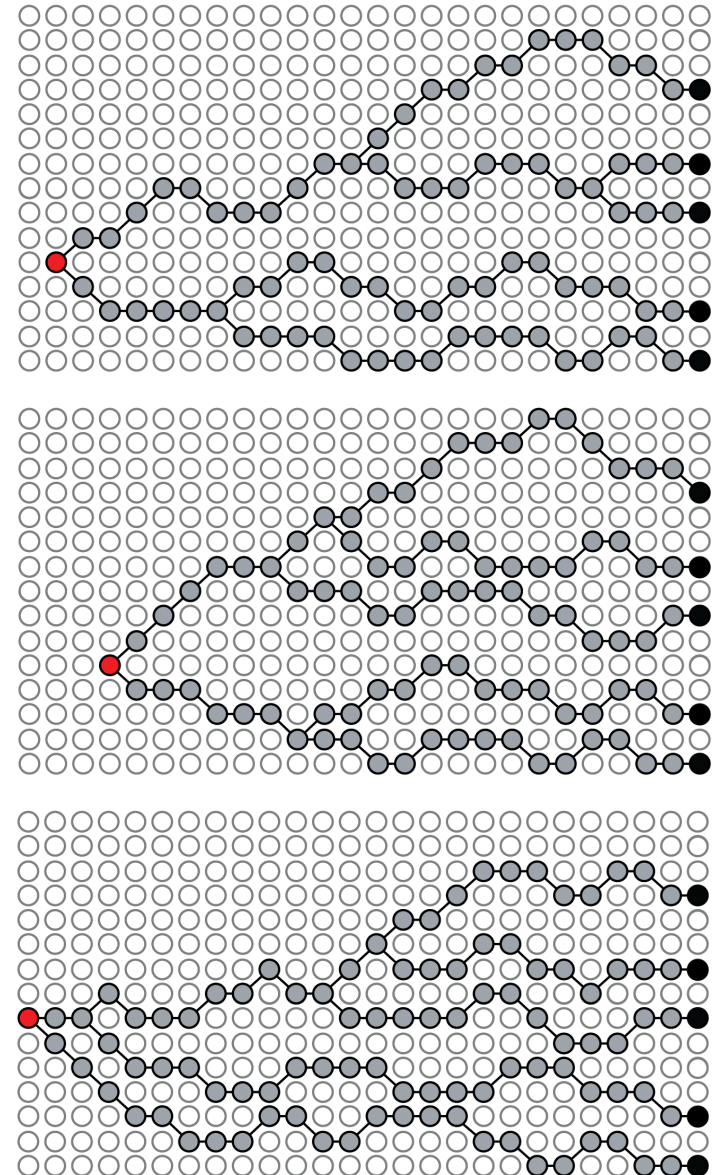

Lecture 2.5

Gene Trees

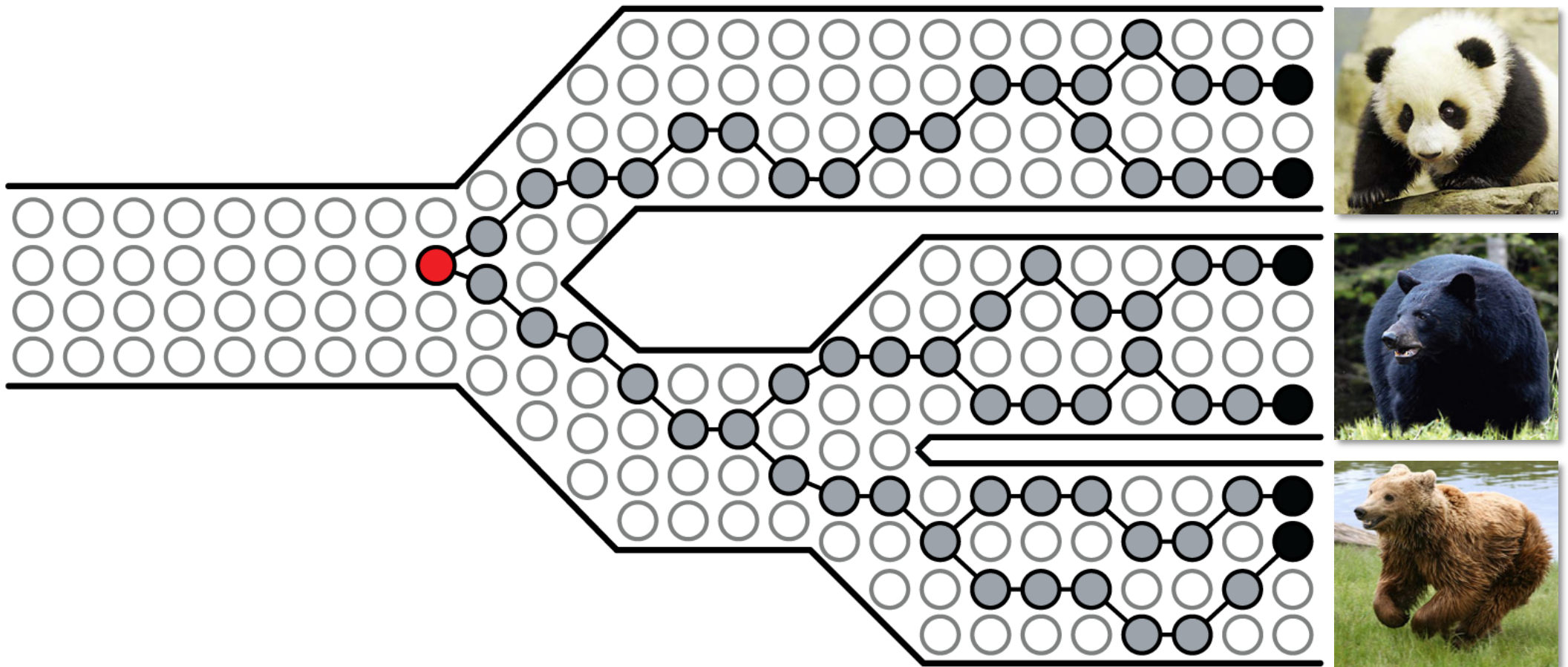
Gene trees in a species

- Genealogies vary stochastically among unlinked loci
- Should not concatenate independent loci in a phylogenetic analysis of intraspecific data
 - Different trees
 - Different coalescence times



