EVE 161:
Microbial Phylogenomics

Class #4:
Phylogeny

UC Davis, Winter 2018
Instructor: Jonathan Eisen
Teaching Assistant: Cassie Ettinger

EVE 161:
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Class #5:
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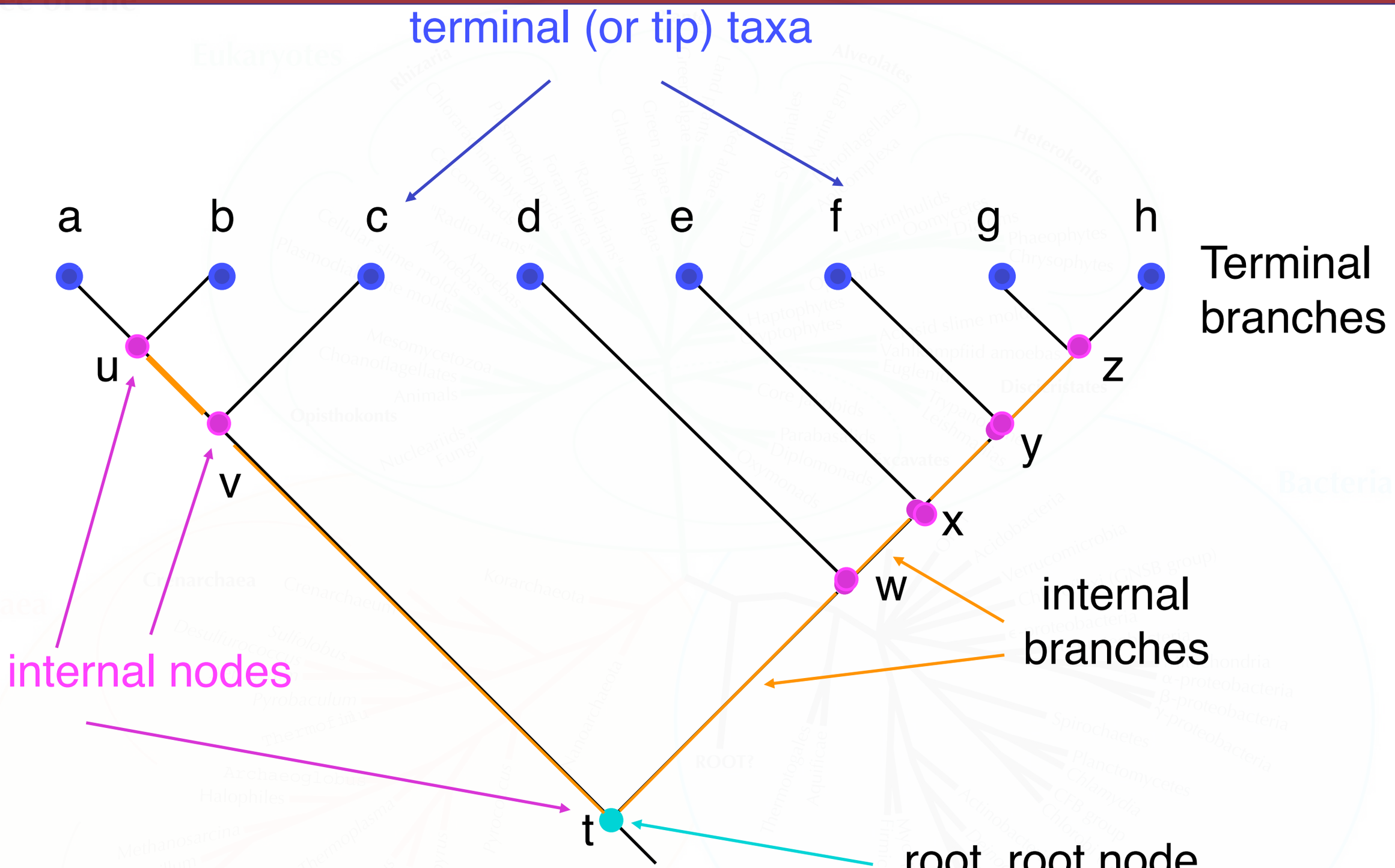
Where we are going and where we have been

- Previous Class:
  - 3. rRNA
- Current Class:
  - 4. Phylogeny
- Next Class:
  - 5. Tree of Life

Phylogeny

Phylogeny

Parts of a phylogenetic tree



Internal nodes represent hypothetical ancestral taxa

Phylogenetic Groups

Monophyletic **Paraphyletic** **Polyphyletic**

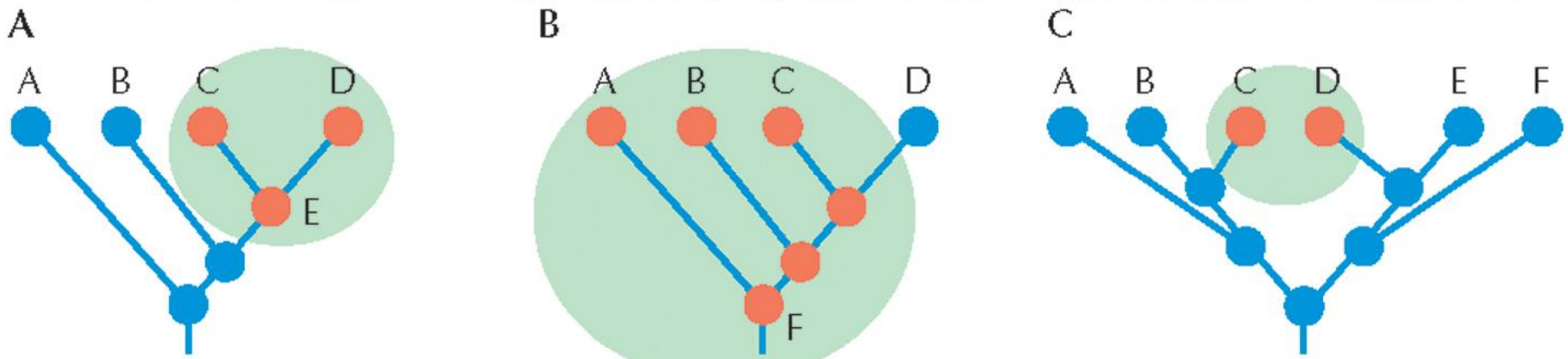


FIGURE 5.3. Different types of phylogenetic groups. In each panel, the phylogenetic group is indicated by a *green shaded circle*. (*A*) Monophyletic group. All species (C and D) in the group share a common ancestor (E) not shared by any of the other species. (*B*) Paraphyletic group. All species in the group share a common ancestor (F), but some species (D) have been excluded from the group. (*C*) Polyphyletic group. A grouping of lineages each more closely related to other species not in the group than they are to each other.

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Sister Taxa
Relatedness

Sequence Alignment

FIGURE 5.16. Example of a multiple sequence alignment, showing alignment of a portion of the RecA proteins from different bacterial species. Amino acids conserved across most or all of the species are highlighted in *red*. *Letters* are the abbreviations of different amino acids (see Fig. 2.23).

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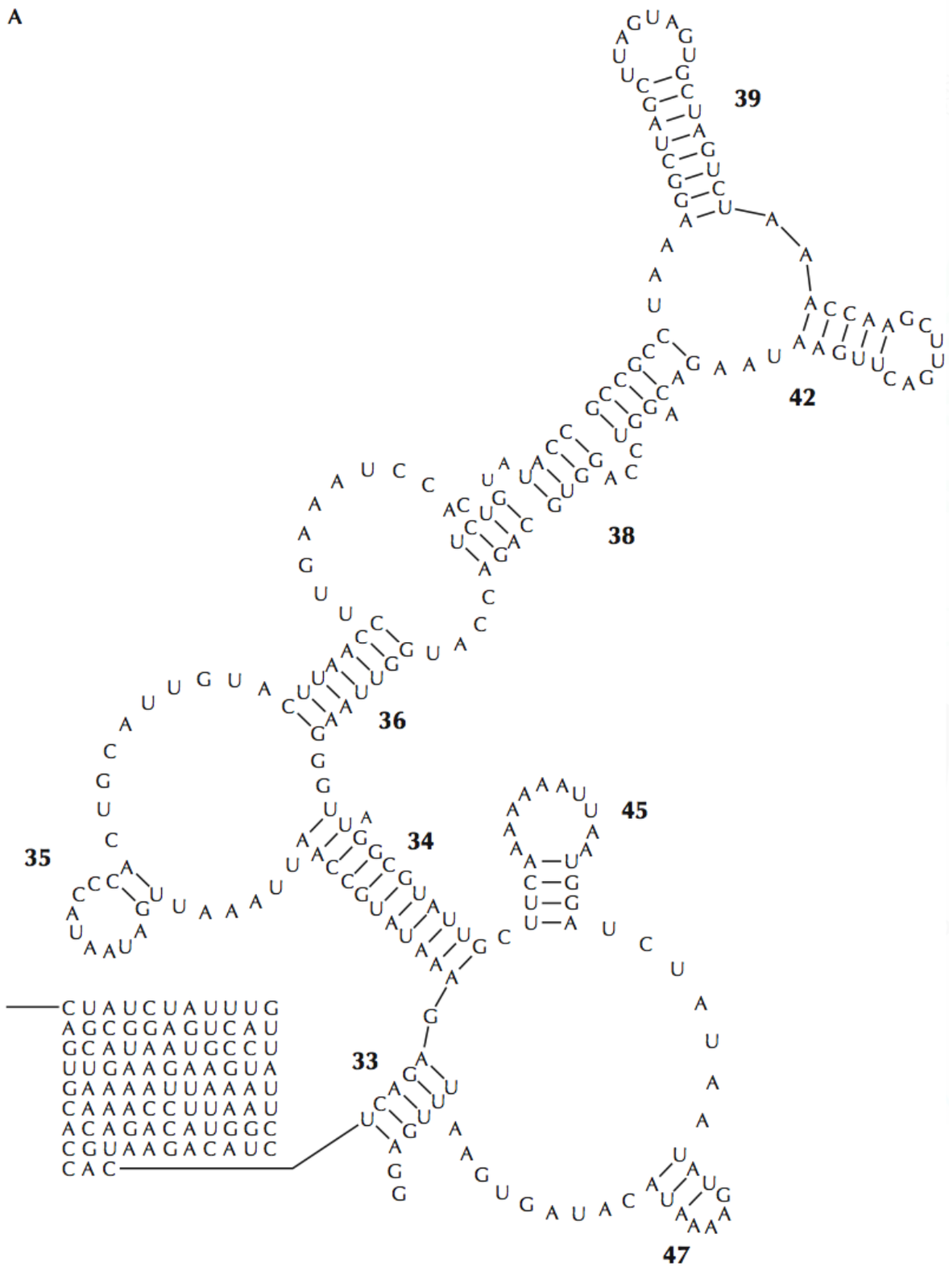
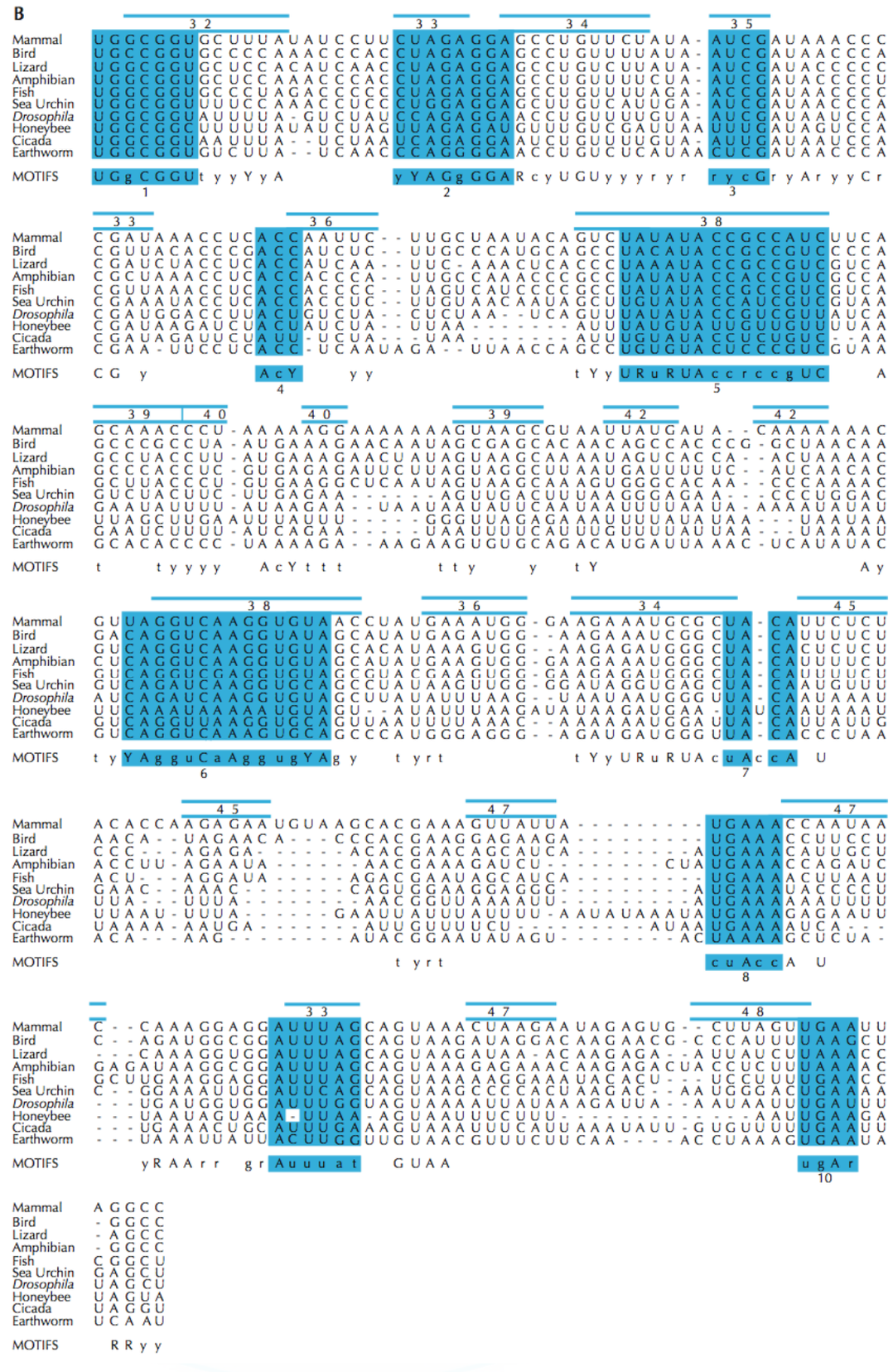
Structure Guided Alignment





Tree reconstruction methods

TABLE 27.4. Molecular phylogenetic methods

Method	Description
Parsimony	Possible trees are compared and each is given a score that is a reflection of the minimum number of character state changes (e.g., amino acid substitutions) that would be required over evolutionary time to fit the sequences into that tree. The optimal tree is considered to be the one requiring the fewest changes (the most parsimonious tree).
Distance	The optimal tree is generated by first calculating the estimated evolutionary distance between all pairs of sequences. These distances are then used to generate a tree in which the branch patterns and lengths best represent the distance matrix.
Maximum likelihood	This method is similar to parsimony methods in that possible trees are compared and given a score. The score is based on how likely the given sequences are to have evolved in a particular tree given a model of amino acid or nucleotide substitution probabilities. The optimal tree is considered to be the one that has the highest probability.
Bayesian	A variant of maximum likelihood in which the likelihood of a tree itself is calculated.

Based on Table 3 in Eisen J.A. 1998. Phylogenomics: Improving functional predictions for uncharacterized genes by evolutionary analysis. *Genome Res.* **8**:163–167.

Distance Phylogenetics

- Calculate distances between taxa
- Use an algorithm to infer a tree from those distances
- Based on principle that divergence occurs after organisms separate

Parimony Phylogenetics

- Based on Principle of Parsimony / Occam's Razor
- Possible trees are given a score of the fewest number of sequence changes required to fit data into tree
- Score for all possible trees
-

Likelihood Phylogenetics

- Based on Bayes' Theorem
- Trying to calculate the Probability of the Data, Given a Hypothesis
- For each tree, calculate probability that the data (e.g., sequence alignment) could come from that tree
- Score for all possible trees

- Prob($H|D$) = Prob(H and D) ÷ Prob(D)
- Prob($H|D$) = **Prob($D|H$)** x Prob(H) ÷ Prob(D)

Bayesian Phylogenetics

- Based on Bayes' Theorem
- Trying to calculate the Probability of the Hypothesis, Given the Data
- For each tree, calculate probability that the tree could come from that data ((e.g., sequence alignment)
- Score for all possible trees

- Prob($H|D$) = Prob(H and D) ÷ Prob(D)
- **Prob($H|D$)** = $\underline{\text{Prob}(D|H)}$ x Prob(H) ÷ Prob(D)

Bayesian

- Based on Bayes' Theorem
- Prob(H|D) = Prob(H and D) ÷ Prob(D)

- **Prob(H|D)** = Prob(D|H) x Prob(H) ÷ Prob(D)

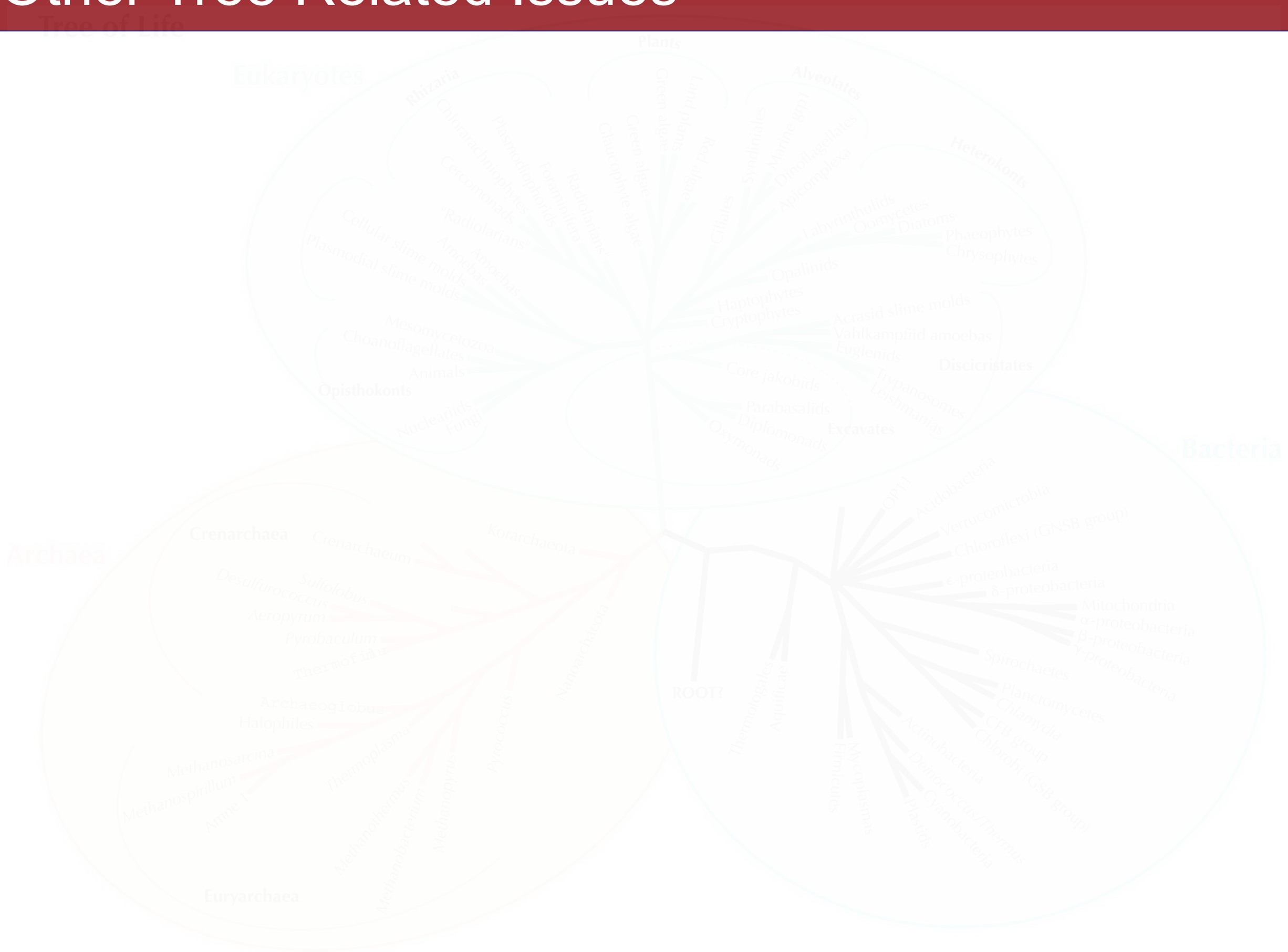
Many possible trees

TABLE 27.5. Number of possible branching patterns versus number of OTUs

Taxa	Rooted Trees[a]	Unrooted Trees[b]
3	3	1
4	15	3
5	105	15
6	945	105
7	10,395	945
8	135,135	10,395
9	2,027,025	135,135
10	34,459,425	2,027,025

[a] $N_r = (2n - 3) \times (2n - 5) \times (2n - 7) \times \cdots \times 3 \times 1 = (2n - 3)!/[2_{n-2} \times (n - 2)!]$.
[b] $N_u = (2n - 3) \times (2n - 5) \times (2n - 7) \times \cdots \times 3 \times 1 = (2n - 5)!/[2_{n-3} \times (n - 3)!]$.

Other Tree Related Issues



Bootstrapping

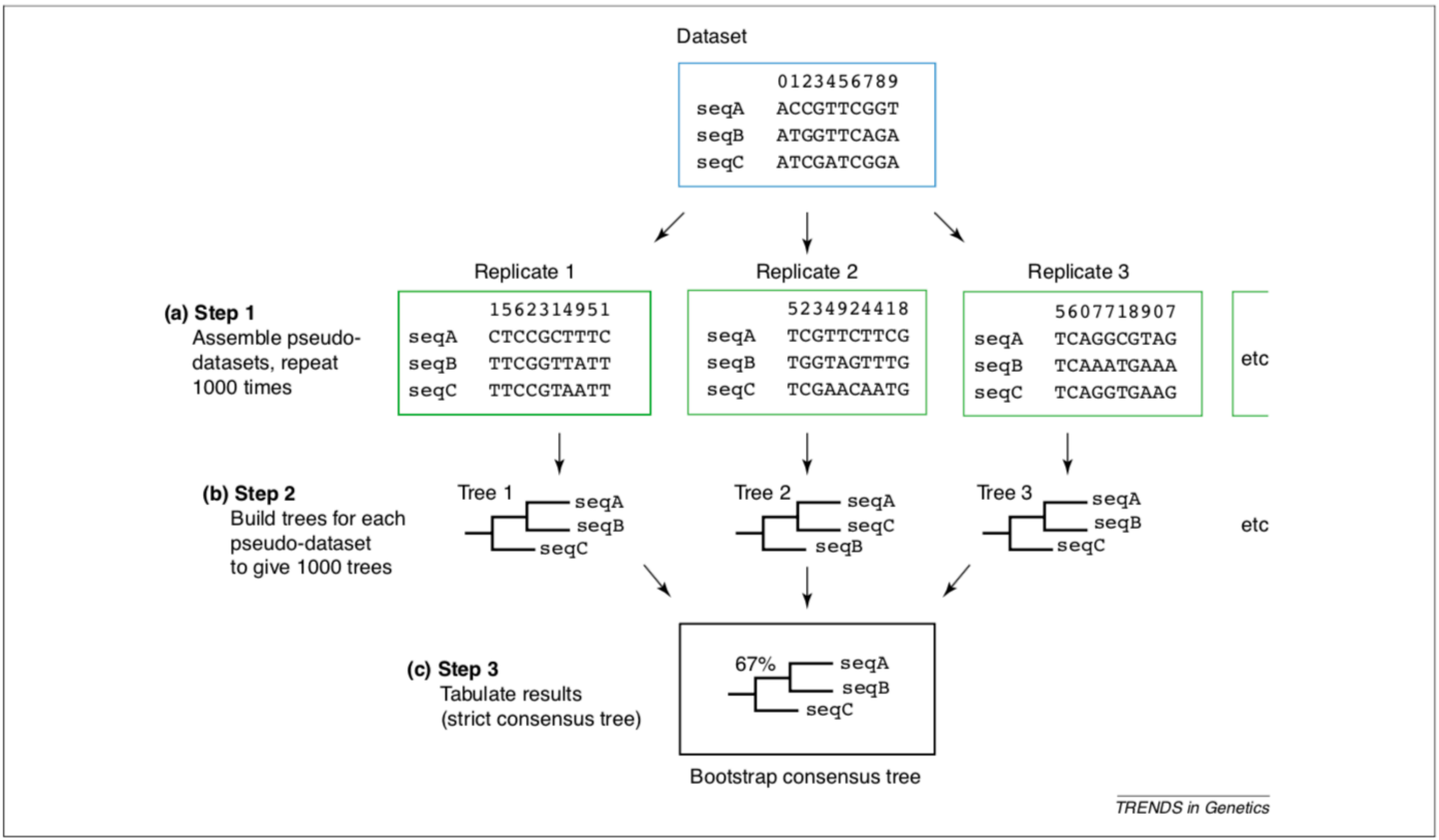


Fig. 6. Bootstrap analysis proceeds in three steps. The dataset is randomly sampled with replacement to create multiple pseudo-datasets of the same size as the original ((a), three are shown in this example). (b) Individual trees are constructed from each of the pseudo-datasets. (c) Each of the pseudo-dataset trees are scored for which nodes (groupings) appear and how often. In this case, a node uniting seqA plus seqB is found in two of the three replicate trees. This gives a bootstrap support for this grouping of 2/3 or 67%.

