

Phylogenetic Biology

Reconciling gene trees

and species trees

Biology 1425

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Brown University

Front matter...

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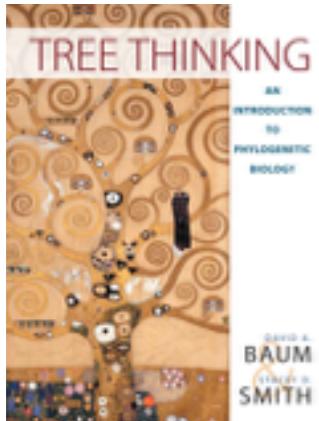
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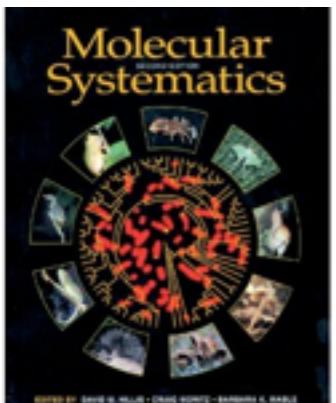
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Sources

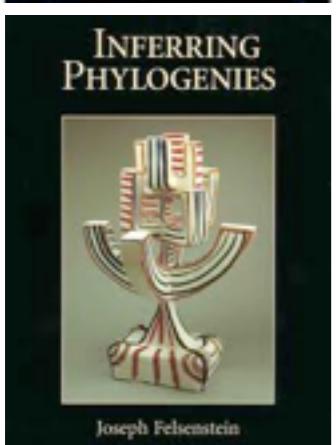
Some non-original content is drawn from:



Baum, D and S. Smith (2012) Tree Thinking: and Introduction to Phylogenetic Biology. Roberts and Company Publishers. ISBN 9781936221165



Swofford, D. L., Olsen, G. J., Waddell, P. J., & Hillis, D. M. (1996). Phylogenetic inference. In: Molecular Systematics, Second Edition. eds: D. M. Hillis, C Moritz, & B. K. Mable. Sinauer Associates. ISBN 9780878932825



Felsenstein, J. (2003) Inferring Phylogenies. Sinauer Associates. ISBN 978-0878931774

Other non-original content is referenced by url.

Reconciling gene trees and species trees

Sometimes gene trees and species trees are congruent...

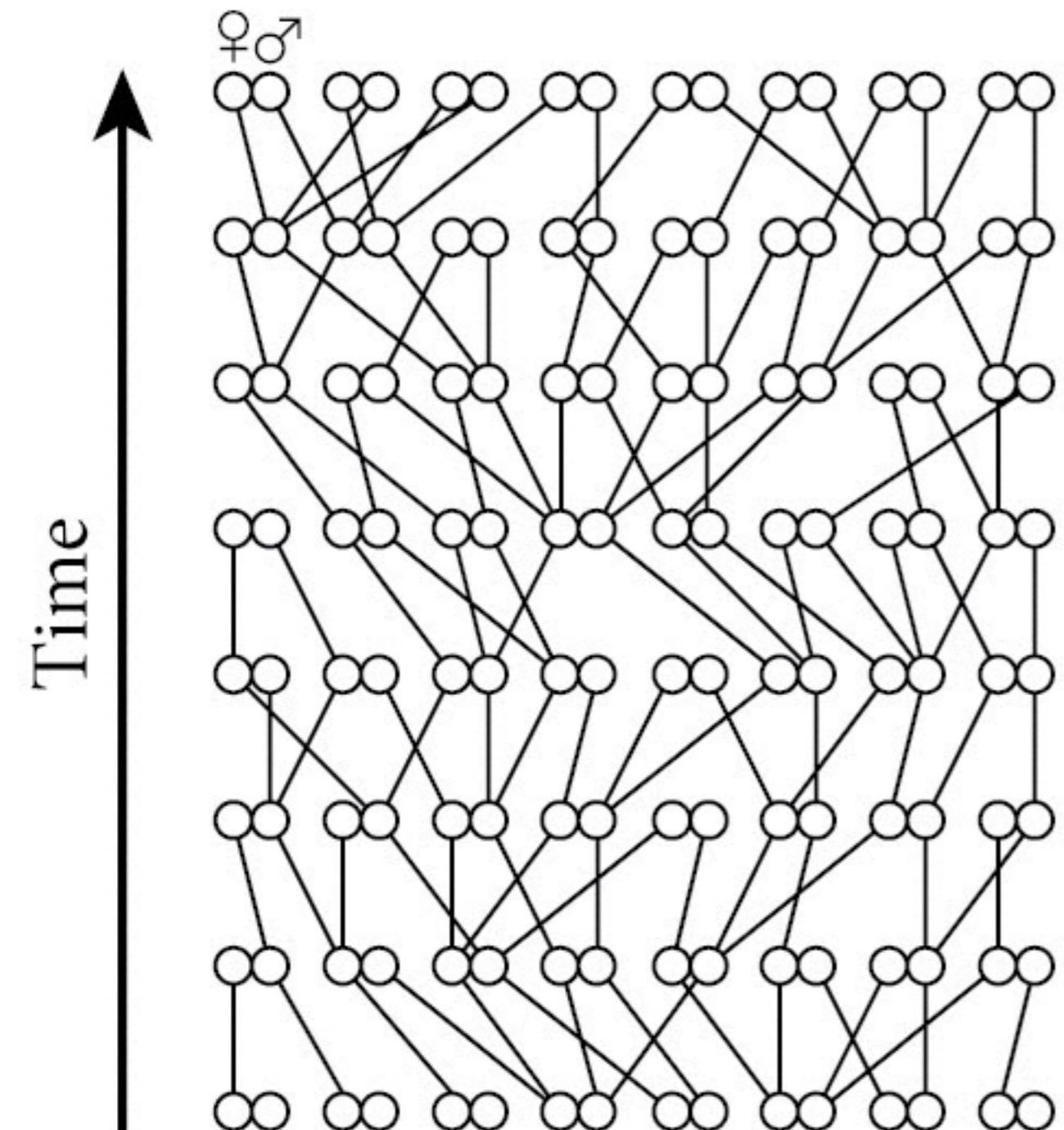
Sometimes gene trees and
species trees are congruent...

Sometimes they aren't.

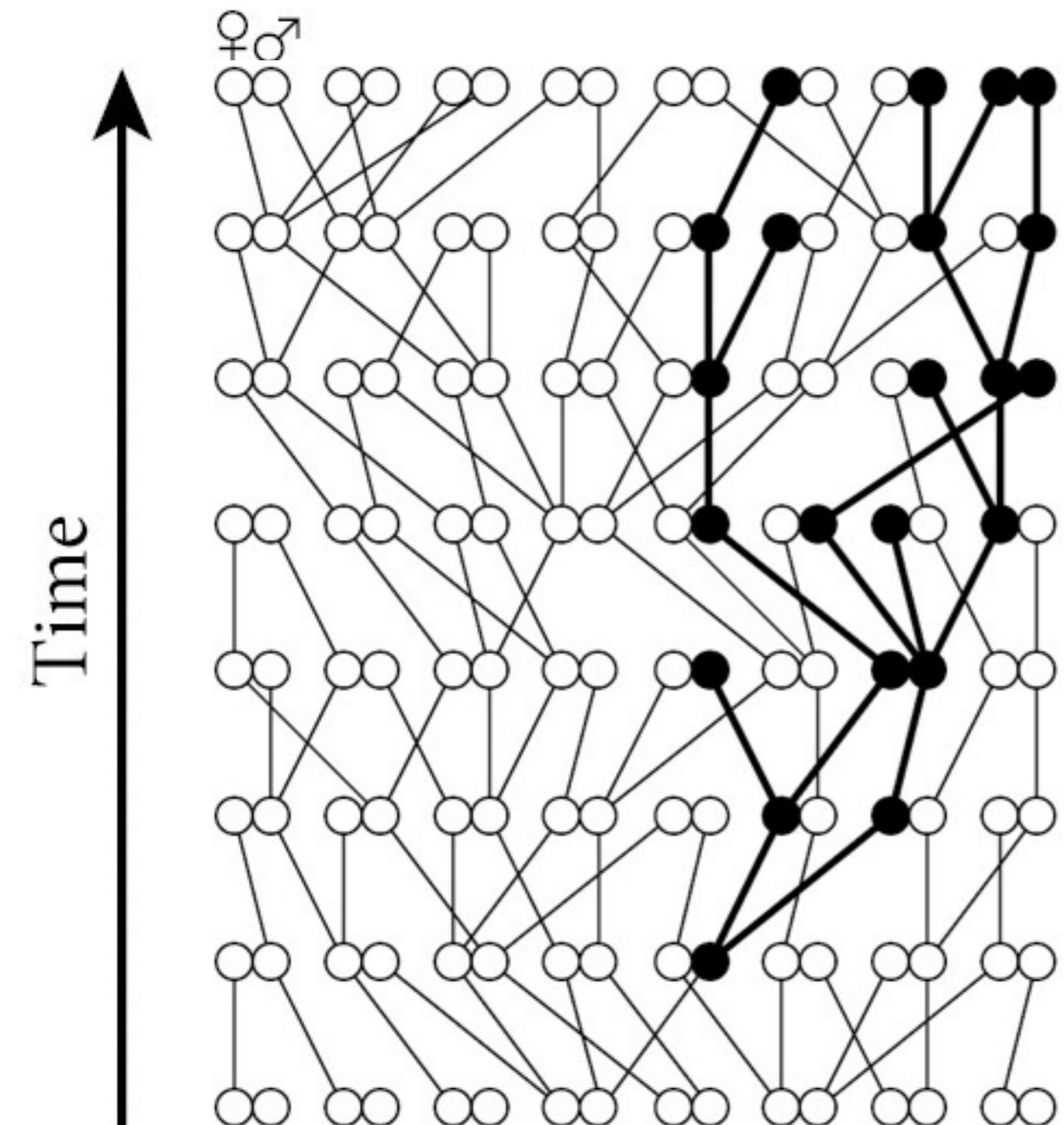
Incongruence can be due to incorrect phylogenetic inference (ie, they do have the same history but this history isn't recovered in analyses of contemporary data).

