PARALLEL SPECIATION OF TWO WESTERN NORTH AMERICAN SKINKS (*PLESTIODON*)

Presentation by Andrew Frank

PREVIOUS WORK

- Parallel cave invasions by amphipod *Gammarus minus*
  - Stable isotope analysis
  - Microsatellite loci

- Cryptic species delimitation of two nemertean worms
  - DNA Barcoding
  - Haplotype network analysis

CURRENT WORK

Speciation &
Population
Genetics

Core Interests

Systematics
& Taxonomy

Deep-Level
Phylogenetics

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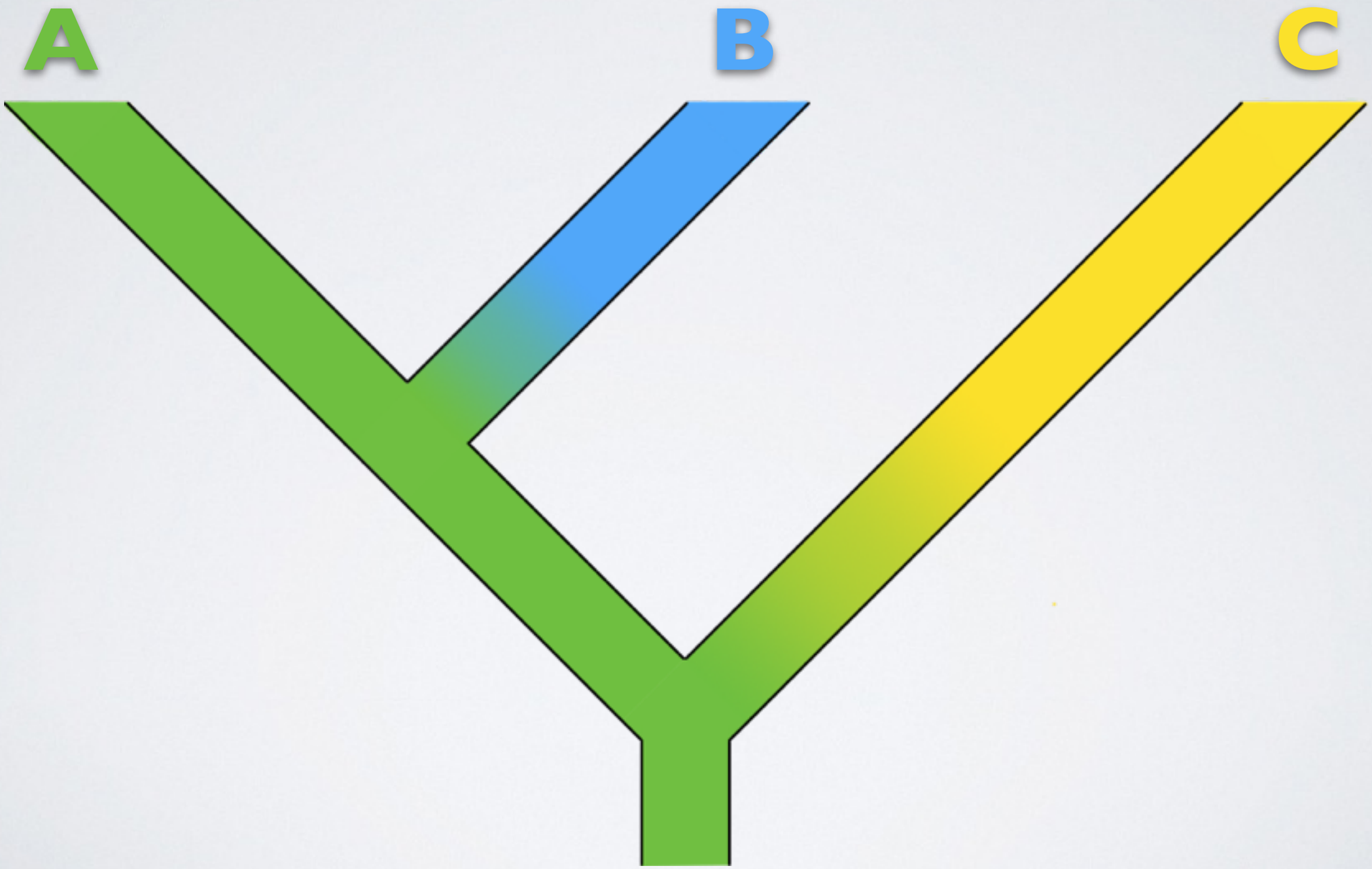
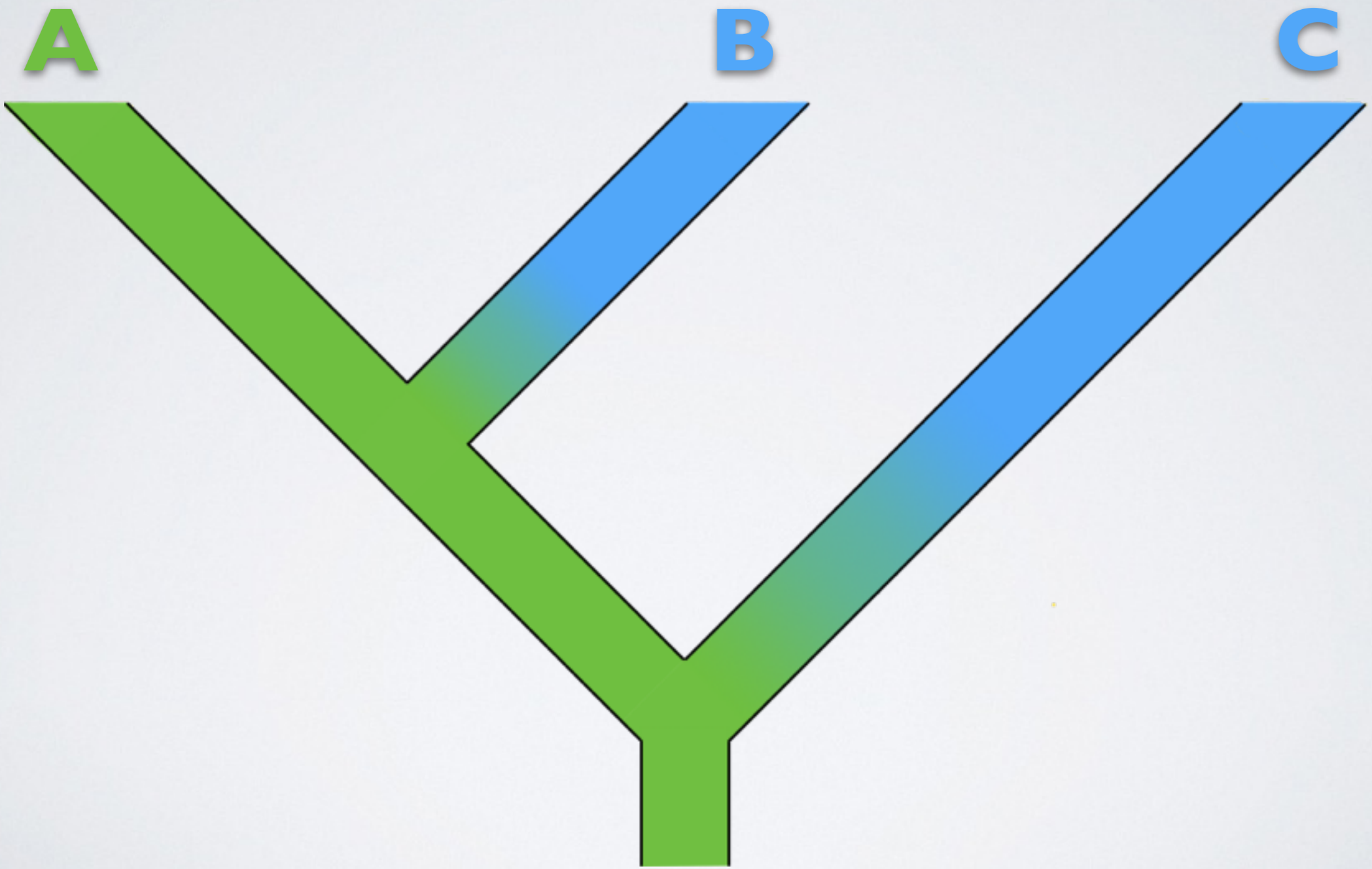
SPECIATION