Bootstrapping

A Bootstrapping

Alignment of sequences

```
Species  1    ATGTTGGATGGTGAT
Species  2    ATGTTGGAAGGAGAA
Species  3    ATGTTAGGAGAAGAA
Species  4    ATGTCAGCAGCCGCC
```

Bootstrapping alignment #1

```
Species  1    ATGTTGGAGGGTAAT
Species  2    ATGTTGGAGGGAAAA
Species  3    ATGTTAGGGGAAAAA
Species  4    ATGTCAGCGGCCCCC
```

Bootstrapping alignment #2

```
Species  1    ATGGGGGATGGTGAT
Species  2    ATGGGGGAAGGAGAA
Species  3    ATGGGAGGAGAAGAA
Species  4    ATGGGAGCAGCCGCC
```

Jacknifing

B Jackknifing

Alignment of sequences

```
Species  1        ATGTTGGATGGTGAT
Species  2        ATGTTGGAAGGAGAA
Species  3        ATGTTAGGAGAAGAA
Species  4        ATGTCAGCAGCCGCC
```

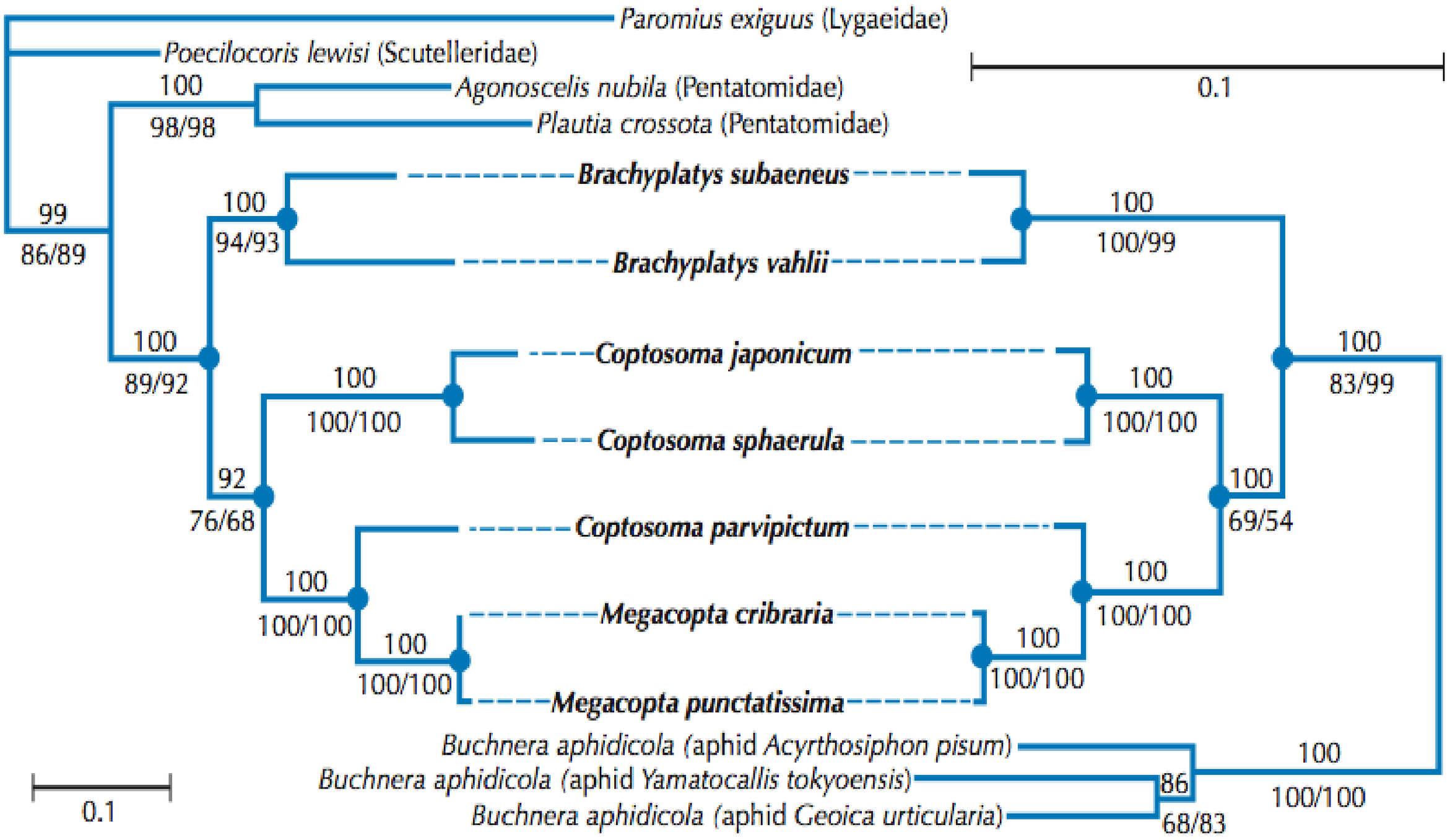
Jackknifed alignment 1 (10 columns kept)

```
Species  1        AT-T-GGA-GG-GA-
Species  2        AT-T-GGA-GG-GA-
Species  3        AT-T-AGG-GA-GA-
Species  4        AT-T-AGC-GC-GC-
```

Jackknifed alignment 2 (10 columns kept)

```
Species  1        --GTTGG--GGT-AT
Species  2        --GTTGG--GGA-AA
Species  3        --GTTAG--GAA-AA
Species  4        --GTCAG--GCC-CC
```

Congruence


Paromius exiguus (Lygaeidae)
Poecilocoris lewisi (Scutelleridae)
Agonoscelis nubila (Pentatomidae)
Plautia crossota (Pentatomidae)
0.1
Brachyplatys subaeneus
Brachyplatys vahlii
Coptosoma japonicum
Coptosoma sphaerula
Coptosoma parvipictum
Megacopta cribraria
Megacopta punctatissima
Buchnera aphidicola (aphid Acyrthosiphon pisum)
Buchnera aphidicola (aphid Yamatocallis tokyoensis)
Buchnera aphidicola (aphid Geoica urticularia)
100
98/98
99
86/89
100
94/93
100
89/92
100
100/100
92
76/68
100
100/100
100
100/100
100
100/99
100
100/100
100
69/54
100
100/100
100
100/100
100
83/99
86
68/83
100
100/100
0.1

Masking

A

```
Protein  1    DEMGLGKK----R--VESTR
Protein  2    DEMGVGKRGH-----LESRK
Protein  3    DDMGLGRWK---R--VESTE
Protein  4    DDMGLGHKKKK-----VDSTK
Mask          11111111100000011111
```

B

```
Protein  1    DEMGLGKKKVESTR
Protein  2    DEMGVGKRLESRK
Protein  3    DDMGLGRKVESTE
Protein  4    DDMGLGHKVDSTK
```

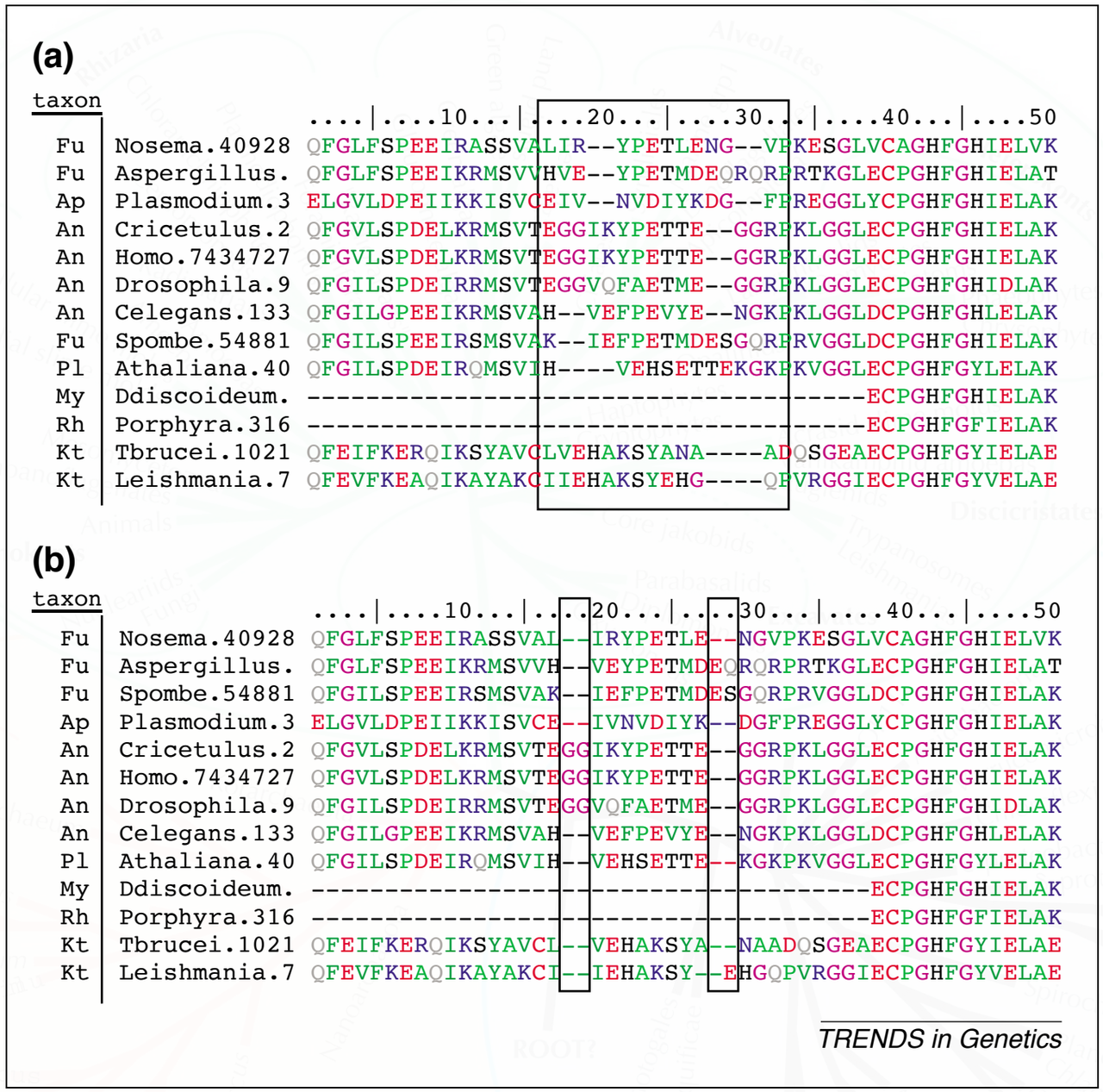
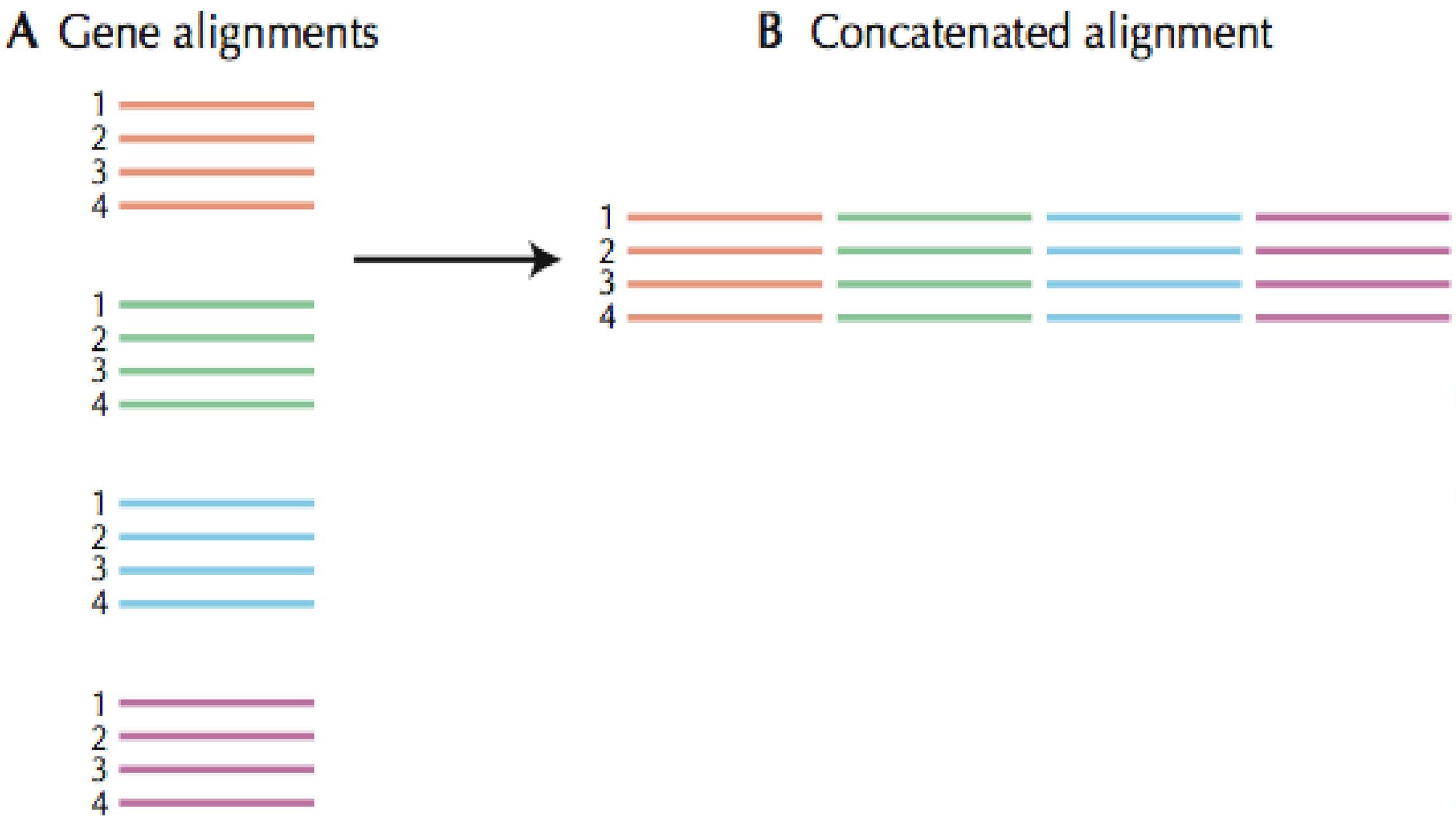


Fig. 5. Refining an alignment. (a) The raw output from a ClustalX alignment of rpb1 sequences, which predicts six insertion/deletion events (boxed), some of which are blatantly inconsistent with known taxonomy. (b) The refined alignment makes much better evolutionary sense, because it shows only two insertion events in well-defined taxonomic groups (animals and higher fungi). Taxon labels are Fu (fungi), An (animals), Pl (green plant), Ap (apicomplexan), Rh (rhodophyte), My (mycetozoan), Kt (kinetoplastids). In (b), the sequence from *Saccharomyces pombe* has been placed adjacent to the other fungi to make these relationships more obvious.

Concatenation



Homoplasy

A

Sequence 1 G A C G A G
Sequence 2 G C C G A C

B

Sequence 1 G A C G A G

↑ G → A at position 5

G A C G G G

↑ G → A at position 2

G G C G G G

Sequence 2 G C C G A C

↑ C → A at position 5

G C C G C C

↑ G → C at position 5

G → C at position 6

G C C G G G } Ancestral sequences

Orthologs and Paralogs

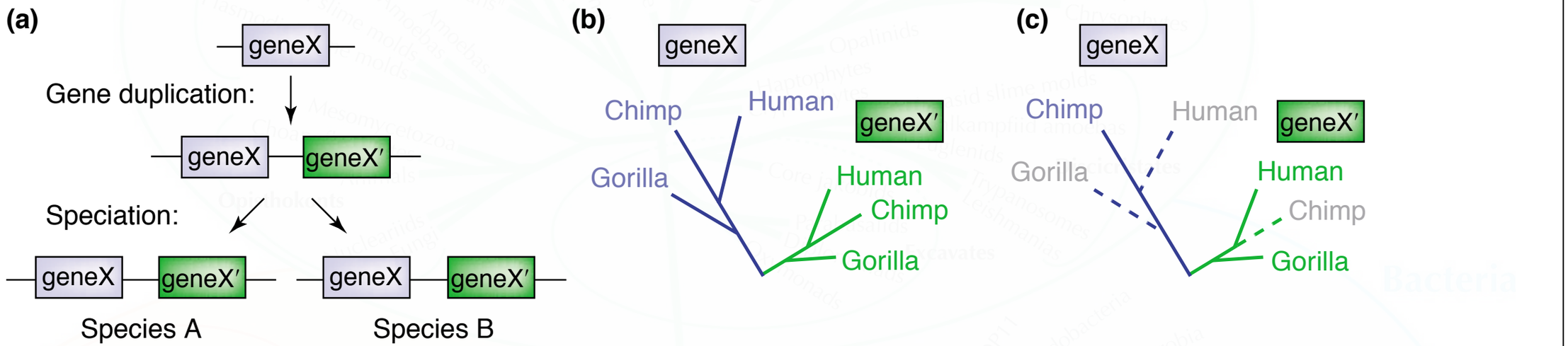
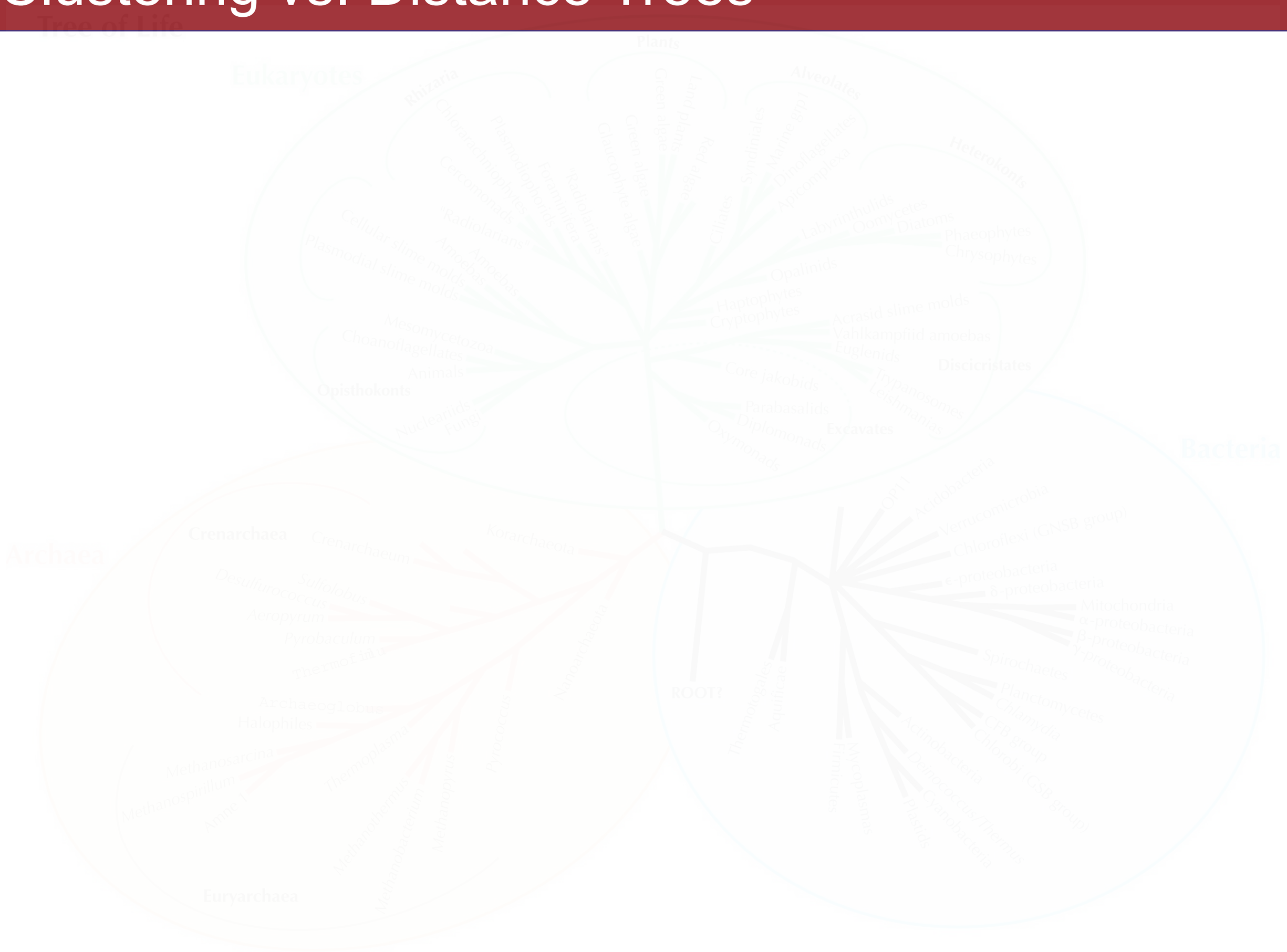


Fig. 3. The problem with paralogues. (a) Paralogous genes are created by gene duplication events. Gene X is duplicated in a common ancestor to species A and B resulting in two paralogous genes, X and X′. All subsequent species inherit both copies of the gene (unless one or the other is lost somewhere along the way). (b) Phylogenetic analysis of the X/X′ gene family gives two parallel phylogenies. All sequences of gene X are orthologues of each other, and all the sequences of gene X′ are orthologues of each other. However, X and X′ are paralogues. Both the X and X′ subtrees show the true relationships among the three species. The subtrees are also each other's natural outgroup, and as a result each subtree is rooted with the other (reciprocally rooting). (c) A tree of the X/X′ gene family can be misleading if not all the sequences are included (because of incomplete sampling or gene loss). If the broken branches are missing, then the true species relationships are misrepresented.

