

Many of the slides that I'll use have been borrowed from Dr. Paul Lewis, Dr. Joe Felsenstein. Thanks!

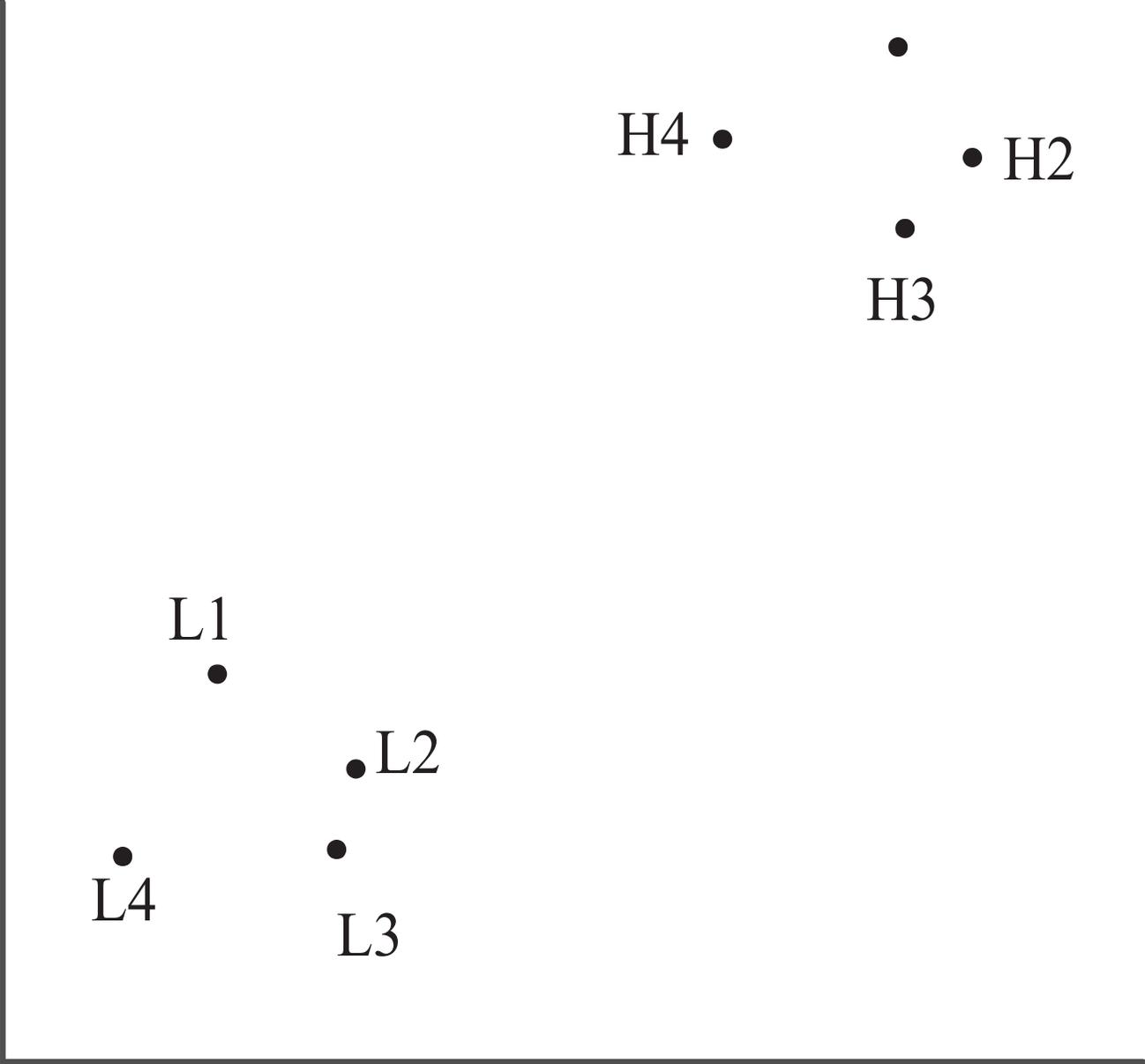
Paul has many great tools for teaching phylogenetics at his web site:

<http://hydrodictyon.eeb.uconn.edu/people/plewis>

Simple test of Bergmann's rule: comparing latitude and mass (I made these data up)

lat. offset = degrees north of the 49th parallel.

species	lat. offset	mass
L1	3.1	5.9
L2	5.4	4.3
L3	5.1	3.1
L4	1.8	3.6
H1	13.5	15.2
H2	14.6	13.5
H3	13.6	12.4
H4	10.8	13.7

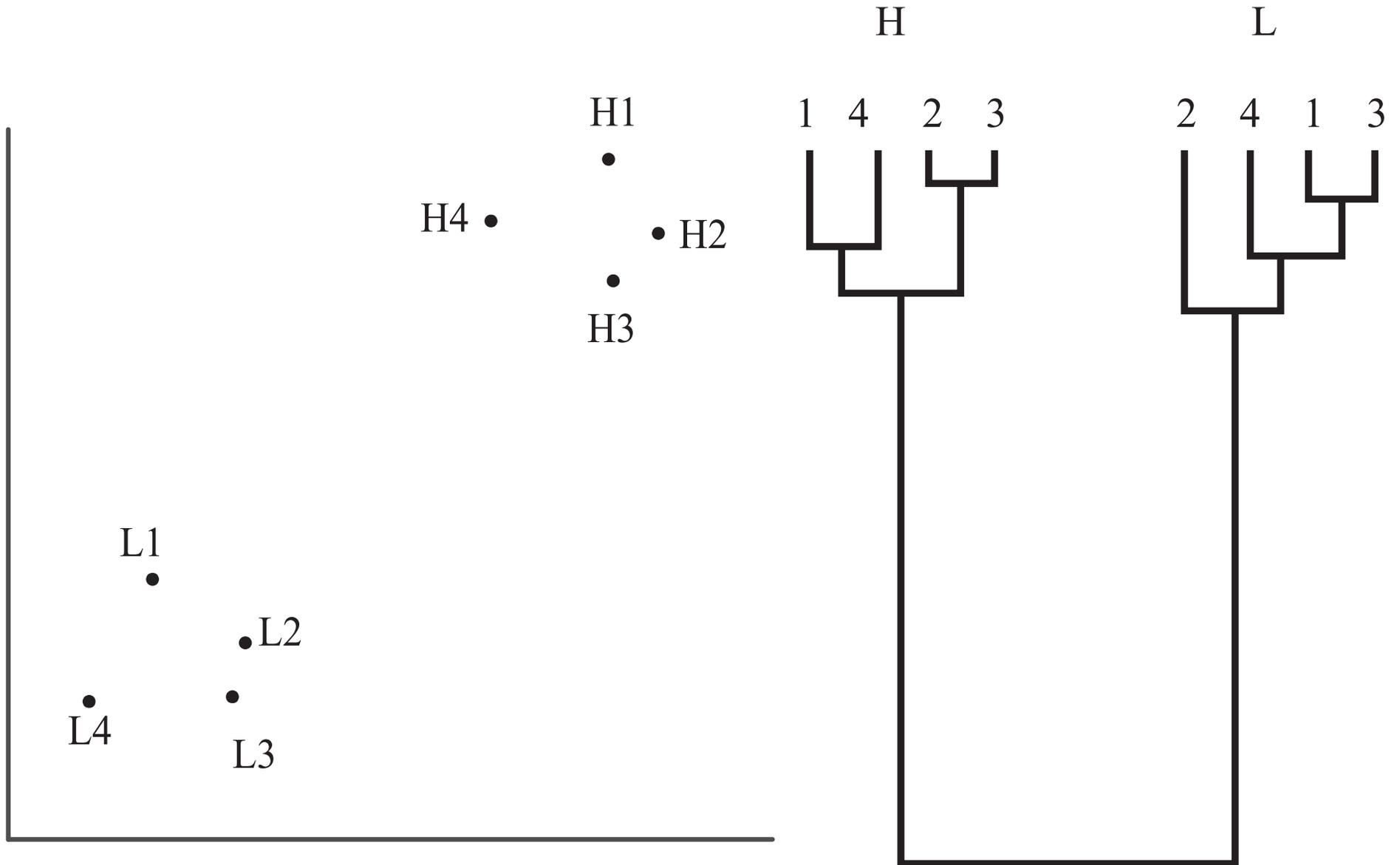


(cue cartoon videos)

