Testing the parallel speciation hypothesis using phylogenomic data in Californian skinks (*Plestiodon*)

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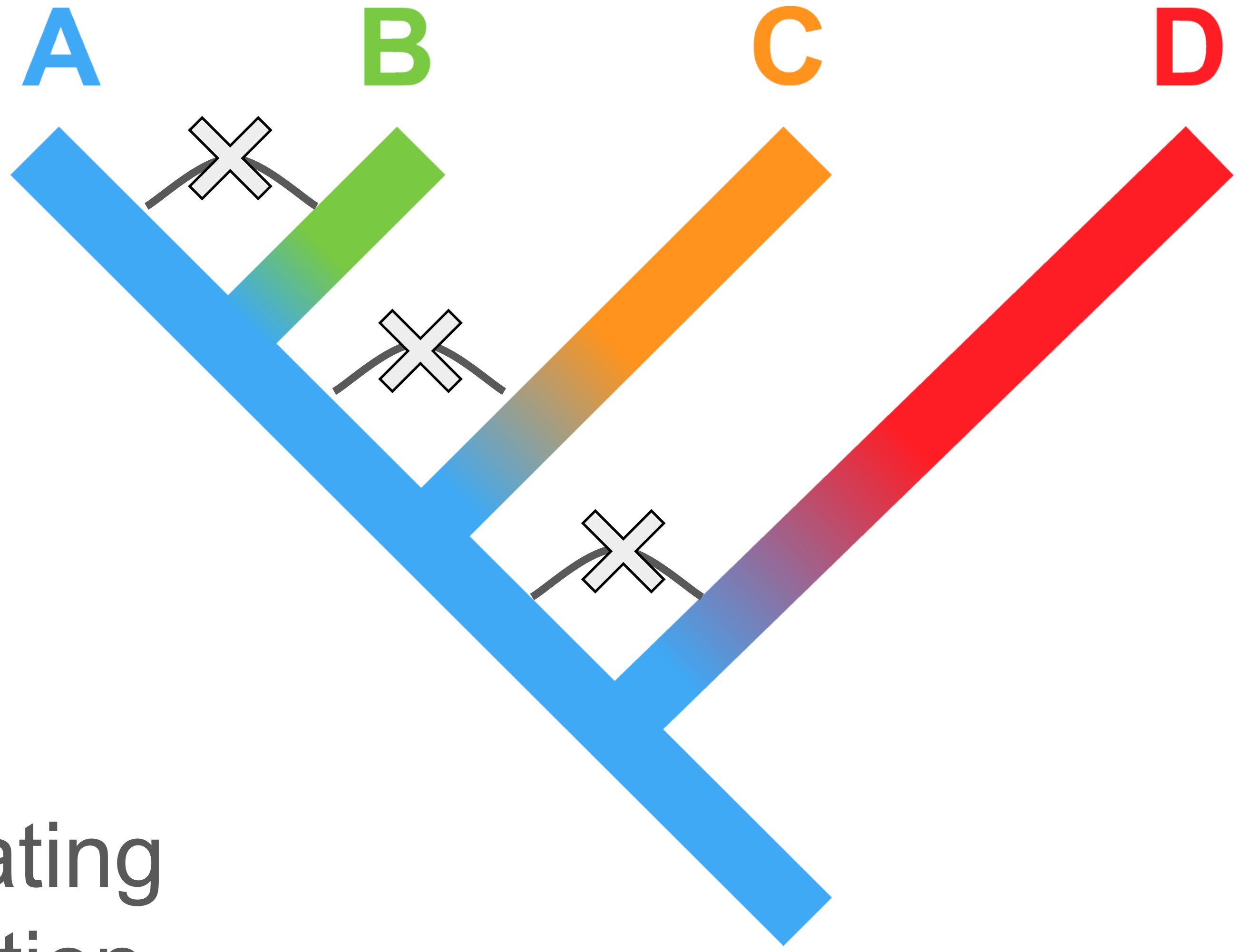
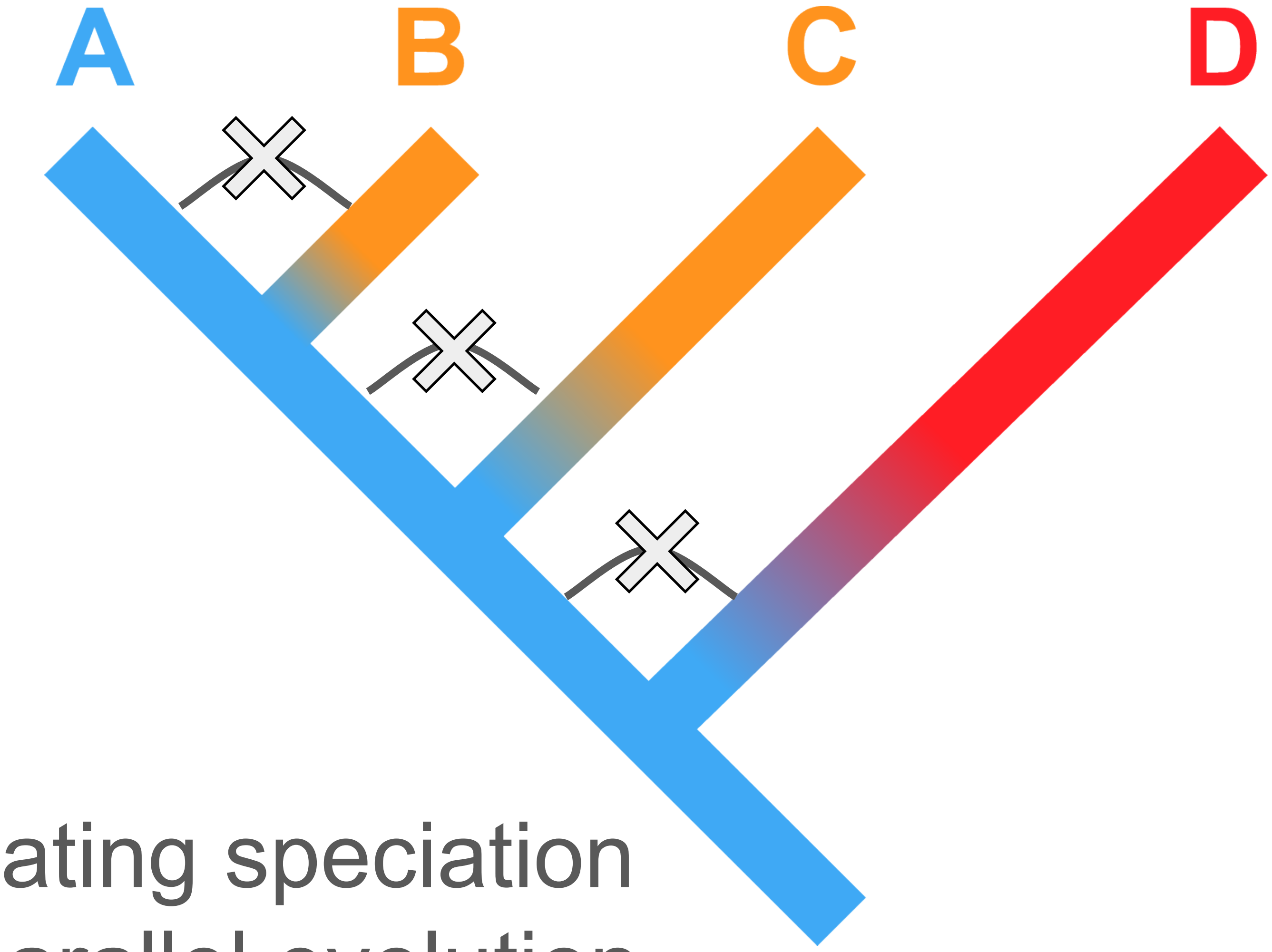
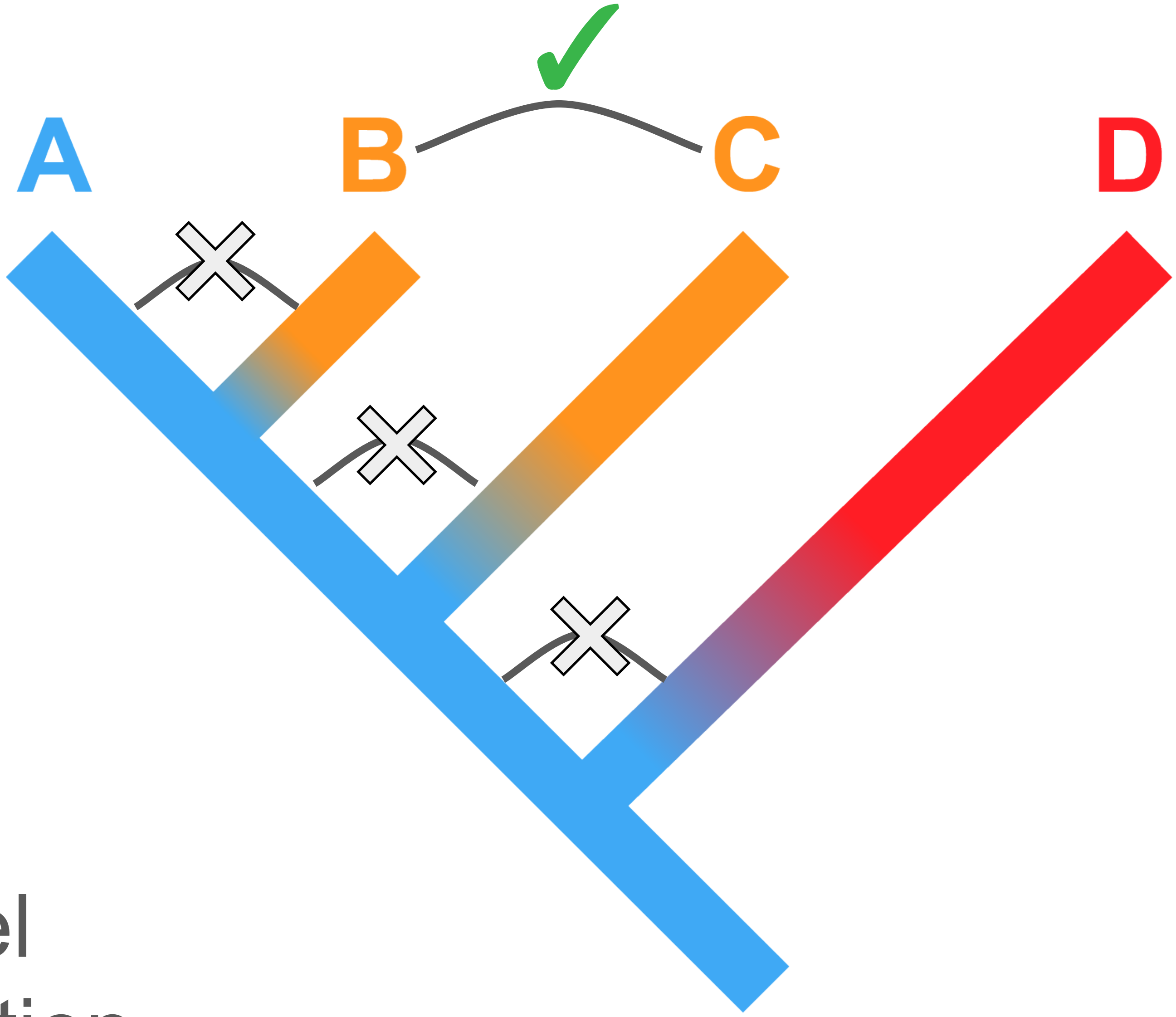
Photo by J. Maughn