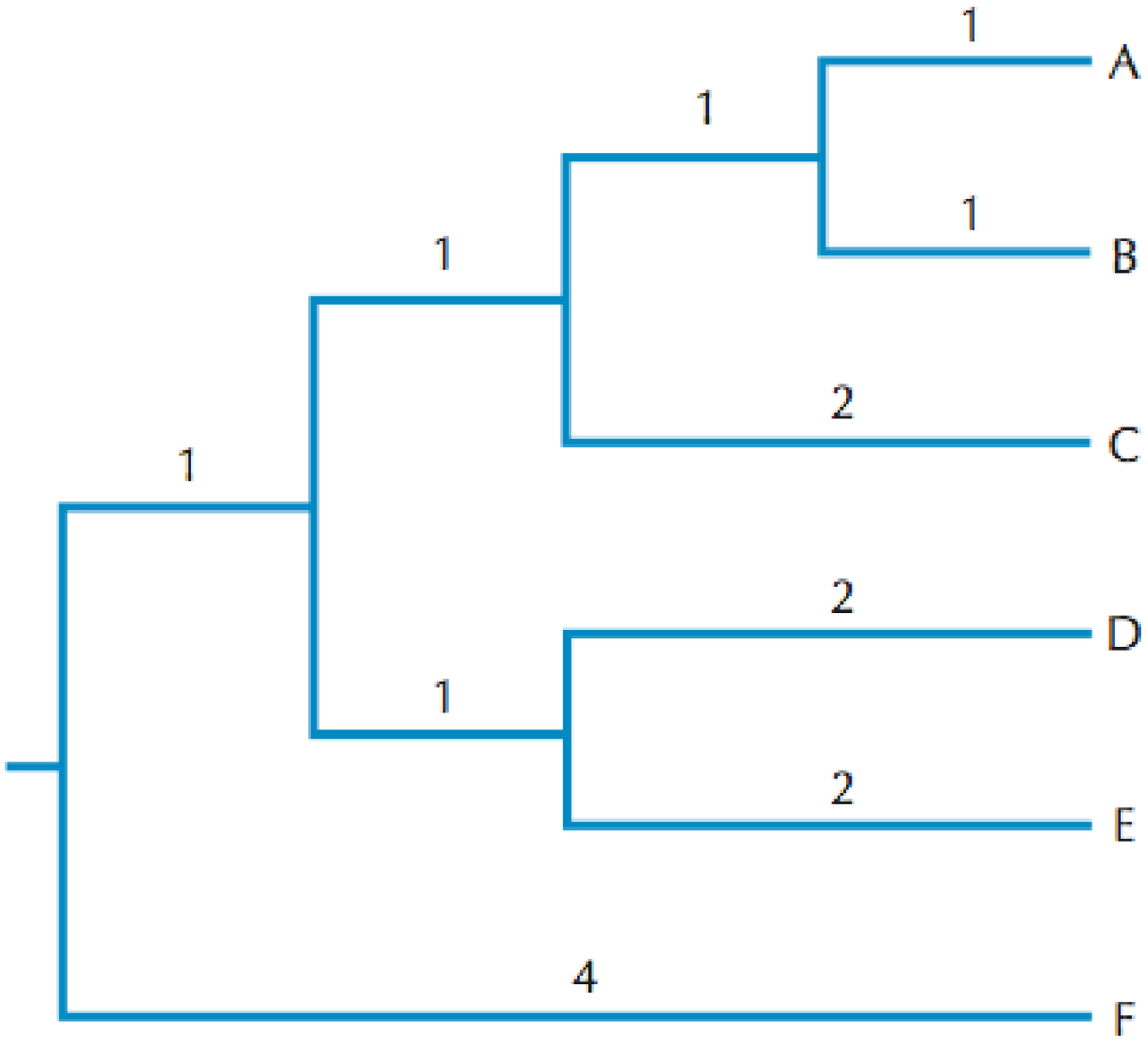
Clustering vs. Distance Trees



UPGMA

Unweighted **P**air **G**roup **M**ethod with **A**rithmetic mean (UPGMA) algorithm

The True Tree



Distance Matrix For True Tree

TABLE 27.6. Distance matrix

OTUs	A	B	C	D	E	F
A	0	2	4	6	6	8
B	2	0	4	6	6	8
C	4	4	0	6	6	8
D	6	6	6	0	4	8
E	6	6	6	4	0	8
F	8	8	8	8	8	0

Collapse Diagonal

TABLE 27.7. Diagonal matrix—Step 1

OTUs	A	B	C	D	E
B	2				
C	4	4			
D	6	6	6		
E	6	6	6	4	
F	8	8	8	8	8

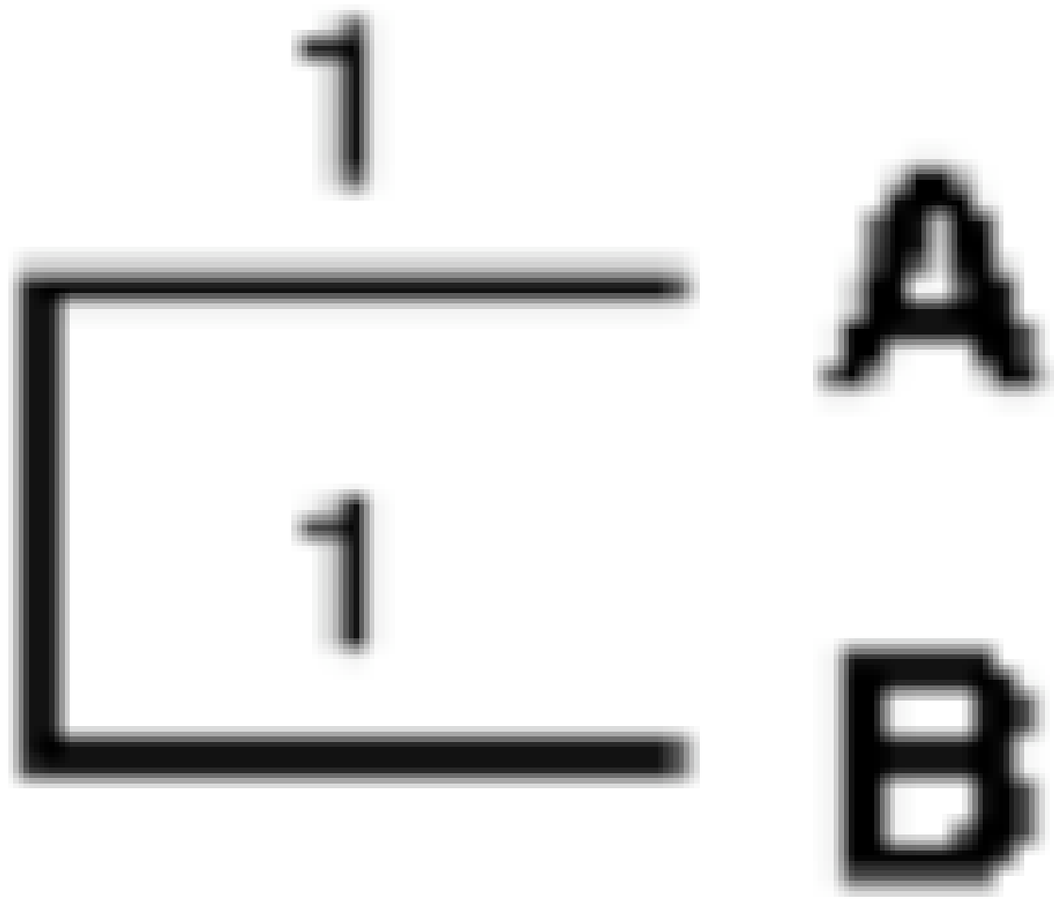
Identify Lowest D

OTUs	A	B	C	D	E
B	**2**				
C	4	4			
D	6	6	6		
E	6	6	6	4	
F	8	8	8	8	8

Join Those Two Taxa

- Create branch with length = D
- 2
- A----------B

Make D from Node Equal



Create New Distance Matrix

- Merge Two OTUs joined in previous step (AB)

- $D_{x,AB} = 0.5 * (D_{x,A} + D_{x,B})$

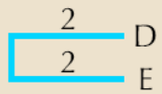
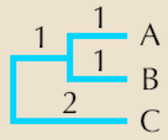
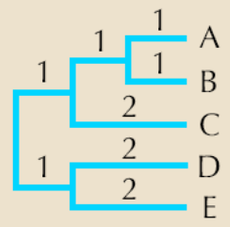
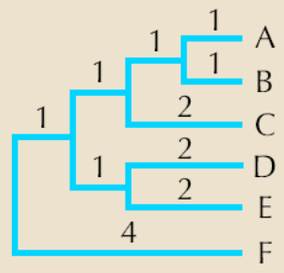
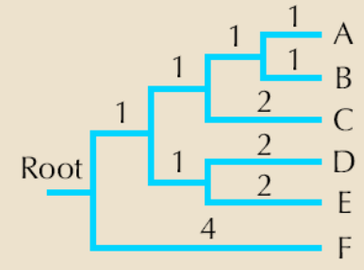
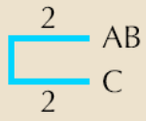
New Matrix

TABLE 27.8. Diagonal matrix—Step 2

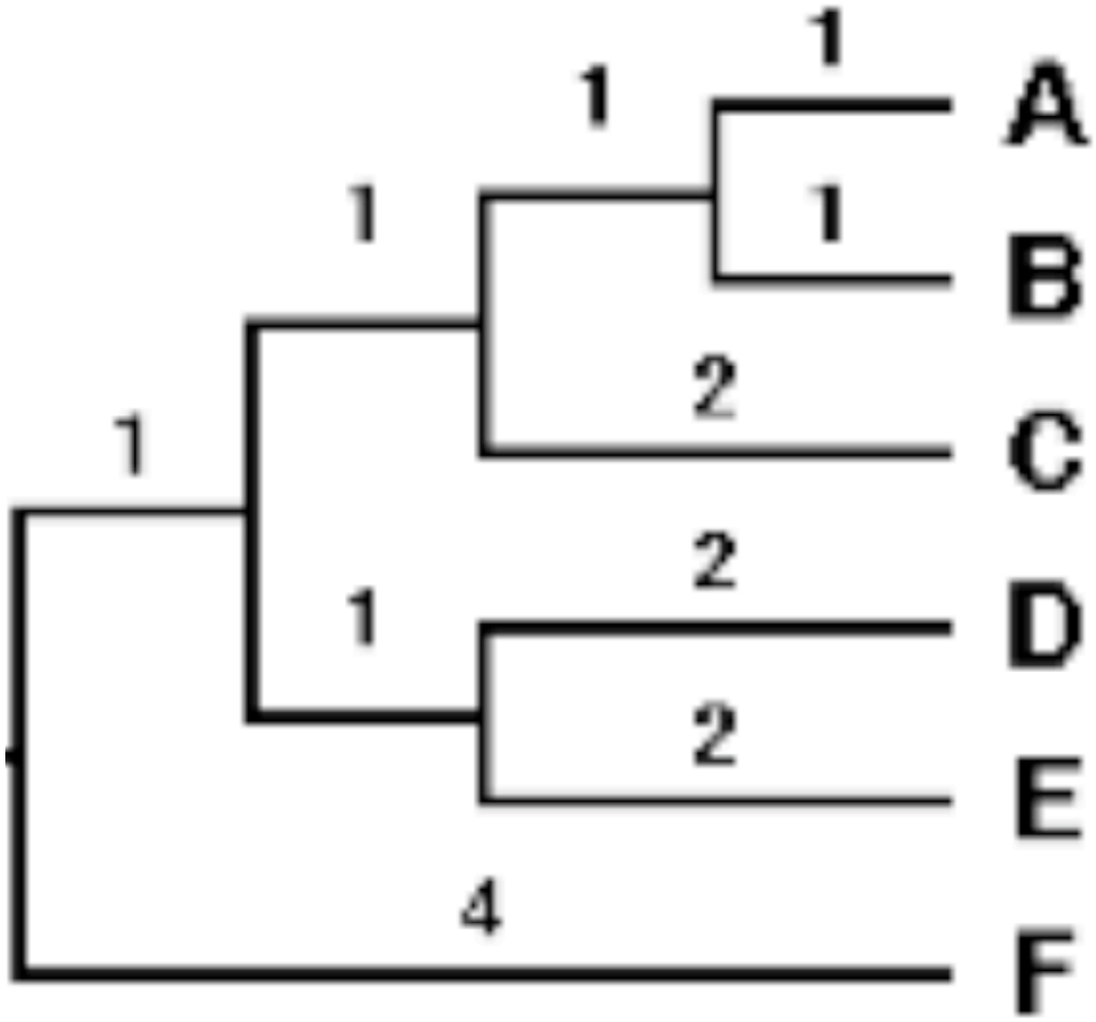
OTUs	AB	C	D	E
C	4			
D	6	6		
E	6	6	4	
F	8	8	8	8

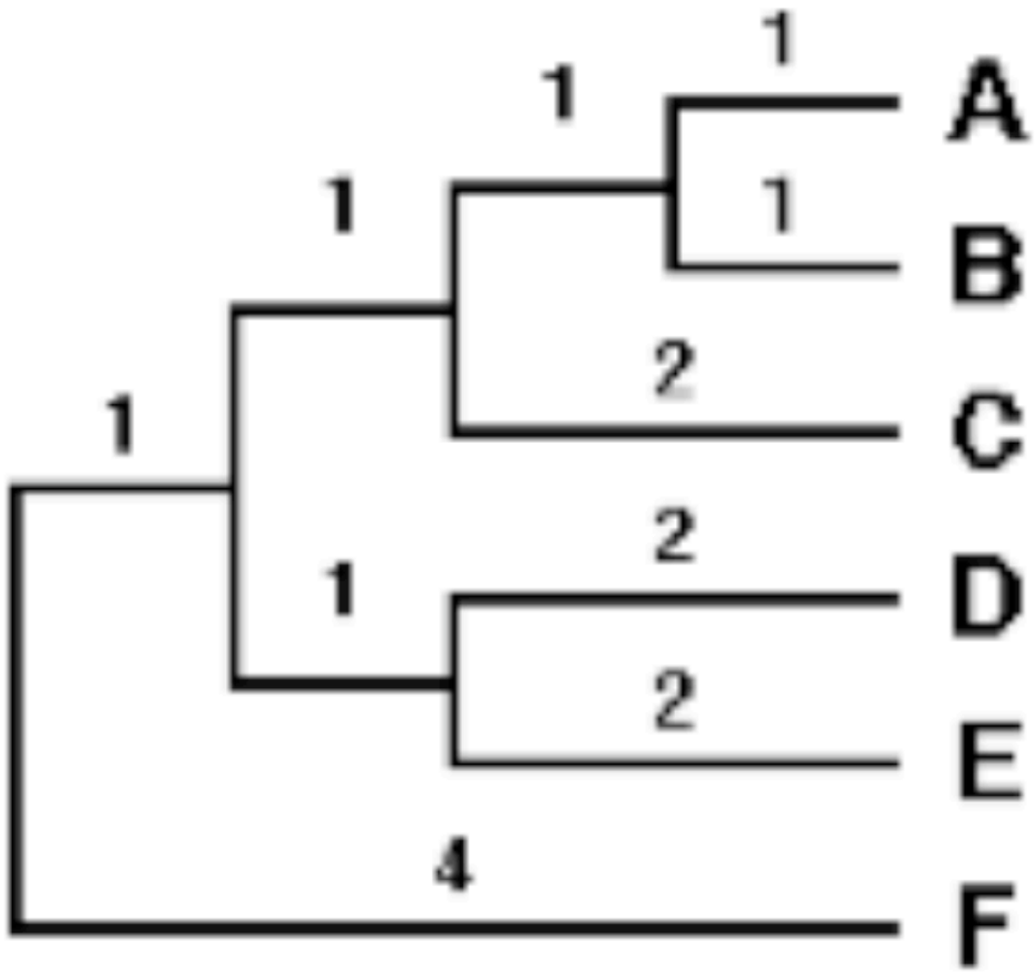
UPGMA

TABLE 27.9. Example of UPGMA tree construction

Step	Cycle 1	Cycle 2	Cycle 3	Cycle 4	Cycle 5	Cycle 6
Distance matrix	OTUs | A B C D E B | 2 C | 4 4 D | 6 6 6 E | 6 6 6 4 F | 8 8 8 8 8	OTUs | AB C D E C | 4 D | 6 6 E | 6 6 4 F | 8 8 8 8	OTUs | AB C DE C | 4 DE | 6 6 DE | 8 8 8	OTUs | ABC DE DE | 6 F | 8 8	OTUs | ABCDE F | 8	No new matrix
Identify smallest D	A↔B = 2 D↔E= 4	AB↔C = 4 C↔DE = 6	AB↔DE = 6	ABC↔DE	ABCDE↔F	
Taxa joined	A and B	D and E	AB and C	ABC and DE	ABCDE and F	
Subtree						
Comments on tree drawing	The distance between A and B is 2 units. A subtree is drawn with the branch point halfway between the two. Thus, each branch is 1 unit in length.	Branching done as in Step 1. Because the distance from AB to C is also 4, that pair could have been selected as well.	First a subtree is drawn with AB and C:  The the AB subtree is attached to the AB branch at a point equal to the length of the A and B branches.	The tree is first done as in Step 3 with the ABC and DE subtrees replacing the branches.	The tree is now complete but unrooted.	The tree can then be rooted using midpoint rooting which tries to balance all the tips to reach the same end point. Note this is the tree that we started with to build the distance matrix.

Compare to True Tree

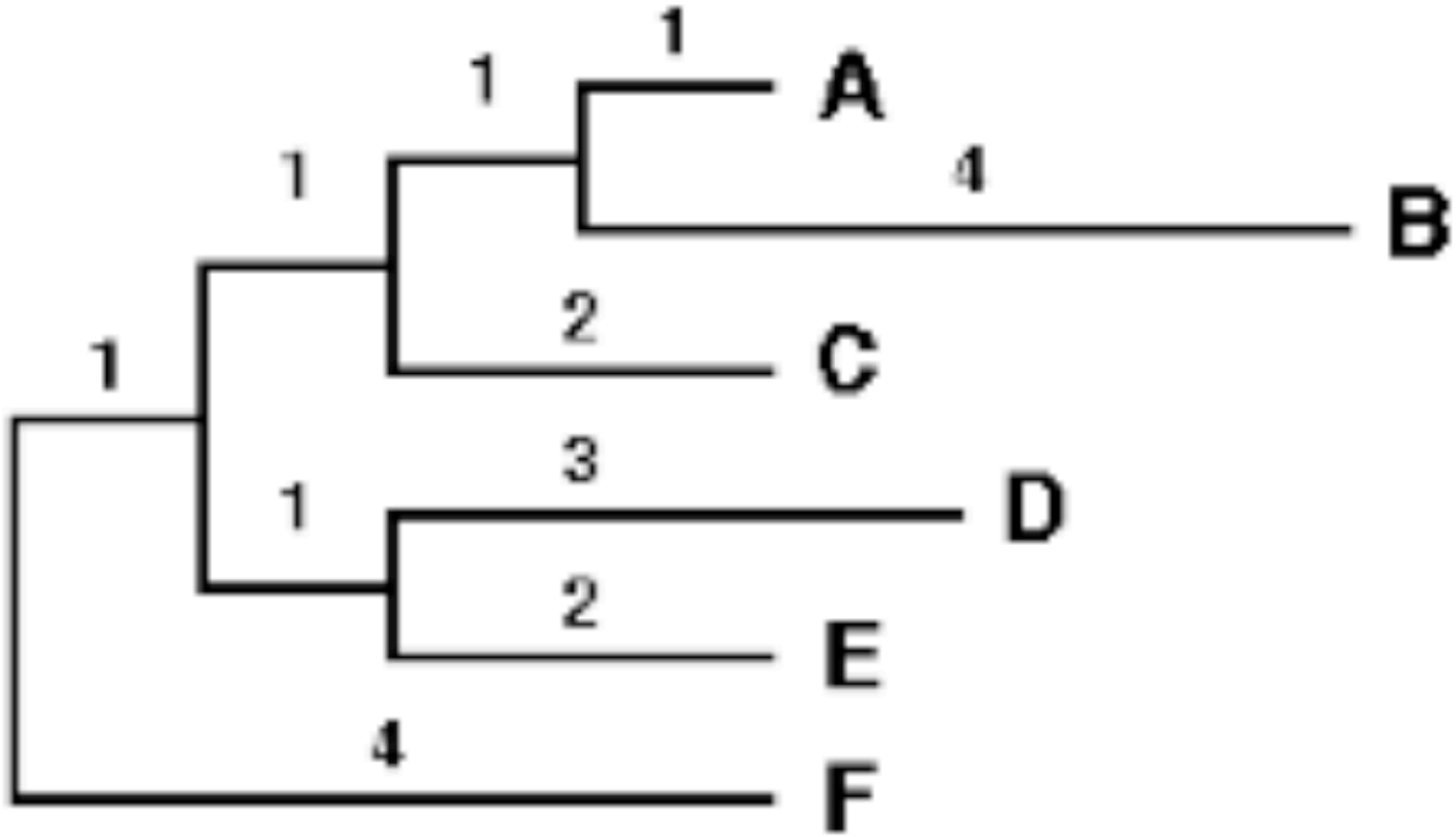




But …

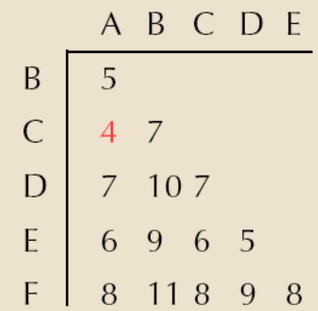
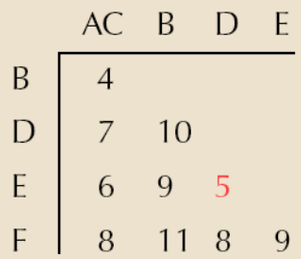
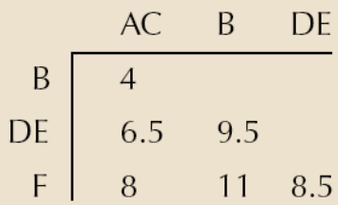
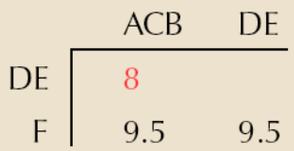
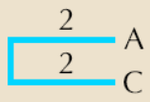
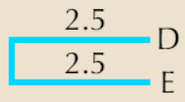
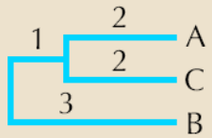
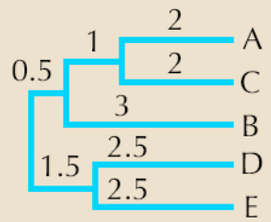
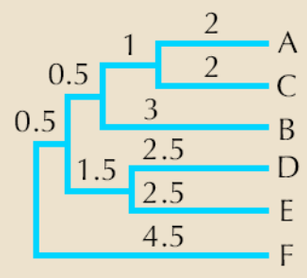
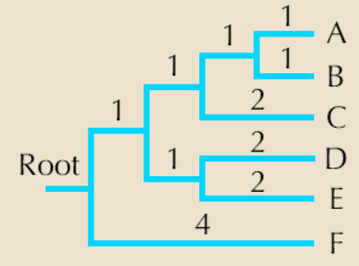
- What is evolutionary rates not equal