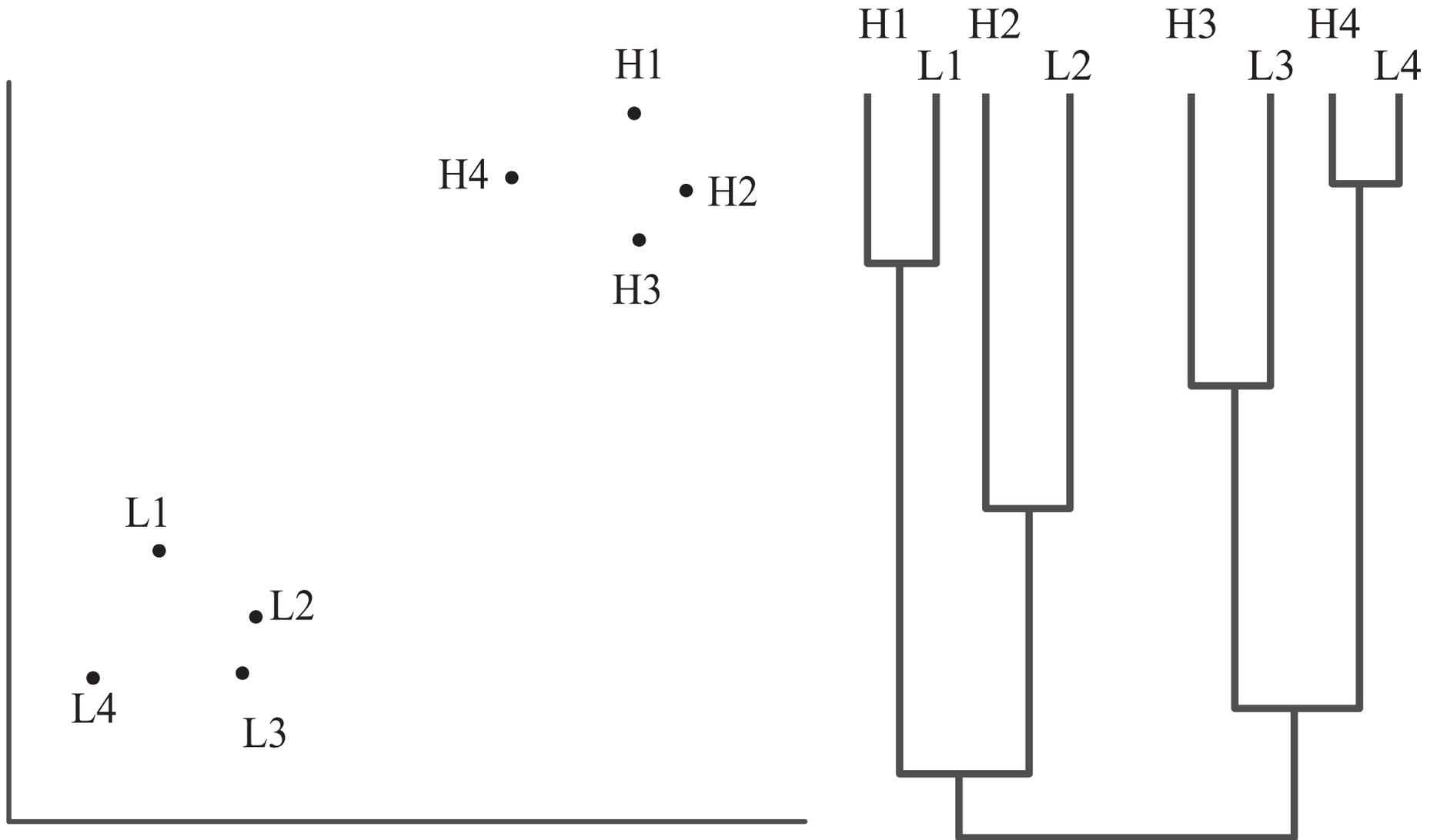
See <http://phylo.bio.ku.edu/slides/no-correl-anim.mov>

