Introduction to Phylogenetics

Marine Biological Laboratory, Woods Hole,
Massachusetts

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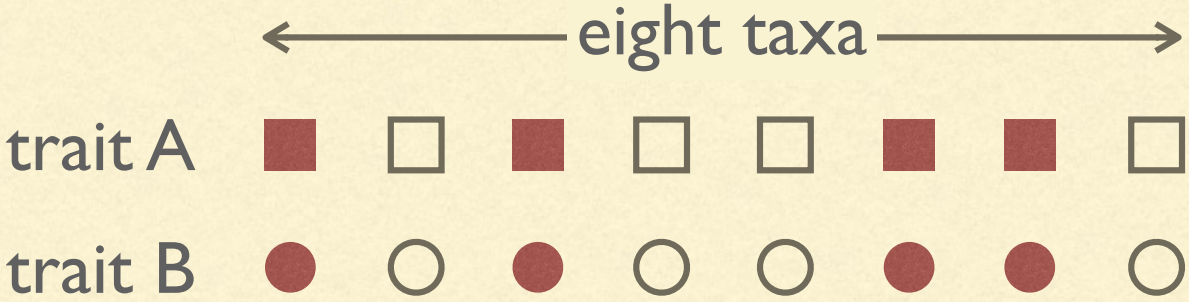
Phylogenetics is key

Dobzhansky, T. 1973. Nothing in **biology** makes sense except in the light of **evolution**. The American Biology Teacher 35:125-129.

Nothing in **evolutionary biology** makes sense except in the light of **phylogeny**. - Society of Systematic Biologists

Perfect correlation

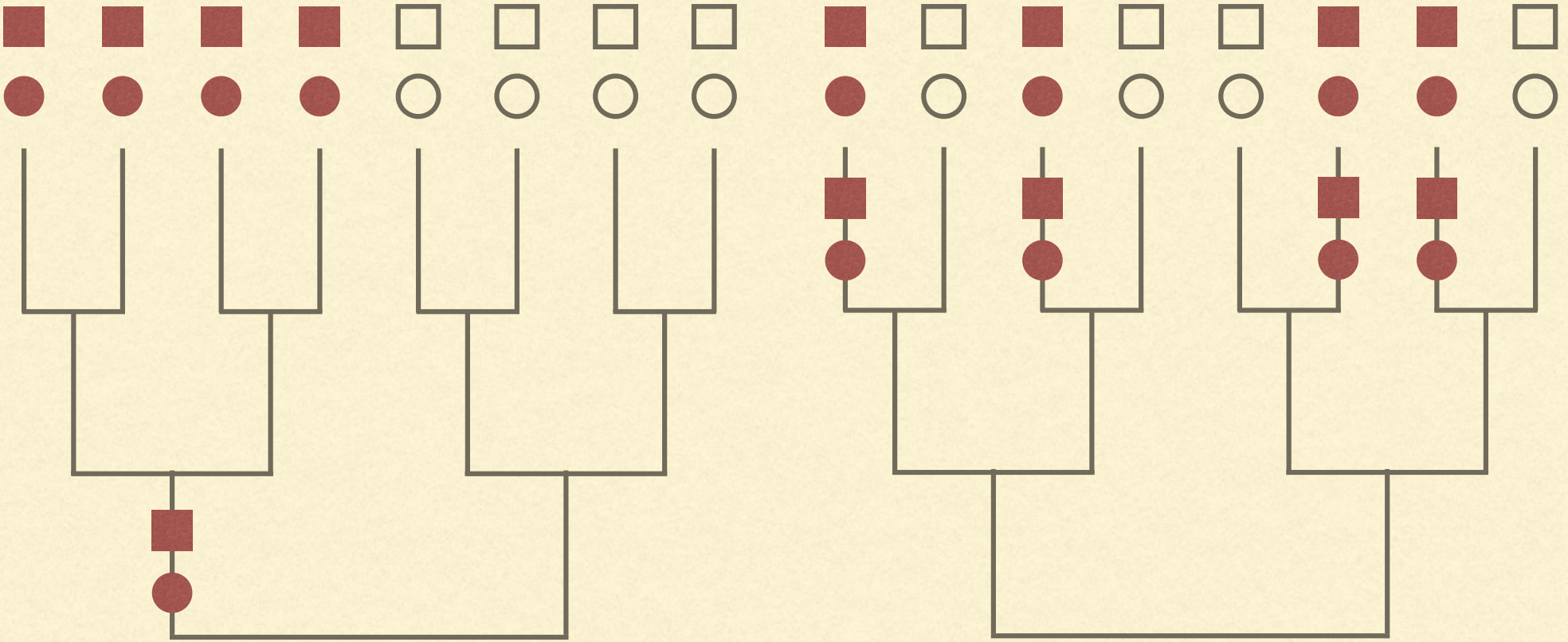


How much importance should we attach to the co-distribution of these two traits?

Two very different explanations

Simple inheritance

Correlated evolution

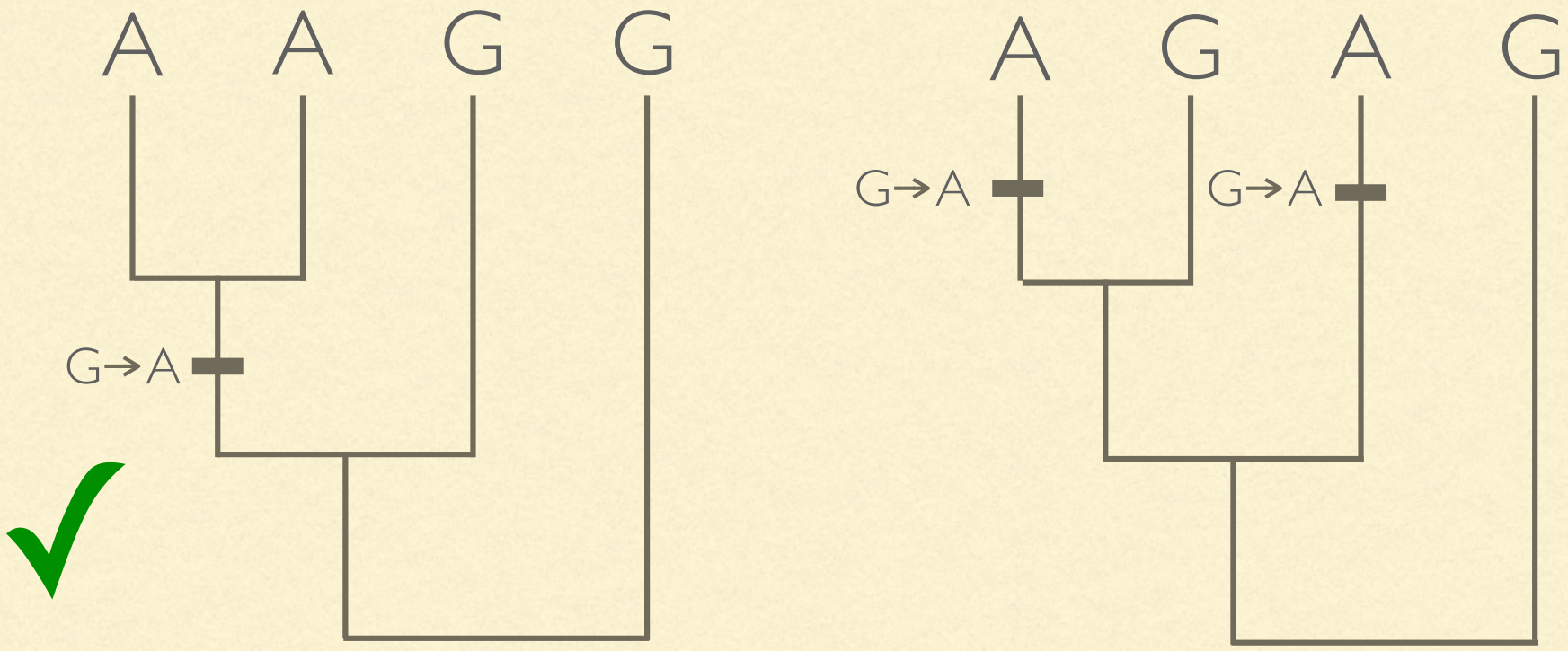


How to estimate a tree

I think that I shall never see
A thing so awesome as the Tree
That links us all in paths of genes
Down into depths of time unseen
--- DAVID MADDISON (2013)

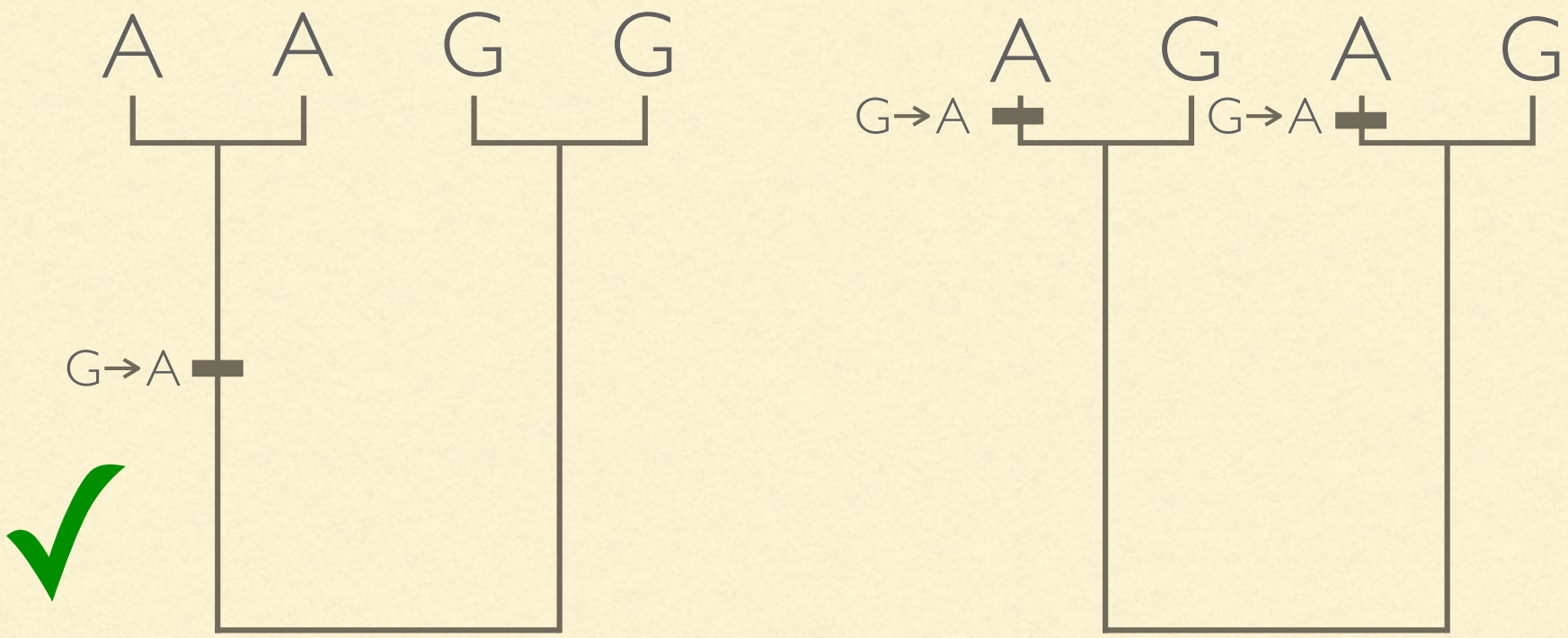
Maddison, D. 2013. The Tree of Life. Systematic Biology 62:179

Which tree is better?



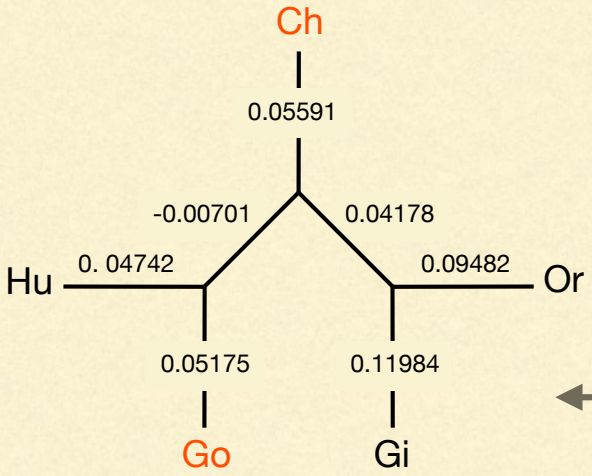
Parsimony criterion says tree requiring fewer changes is better

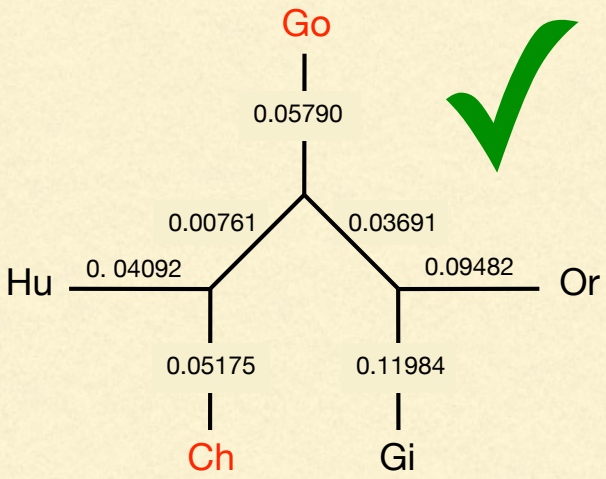
Which tree is better?



Likelihood criterion says tree that makes us less surprised at the observed data is better

Which tree is better?