There are also multiple biological reasons that gene trees can really differ from each other and from the species tree.

Incomplete lineage sorting



Nodes are alleles. Pairs of nodes are individuals.
Edges indicate inheritance of alleles



Any set of alleles in one generation can be traced back to a common ancestor in a previous generation - coalescence.

What is the average time to coalescence?

$$E(T) = 2N$$

Where:

N is the population size.

T is the number of generations

coaltrace

Simulating genealogies using charged particles

Source code

 github.com/trvrb/coaltrace

Contributors



Latest commits

- 20 Apr 2015 - Update processing.js.
- 25 Jul 2014 - Back to dark background.
- 25 Jul 2014 - Switch to white background.
- 25 Jul 2014 - Add stub page.
- 18 Oct 2013 - Update readme.

Pages

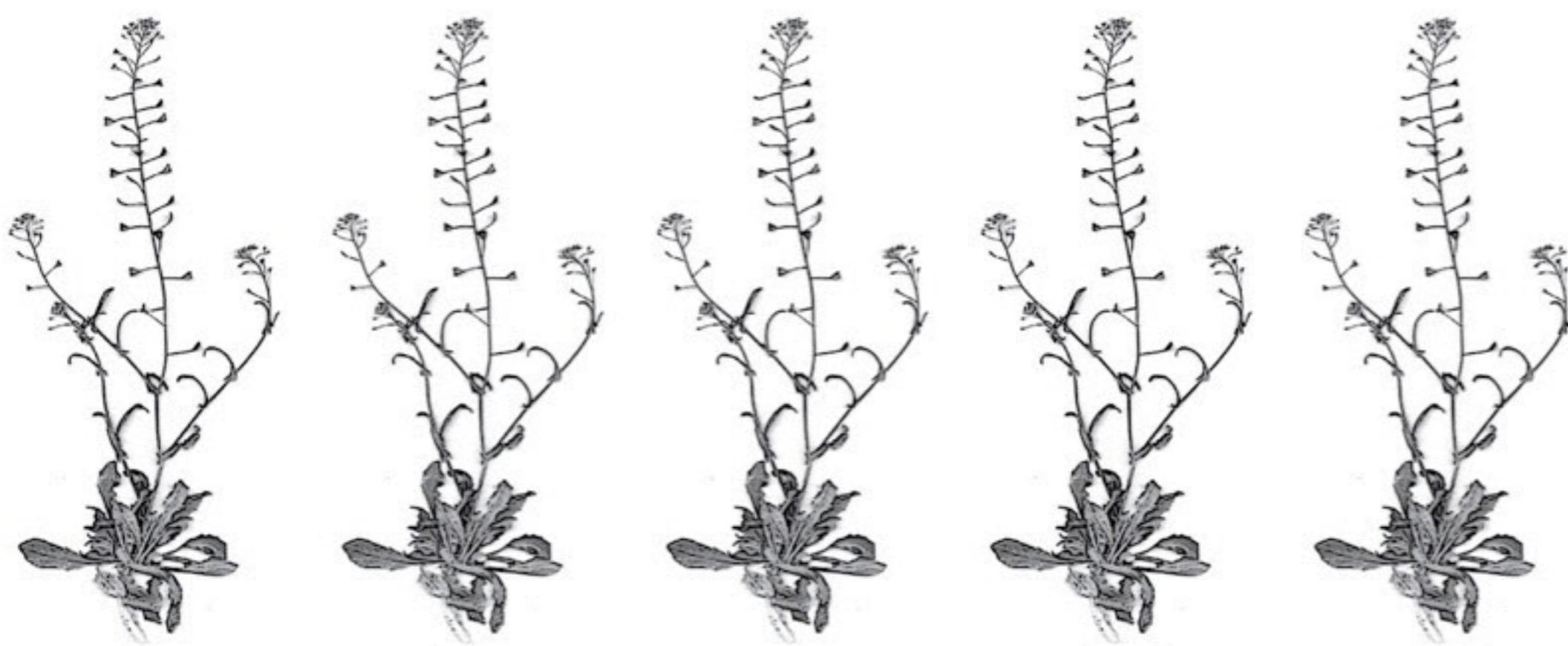


<http://bedford.io/projects/coaltrace/>

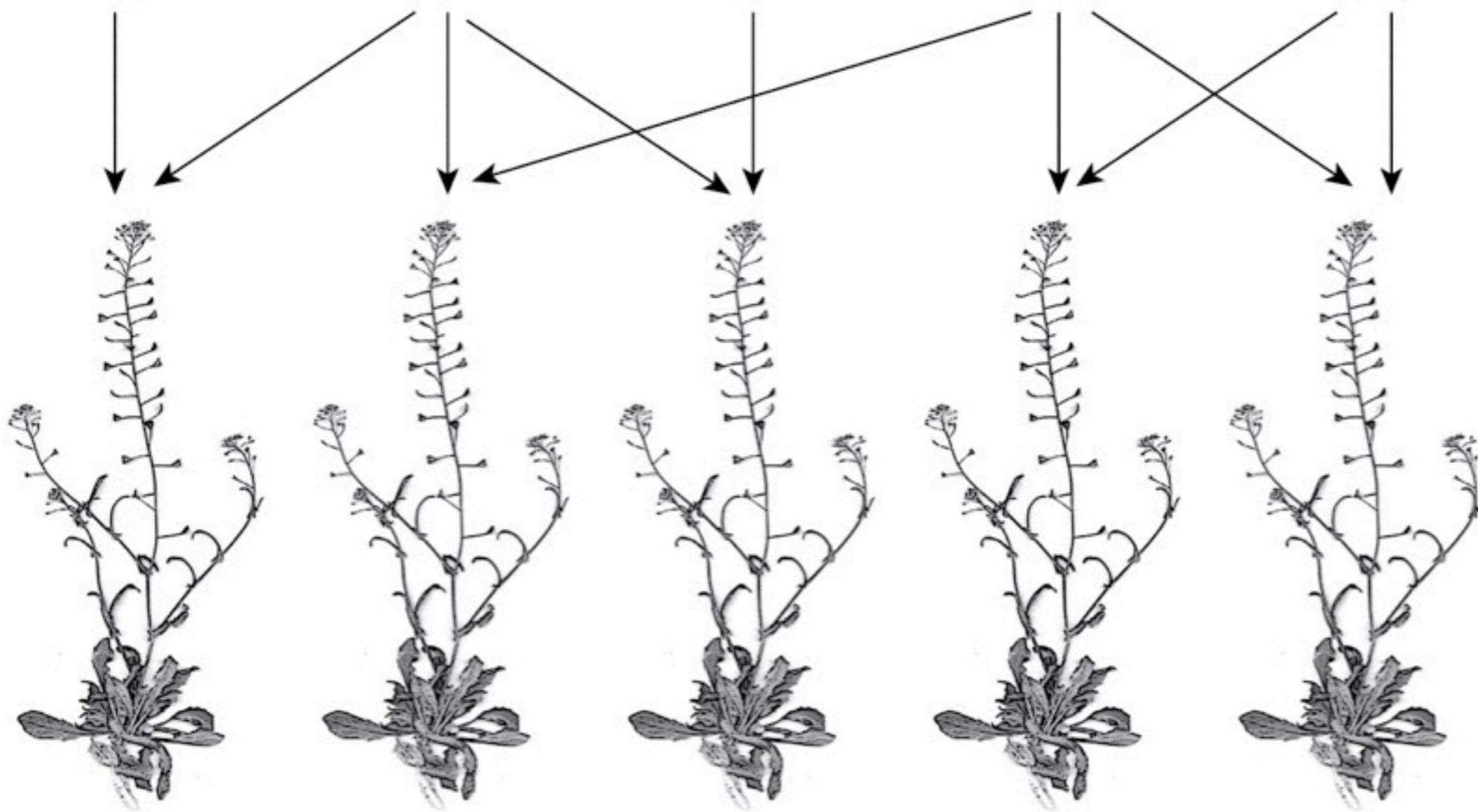
For any group of individuals in a sexual population, different genes will have different histories.