and <http://phylo.bio.ku.edu/slides/correl-anim2.mov>

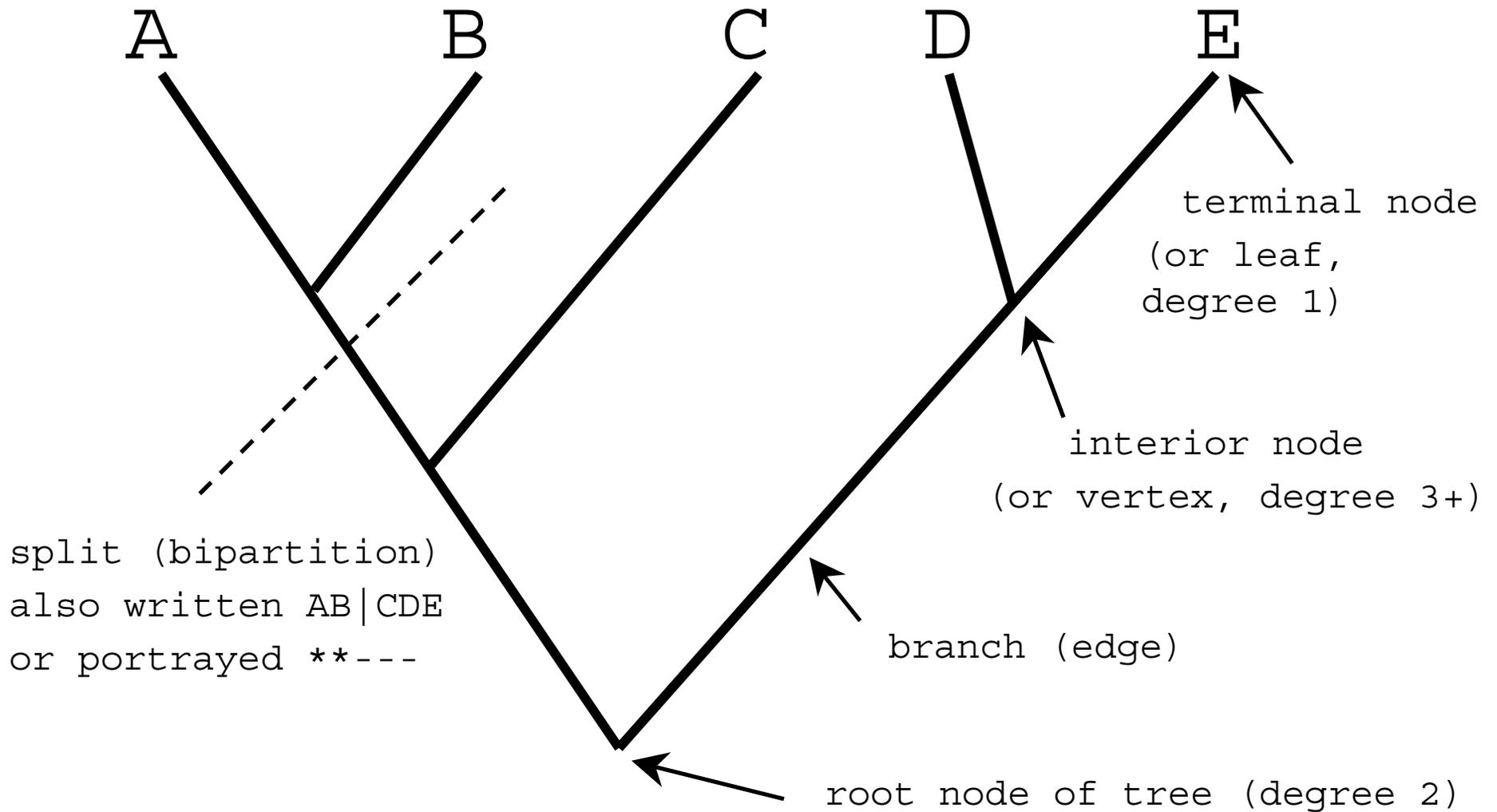
No (or little) evidence for correlation



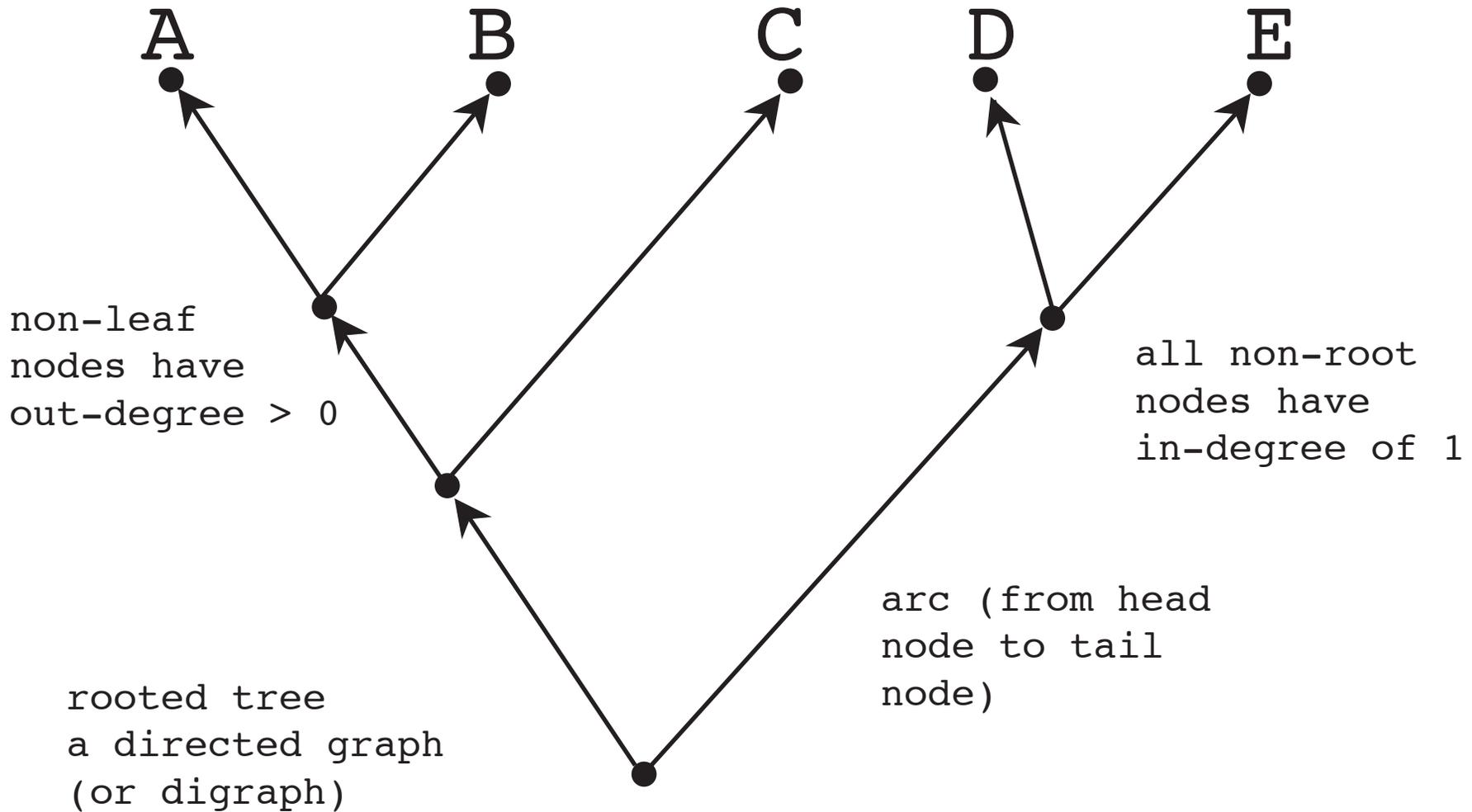
Evidence for correlation



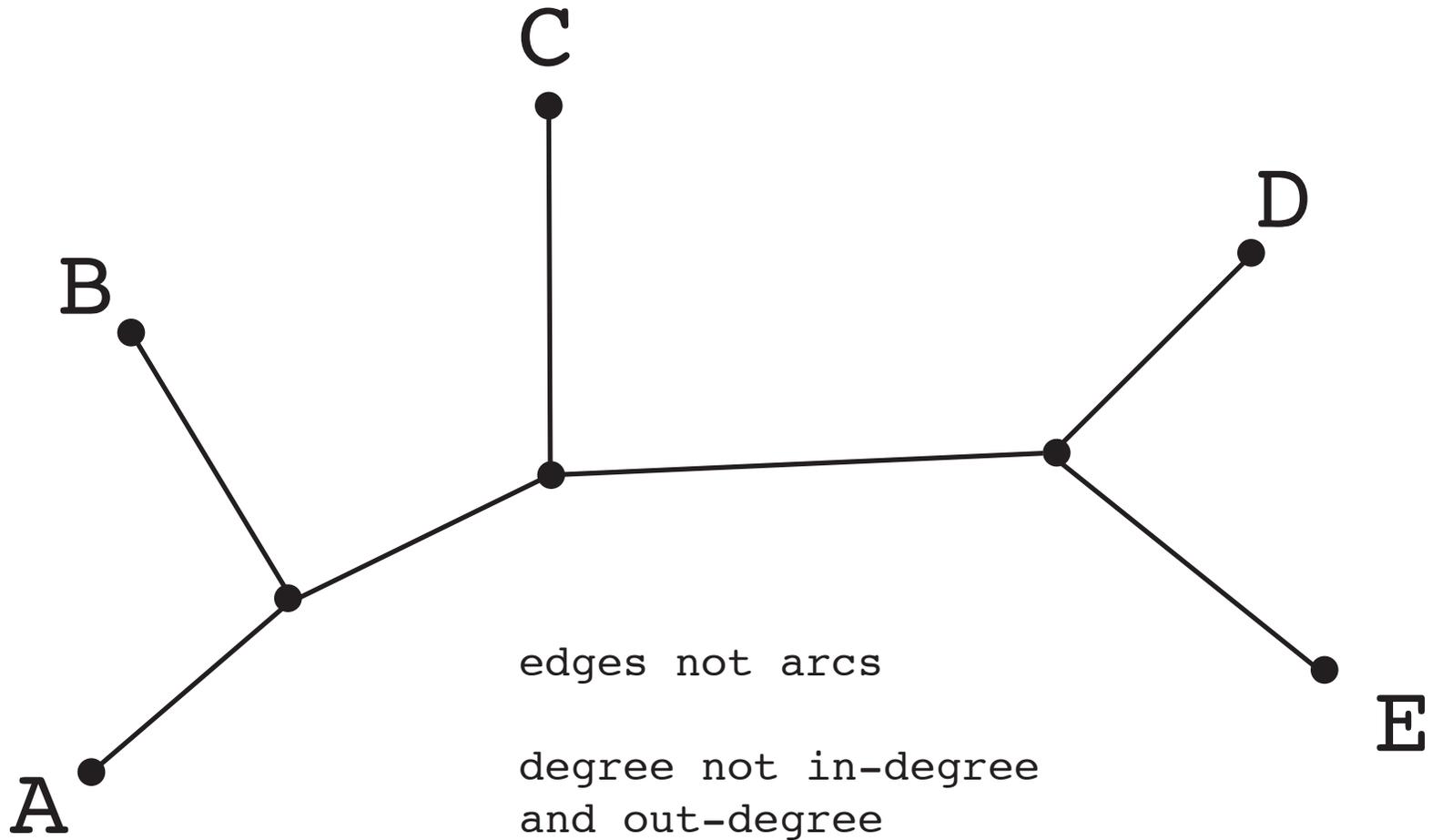
Tree terminology



Rooted tree terminology



Rooted tree terminology



Tree terms

A tree is a connected, acyclic graph.