Unequal rates

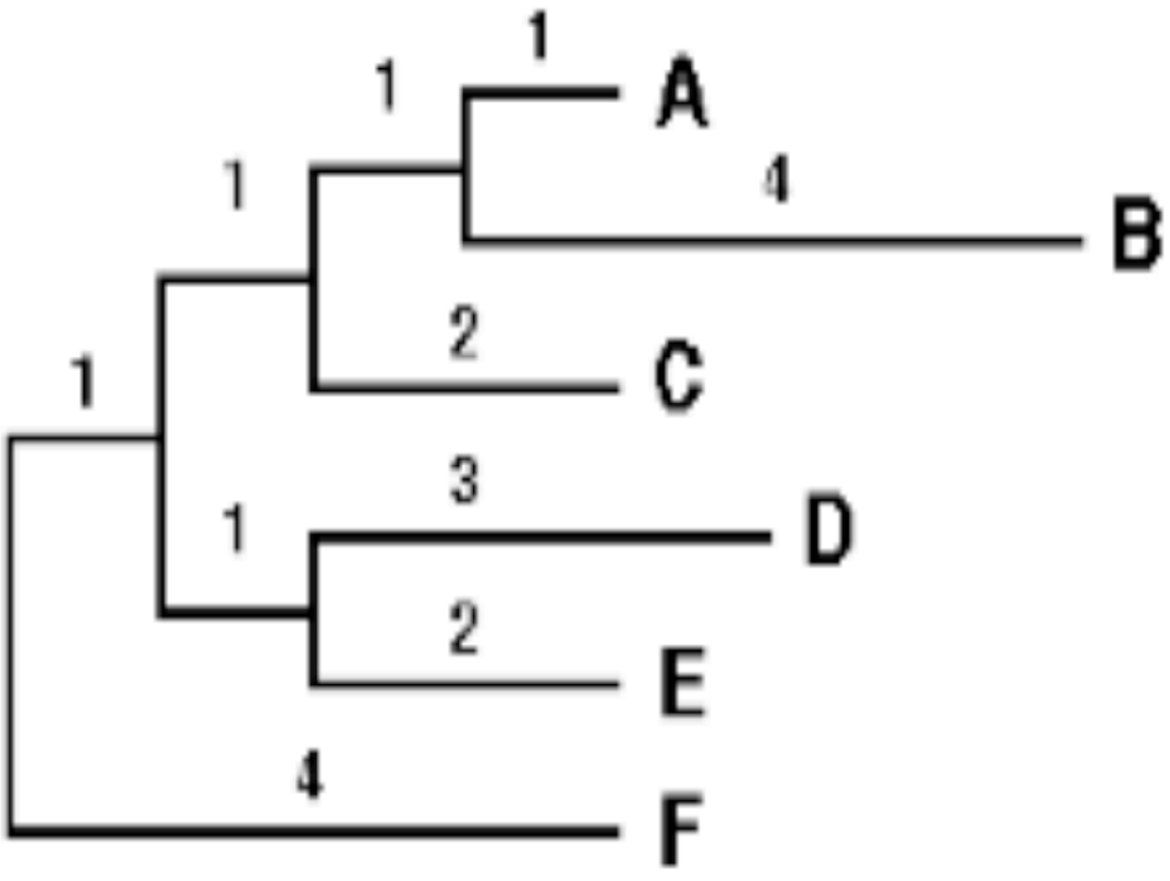


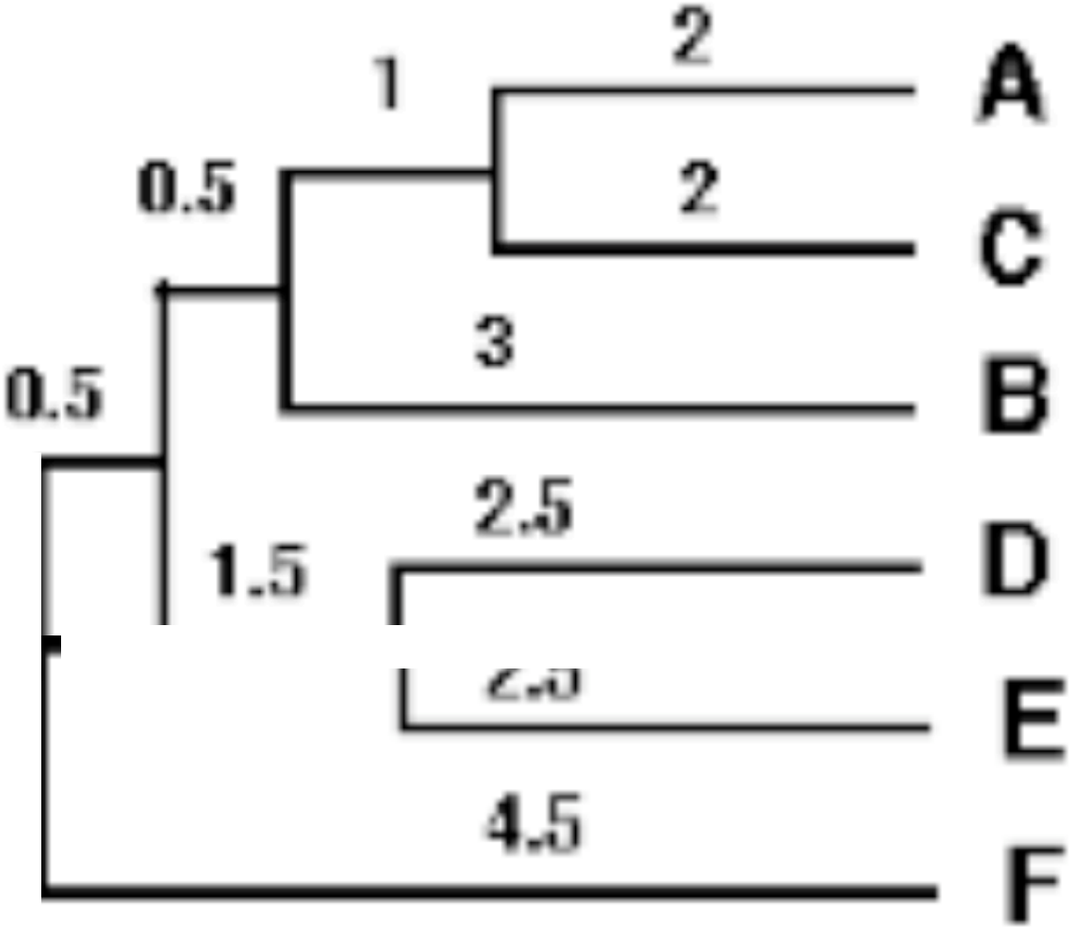
UPGMA with Unequal rates

TABLE 27.10. UPGMA tree construction errors

	Cycle 1	Cycle 2	Cycle 3	Cycle 4	Cycle 5	Cycle 6
Distance matrix						No new matrix
Identify smallest D	A↔C = 4	D↔E = 5	AC↔B = 4	ACB↔DF = 8	ABCDE↔F = 9	
Taxa joined	A and C	D and E	A and C with B	ABC with DE	ABCDE with F	
Subtree						
Comments					Note how this is not the same as the starting tree.	

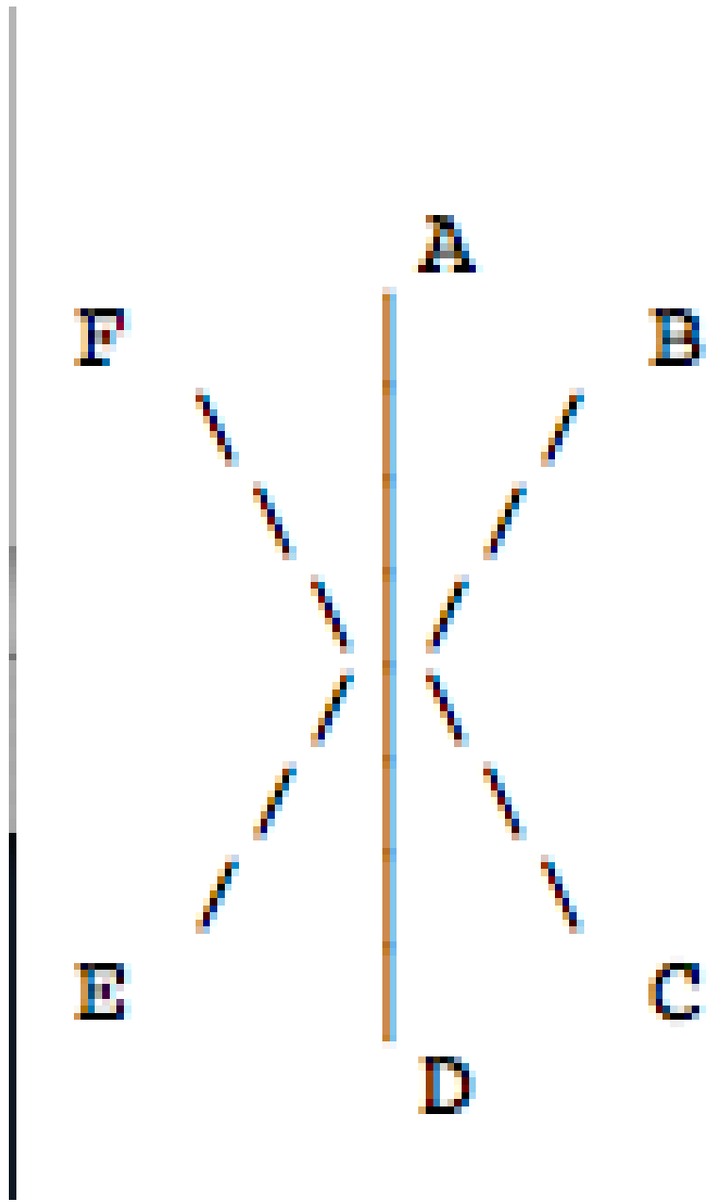
Compare to True Tree





Neighbor Joining

Start with Star Tree



Calculate S

- For each OTU, calculate a measure (S) as follows.
- S is the sum of the distances (D) between that OTU and every other OTU, divided by N-2 where N is the total number of OTUs.
- This is a measure of the distance an OTU is from all other OTUs

Calculate Pairwise Distances

- Calculate the distance D_{ij} between each OTU pair (e.g., I and J).

Identify Closest Pair

- Identify the pair of OTUs with the minimum value of $D_{ij} - S_i - S_j$

Joining Taxa

- As in UPGMA, join these two taxa at a node in a subtree.

Calculate Branches

- Calculate branch lengths. Unlike UPGMA, neighbor joining does not force the branch lengths from node X to I (D_{xi}) and to J (D_{xj}) to be equal, i.e., does not force the rate of change in those branches to be equal. Instead, these distances are calculated according to the following formulas
- $D_{xi} = 1/2\ D_{ij} + 1/2\ (S_i - S_j)$
- $D_{xj} = 1/2\ D_{ij} + 1/2\ (S_j - S_i)$

Calculate New Matrix

- Calculate a new distance matrix with I and J merged and replaced by the node (X) that joins them. Calculate the distances from this node to the other tips (K) by:

- $D_{xk} = (D_{ik} + D_{jk} - D_{ij})/2$

Distance Matrix

	A	B	C	D	E
B	5				
C	4	7			
D	7	10	7		
E	6	9	6	5	
F	8	11	8	9	8

S

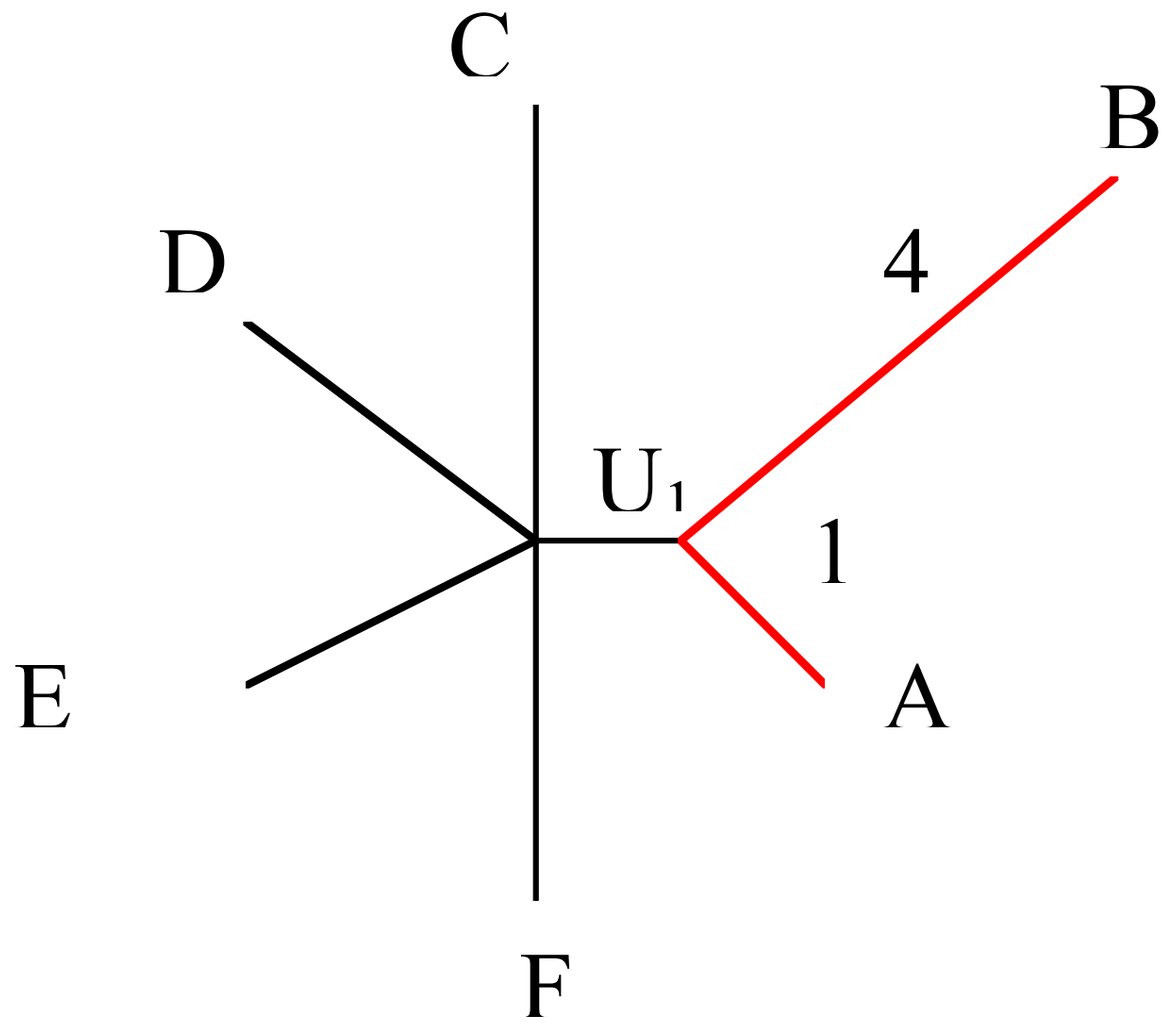
- $S_A = (5+4+7+6+8) / 4 =$ 7.5
- $S_B = (5+7+10+9+11) / 4 =$ 10.5
- $S_C = (4+7+7+6+8) / 4 =$ 8
- $S_D = (7+10+7+5+9) / 4 =$ 9.5
- $S_E = (6+9+6+5+8) / 4 =$ 8.5
- $S_F = (8+11+8+9+8) / 4 =$ 11

M

- $M_{ij} = D_{ij} - S_i - S_j$
- Smallest are
- $M_{AB} = 5 - 7.5 - 10.5 = -13$
- $M_{DE} = 5 - 9.5 - 8.5 = -13$
- Choose one of these (AB here)

New Tree

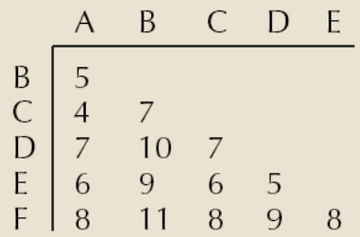
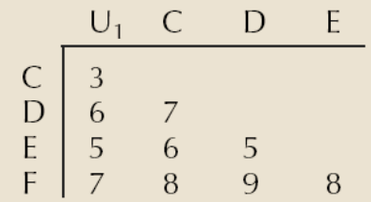
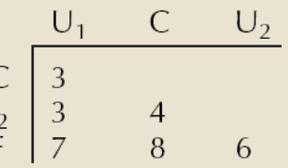
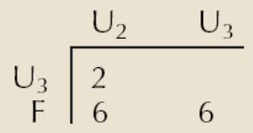
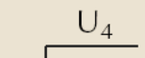
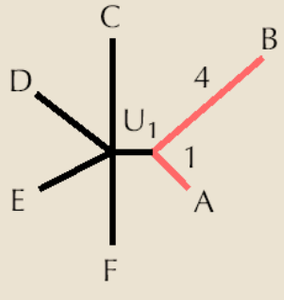
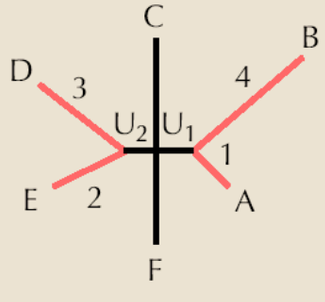
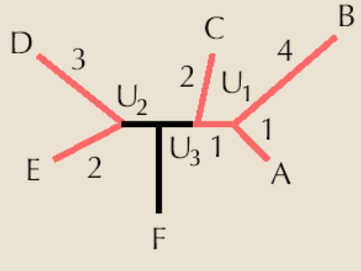
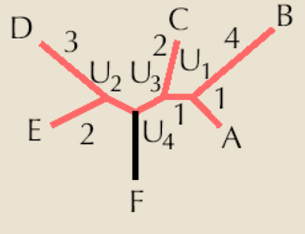
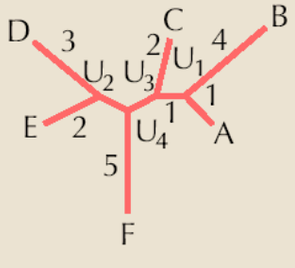
- Create a node (U) that joins pair with lowest M_{ij} such that
- $S_{IU} = D_{IJ}/2 + (S_I - S_J) / 2$
- Merge U with other taxa
- Join I and J according to S above and make all other taxa in form of a star


C
B
D
4
U_1
1
E
A
F

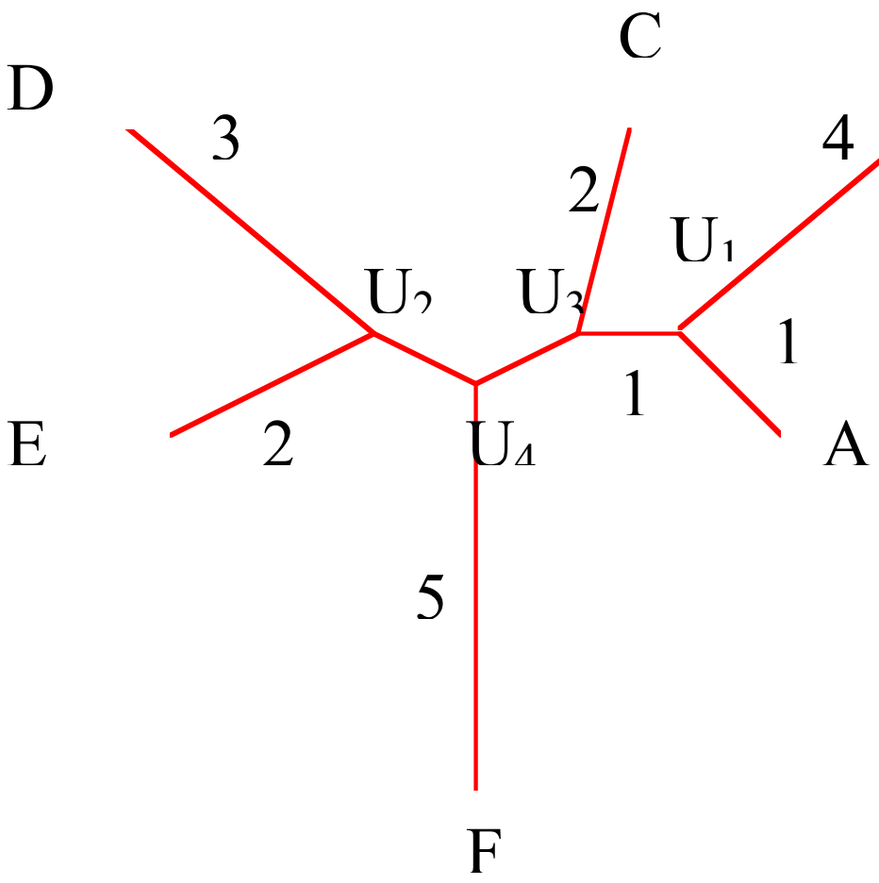
New Matrix

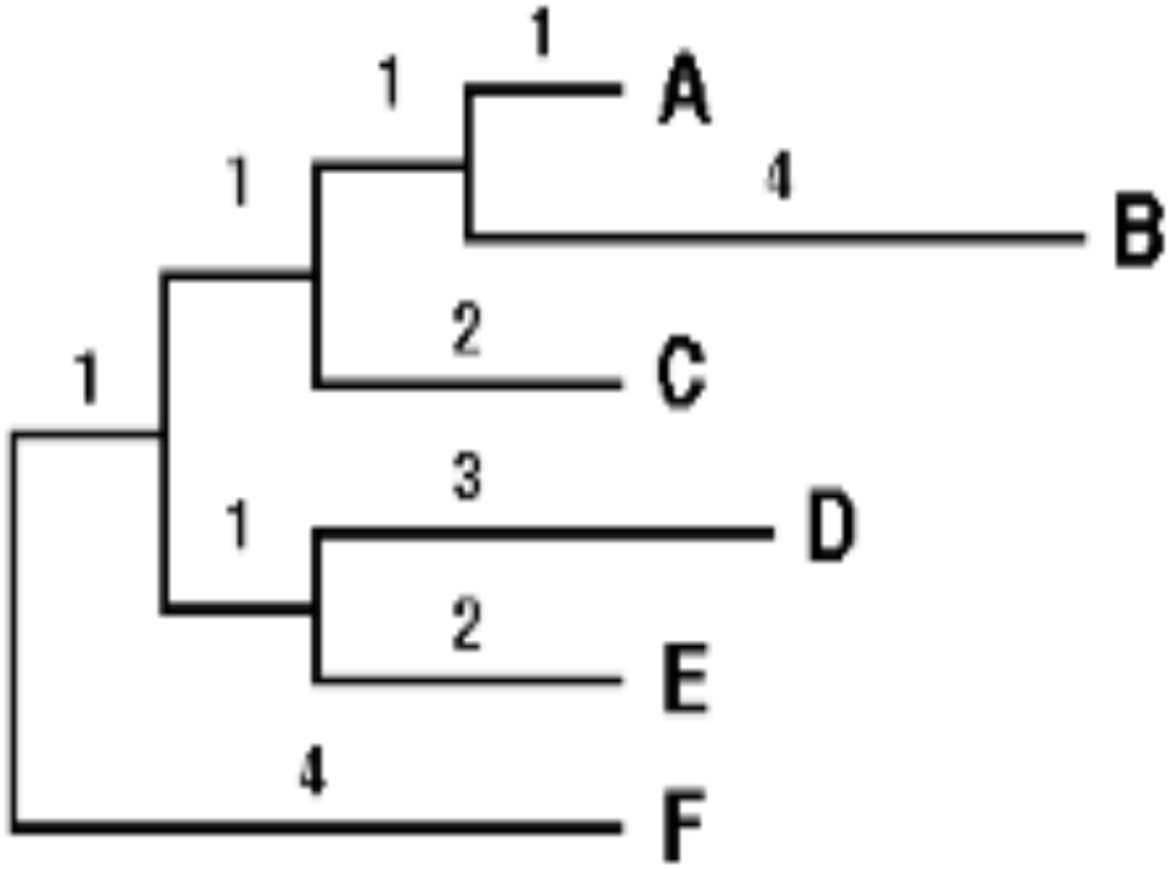
- $D_{XU} = D_{IX} + D_{JX} - D_{IJ}$ where I and J are those selected from above.