Bifurcating
speciation

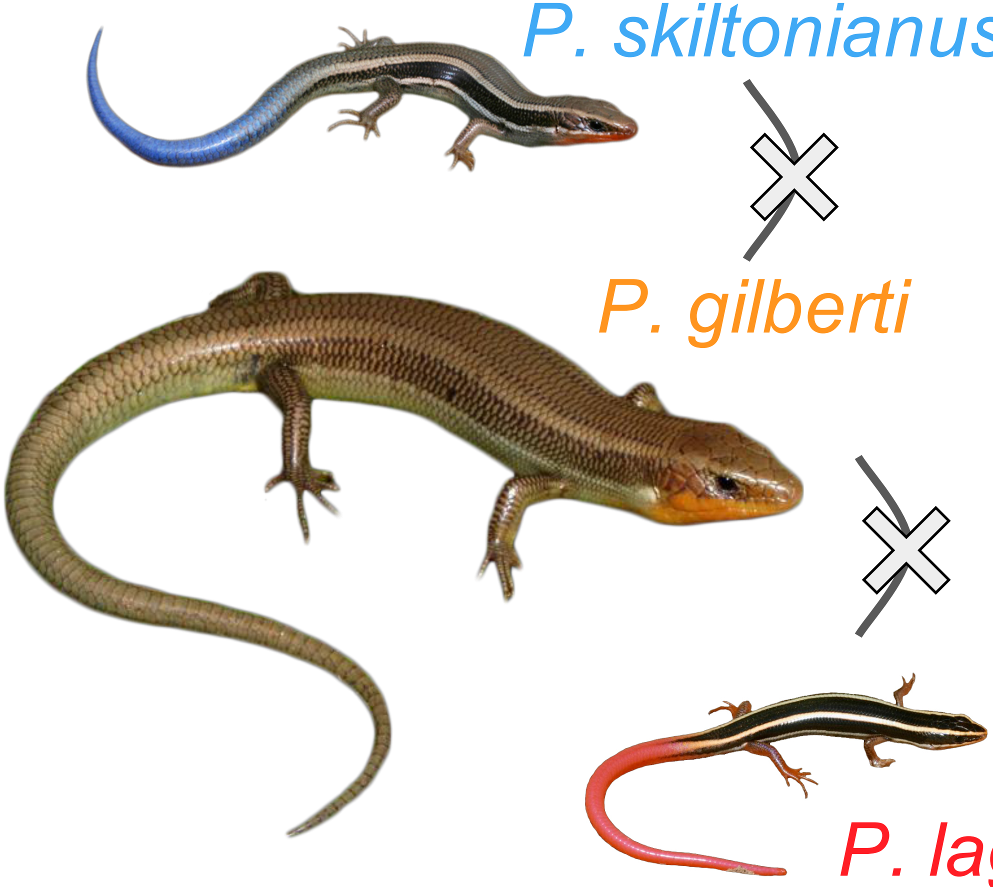


Bifurcating speciation with parallel evolution



Parallel speciation

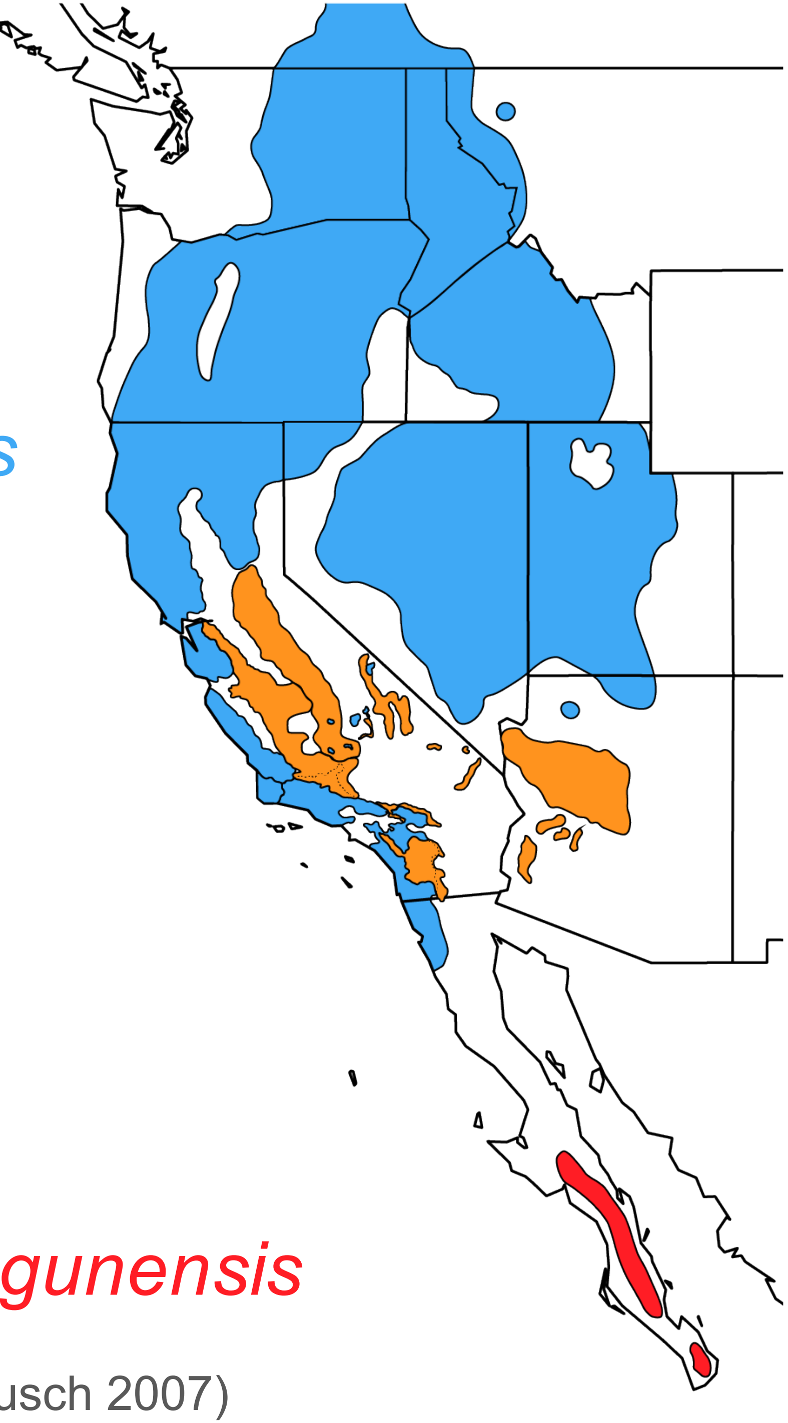
The *Plestiodon skiltonianus* species complex



P. skiltonianus

P. gilberti

P. lagunensis



(Reeder and Richmond 2002; Richmond and Jockusch 2007)

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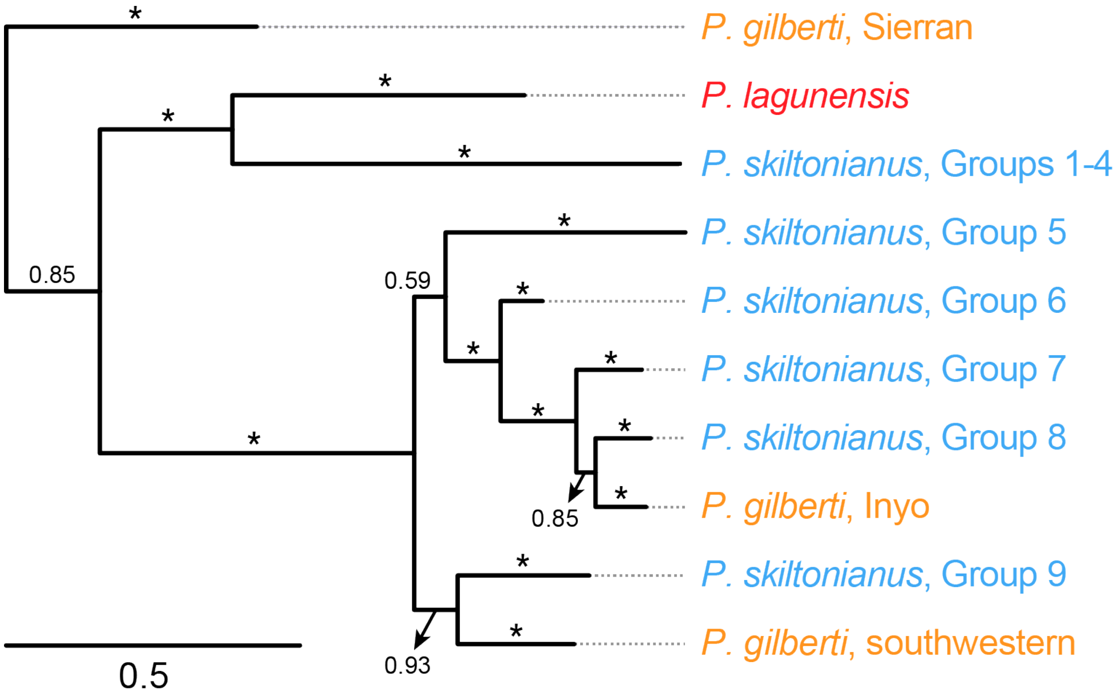
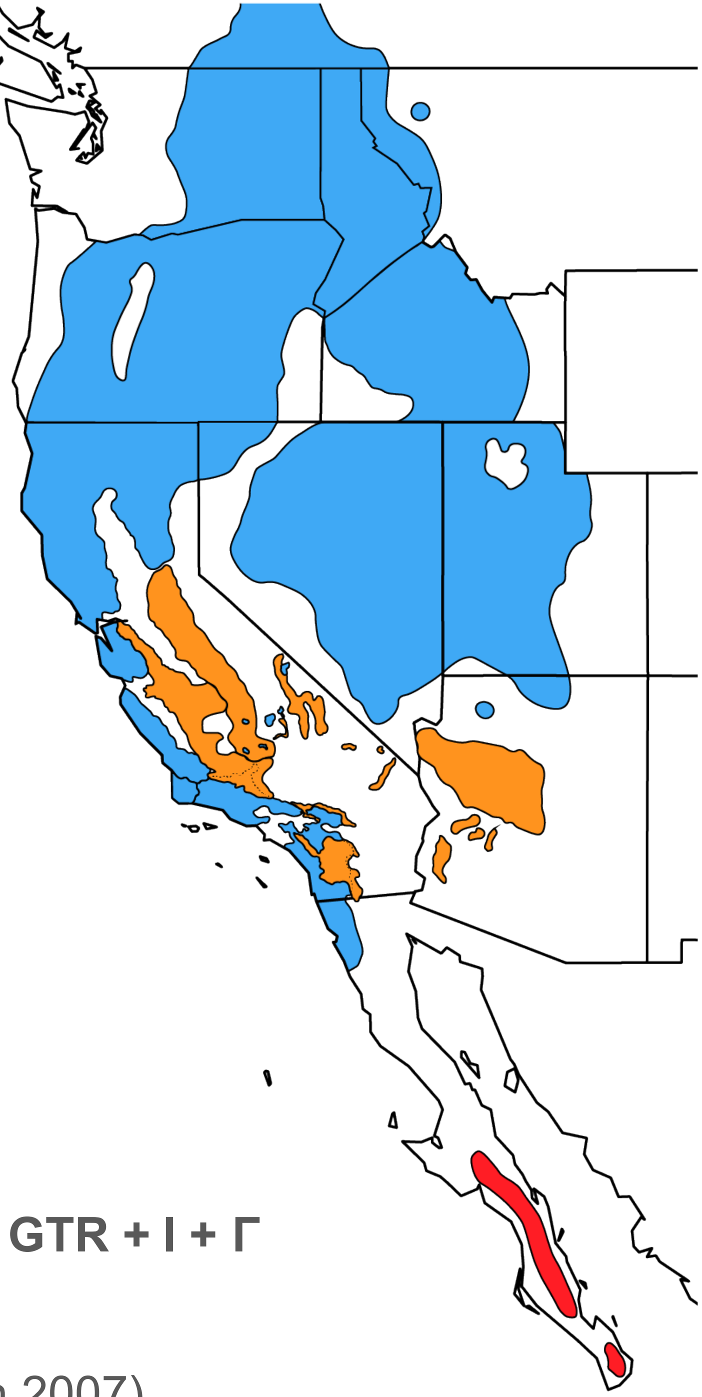




MrBayes, tRNA & ND4 mtDNA loci, HKY + I + Γ & GTR + I + Γ

* denotes >= 95 pp

(Reeder and Richmond 2002; Richmond and Jockusch 2007)

Hypothesis: The 3 mtDNA clades of *P. gilberti* have undergone parallel speciation

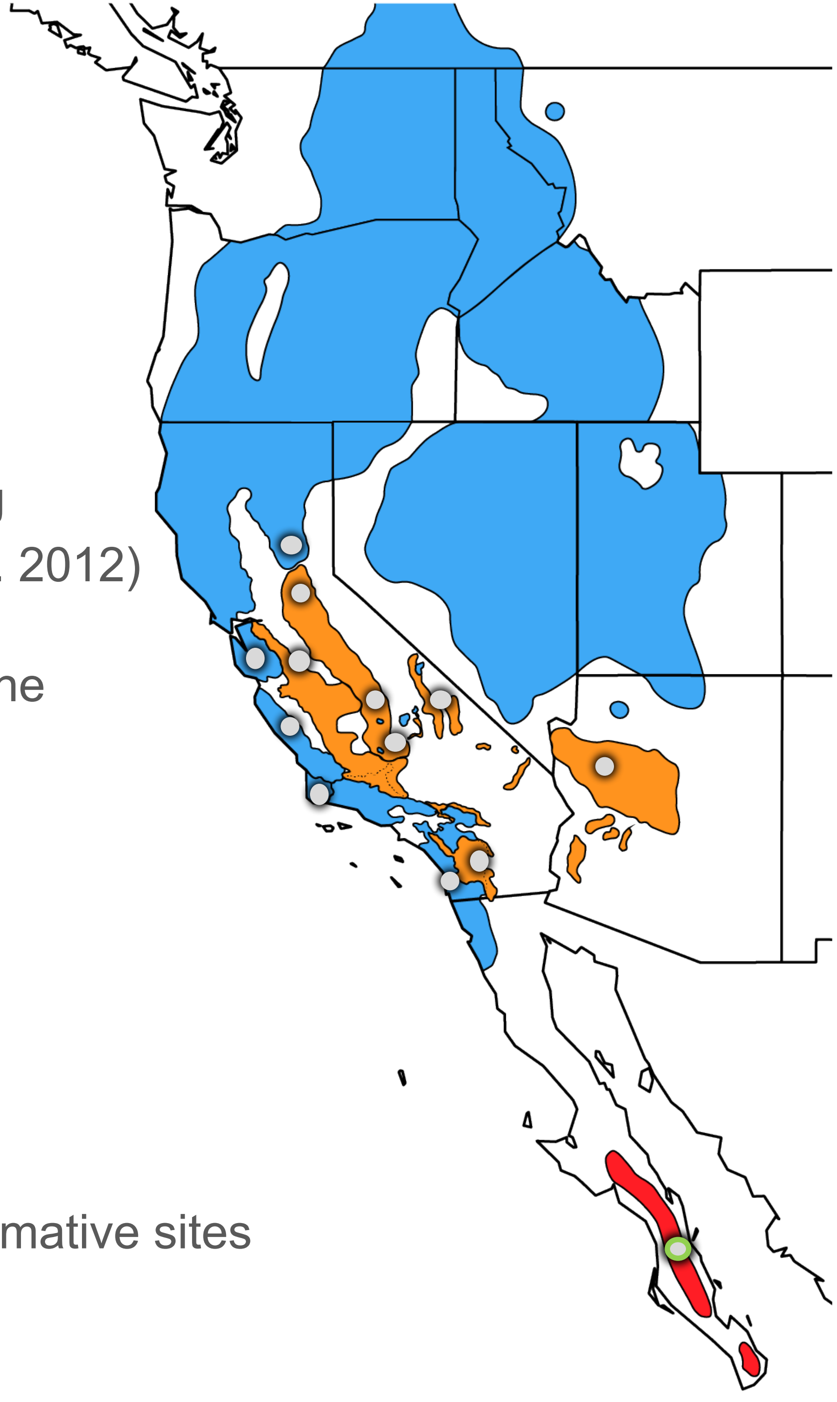
✓ 1. **Reproductive isolation** from non-parallel descendant populations.

✓ 2. **Reproductive compatibility** with descendant populations that share the parallel trait.

? 3. **Independent origins** of parallel traits responsible for reproductive isolation.

Goal: Test the independent origins of *P. gilberti* using modern phylogenomic techniques.

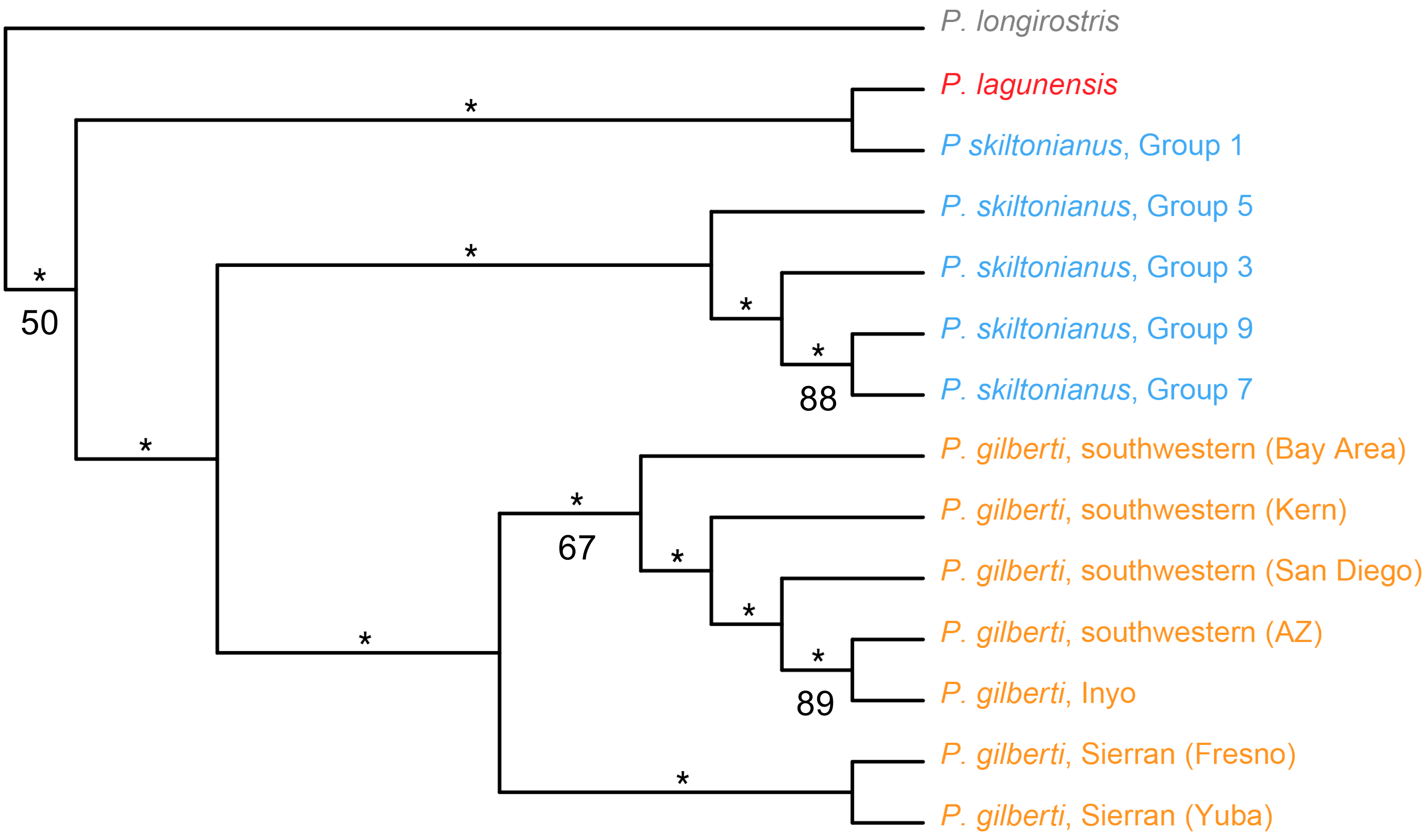
Testing independent origins of *Plestiodon gilberti*



