15.xi.

1. optimization (continued…)

2. mono-, para-, & polyphyly

3. trees & their form

4. consensus- & compromise trees

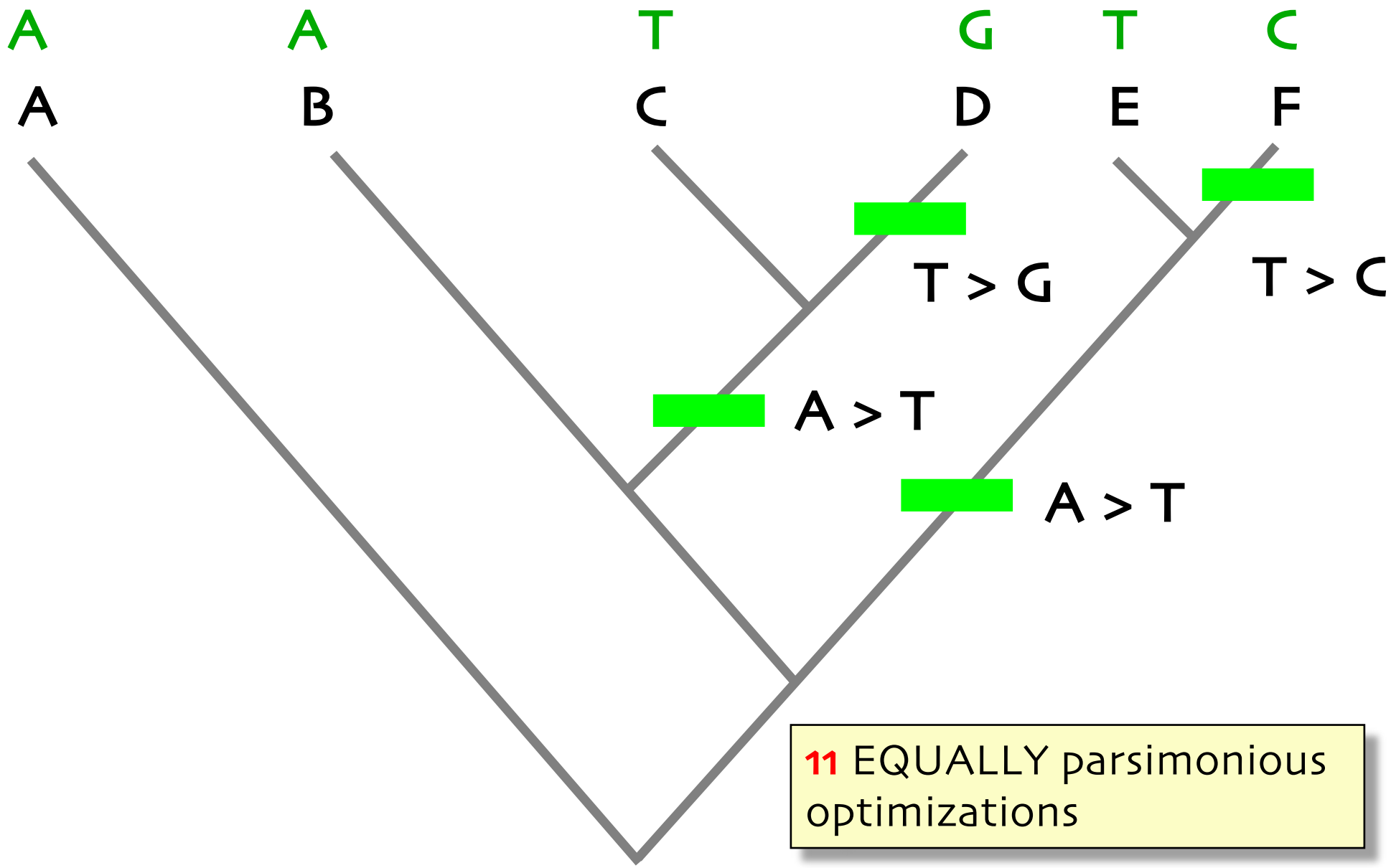
5. summary

OPTIMIZATION

HTU, Hypothetical Taxonomic Unit

possible character state reconstructions for internal nodes (HTU)

MPR, Most Parsimonious Reconstruction set


A
A
T
G
T
C
A
B
C
D
E
F
T > G
T > C
A > T
A > T
11 EQUALLY parsimonious optimizations

OPTIMIZATION

programs to find ALL equally parsimonious character state reconstructions MacClade, Mesquite

Swofford, D. L. & Maddison, W. P. 1987. Reconstructing ancestral character states under Wagner parsimony. *Mathematical Biosciences* 87: 199-229.

…frequently … we are interested not only in the branching pattern but also in the evolutionary hypothesis: a phylogeny coupled with the reconstructed states of the characters in the hypothetical ancestors…

…when multiple, equally parsimonious character-state reconstructions exist, we must be careful in interpreting **any ONE** solution…

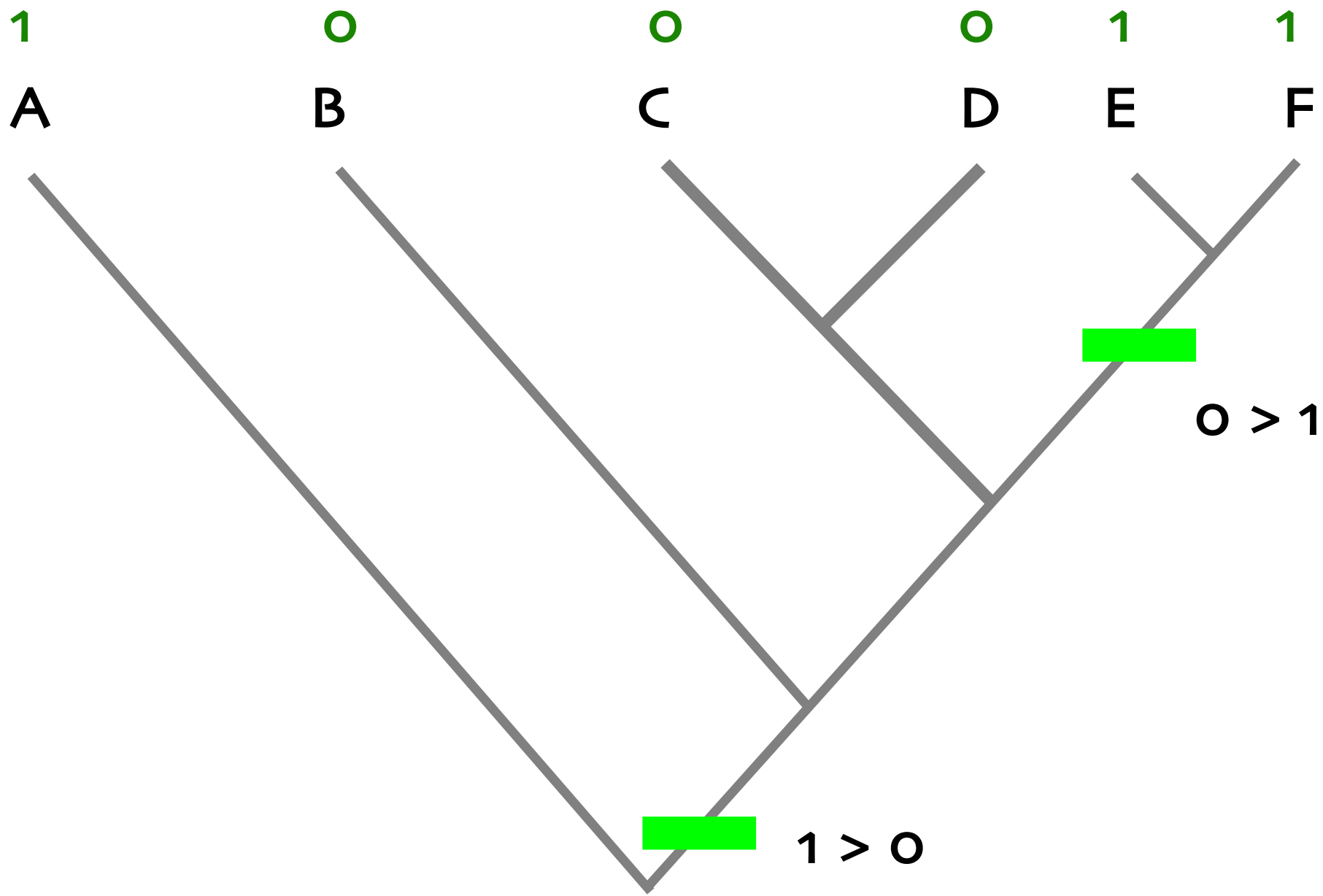
OPTIMIZATION

HTU, Hypothetical Taxonomic Unit

possible character state reconstructions for internal nodes (HTU)

MPR, Most Parsimonious Reconstruction set

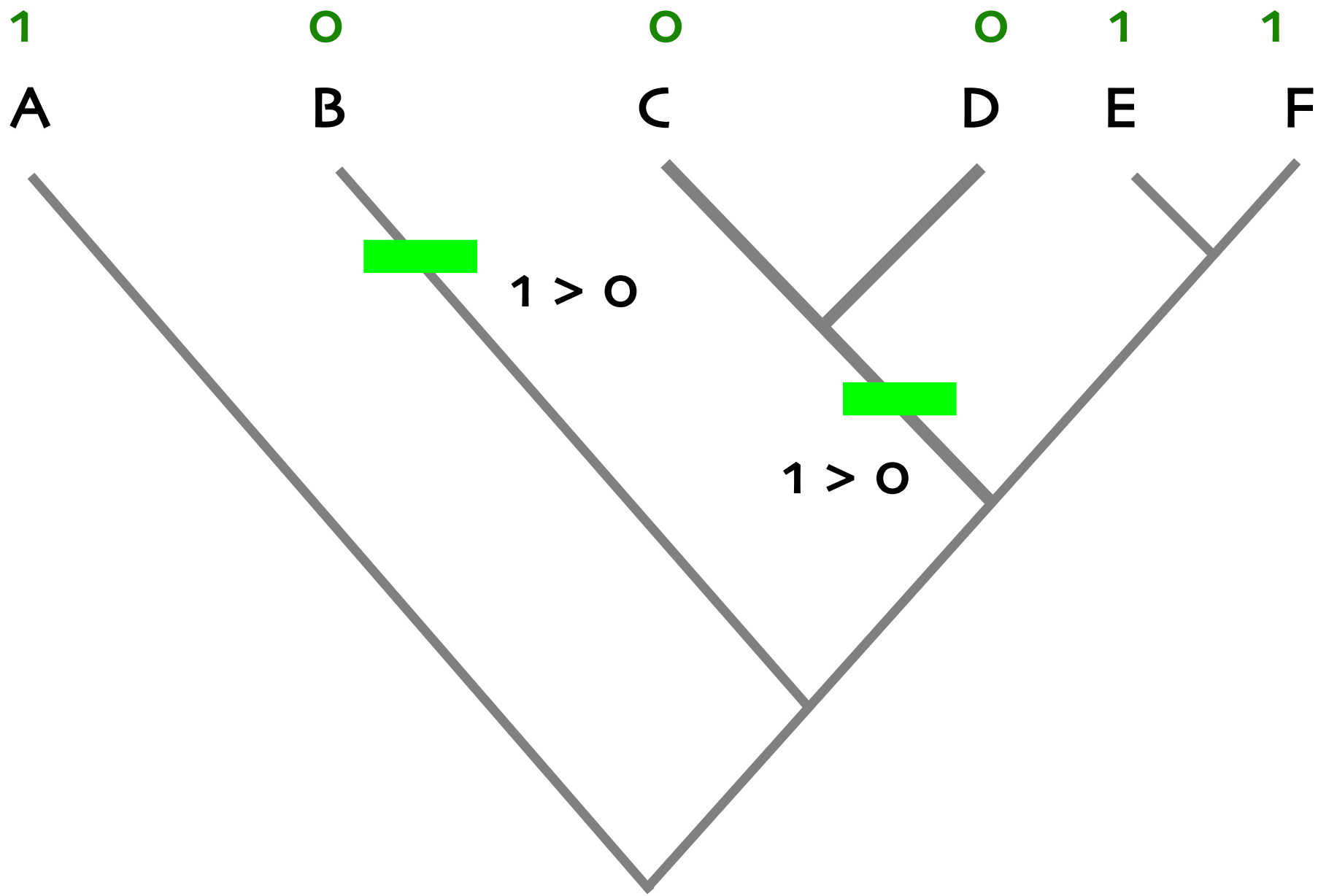
practical consequences of different reconstructions?


1
0
0
0
1
1
A
B
C
D
E
F
0 > 1
1 > 0

ACCTRAN optimization

ACCelarated TRANsformation

favors reversals, changes are assumed to have taken place as early as possible

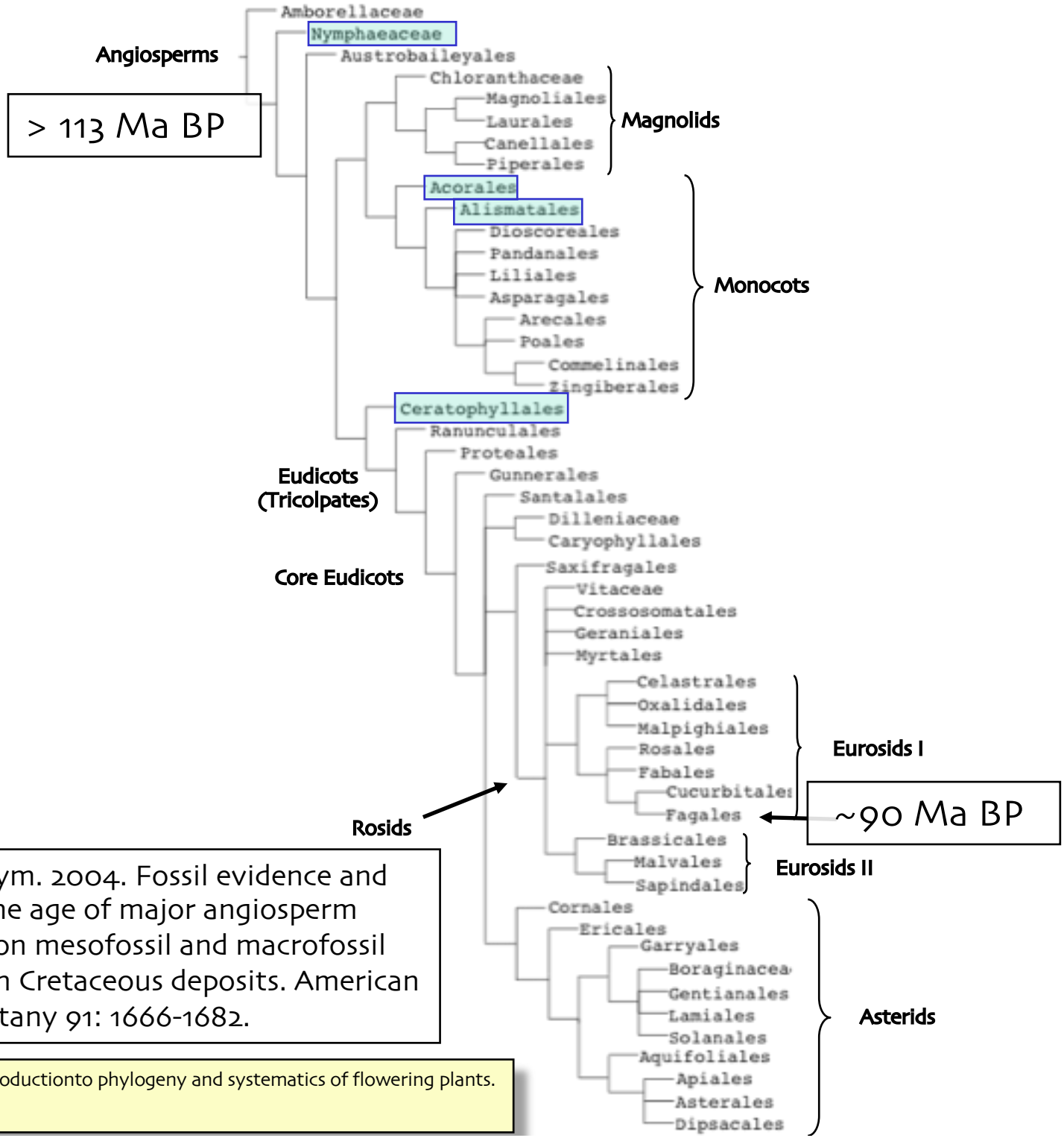

1
0
0
0
1
1
A
B
C
D
E
F
1 > 0
1 > 0

DELTRAN optimization

DELayed TRANsformation

favors parallelism, changes are assumed to have taken place as late as possible

EQUALLY parsimonious optimizations might posit changes on a tree that are VERY FAR from each other in time



Crepet, W.L. ym. 2004. Fossil evidence and phylogeny: the age of major angiosperm clades based on mesofossil and macrofossil evidence from Cretaceous deposits. American Journal of Botany 91: 1666-1682.

Bremer, K. ym. 2003. Introductionto phylogeny and systematics of flowering plants. Acta Univ. Upsal. 33: 2.

Lipscomb page 32:

The first tree has a **DELTRAN** (DELays the TRANsformation of characters on a tree) optimization - the character is optimized as far from the root as possible.

Lipscomb page 32:

The **second** tree has a **DELTRAN** (DELays the TRANsformation of characters on a tree) optimization - the character is optimized as far from the root as possible.

Wagner optimization

Farris, J.S. 1970. Methods for computing Wagner trees.
Systematic Zoology 19: 83-92.

Fitch parsimony
Wagner "
Dollo "
Camin-Sokal "
Sankoff "

Fitch, W.M. 1971. Toward defining the course of evolution :
minimal change for a specific tree topology.
Systematic Zoology 20: 406-416.