TABLE 27.11. Neighbor-joining example

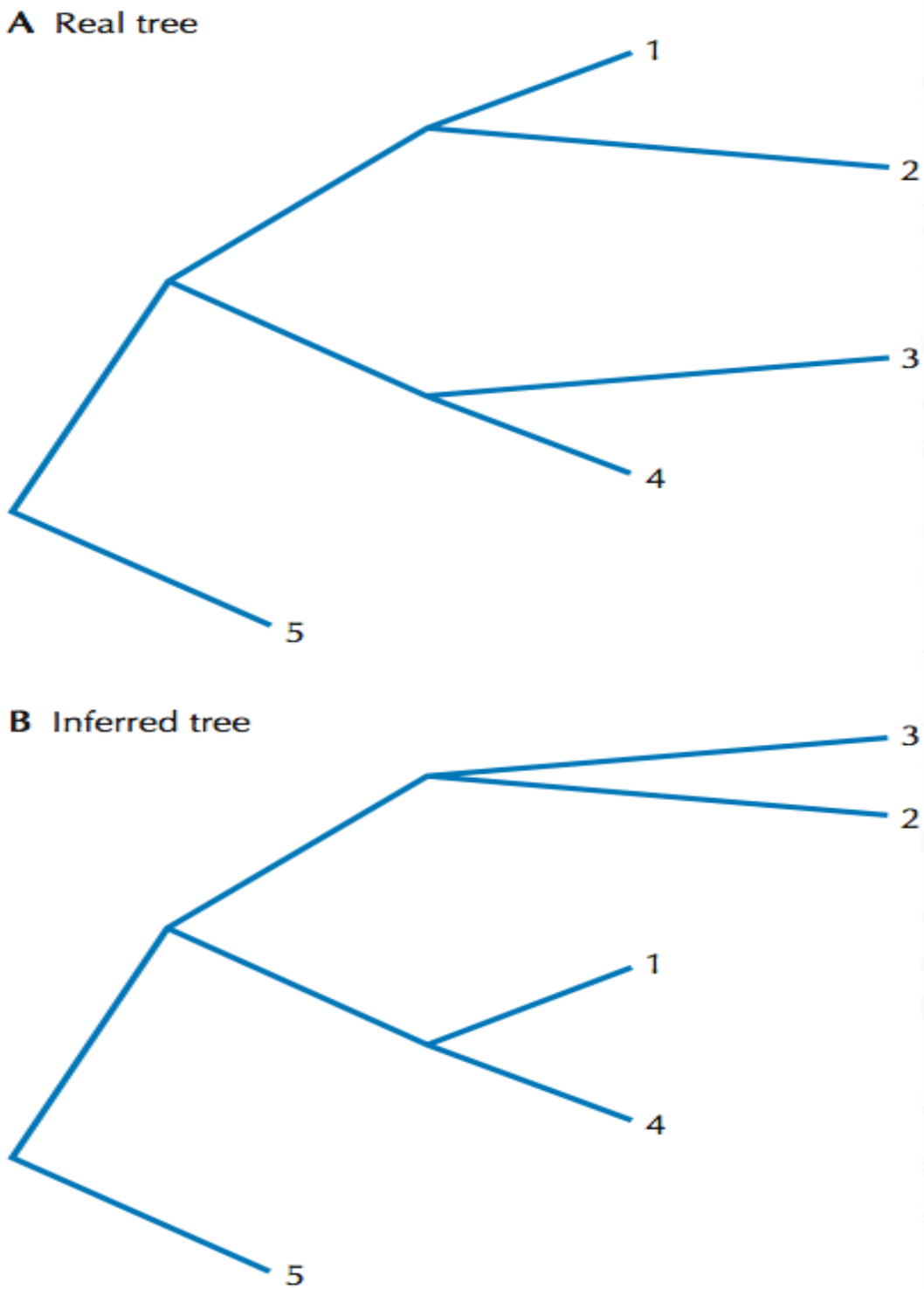
	Cycle 1	Cycle 2	Cycle 3	Cycle 4	Cycle 5
Distance matrix					
Step 1					
S calculations S_x = (sum all D_x)/(N – 2), where N is the # of OTUs in the set.	$S_A = (5+4+7+6+8)/4 = 7.5$ $S_B = (5+7+10+9+11)/4 = 10.5$ $S_C = (4+7+7+6+8)/4 = 8$ $S_D = (7+10+7+5+9)/4 = 9.5$ $S_E = (6+9+6+5+8)/4 = 8.5$ $S_F = (8+11+8+9+8)/4 = 11$	$S_{U_1} = (3+6+5+7)/3 = 7$ $S_C = (3+7+6=8)/3 = 8$ $S_D = (6+7+5+9)/3 = 9$ $S_E = (5+6+5+8)/3 = 8$ $S_F = (7+8+9+8)/3 = 10.6$	$S_{U_1} = (3+3+7)/2 = 6.5$ $S_C = (3+4+8)/2 = 7.5$ $S_{U_2} = (3+4+6)/2 = 6.5$ $S_F = (7+8+6)/2 = 10.5$	$S_{U_2} = (2+6)/1 = 8$ $S_{U_3} = (2+6)/1 = 8$ $S_F = (6+6)/1 = 12$	Because N – 2 = 0, we cannot do this calculation.
Step 2					
Calculate pair with smallest (M), where $M_{ij} = D_{ij} - S_i - S_j$.	Smallest are $M_{AB} = 5 - 7.5 - 10.5 = -13$ $M_{DE} = 5 - 9.5 - 8.5 = -13$ Choose one of these (AB here).	Smallest is $M_{CU_1} = 3 - 7 - 8 = -12$ $M_{DE} = 5 - 9 - 8 = -12$ Choose one of these (DE here).	Smallest is $M_{CU_1} = 3 - 6.5 - 7.5 = -11$	Smallest is $M_{U_2F} = 6 - 8 - 12 = -14$ $M_{U_3F} = 6 - 8 - 12 = -14$ $M_{U_2U_3} = 2 - 8 - 8 = -14$ Choose one of these ($M_{U_2U_3}$ here).	
Step 3					
Create a node (U) that joins pair with lowest M_{ij} such that $S_{IU} = D_{ij}/2 + (S_i - S_j)/2$.	U_1 joins A and B: $S_{AU_1} = D_{AB}/2 + (S_A - S_B)/2 = 1$ $S_{BU_1} = D_{AB}/2 + (S_B - S_A)/2 = 4$	U_2 joins D and E: $S_{DU_2} = D_{DE}/2 + (S_D - S_E)2 = 3$ $S_{EU_2} = D_{DE}/2 + (S_E - S_D)/2 = 2$	U_3 joins C and U_1: $S_{CU_3} = D_{CU_1}/2 + (S_C - S_{U_1})/2 = 2$ $S_{U_1U_3} = D_{CU_1}/2 + (S_{U1} - S_C)/2 = 1$	U_4 joins U_2 and U_3: $S_{U_2U_4} = D_{U_2U_3}/2 + (S_{U2} - S_{U3})/2 = 1$ $S_{U_3U_4} = D_{U_2U_3}/2 + (S_{U3} - S_{U2})/2 = 1$	For last pair connect with branch = D. Here $D_{U_4F} = 5$.
Step 4					
Join i and j according to S above and make all other taxa in form of a star. Branches in black are of unknown length. Branches in red are of known length.					
Step 5					**Comments**
Calculate new distance matrix of all other taxa to U with $D_{xU} = D_{ix} + D_{jx} - D_{ij}$, where i and j are those selected from above.					Note this is the same tree we started with (drawn in unrooted form here).

Compare to True Tree



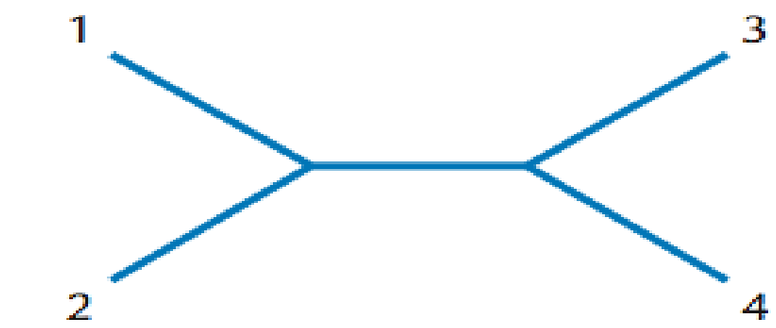


Long branch attraction

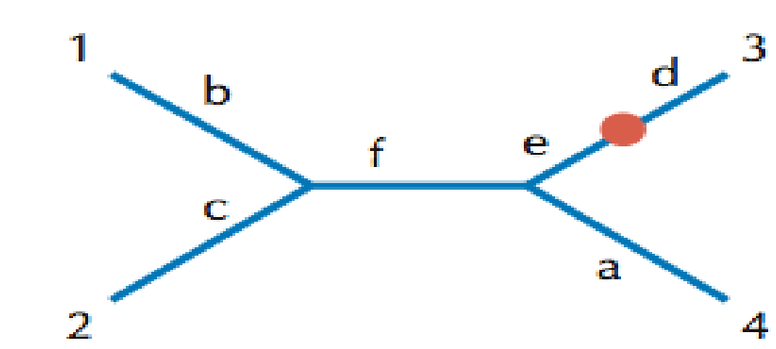


Rooting

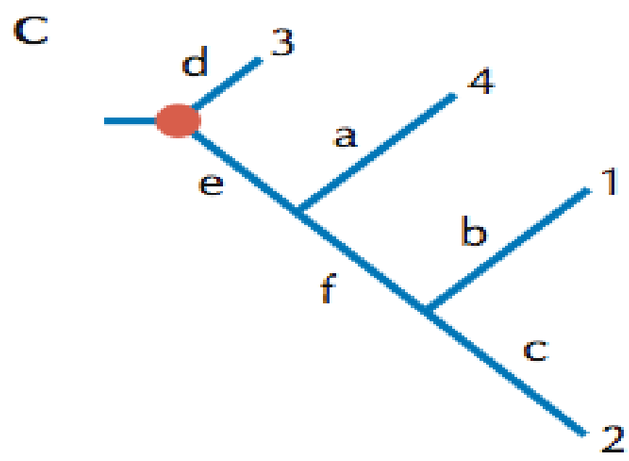
A



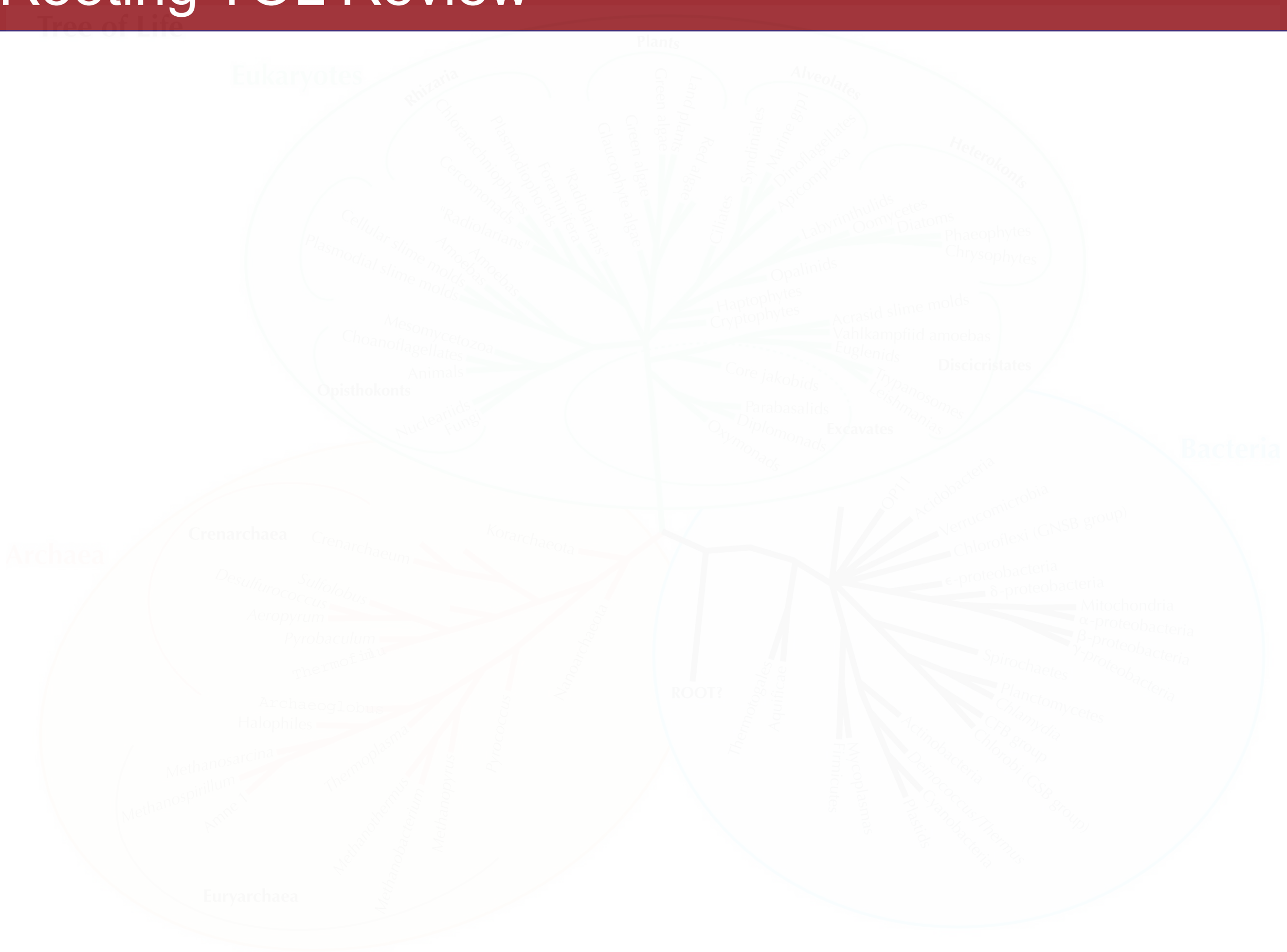
B



C



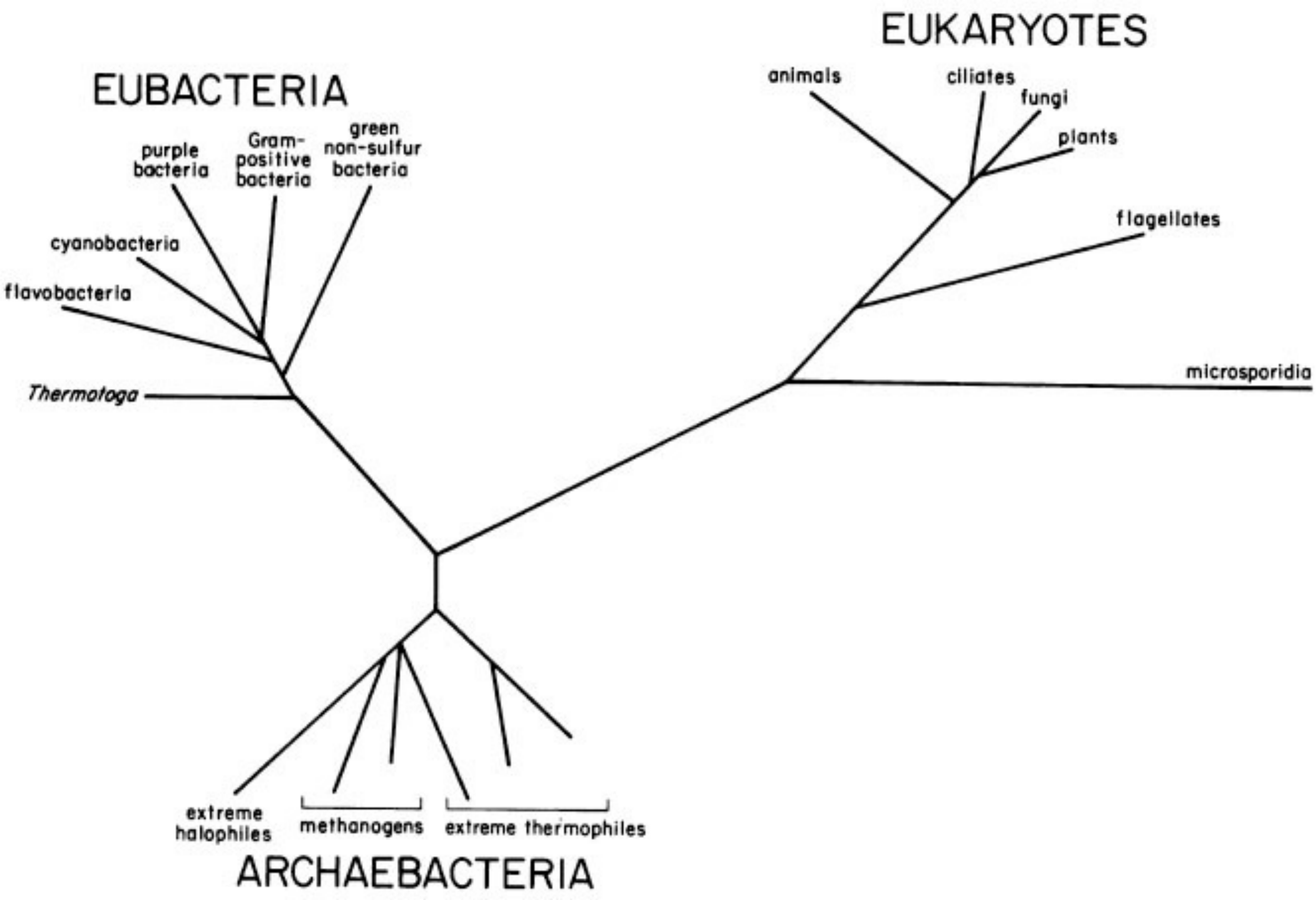
Rooting TOL Review



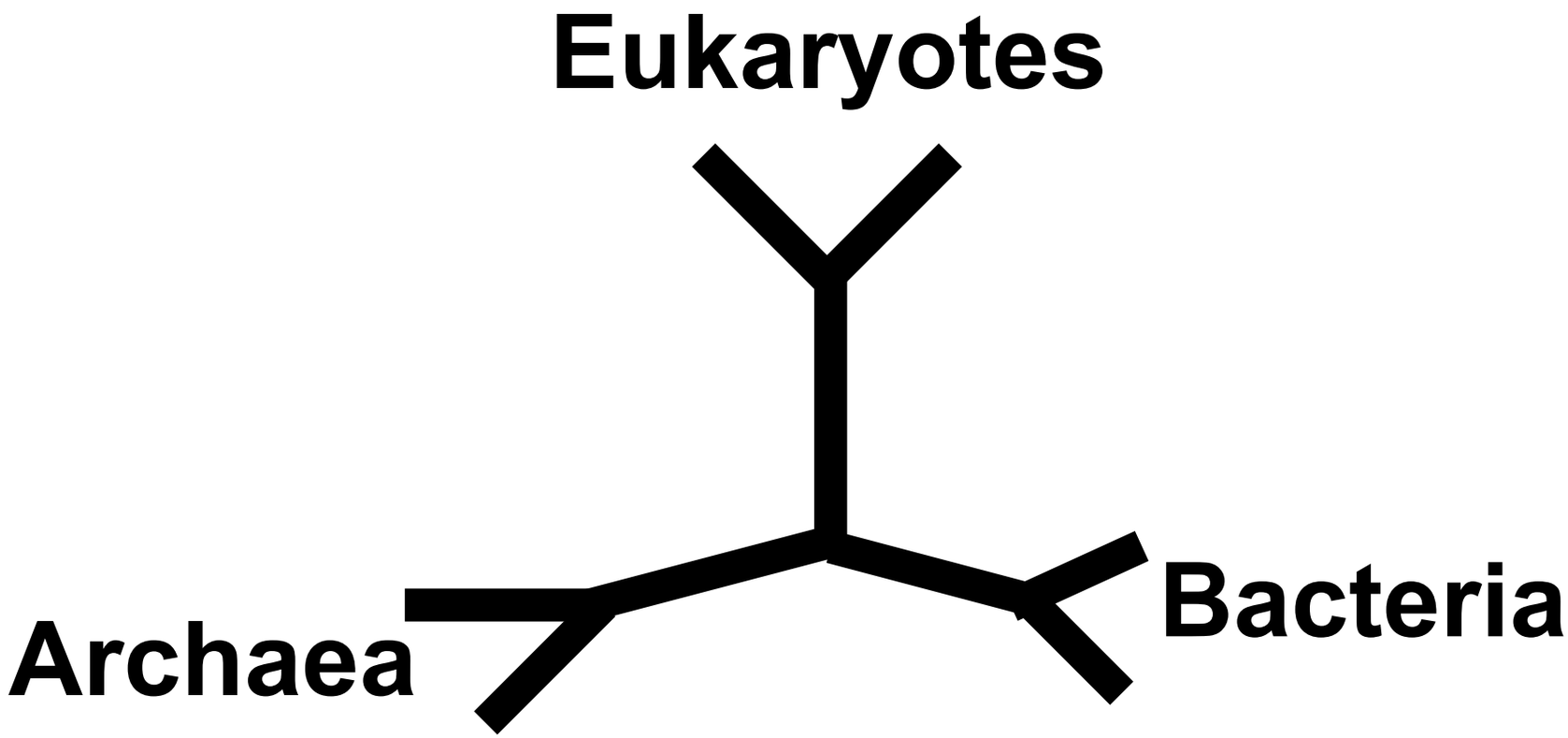
Other Tree Issues

- More characters vs. more taxa
- Lateral gene transfer
- Polytomies
- Paralogs and Orthologs
- Species Tree vs. Gene Tree
- Networks vs. Trees
- Clusters vs. Trees
-

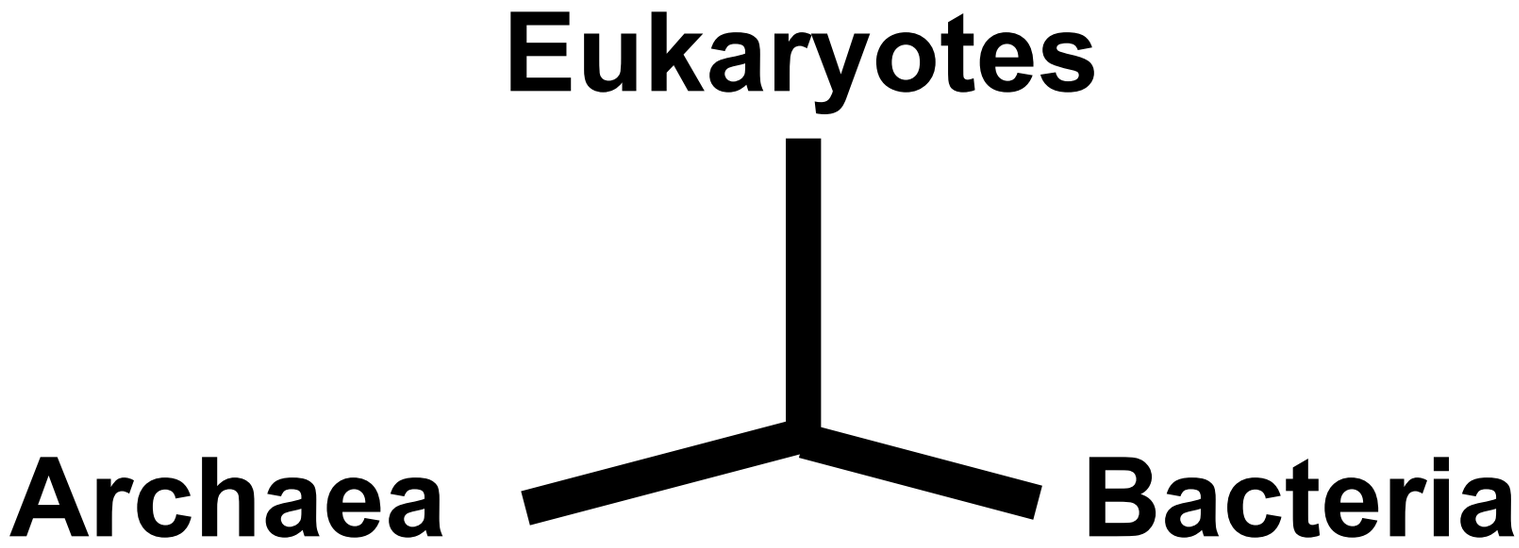
Unrooted Tree of Life from Woese



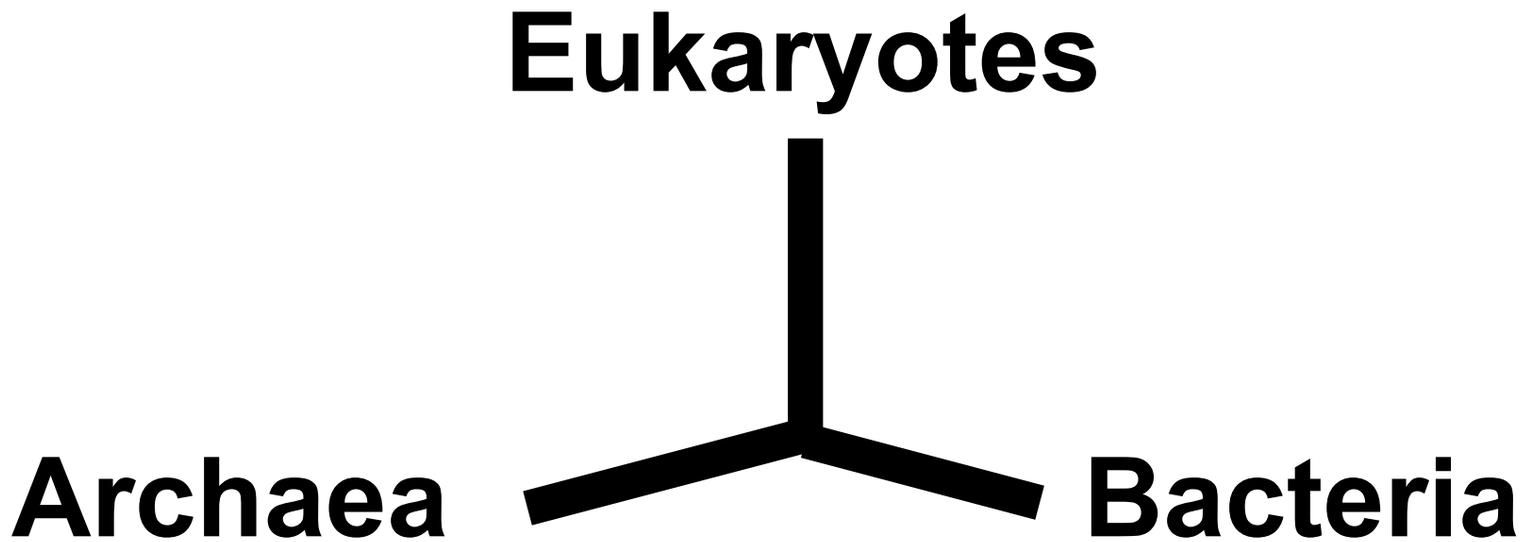
Simplified Three Domain Unrooted Tree of Life