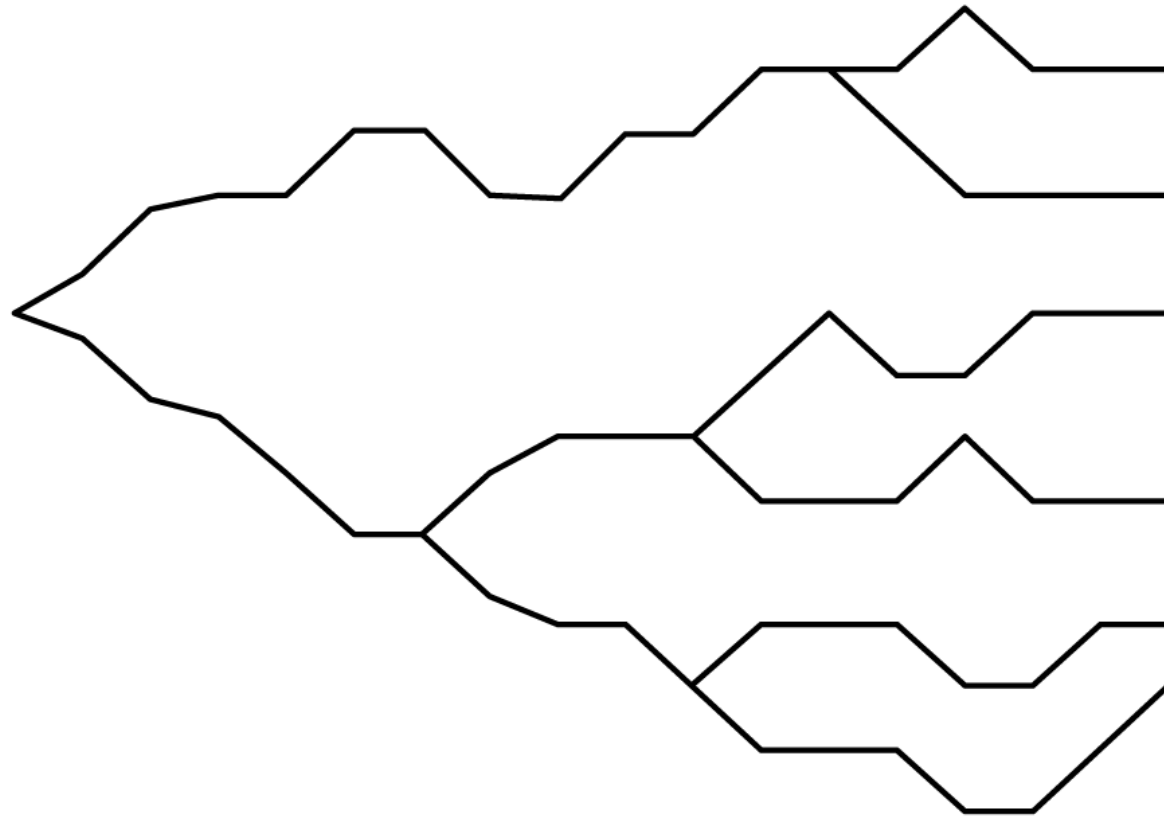
Gene trees in multiple species

- Gene trees are embedded in the species tree



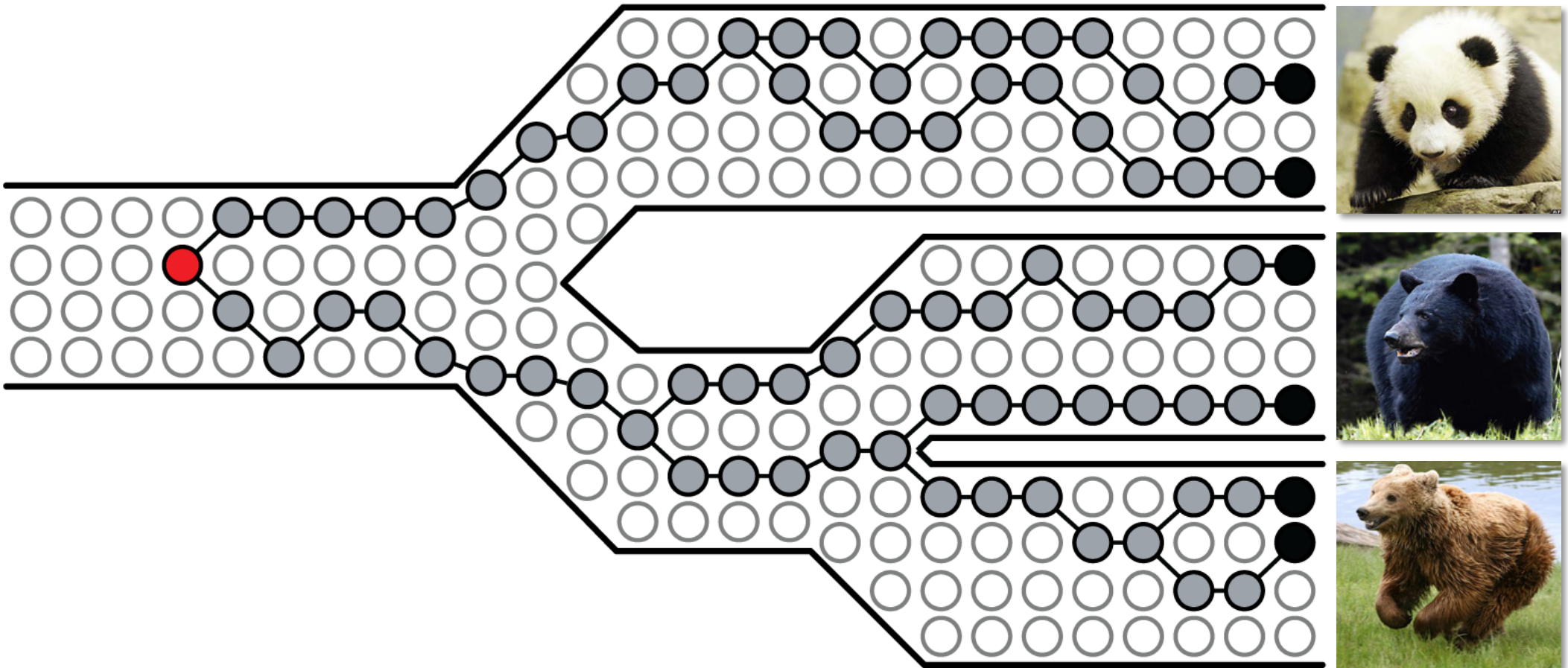
Gene trees in multiple species

- Gene trees are embedded in the species tree



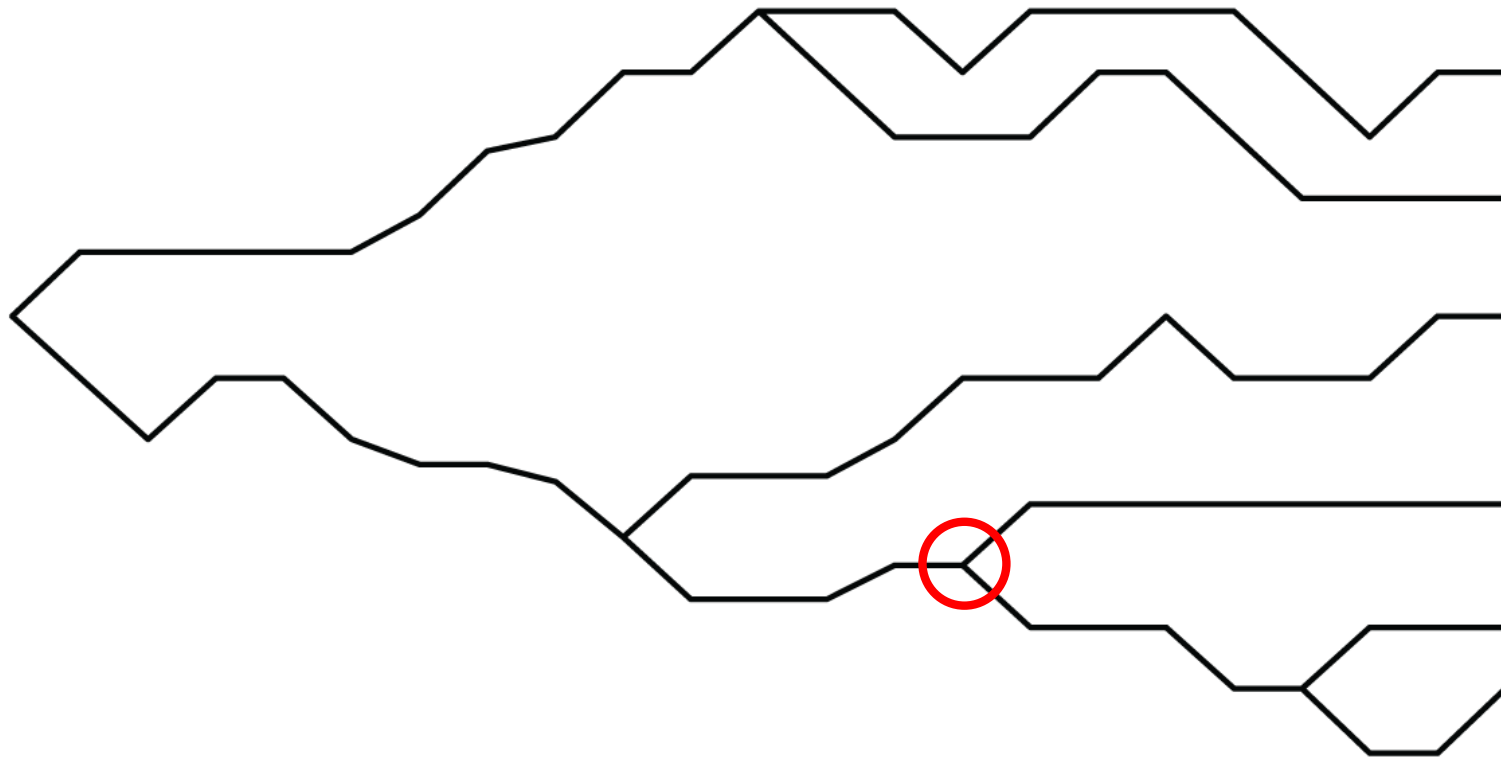
Gene trees in multiple species

- Incomplete lineage sorting



Gene trees in multiple species