SS = 0.00003

SS = 0.0003

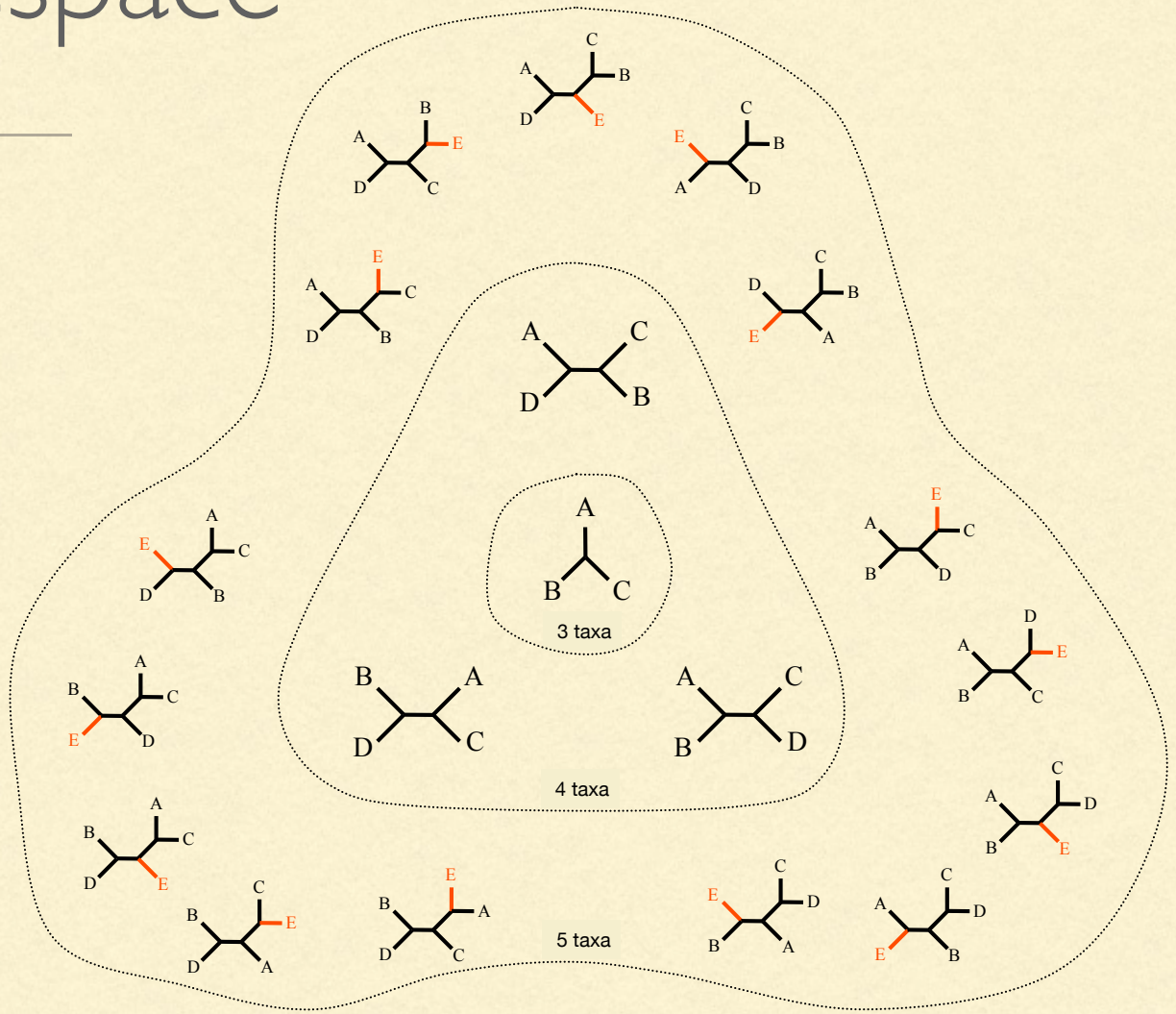
$(0.10928 - 0.10643)^2$

Taxon Pair	distance (data)	distance (tree)	squared differences
Hu-Ch	0.09267	0.09267	0
Hu-Go	0.10928	0.10643	0.000008123
Hu-Or	0.17848	0.18026	0.000003168
Hu-Gi	0.2042	0.20528	0.000001166
Ch-Go	0.1144	0.11726	0.00000818
Ch-Or	0.19413	0.19109	0.000009242
Ch-Gi	0.21591	0.21611	0.00000004
Go-Or	0.18836	0.18963	0.000001613
Go-Gi	0.21592	0.21465	0.000001613
Or-Gi	0.21466	0.21466	0
			0.000033144

Least squares criterion says tree that better matches pairwise distances is better

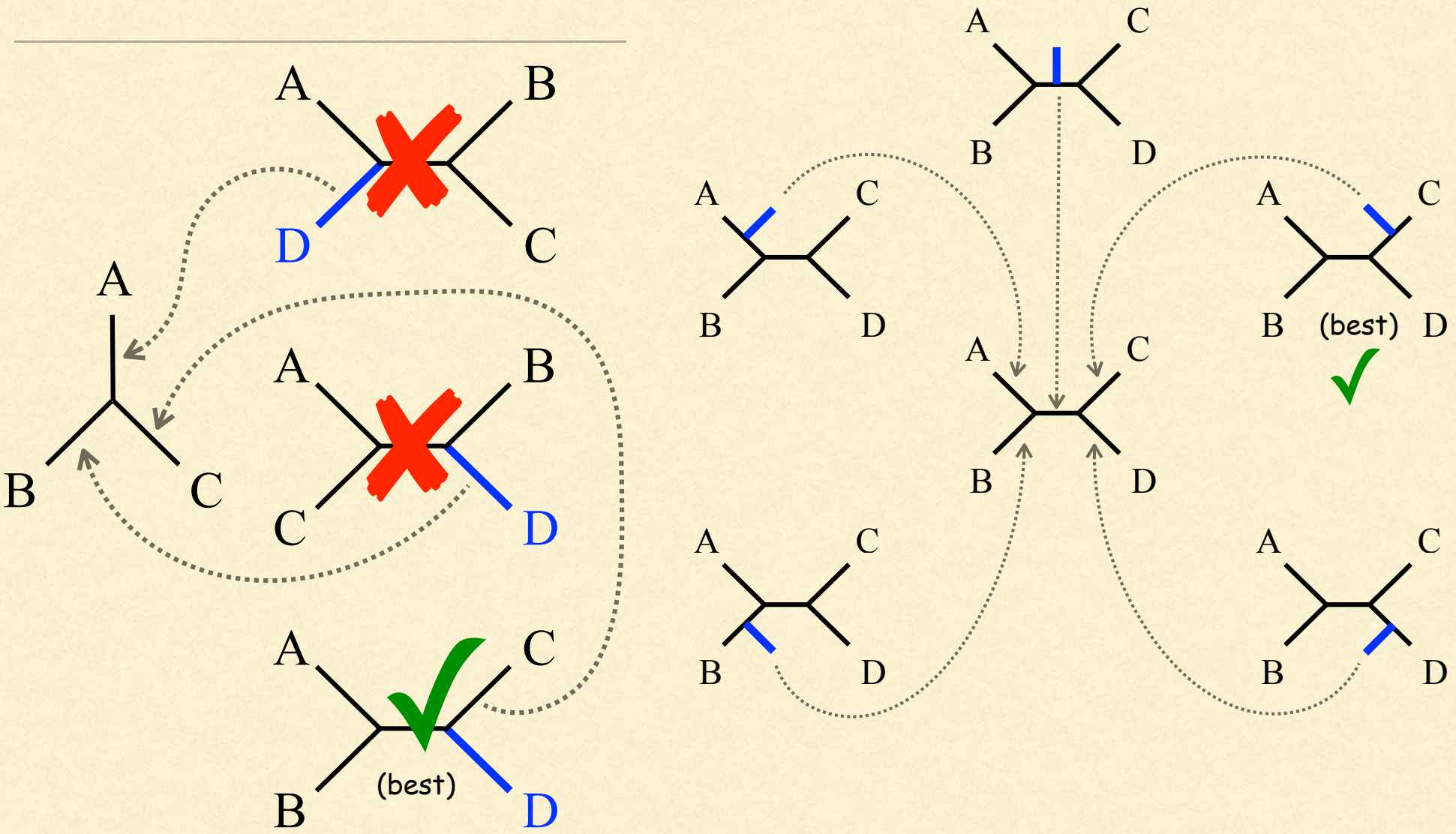
Searching treespace

Taxa	Number of unrooted trees
4	3
5	15
6	105
7	945
8	10,395
9	135,135
10	2,027,025
11	34,459,425
12	654,729,075
13	13,749,310,575
14	316,234,143,225
15	7,905,853,580,625
16	213,458,046,676,875
17	6,190,283,353,629,375
18	191,898,783,962,510,625
19	6,332,659,870,762,850,625
20	221,643,095,476,699,771,875
21	8,200,794,532,637,891,559,375
22	319,830,986,772,877,770,815,625
23	13,113,070,457,687,988,603,440,625

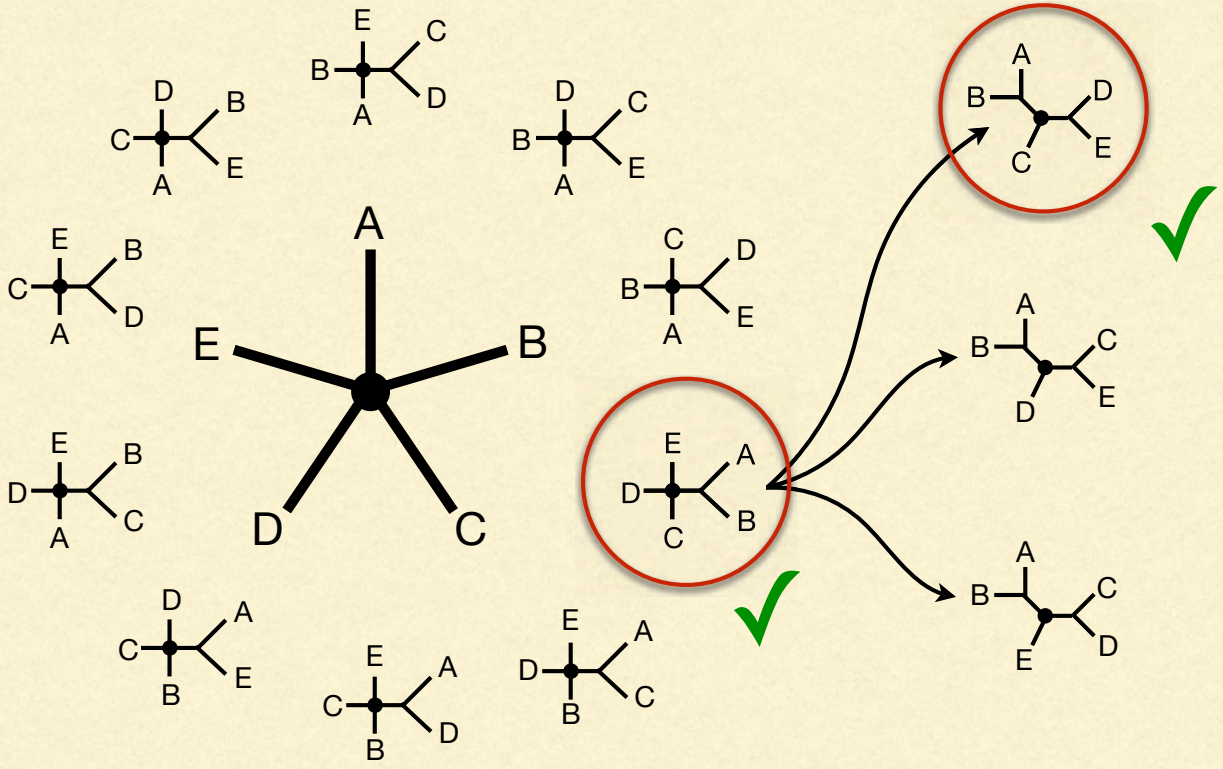


← 83.2 billion years @ 5 million trees/sec

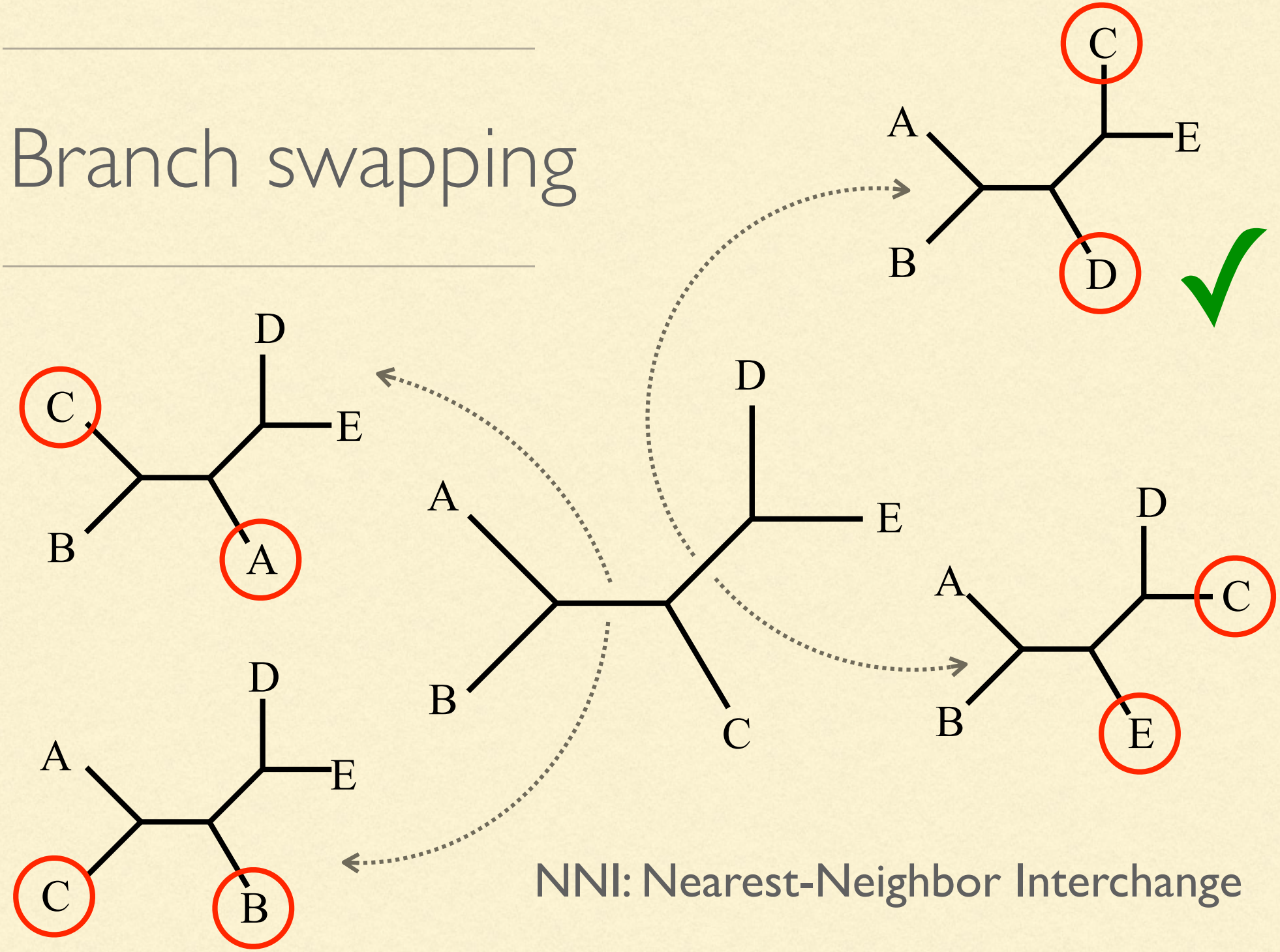
Stepwise addition



Star decomposition (e.g. Neighbor Joining)