Simplified Three Domain Unrooted Tree of Life

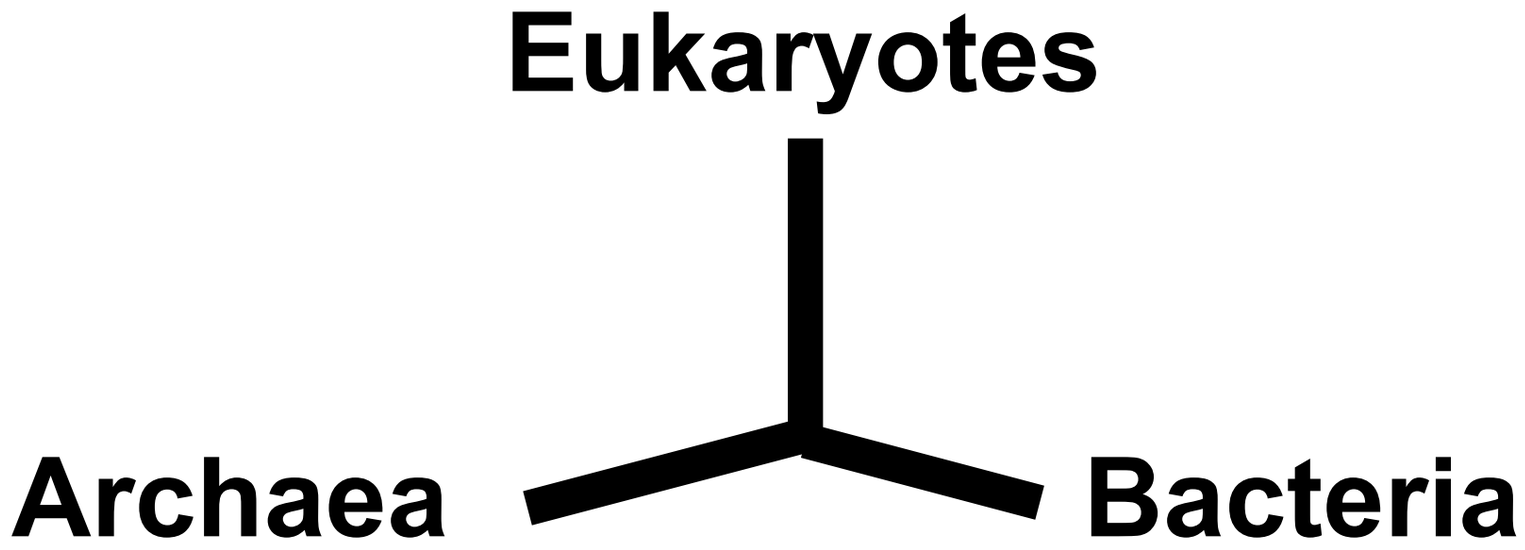


Simplified Three Domain Unrooted Tree of Life



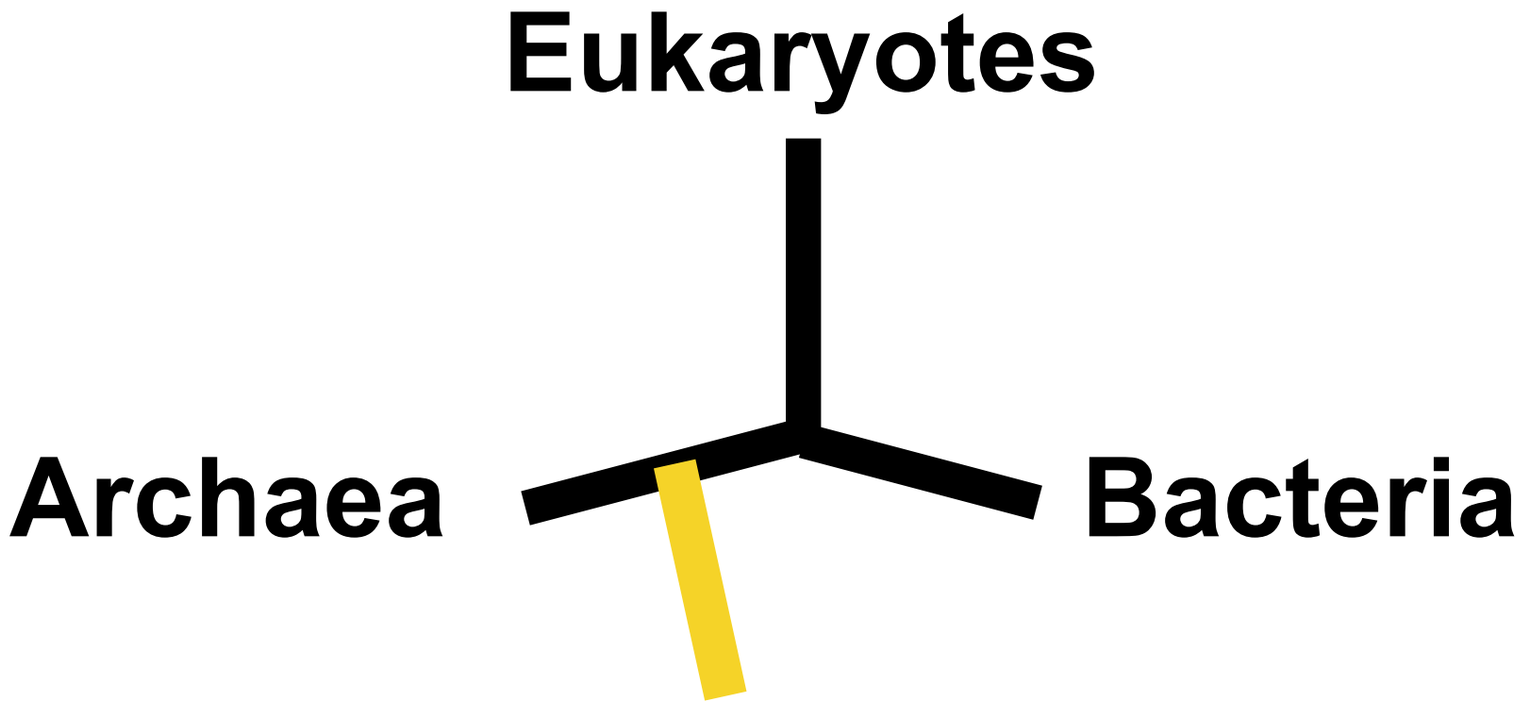
Can You Tell Which Groups are Sister Taxa from this?

Simplified Three Domain Unrooted Tree of Life

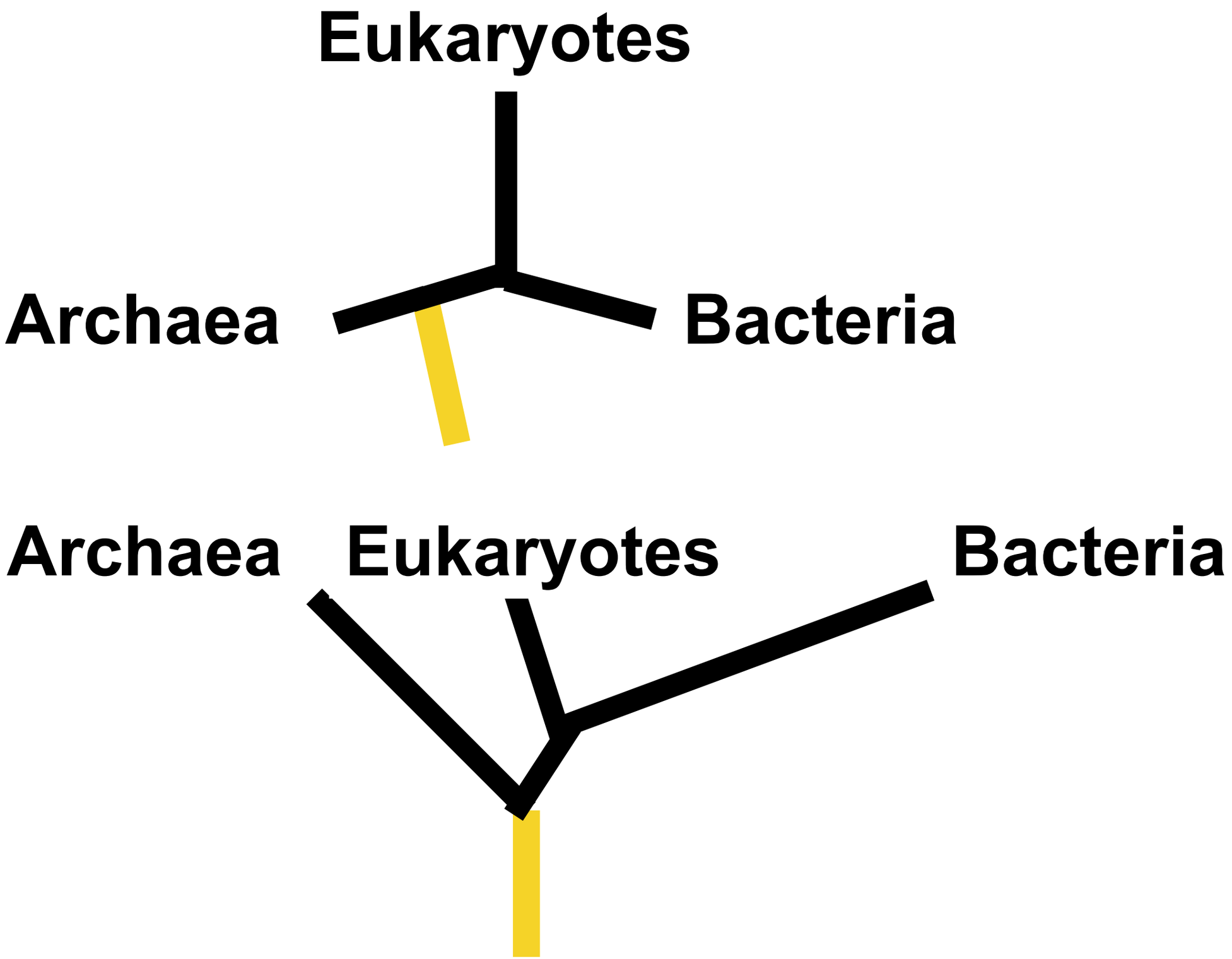


What is Missing?

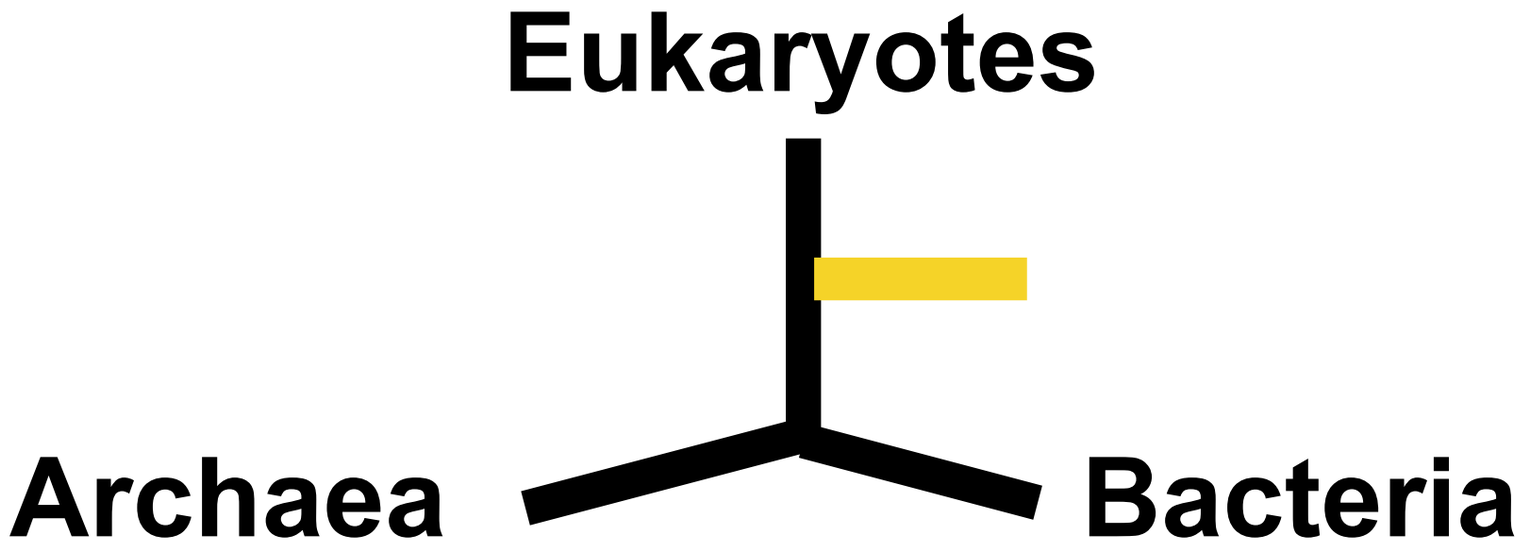
Simplified Three Domain Unrooted Tree of Life



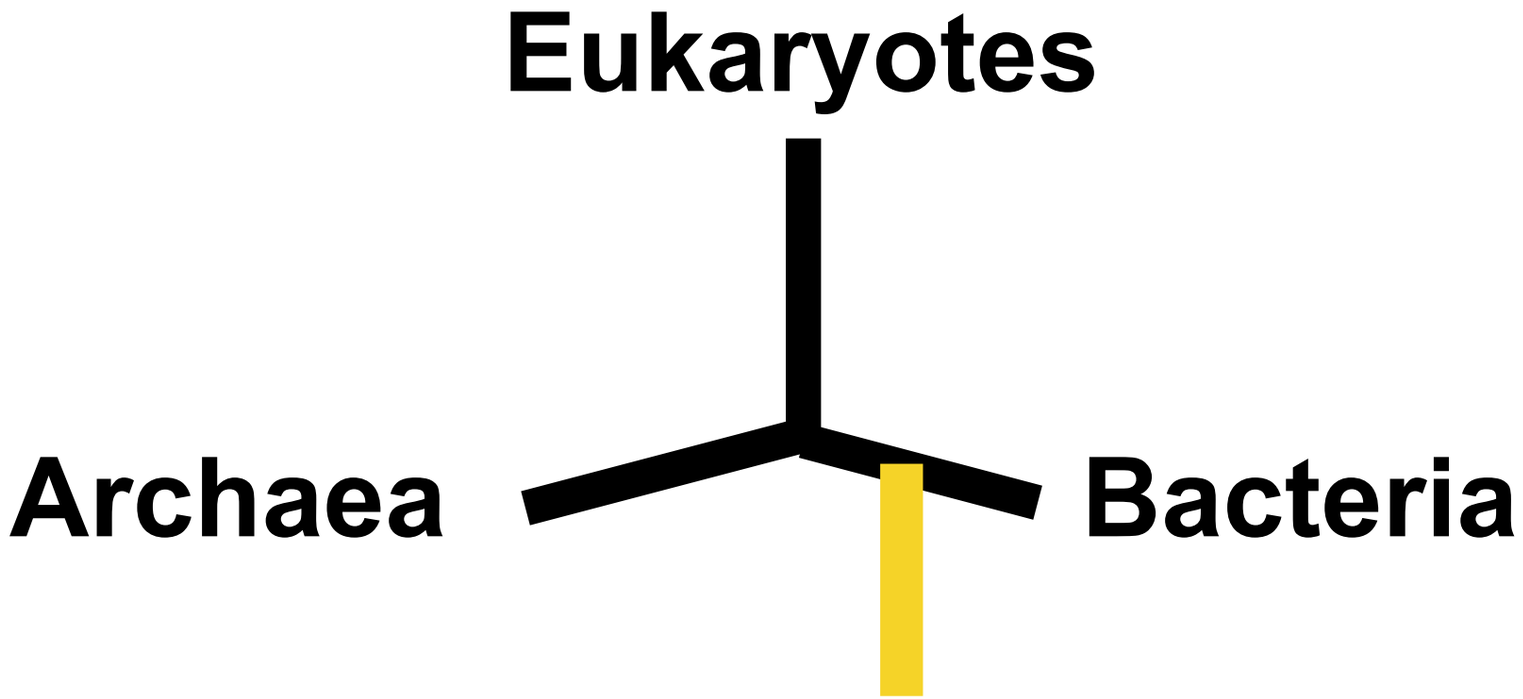
Simplified Three Domain Unrooted Tree of Life



Simplified Three Domain Unrooted Tree of Life

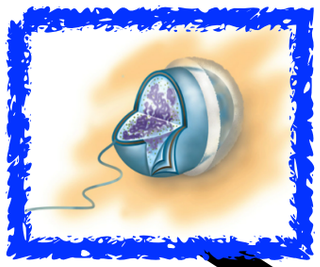


Simplified Three Domain Unrooted Tree of Life

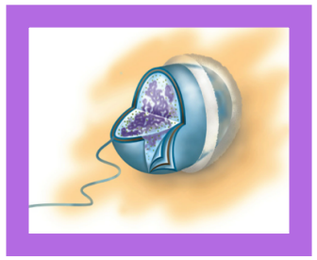


A Polytomous Three Domain Tree of Life

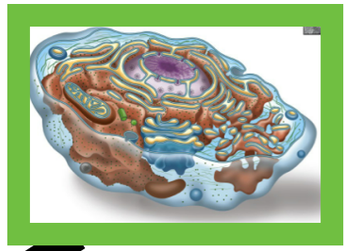
Bacteria



Archaea



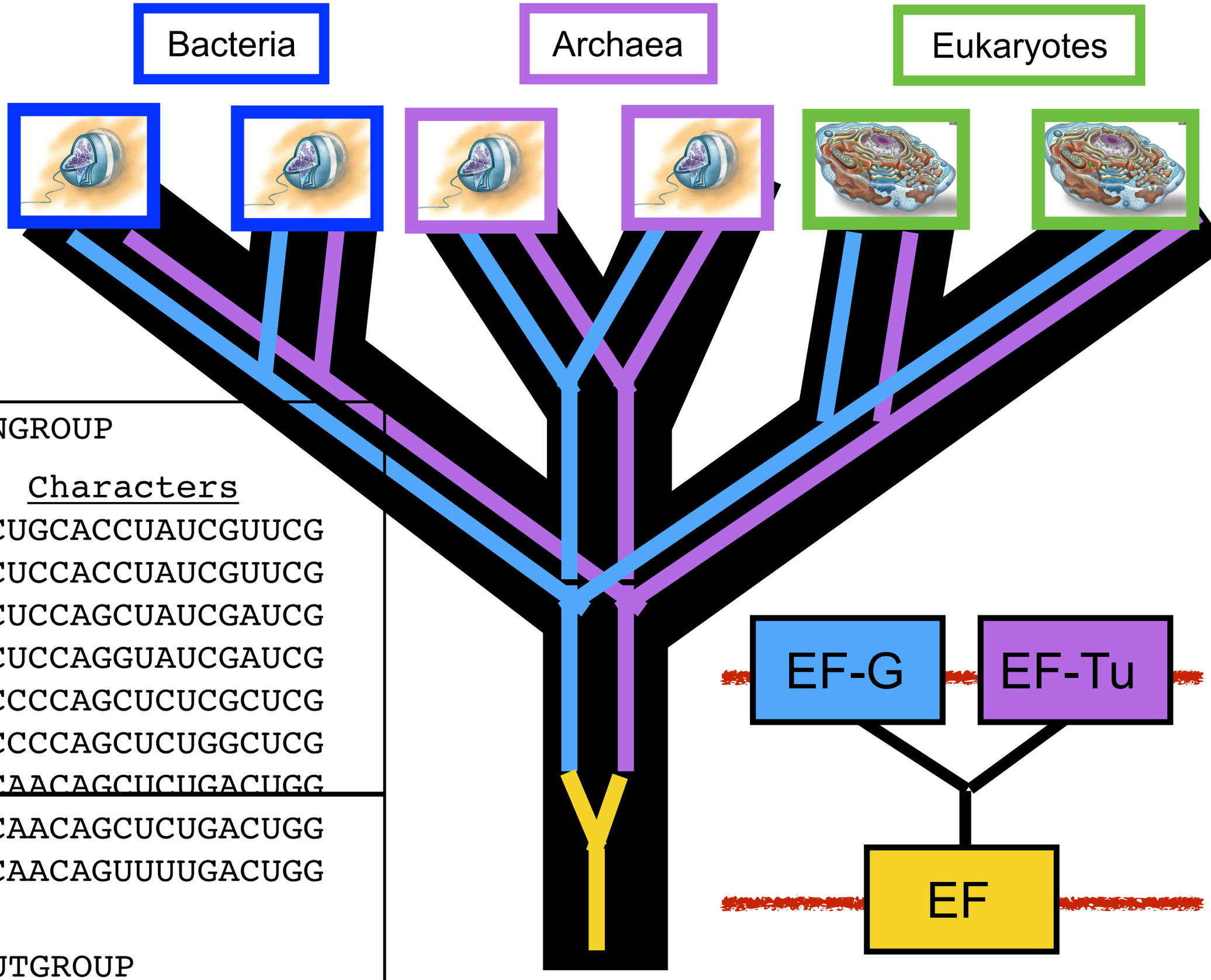
Eukaryotes



Polytomy

Gene Duplications Prior to MRCA of All Life

Sandra Baldauf



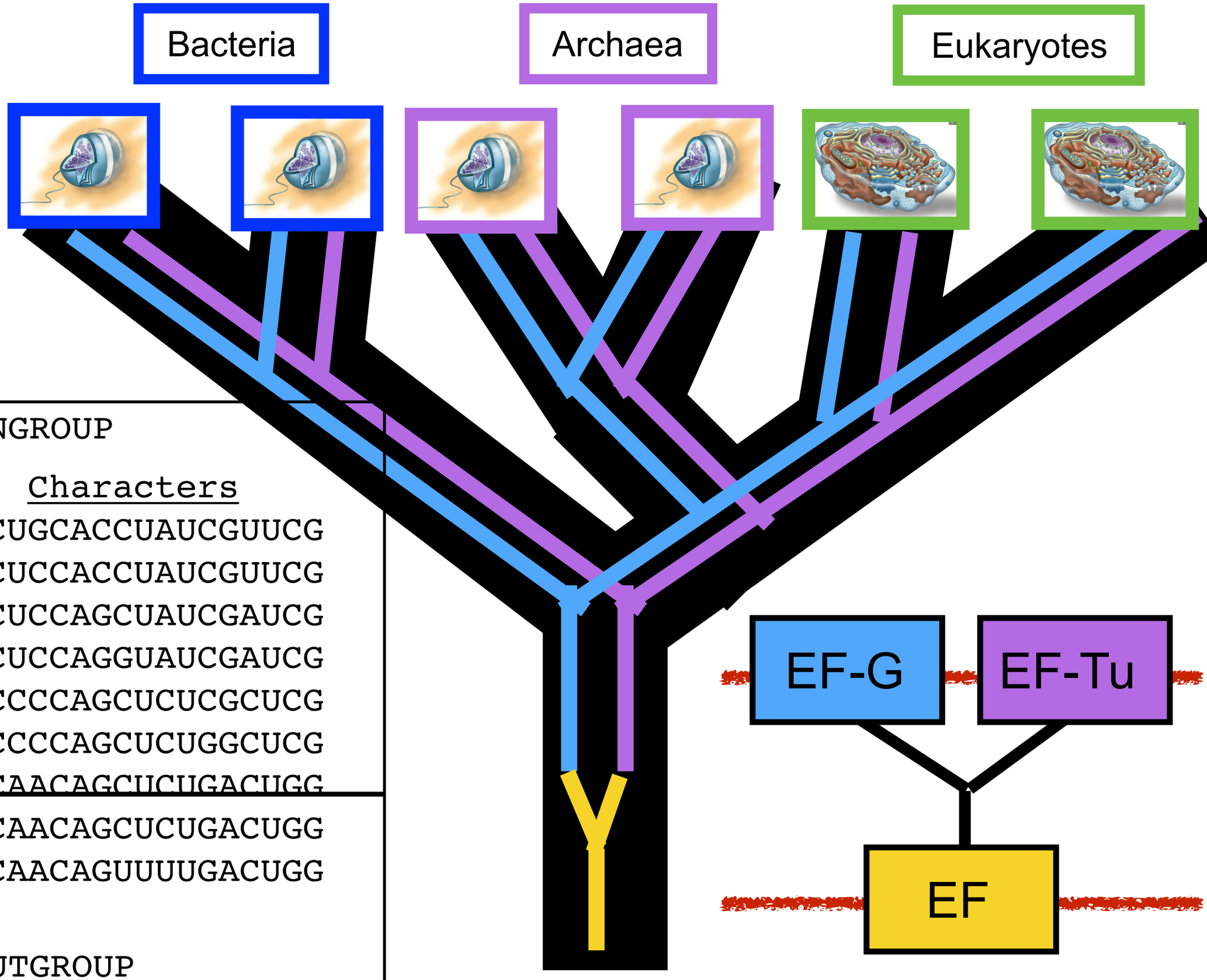
INGROUP

Taxa	Characters
B1 EFG	ACUGCACCUAUCGUUCG
B2 EFG	ACUCCACCUAUCGUUCG
E1 EFG	ACUCCAGCUAUCGAUCG
E2 EFG	ACUCCAGGUAUCGAUCG
A1 EFG	ACCCCAGCUCUCGCUCG
A2 EFG	ACCCCAGCUCUGGCUCG
B1 EF2	ACAACAGCUCUGACUGG
E1 EF2	CCAACAGCUCUGACUGG
A1 EF2	ACAACAGUUUUGACUGG