Bifurcating Speciation



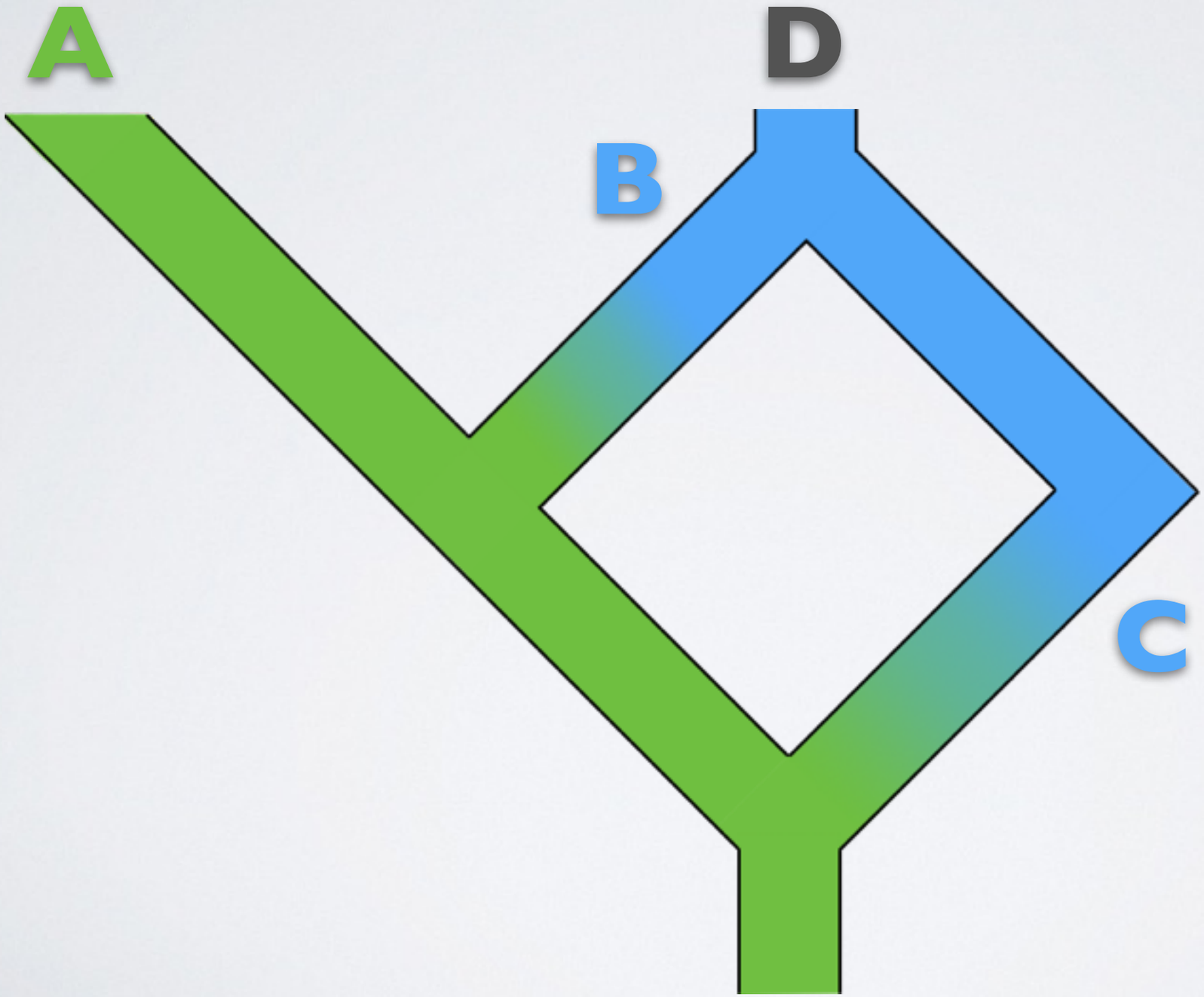
SPECIATION

Parallel Evolution



SPECIATION

Parallel Speciation



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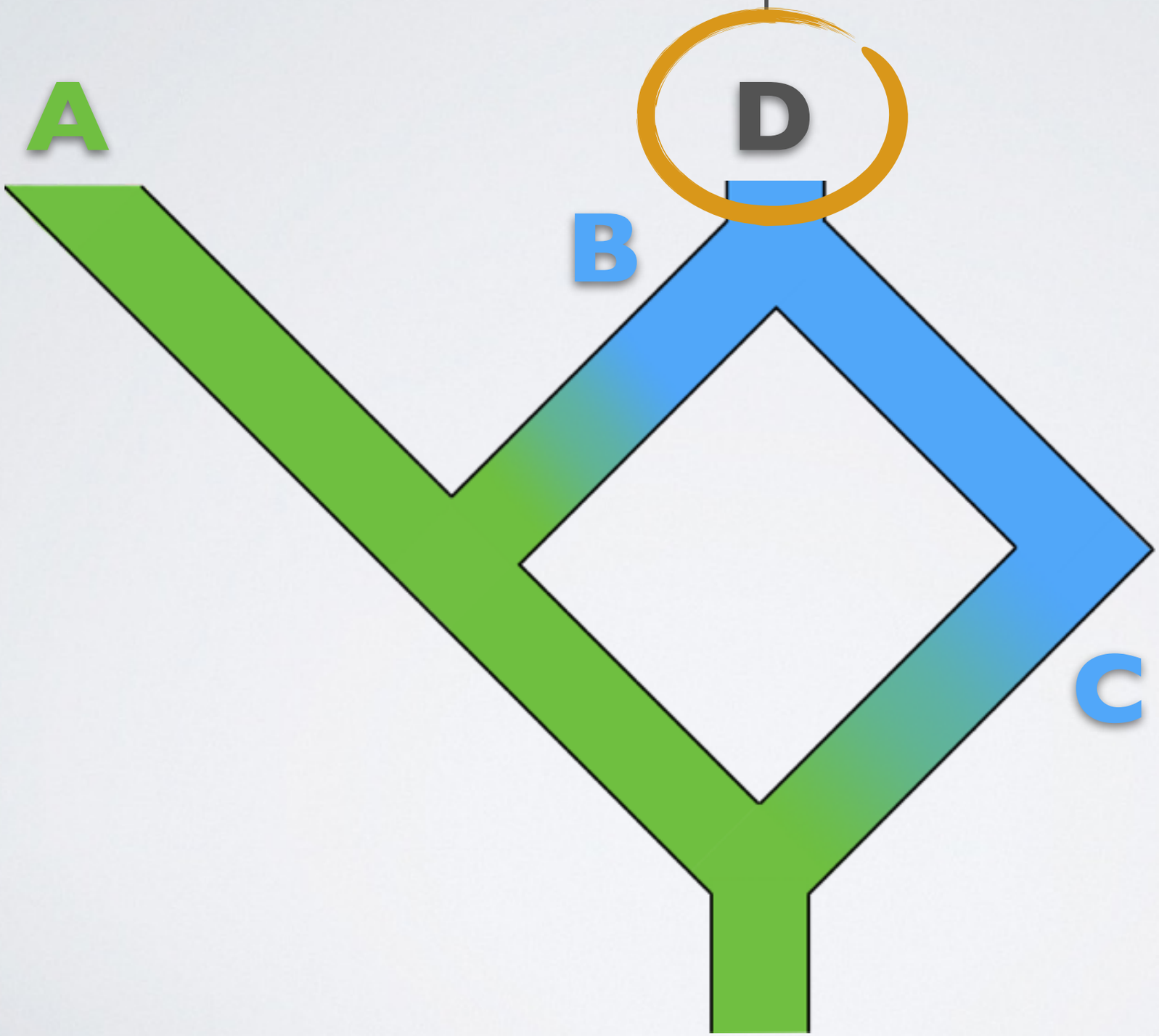

B and **C** are more reproductively compatible than either is with **A**, resulting in the new lineage **D**

P. SKILTONIANUS GROUP

(Photos by Gary Nafis)

P. SKILTONIANUS GROUP

- Small bodied adults
- Mesic
- Coastal
- High elevations

(Photos by Gary Nafis)

P. SKILTONIANUS GROUP

- Small bodied adults
- Mesic
- Coastal
- High elevations

- Large bodied adults
- Xeric
- Inland
- Low elevations

(Photos by Gary Nafis)

P. SKILTONIANUS GROUP

Plestiodon skiltonianus

Plestiodon gilberti

Adult

(Photos by Gary Nafis)

P. SKILTONIANUS GROUP

	Juvenile	Adult
Plestiodon skiltonianus		
Plestiodon gilberti		

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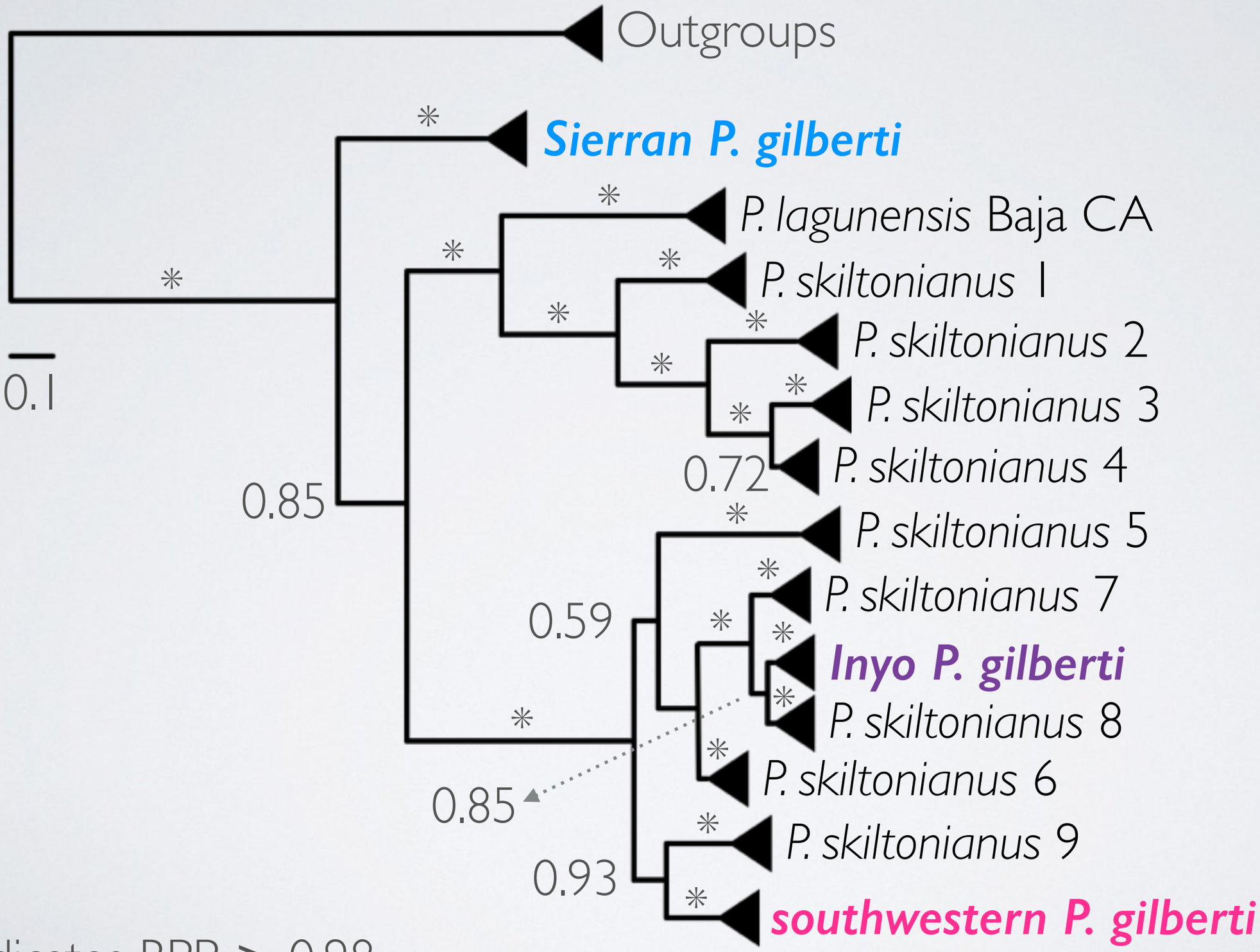
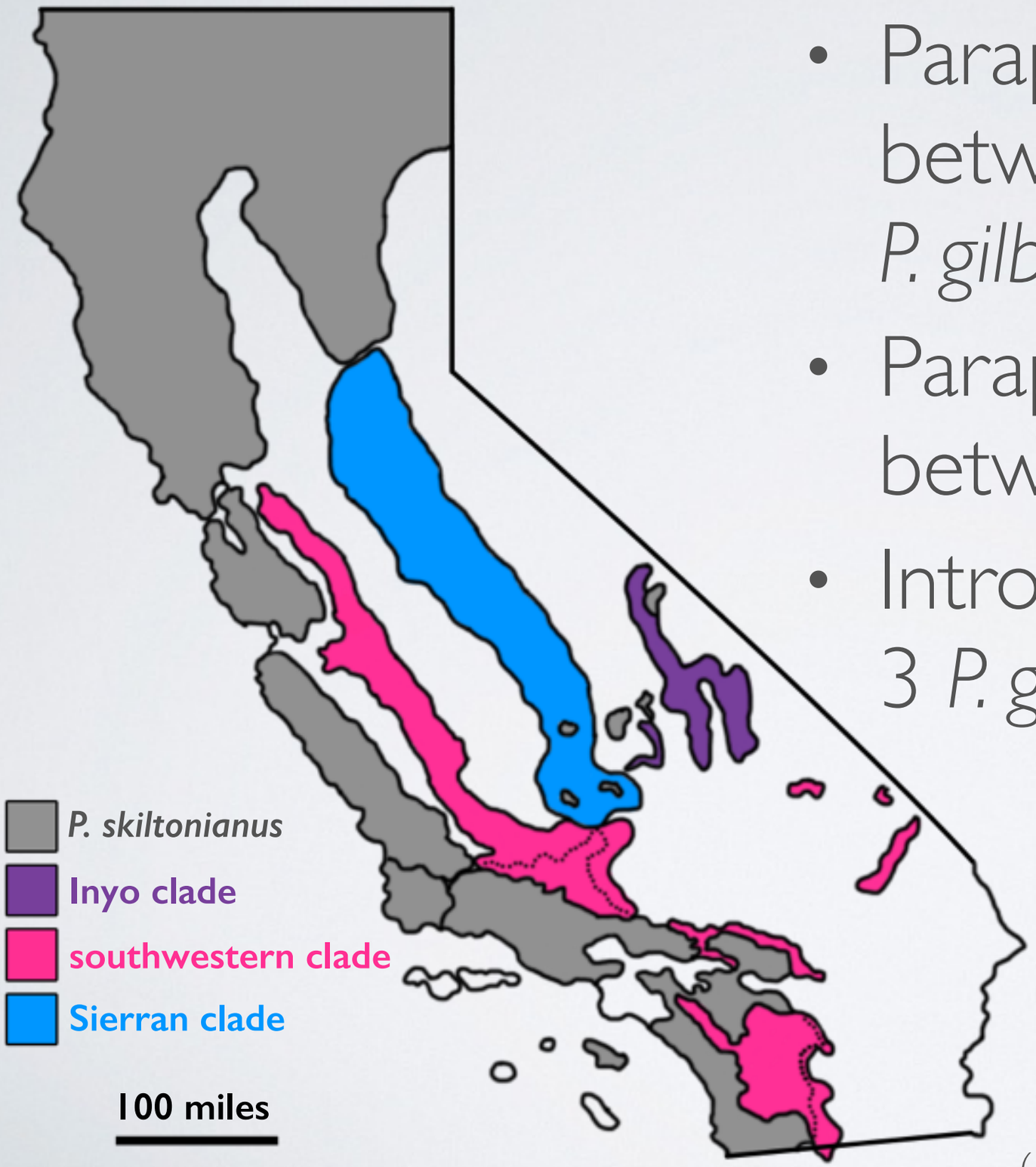
MITOCHONDRIAL TREE