Data:

- Sequence hundreds of nuclear loci using anchored phylogenomics (Lemmon et al. 2012)
- 14 representative samples from across the *P. skiltonianus* complex
    - 387 phased loci
    - 1662 bp, mean locus length
    - 646442 sites
    - 5.4% total missing data
    - 12406 total phylogenetically informative sites

Coalescent-based species tree results

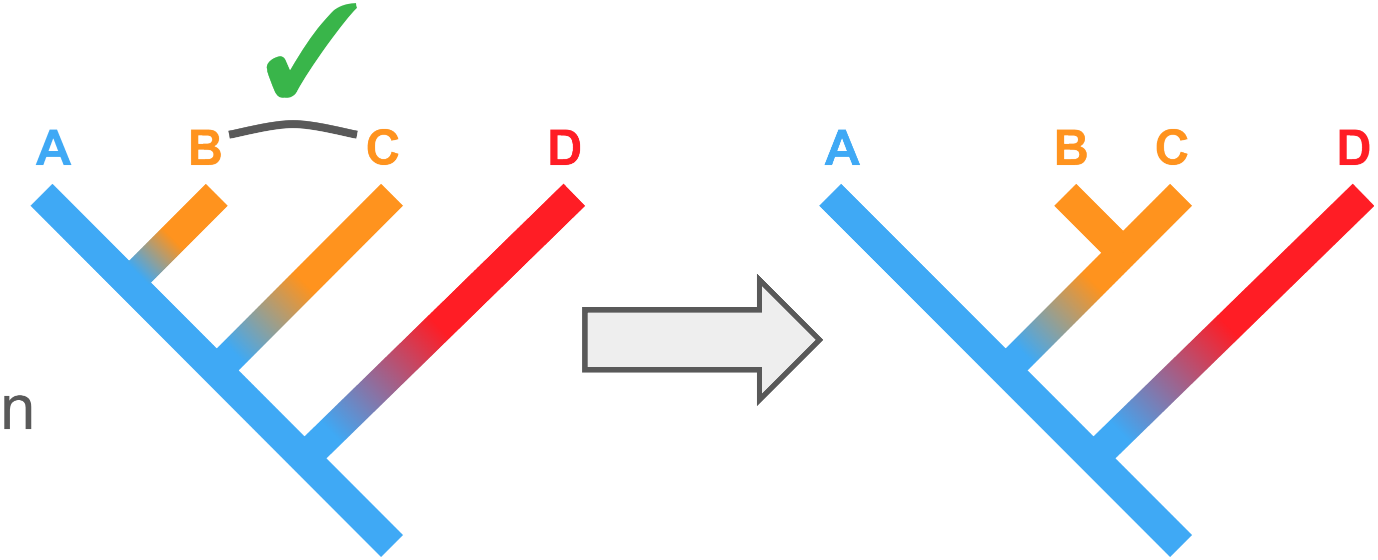


ASTRAL II w/ RAxML anchored loci gene trees; SVDquartets w/ anchored loci

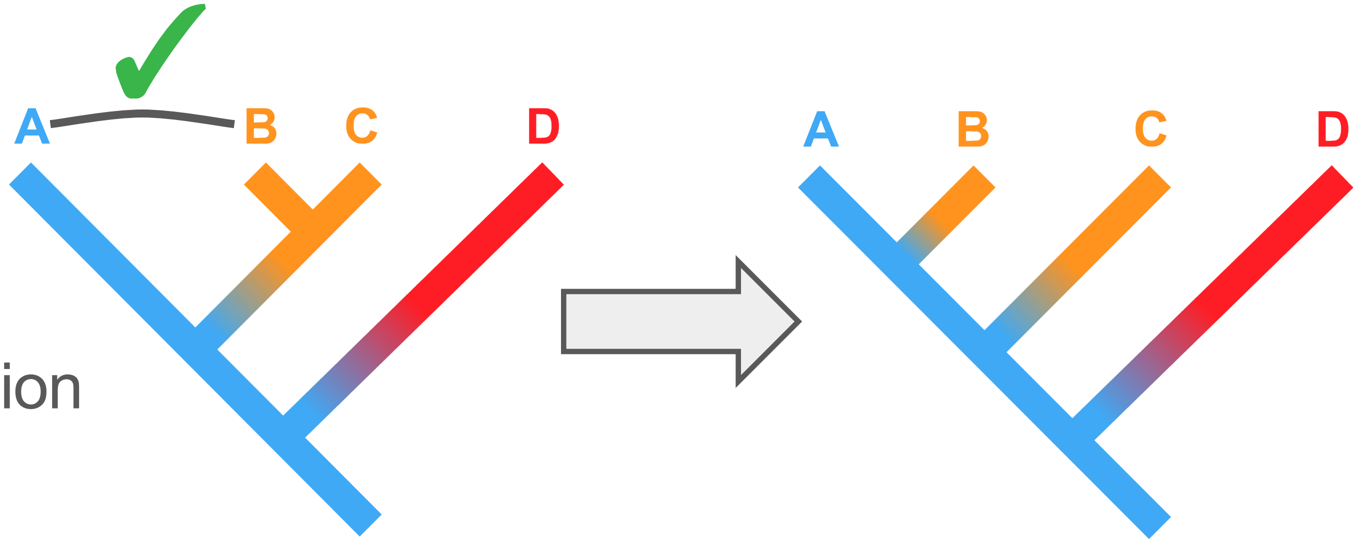
* denotes >= 95 bootstrap support, lower SVDquartet support values reported below

What’s the true evolutionary history?

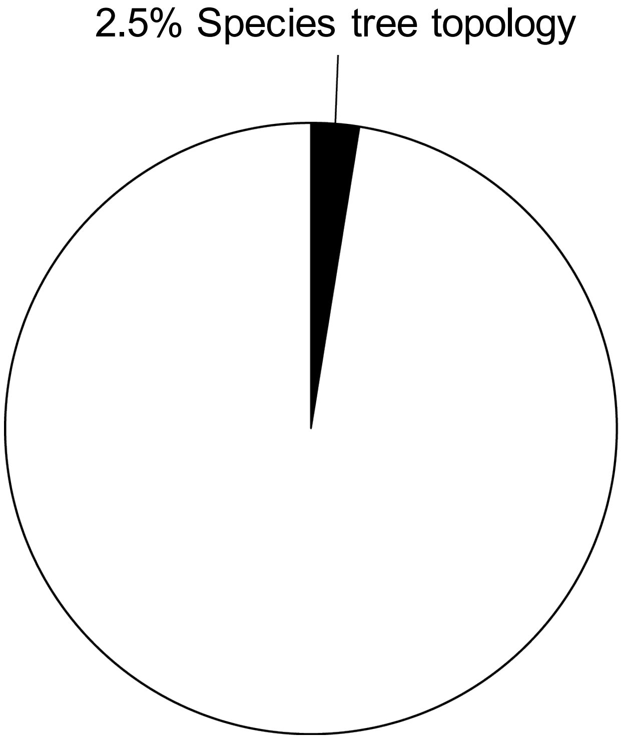
Scenario 1:
Parallel speciation
(Leaché et al., 2013)

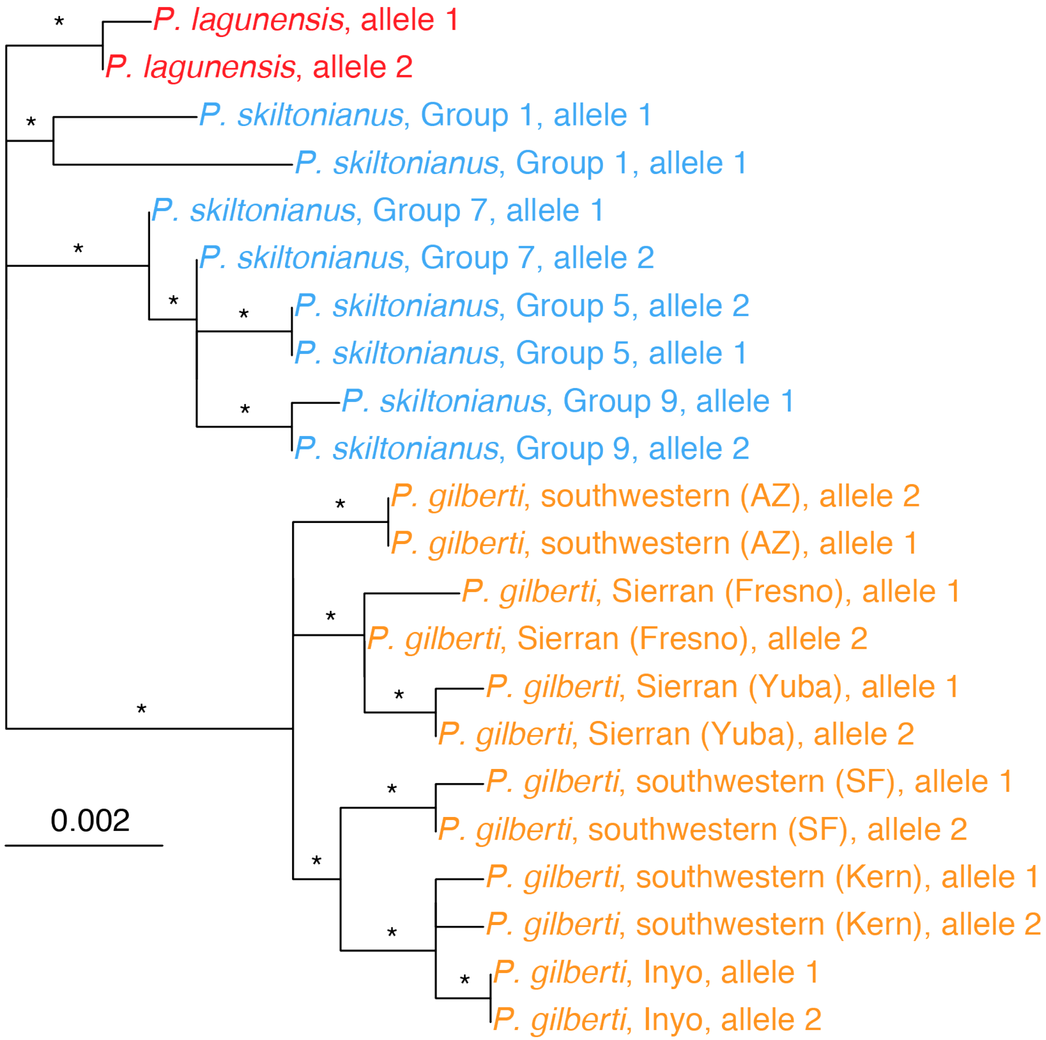


Scenario 2:
mtDNA introgression



The distribution of gene tree topologies





MrBayes, anchored loci

Unpartitioned models fit with PartitionFinder, * denotes >= 95 pp

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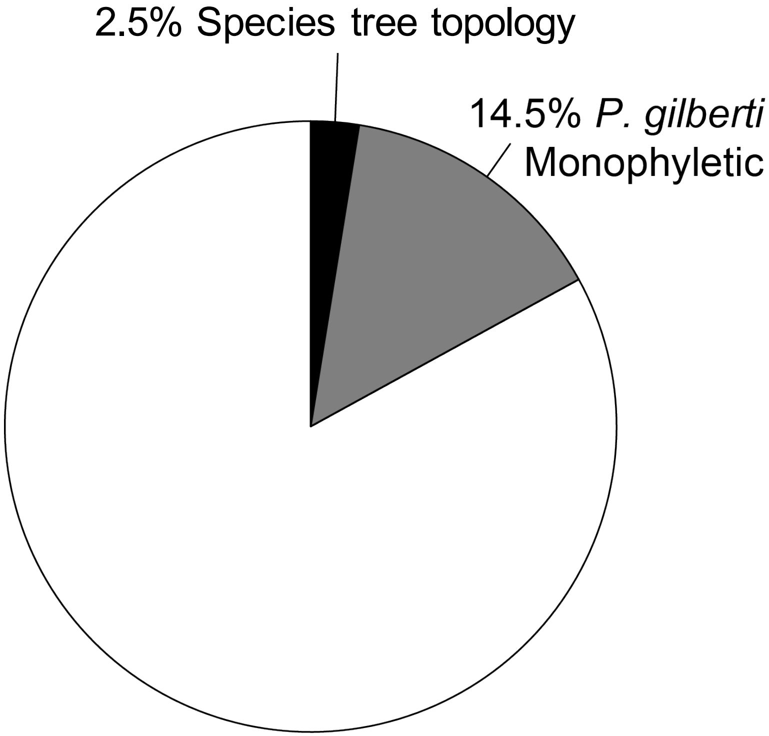