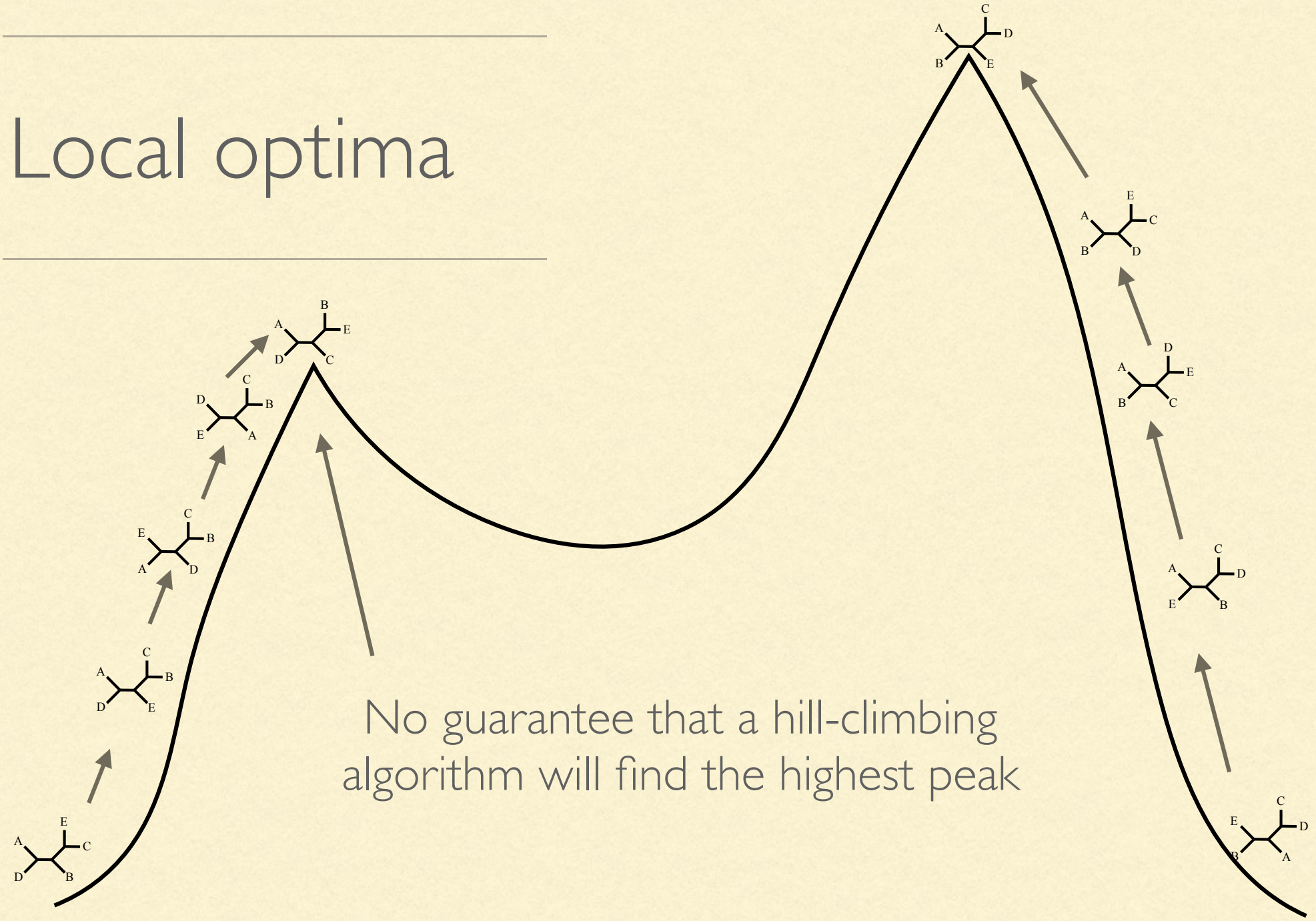


Branch swapping



NNI: Nearest-Neighbor Interchange

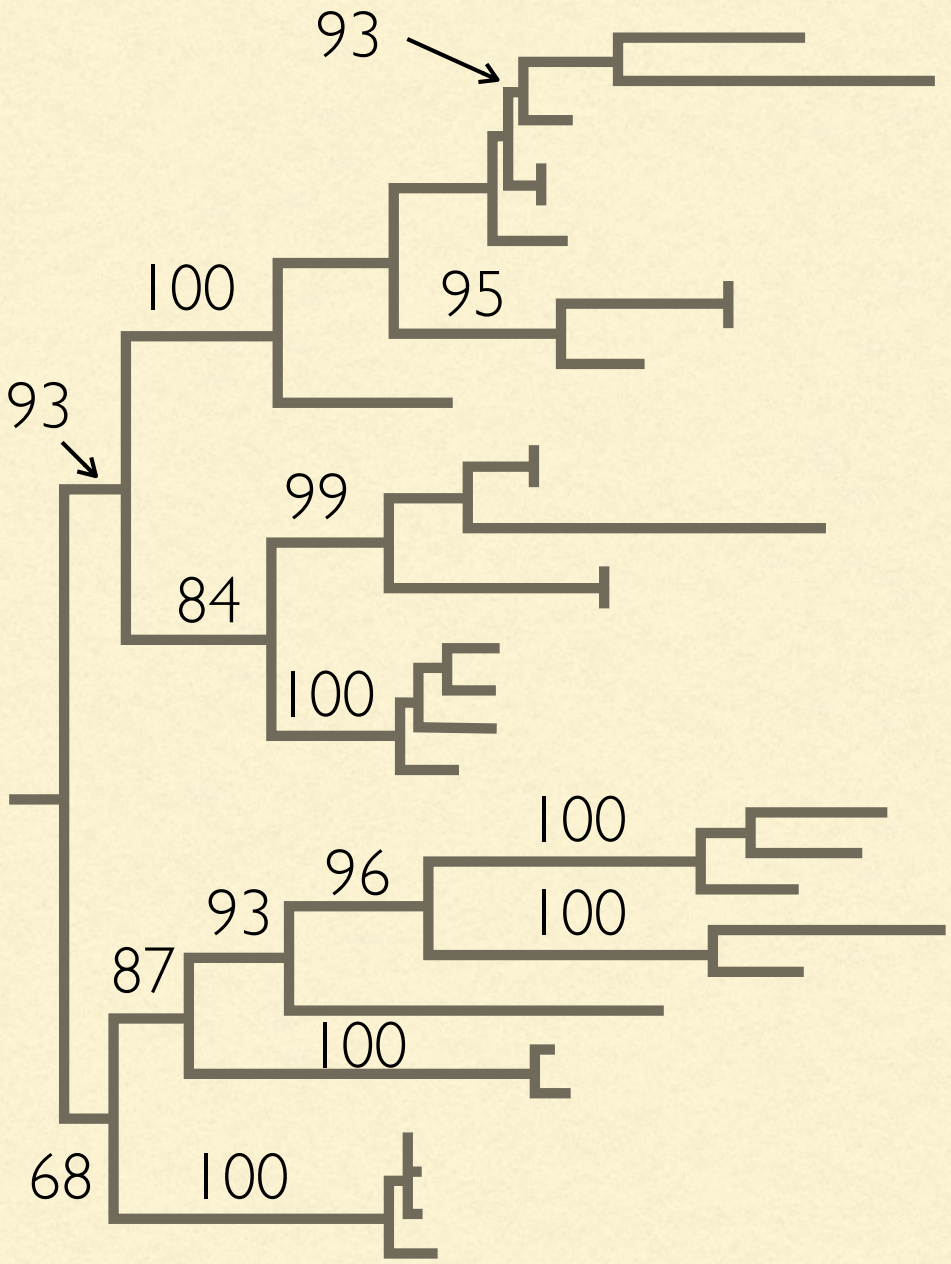
Local optima



Support

Not all parts of a tree are equally well supported by the data.

Support values on the branches tell us how confident we can be in the clade defined by that branch.