* indicates BPP ≥ 0.98

(Adapted from Richmond et al. 2007)

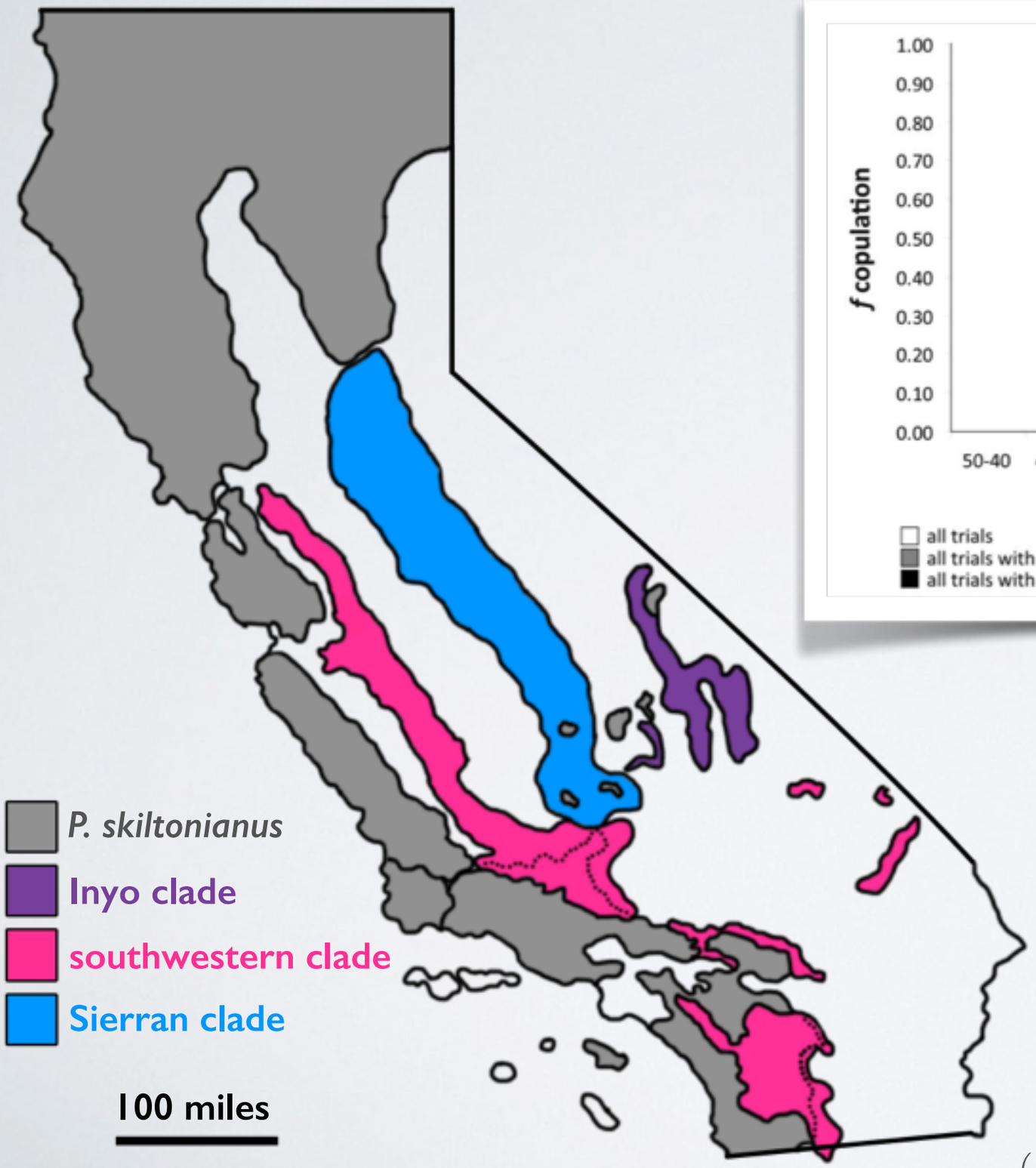
ISOLATION BY SIZE

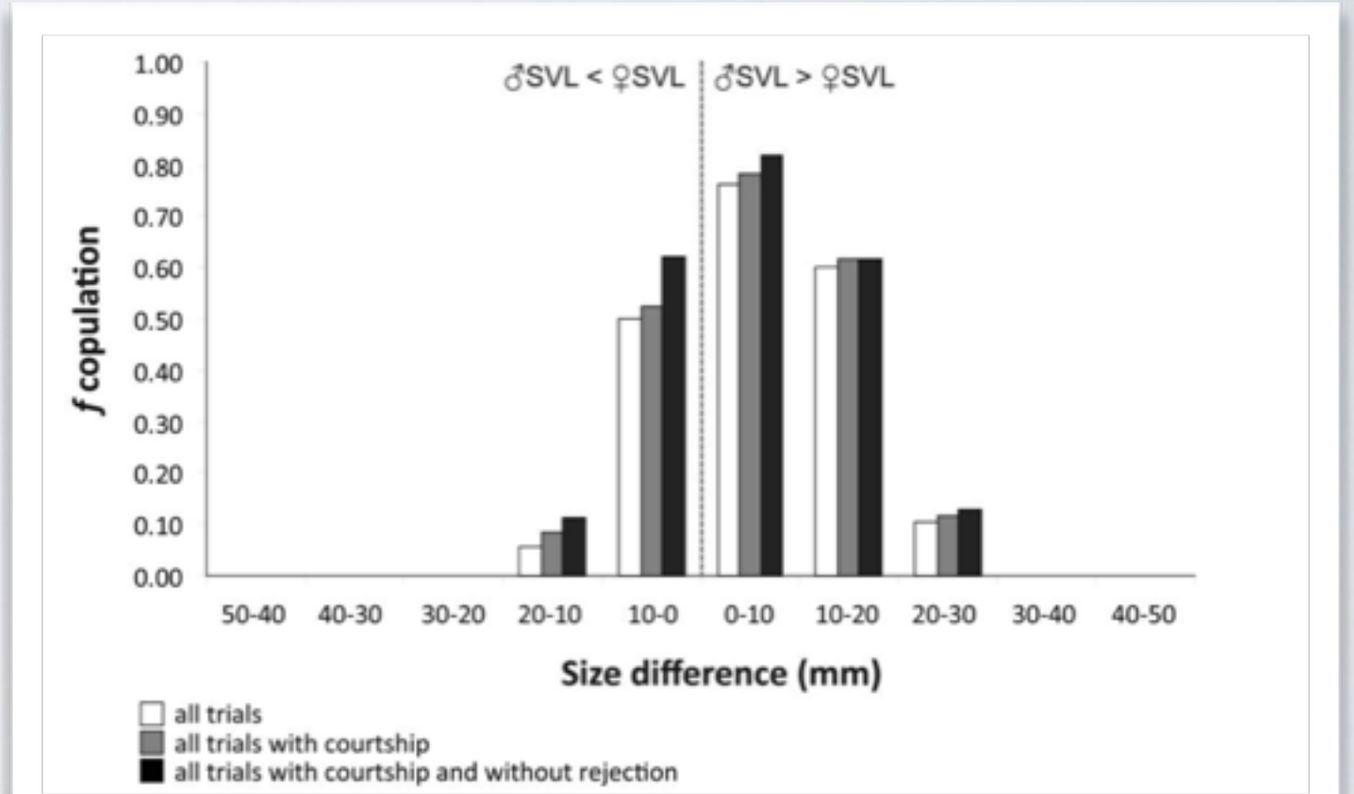


- Parapatric distribution between *P. skiltonianus* and *P. gilberti*
- Parapatric distribution between 3 *P. gilberti* clades
- Introgression between the 3 *P. gilberti* clades