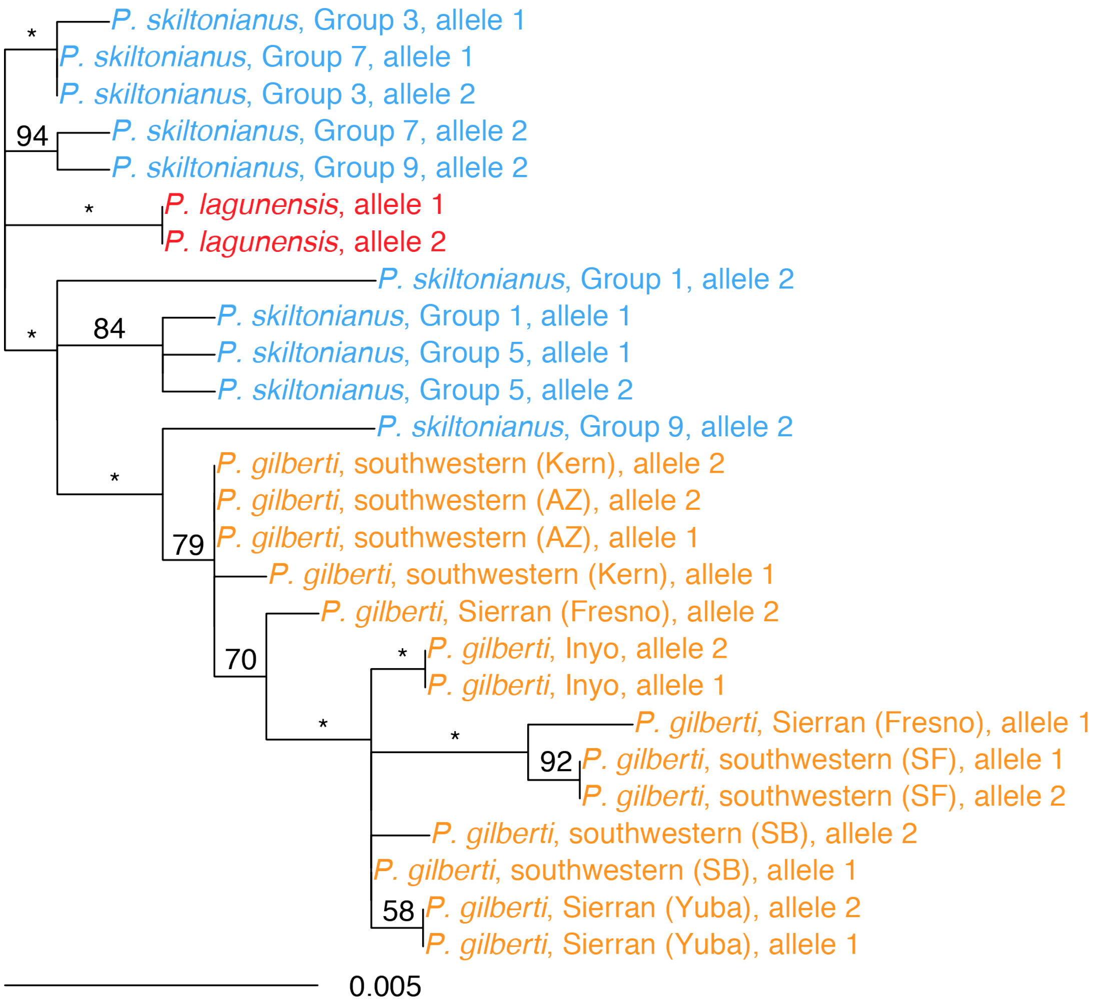

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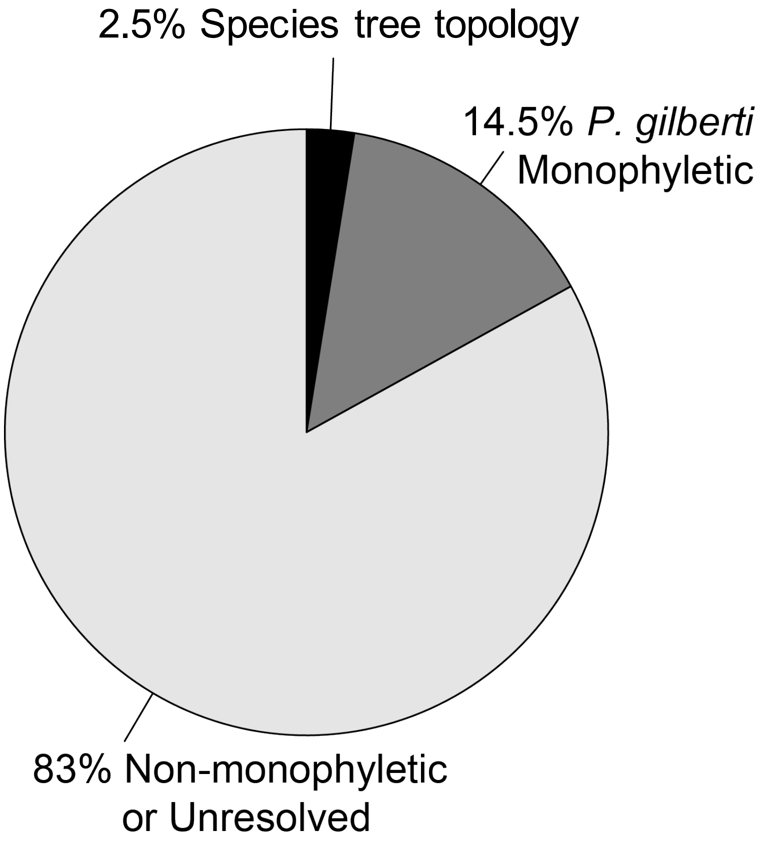

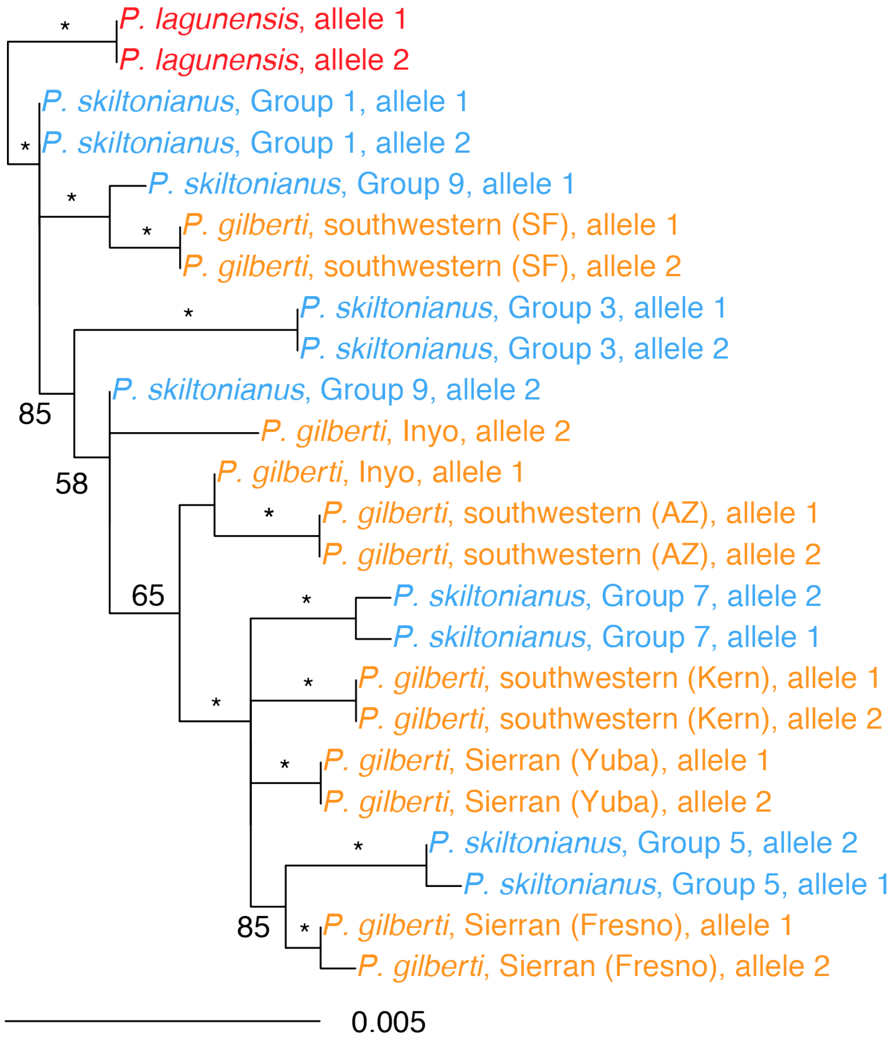

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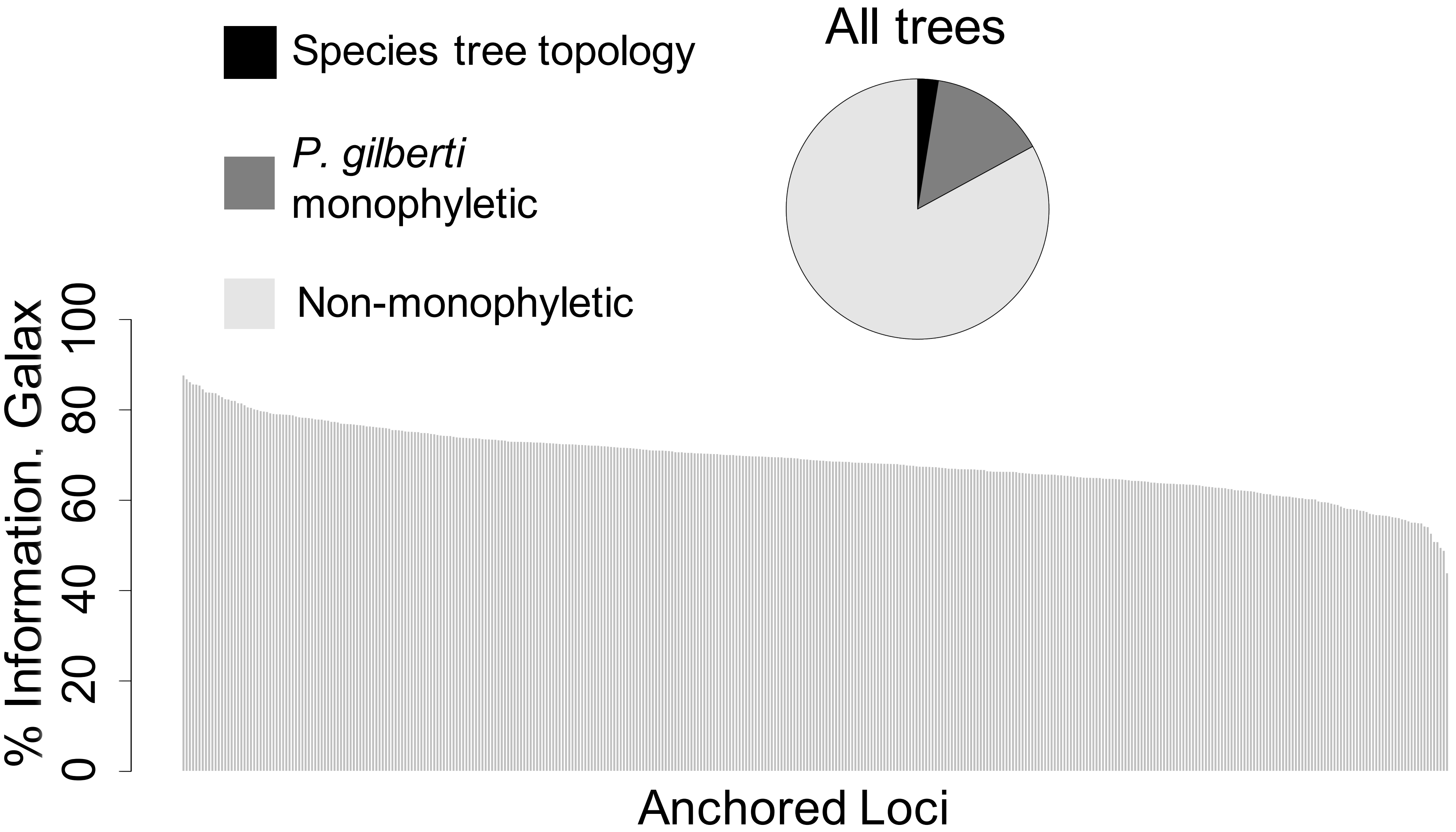
The distribution of gene tree topologies, as low information trees are removed



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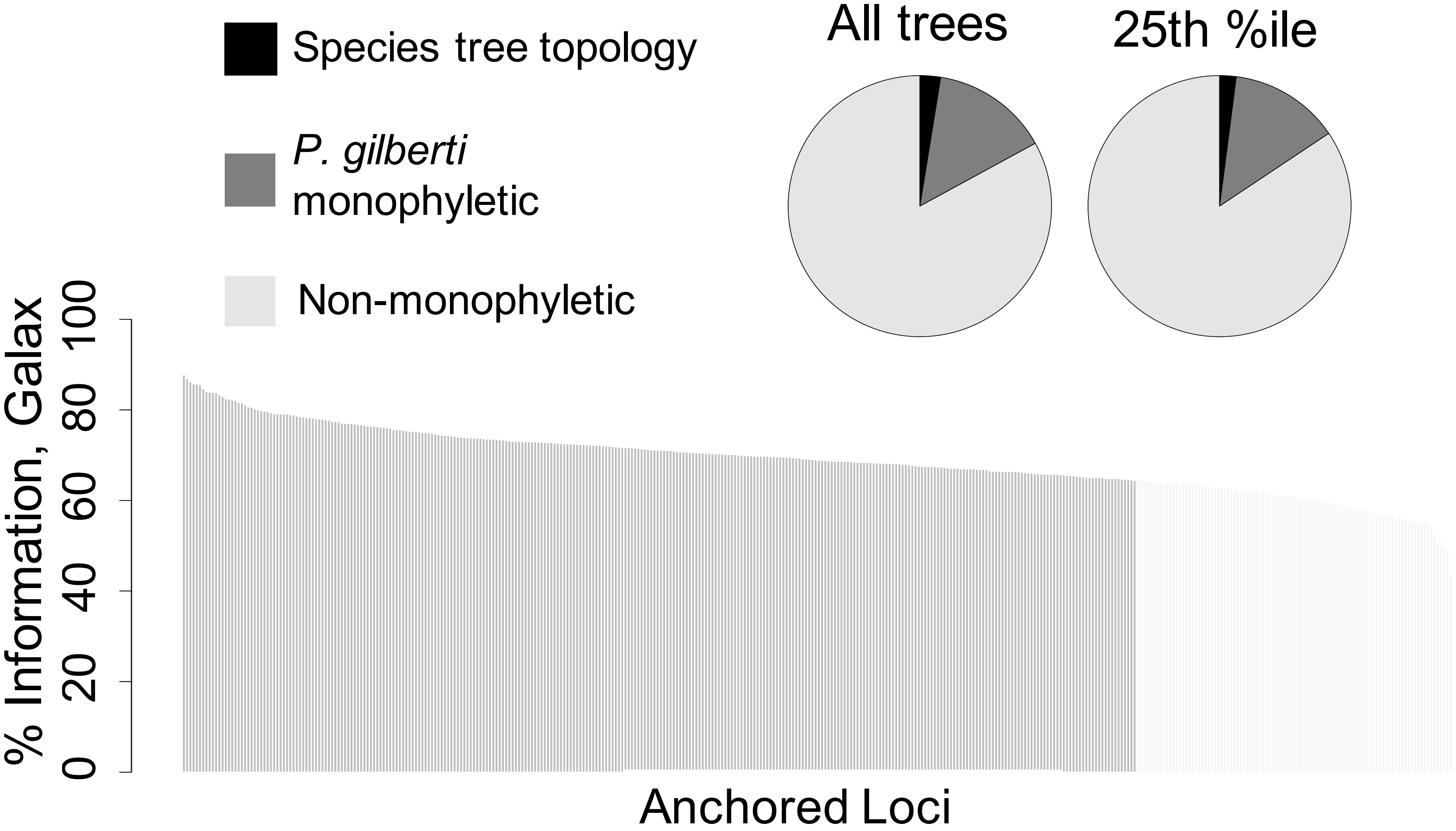