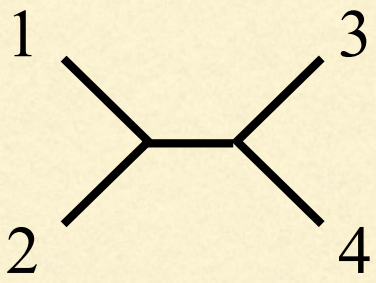
Bootstrap support

sites sampled with replacement

	1	2	3	4	5	6	7	8
1	A	G	G	C	G	T	A	C
2	A	A	G	C	G	T	A	T
3	A	G	T	C	A	C	G	G
4	A	A	T	C	G	C	G	G

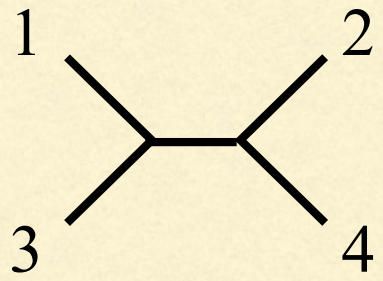
✗ ✗ ✗

original data

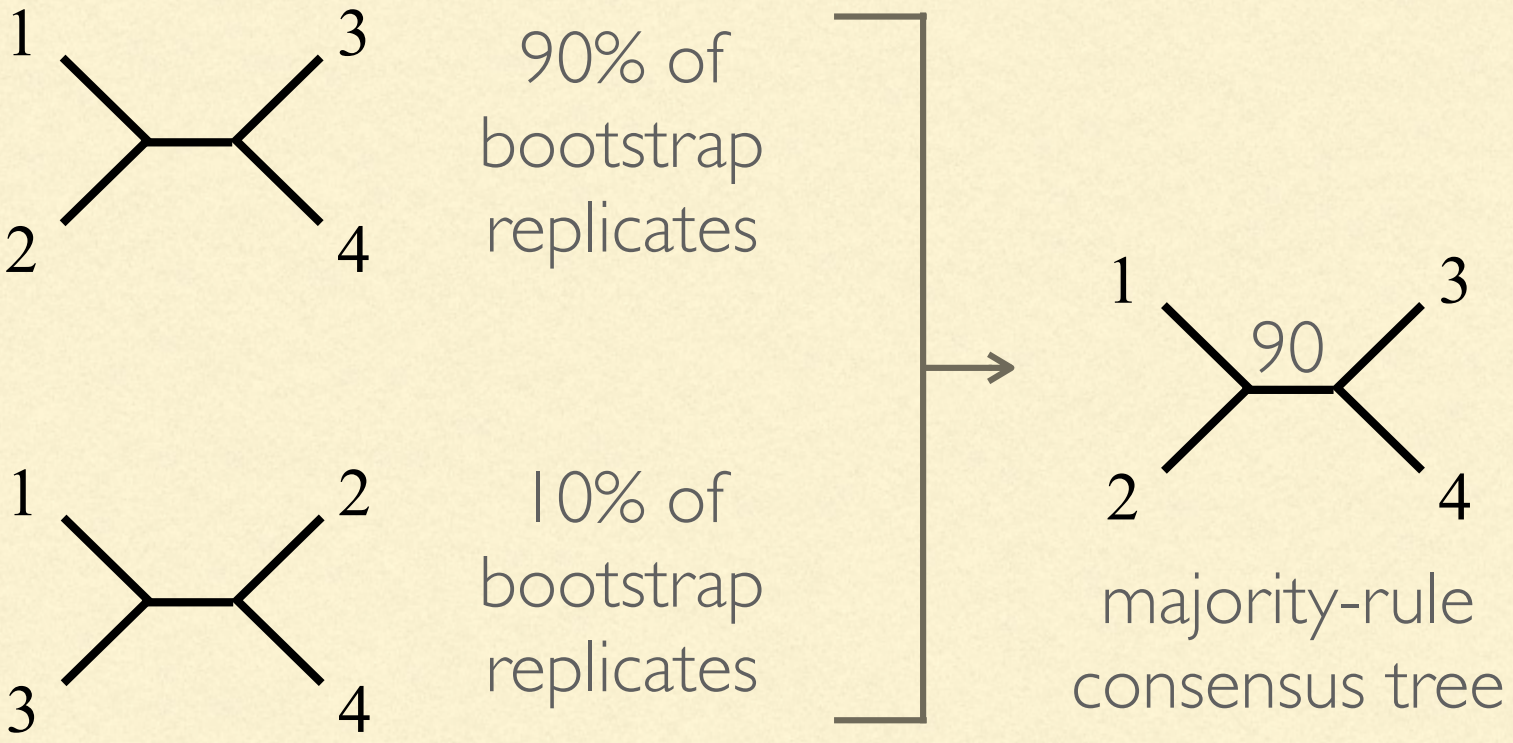


	1	2	3	4	5	6	7	8
1	G	G	C	G	G	C	G	G
2	G	A	C	A	G	T	A	G
3	T	G	C	G	A	G	G	A
4	T	A	C	A	G	G	A	G

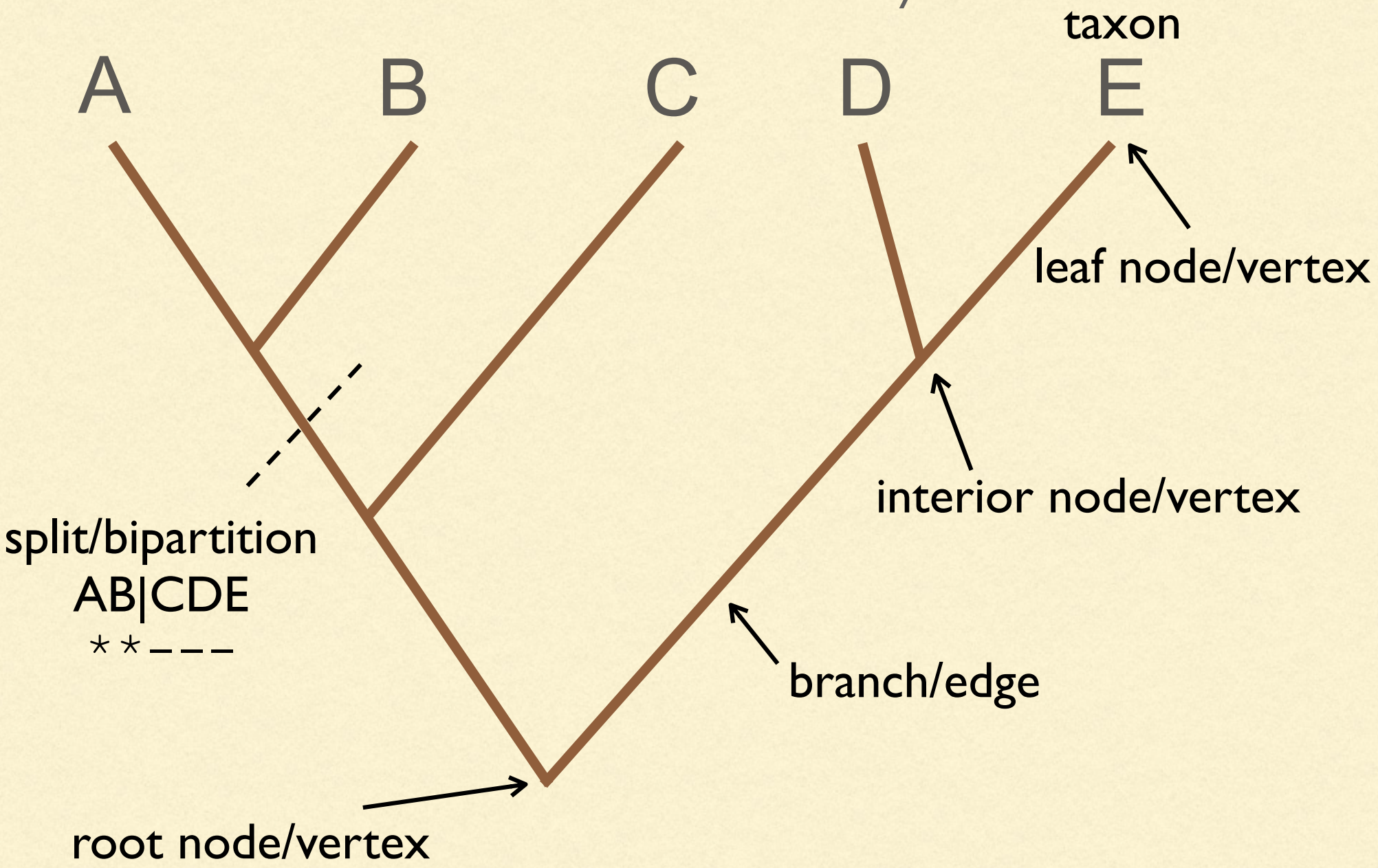
bootstrap replicate



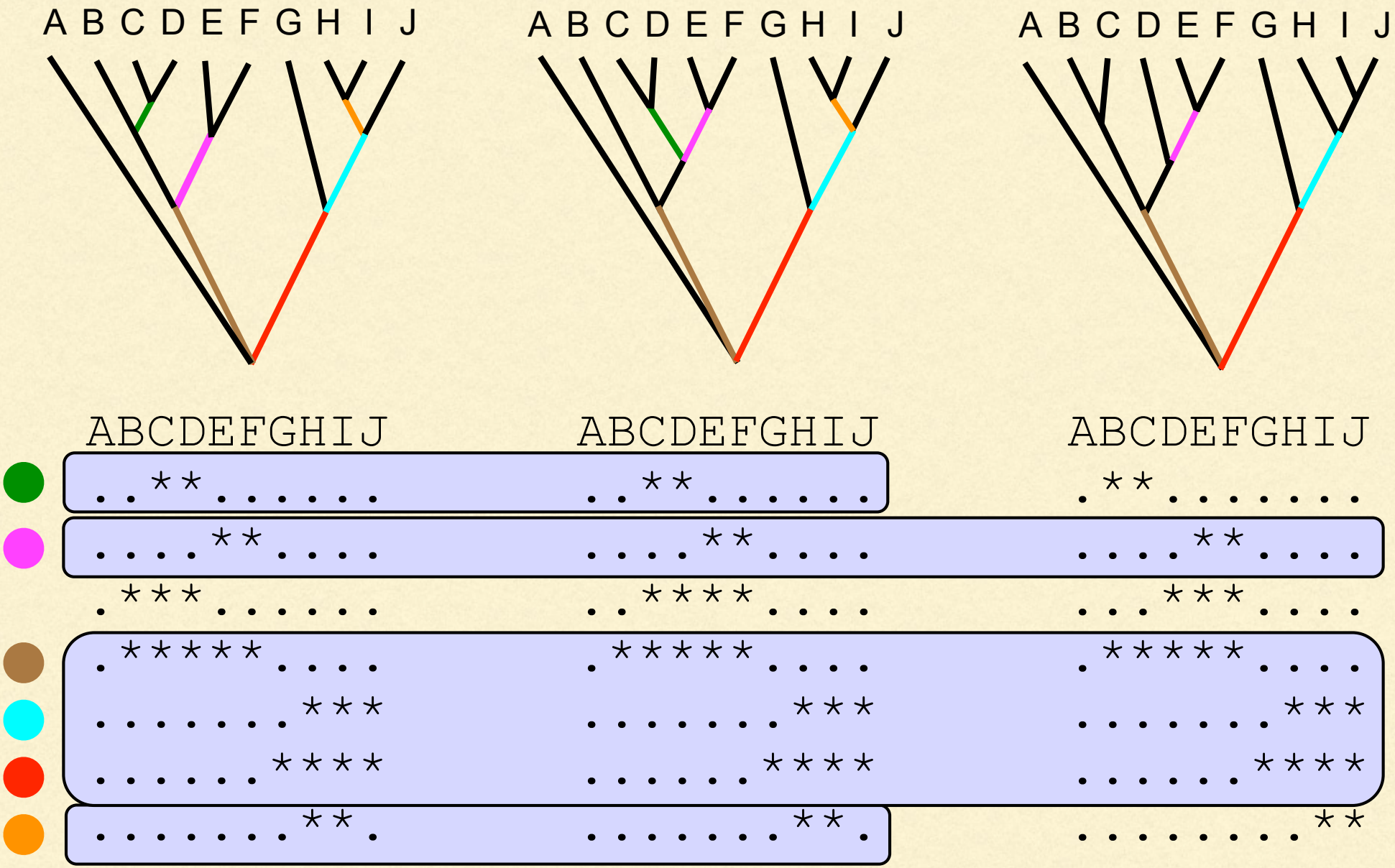
Consensus trees

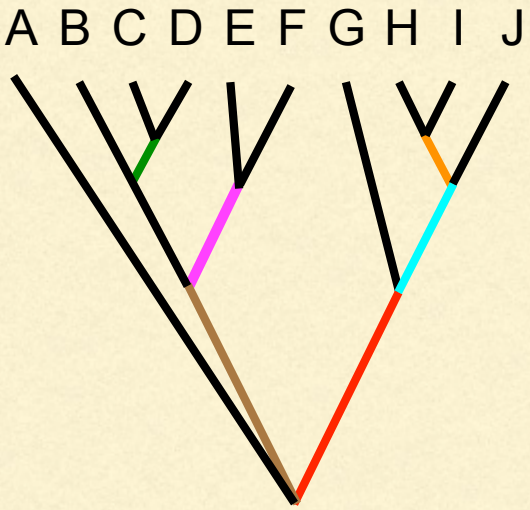


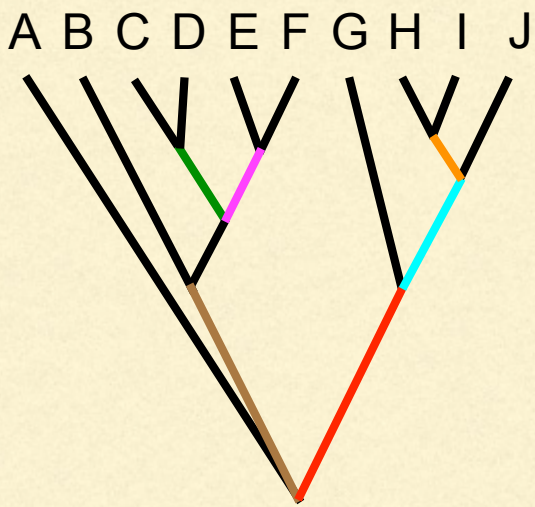
Tree anatomy

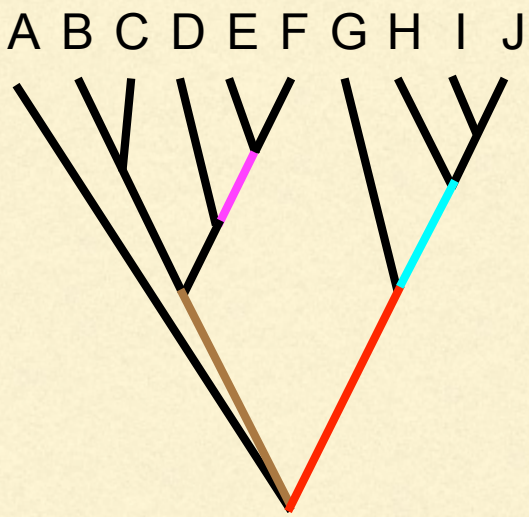


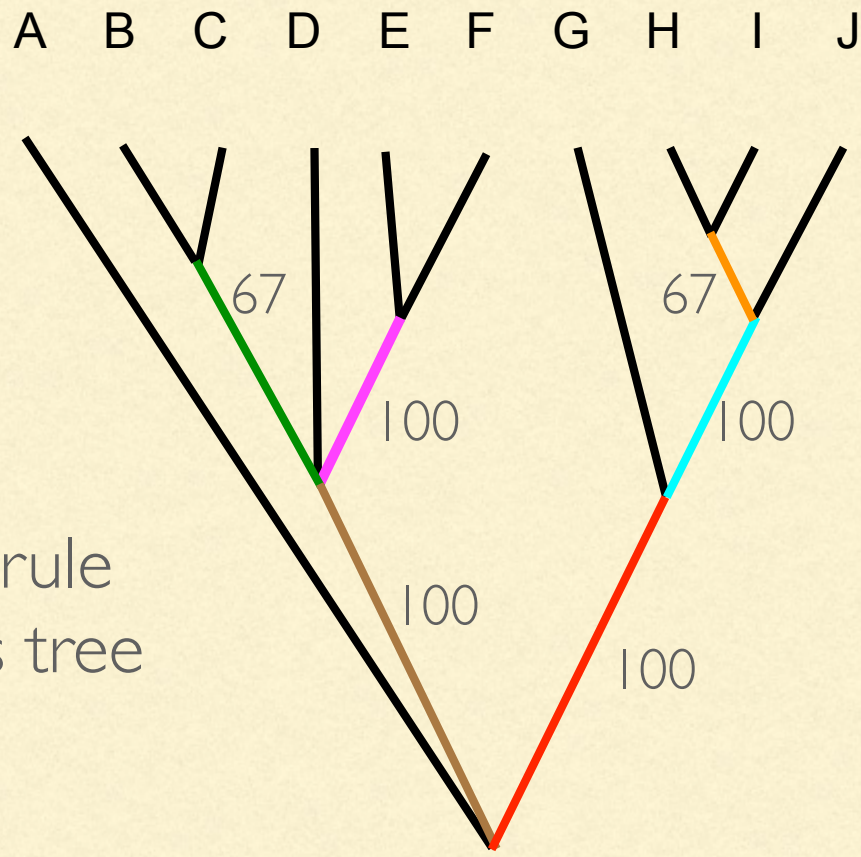
Consensus trees







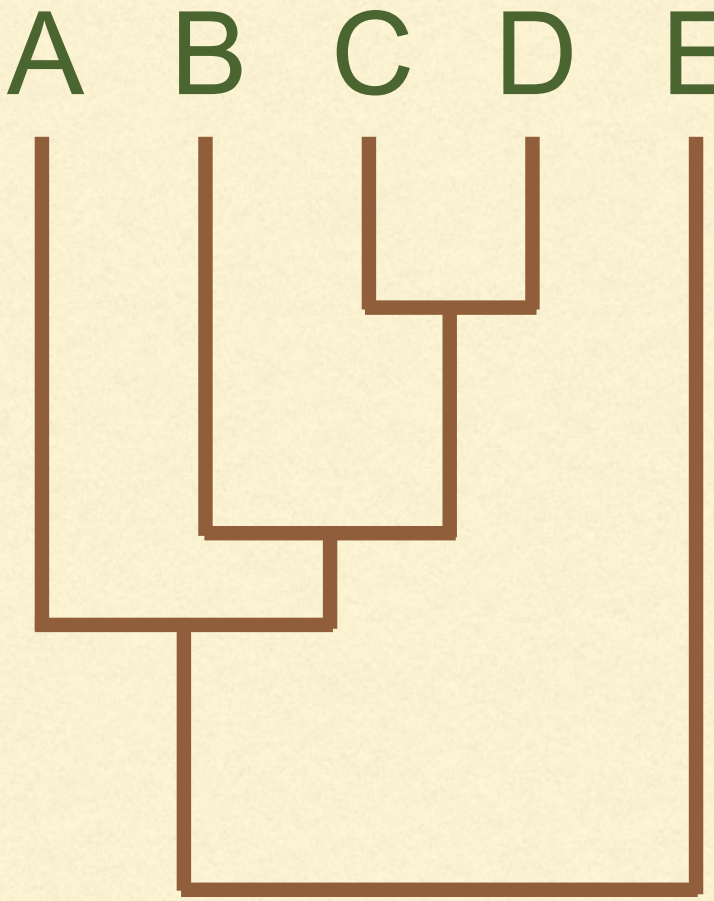




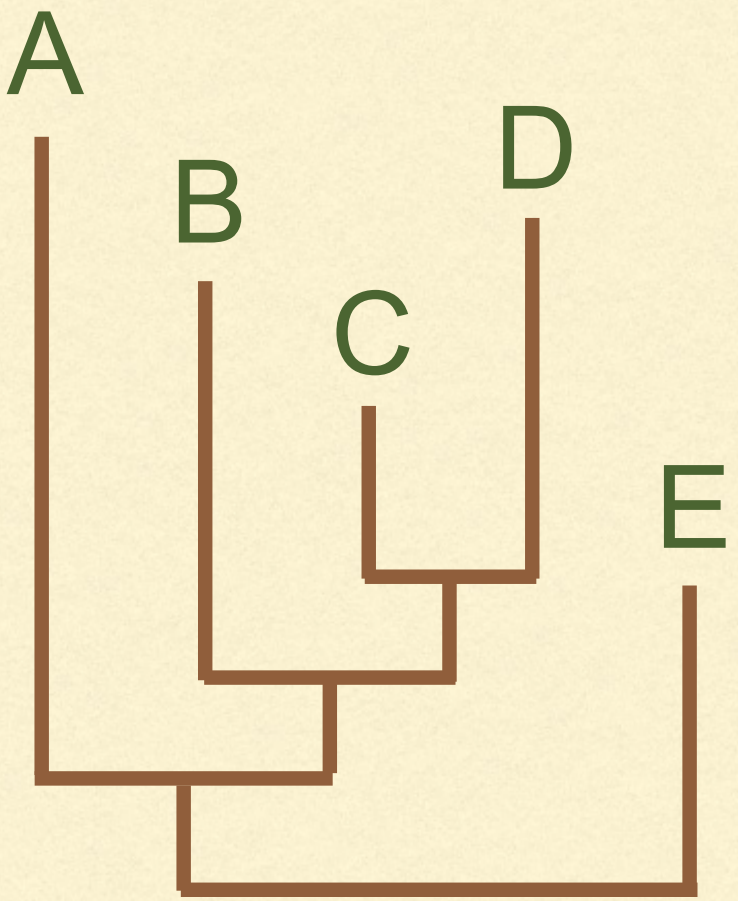
majority rule
consensus tree

% of input trees

Edge lengths



edge lengths are
time only



edge lengths are
rate x time

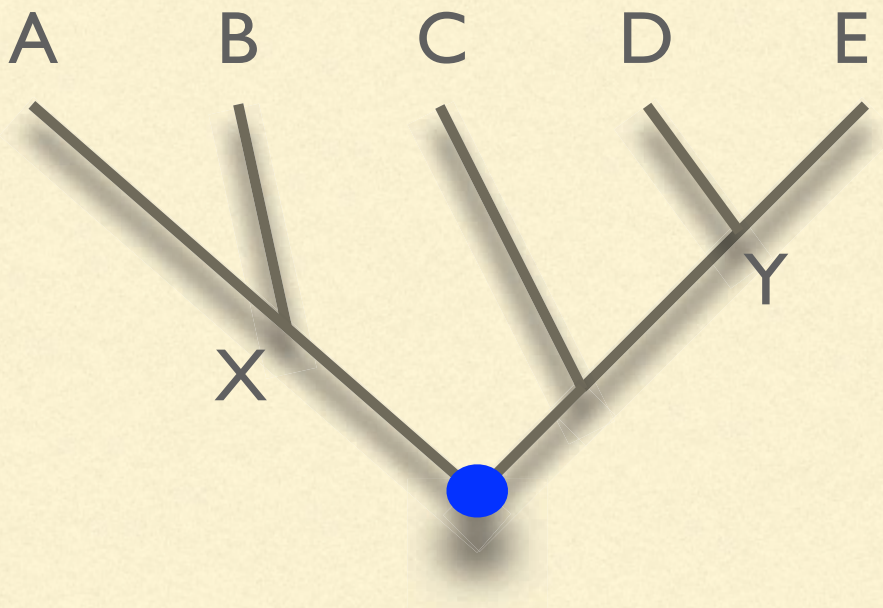
Newick descriptions


```
#NEXUS

Begin trees;
        Translate
                1 Chlamydopodium_vacuolatum_EF113426,
                2 Protosiphon_sp_FRT2000_JN880462,
                3 Protosiphon_botryoides_UTEX_B99_JN880463,
                4 Protosiphon_botryoides_UTEX_B461_JN880464,
                5 Protosiphon_botryoides_f_parieticola_UTEX_46_JN880465,
                6 Protosiphon_botryoides_UTEX_47_JN880466
                ;
tree 'PAUP_1' = [&U] (1:0.104899,((2:0.009446,
(4:0.001635,6:7.29892e-07):0.030410):0.005612,3:0.007100):0.002552,5:0.001416);
End;
```