(Adapted from Richmond et al. 2007 & Richmond 2011)

ISOLATION BY SIZE





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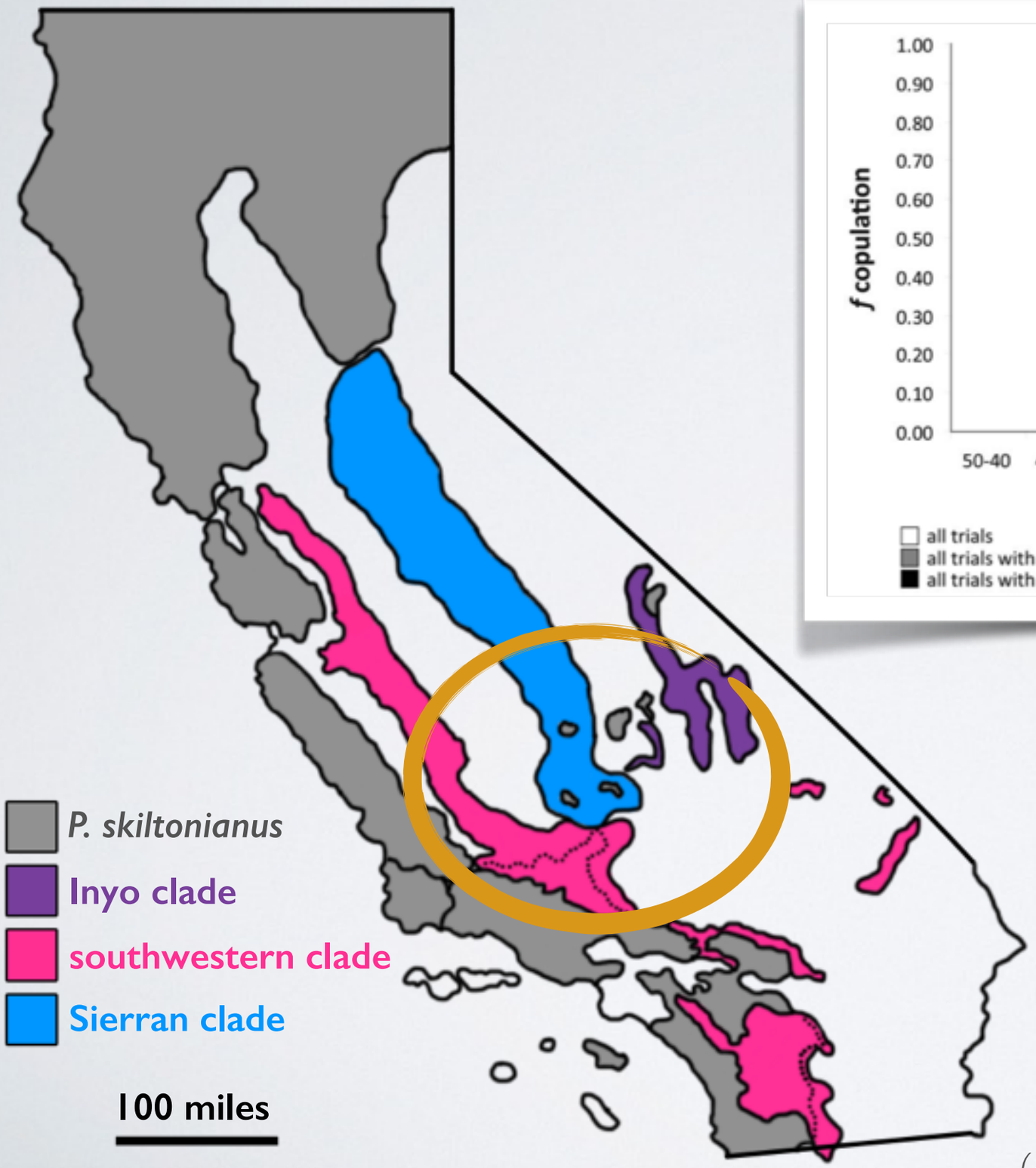
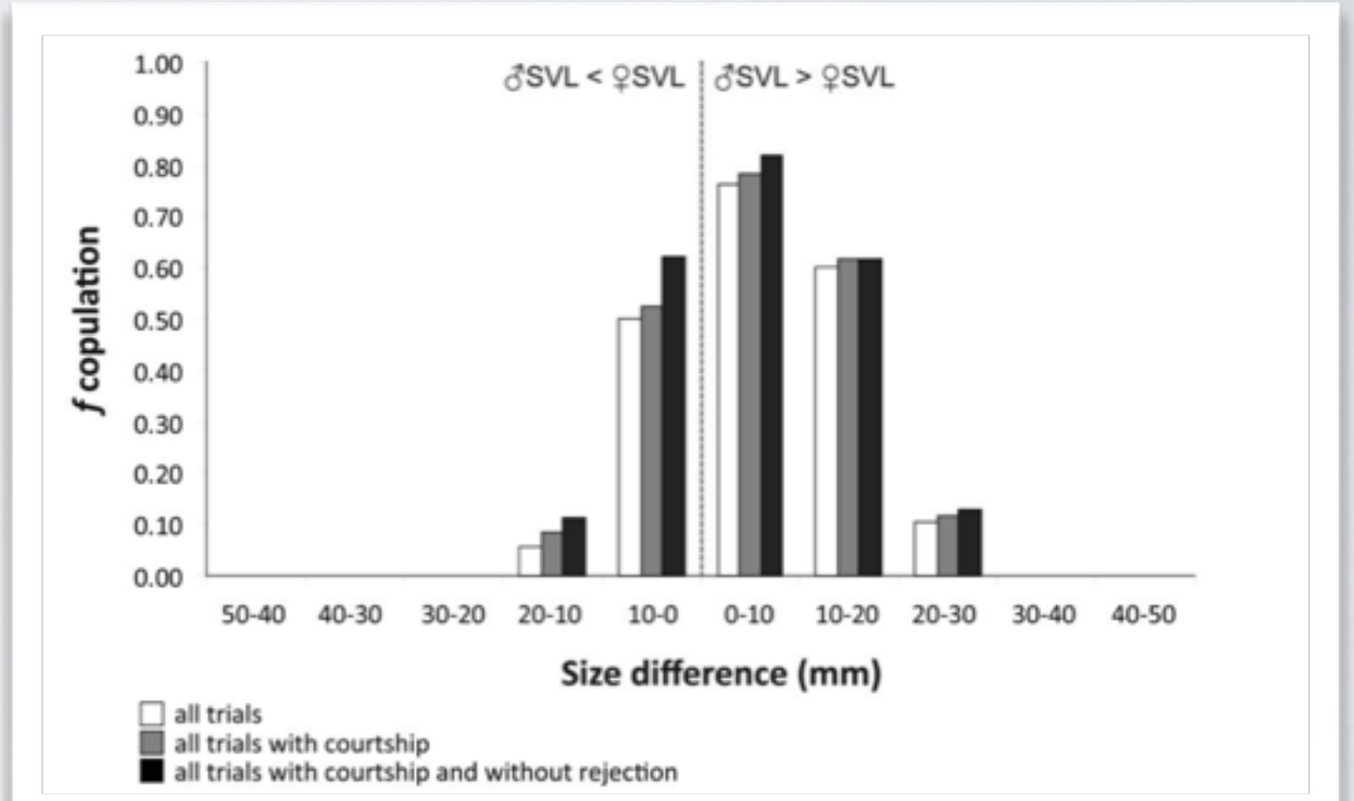
ISOLATION BY SIZE





- AFLP data suggests isolation-by-distance across *P. gilberti* contact zone

(Adapted from Richmond et al. 2007 & Richmond 2011)

PARALLEL SPECIATION CRITERIA

Clades have…

- ☐ reproductive incompatibility with a divergent sister clade
- ☐ reproductive compatibility with one or more convergent sister clades
- ☐ independent origins