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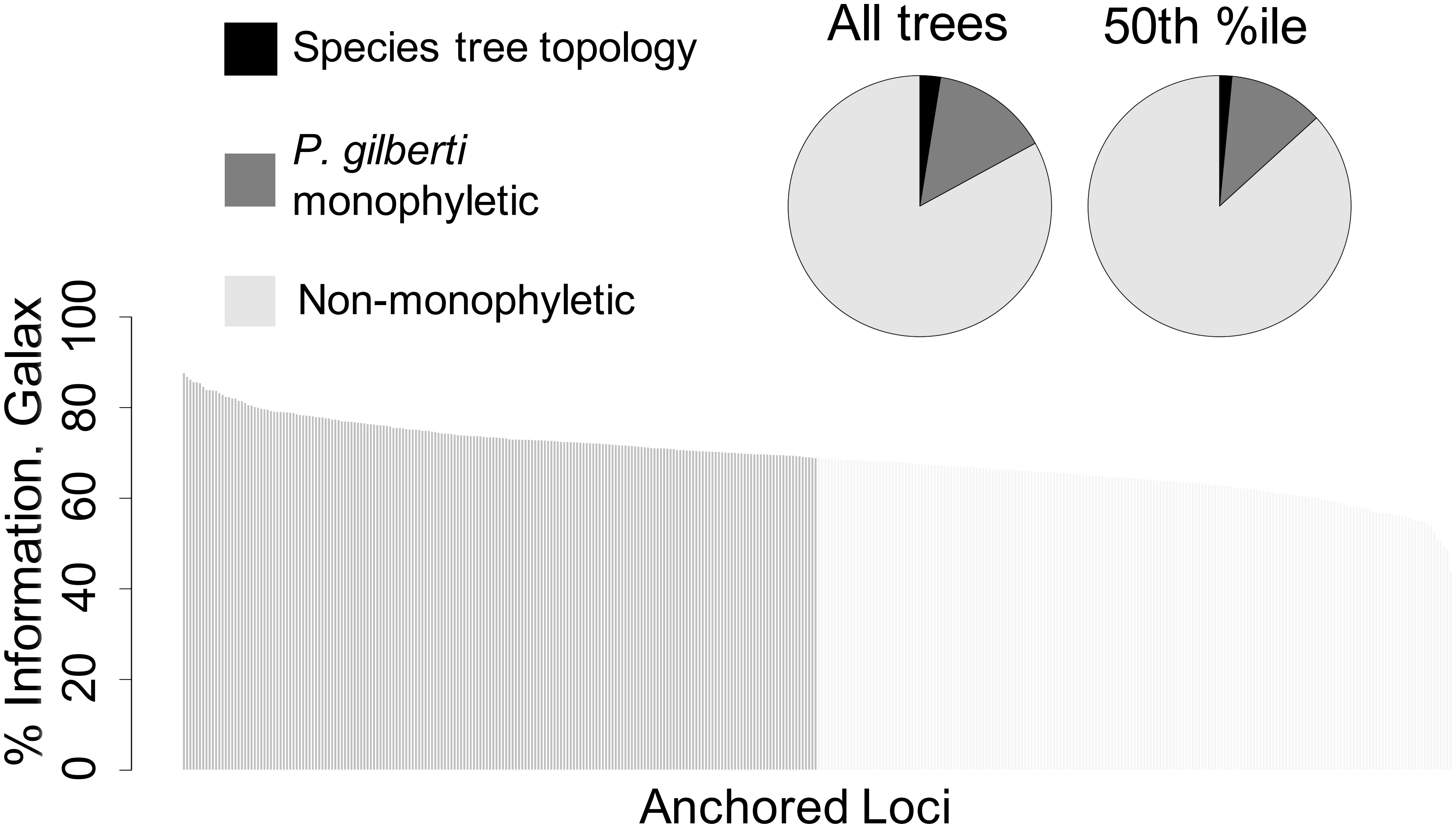

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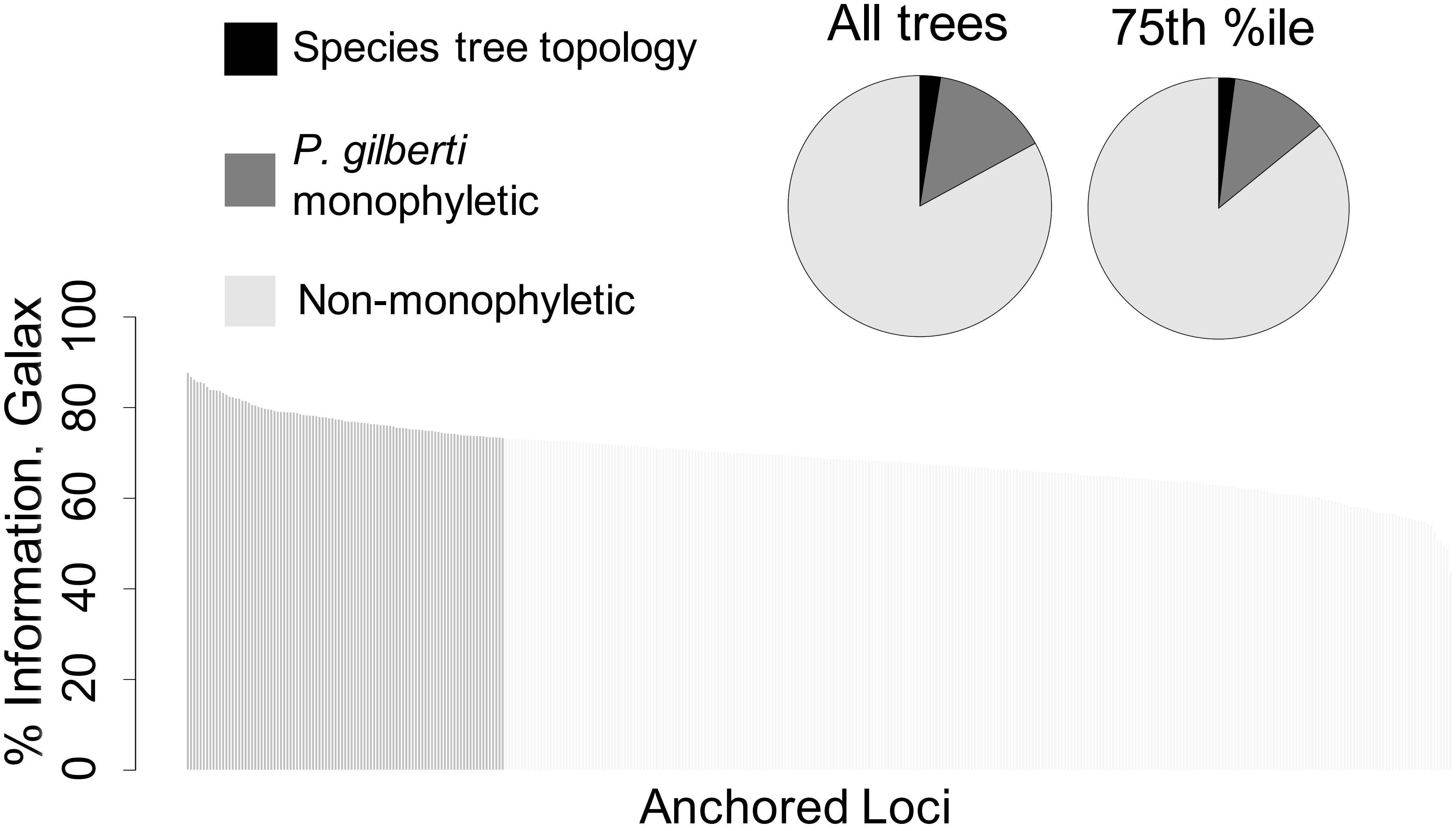

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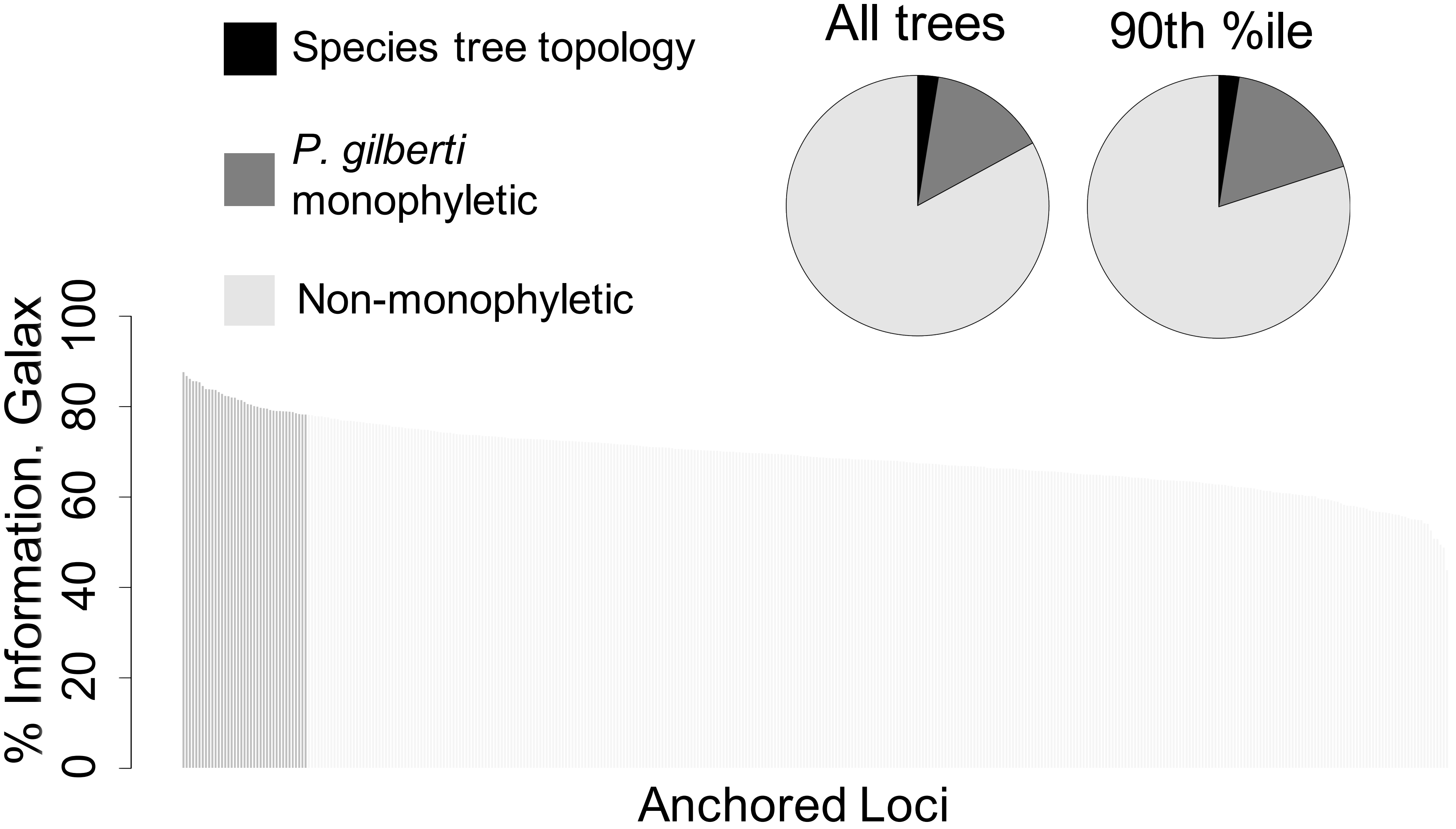


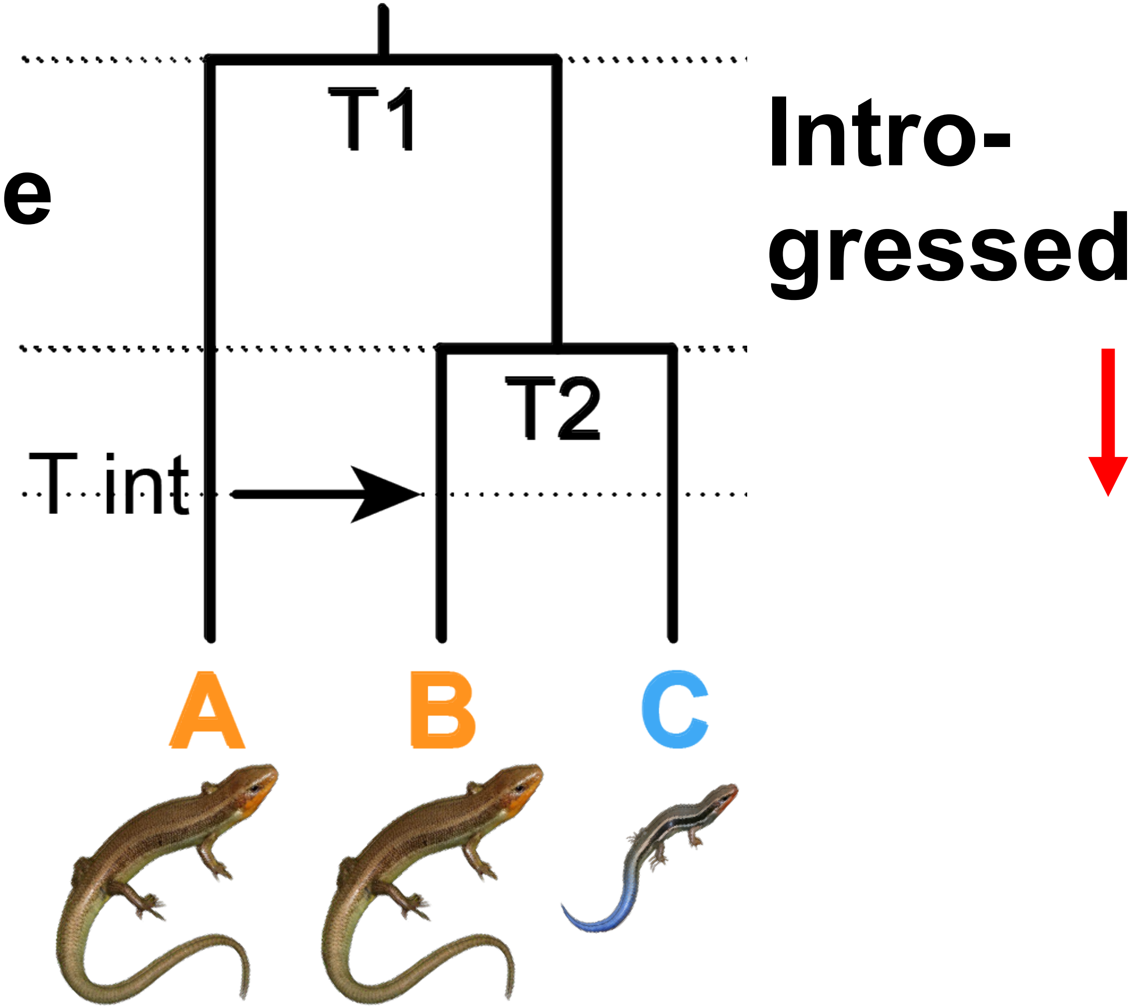
Can you pick up signals of introgression in the presence of incomplete lineage sorting?