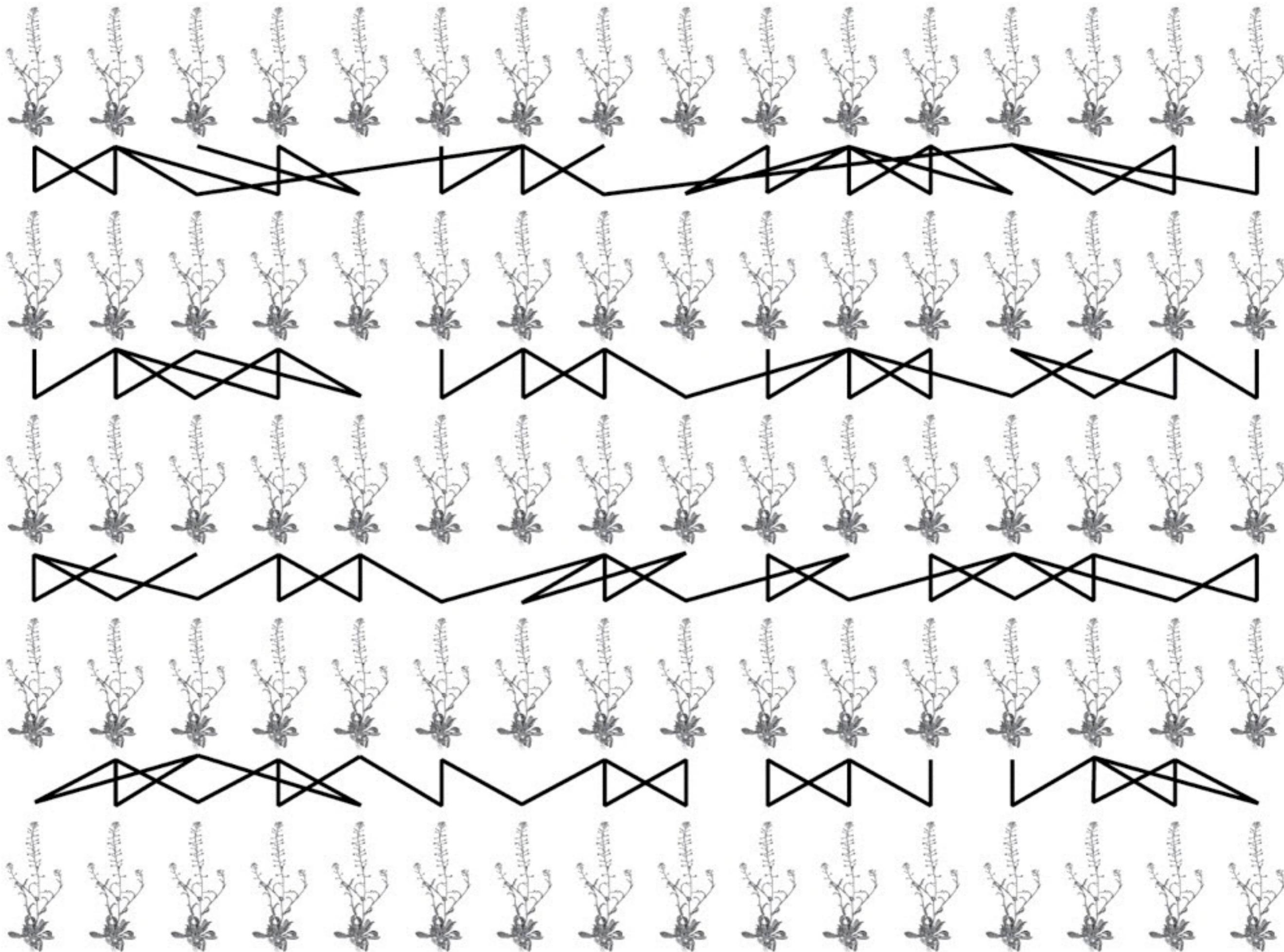
This can be the case for phylogenetic trees, if a branch is not long relative to the expected coalescence time.