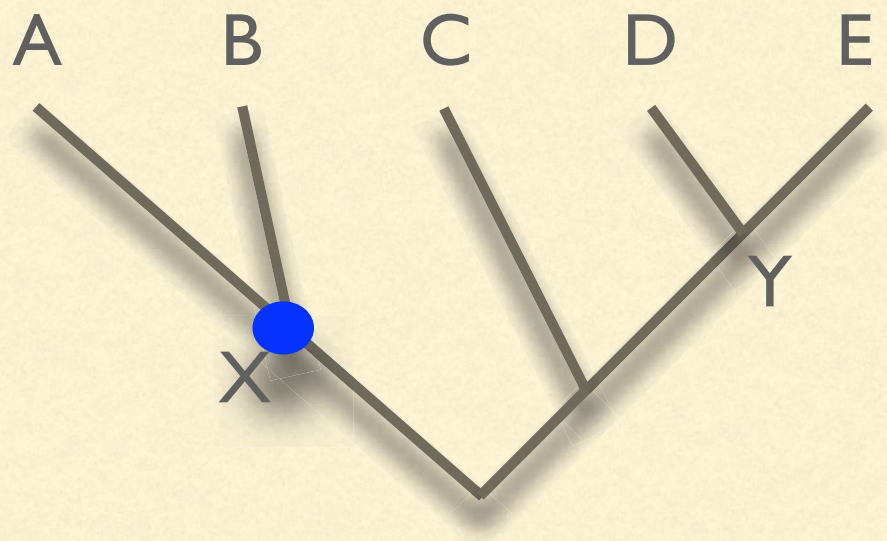
https://en.wikipedia.org/wiki/Newick_format

Newick tree descriptions



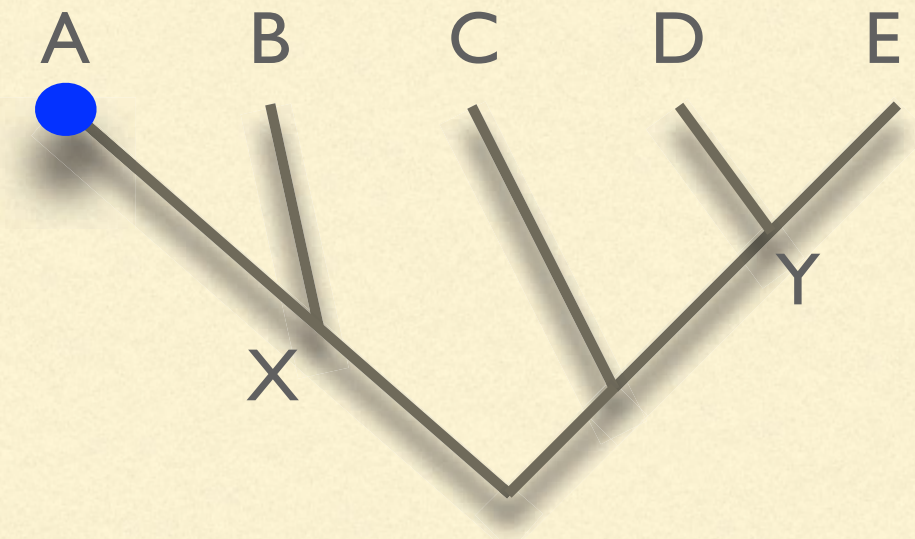
((A,B)X,(C,(D,E)Y))

Newick tree descriptions



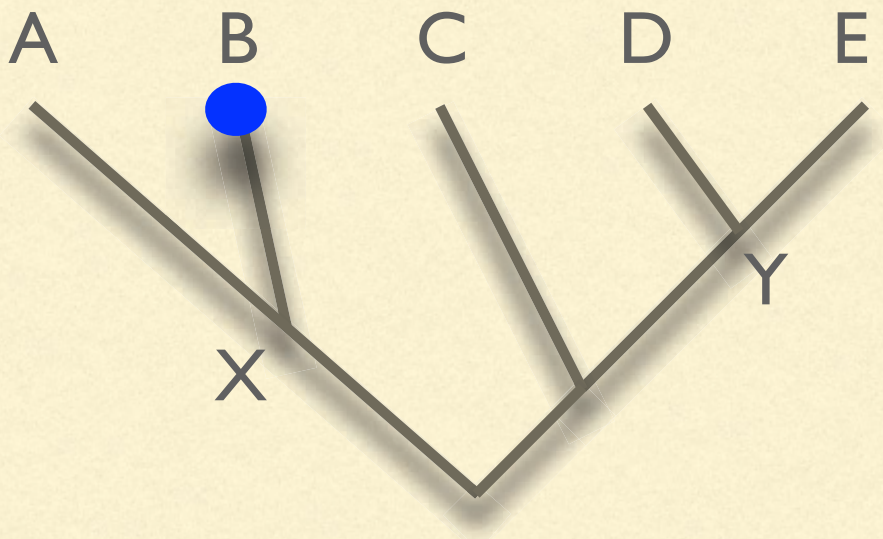
((A,B)X,(C,(D,E)Y))

Newick tree descriptions



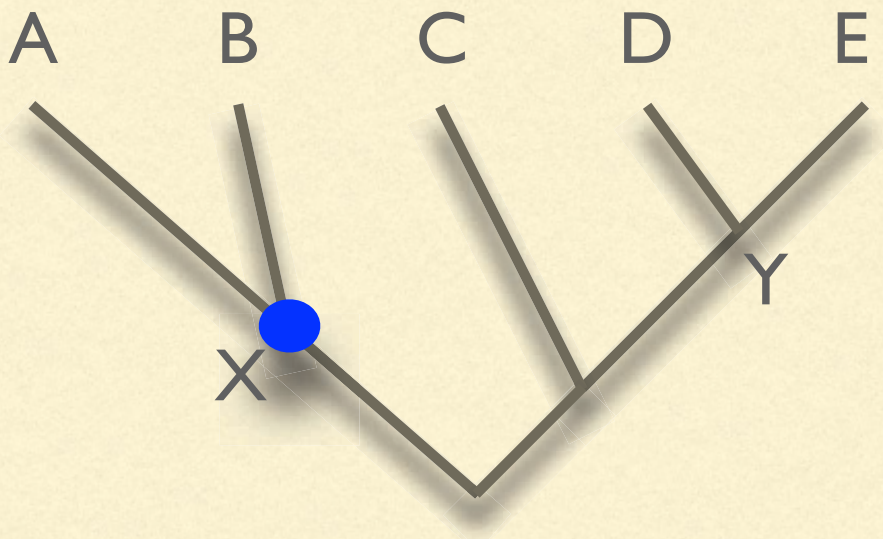
((**A**,B)X,(C,(D,E)Y))

Newick tree descriptions



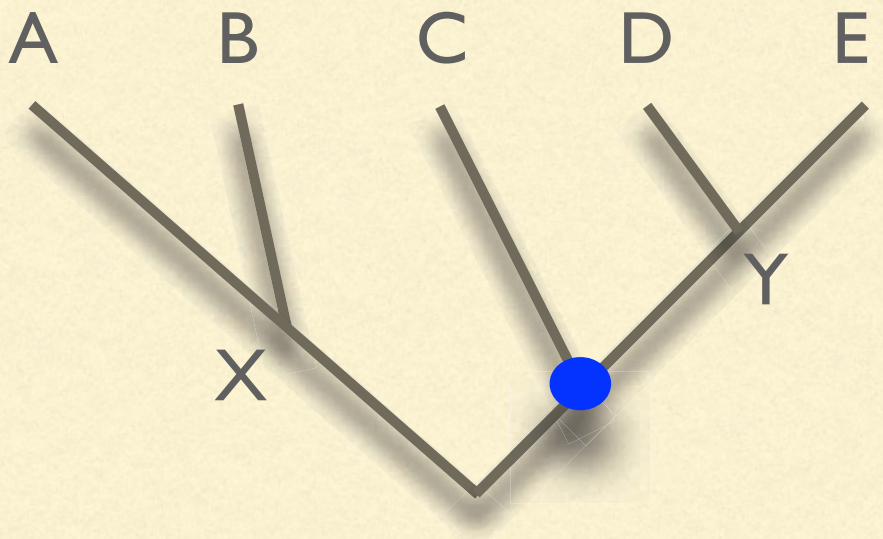
((A,**B**)X,(C,(D,E)Y))

Newick tree descriptions



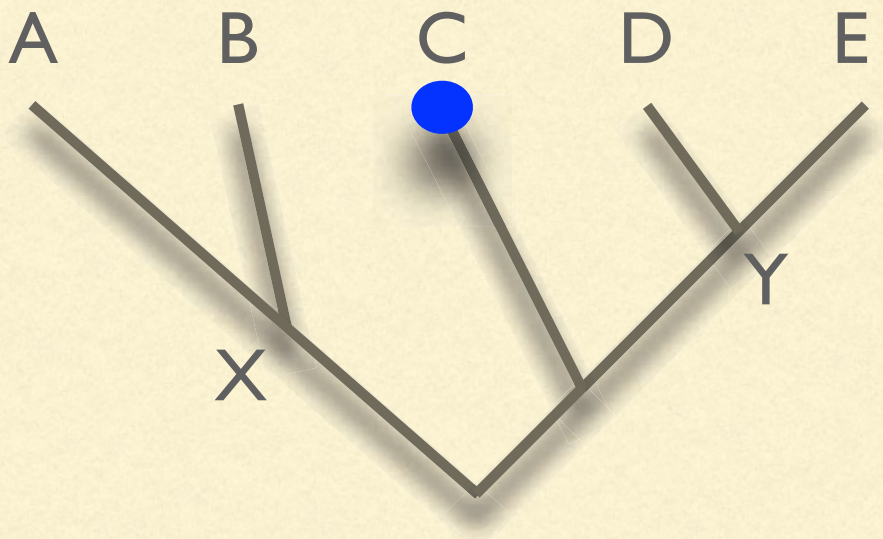
((A,B)**X**,(C,(D,E)Y))

Newick tree descriptions



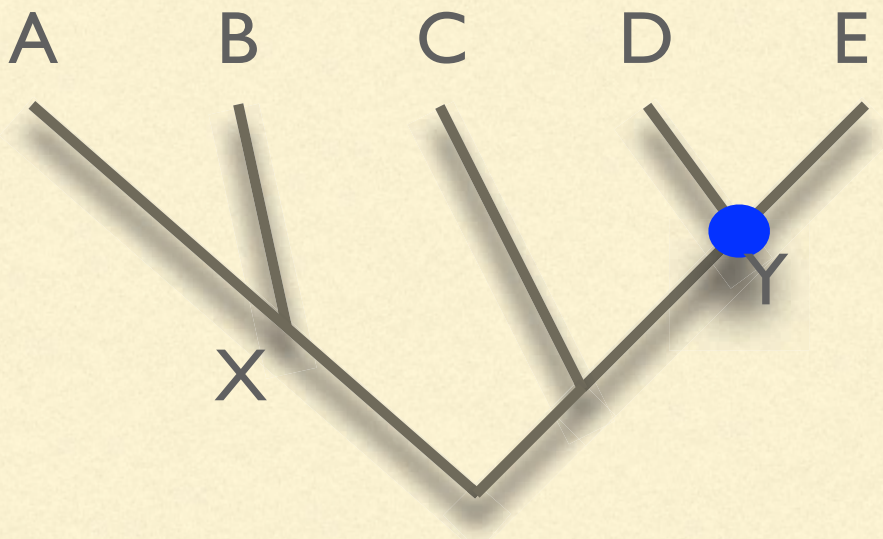
((A,B)X,(C,(D,E)Y))

Newick tree descriptions



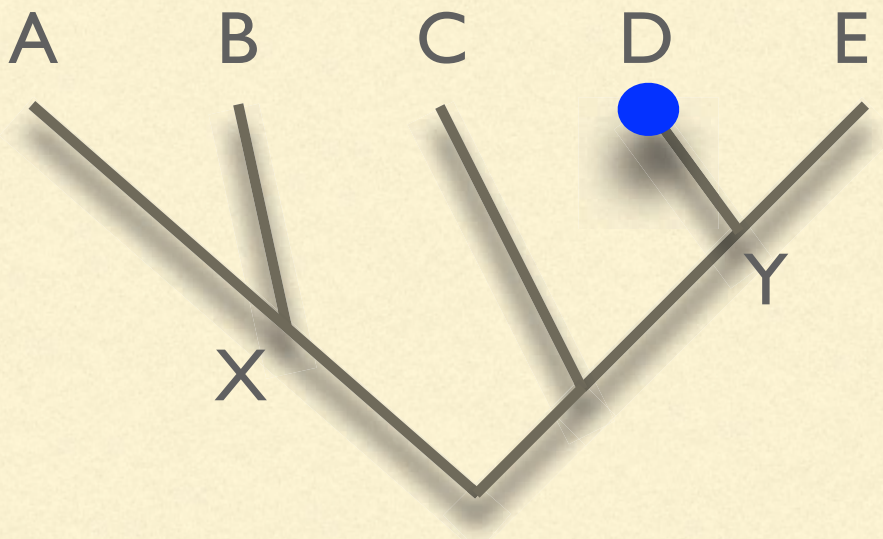
((A,B)X,**(C**,(D,E)Y))

Newick tree descriptions



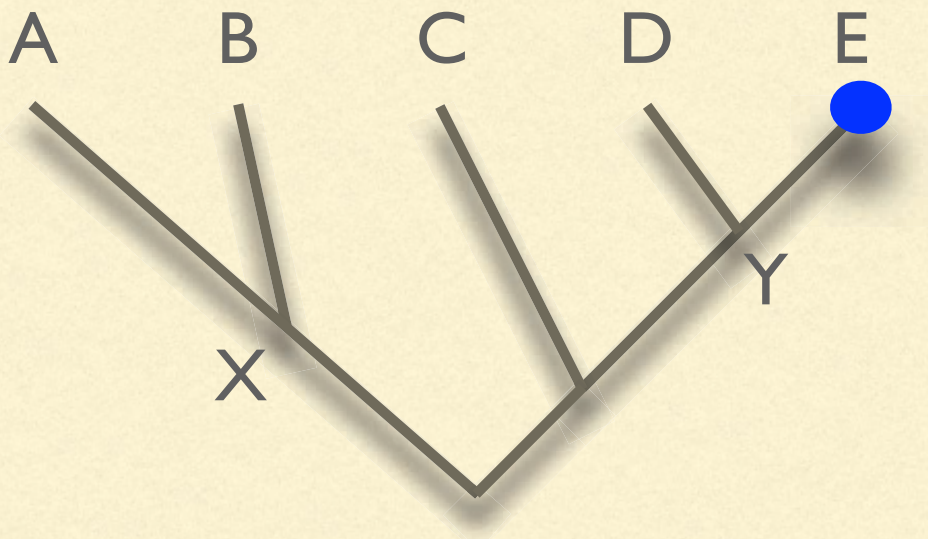
((A,B)X,(C,(D,E)Y))