Approach 1. The gene trees with the earliest divergences have the original branching history. (Leaché et al. 2013, Fontaine et al. 2015)

Approach 2. Estimate the phylogenetic network. (PhyloNet, Yu et al. 2014)

Approach 1. The gene trees with the earliest divergences have the original branching history

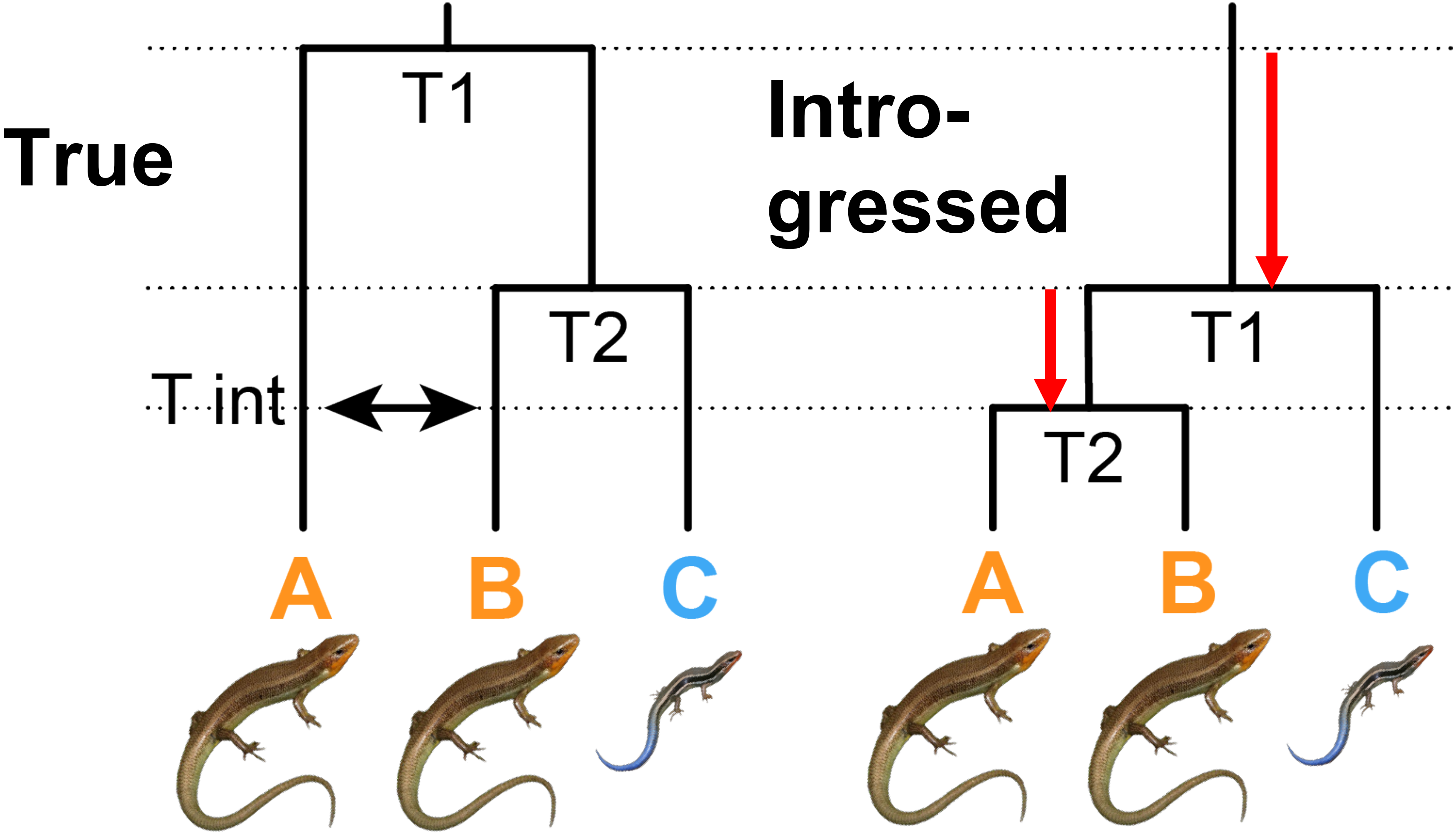
True



Intro-gressed

(Leaché et al. 2013, Fontaine et al. 2015)

Approach 1. The gene trees with the earliest divergences have the original branching history



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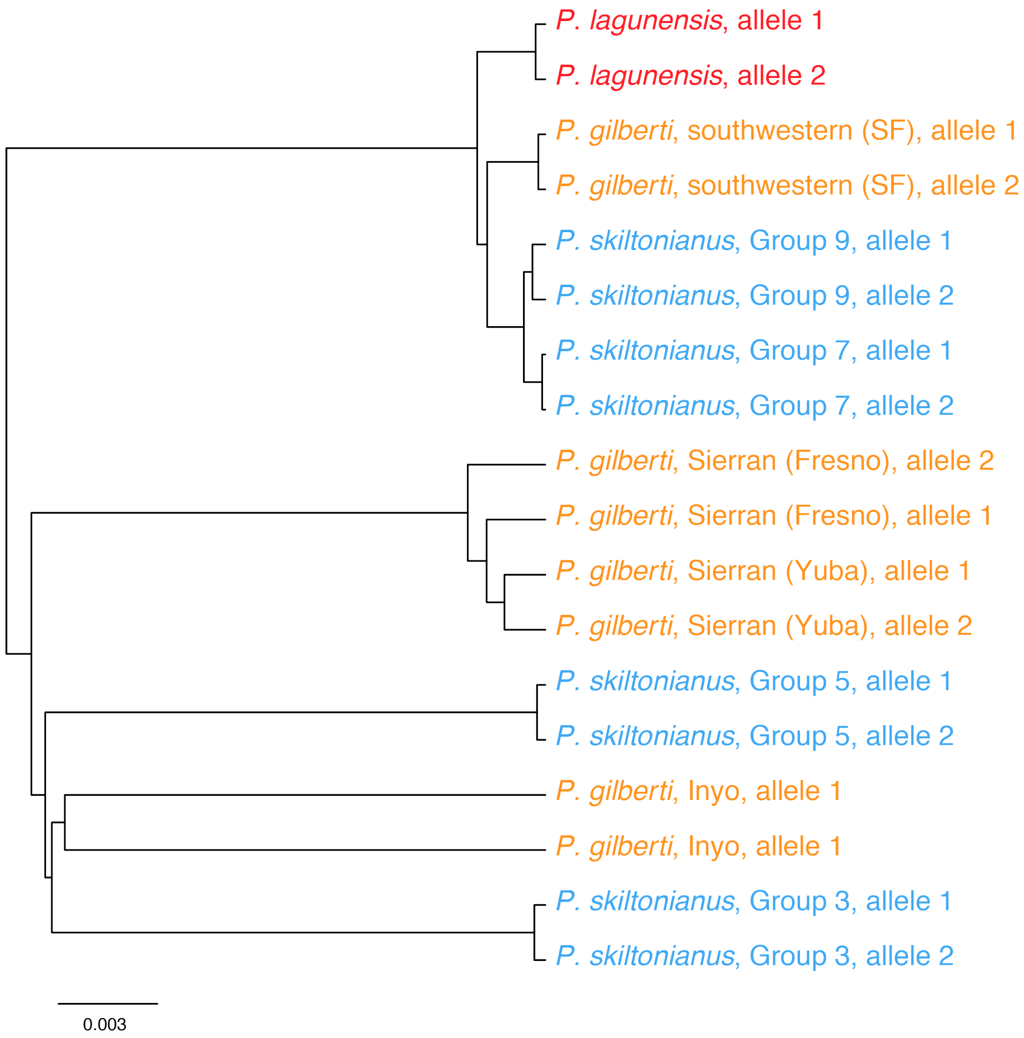
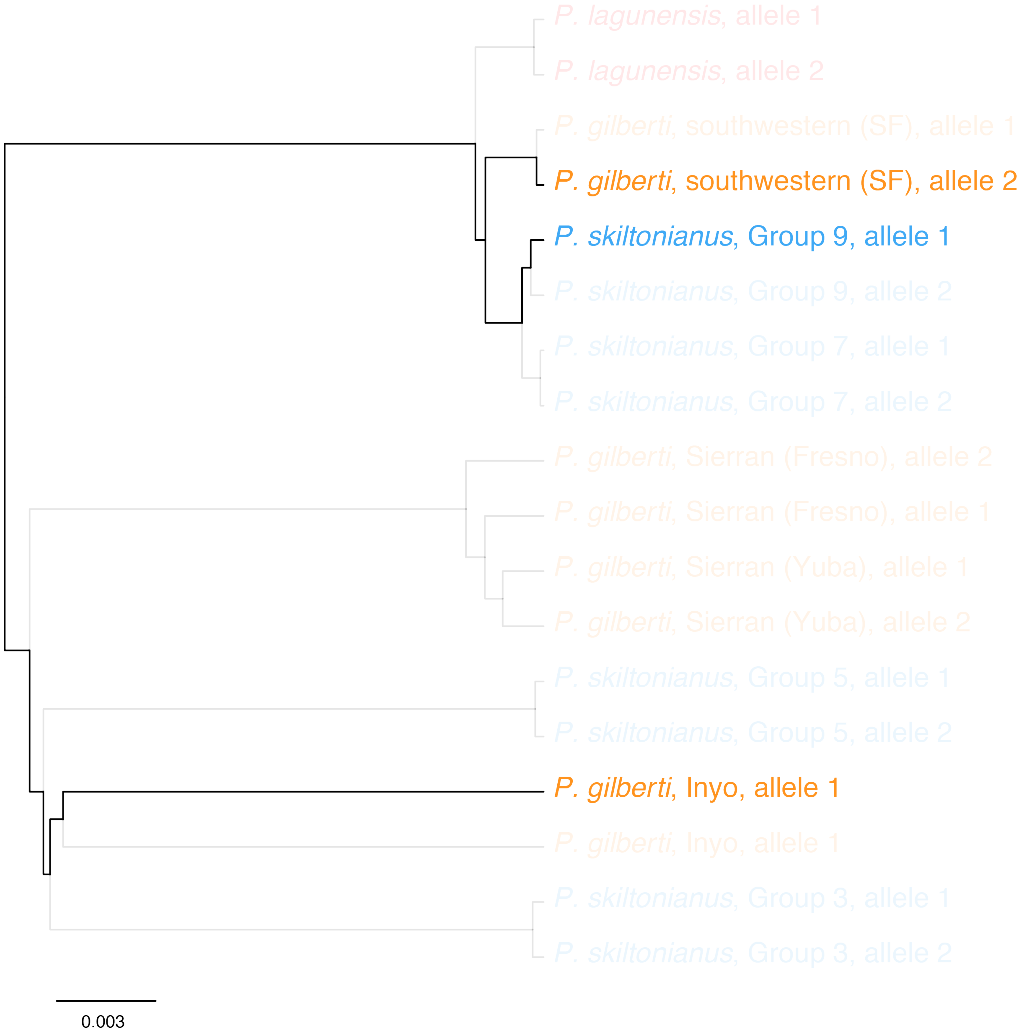


BEAST

HKY, strict clock for all loci

Approach 1. The gene trees with the earliest divergences have the original branching history



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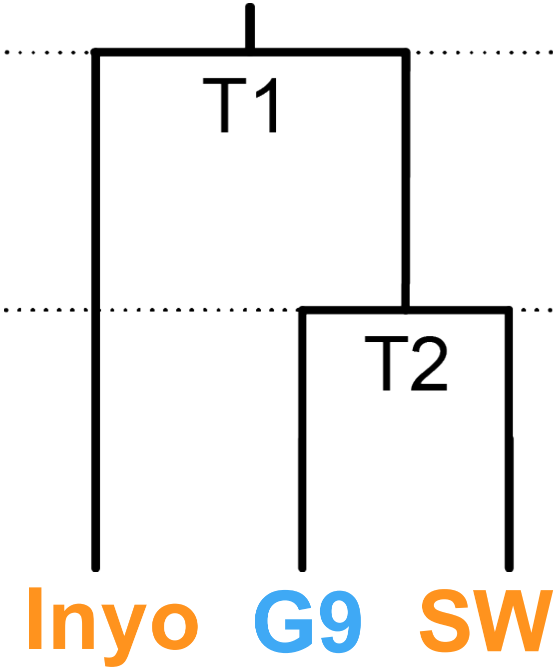

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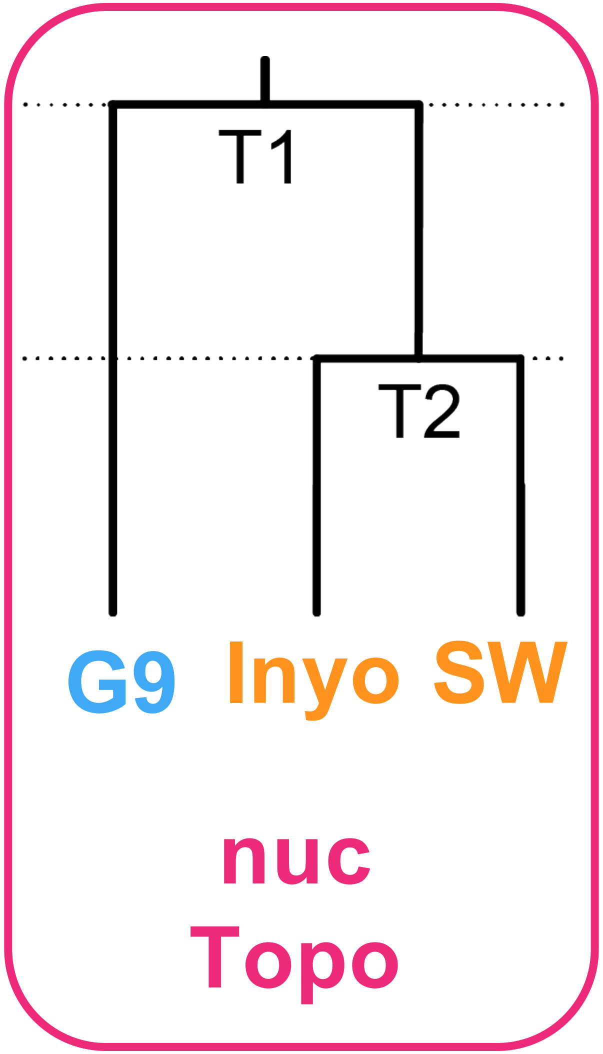