- Incomplete lineage sorting



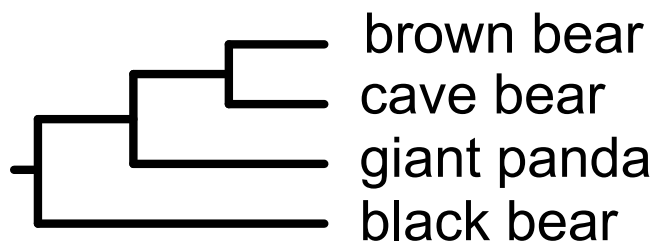
Species tree

- **Incomplete lineage sorting** can lead to gene trees that do not match the species tree
- We can infer the species tree from multiple gene trees
- Three approaches
 1. Consensus
 2. Concatenation
 3. Species-tree methods

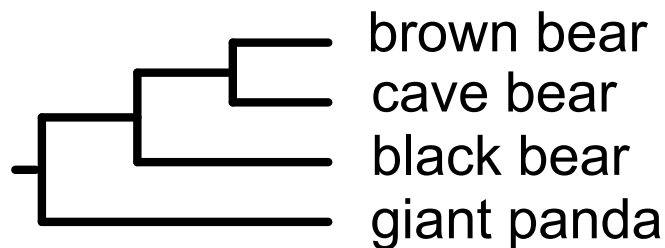
Species tree

1. Consensus