Newick tree descriptions



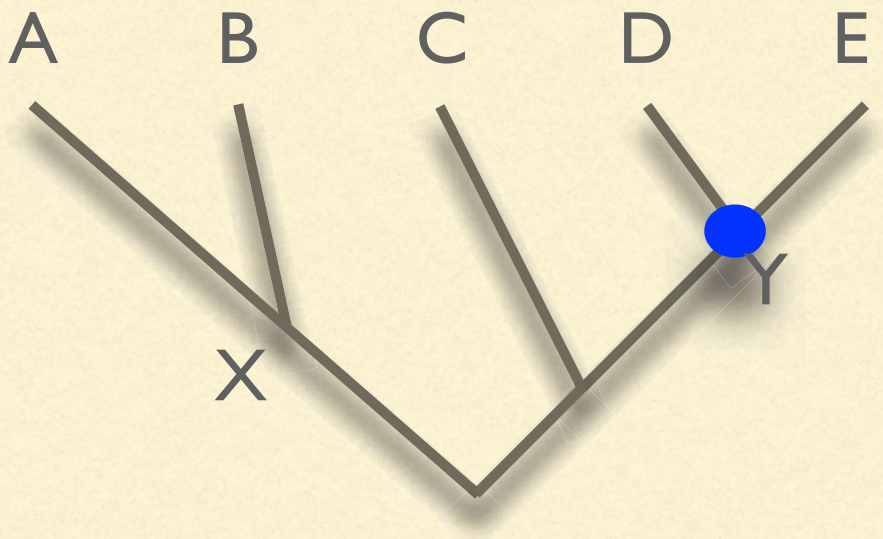
((A,B)X,(C,**(D**,E)Y))

Newick tree descriptions



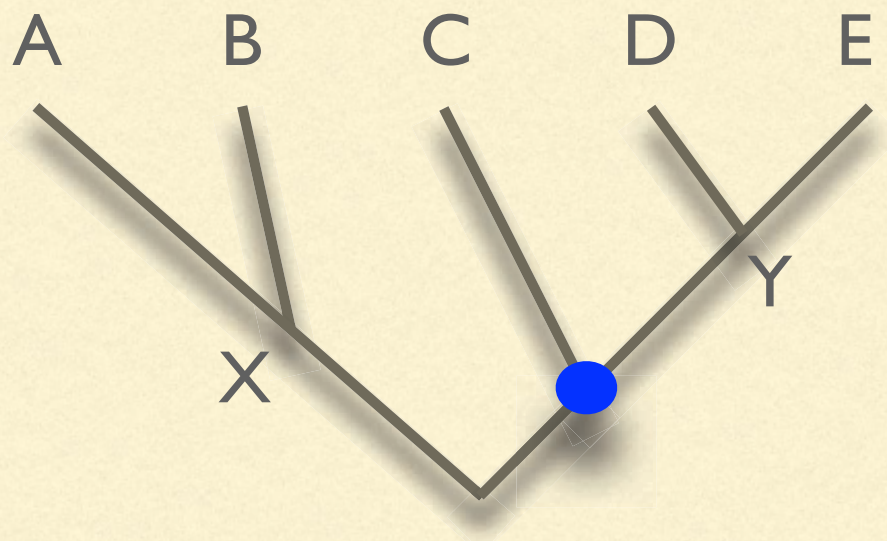
((A,B)X,(C,(D,**E**)Y))

Newick tree descriptions



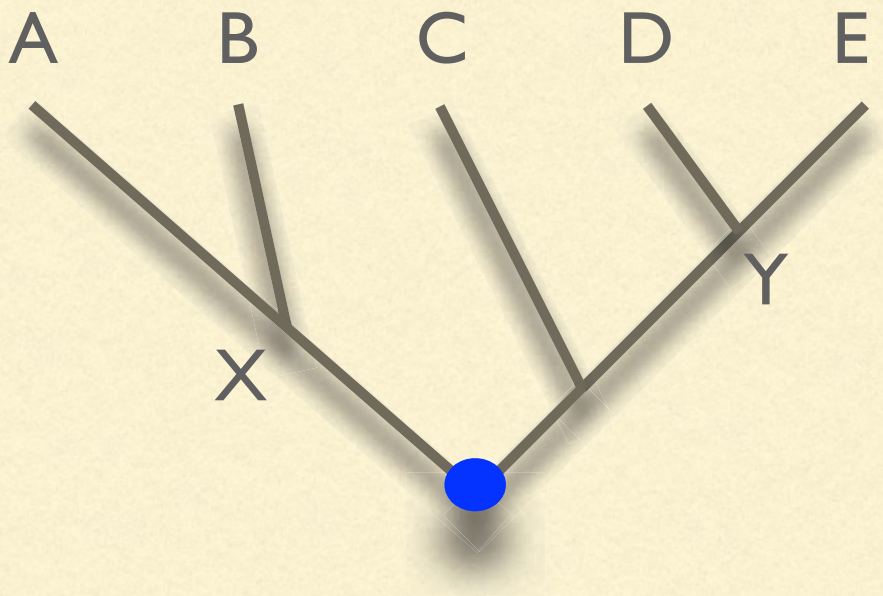
((A,B)X,(C,(D,E)**Y**))

Newick tree descriptions



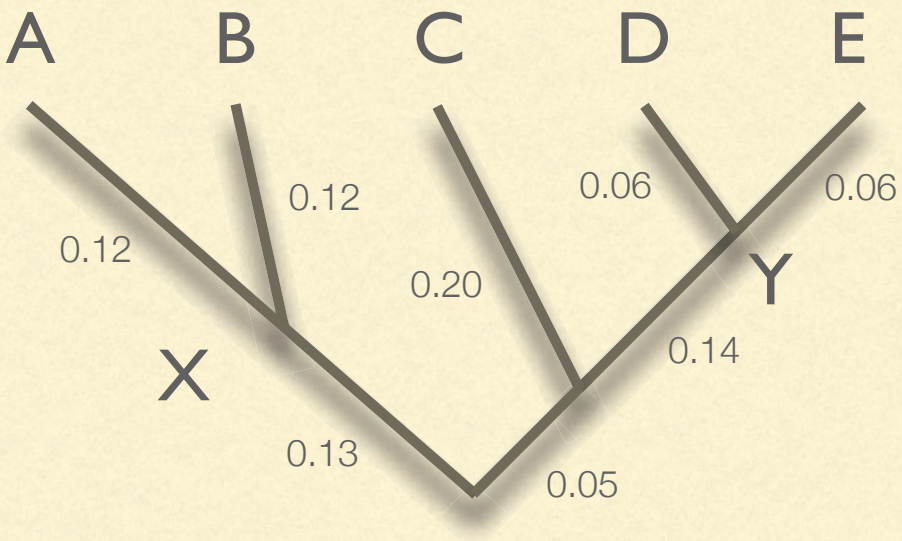
((A,B)X,(C,(D,E)Y))

Newick tree descriptions



((A,B)X,(C,(D,E)Y))

Newick tree descriptions

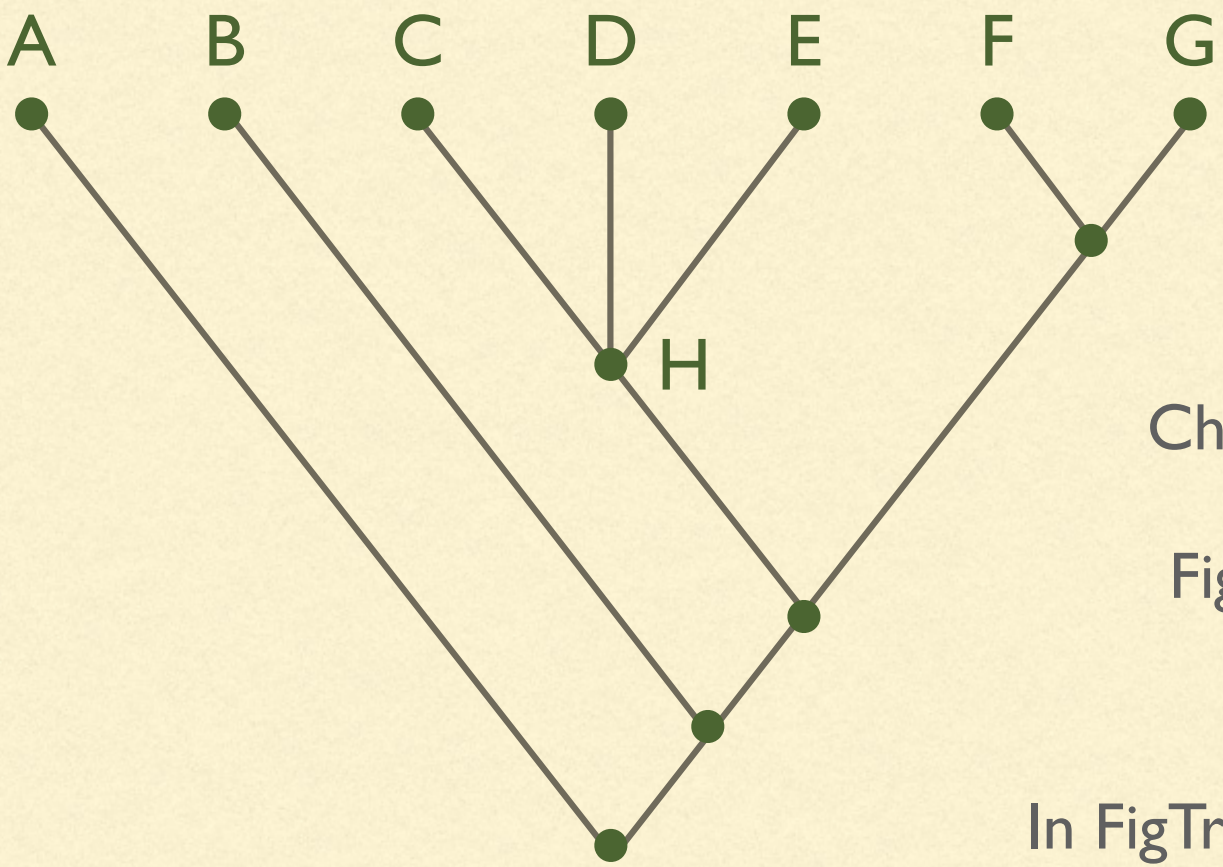


((A:.12,B:.12)X:.13,(C:.2,(D:.06,E:.06)Y:.14):.05)

edge lengths follow colon after node name (if present)

Newick challenge

Create a newick tree description for this tree (just the topology, no branch lengths)

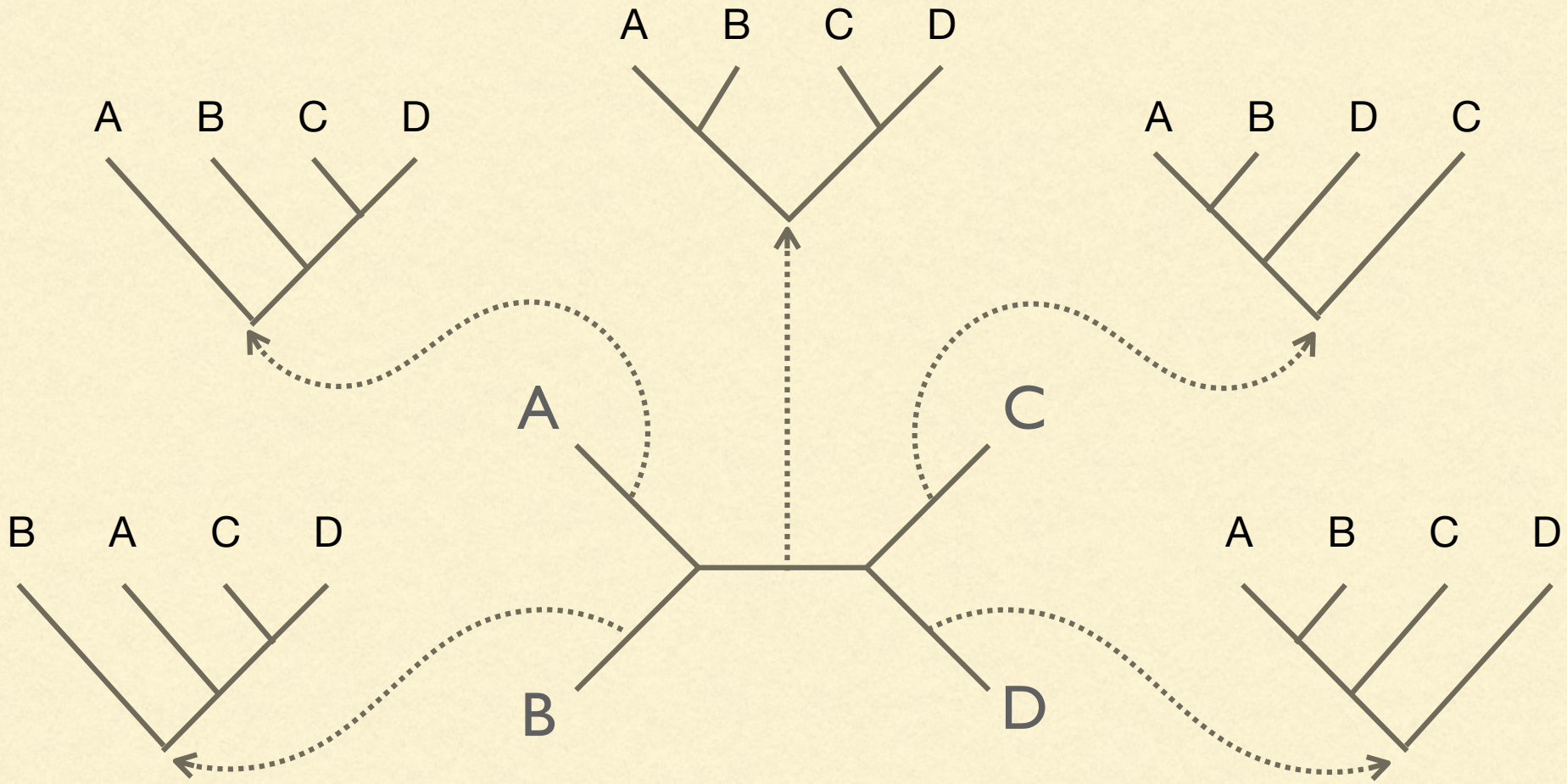


Check your work by pasting your newick string into FigTree (https://github.com/rambaut/figtree/releases)

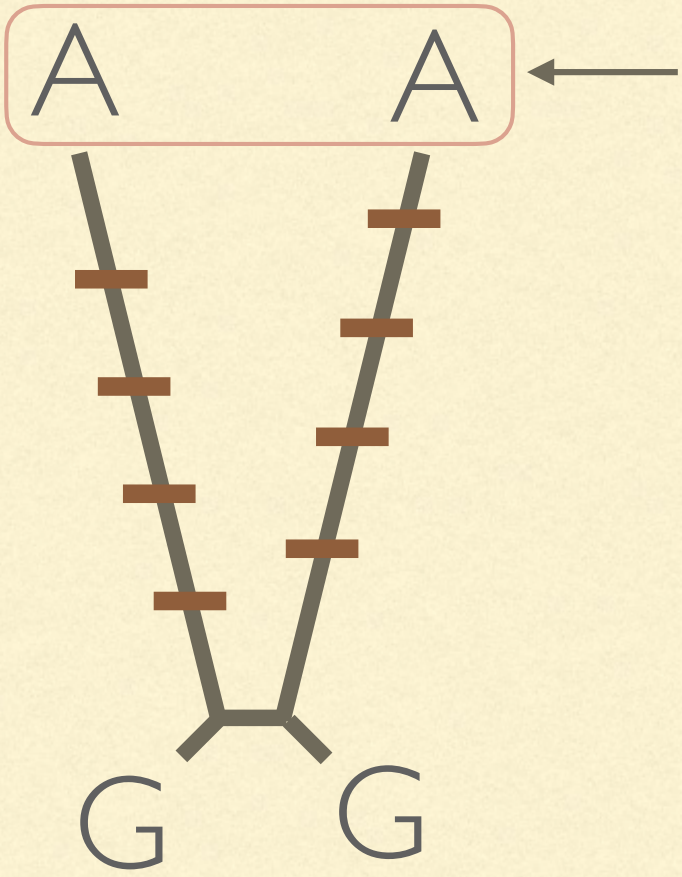
In FigTree, check Node labels and choose display = label" to see the "H"