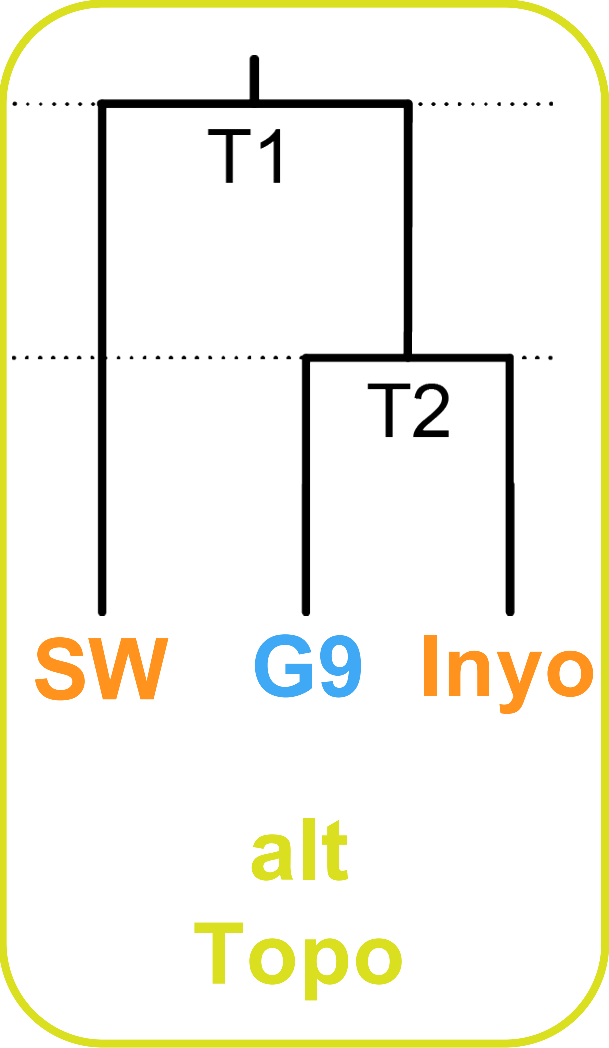

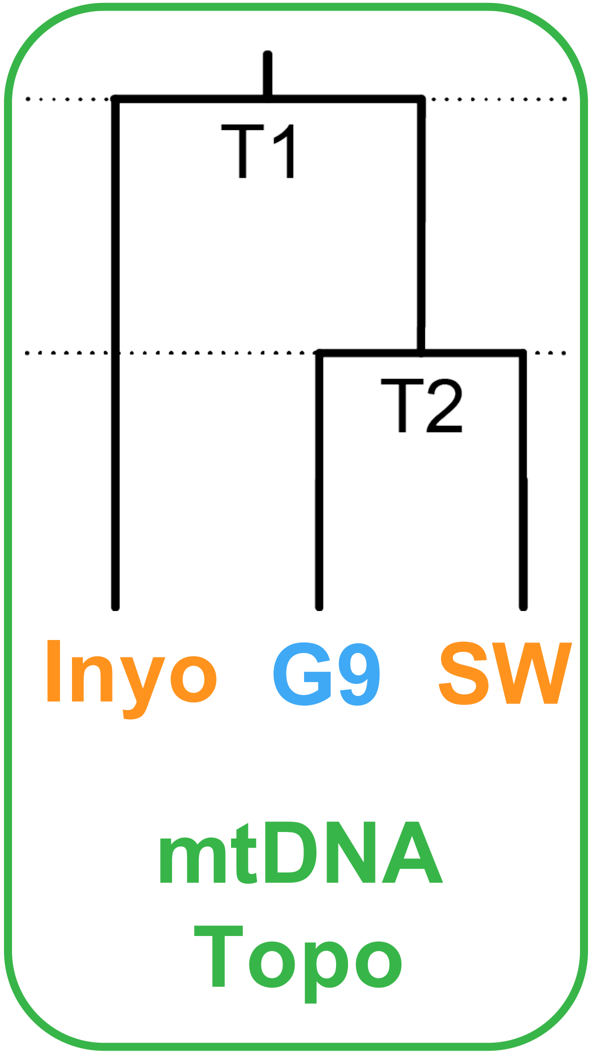

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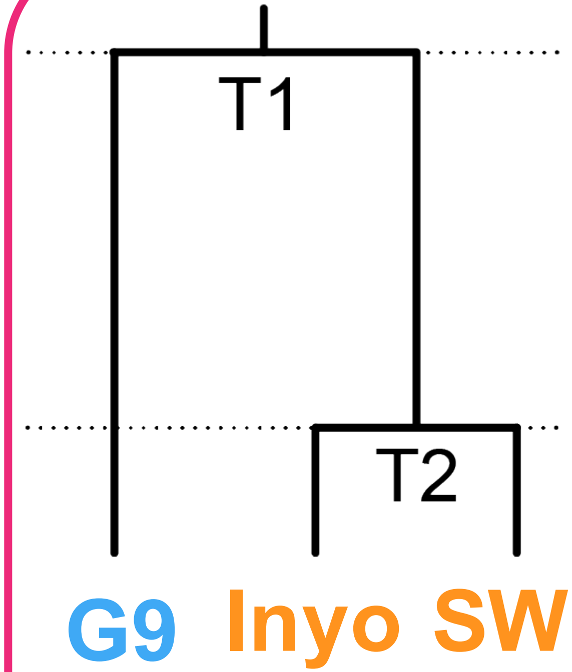
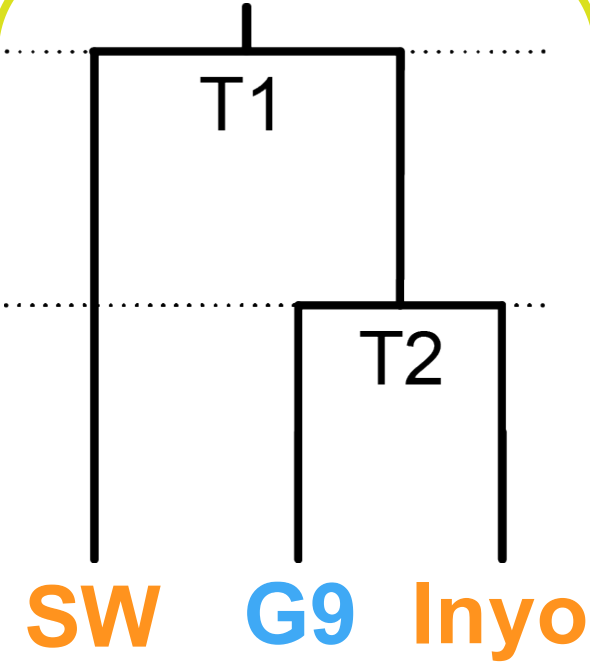
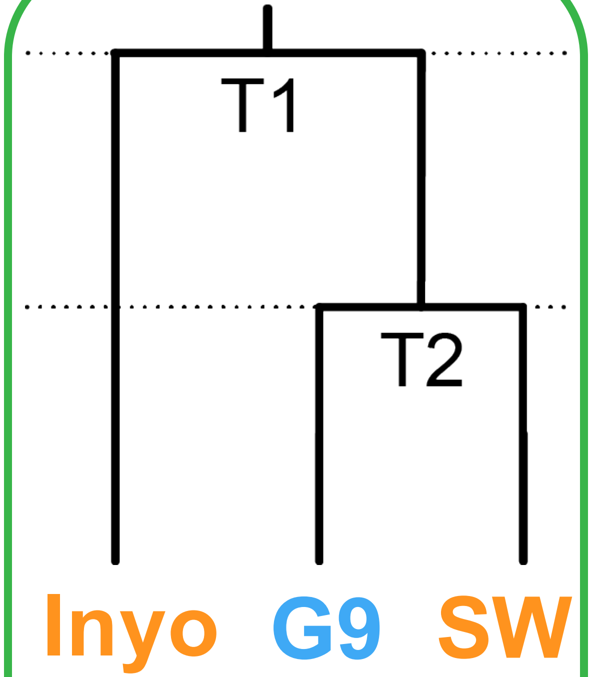


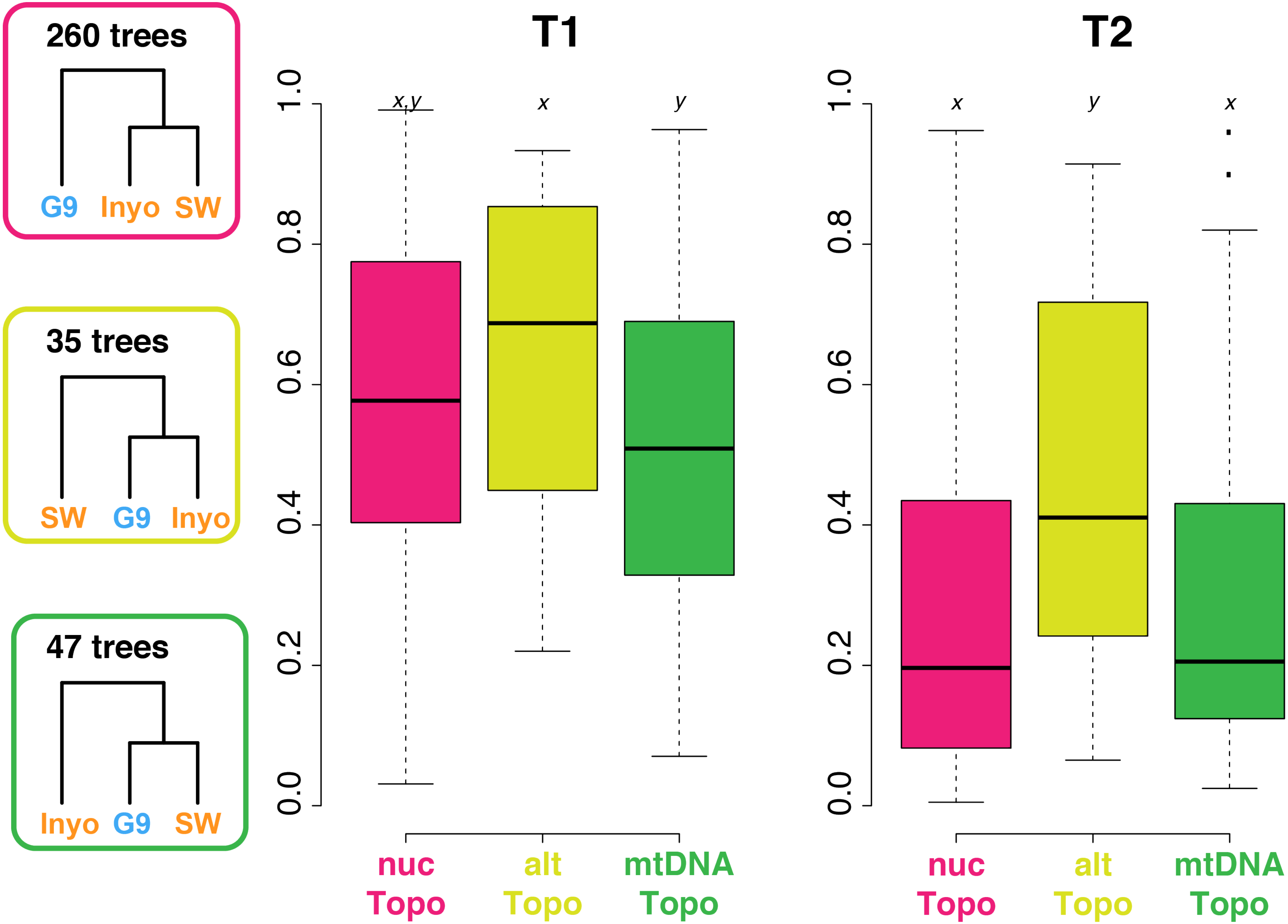
**nuc
Topo**

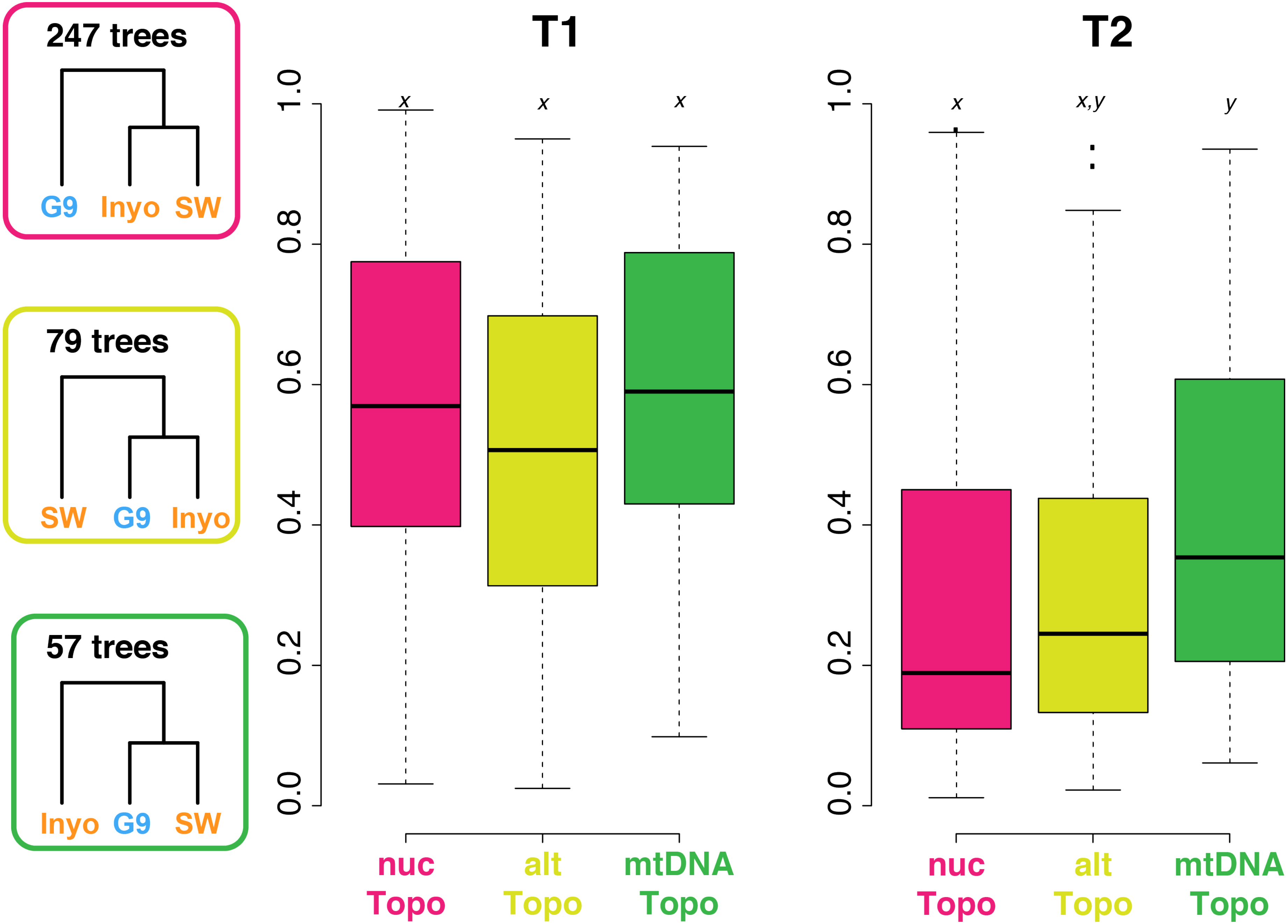


**alt
Topo**



**mtDNA
Topo**


260 trees
G9
Inyo
SW
35 trees
SW
G9
Inyo
47 trees
Inyo
G9
SW
T1
T2
1.0
0.8
0.6
0.4
0.2
0.0
x,y
x
y
x
y
x
nuc Topo
alt Topo
mtDNA Topo
nuc Topo
alt Topo
mtDNA Topo


247 trees
G9
Inyo
SW
79 trees
SW
G9
Inyo
57 trees
Inyo
G9
SW
T1
T2
1.0
0.8
0.6
0.4
0.2
0.0
x
x
x
x
x,y
y
nuc Topo
alt Topo
mtDNA Topo
nuc Topo
alt Topo
mtDNA Topo

Approach 2. Estimate the phylogenetic network.

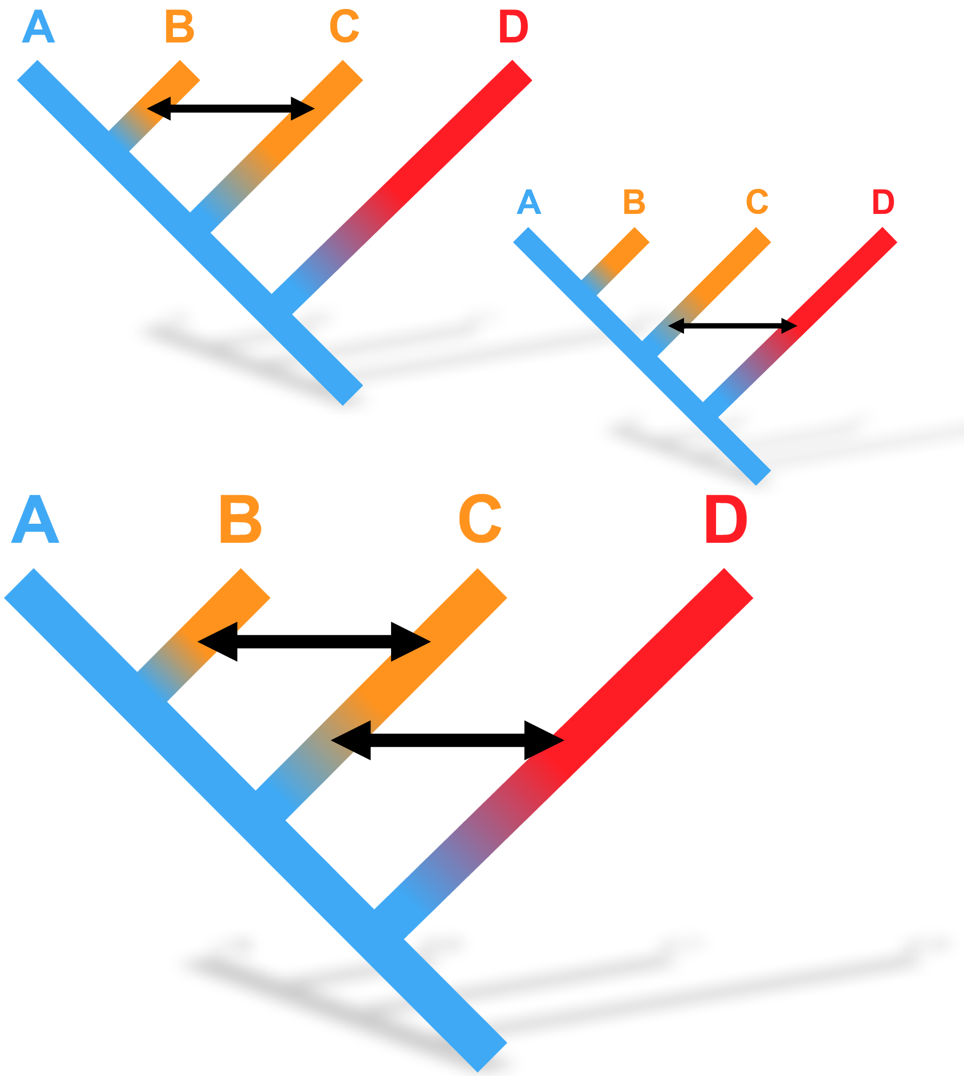
Phylogenetic Networks: Trees where a given node can have >1 parent nodes.

