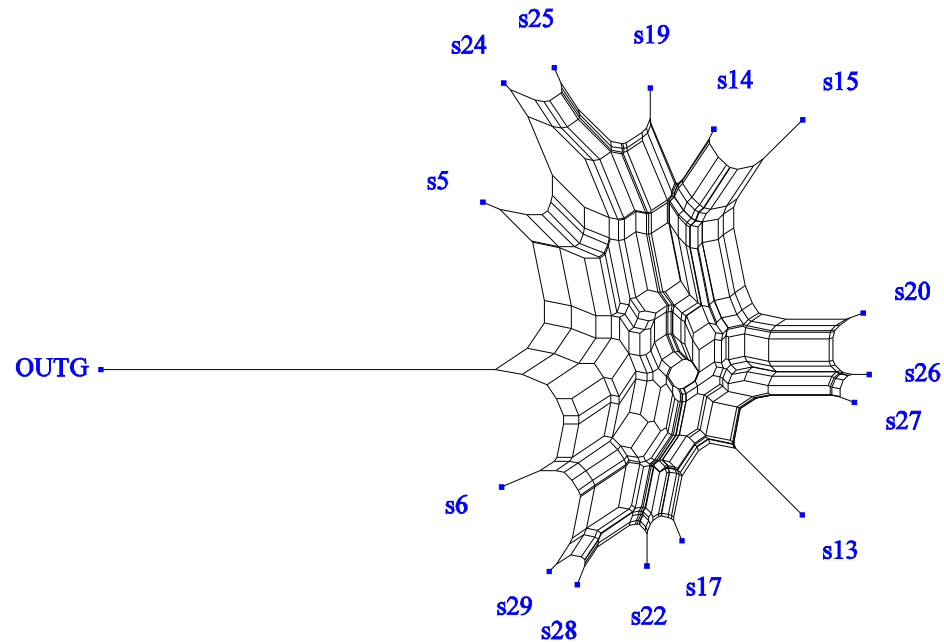
Phylogeny: 20-taxon 1-hybrid network



NeighborNet: False Positives

Title: splitstree.in

Date : Thu Mar 06 22:30:46 2003



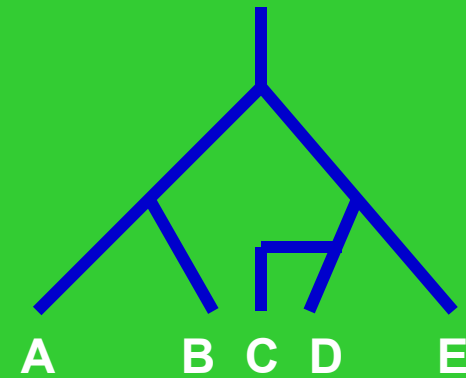
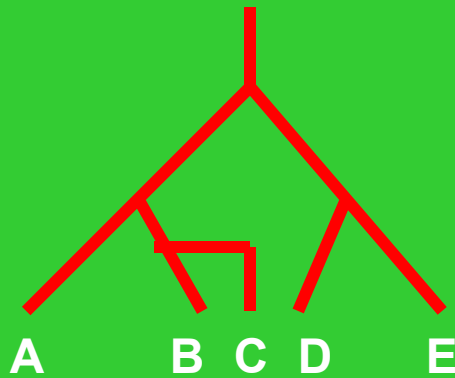
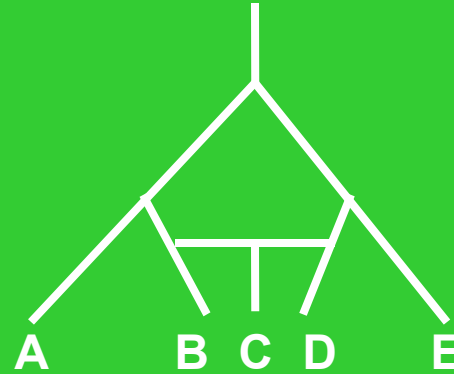
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Open Problems in Hybrid Speciation

- **Detecting reticulation**
- **Representing reticulate evolutionary scenarios**
- **Inferring reticulate evolution**
- **Visualization**