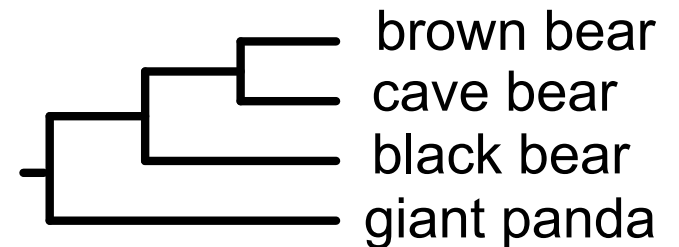
Estimate genealogy from each locus and find the consensus



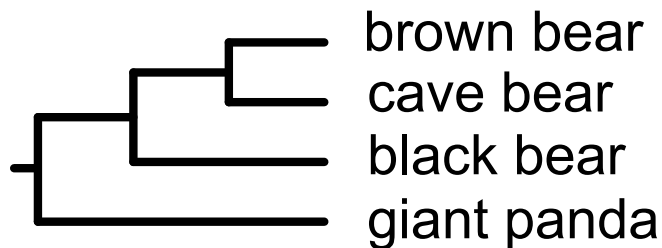
Locus 1



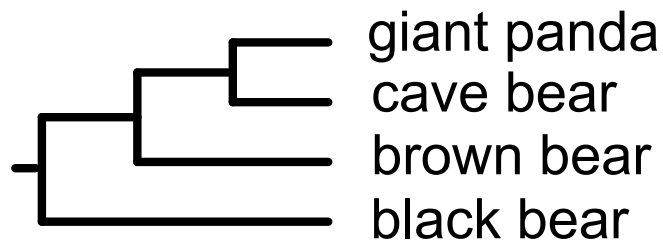
Locus 2



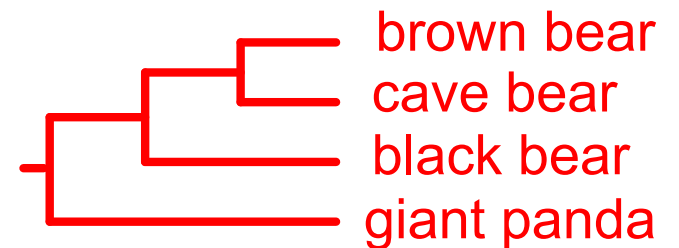
Locus 5



Locus 4



Locus 5



Consensus

But the most frequent gene tree does not always match the true species tree (anomaly zone)