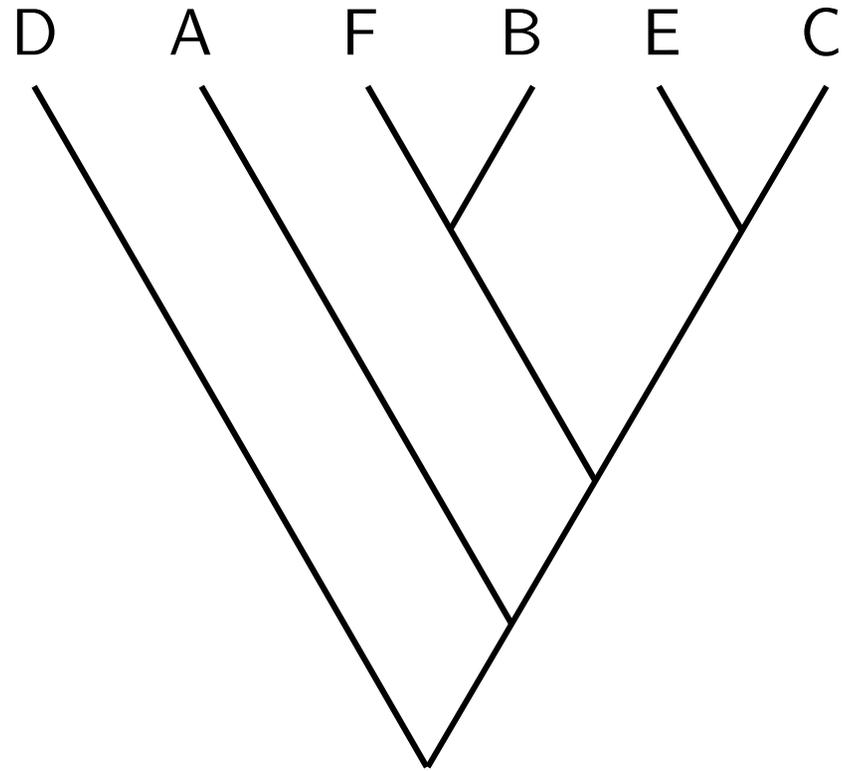
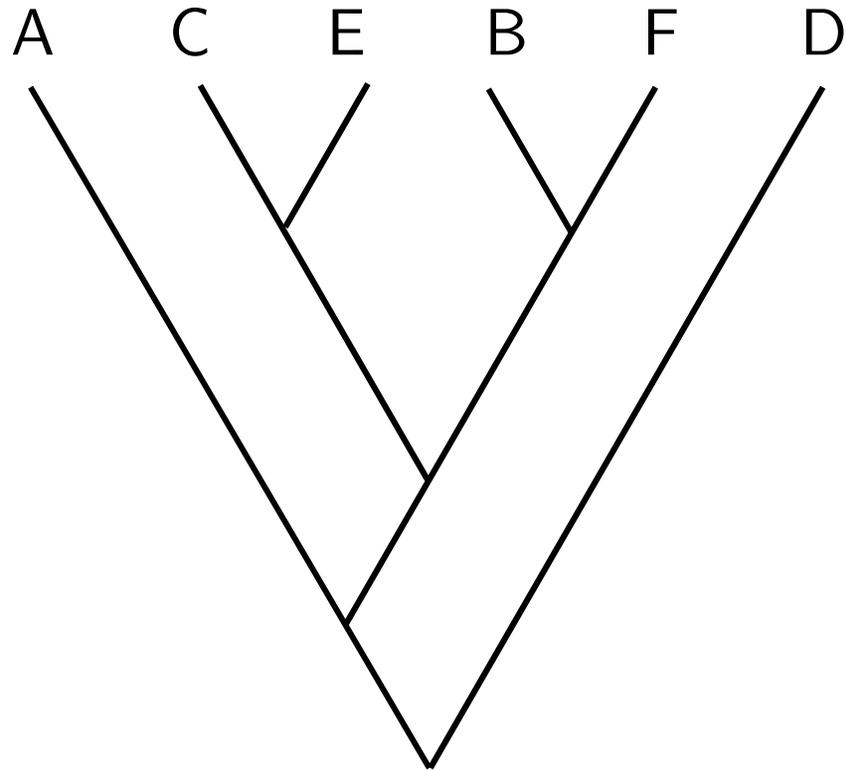
A rooted tree is a connected, acyclic directed graph.

A polytomy or multifurcation is a node with a degree > 3 (in an unrooted tree), or a node with an out-degree > 2 (in a rooted tree).

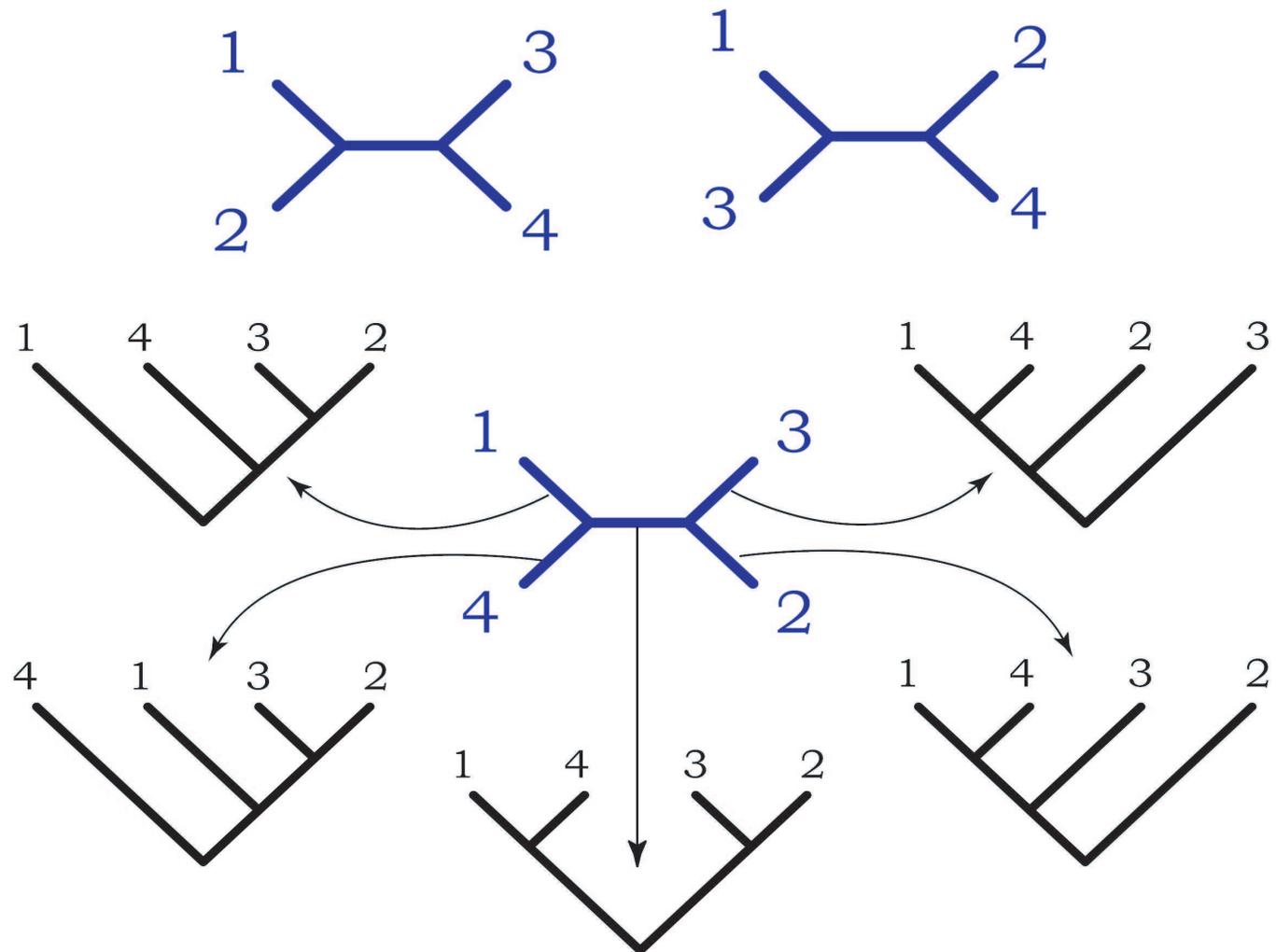
Collapsing an edge means to merge the nodes at the end of the branch (resulting in a polytomy in most cases).