Rooted vs unrooted

rooting and **adding a taxon** increase treespace by the same amount

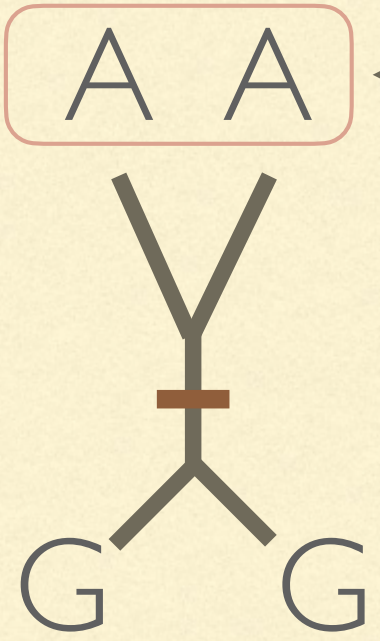


Challenges: model violations



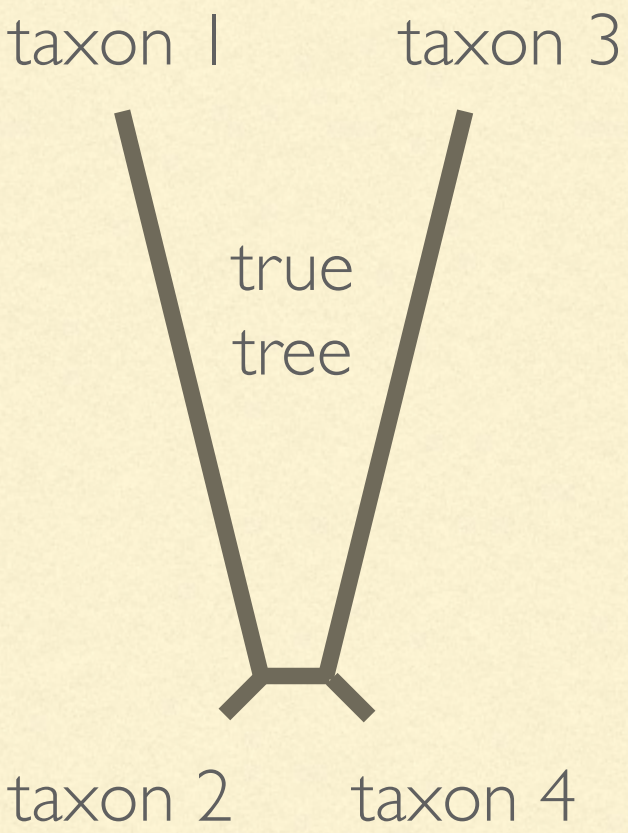
Long external branches favor a **convergence explanation** of this similarity

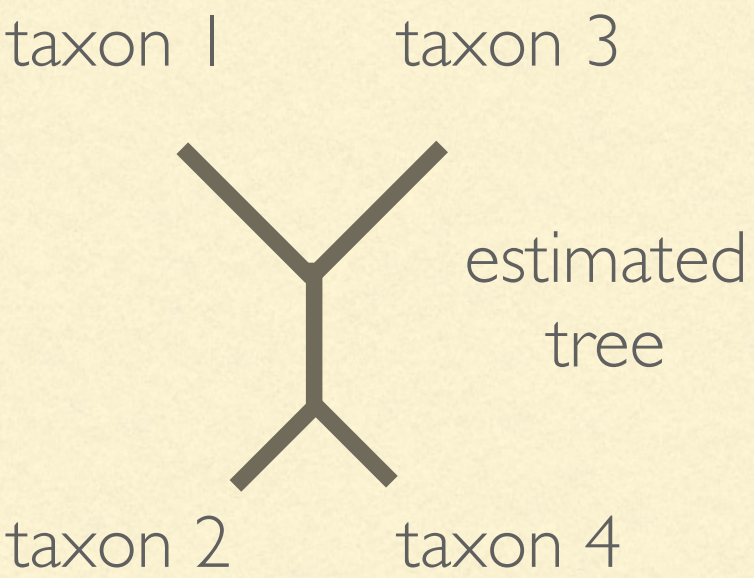
Challenges: model violations



Short external branches favor an **inheritance explanation** of this similarity

Challenges: model violations

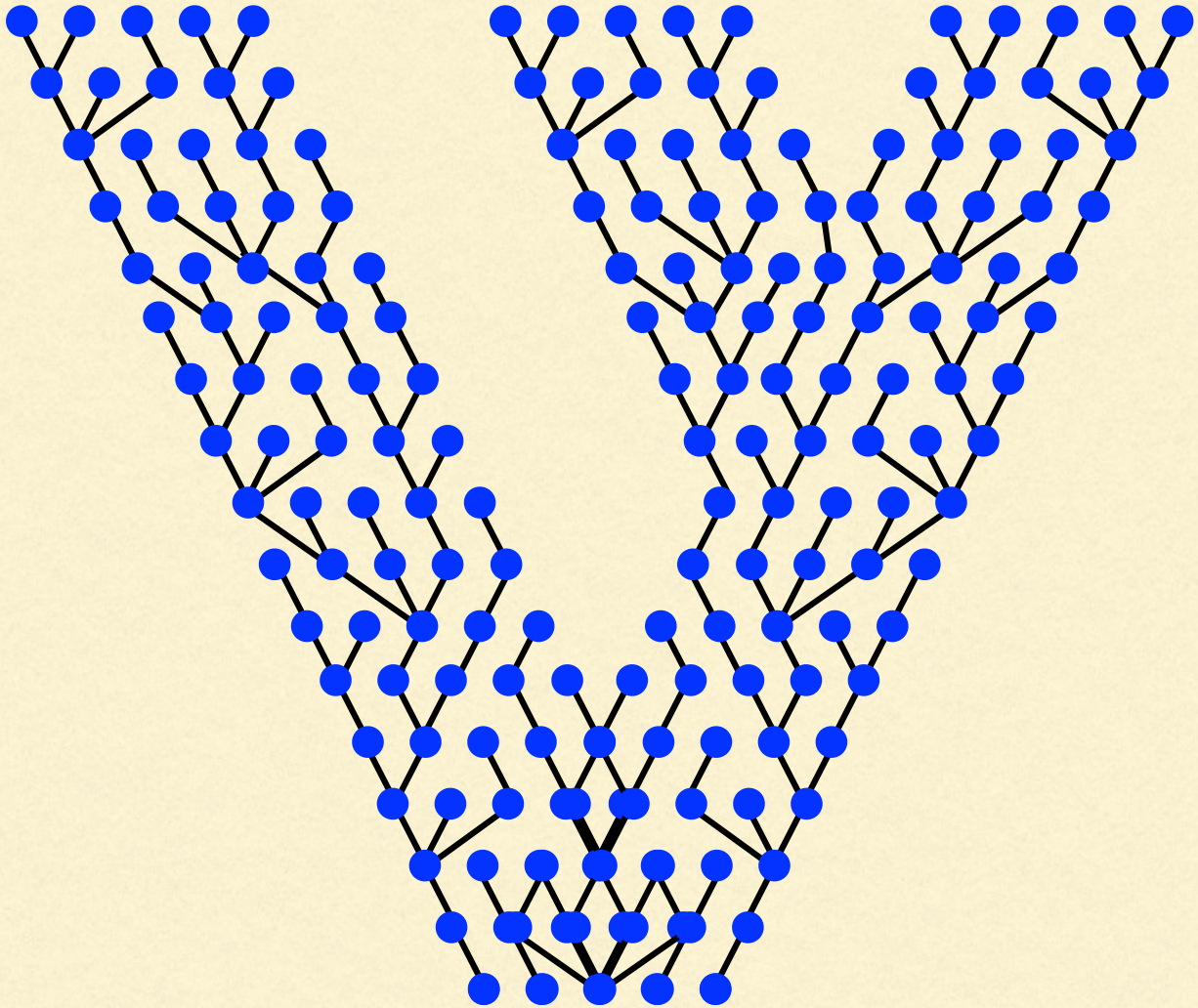




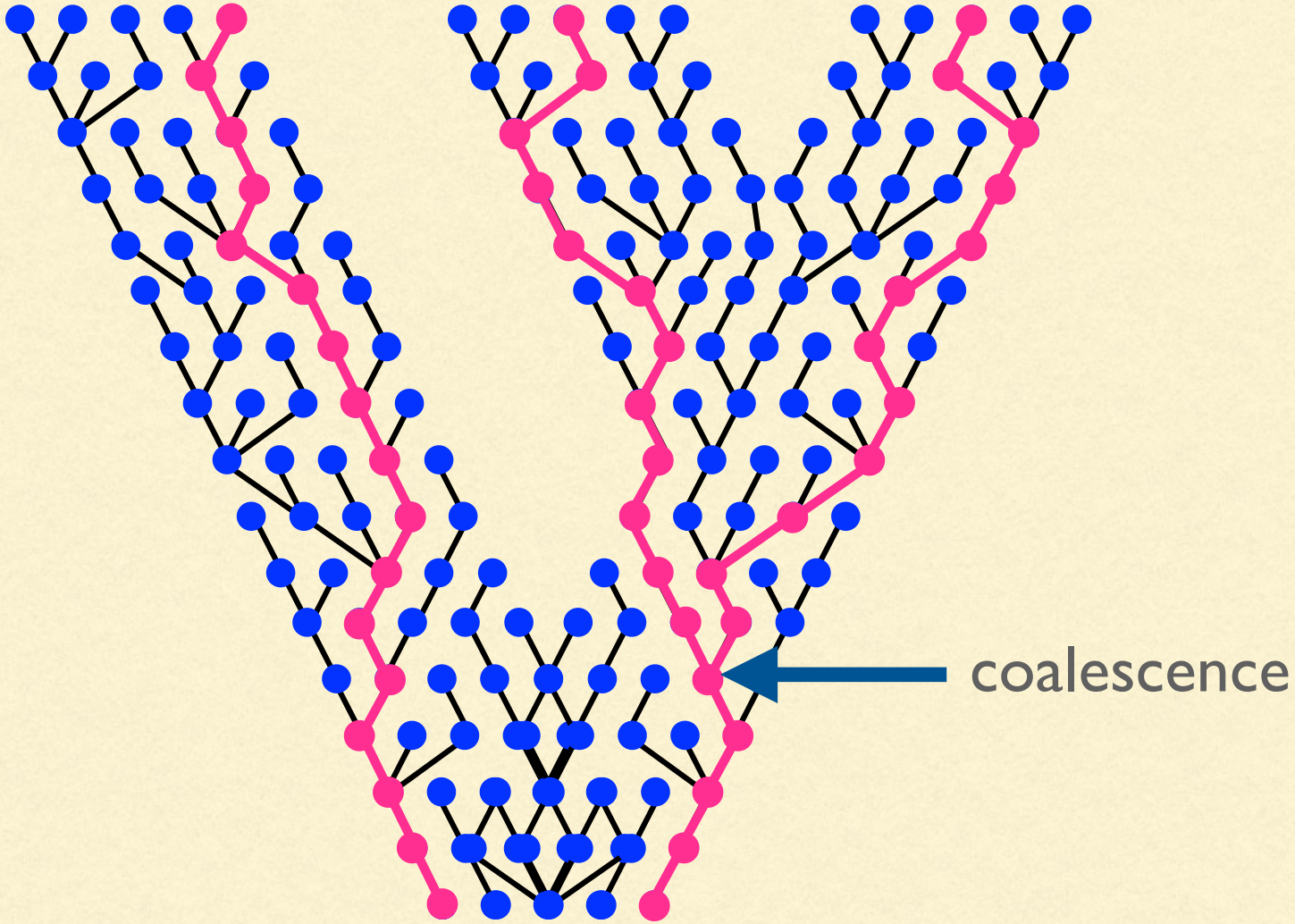
Models that are too simple often underestimate branch lengths

Long branch attraction

Challenges: deep coalescence



Challenges: deep coalescence

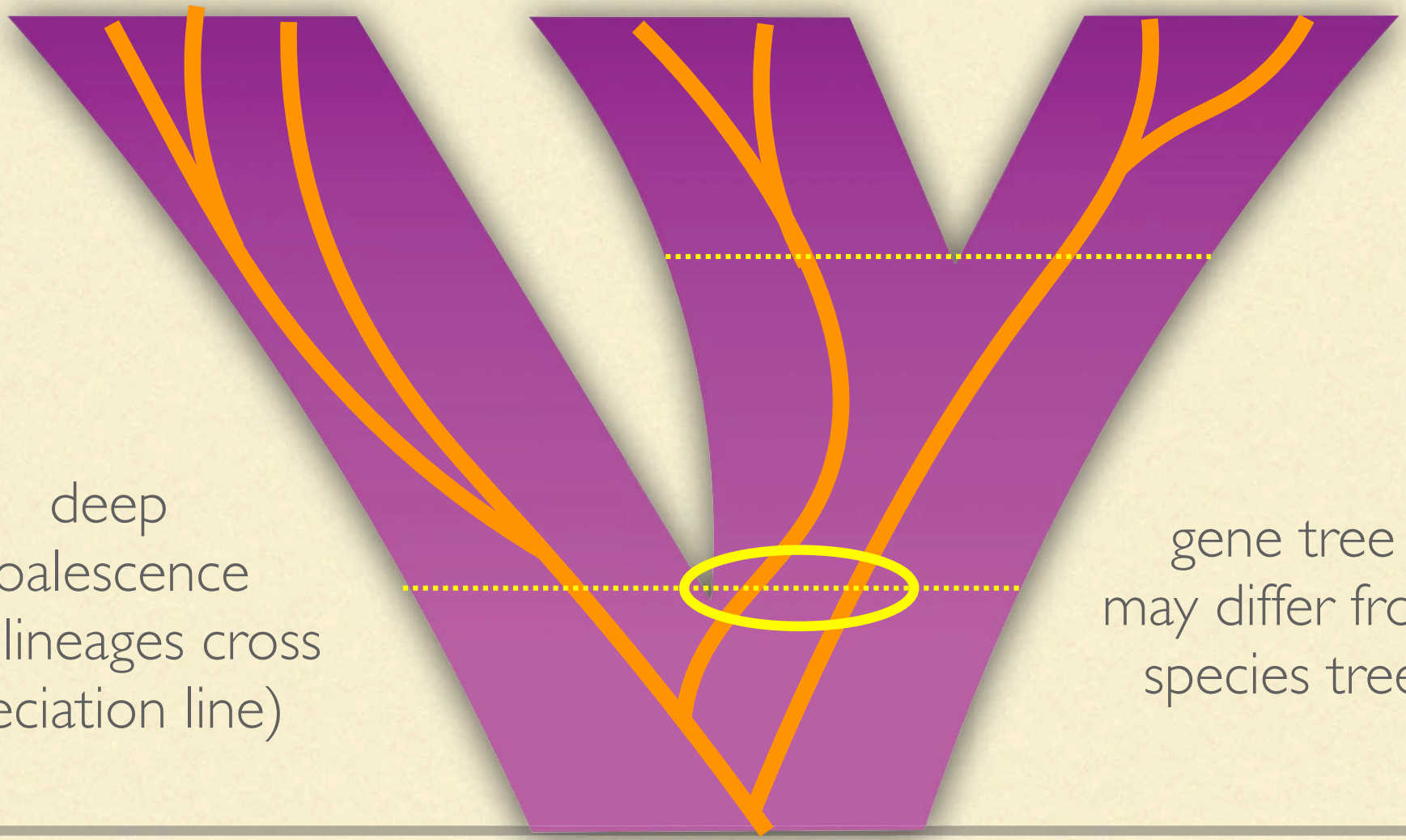


Challenges: deep coalescence

no deep coalescence (always only one lineage crosses speciation line)