OUTGROUP

Gene Duplications Prior to MRCA of All Life

Sandra Baldauf

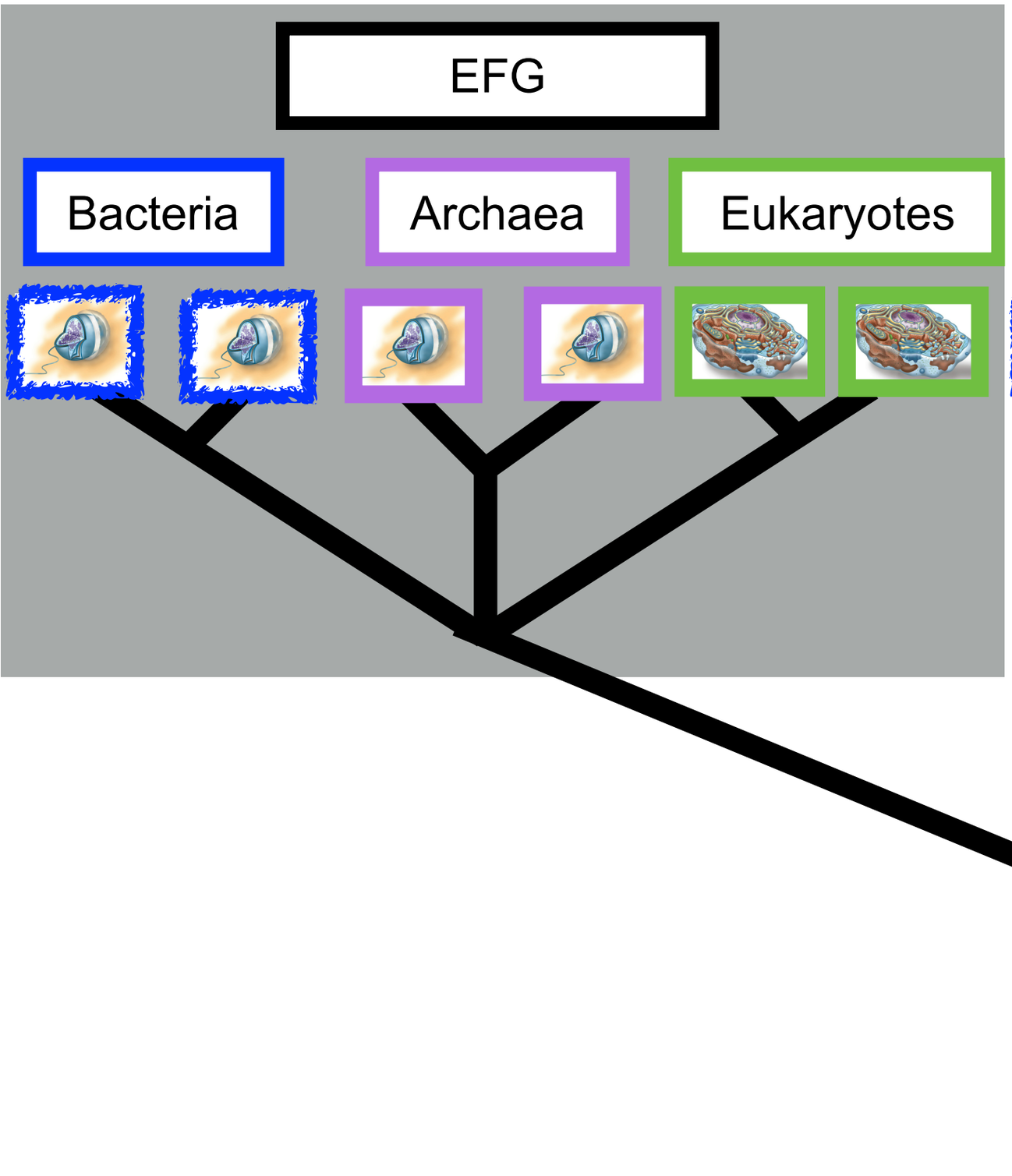


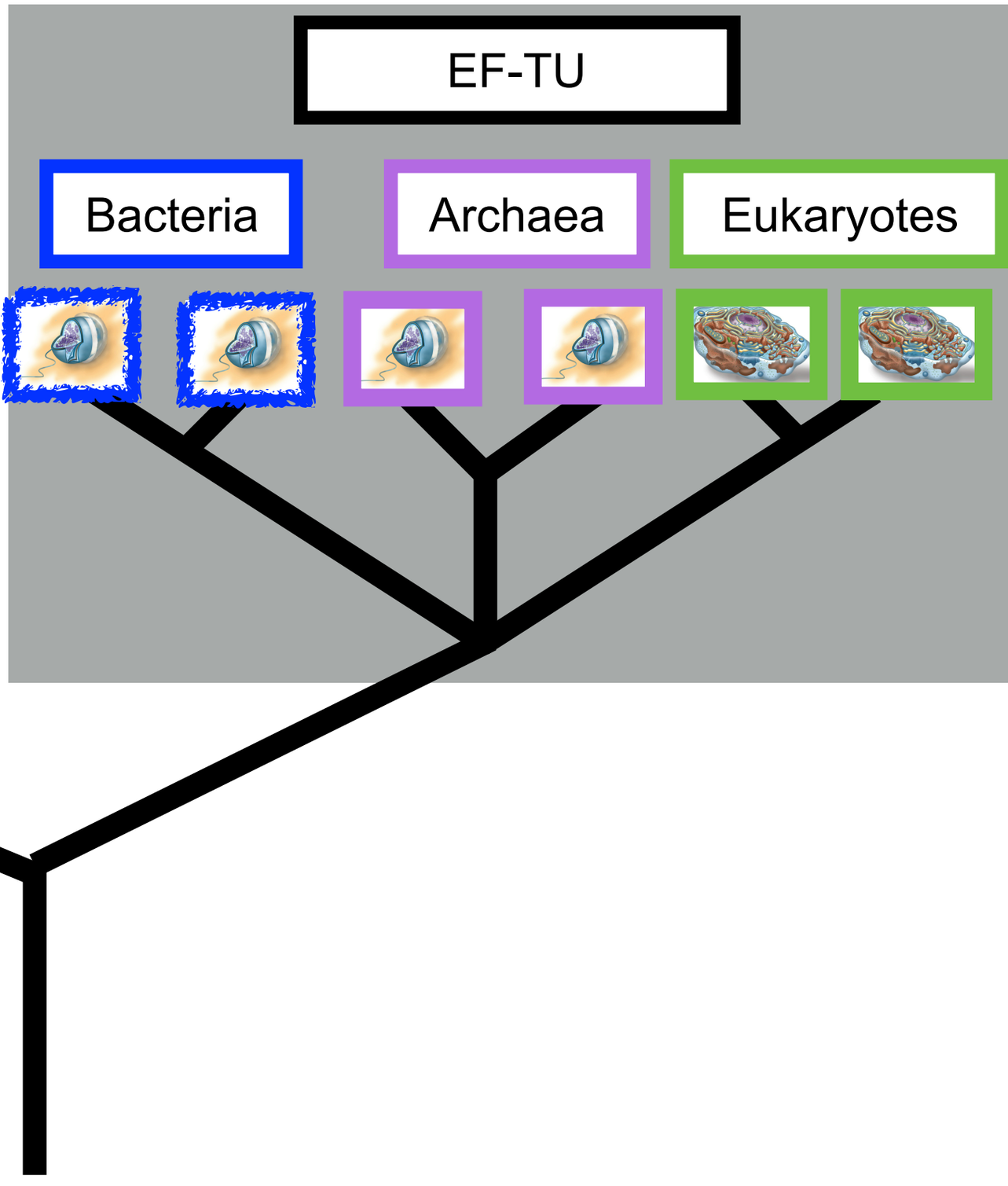
INGROUP

Taxa	Characters
B1 EFG	ACUGCACCUAUCGUUCG
B2 EFG	ACUCCACCUAUCGUUCG
E1 EFG	ACUCCAGCUAUCGAUCG
E2 EFG	ACUCCAGGUAUCGAUCG
A1 EFG	ACCCCAGCUCUCGCUCG
A2 EFG	ACCCCAGCUCUGGCUCG
B1 EF2	ACAACAGCUCUGACUGG
E1 EF2	CCAACAGCUCUGACUGG
A1 EF2	ACAACAGUUUUGACUGG

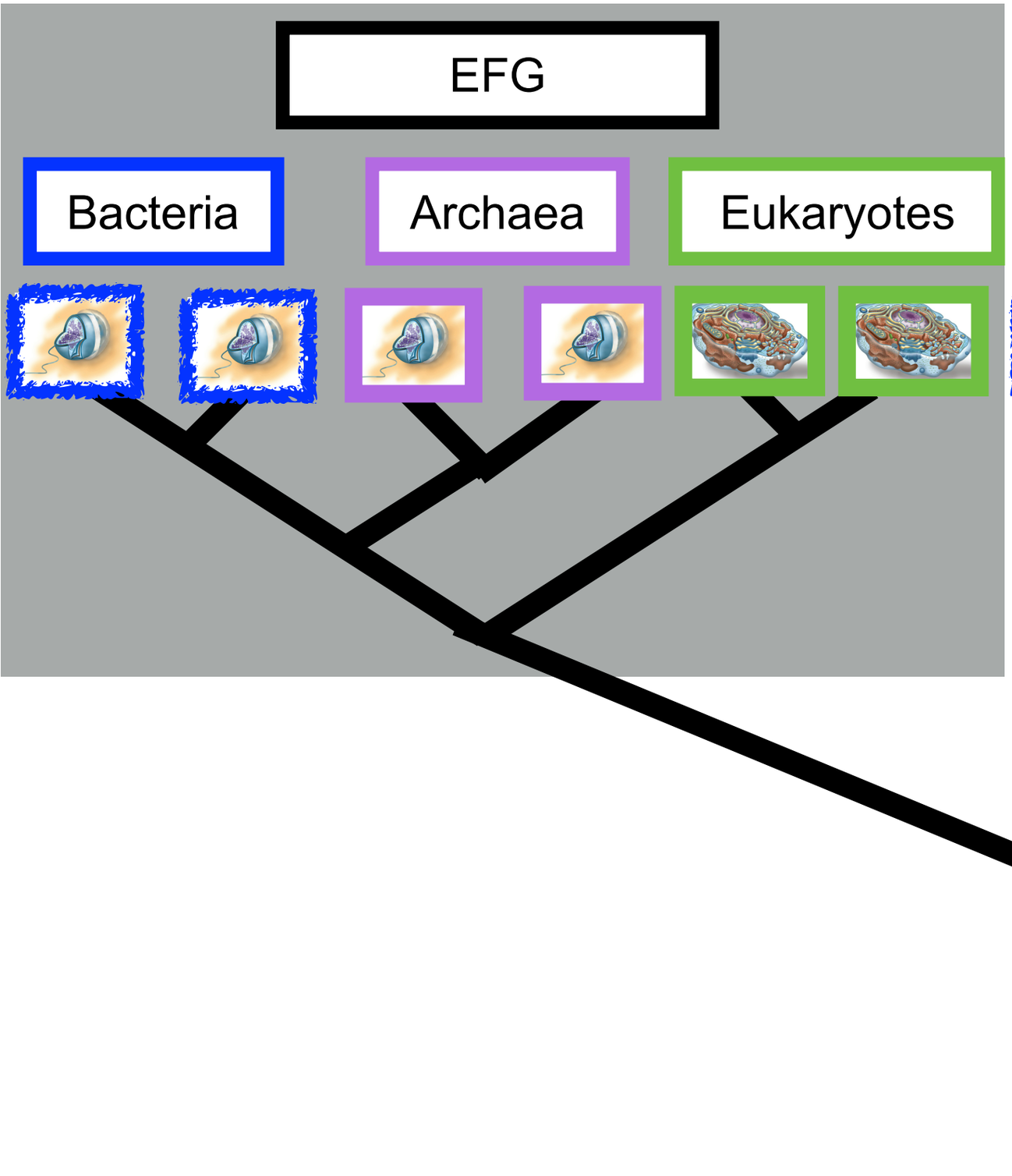
OUTGROUP

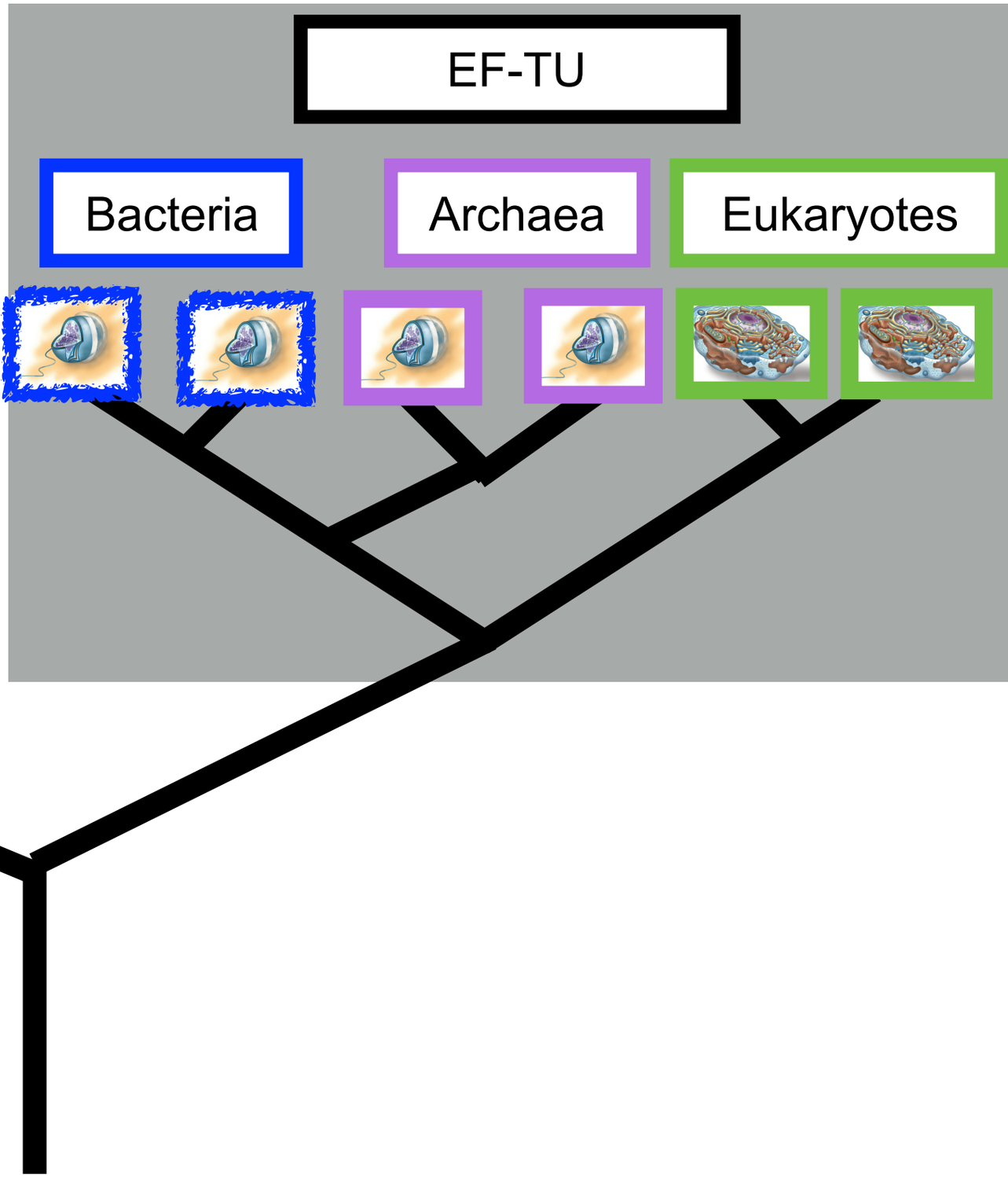
Semi-resolved Phylogeny of Elongation Factors