Analysing multiple loci

2. Concatenation

Assume that all loci share the same evolutionary history



But this ignores the occurrence of different gene trees

Species tree

3. Species-tree methods

Estimate the species tree based on gene trees

- Gene trees are independent realisations of a stochastic process (the coalescent) on the same species tree
- Various methods
 - **BEAST* co-estimates gene trees and the species tree

BIOINFORMATICS

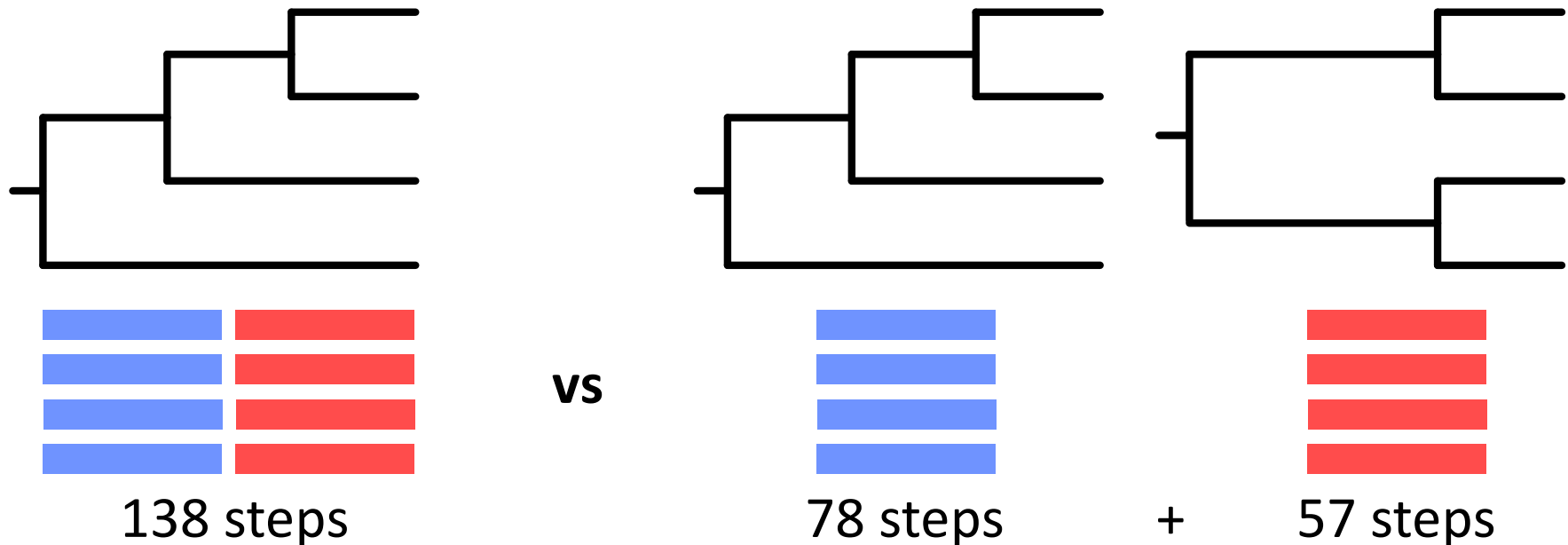
Vol. 30 ECCB 2014, pages i541–i548
doi:10.1093/bioinformatics/btu462