Emil Hans WILLI HENNIG

*20.4.1913 †5.11.1976

Hennig, W. 1950. Grundzüge einer Theorie der phylogenetischen Systematik

Hennig, W. 1966. Phylogenetic systematics

CLADISTIC revolution

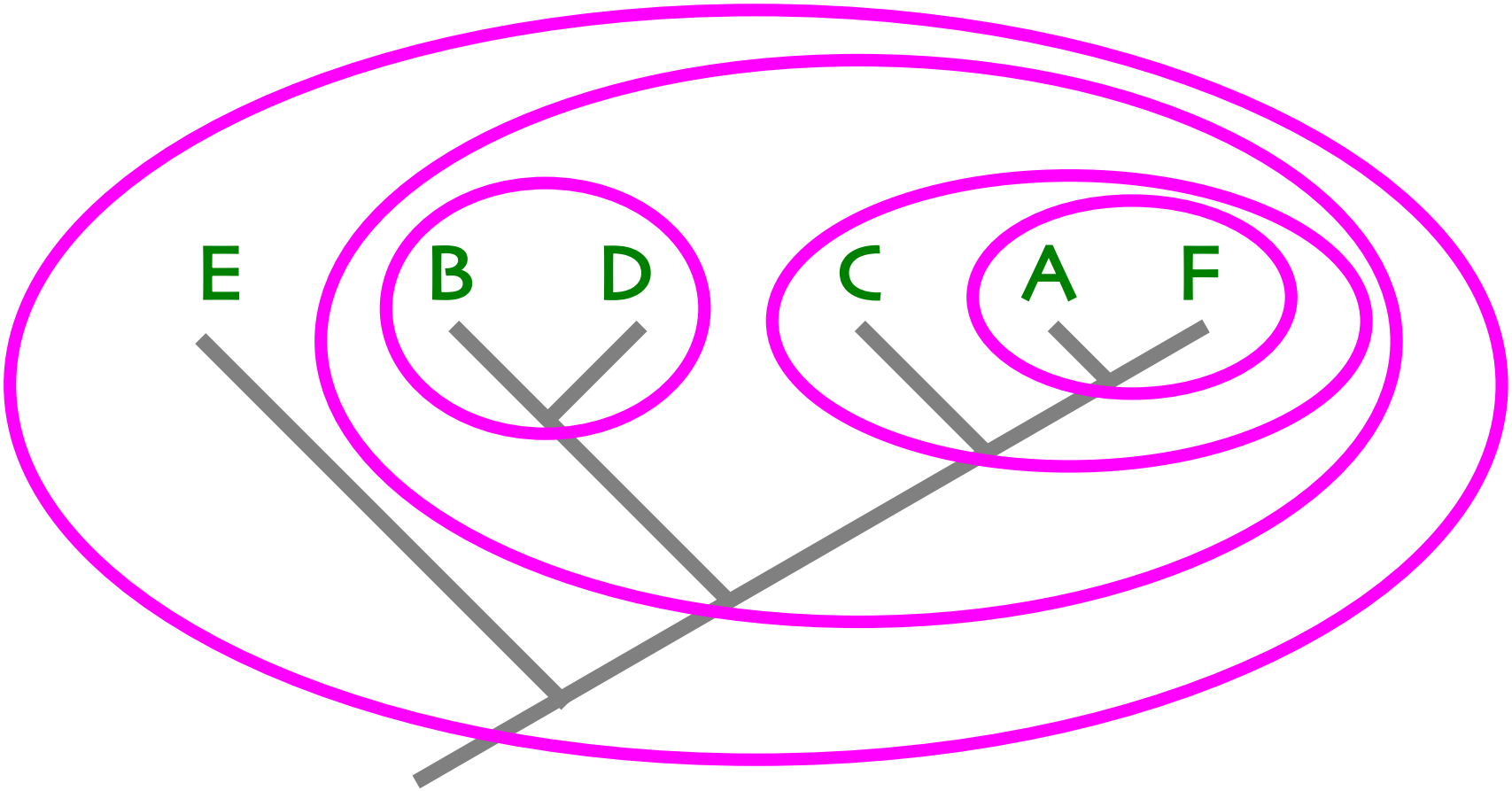
CLEAR, EXPLICIT & LOGICAL presentation of basic principles of phylogenetic analysis

SYNAPOMORPHY

MONOPHYLY

PARAPHYLY

MONOPHYLY, paraphyly, polyphyly

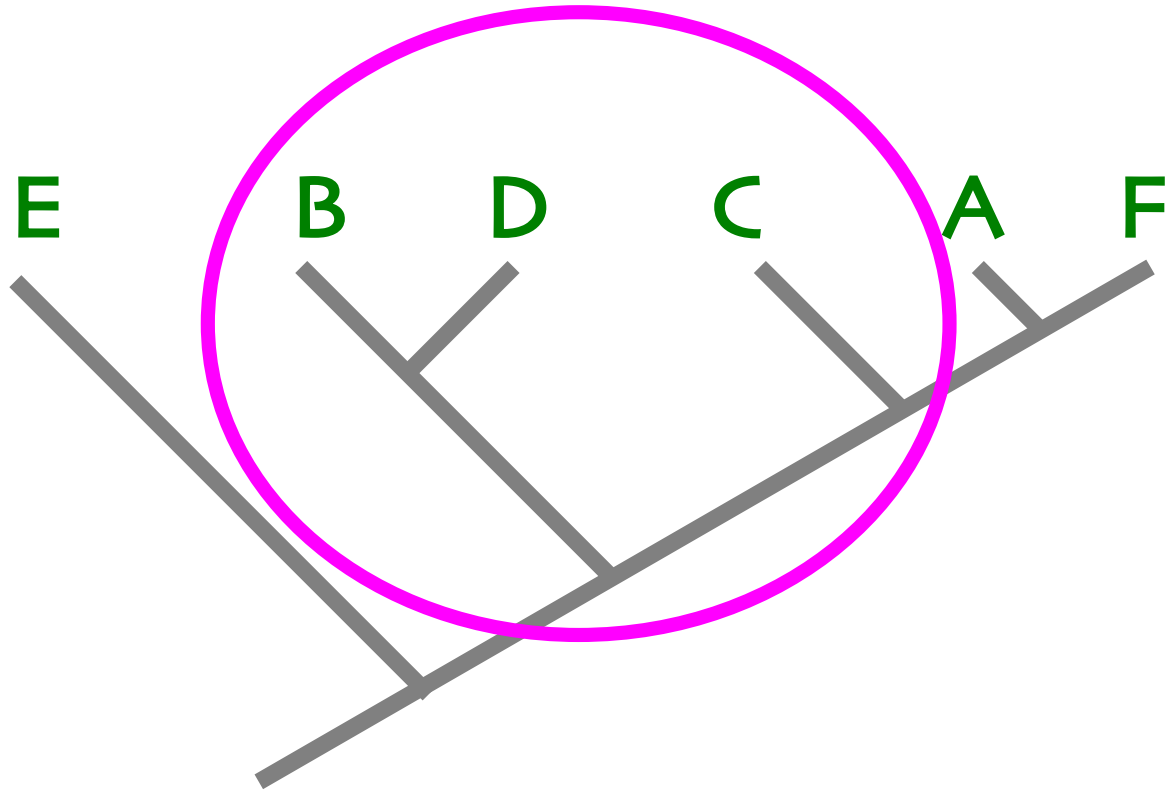


MONOPHYLY, paraphyly, polyphyly

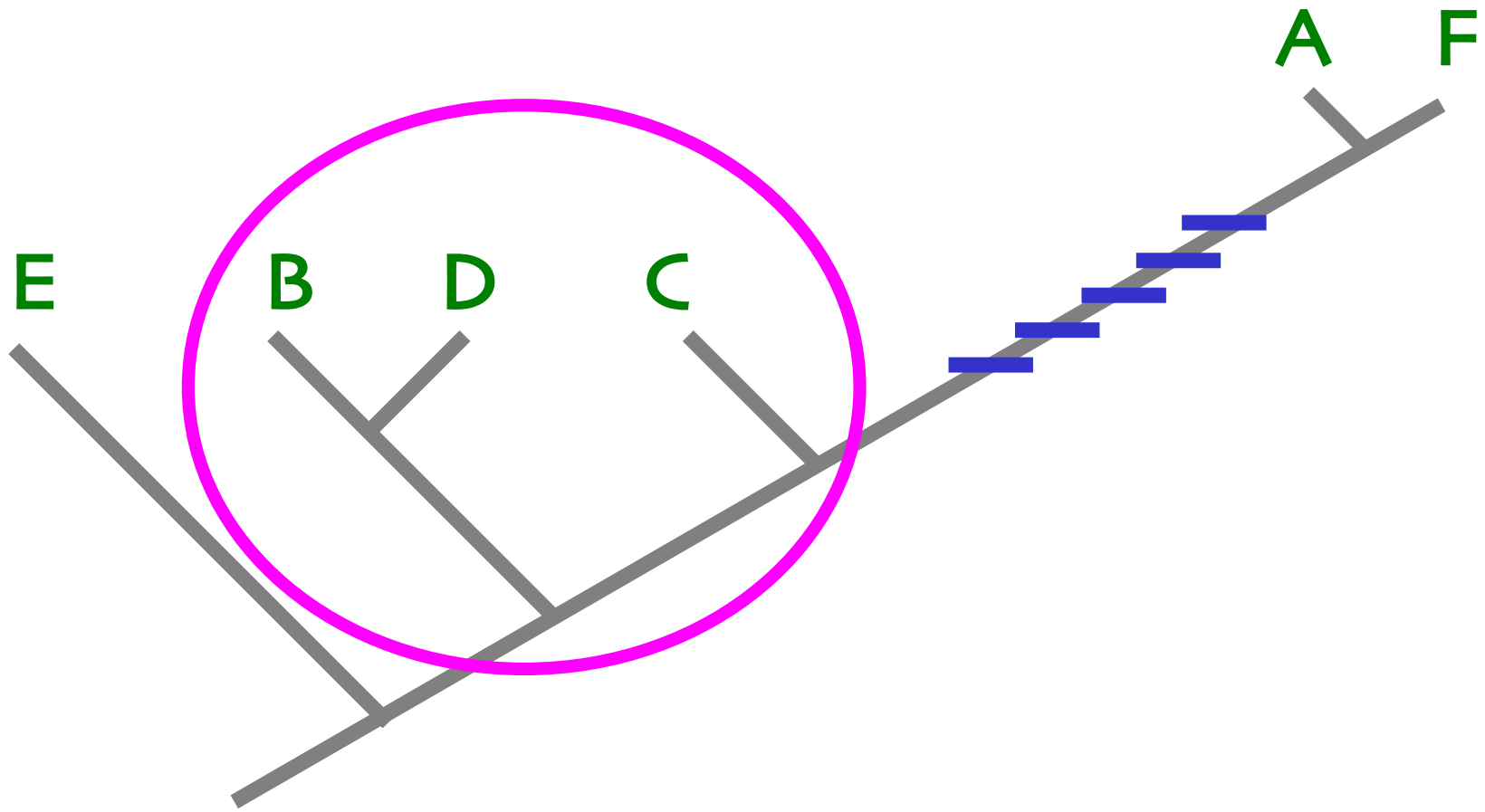
1. Monophyletic group includes ALL descendants of the common ancestor

2. In paraphyletic group 1 or more of the descendants are left out

MONOPHYLY, paraphyly, polyphyly



MONOPHYLY, paraphyly, polyphyly



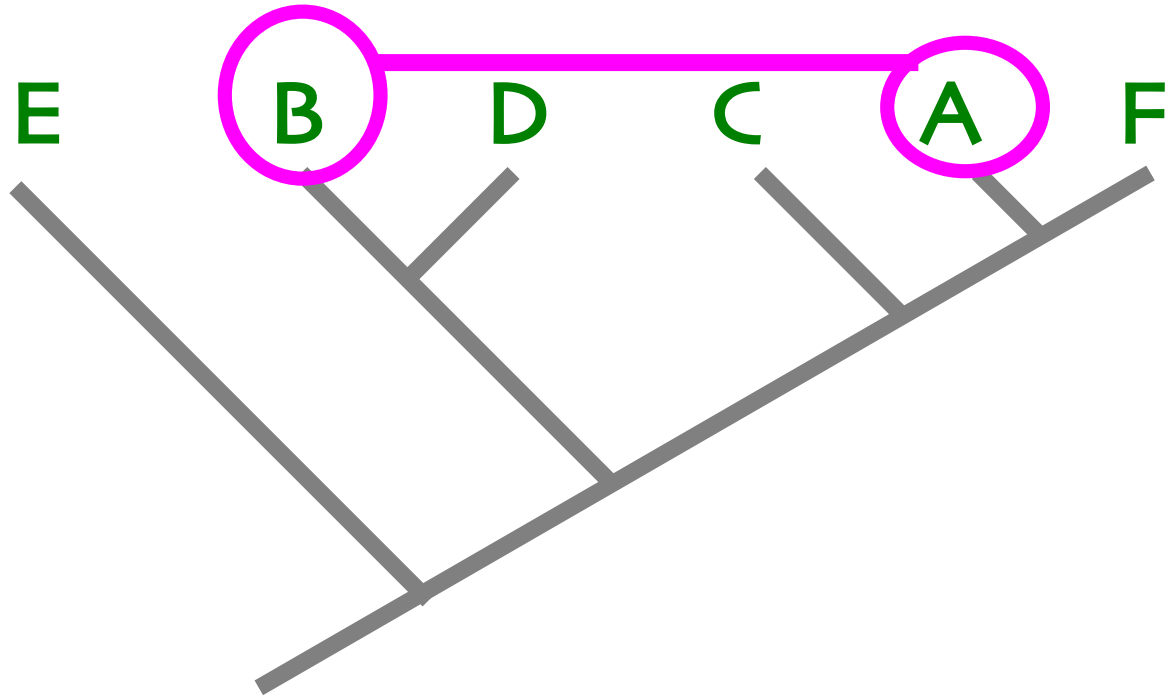
MONOPHYLY, paraphyly, polyphyly

1. Monophyletic group includes ALL descendants of the common ancestor

2. In paraphyletic group 1 or more of the descendants are left out

3. In polyphyletic group common ancestor is left out

MONOPHYLY, paraphyly, polyphyly



MONOPHYLY, paraphyly, polyphyly

1. Monophyletic group is defined by
   SYNAPOMORPHY

2. Paraphyletic group by **plesiomorphy**

   &

3. Polyphyletic group by **homoplasy**

MONOPHYLY, paraphyly, polyphyly

1. Monophyletic groups provide PRECISE information about relationships

2. Paraphyletic group imprecise

&

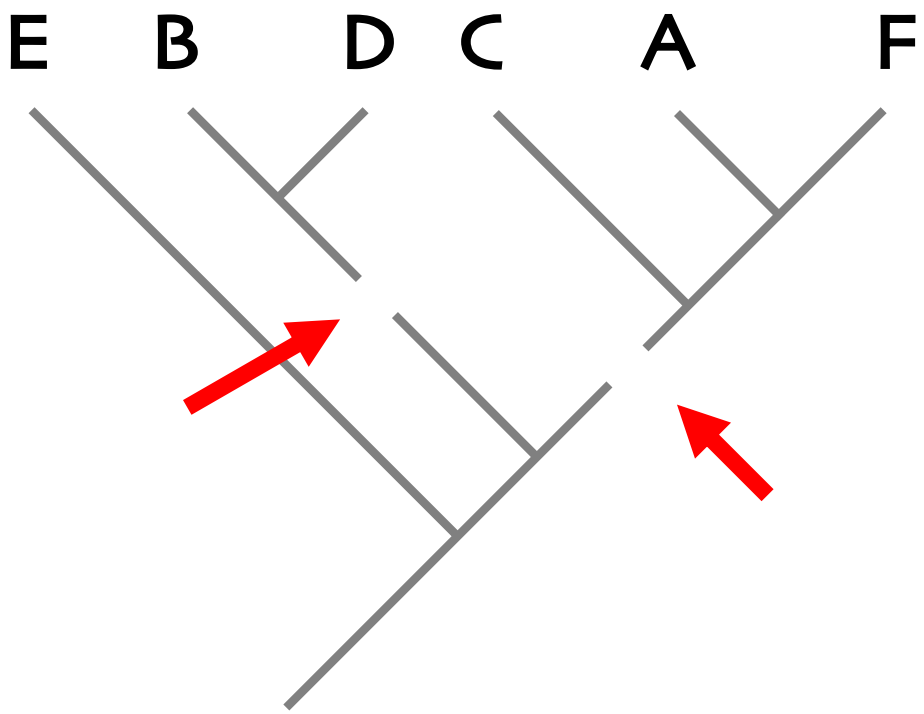
3. Polyphyletic groups **MISLEADING** information

MONOPHYLY, paraphyly, polyphyly

1. Monophyletic group can be separate from tree with 1 cut

WHOLE parts of Tree of Life

MONOPHYLY, paraphyly, polyphyly

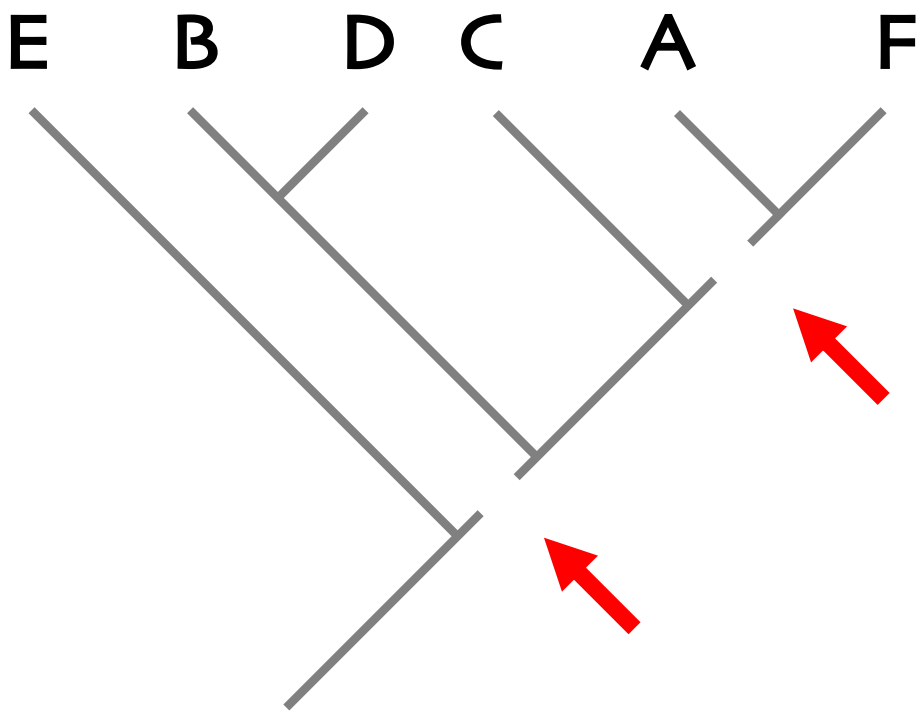


MONOPHYLY, paraphyly, polyphyly

1. Monophyletic group can be separate from tree with 1 cut

2. Paraphyletic with 2

MONOPHYLY, paraphyly, polyphyly



MONOPHYLY, paraphyly, polyphyly

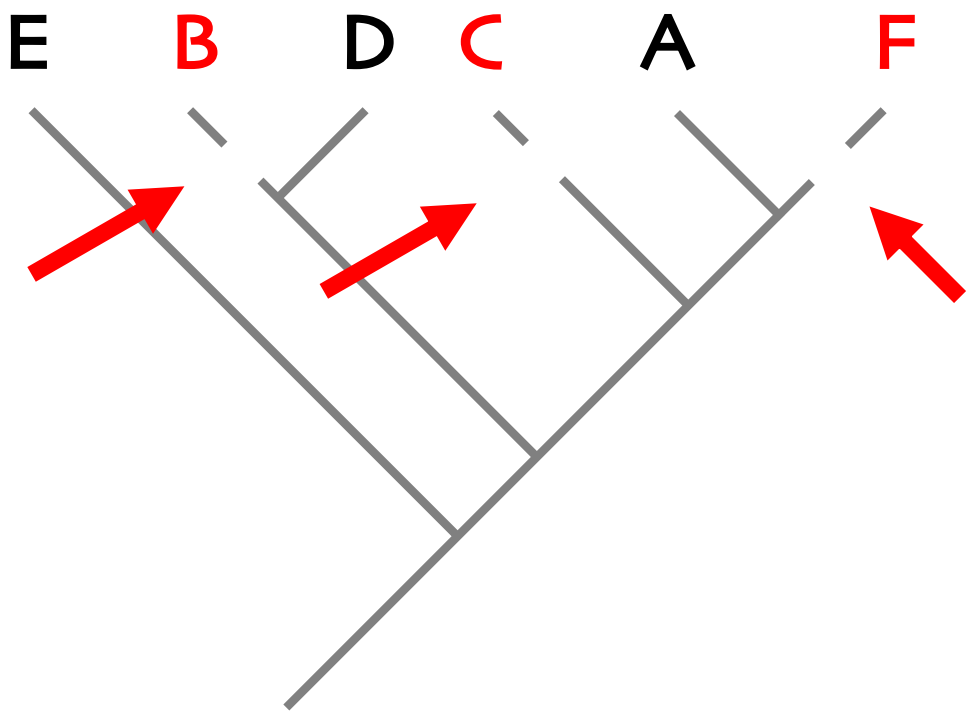
1. Monophyletic group can be separate from tree with 1 cut