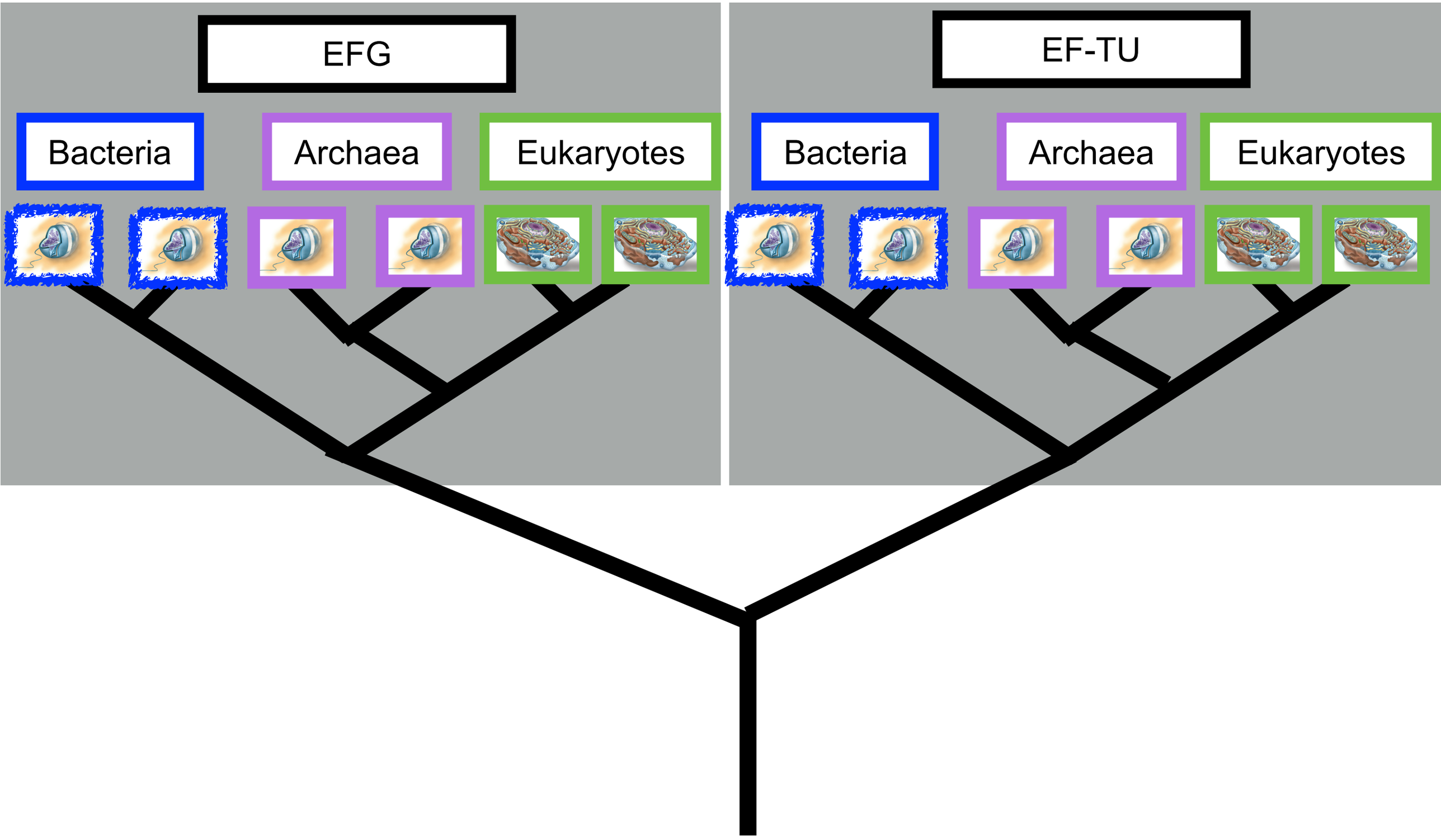


If AB Together Should Be For Both EF2 and EFG

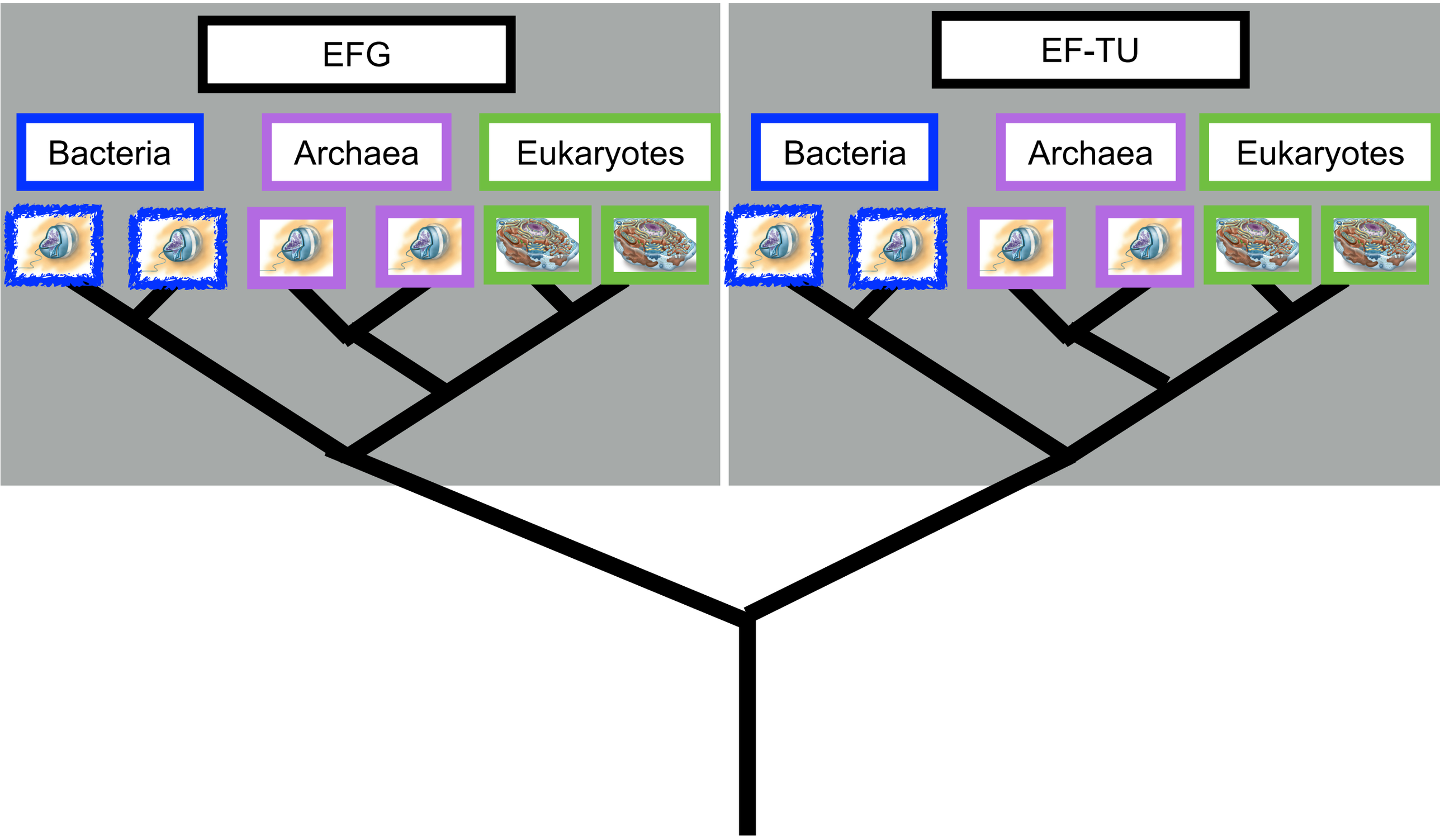




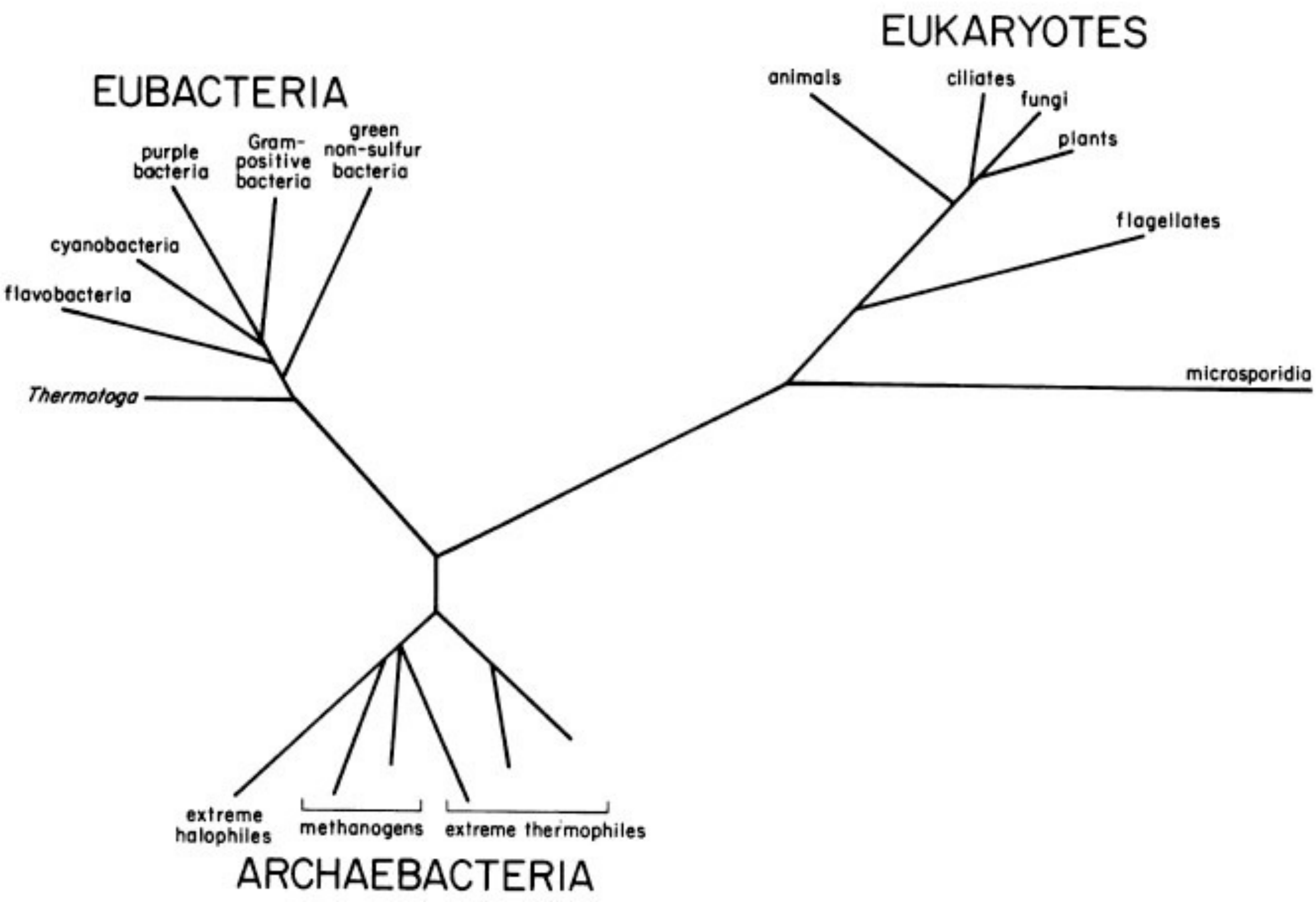
If AE Together Should Be For Both EF2 and EFG



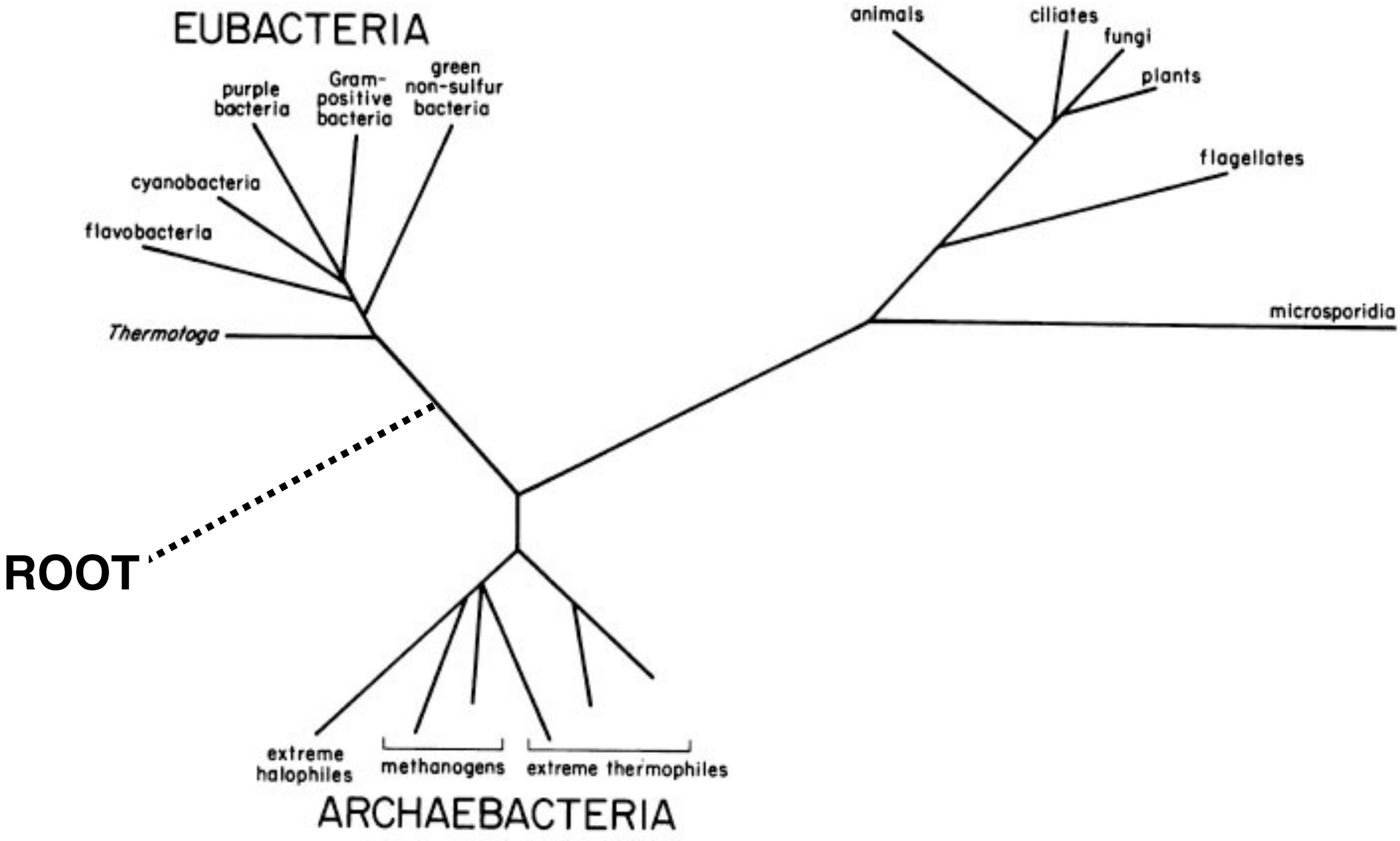
WInner


EFG
Bacteria
Archaea
Eukaryotes
EF-TU
Bacteria
Archaea
Eukaryotes

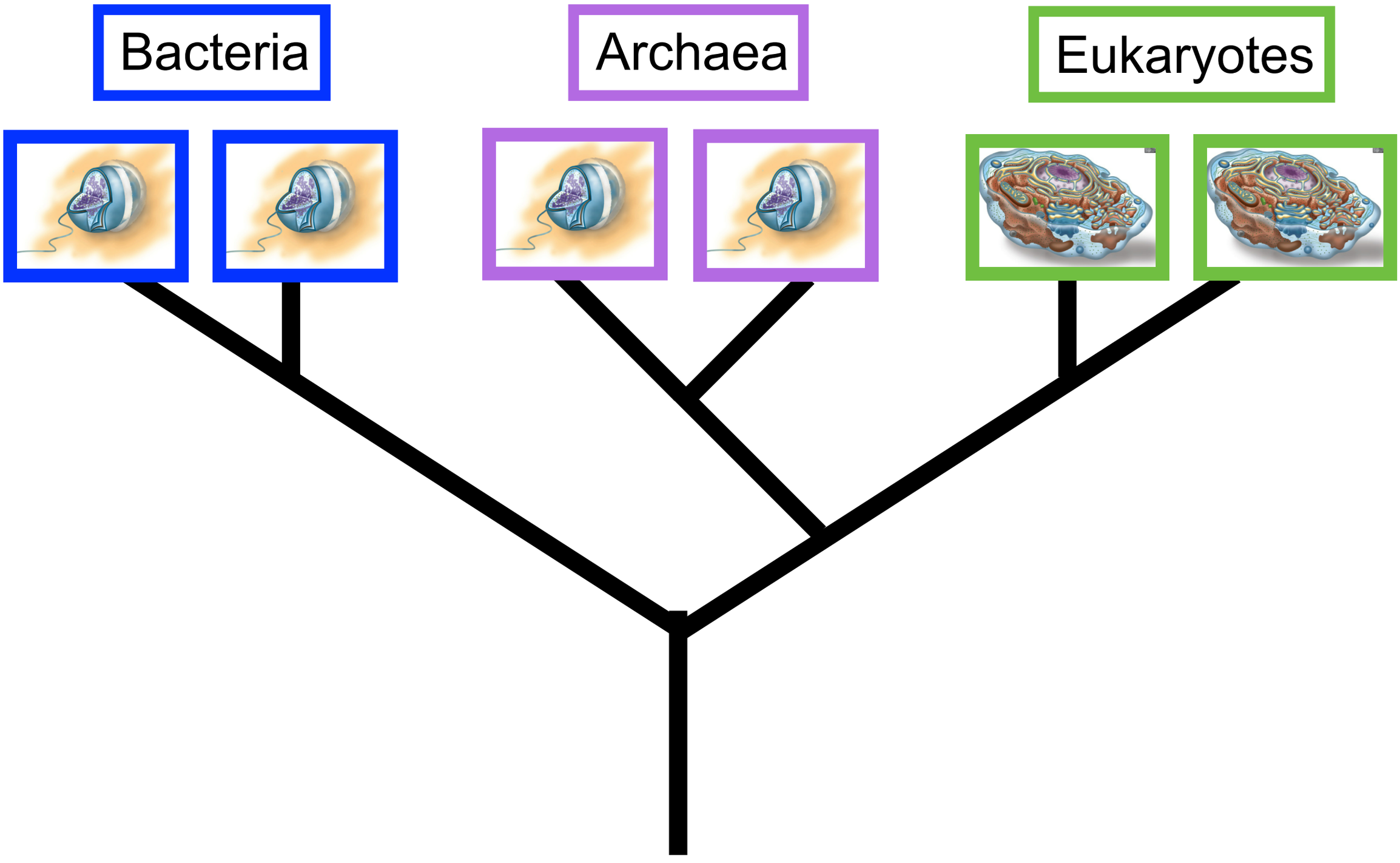
Unrooted Tree of Life from Woese



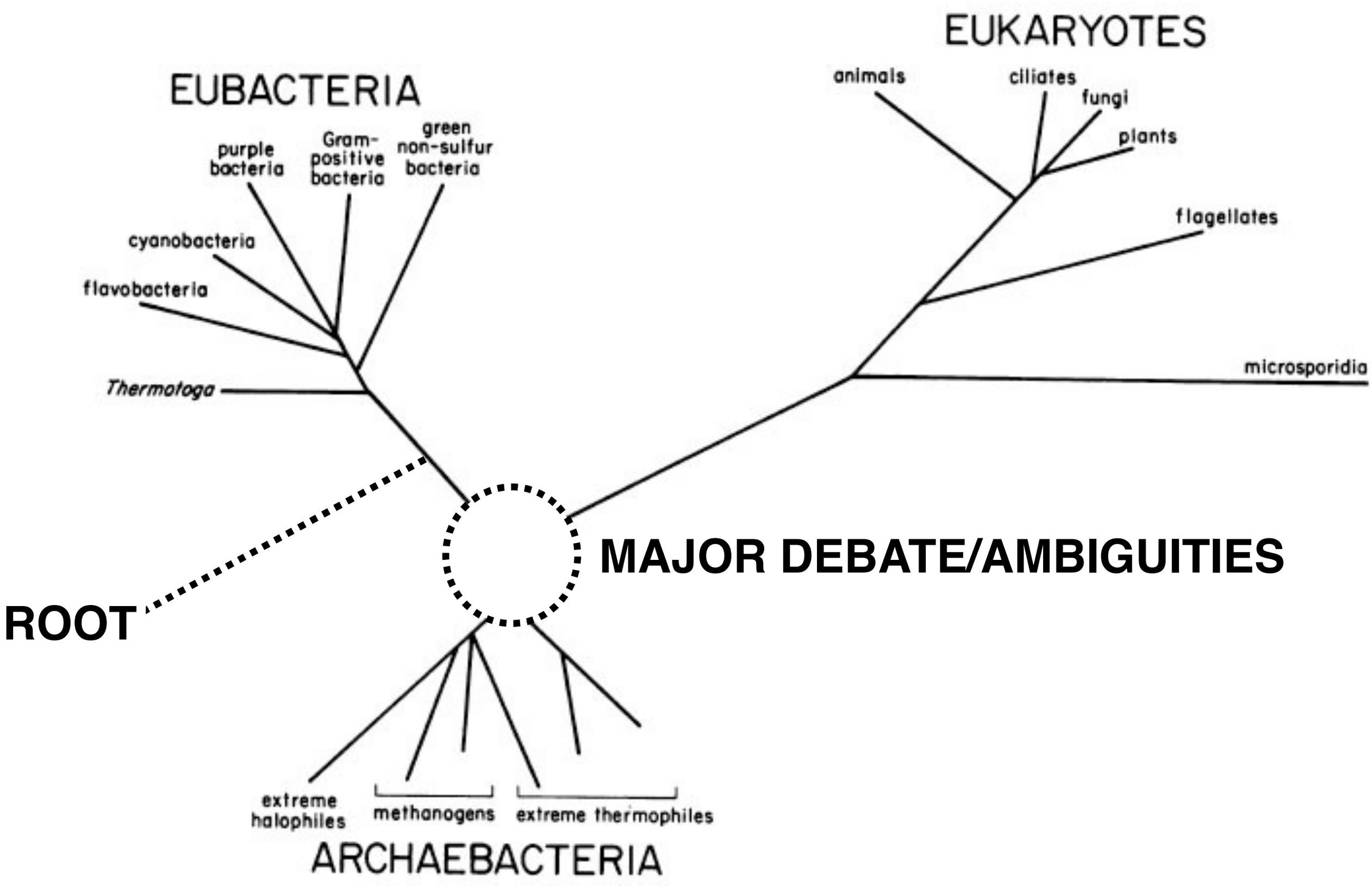
Unrooted Tree of Life from Woese



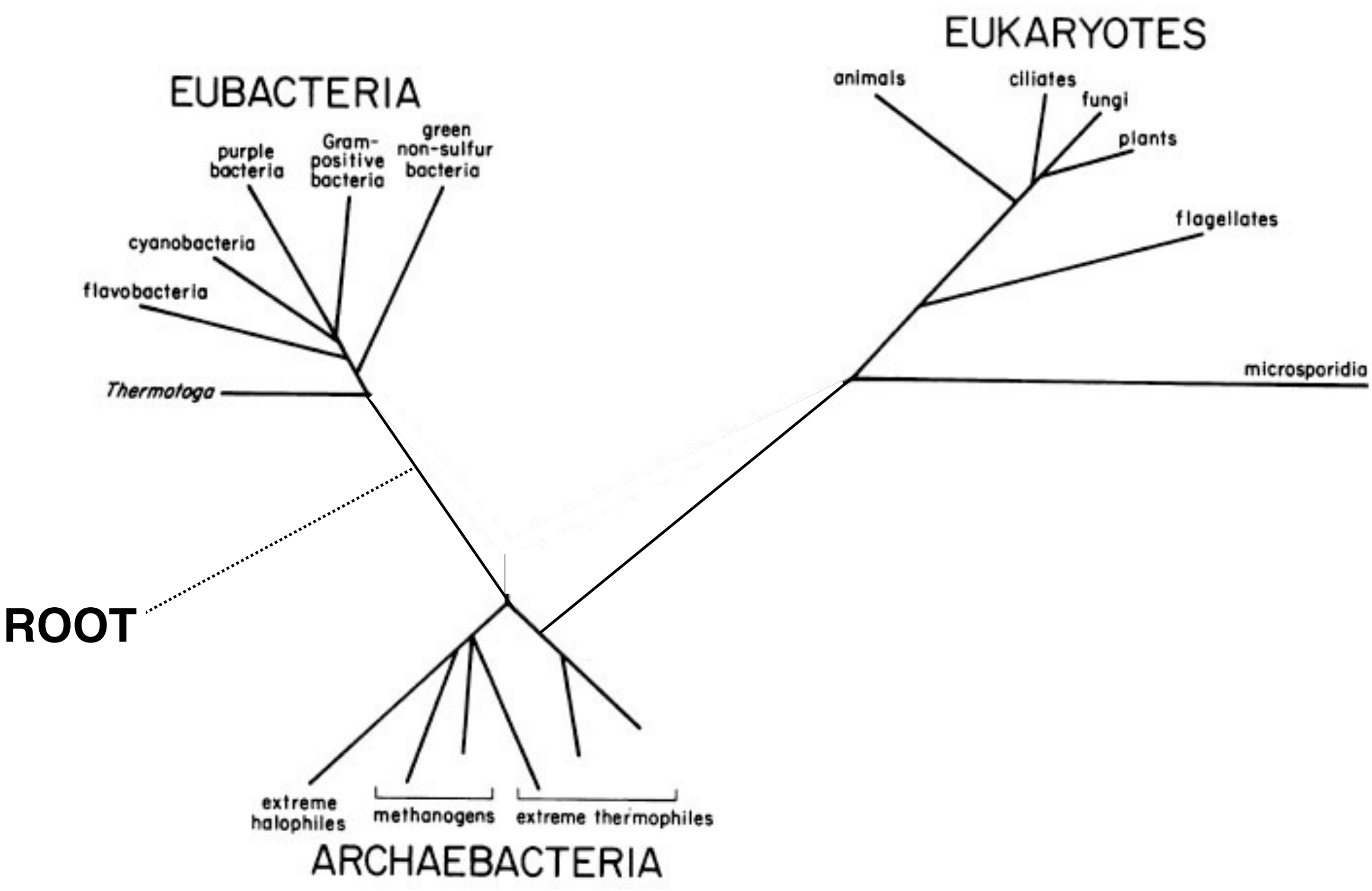
Rooted Three Domain Tree of Life



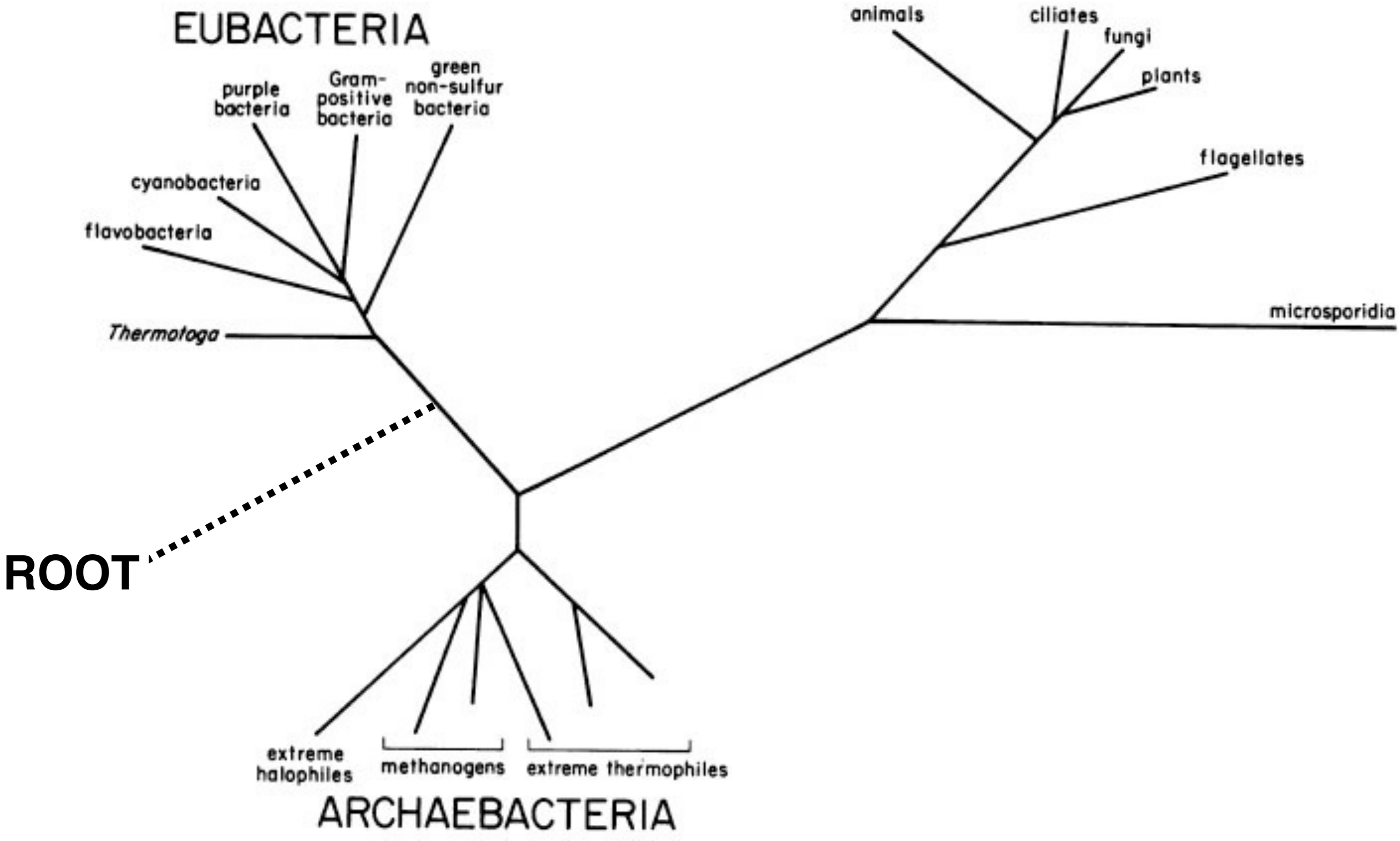
Unrooted Tree of Life from Woese



Alternative Position of Eukaryote Branch



Unrooted Tree of Life from Woese



Diversity Within Each Domain