ASTRAL: genome-scale coalescent-based species tree estimation

S. Mirarab¹, R. Reaz¹, Md. S. Bayzid¹, T. Zimmermann^{1,2}, M. S. Swenson³ and
T. Warnow^{1,*}

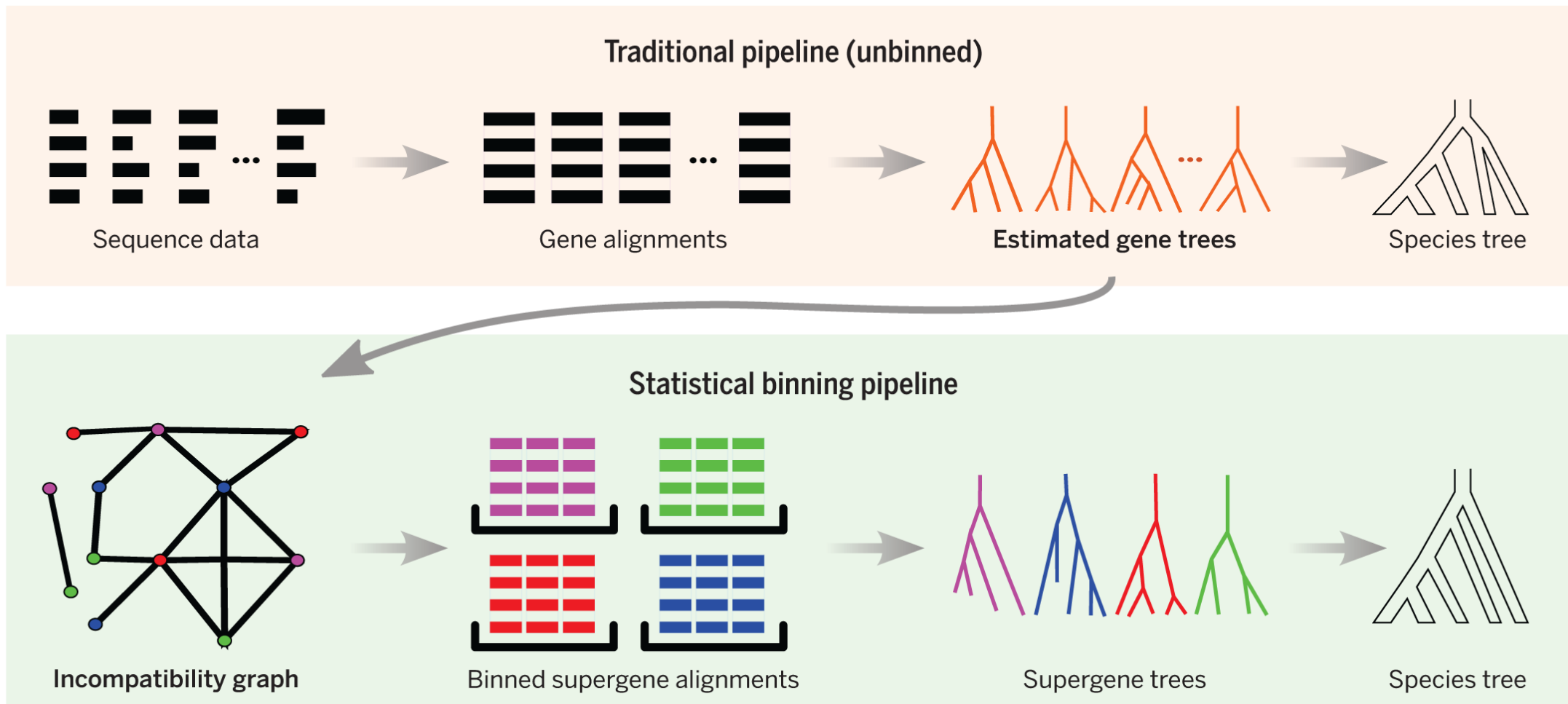
Partition-homogeneity test

- Test for phylogenetic congruence across markers
- Partition-homogeneity (incongruence length difference) test