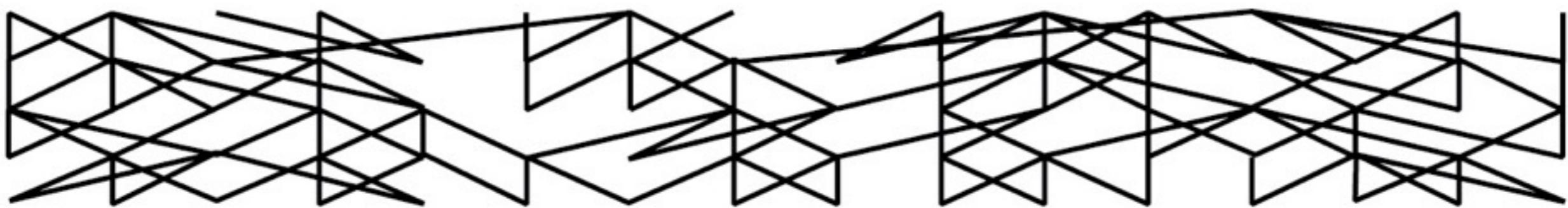
Parents—
Generation 1

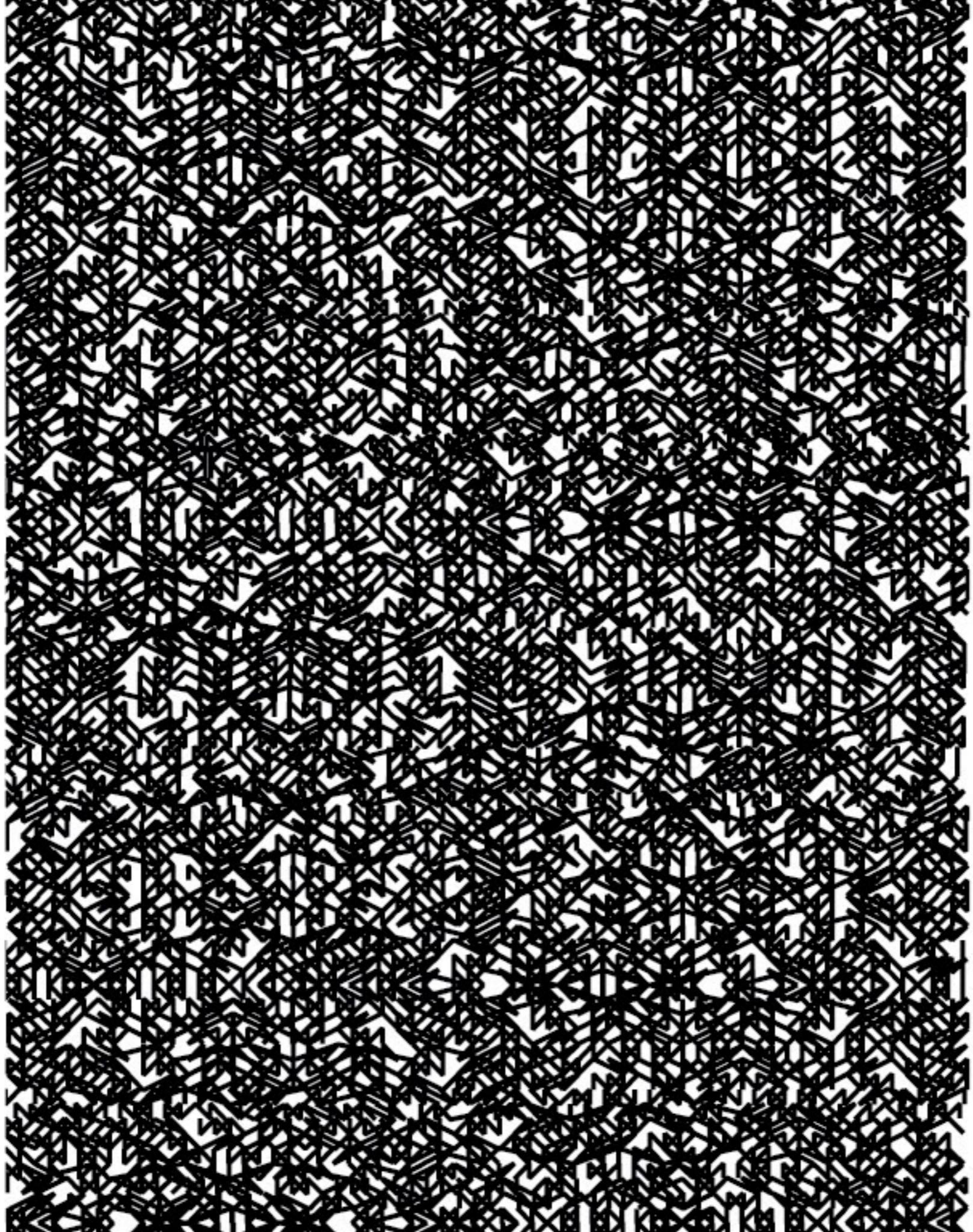


Offspring—
Generation 2







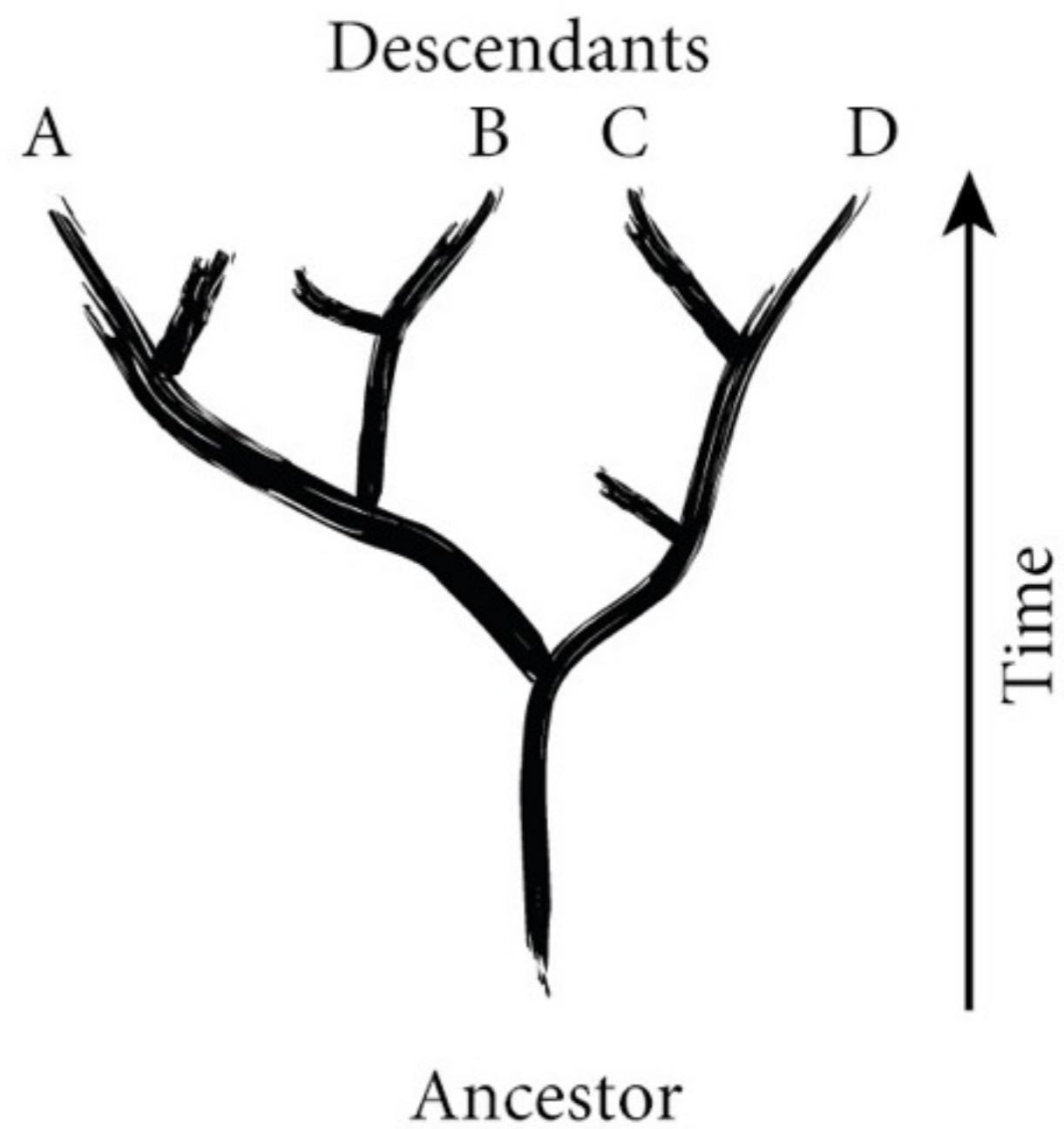
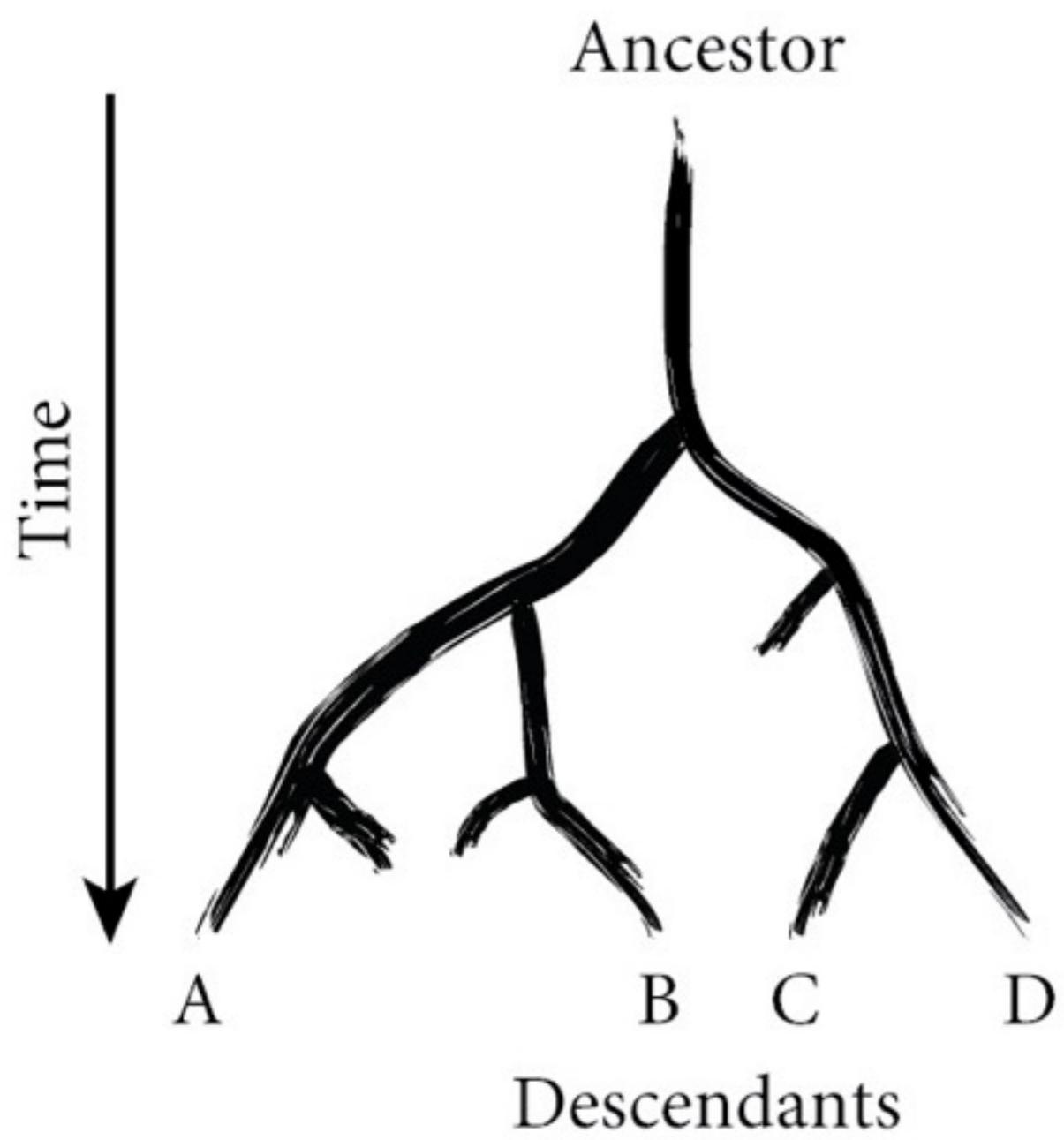


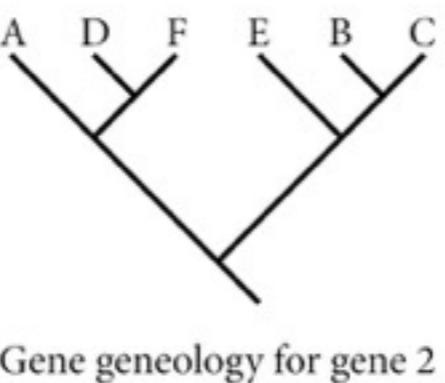
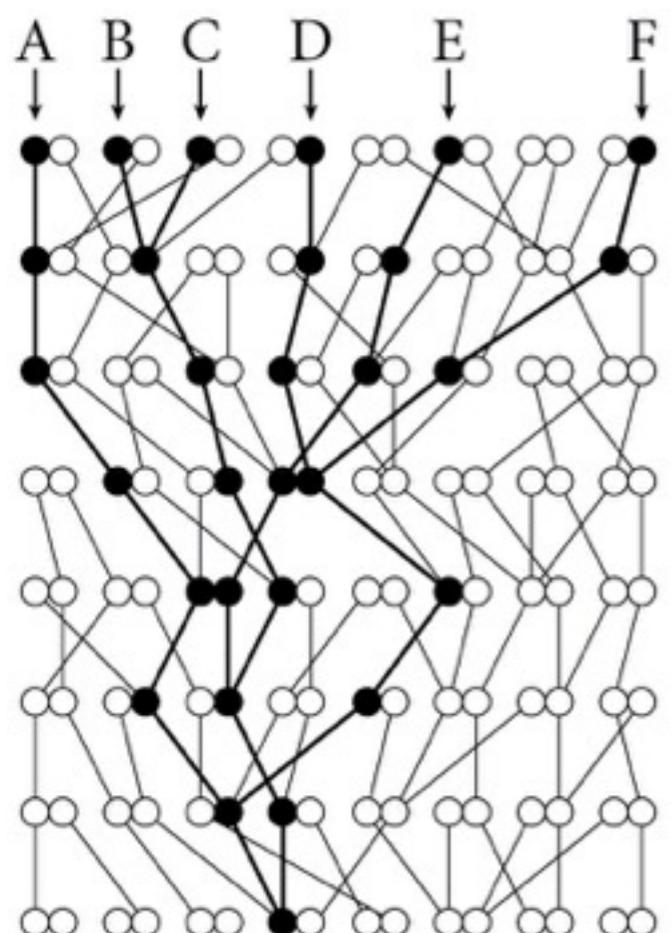
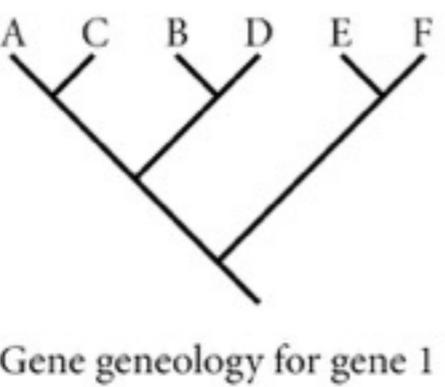
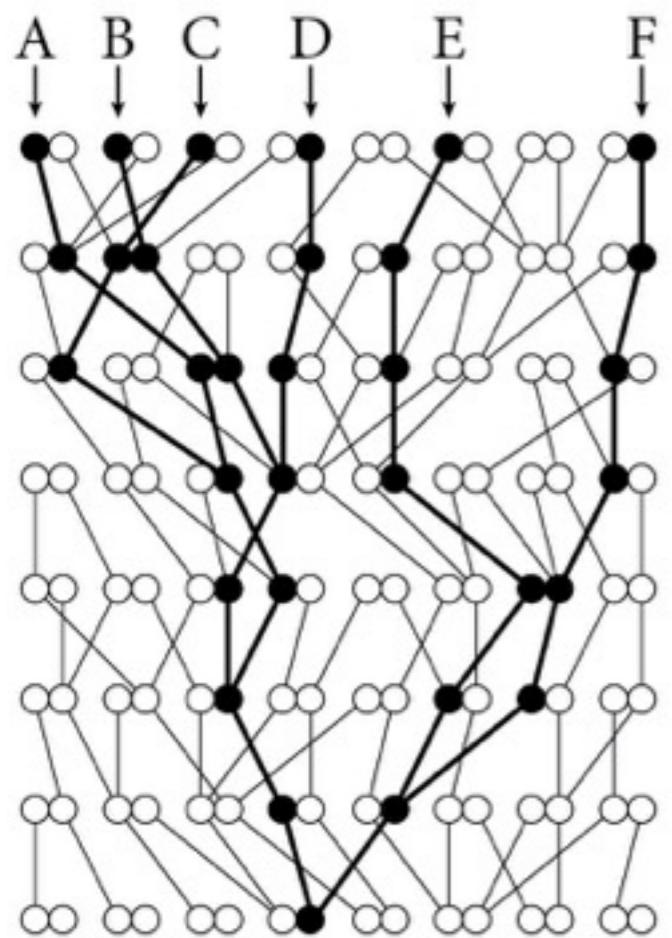