2. Paraphyletic with 2

   &

3. Polyphyletic with $\geq$ 2

MONOPHYLY, paraphyly, polyphyly

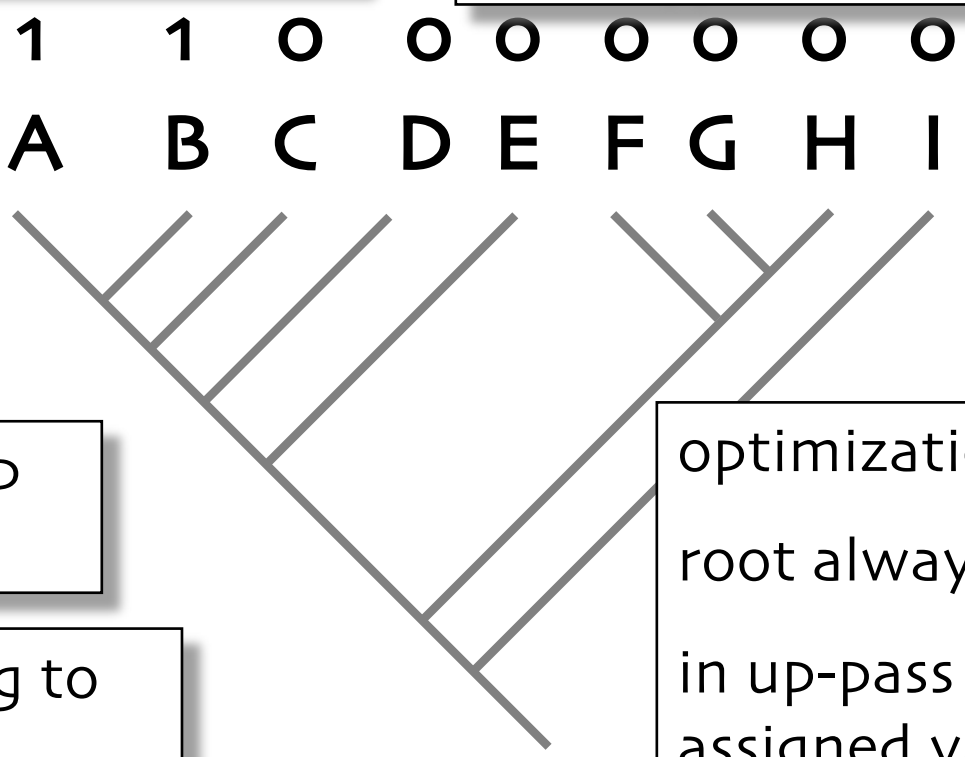


MONOPHYLY, paraphyly, polyphyly

Farris, J.S. 1974. Formal definitions of paraphyly and polyphyly. *Systematic Zoology* 23: 548-554

group membership character

defined groups inspected on the tree currently accepted as the best hypothesis about phylogeny



member of group
ch. state = 1

does NOT belong to group = 0

optimization (down & up)

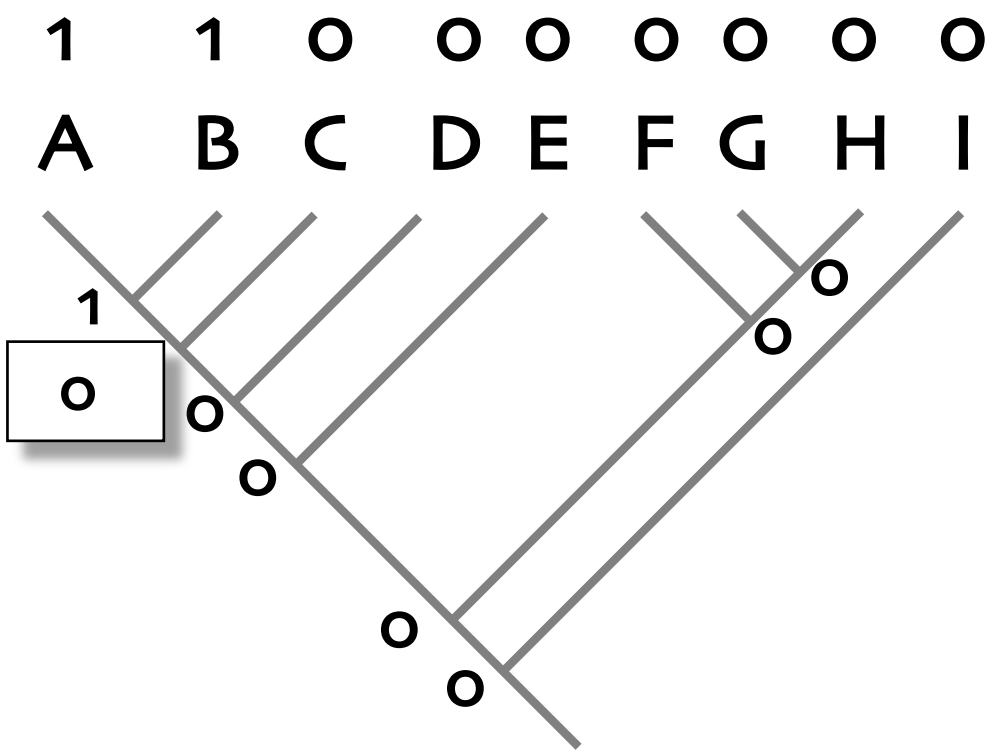
root always signed 0

in up-pass always assigned value of the immediate ancestor

MONOPHYLY, paraphyly, polyphyly

change 0 > 1 only once -->

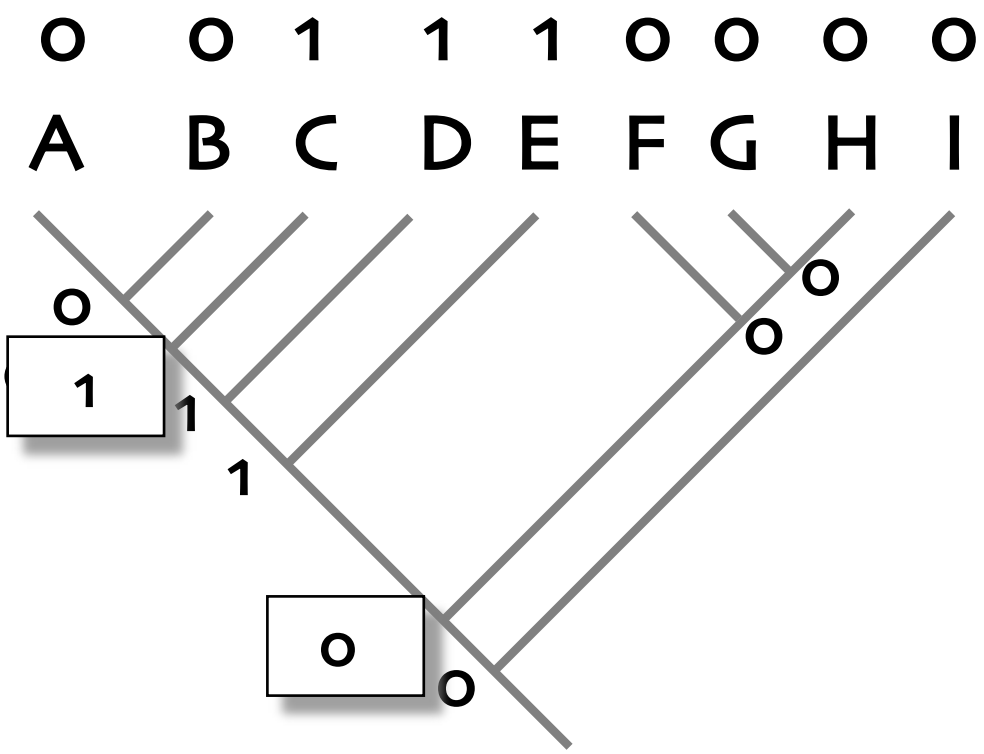
group monophyletic (A & B)



MONOPHYLY, paraphyly, polyphyly

change 1 > 0 -->

group paraphyletic (C, D & E)

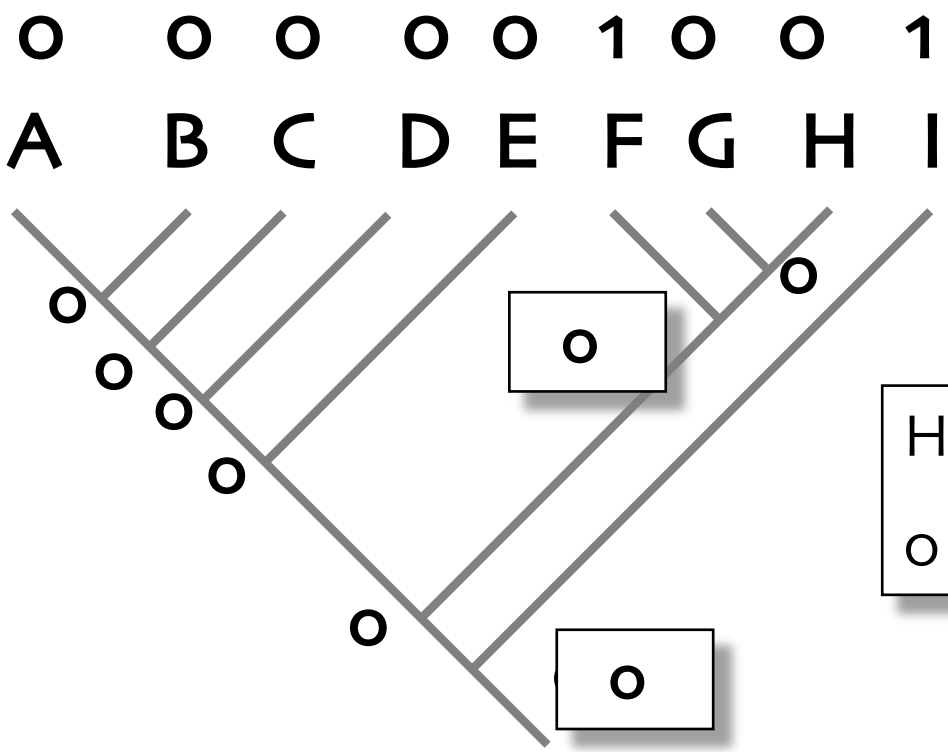


MONOPHYLY, paraphyly, polyphyly

Group membership matrices
can be produced with e.g. TNT

all other changes -->

group polyphyletic (F & I)



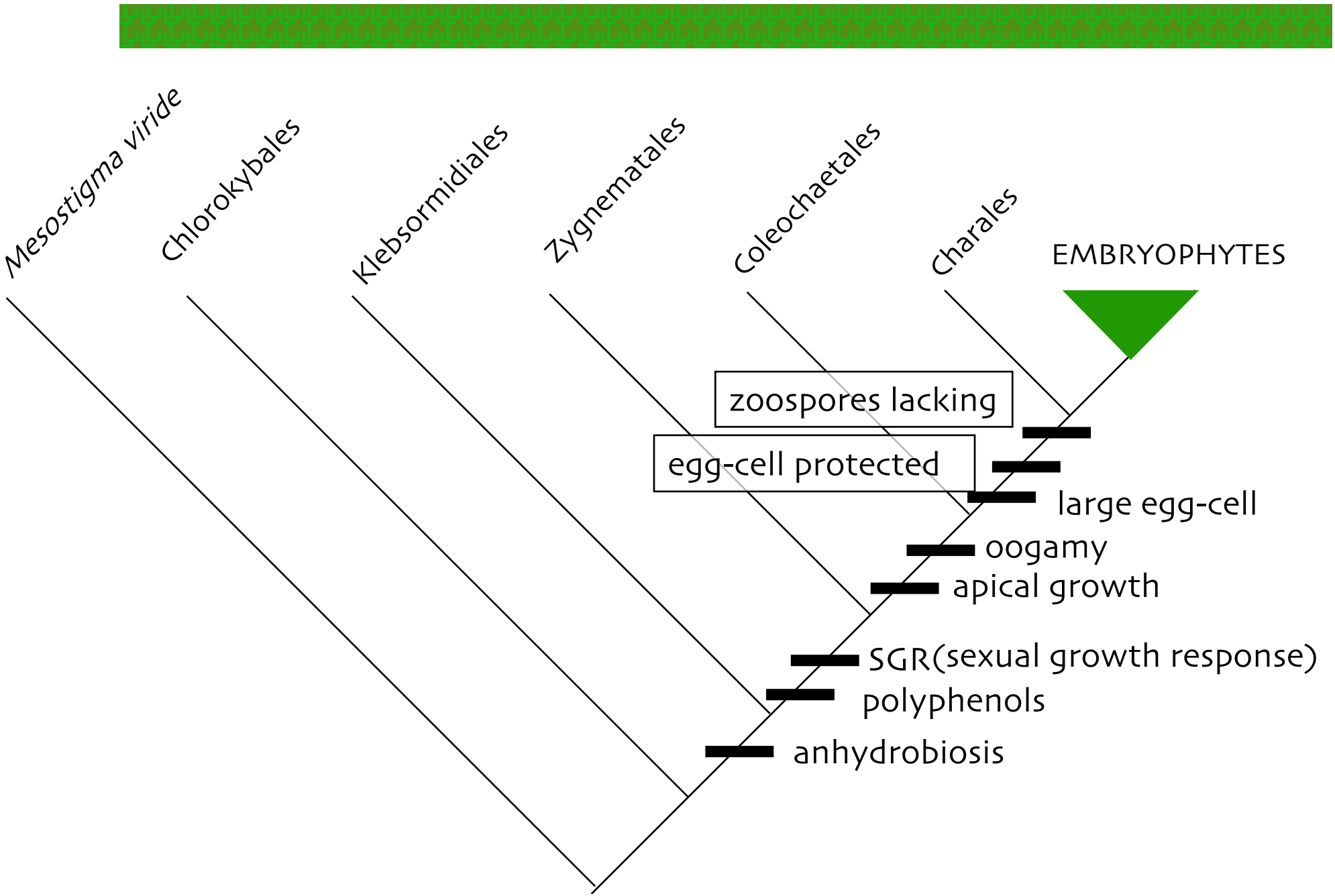
Here change

0 > 1 2x

MONOPHYLY, paraphyly, polyphyly

paraphyletic groups give too COMPLICATED explanation about evolutionary history of characters

EMBRYOPHYTES



MONOPHYLY, paraphyly, polyphyly

"Green algae"

- numerous "green algal" orders e.g.
  - Chlorokybales
  - Klebsormidiales
  - Zygnematales
  - Coleochaetales
  - Charales

Embryophytes

- Hepatics
- Mosses
- Hornworts
- Polysporangiophytes

MONOPHYLY, paraphyly, polyphyly

Paraphyletic groups give too COMPLICATED explanation about evolutionary history

&

polyphyletic groups too SIMPLE

e.g. Homeothermia

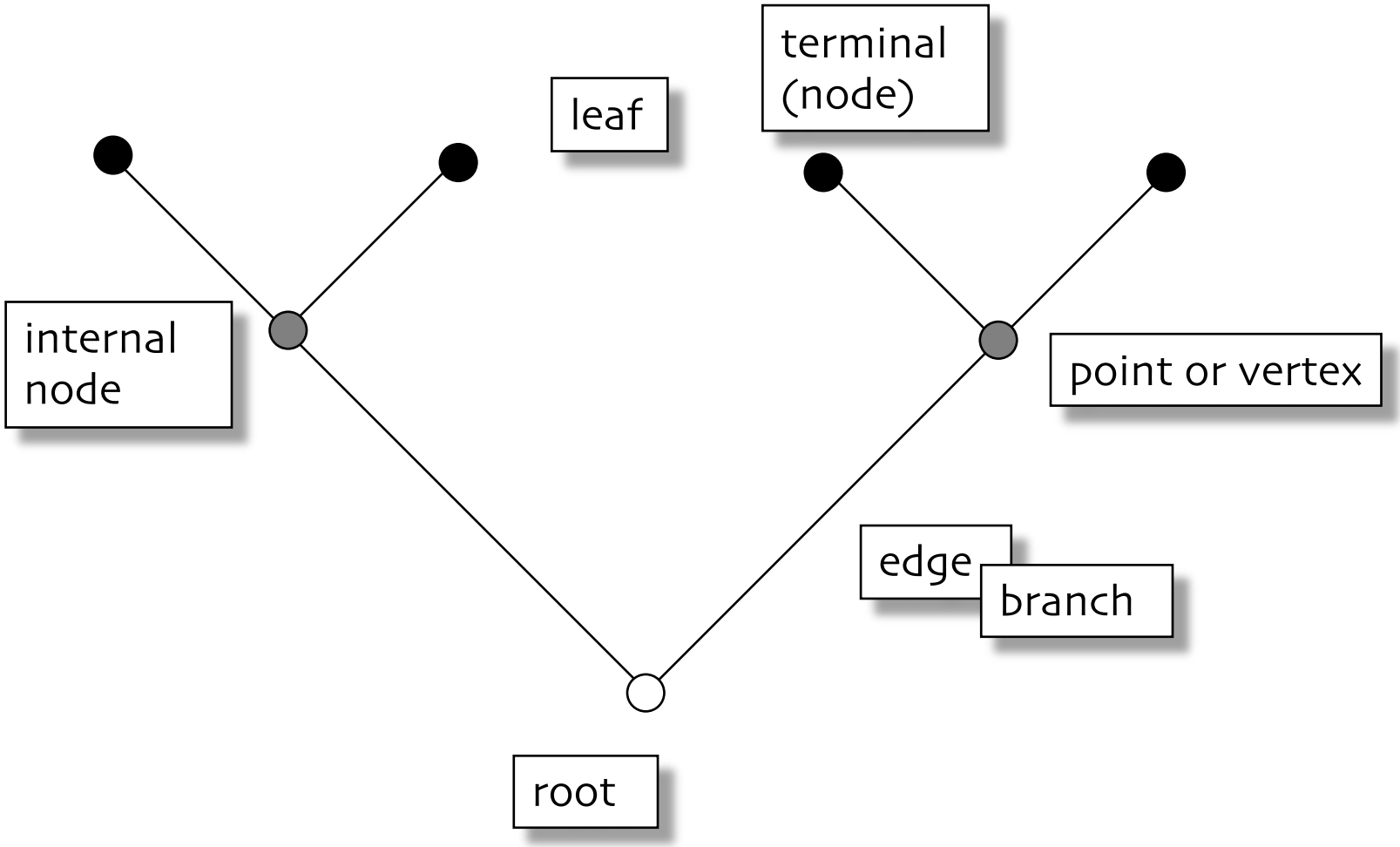
use of these kind of groups in classification is ***misleading***

SIMULTANEOUS USE IS ALWAYS DANGEROUS

SEKAKÄYTTÖ ON AINA VAARALLISTA!!!