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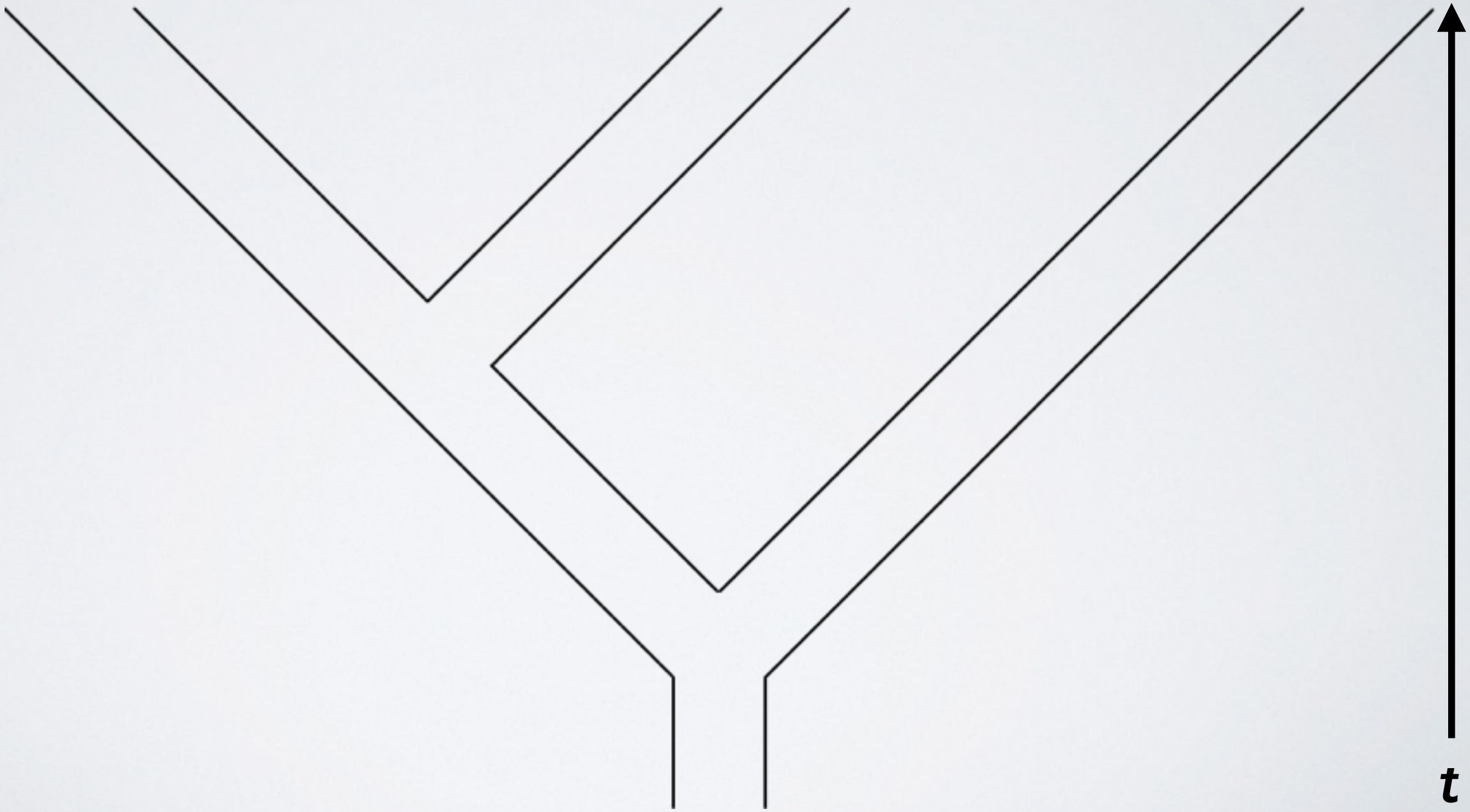
COALESCENCE TIME DISTRIBUTIONS

Bifurcating Speciation



(Adapted from Leaché et al. 2013)

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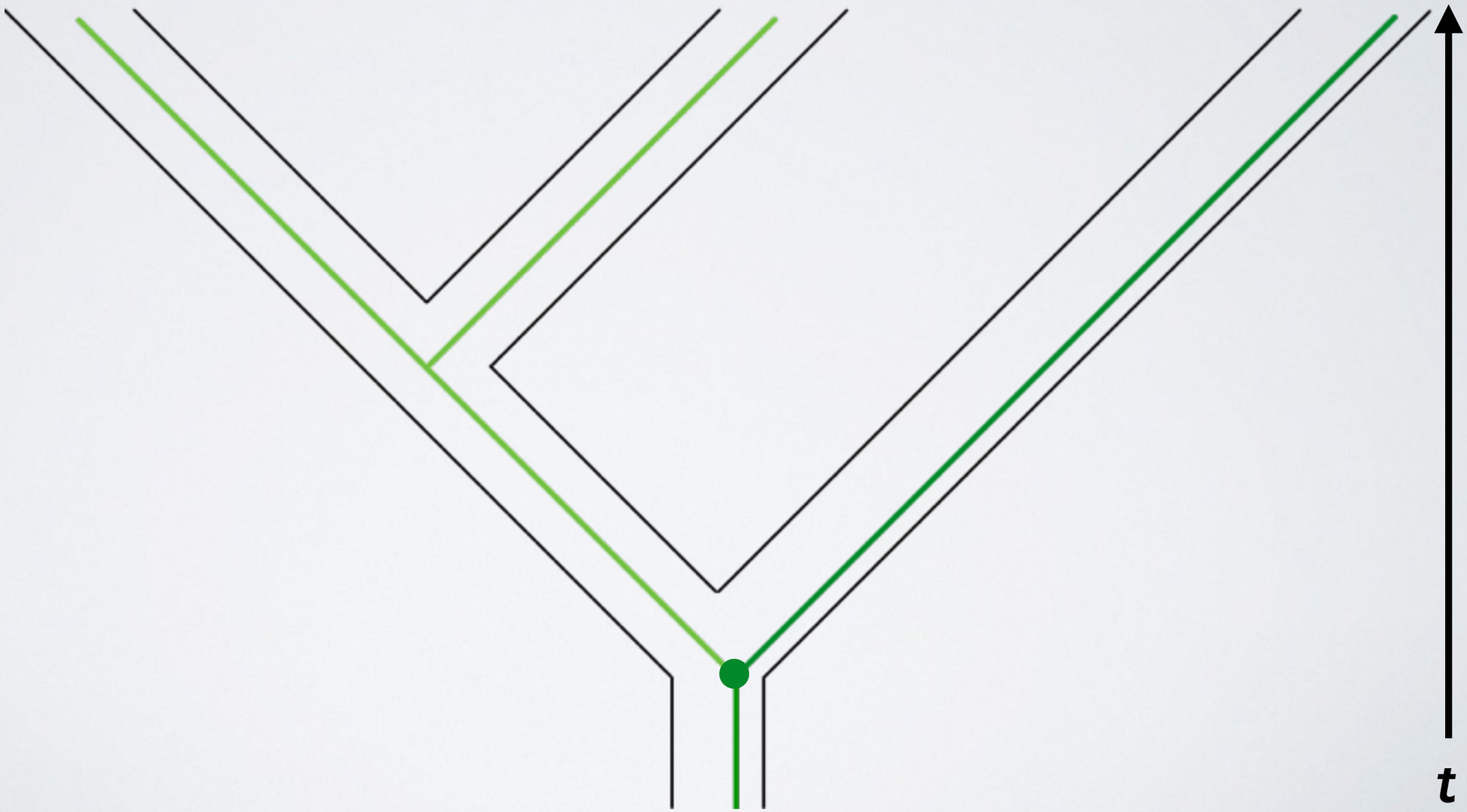

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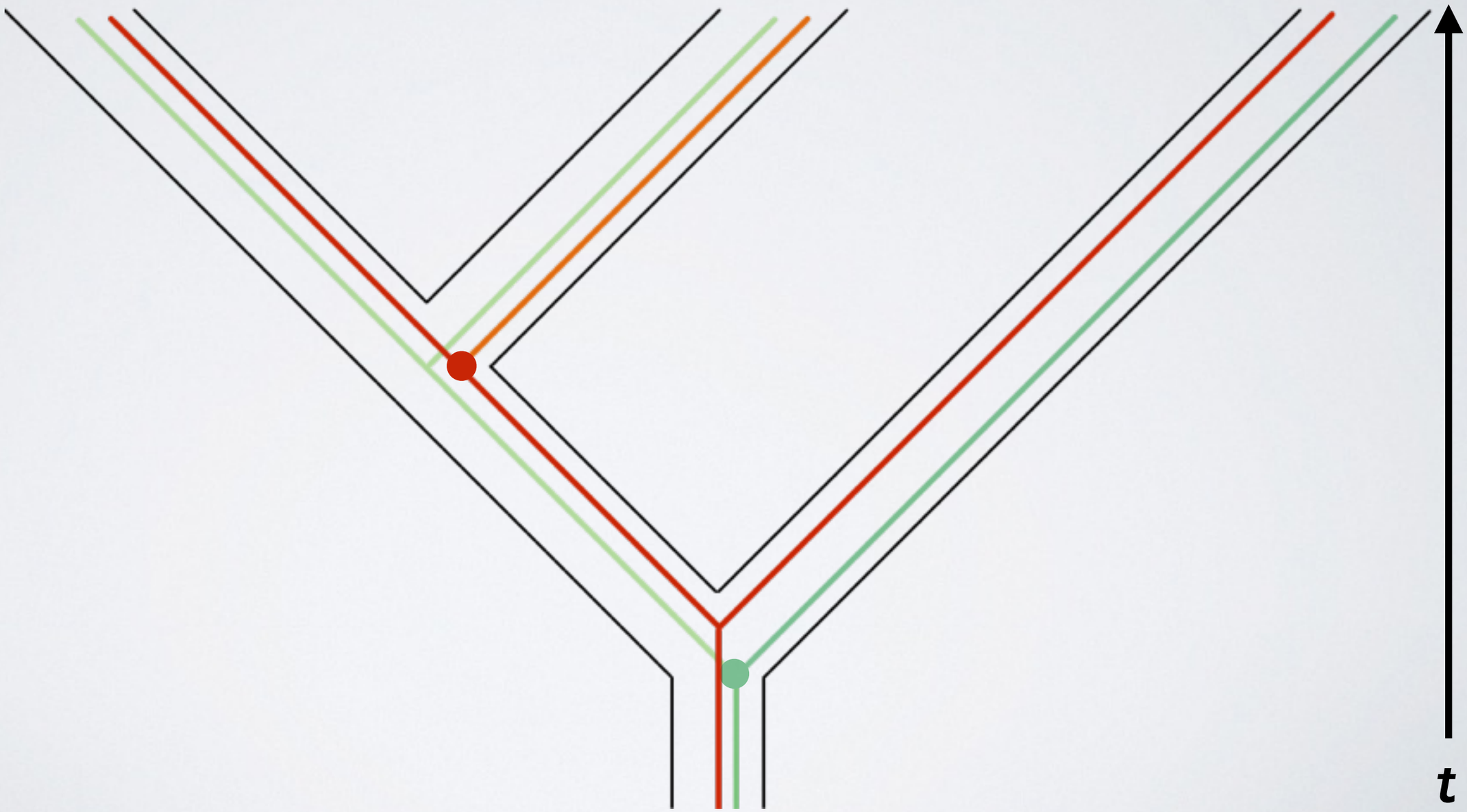