Past



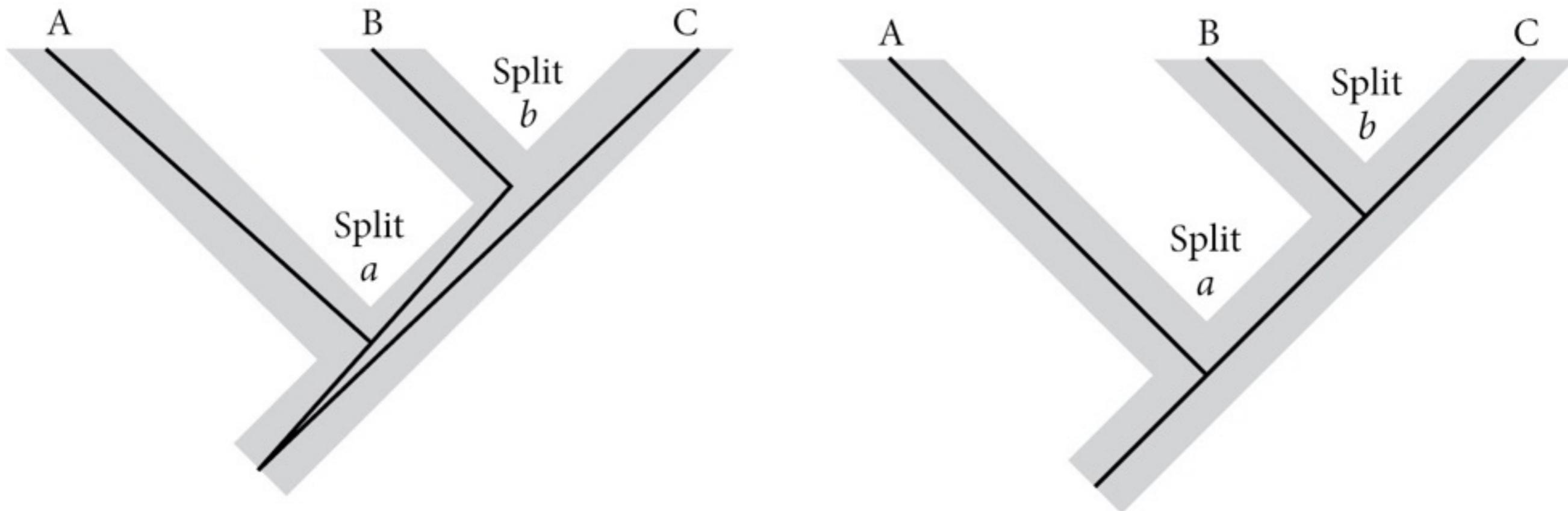
Present

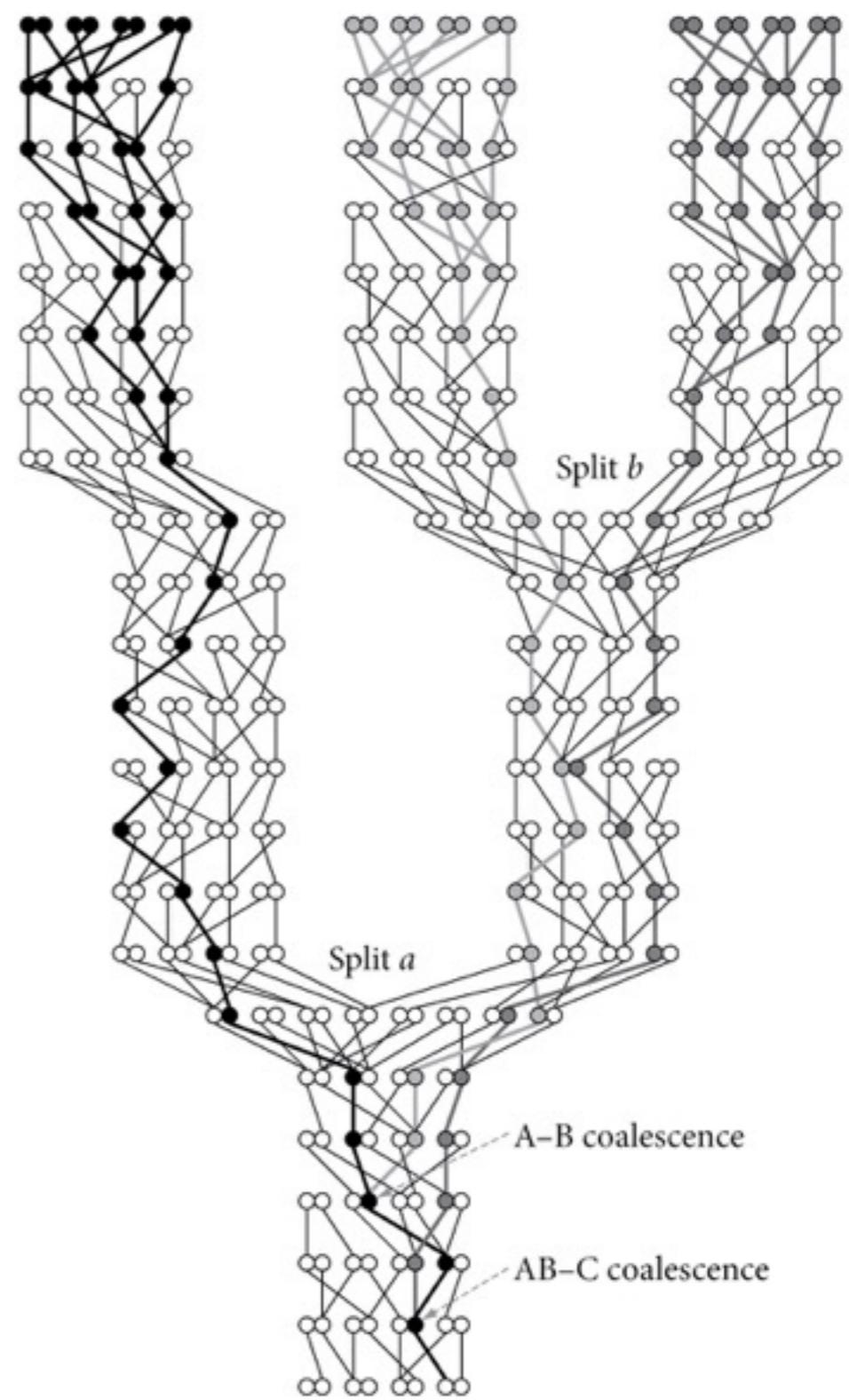
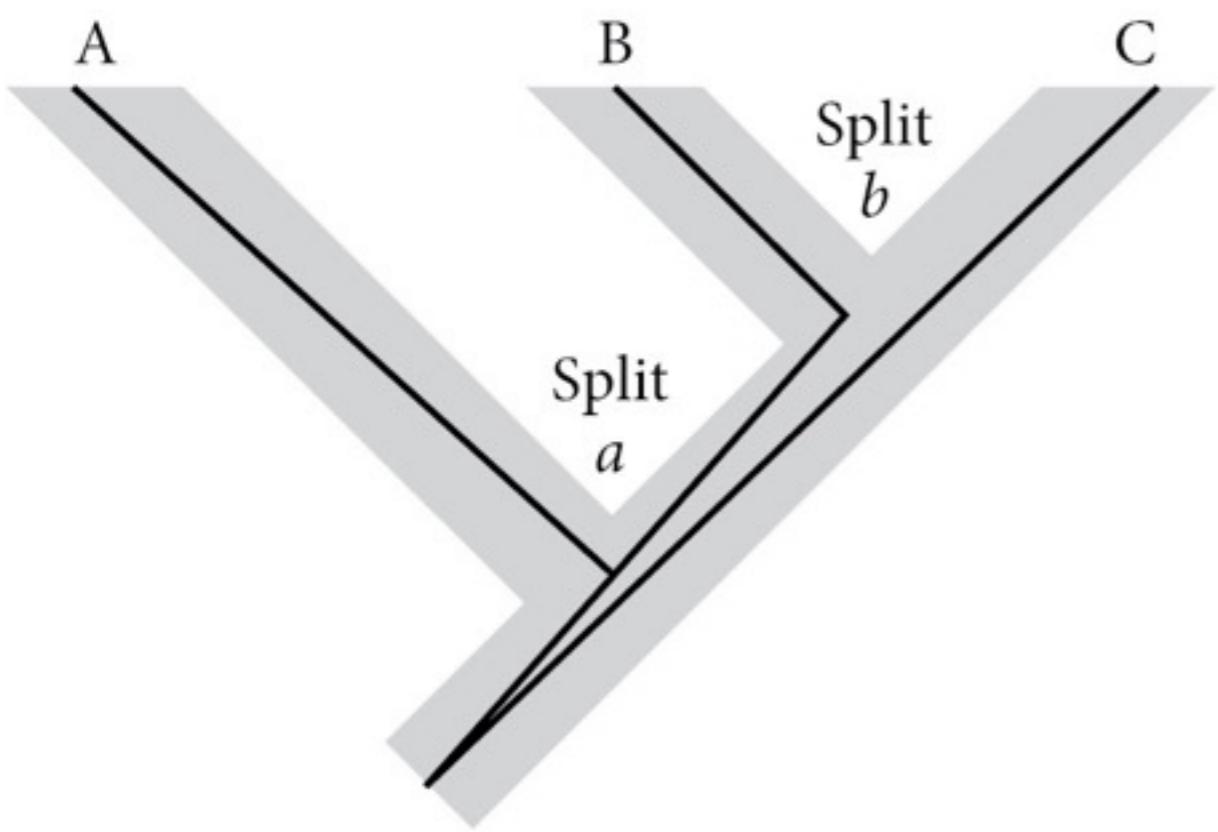




Baum and Smith 2012, Figure 6.3

Phylogenies of different genes can differ...





Baum and Smith 2012, Figures 6.6-6.7

Usually coalescence focuses on the excess contribution by a small number of individuals to future generations, but that also means there are many that under contribute.

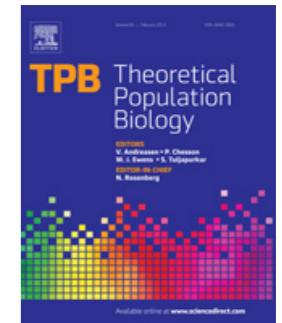
In sexual populations, this means there are some “ghost” ancestors that are ancestors to the entire future population, but make no genetic contribution to it.



