Why don't my trees work?

Previous work

Check distribution of gene trees
  -need 30+ trees
  -AGTs must be quantified
Divergence times
  -too much variance in real coalescence times
MIGRATE: Bayesian analysis for gene flow
  -treats hybridization as 'gene flow' between unrelated
  groups
Species cohesion
  -some genes under stabilizing selection
Linkage disequilibrium
  -based on sexual recombination

What you need

Species tree

At least one sequence locus from each taxon
 (Effects of recombination untested)

Evolutionary process priors

What to do

- Simulate evolution using your species tree

- Analyze test statistic

  - Minimum sequence-sequence distance

- Repeat many times to get a distribution on the test statistic

Ranunculus analysis

- Formation of Southern Alps

  - Constrains priors

- Small, relatively isolated pockets

  - Increases effective population size

One hybridization

Other incongruence
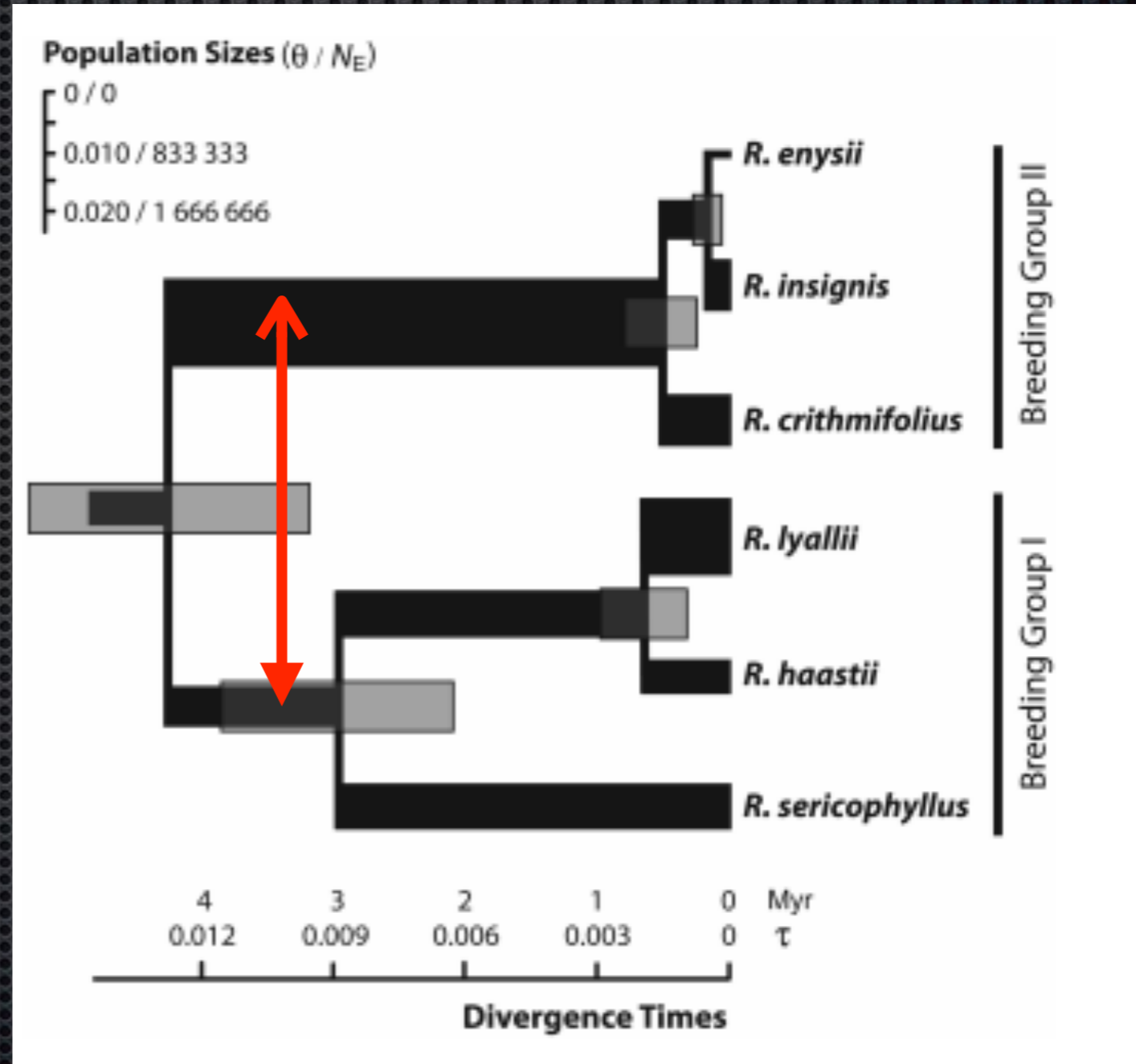
Issues

* MCMCcoal species tree strictly inaccurate under hybridization

    * Hybridization later detected

* Some hybridizations undetectable

* Gene tree parsimony is statistically inconsistent

    * Gene trees themselves maximally parsimonious

* Recombination has entirely unknown effects

    * nrITS locus used in this study exhibits recombination/selection elsewhere

Why do this at all?

It's complicated
It's inaccurate

What's the point of species trees if we can't find hybridizations?