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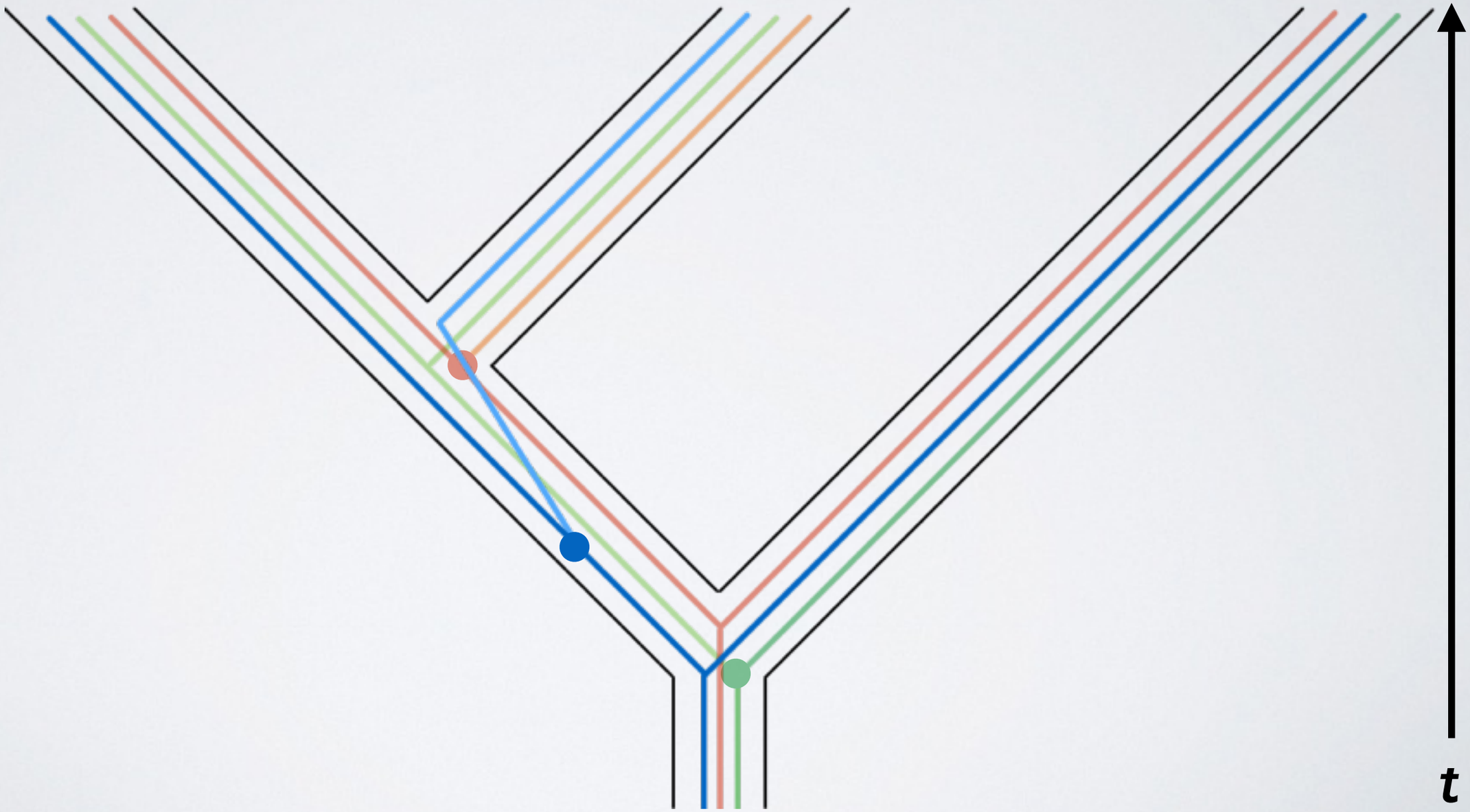

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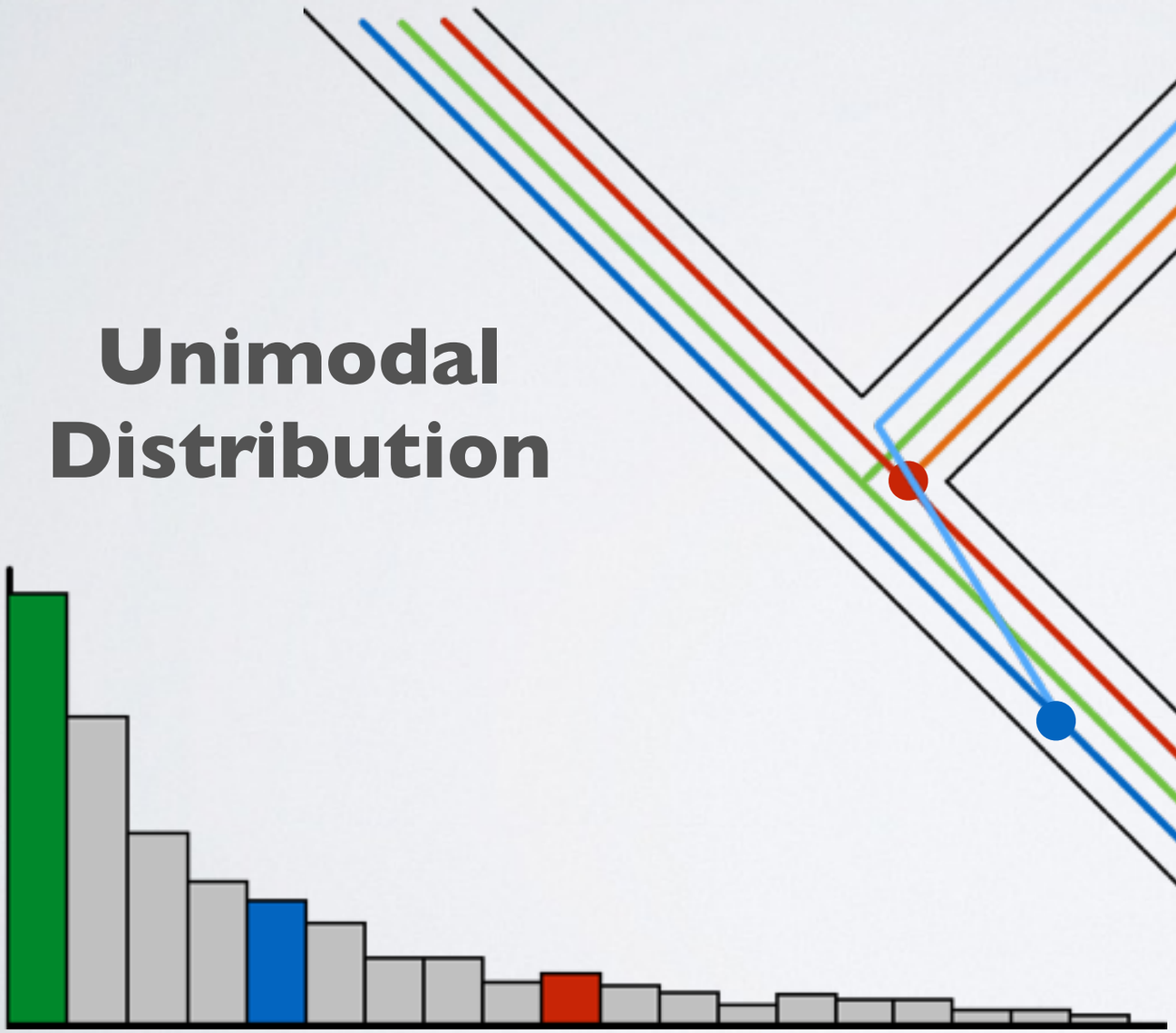
COALESCENCE TIME DISTRIBUTIONS