Contents lists available at ScienceDirect

Theoretical Population Biology

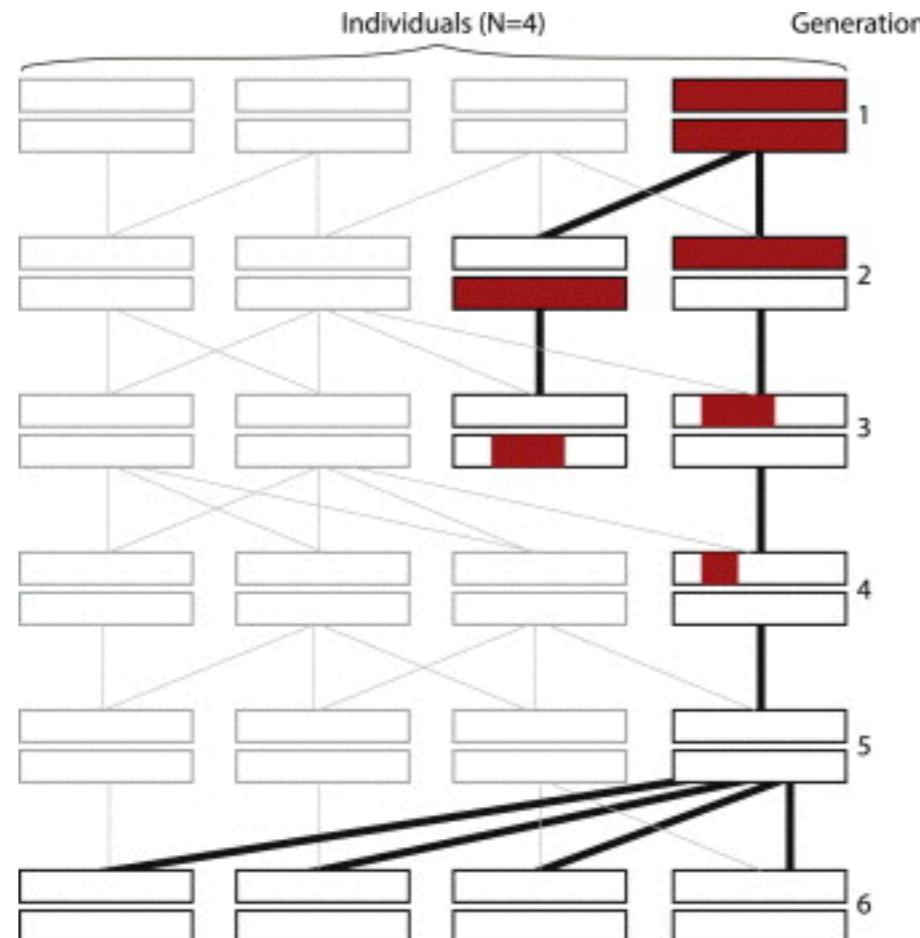
journal homepage: www.elsevier.com/locate/tpb



The existence and abundance of ghost ancestors in biparental populations



Simon Gravel ^{a,*}, Mike Steel ^b



Gene duplication and loss

Species A



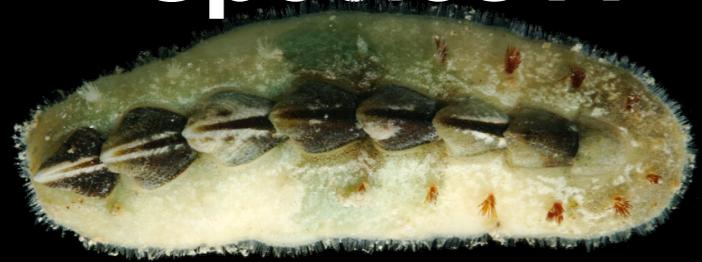
Species B



Species C



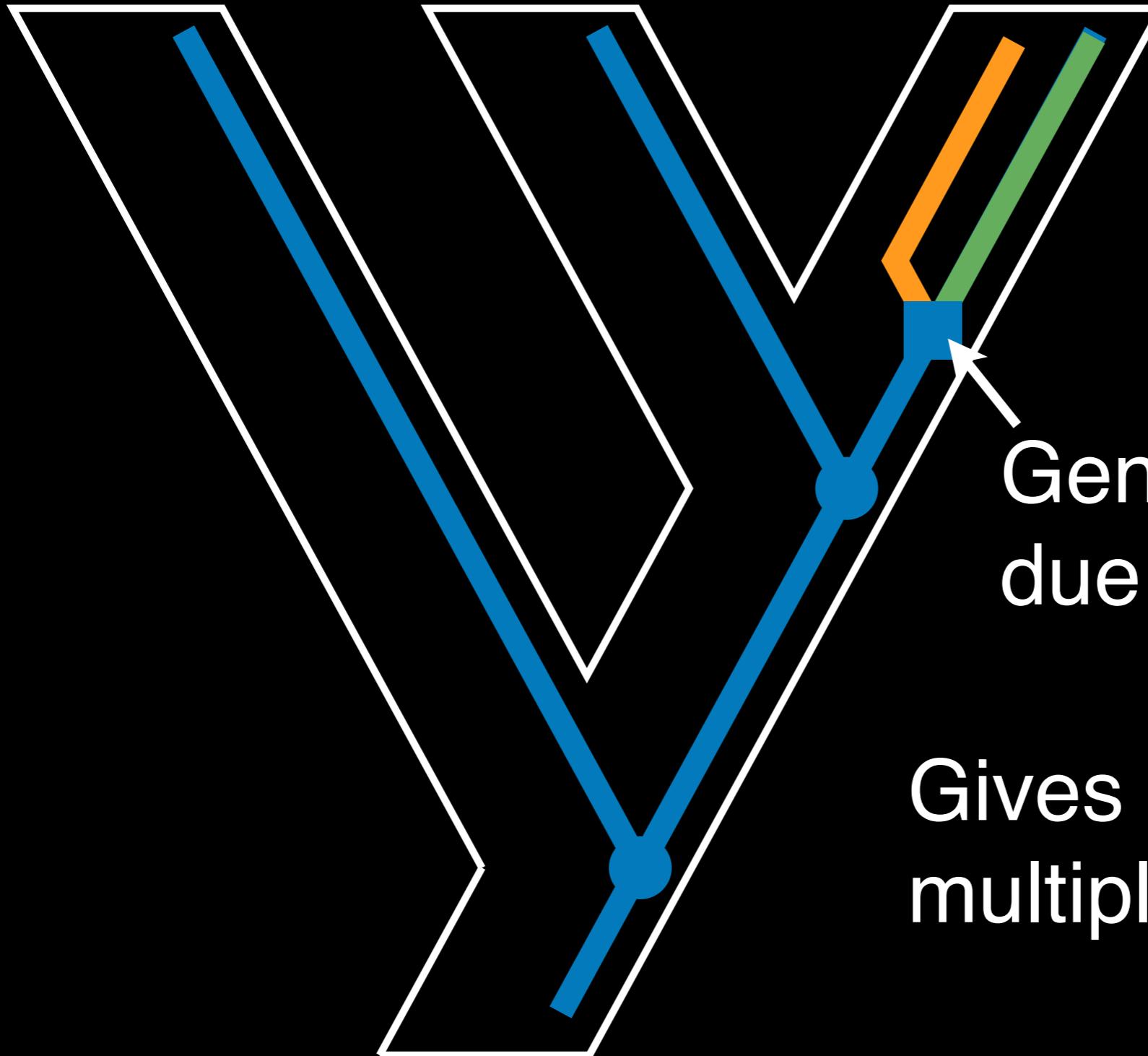
Species A



Species B



Species C



Gives rise to
multiple “paralogs”