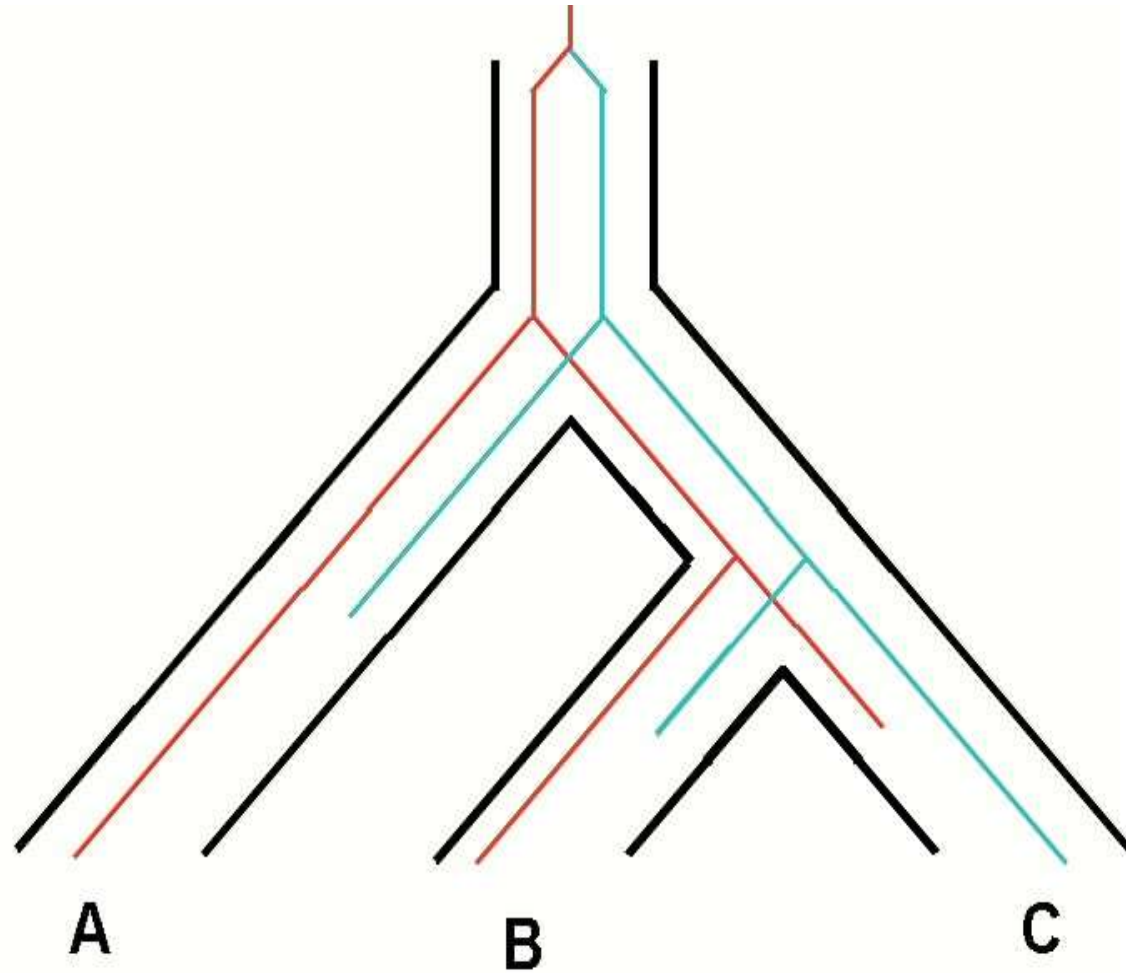
Deciding Whether to Combine Datasets



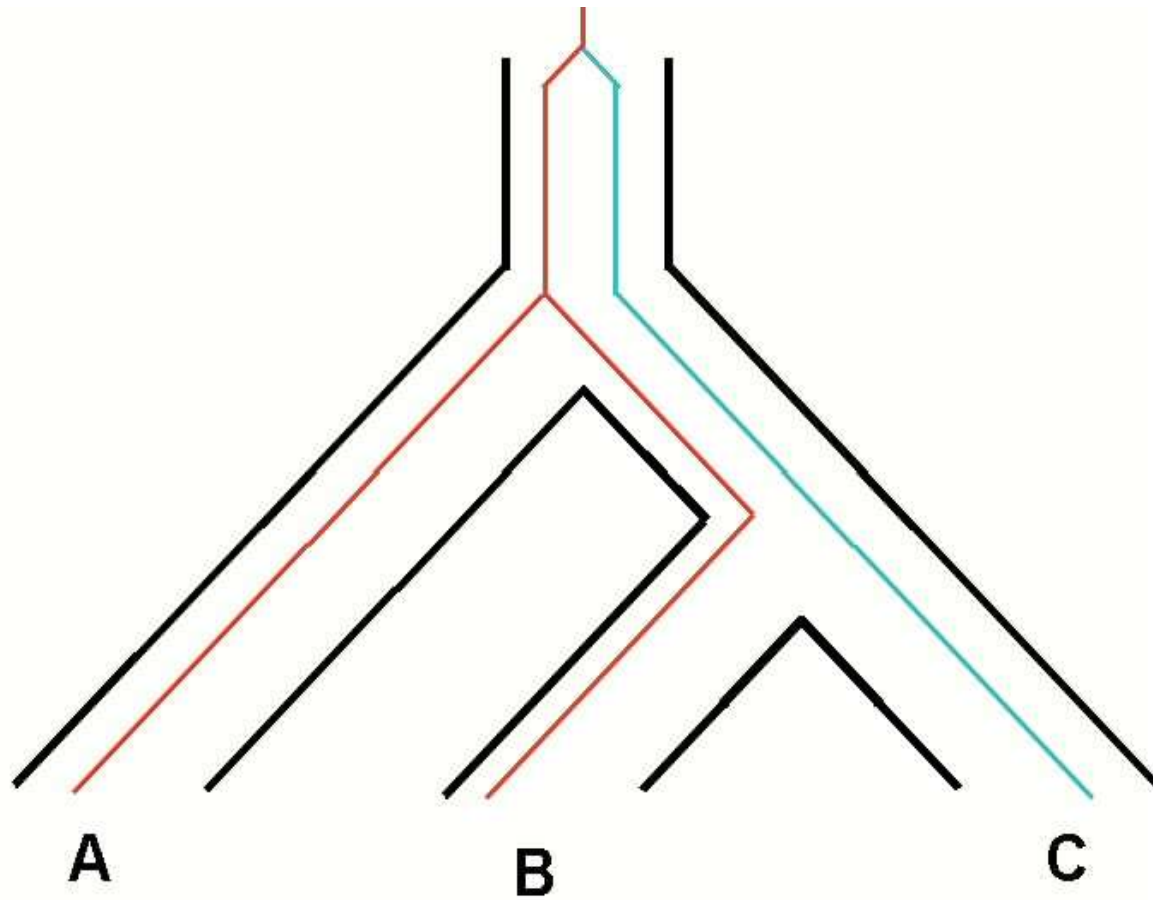
Population Genetic Issues

- **Population genetic reticulation masquerading as hybrid speciation**
 - Meiotic recombination
 - Sexual recombination
- **Lineage sorting**
- **Resolving this will require combining coalescent models with phylogenetic models**