Refining a polytomy means to “break” the node into two nodes that are connected by an edge.

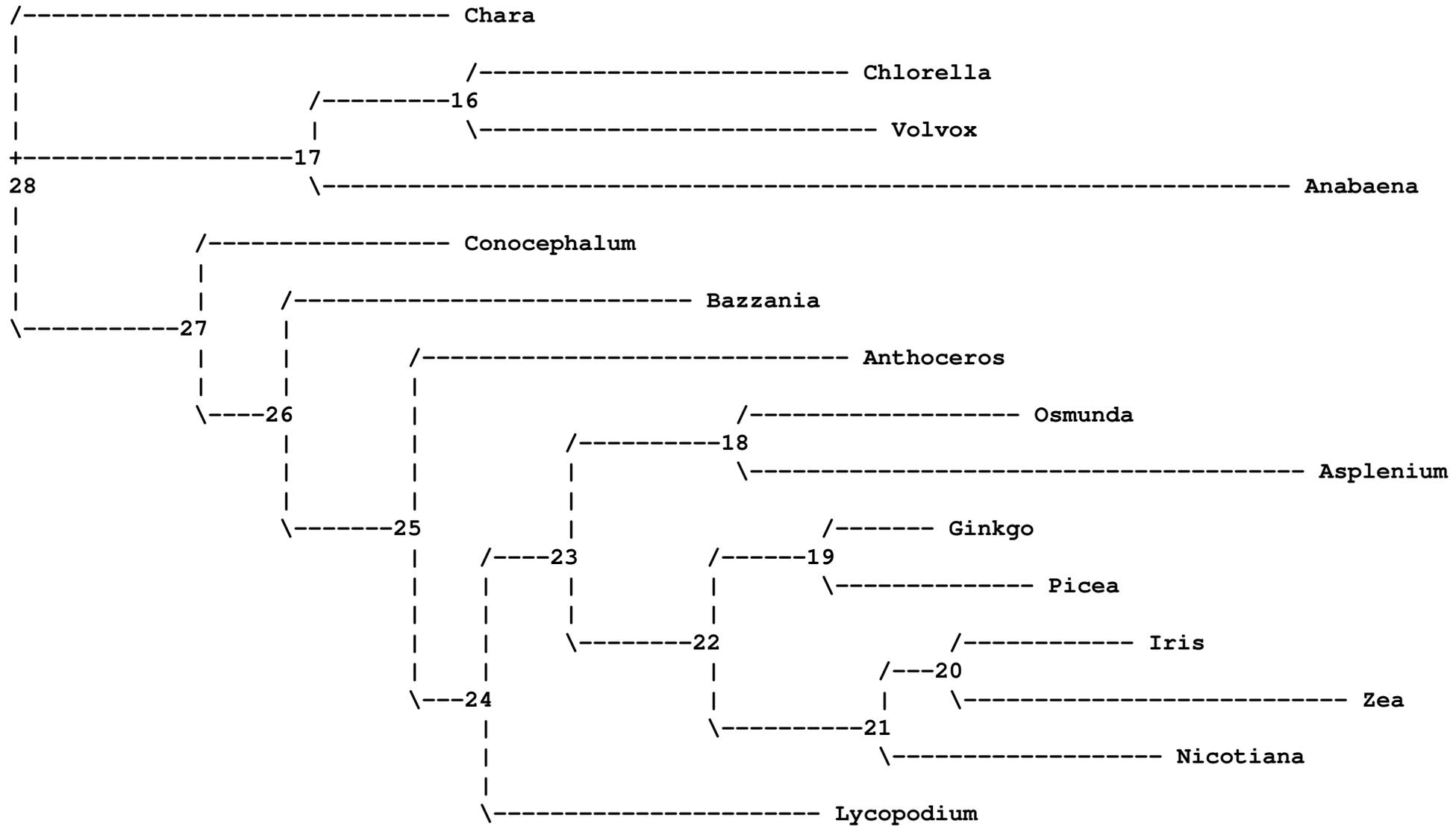
Branch rotation does not matter



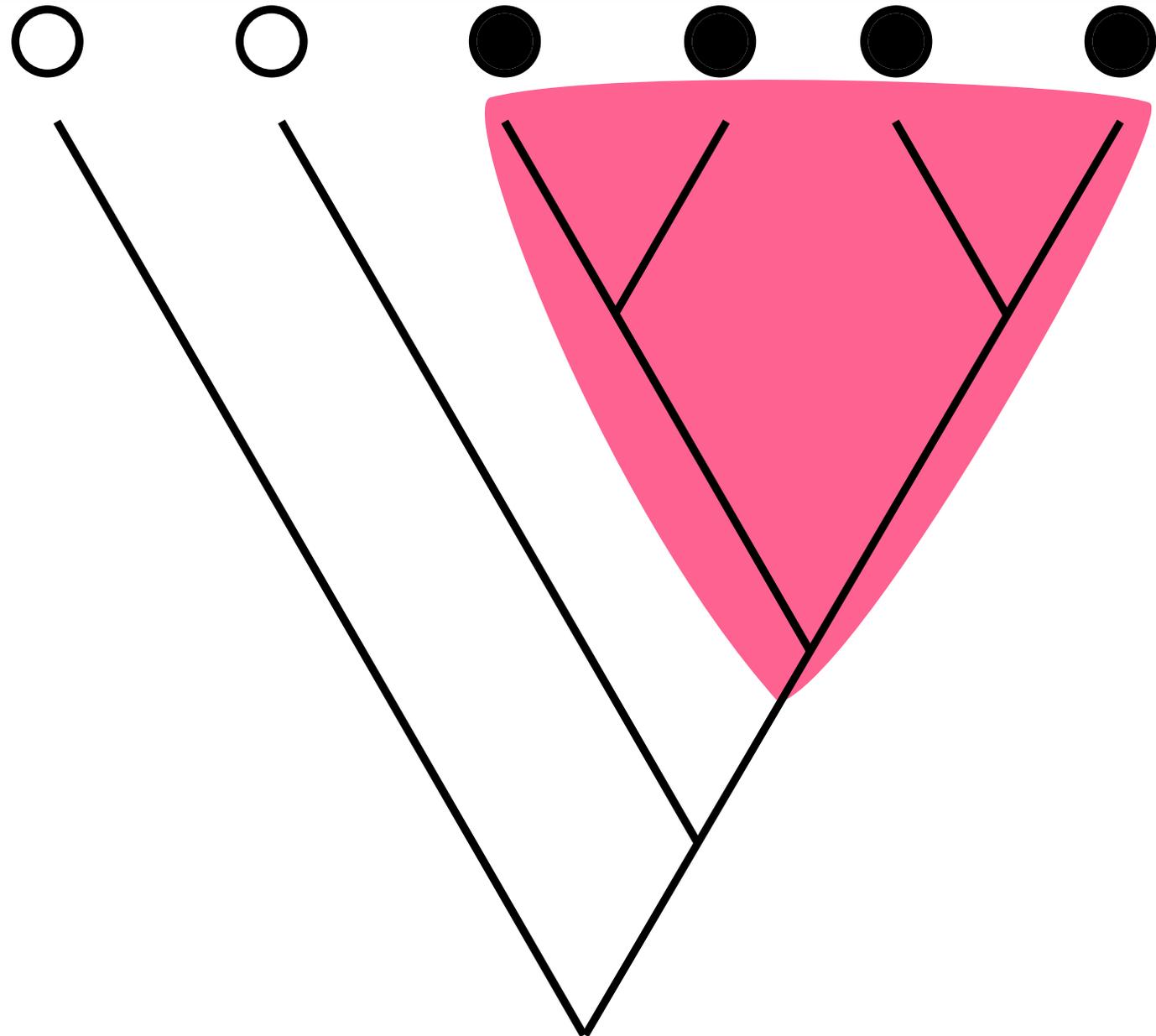
An unrooted tree maps to *several* rooted trees