What are trees?

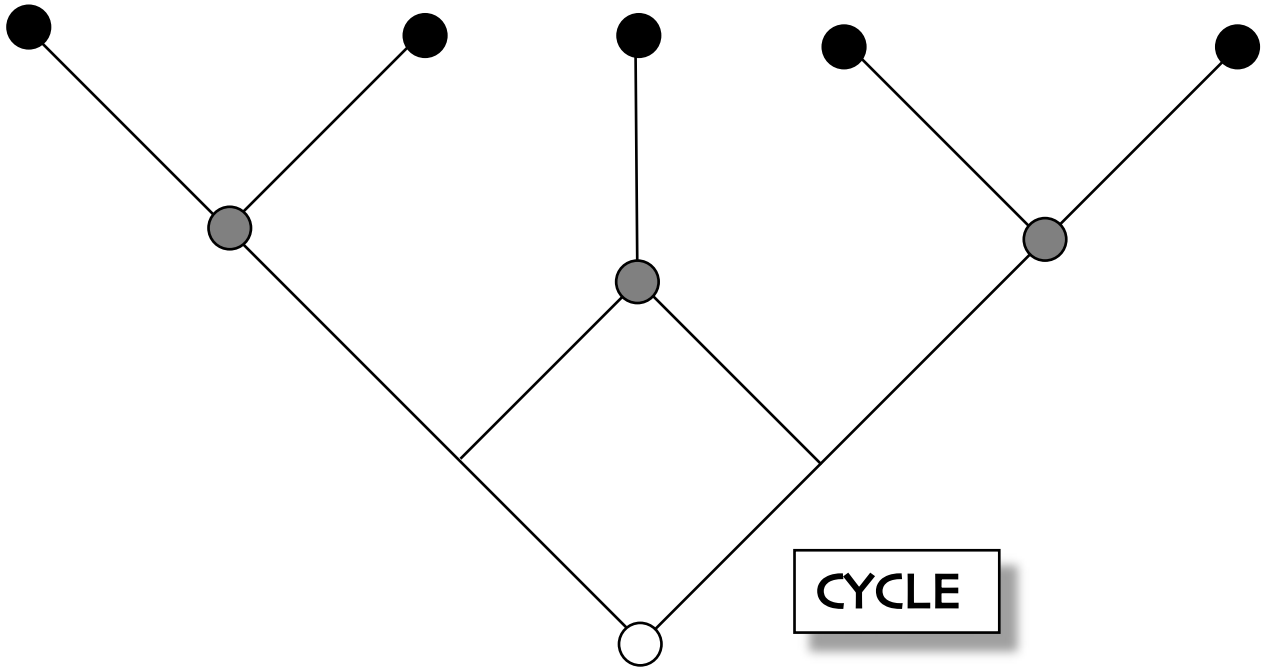
acyclic connected GRAPH



Page & Holmes 1998.
Molecular evolution

Network

cyclic connected GRAPH

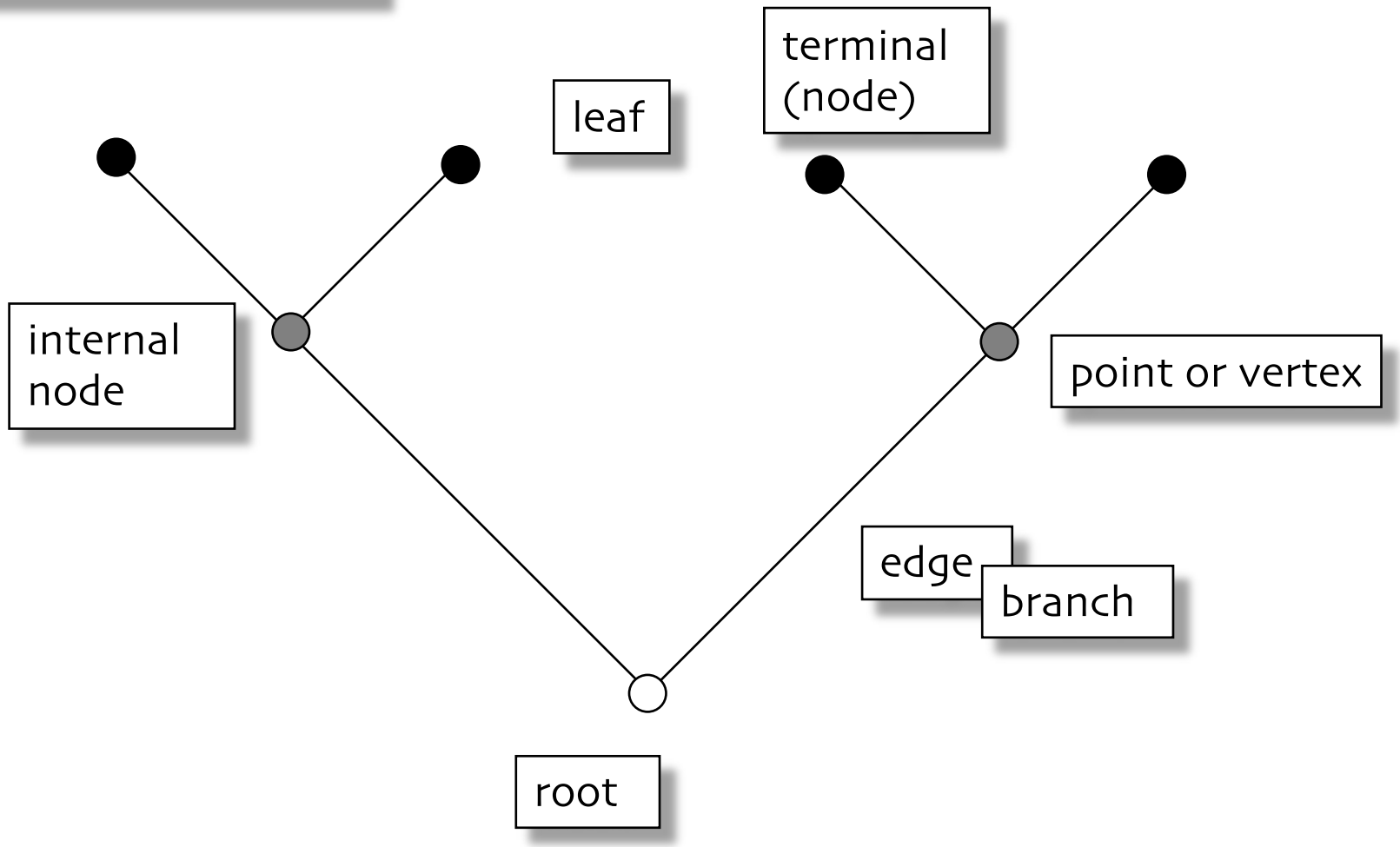


Page & Holmes
1998. Molecular

What are trees?

acyclic connected GRAPH

Steiner trees

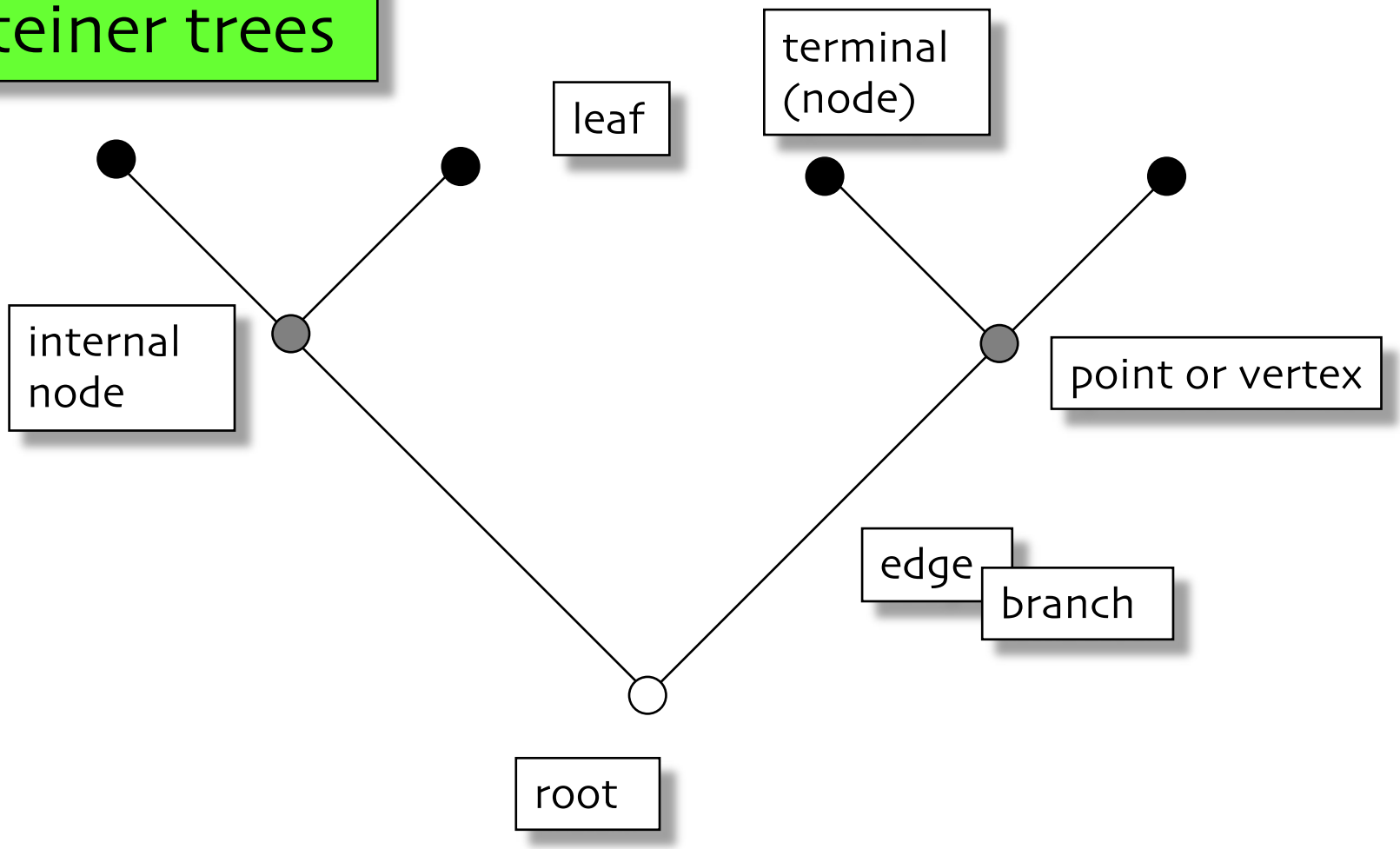


Page & Holmes 1998.
Molecular evolution

What are trees?