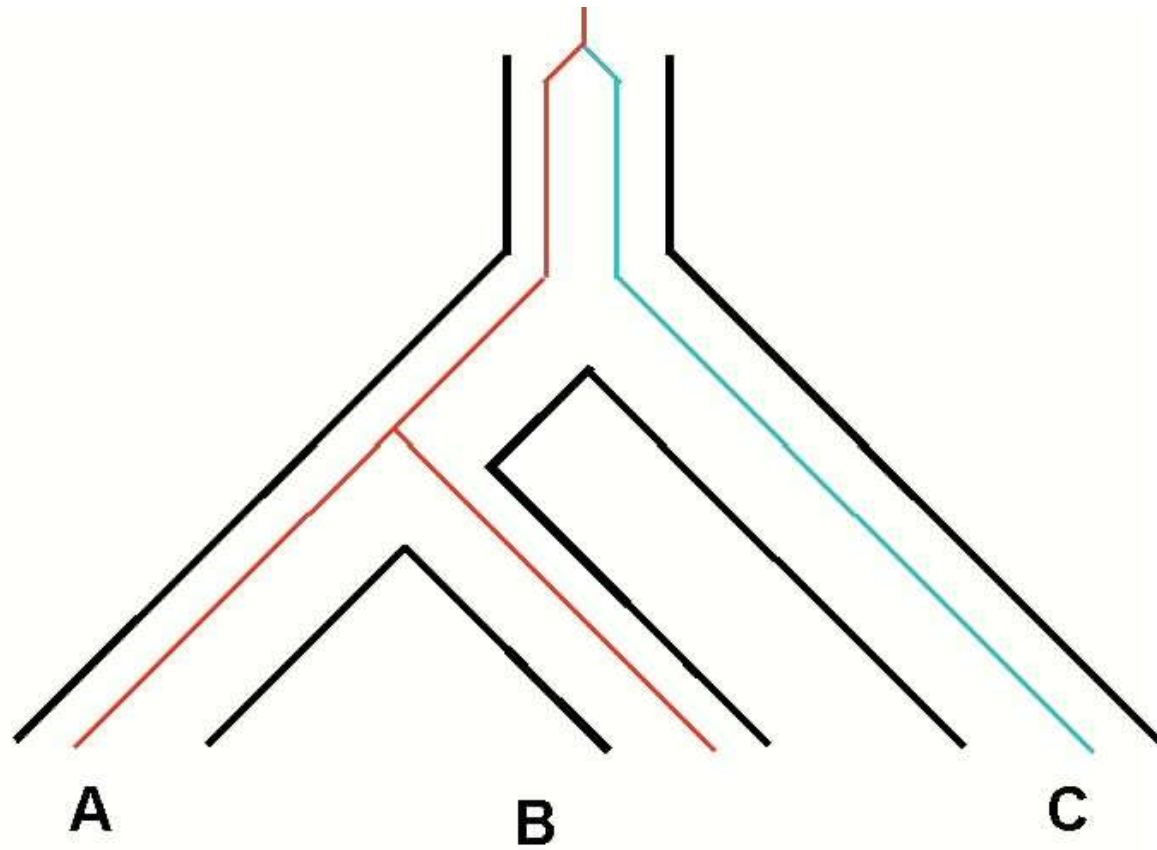
Lineage Sorting: Gene Tree/Species Tree



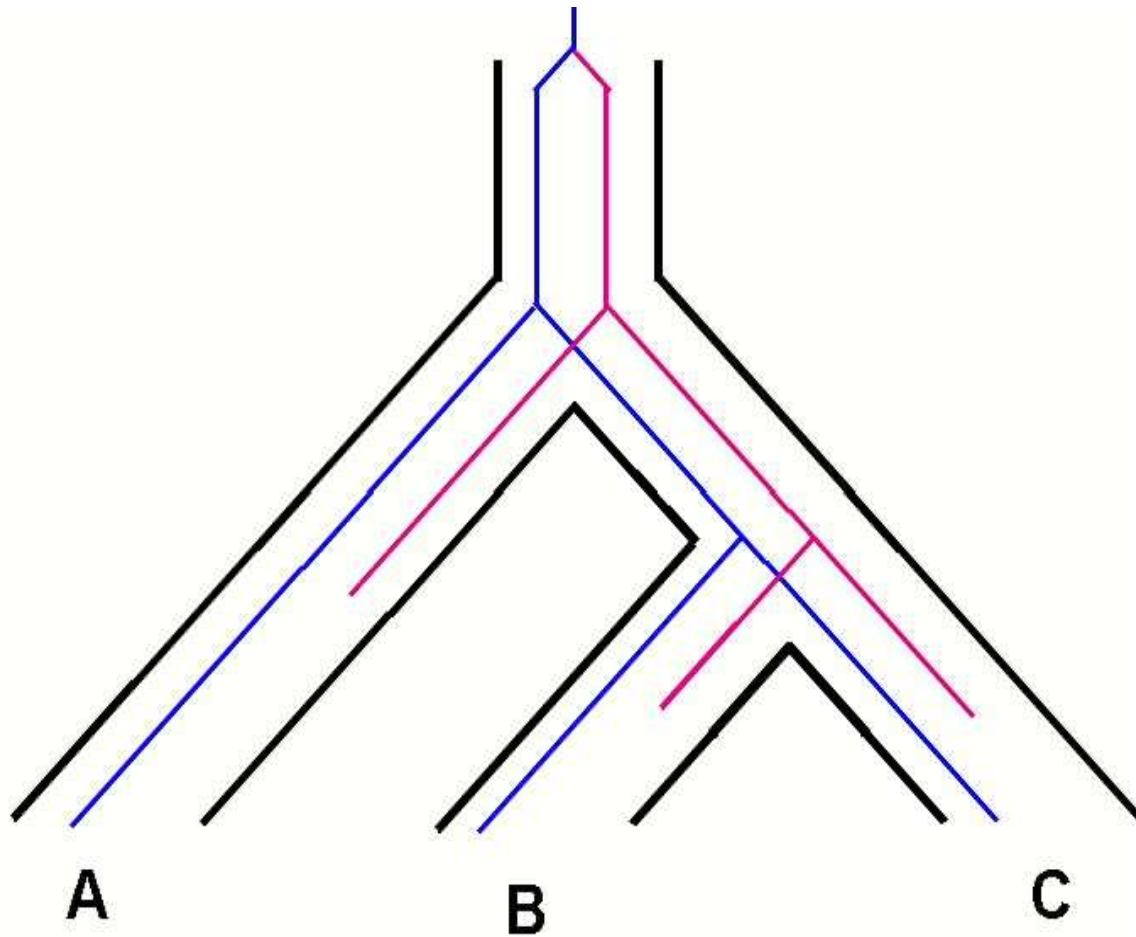
Gene Tree/Species Tree



Gene Tree/Species Tree



Gene Tree/Species Tree



Gene Tree/Species Tree