PhyloNet: a maximum likelihood approach to searching “network space” for the optimal network, using gene tree topologies.

Estimating the maximum likelihood network is computationally expensive…

- ~ 64 GB of RAM for 24 hours to estimate network for 38 loci with 11 taxa!

But is sped up using maximum pseudolikelihoods…



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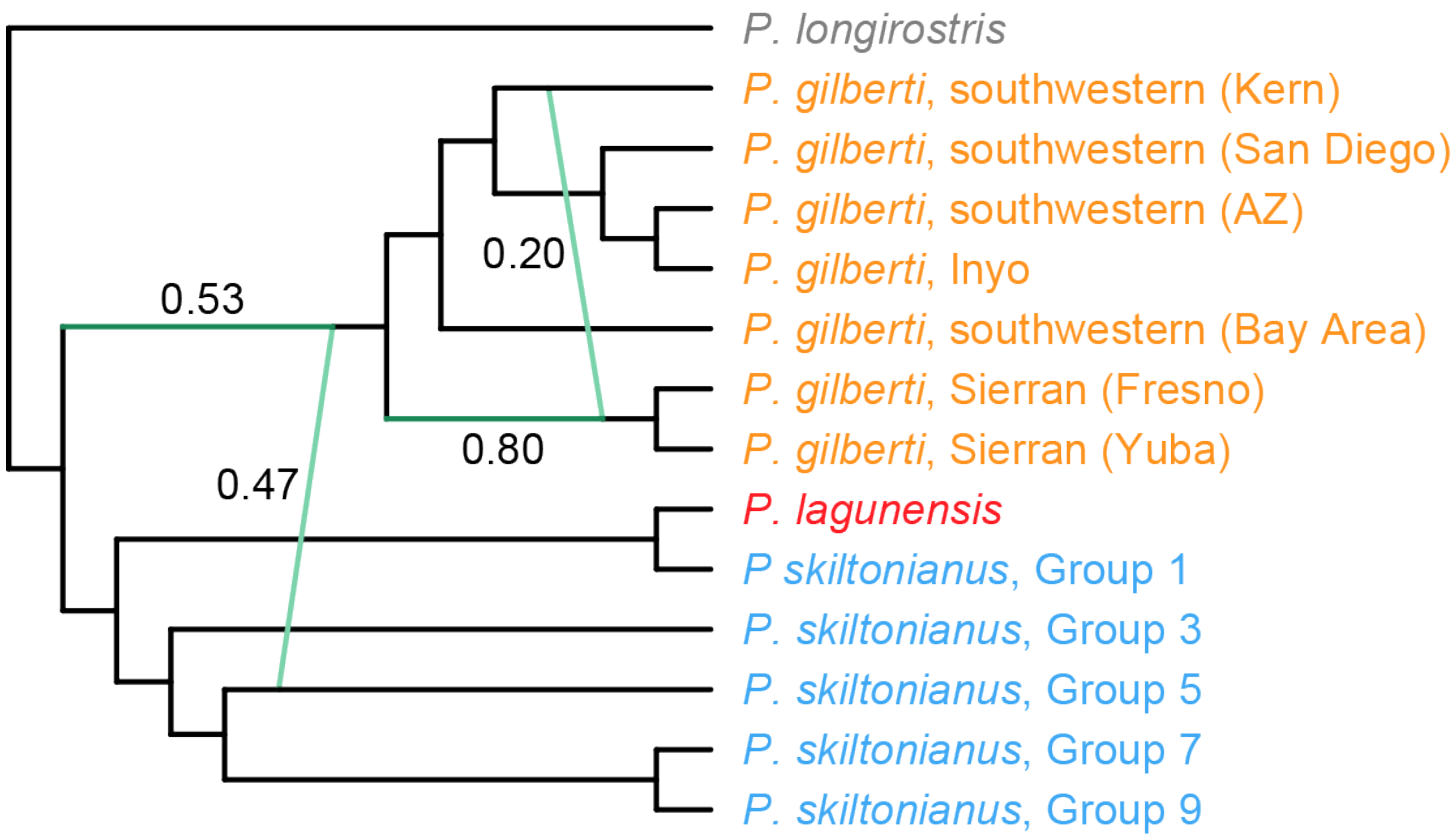

PhyloNet, Maximum Pseudolikelihood, anchored loci with random allele selection
Branch lengths not shown; numbers are inheritance probabilities for reticulations

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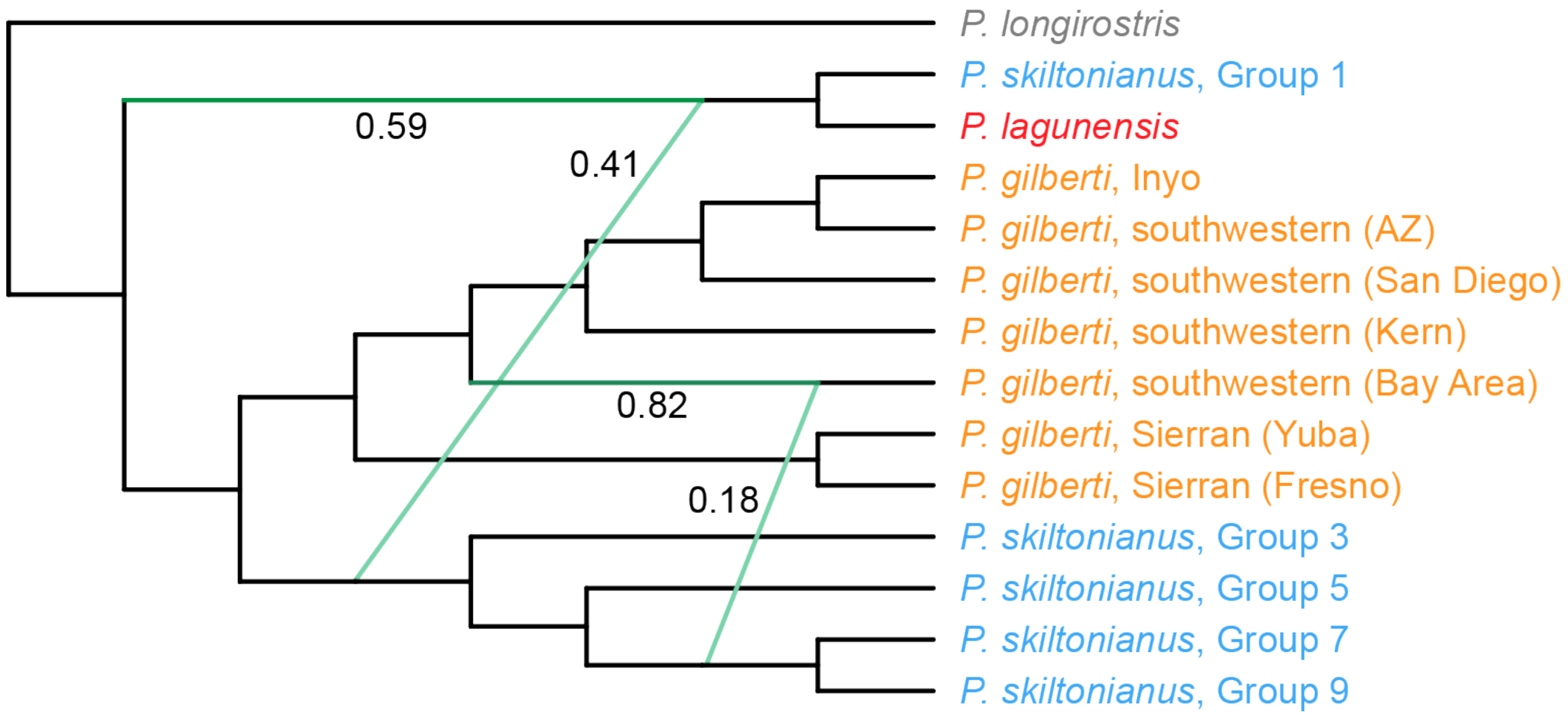
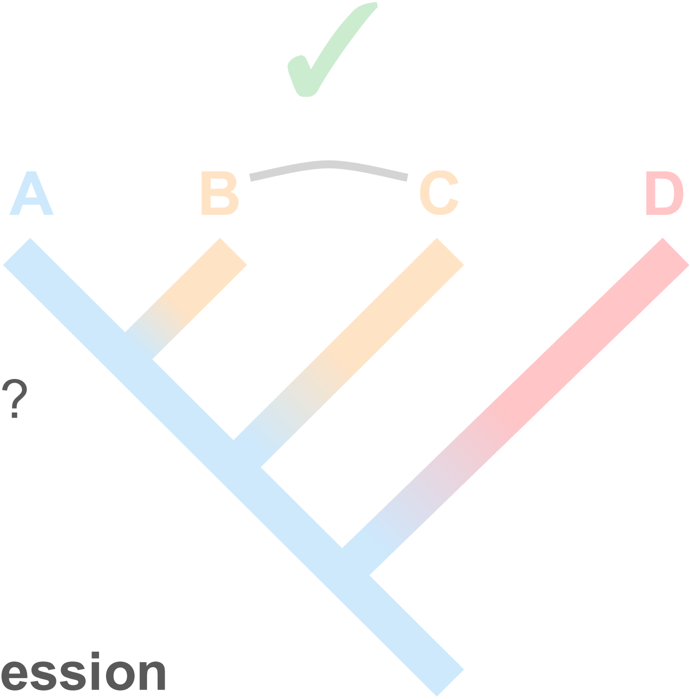


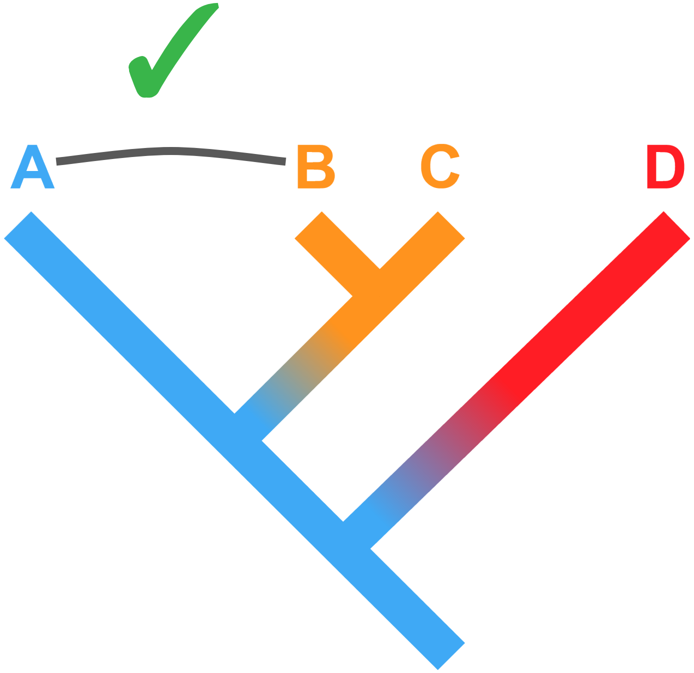
PhyloNet, Maximum Pseudolikelihood with mapped alleles, anchored loci
Branch lengths not shown; numbers are inheritance probabilities for reticulations

A Case of Tangled Speciation



Does *P. gilberti* actually represent 3 independent evolutions of large body size?

- Species tree … **No**
- T1T2 test … **No, with exceptions**
- Phylogenetic networks ... **No, but introgression**



Then how do these species break the mechanical prezygotic barrier?

- Networks imply ancestral introgressions, prior to body size divergence?
- Maybe it was never as strong as we assumed…

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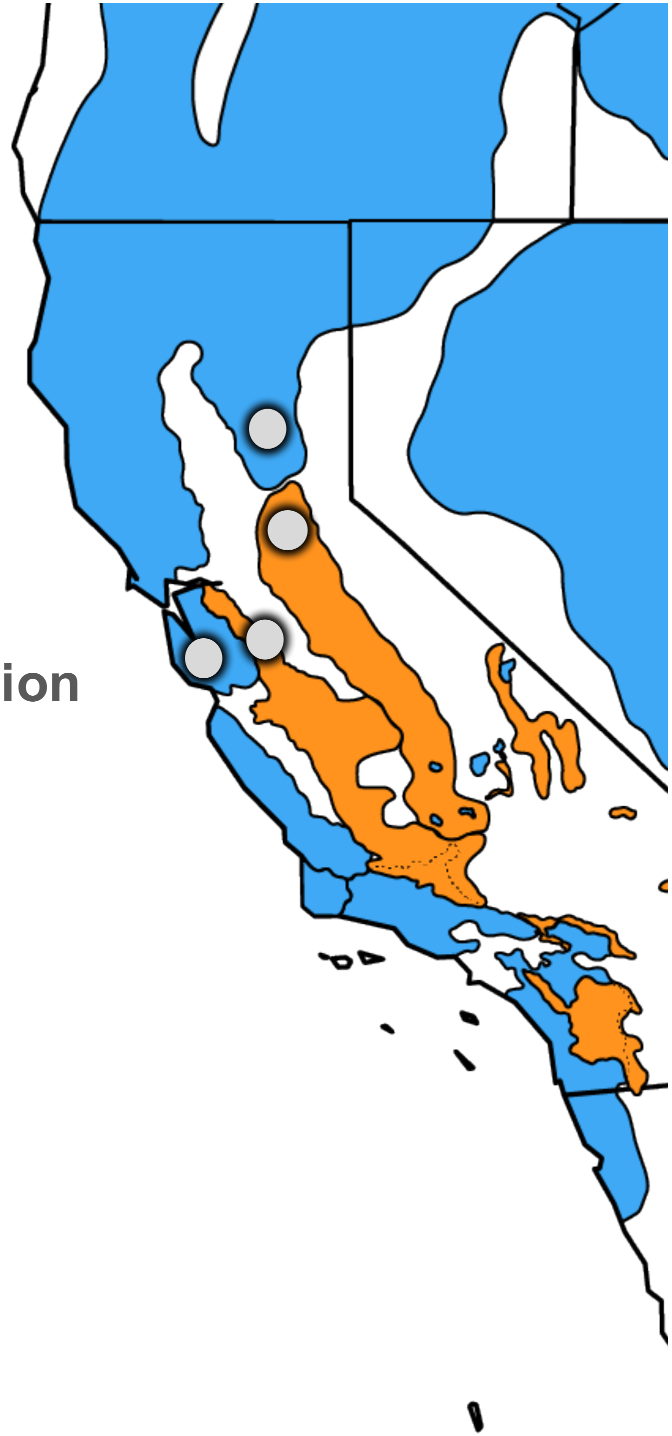

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