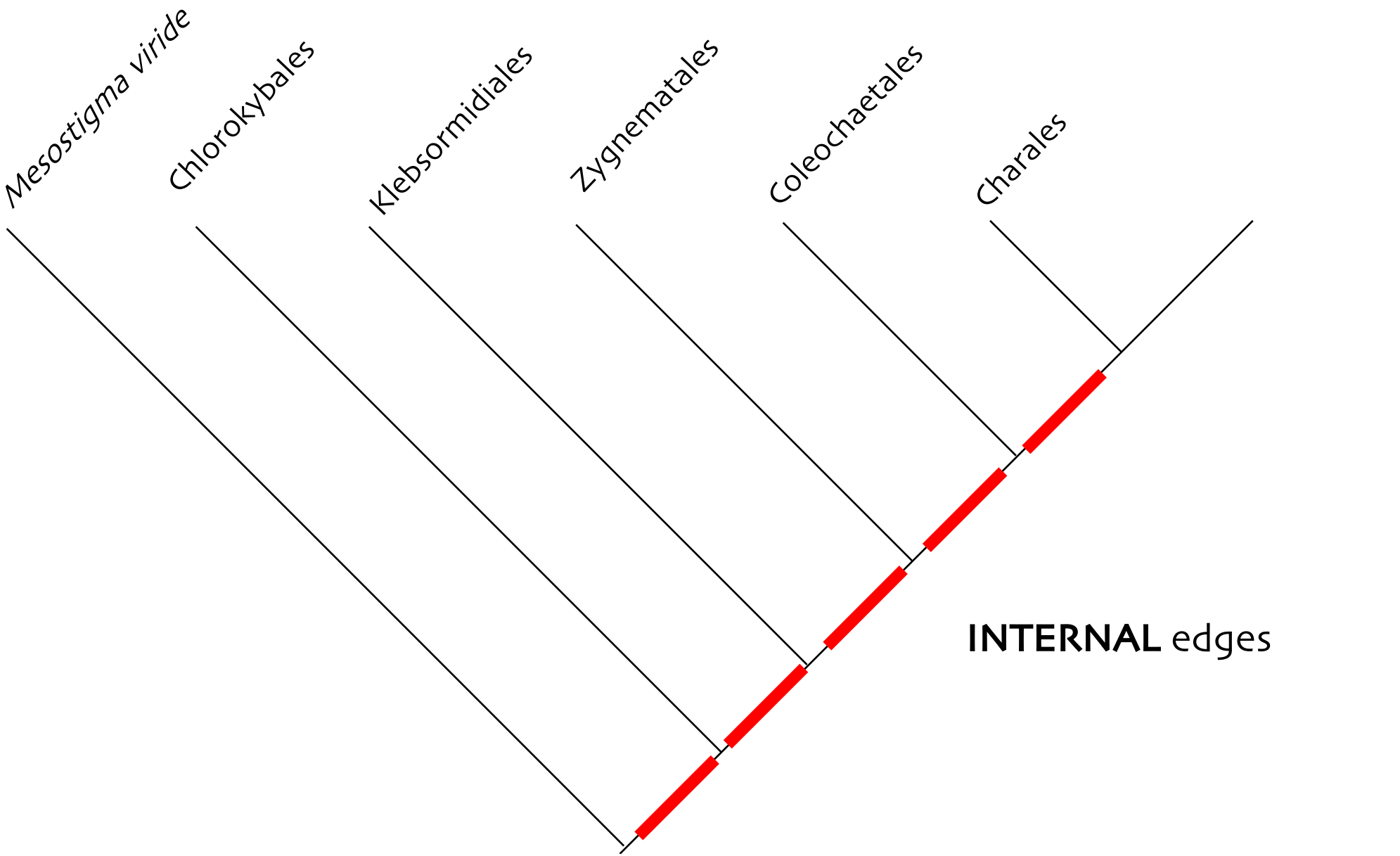
acyclic connected GRAPH

rectilinear Steiner trees

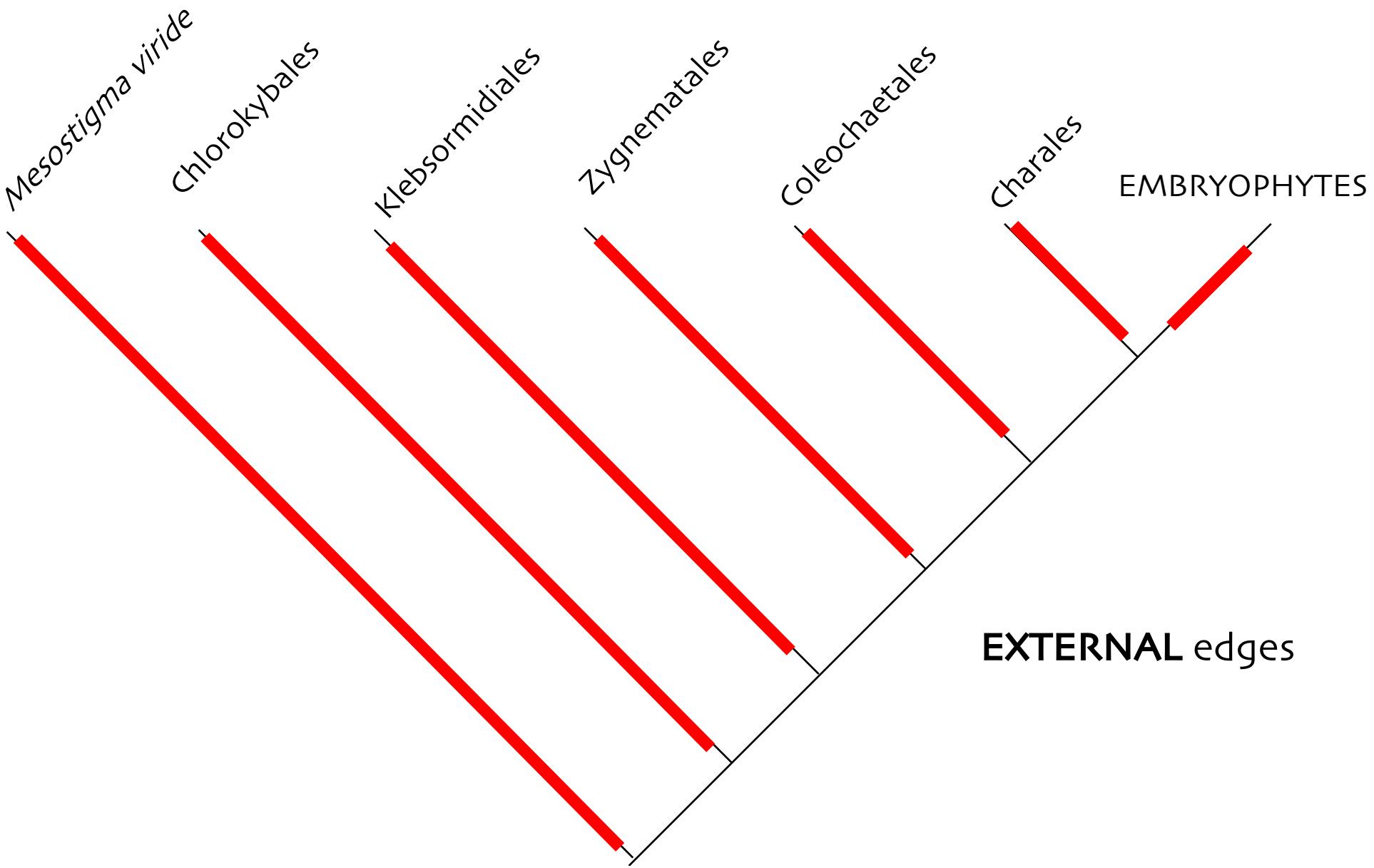


Page & Holmes 1998.
Molecular evolution

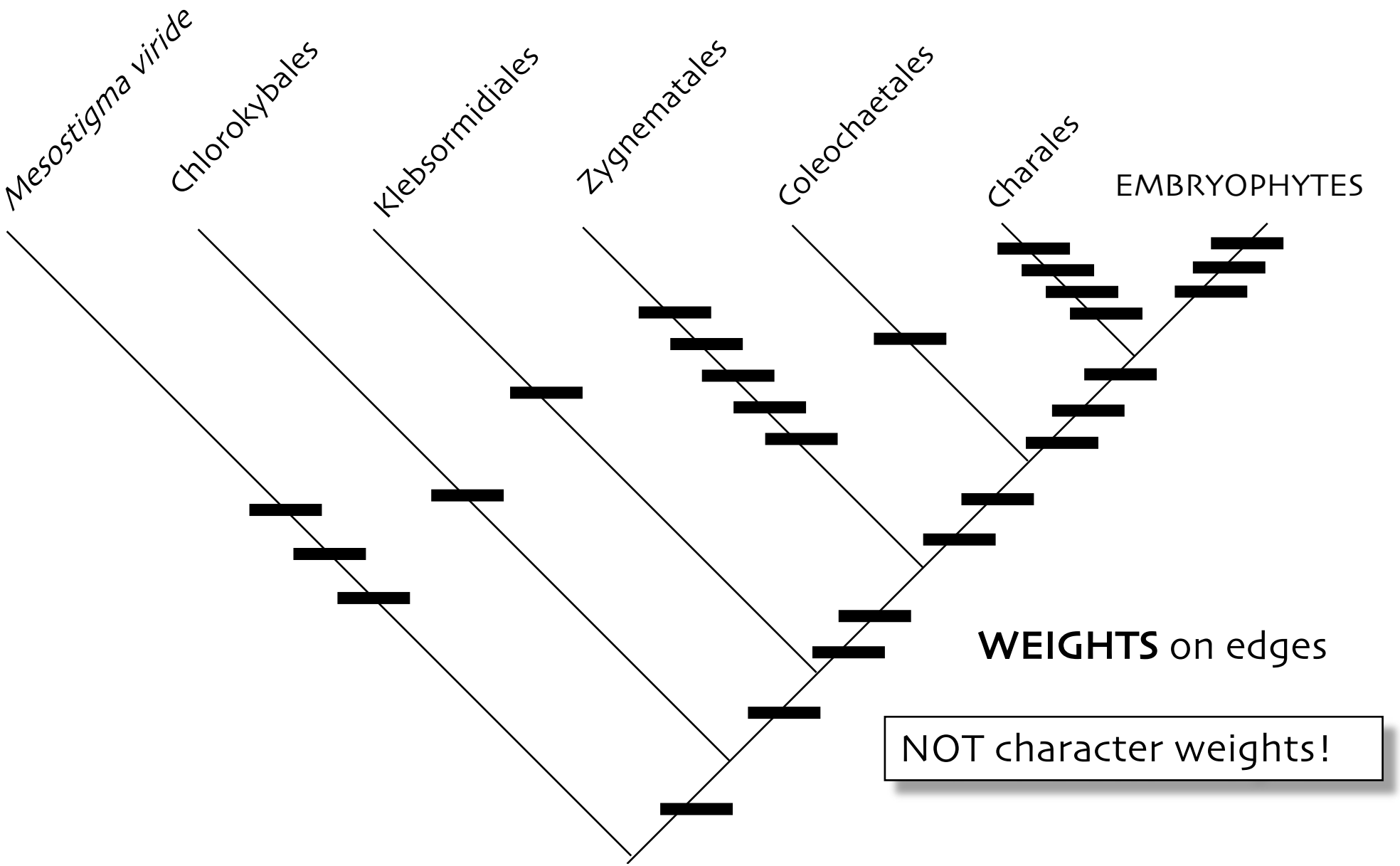
EMBRYOPHYTES

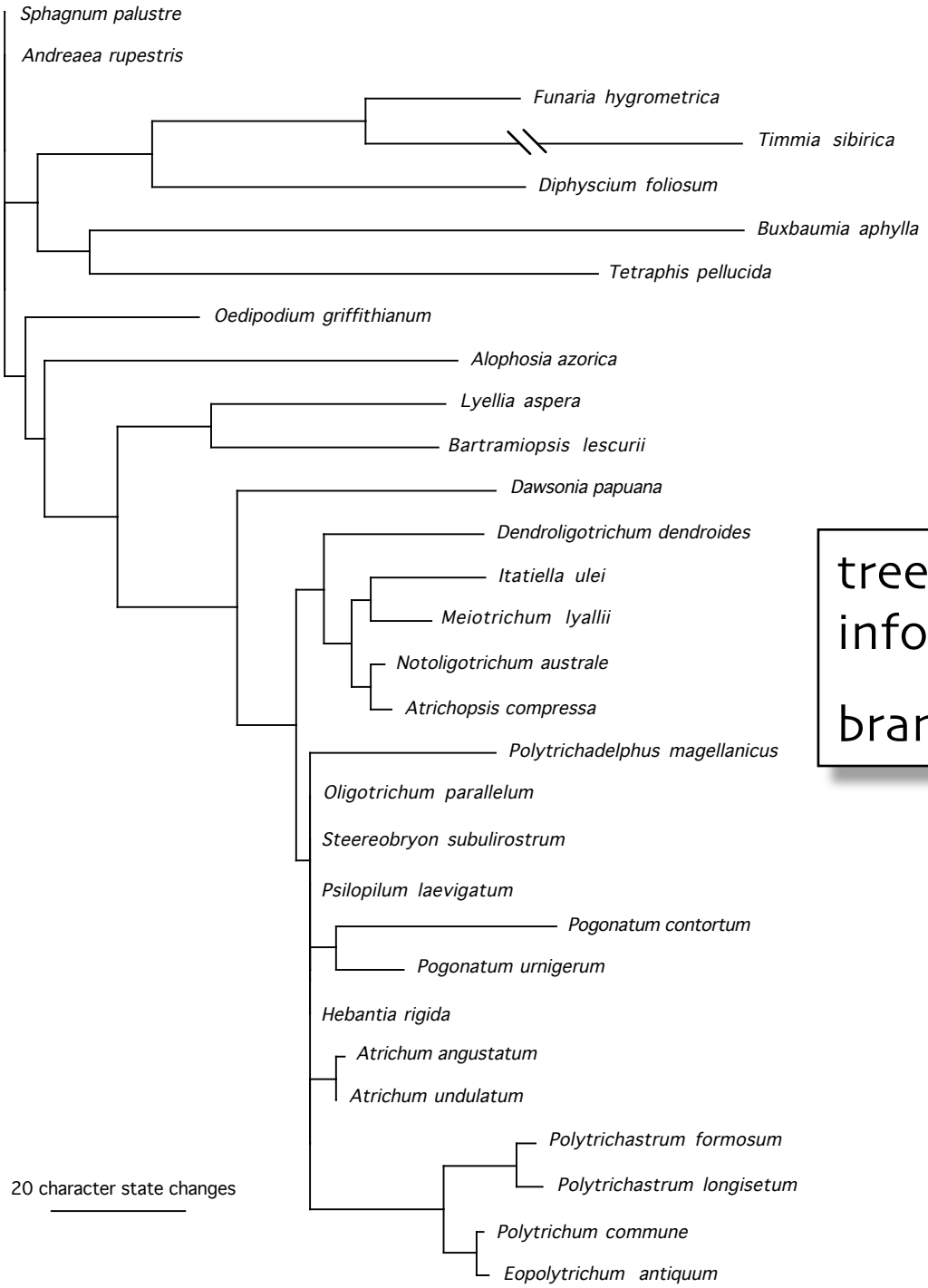


EMBRYOPHYTES



EMBRYOPHYTES

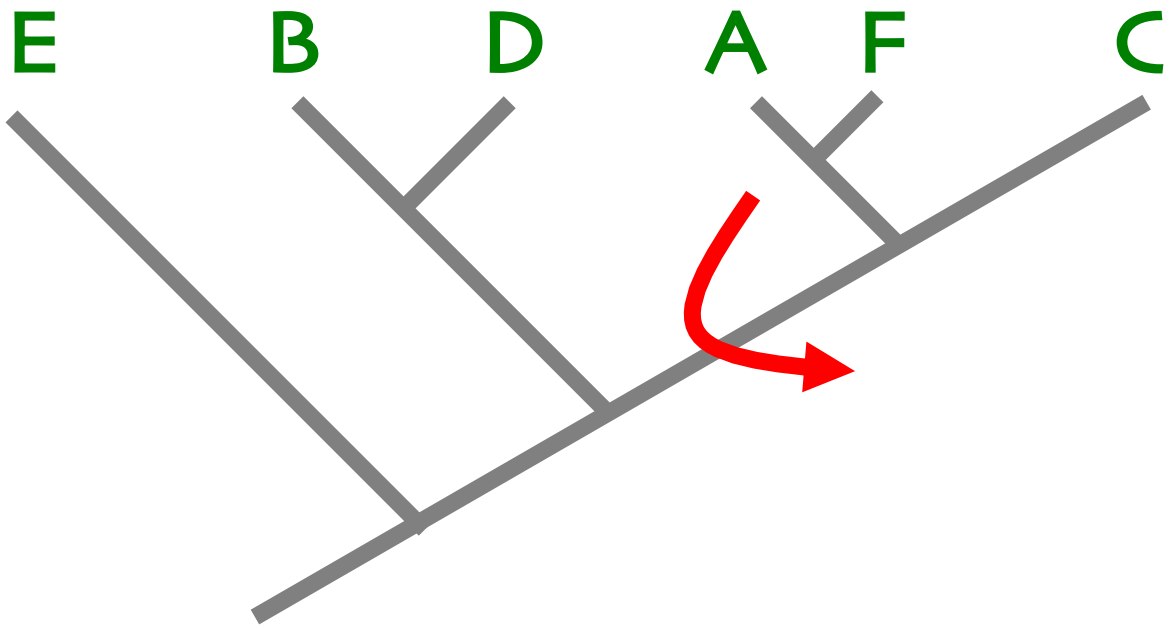




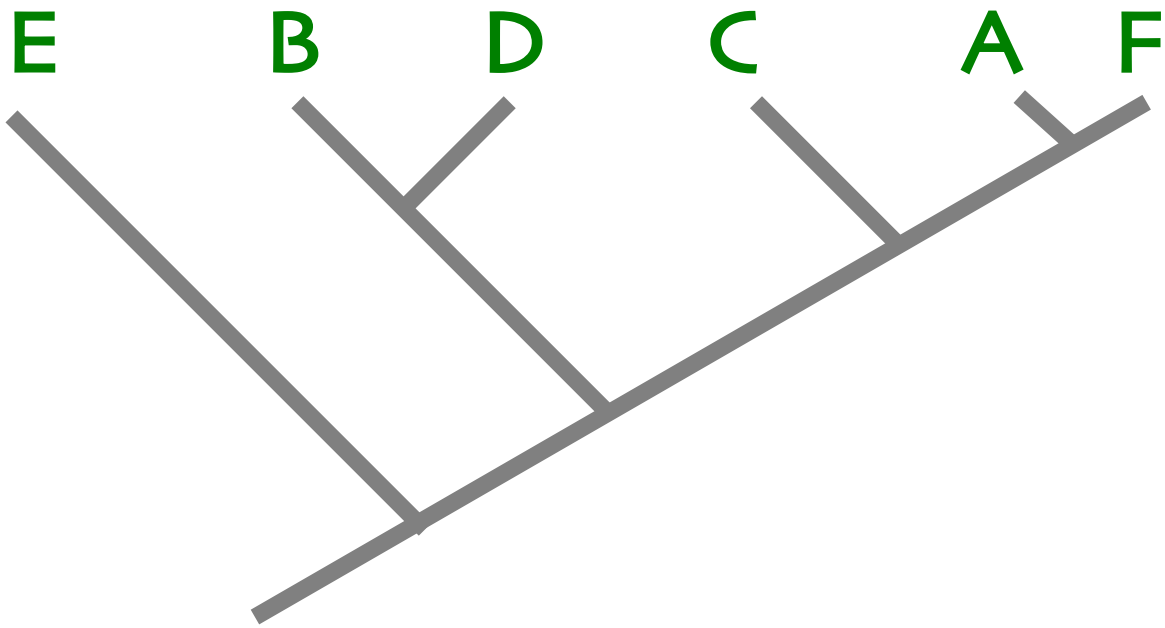
tree with additional information:

branch length

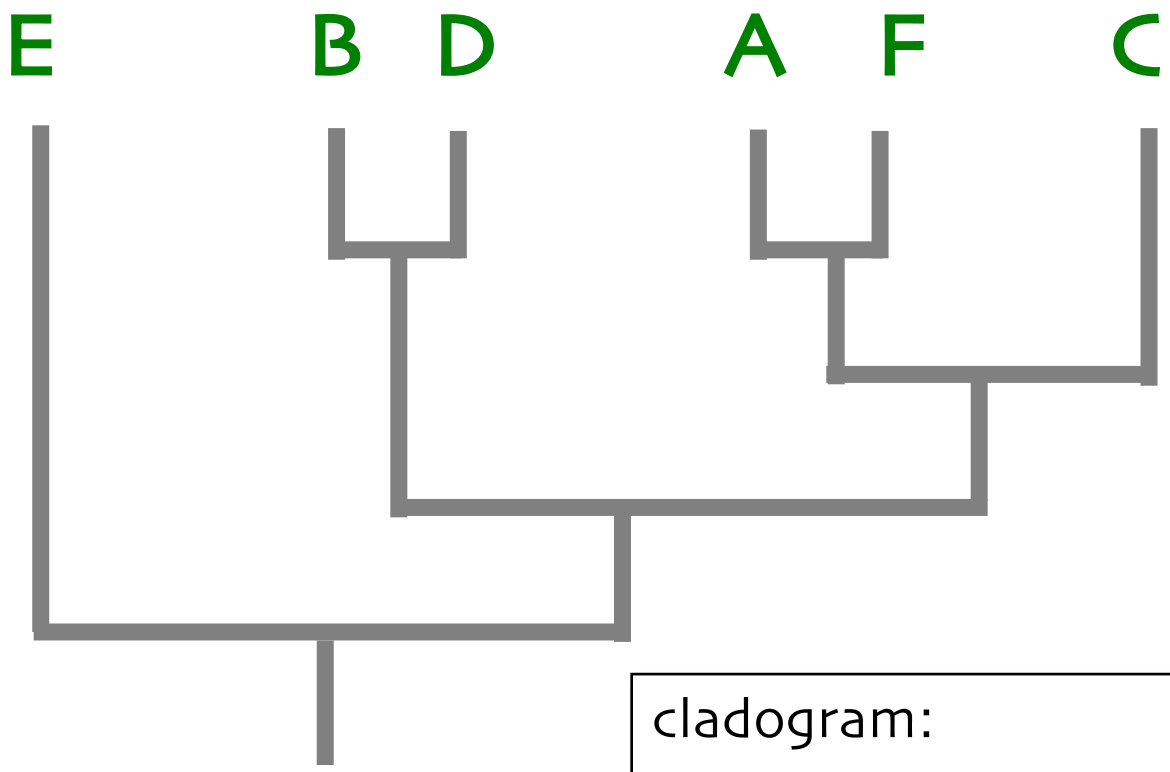
TREES & their form



TREES & their form



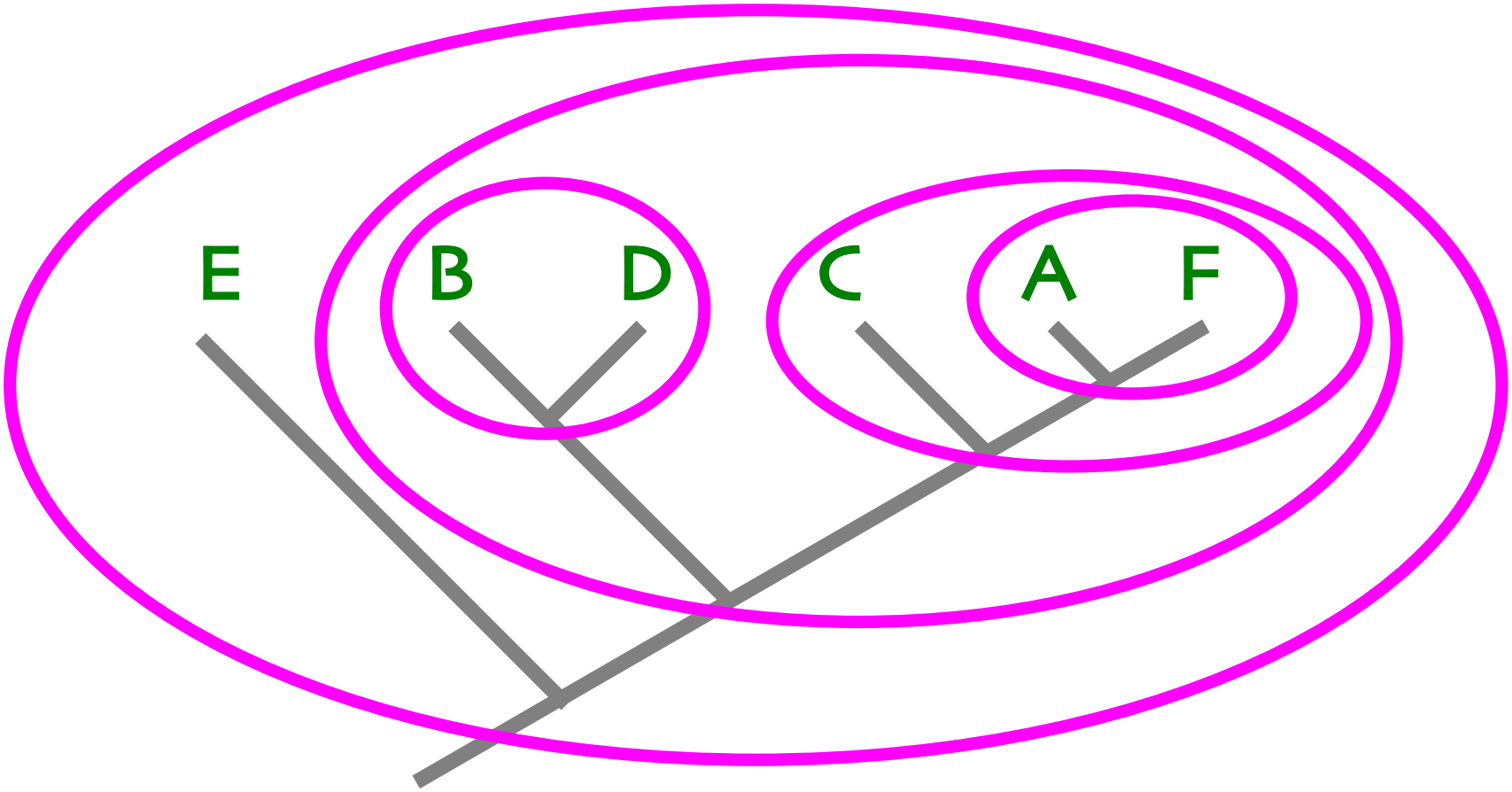
TREES & their form



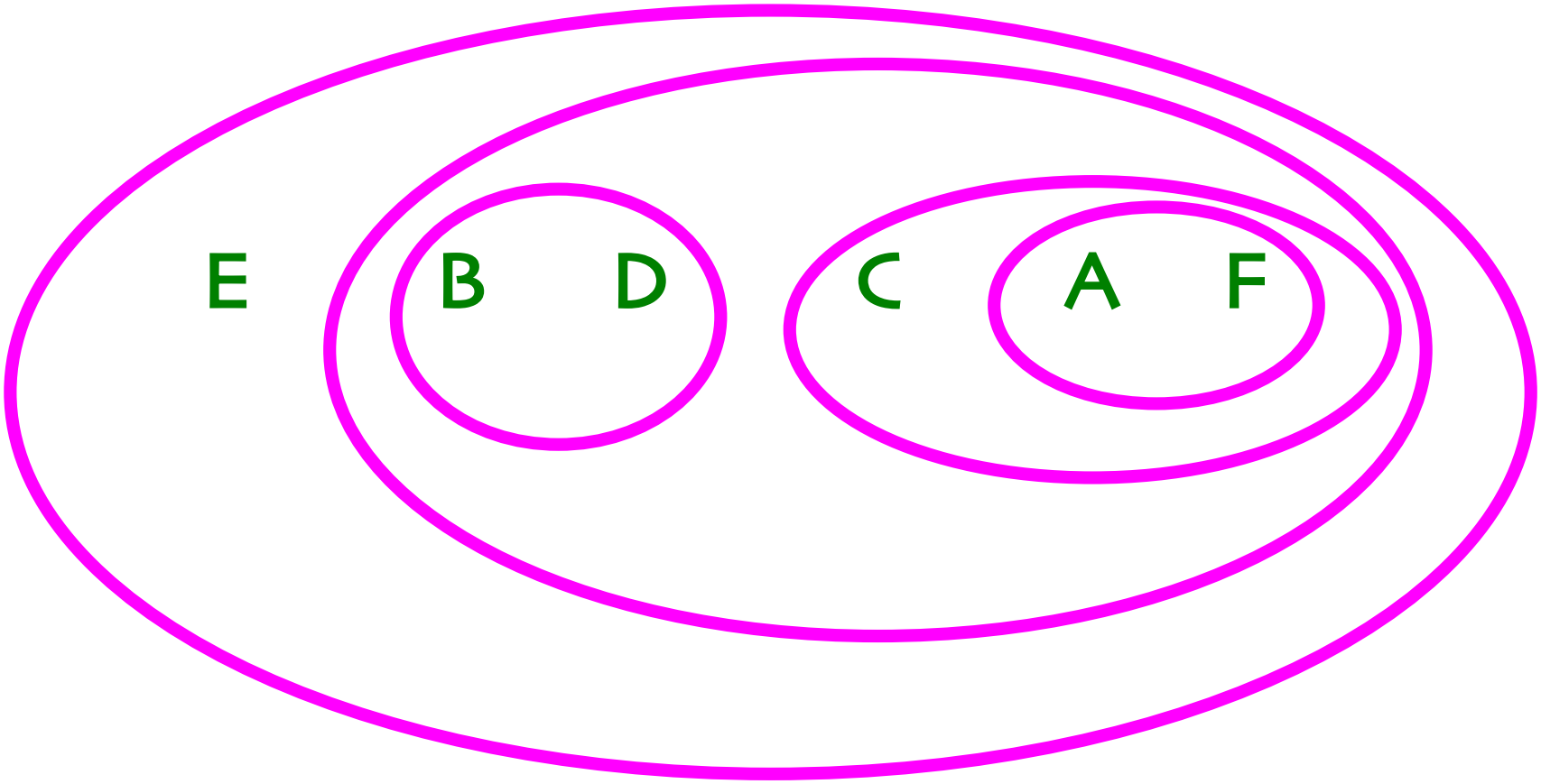
cladogram:

only branching ORDER matter

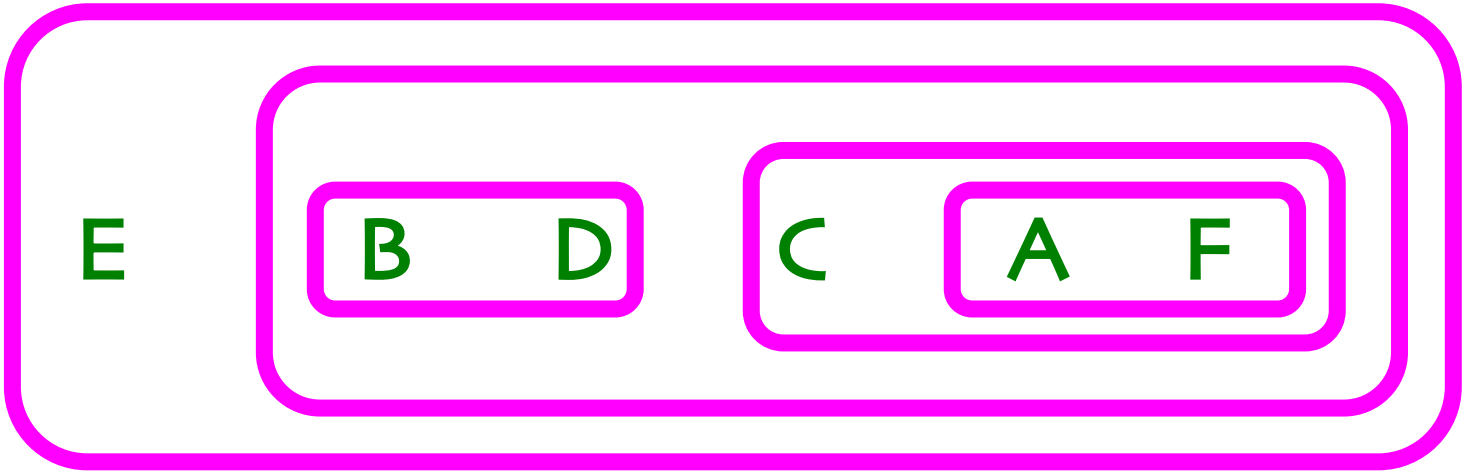
TREES & their form



TREES & their form

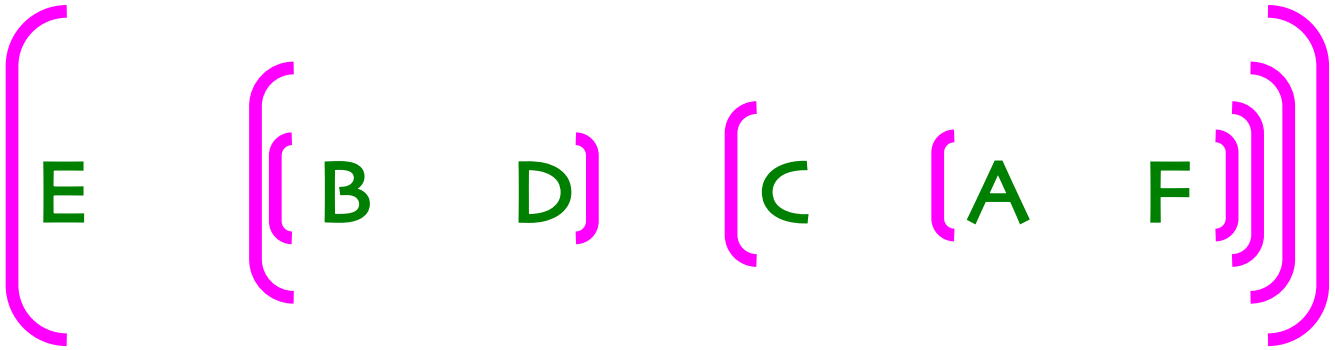


TREES & their form



Venn diagram

TREES & their form



From Venn diagram ---->

TREES & their form

(E ((B D) (C (A F))))

parenthetical notation

TREES & their form

Enables presentation of trees as part of normal text

(E ((B D) (C (A F))))

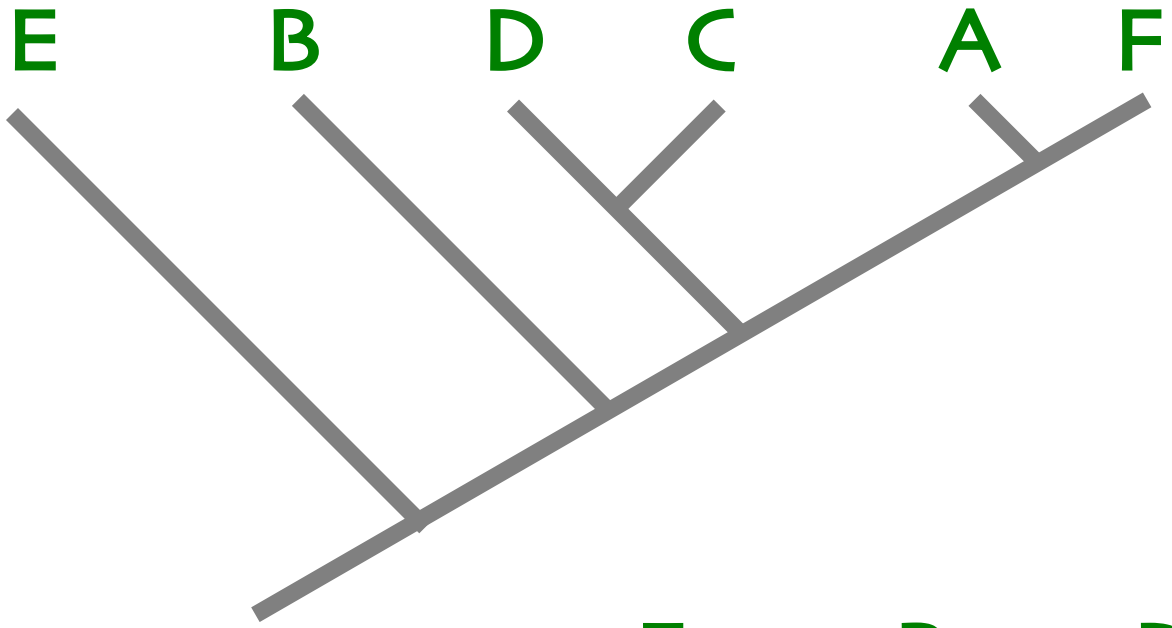
naturally used also in programming

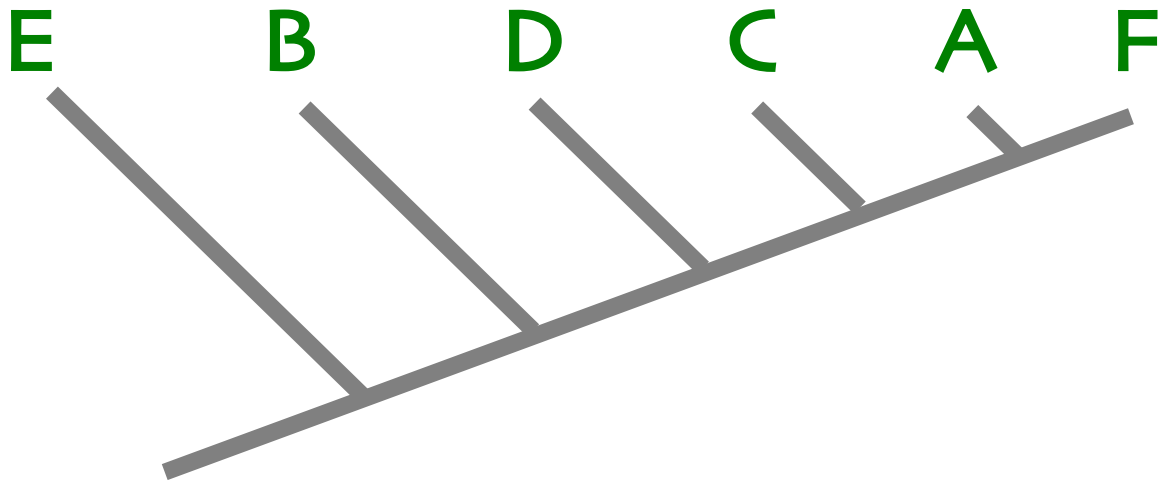
Consensus-, compromise- & "super"trees

ONLY trees treated & compared, **NOT CHARACTERS**

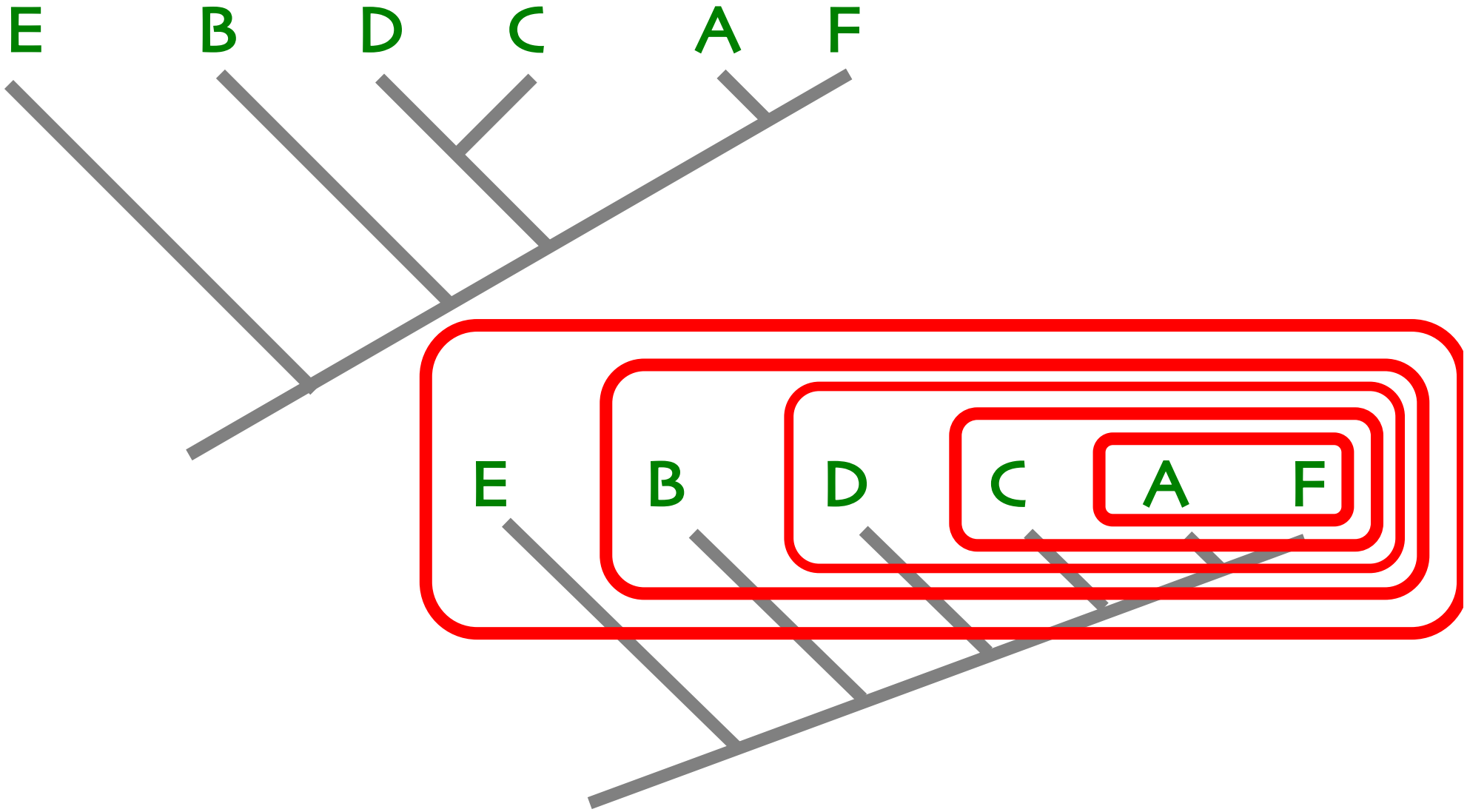
Consensus trees

Sokal, R. R. & Rohlf, F. J. 1981. Taxonomic congruence in the Leptopodomorpha re-examined. *Systematic Zoology* 30: 309-325.