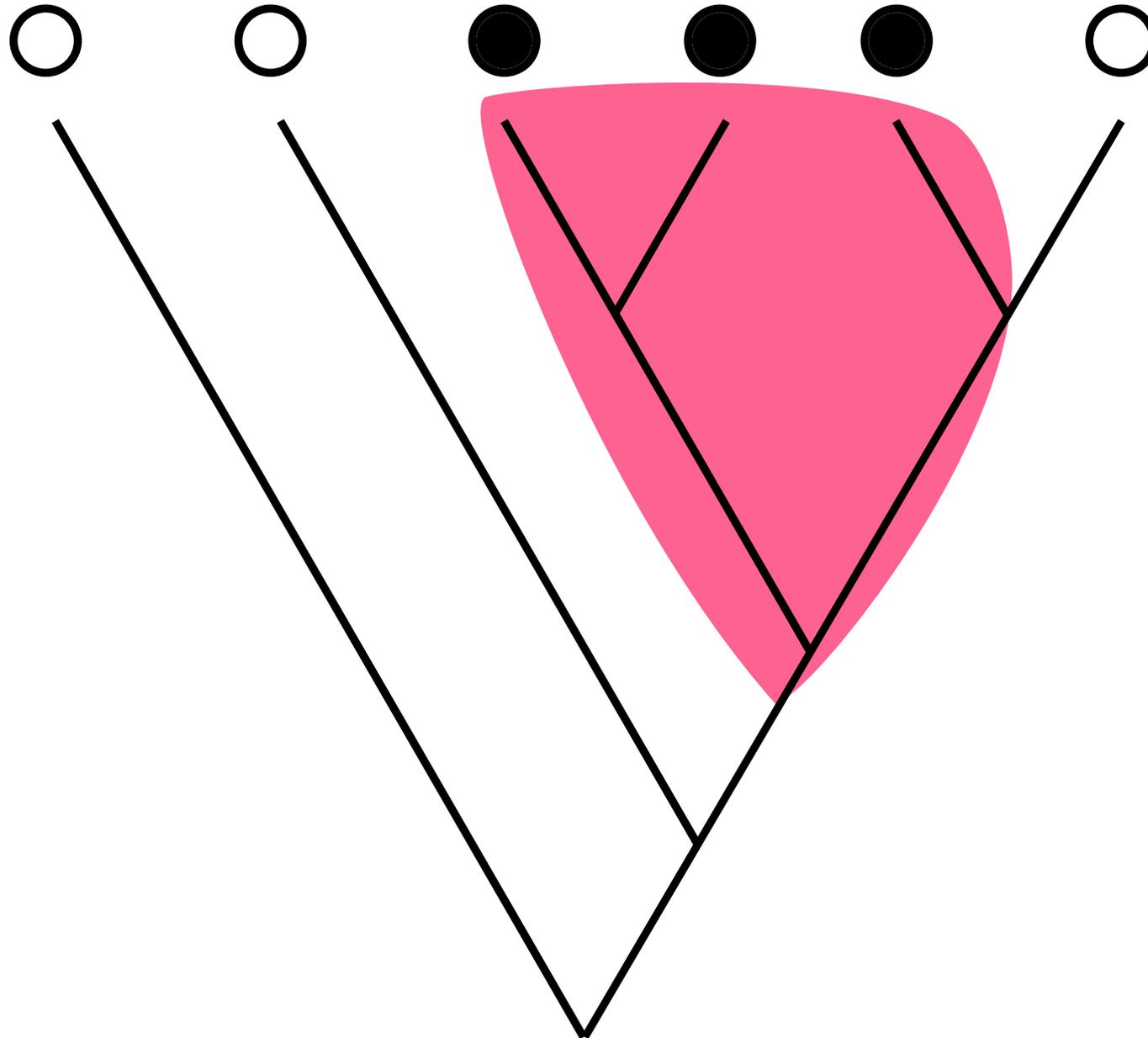
Warning: software often displays unrooted trees like this:



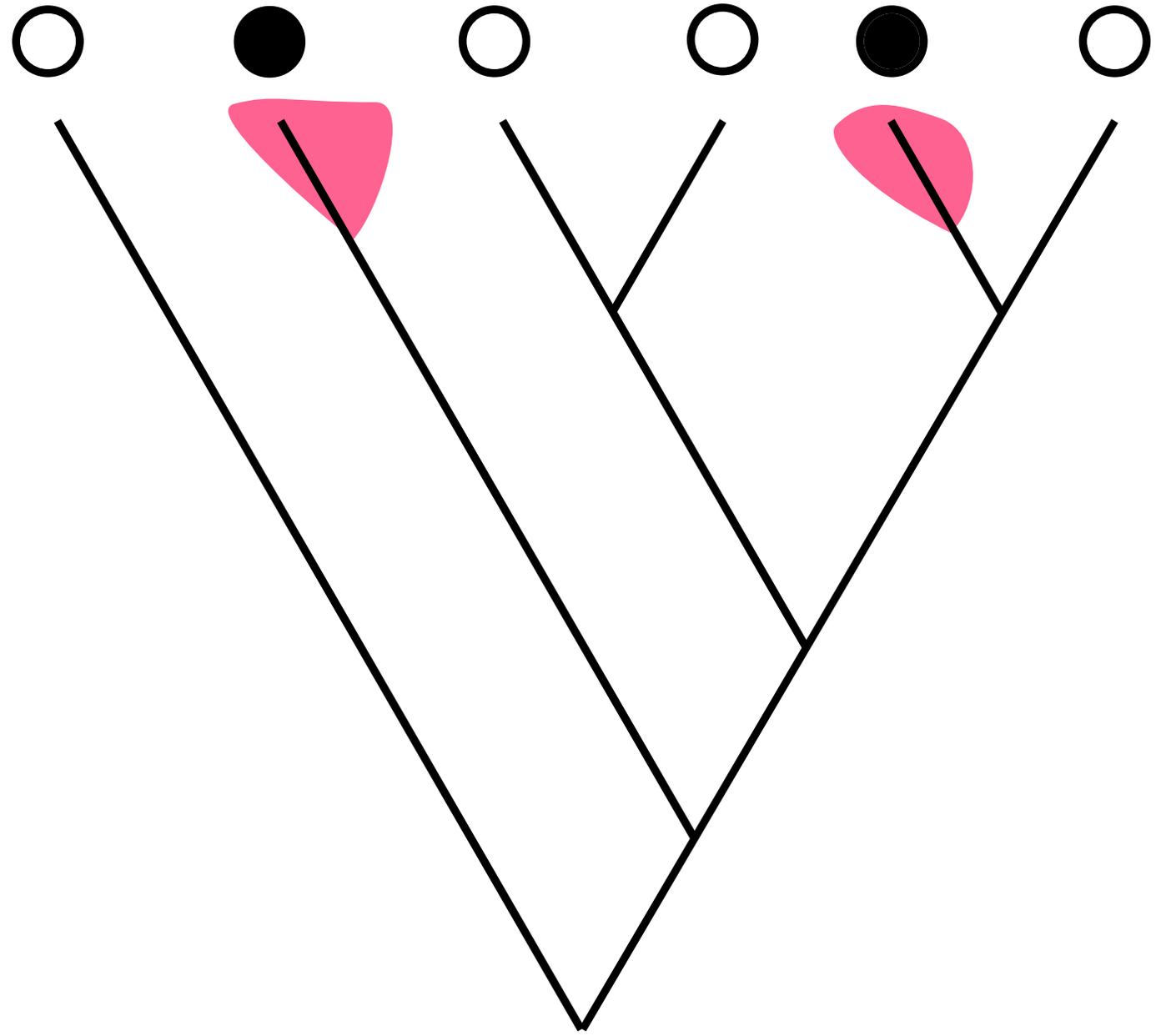
Monophyletic groups (“clades”): the basis of phylogenetic classification



Paraphyletic groups: error of omitting some species



Polyphyletic groups: error of grouping “unrelated” species



Homework #1 – (due Friday, August 27)

Draw an unrooted tree from the table of splits shown on the next page. The frequencies shown in the table represent bootstrap proportions. We'll cover bootstrapping later in the course – for now you can treat the “Freq” column as label for the branches.