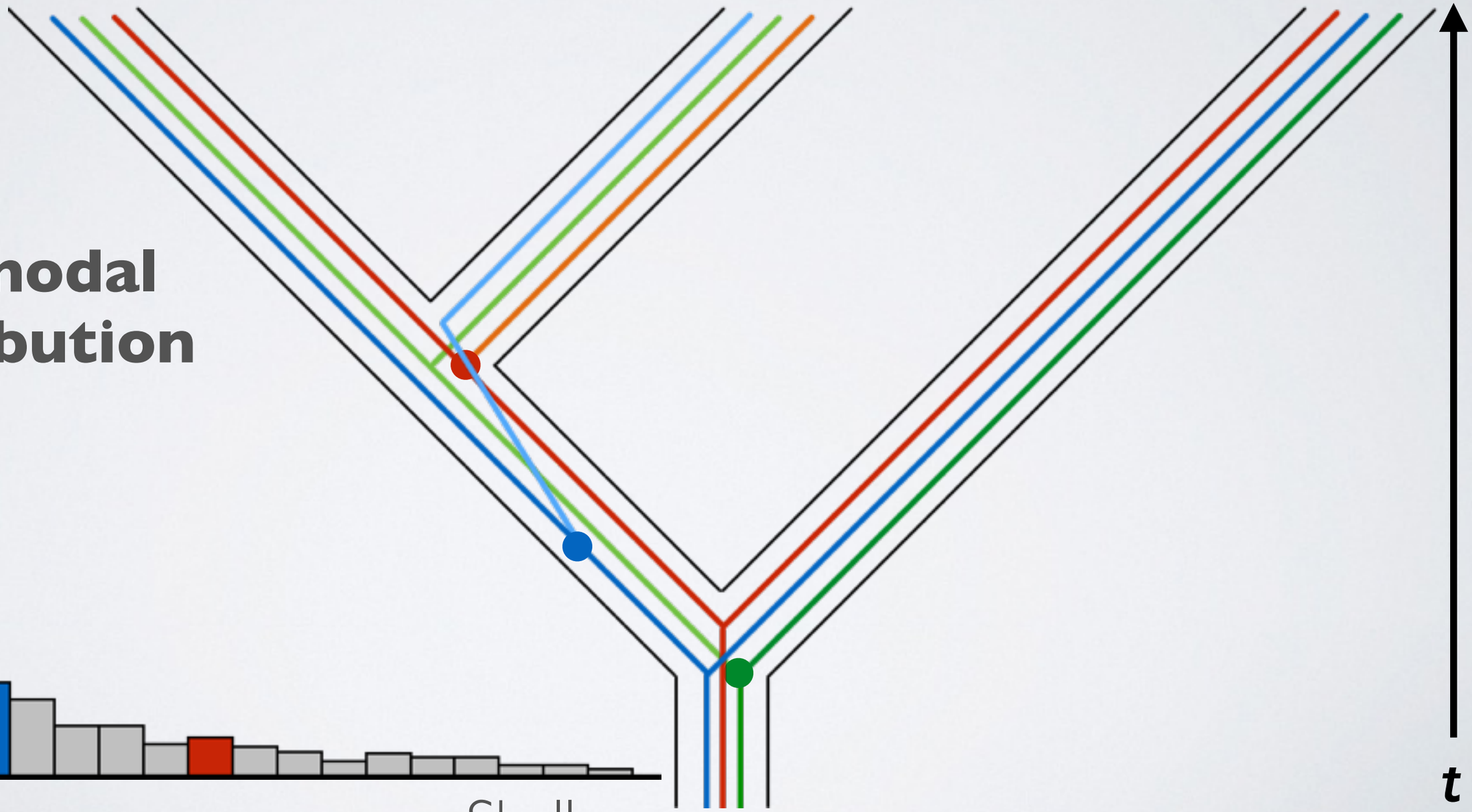
Bifurcating Speciation

Unimodal Distribution



Deep

Shallow



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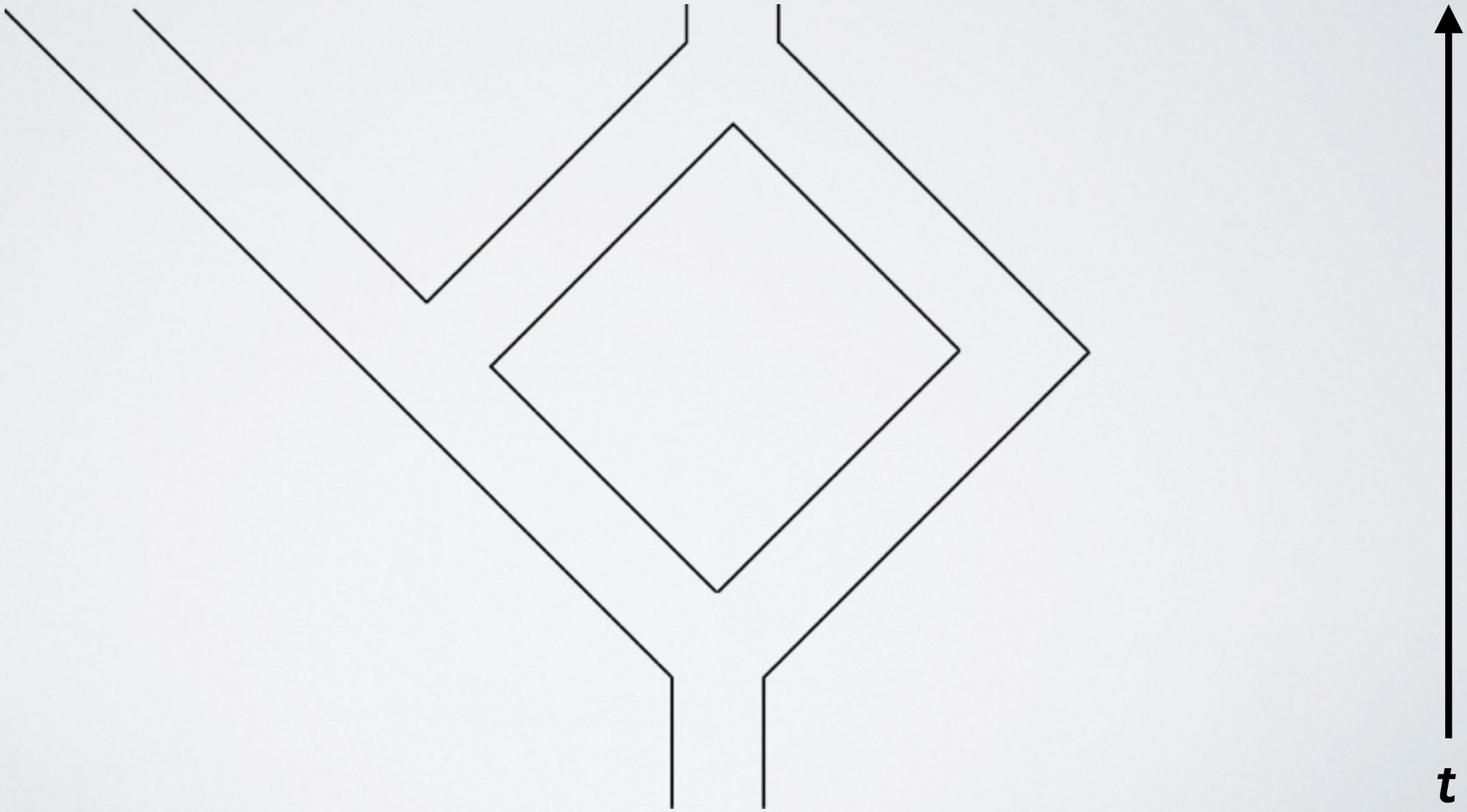
COALESCENCE TIME DISTRIBUTIONS

Parallel Speciation



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COALESCENCE TIME DISTRIBUTIONS

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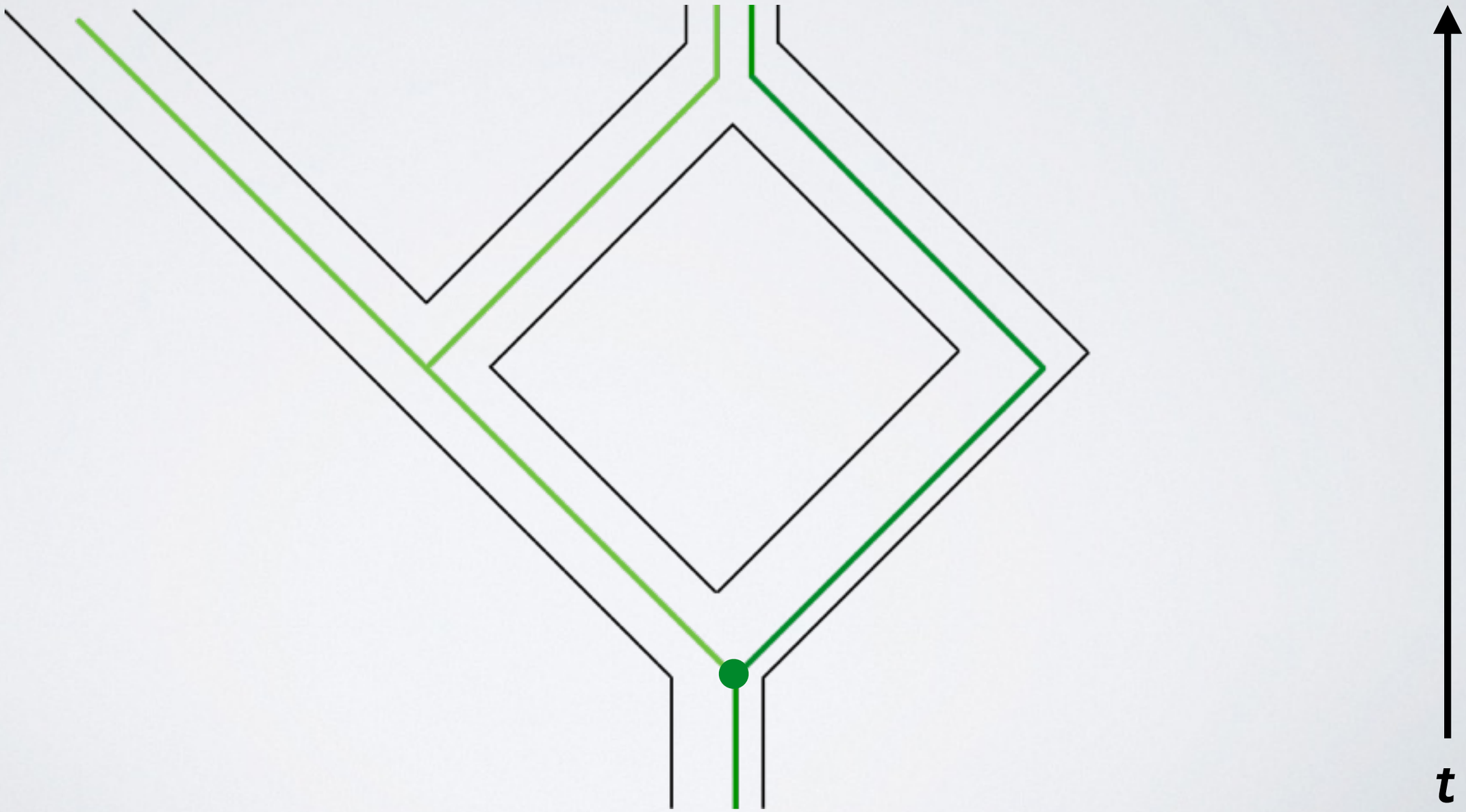