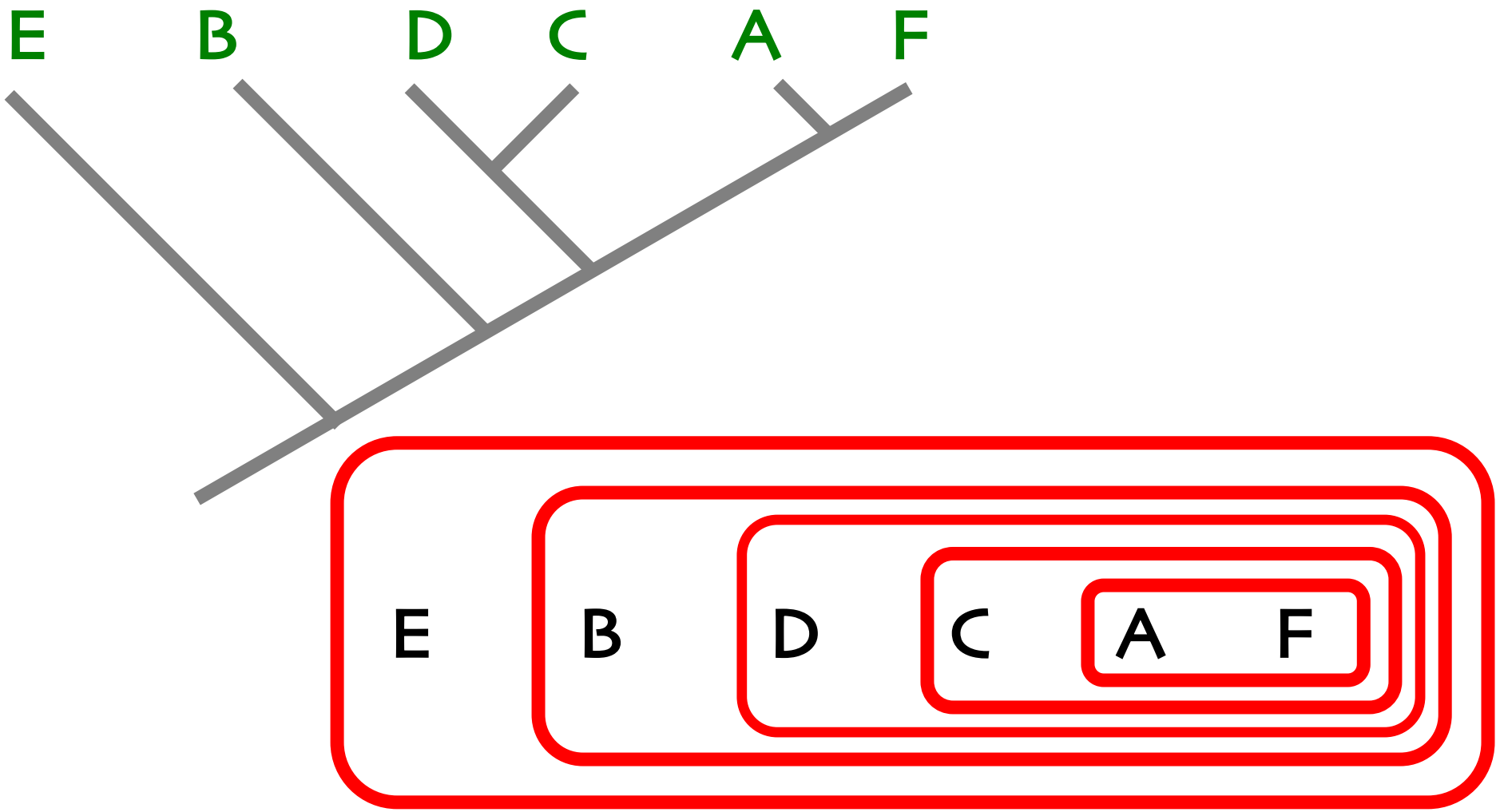




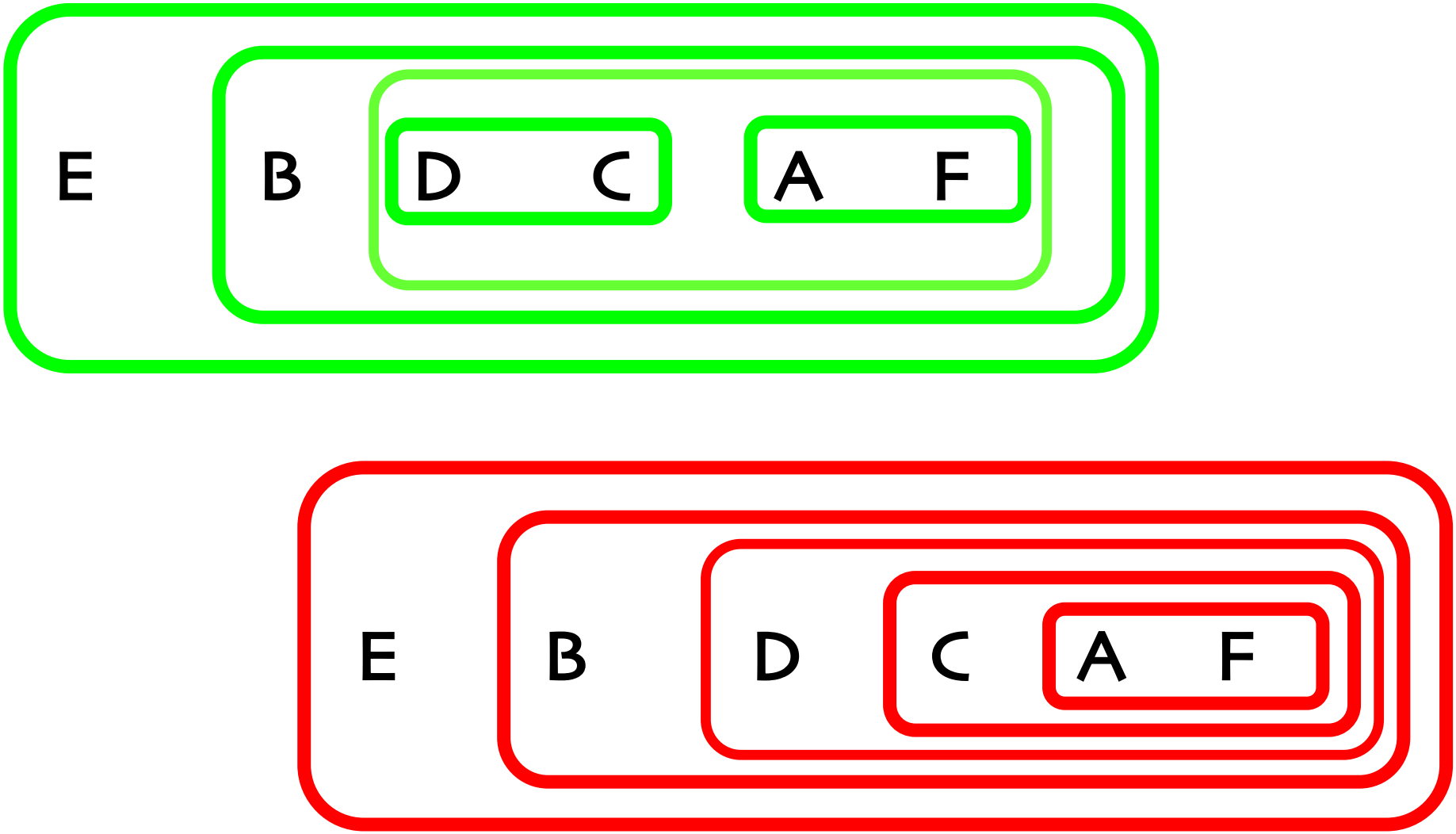
Consensus trees



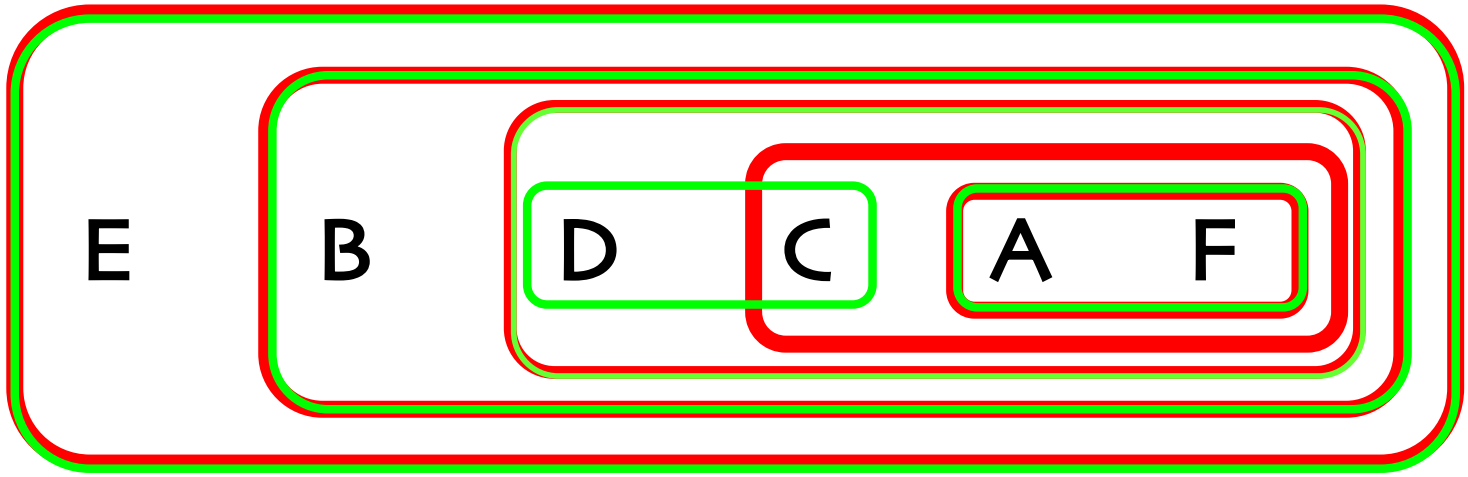
Consensus trees



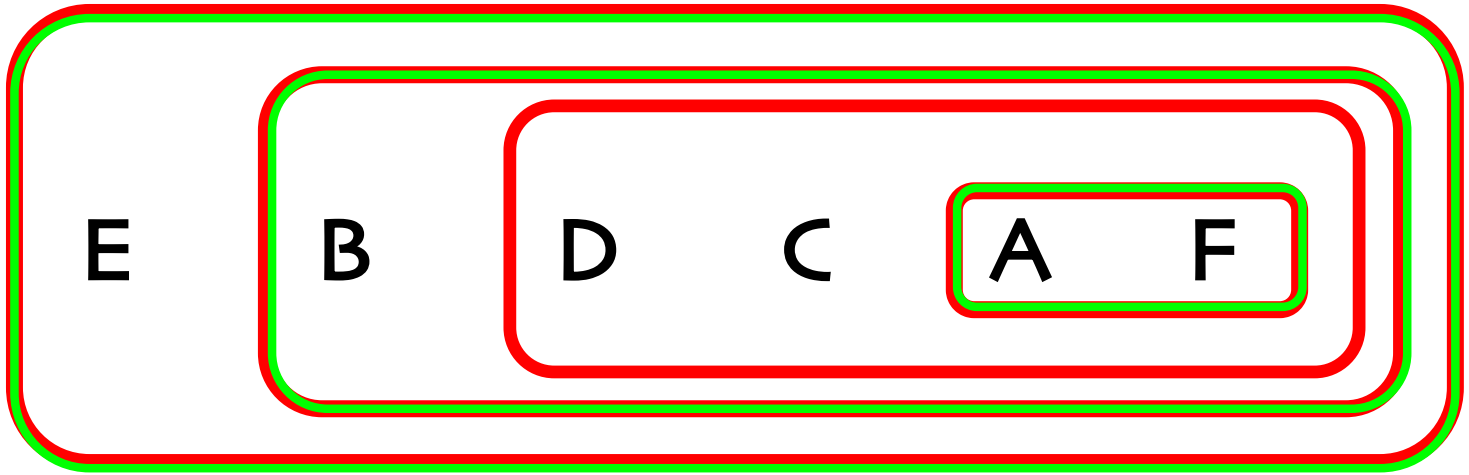
Consensus trees



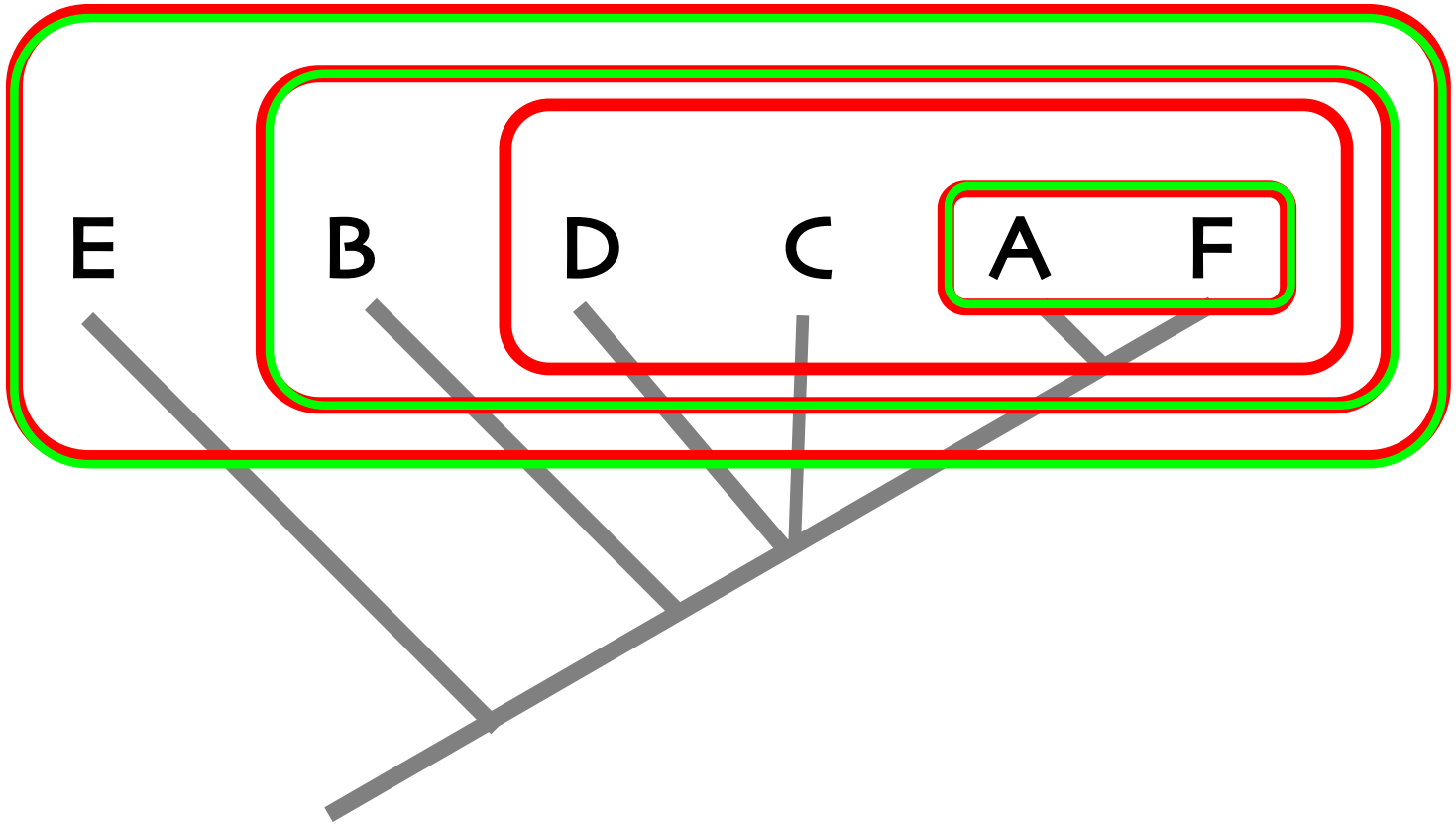
Consensus trees



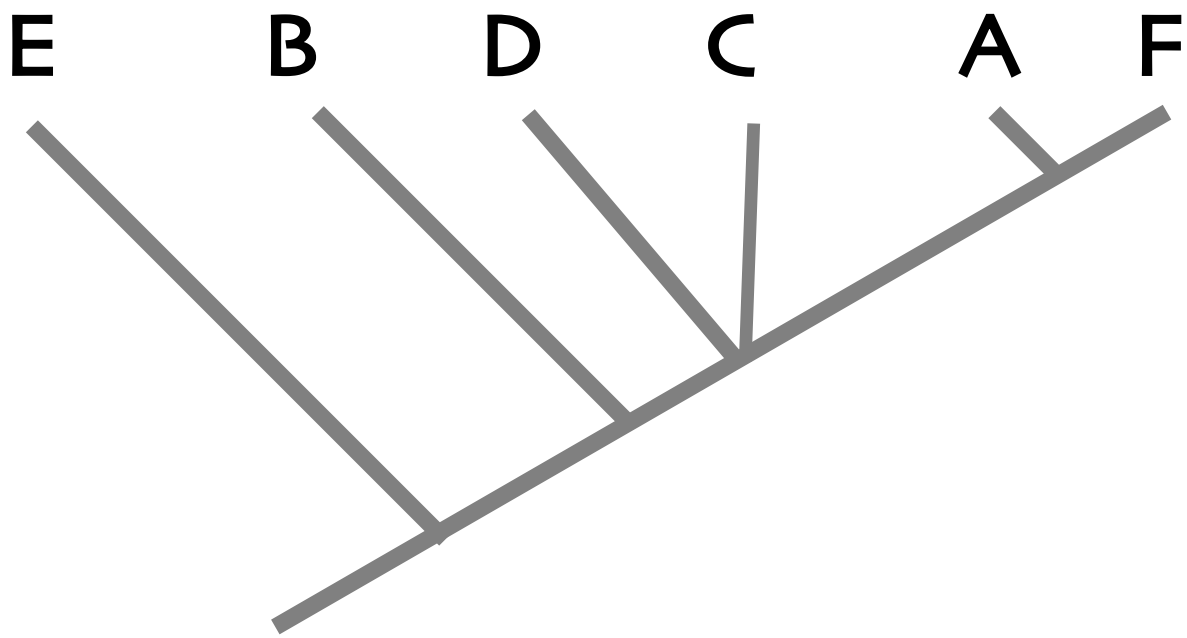
Consensus trees



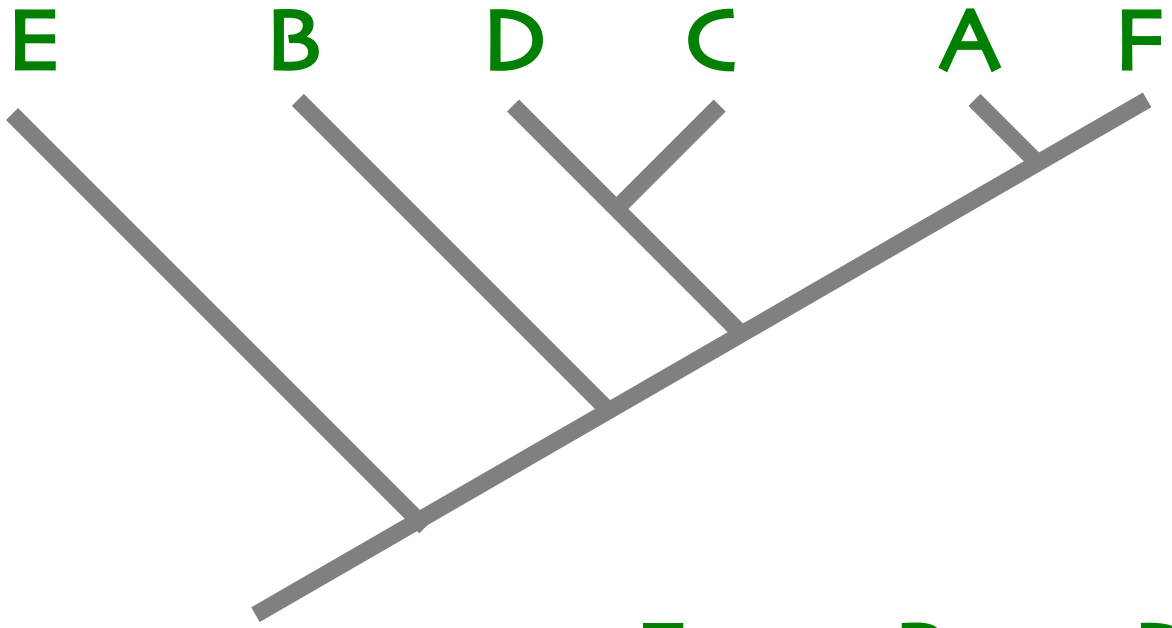
Consensus trees



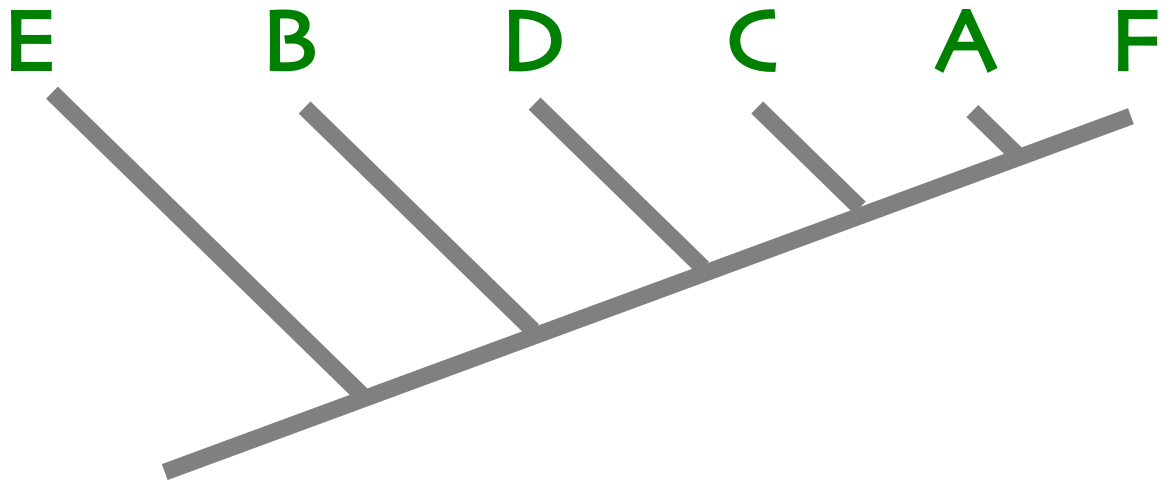
Consensus trees



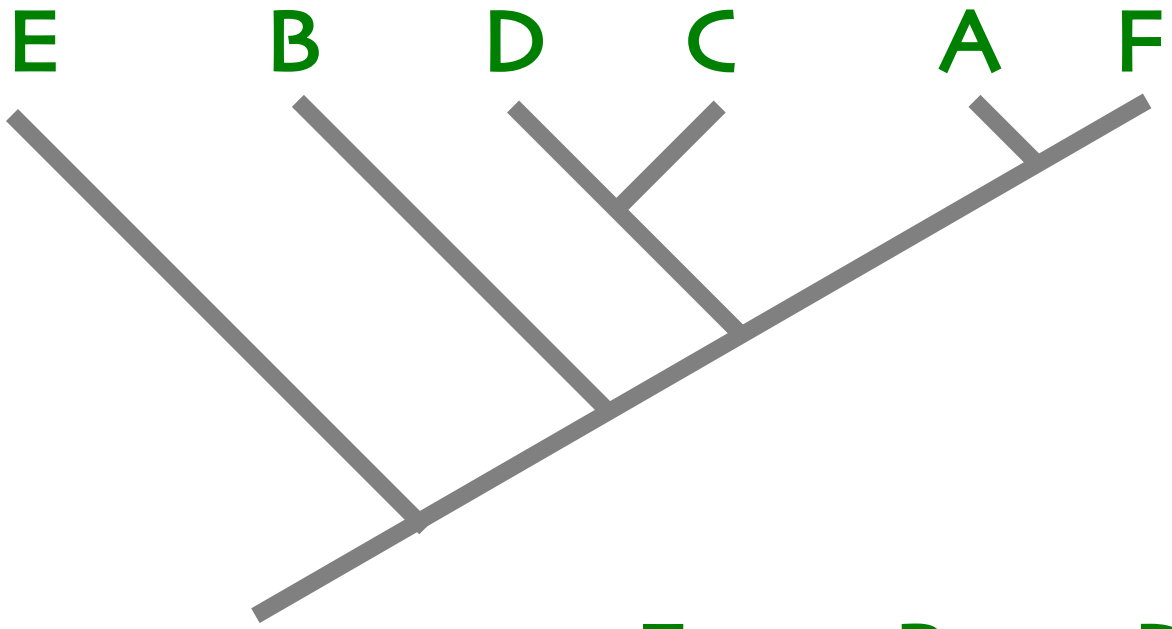
Consensus trees



(E (B (D C) (A F))))