Start at the first row and add splits until you cannot add any more splits to the tree.

Make sure to label the leaves of the tree with the taxon number and the edges with the value found in the “Freq” column.

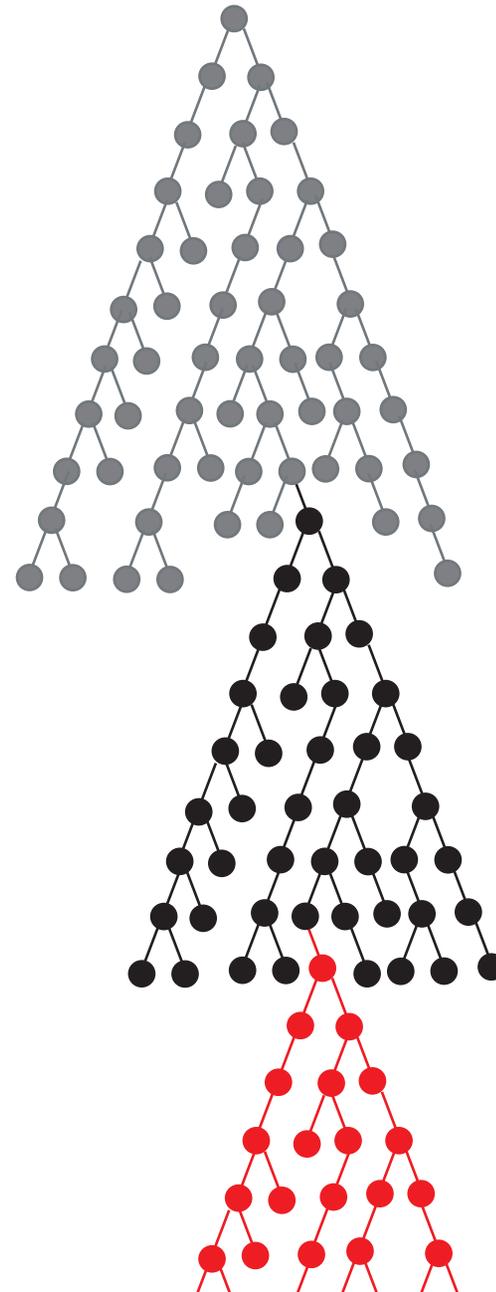
000000000111111 123456789012345	Freq
.....*.*.*	100
.....**.....	99
.**.....*.	97
.....***.*.*	94
.....*.....*..	78
..*****.*	67
.**.....	61
.....*.*****.*	60
.....*...*	56
..*.*......	41
.....*.*..	39
..*.....*.	37
.....*****.*	33

/end-of-homework

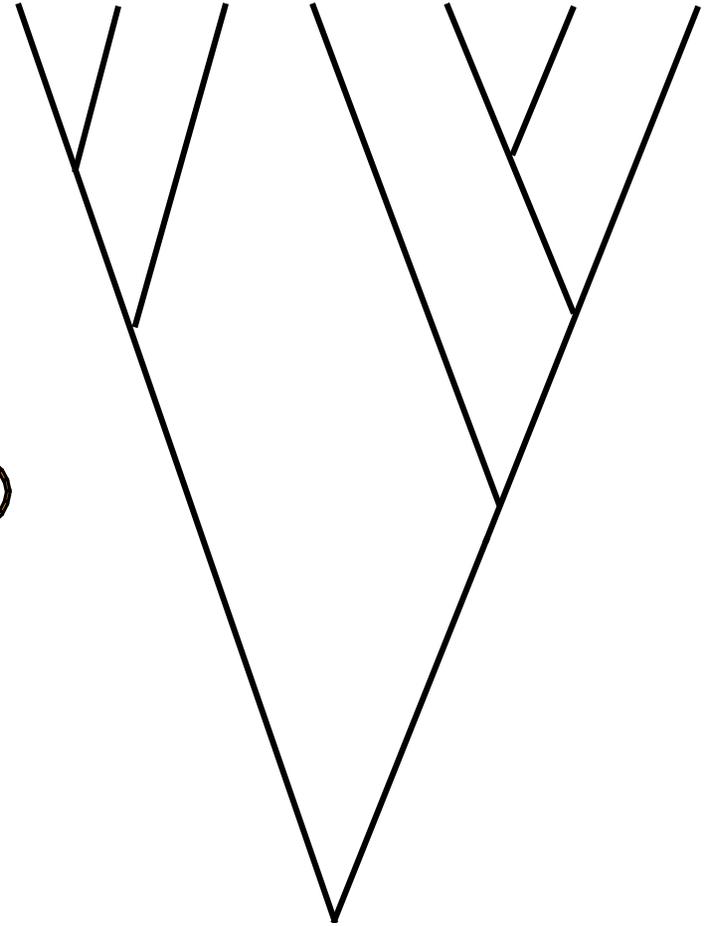
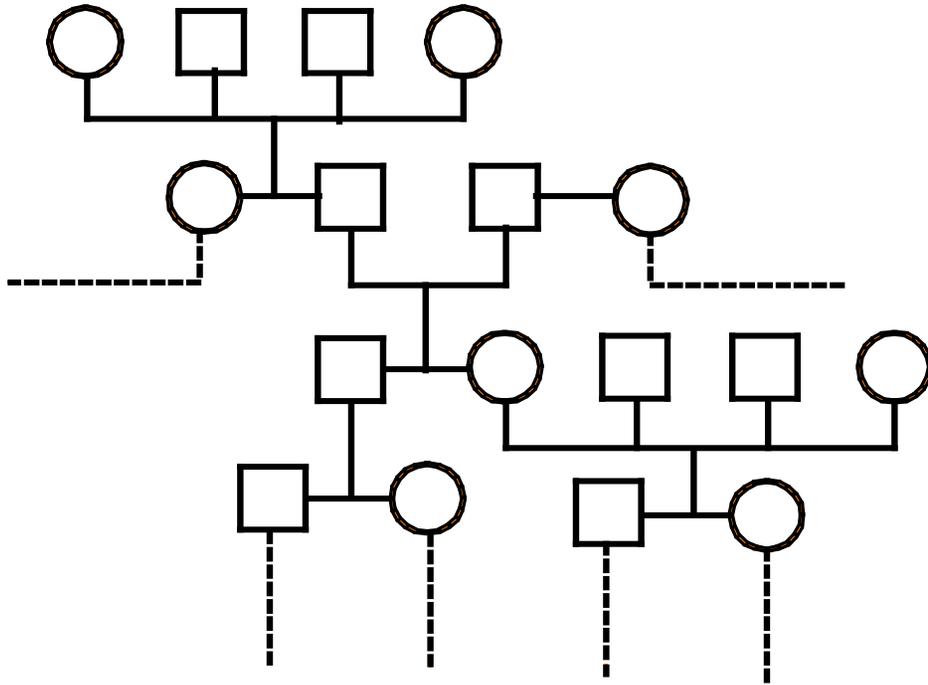
We use trees to represent genealogical relationships in several contexts.