gene tree matches species tree

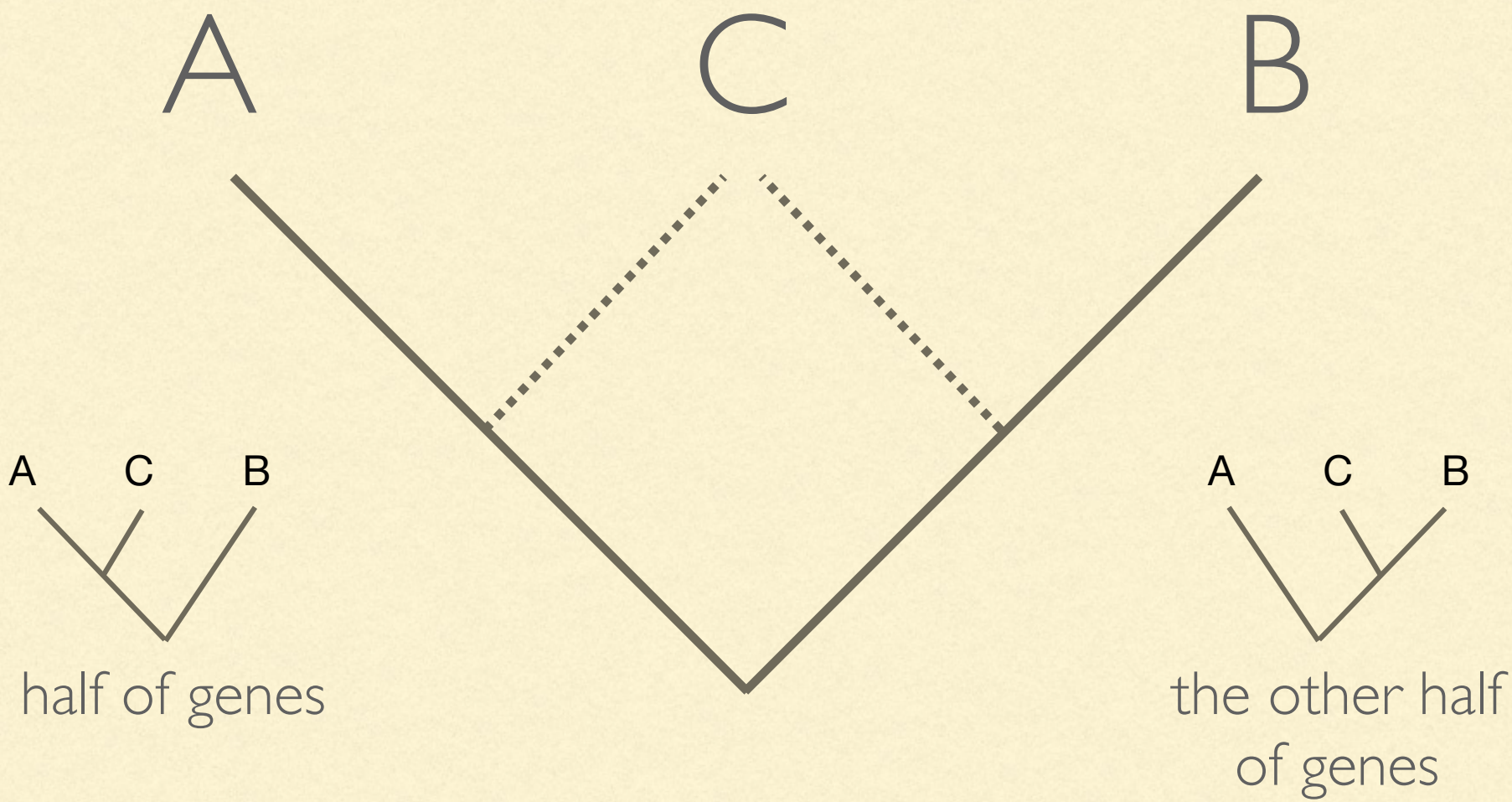
Challenges: deep coalescence



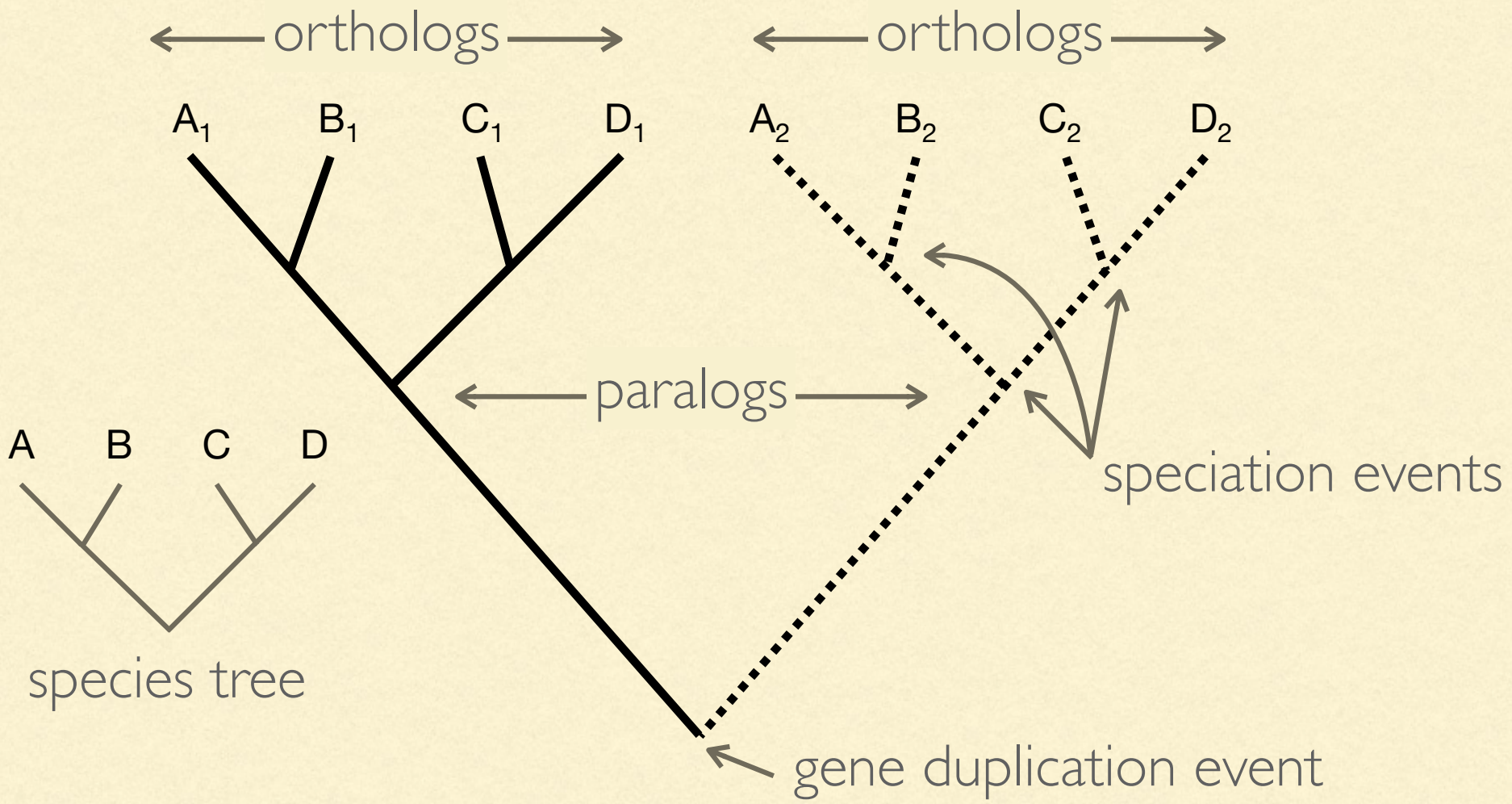
deep coalescence (2+ lineages cross speciation line)

gene tree may differ from species tree

Challenges: hybridization

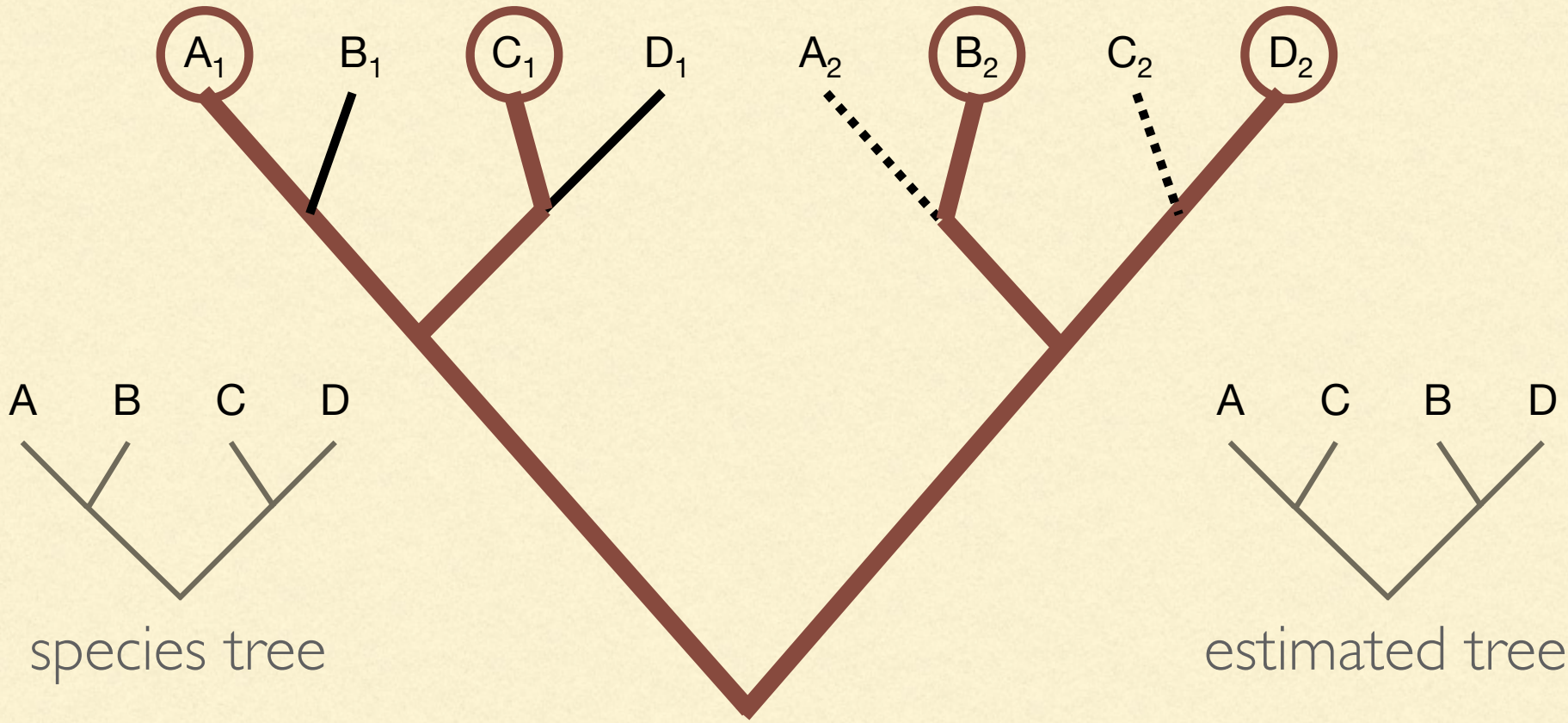


Challenges: paralogy



Challenges: paralogy

sampled sequences are a mixture of orthologs and paralogs



Overview of the Workshop

Sun	Mon	Tue	Wed	Thu	Fri	Sat
					24	25
26	27	28	29	30	31	1
2	3					

Today (Saturday): **Lewis**, **Huelsenbeck**

Intro to phylogenetics, likelihood and likelihood models:

Computing introduction, sequence alignment:

Tonight: **Kong**, **Fauskee**, **Milkey, Adesina, Petrucci**


Kevin


Blake


Analisa


Teejay


Bruno

Under the hood

C++ Programming subworkshop (optional):

Mornings 8-9am: **Huelsenbeck**

Model selection and maximum likelihood

Model selection:

Sunday morning: **Lewis**, **Swofford**

PAUP* lab:

Sunday afternoon: **Swofford**

IQ-TREE: ML inference on a large scale

Sunday evening: **TAs**

RevBayes

Introduction to Bayesian statistics

Monday morning: **Lewis**

RevBayes: Graphical models, tree estimation:

Monday afternoon: **Brown**

RevBayes: Divergence time estimation:

Monday evening lecture/lab: **Heath**

Coalescence, species trees

Introduction to coalescent theory:

Tuesday morning: **Beerli**

Species tree estimation lab:

Tuesday afternoon/evening: **Kubatko, Swofford**

Open lab:

Tuesday evening

Migration, phylogeography, dinner party, and free day!

MIGRATE: population structure and migration:

Wednesday morning: **Beerli**

Phylogeography, pangenomes, evolution, and phylogenetics:

Wednesday afternoon: **Edwards**

Course **Dinner Party**

Wednesday evening

Free day: Thursday all day

Sleep, visit Martha's Vineyard, whale watching...

Selection

Sun	Mon	Tue	Wed	Thu	Fri	Sat
					24	25
26	27	28	29	30	31	1
2	3					

Selection and codon models:

- Friday morning: **Bielawski**

Adaptive protein evolution:

- Friday afternoon: **Chang**

PAML lab:

- Friday evening: **Bielawski**

Machine learning, phylodynamics, and networks

Machine learning:

- Saturday morning: **Smith**

Phylodynamics of infectious disease:

- Saturday afternoon: **Gill**

Network models

- Saturday evening: **Solís-Lemus**

Phylogenomics, ants, and applications

Phylogenomics, ants and their gut microbiomes:

Sunday morning: **Moreau**

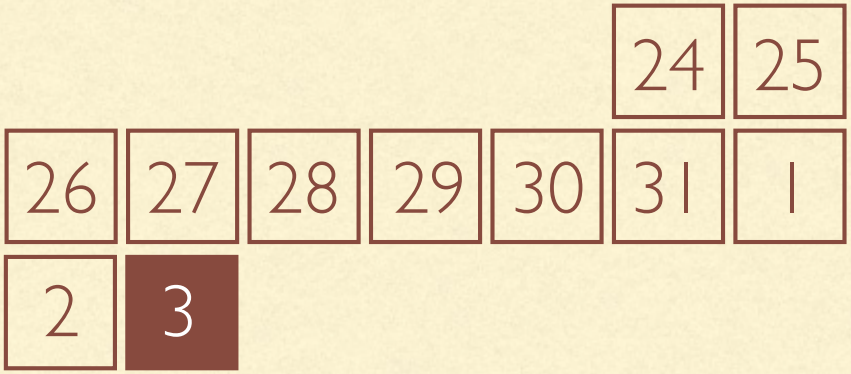
Open Tree of Life, phylogenomics, gene tree updating:

Sunday afternoon: **McTavish**

Evolutionary applications of genomics

Sunday evening: **Knowles**

Ethics



Scientific ethics:

Monday morning: **Swofford**, **Bielawski**

Open lab:

Your last chance to ask questions