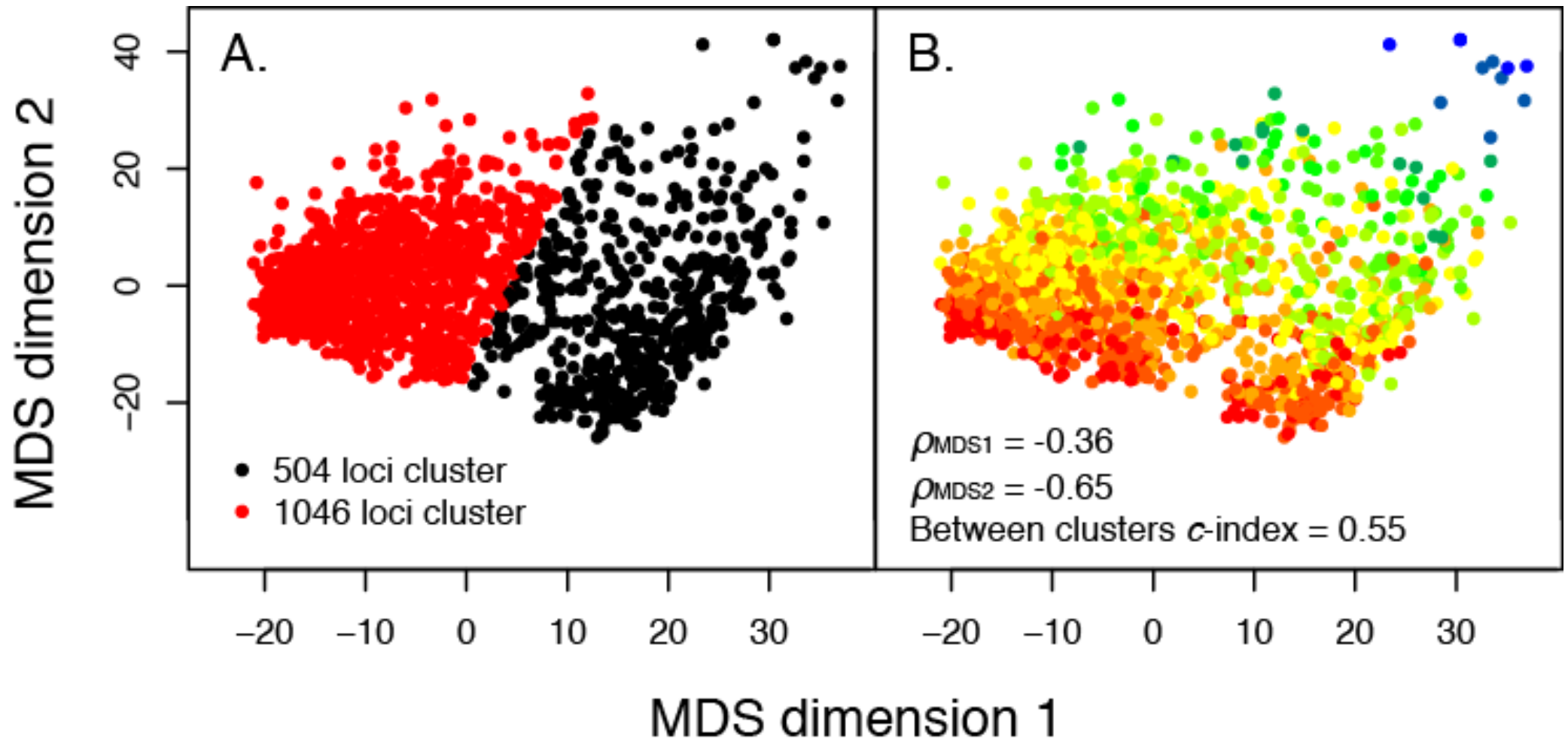
Species tree

- Statistical binning



Species tree

- Topology clustering



Useful references

- **Statistical binning enables an accurate coalescent-based estimation of the avian tree**
Mirarab et al. (2014) *Science*, 346: 1337.
- **Lineage sorting in apes**
Mailund et al. (2014) *Annu Rev Genet*, 48: 519–535.
- **Estimating phylogenetic trees from genome-scale data**
Liu et al. (2015) *Annals New York Acad Sci*, 1360: 36–53.
- **Analysis of phylogenomic tree space resolves relationships among marsupial families**
Duchêne et al. (2018) *Syst Biol*, 67: 400–412.