Domain	Sampling	tree	The cause of splitting
Pop. Gen.	> 1 indiv/sp. Few species	Gene tree	> 1 descendants of a single gene copy
Phylogenetics	Few indiv/sp. Many species	Phylogeny	speciation
Mol. Gen.	> 1 locus/sp. > 1 species	Gene tree. Gene family tree	speciation or duplication

Phylogenies are an inevitable result of molecular genetics



Two types of genealogies



Genealogies within a population

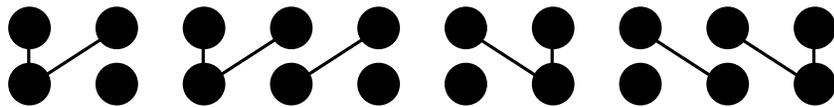
Present



Past

Genealogies within a population

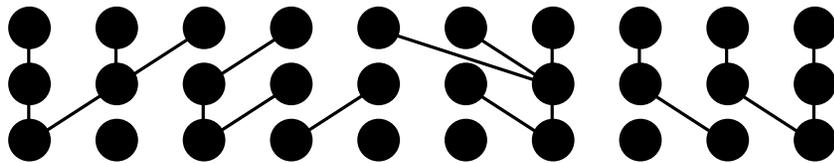
Present



Past

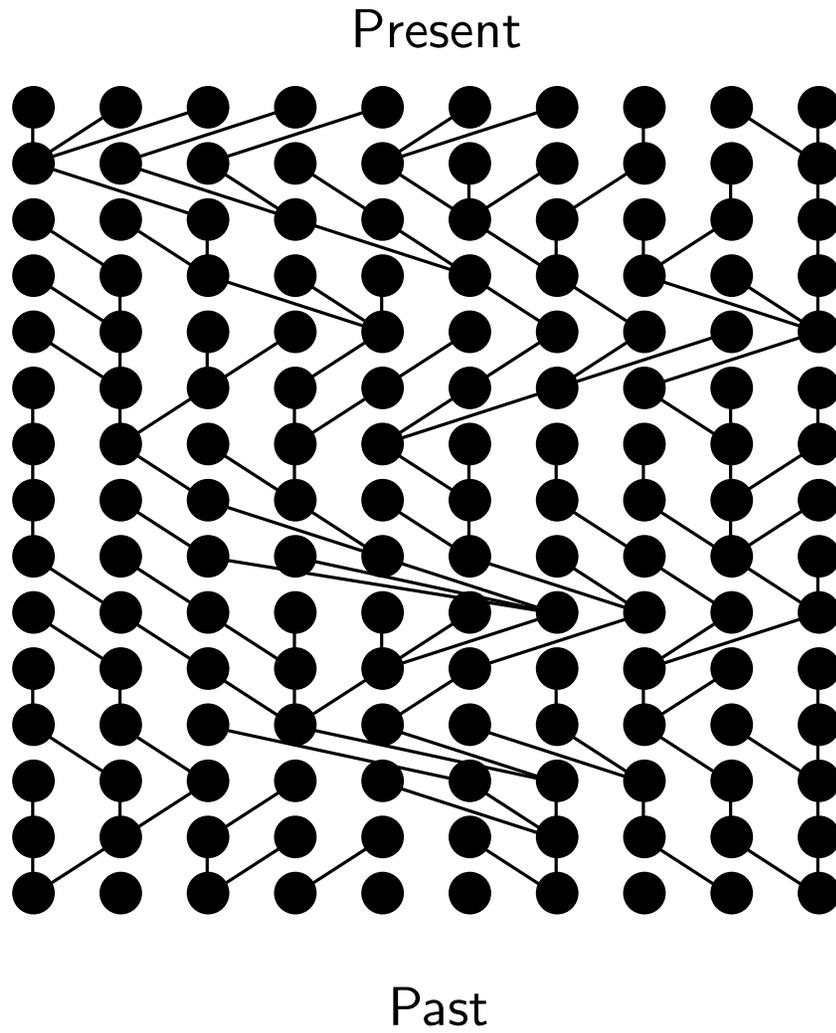
Genealogies within a population

Present

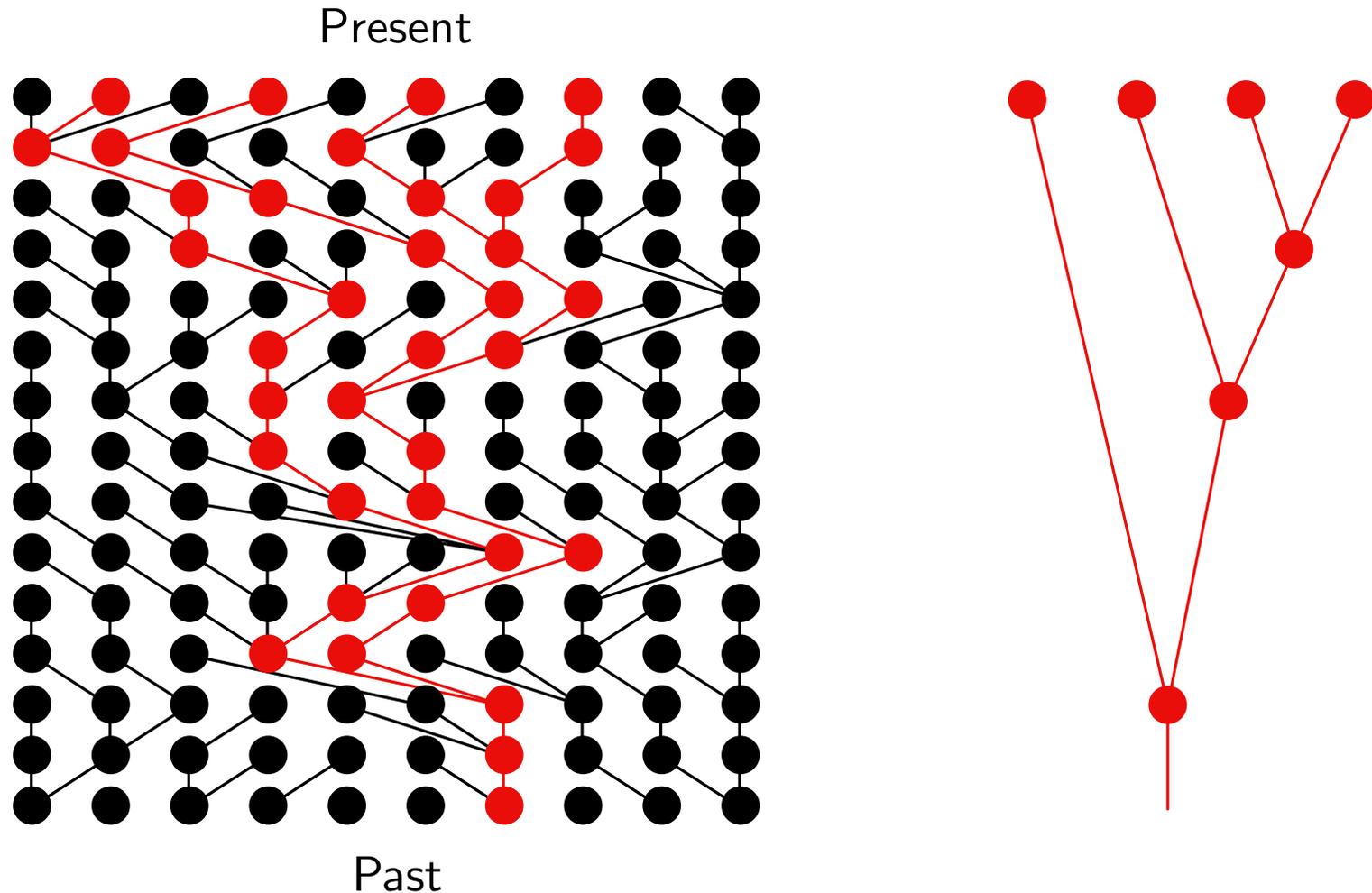


Past

Genealogies within a population



Genealogies within a population



Biparental inheritance would make the picture messier, but the genealogy of the gene copies would still form a tree (if there is no recombination).

terminology: genealogical trees within population or species trees

It is tempting to refer to the tips of these gene trees as alleles or haplotypes.

- allele – an alternative form a gene.
- haplotype – a linked set of alleles

But both of these terms require a differences in sequence.

The gene trees that we draw depict genealogical relationships – regardless of whether or not nucleotide differences distinguish the “gene copies” at the tips of the tree.