Gene divergence
due to duplication

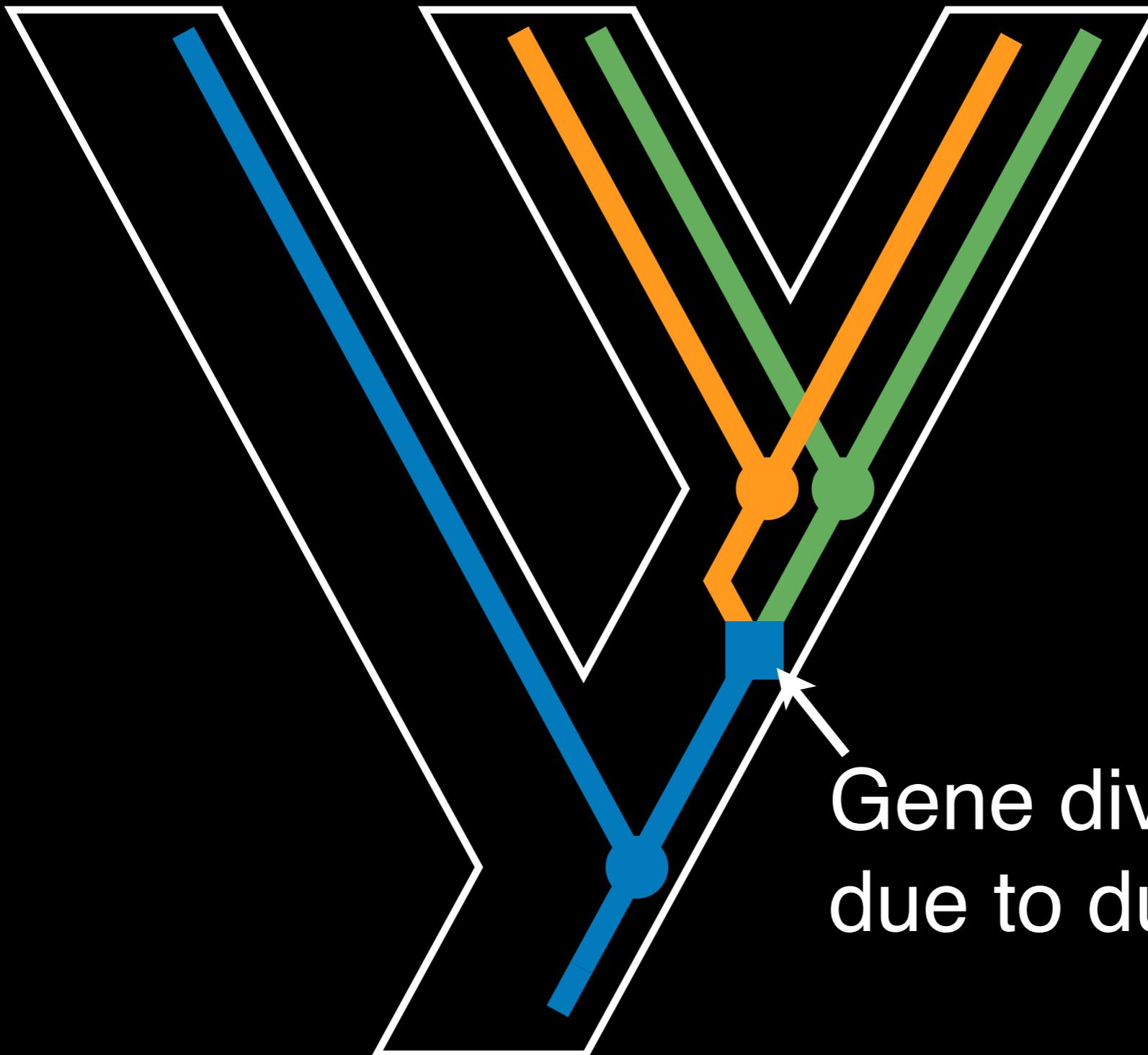
Species A



Species B



Species C



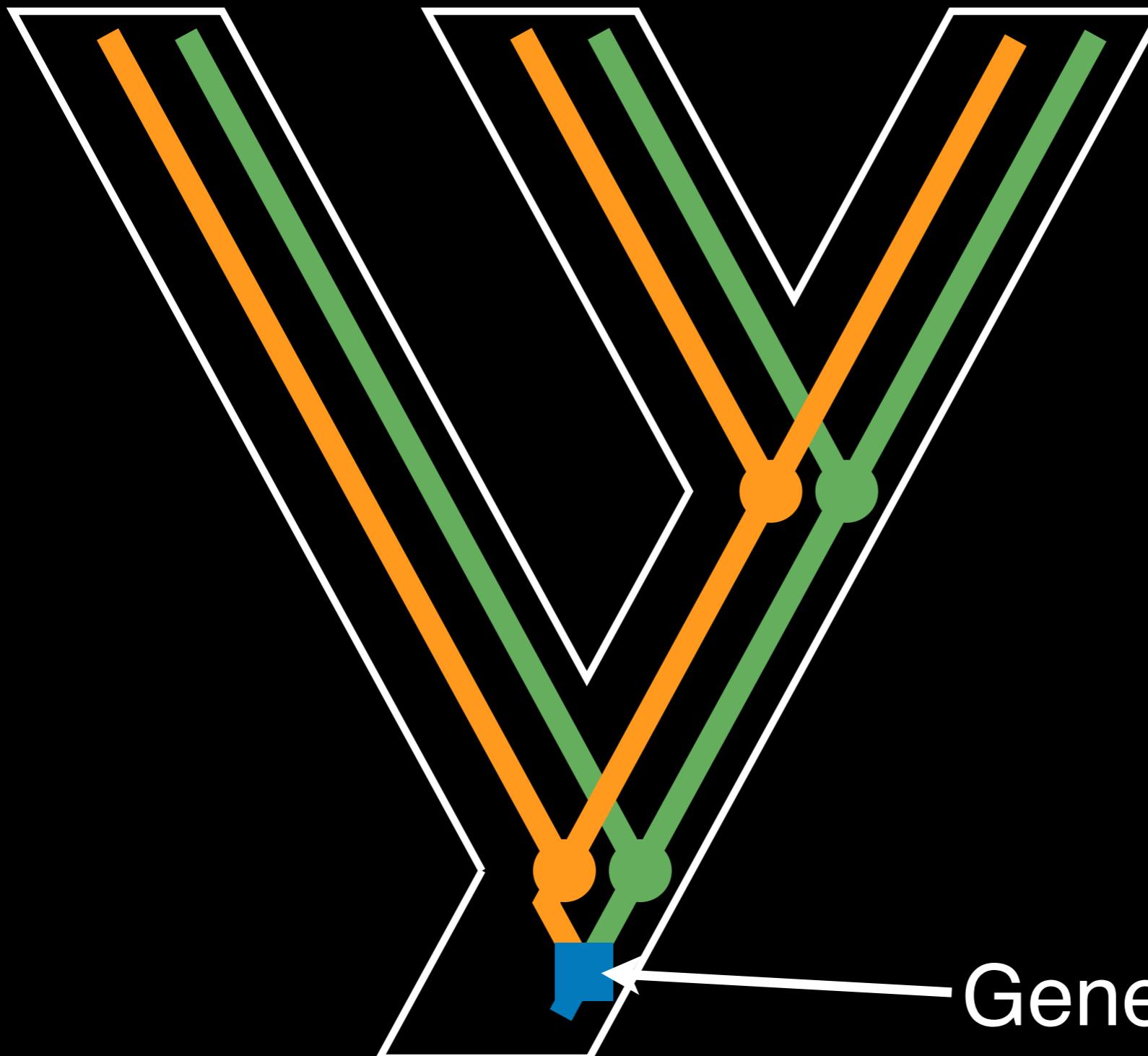
Species A



Species B



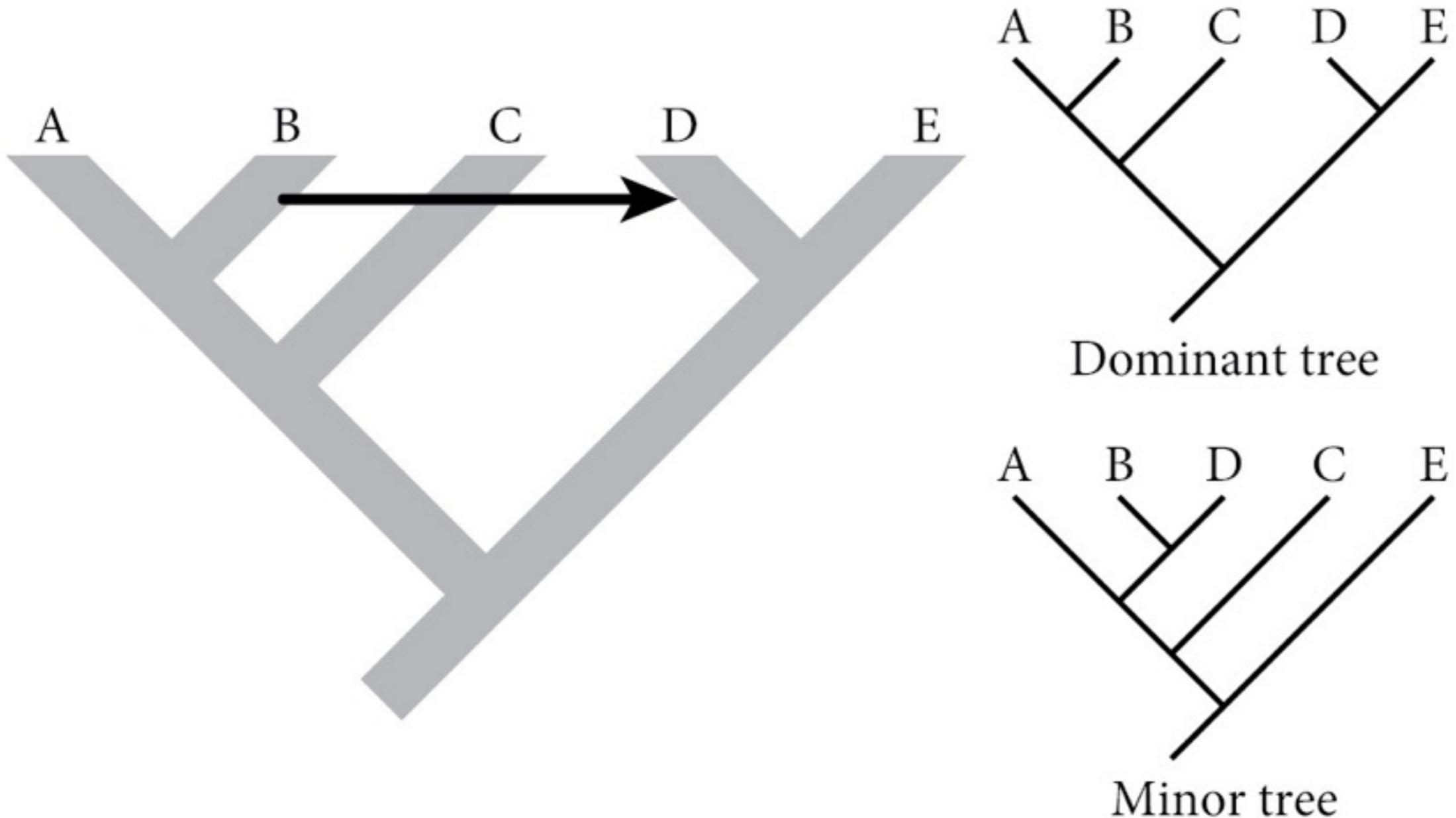
Species C



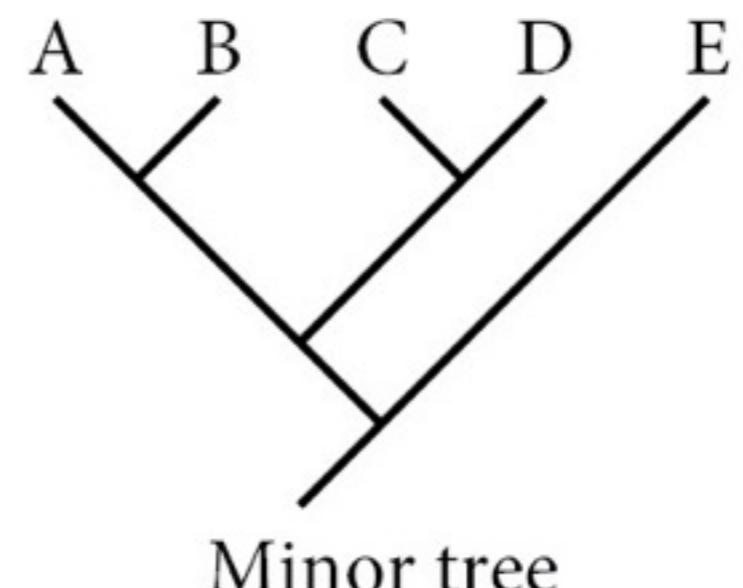