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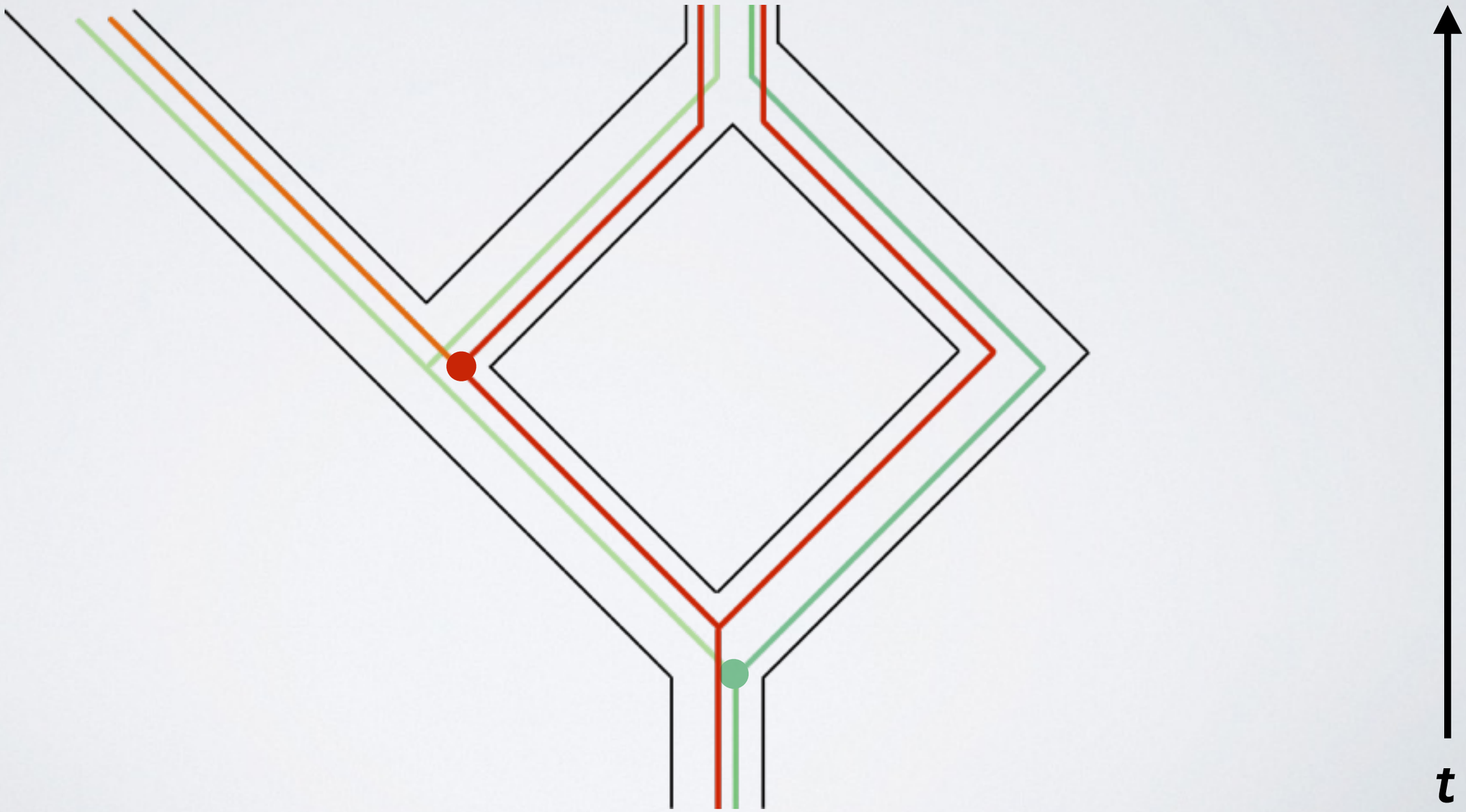

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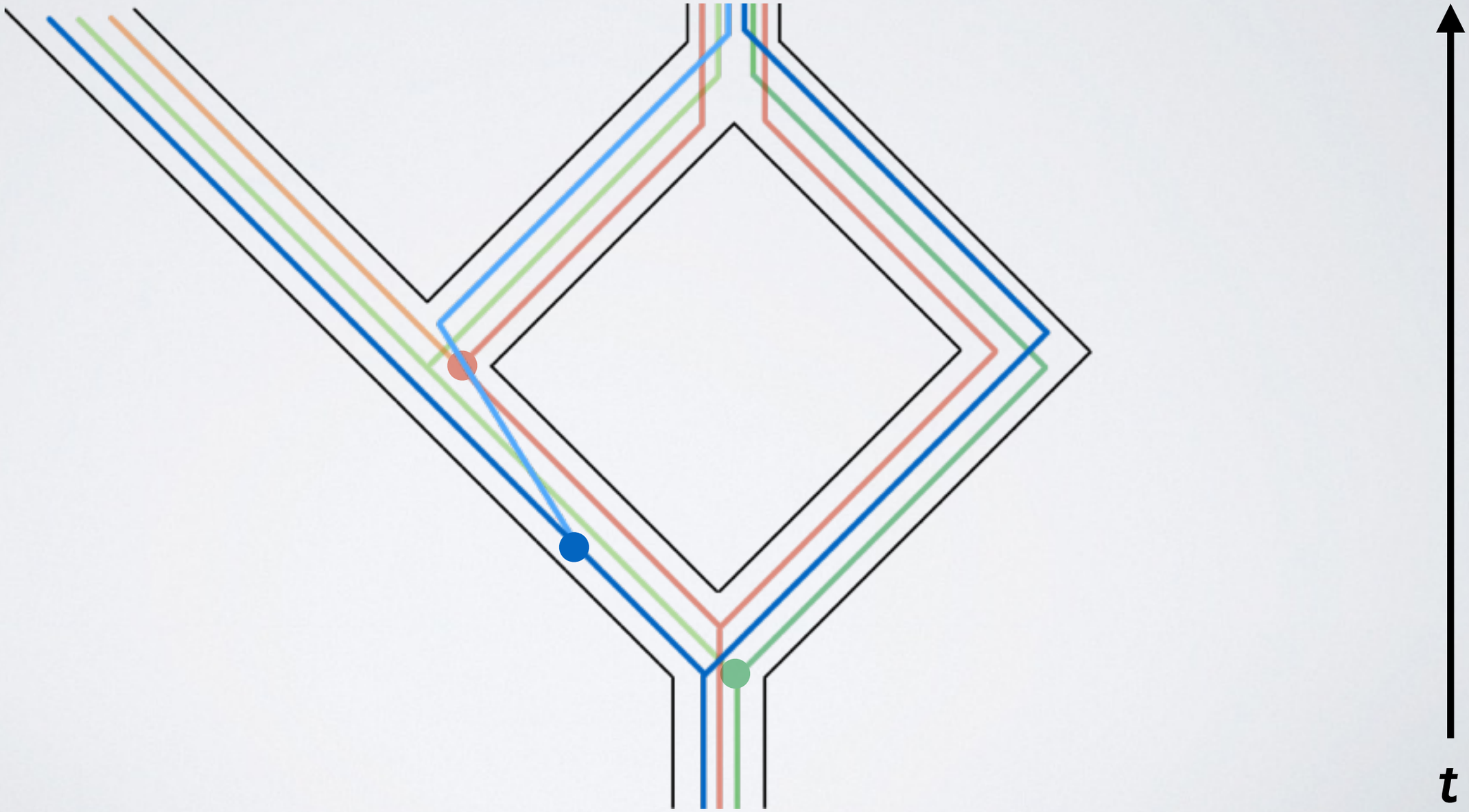

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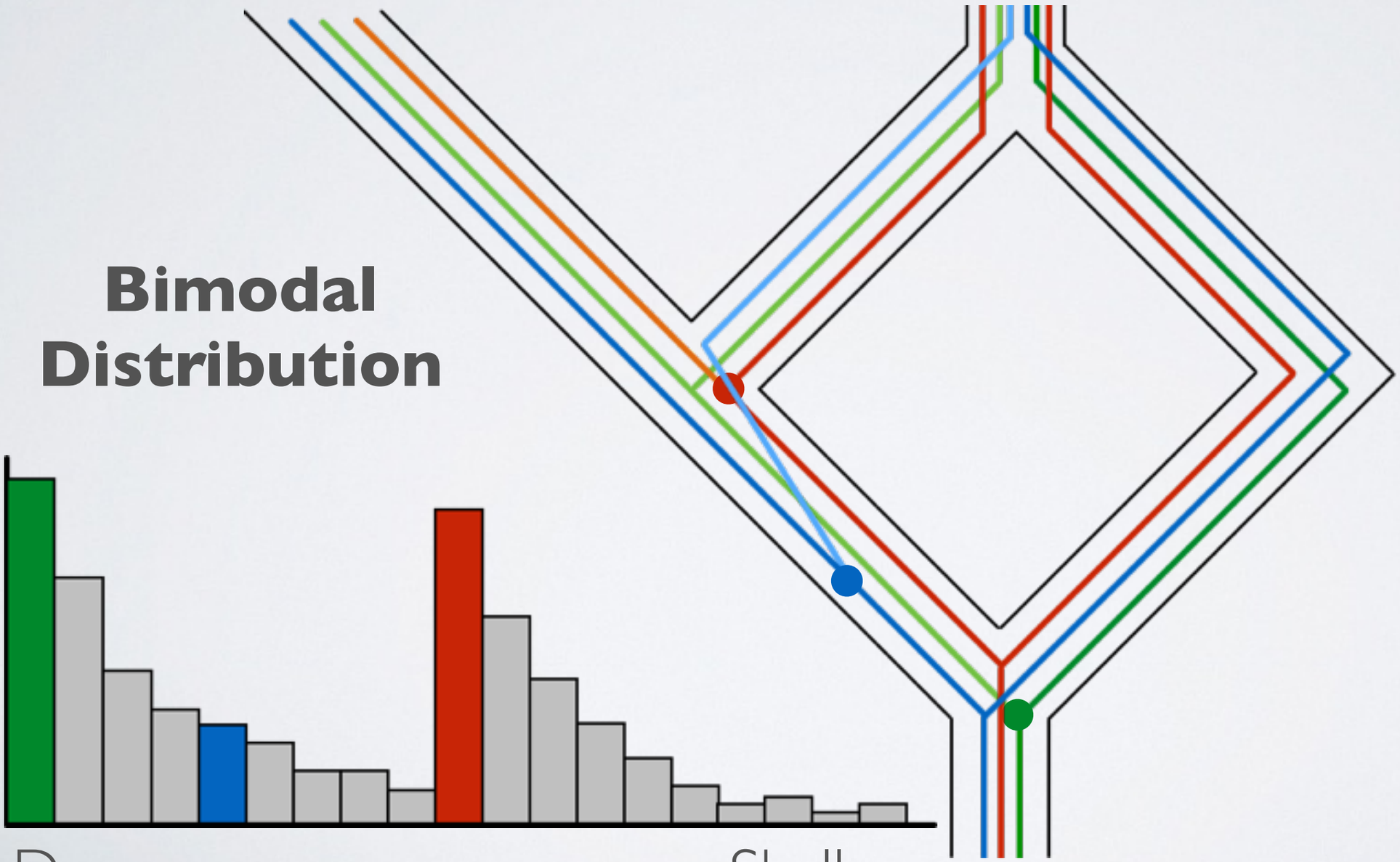

Bimodal Distribution

Deep

Shallow

(Adapted from Leaché et al. 2013)

HOW DO I GET COALESCENCE TIME DISTRIBUTIONS?

"Identifying a bimodal distribution in gene tree coalescent times with empirical data, which is suggestive of genetic exchange, **will require more loci than are typically available**, but this constraint is vanishing as more studies shift towards new sequencing technologies." (Leaché et al. 2013)

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Leverage anchored phylogenomics to capture ~500 loci

NEXT STEPS

- Sample from allopatric portions of *P. skiltonianus* and *P. gilberti* ranges, including from well-separated portions of the different *P. gilberti* mitochondrial lineages

- Use anchored phylogenomics to capture sequence data from ~500 loci for each sample

- Generate a distribution of coalescence times across all loci, and gene tree topologies for each loci using BEAST

THANK YOU!

Thanks to…