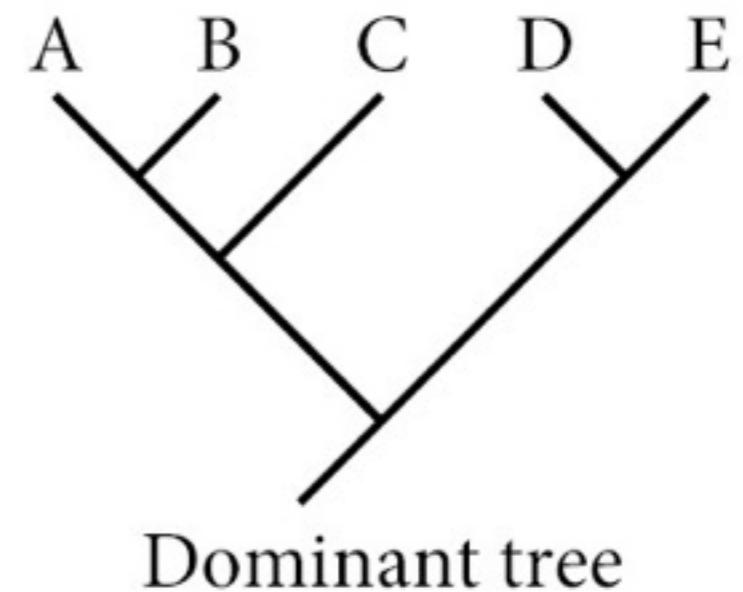
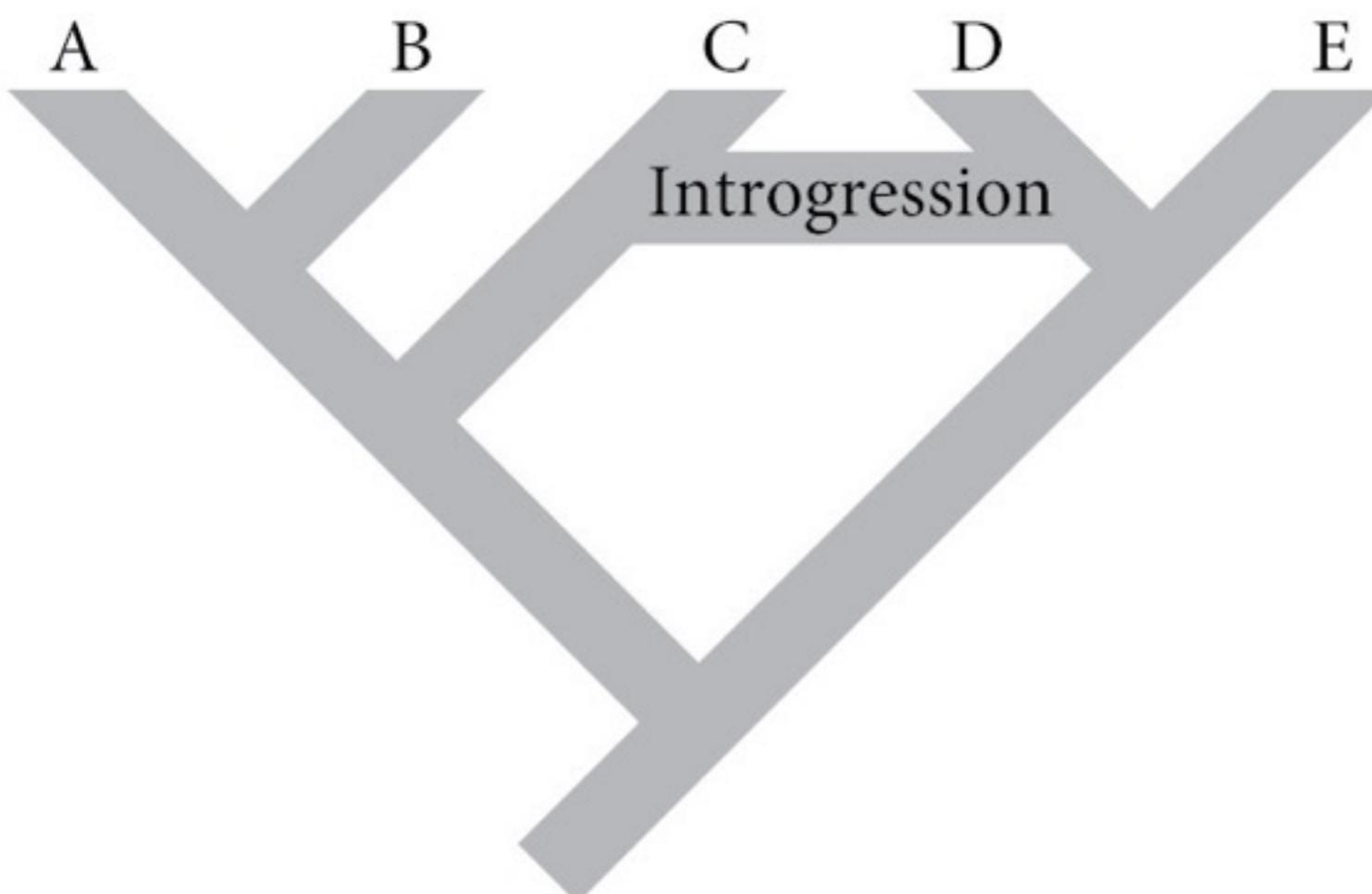
Gene divergence
due to duplication

Reticulation

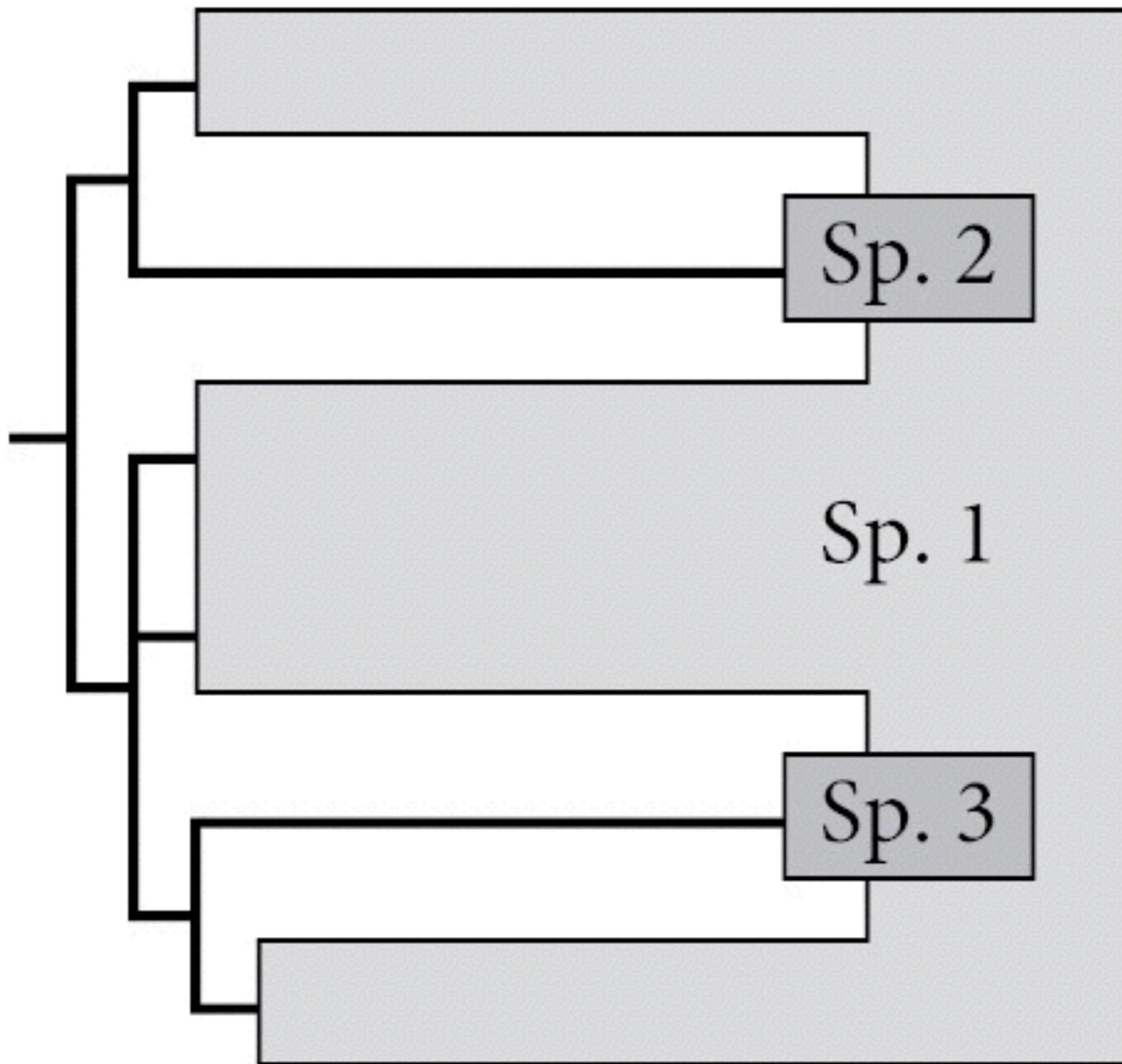
Lateral (aka horizontal) gene transfer



Introgression



Species paraphyly



Baum and Smith 2012, Figures 6.20