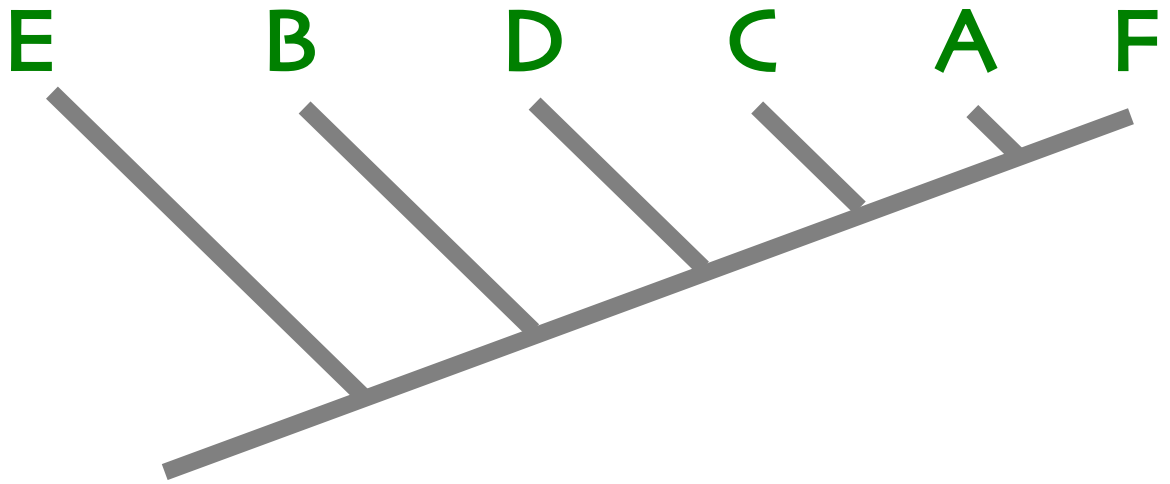


Consensus trees

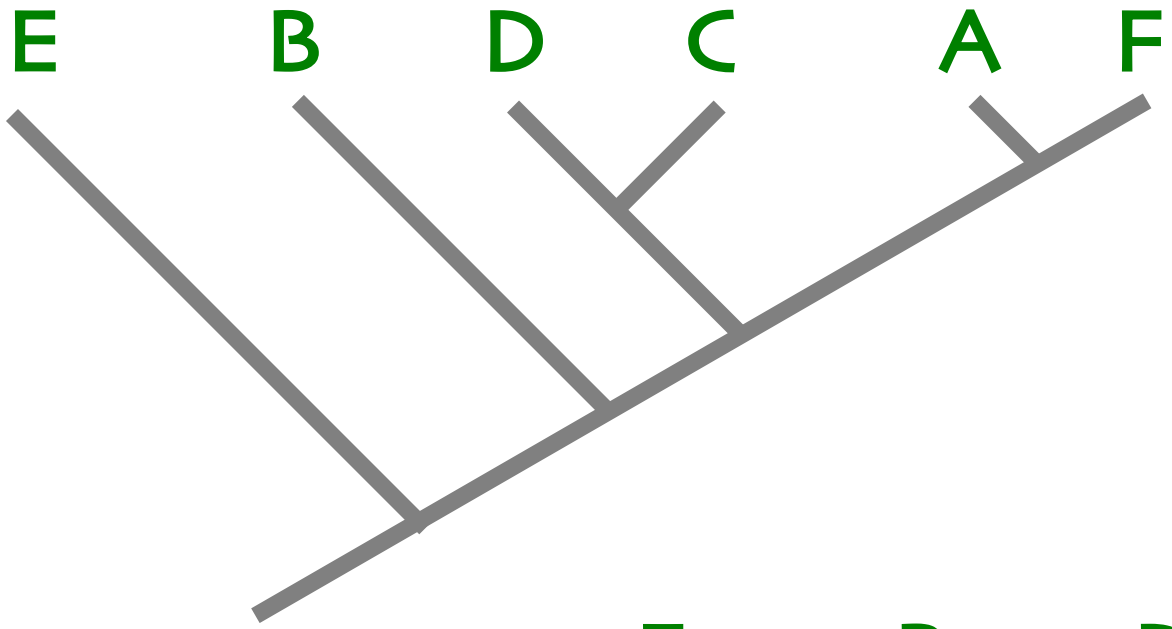


(E B D C A F)
(B D C A F)
(D C A F)
(D C)
(A F)

(E B D C A F)
(B D C A F)
(D C A F)
(C A F)
(A F)

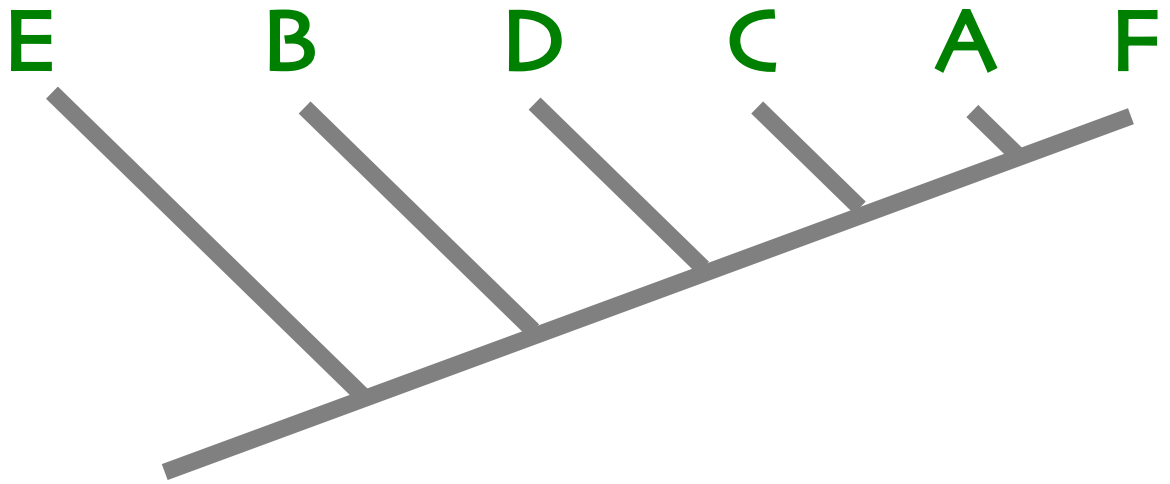


Consensus trees



(E B D C A F)
(B D C A F)
(D C A F)
~~(D C)~~
(A F)

(E B D C A F)
(B D C A F)
(D C A F)
~~(C A F)~~
(A F)



Consensus trees

(E (B (D C (A F))))

(E B D C A F)

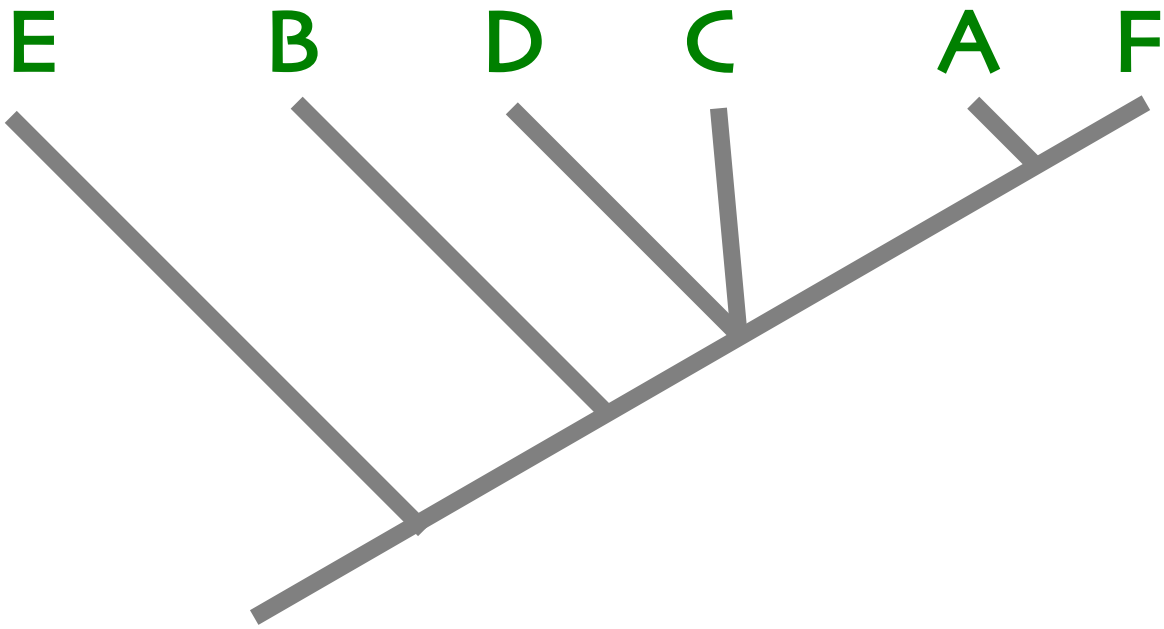
(B D C A F)

(D C A F)

(A F)

Consensus trees

(E (B (D C (A F))))



(E B D C A F)

(B D C A F)

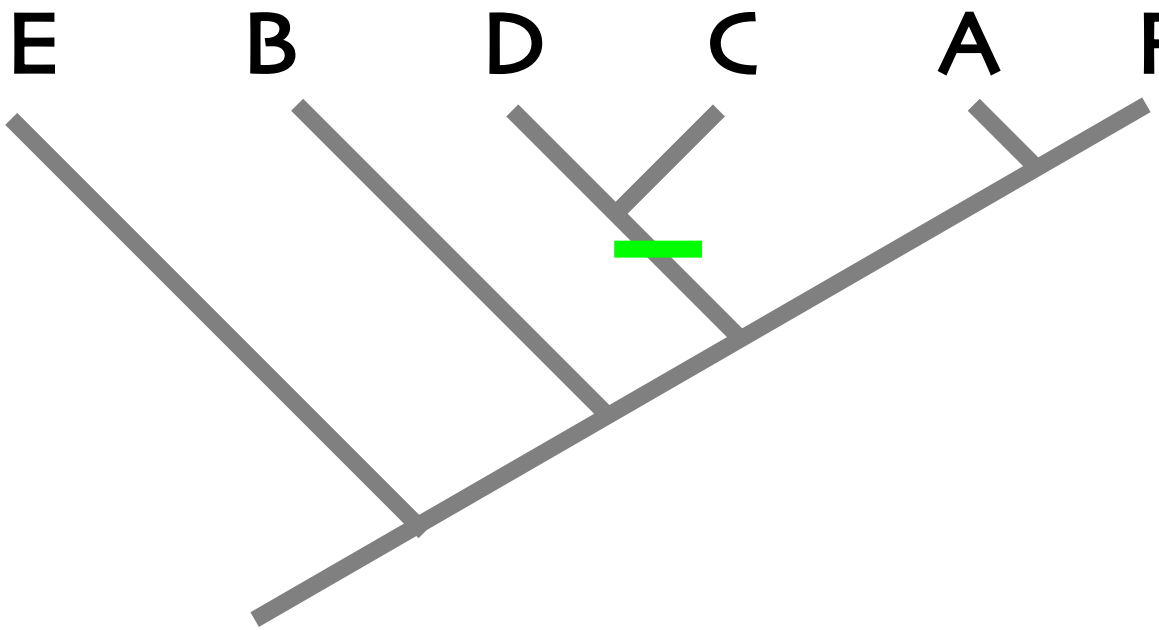
(D C A F)

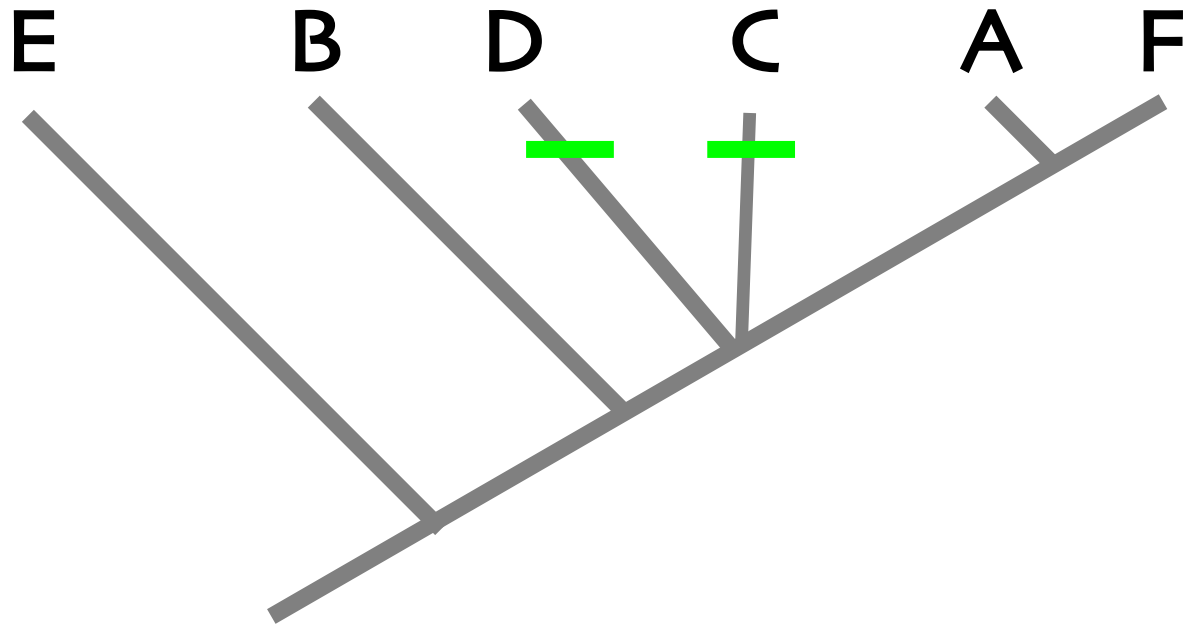
(A F)

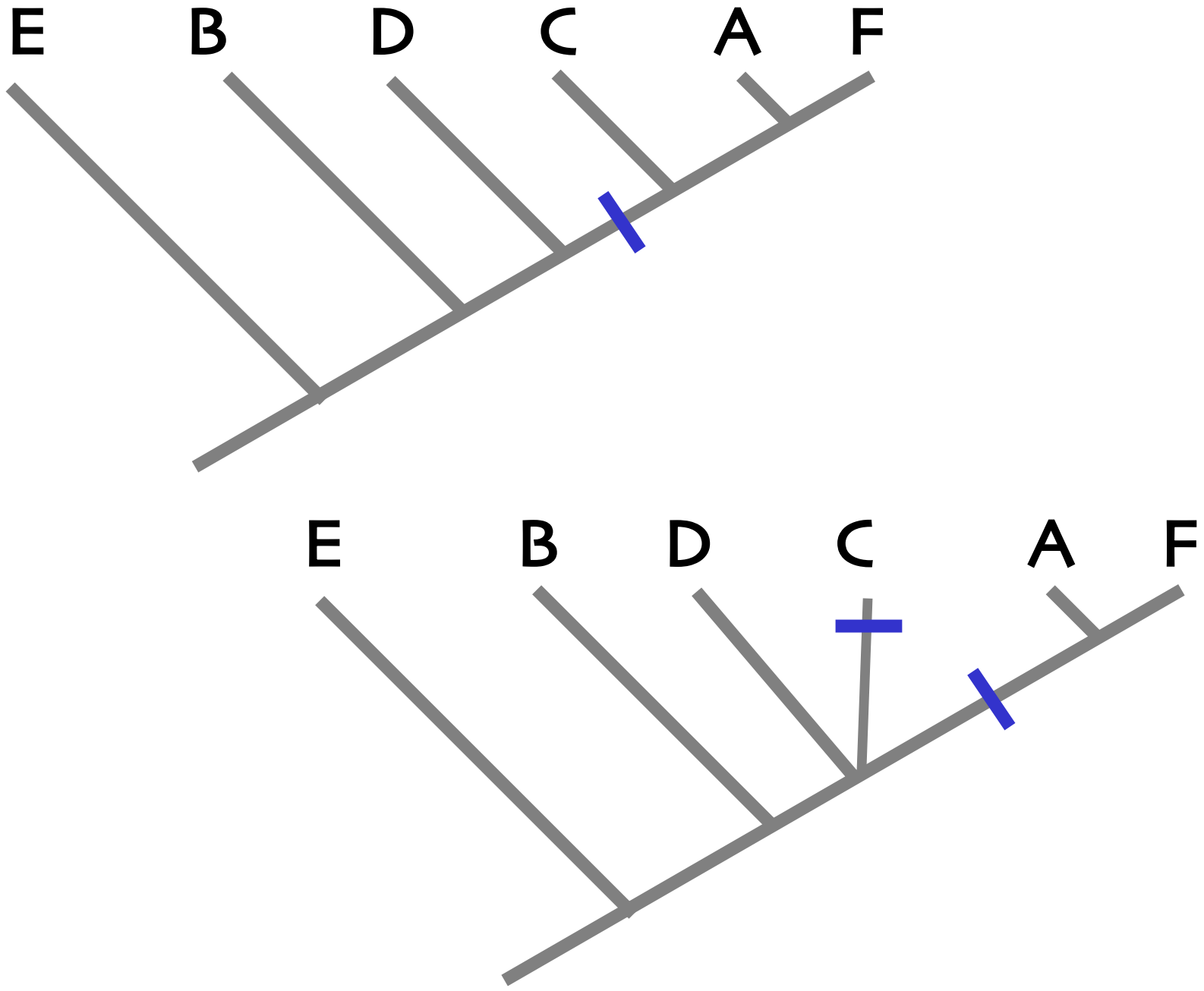
Consensus trees

consensus tree is ALWAYS ONLY SUMMARY

it is **ALWAYS more complicated** than any of the original trees


E
B
D
C
A
F


E
B
D
C
A
F


E
B
D
C
A
F
E
B
D
C
A
F

Consensus trees

consensus tree is ALWAYS ONLY SUMMARY

it is **ALWAYS more complicated** than any of the original trees

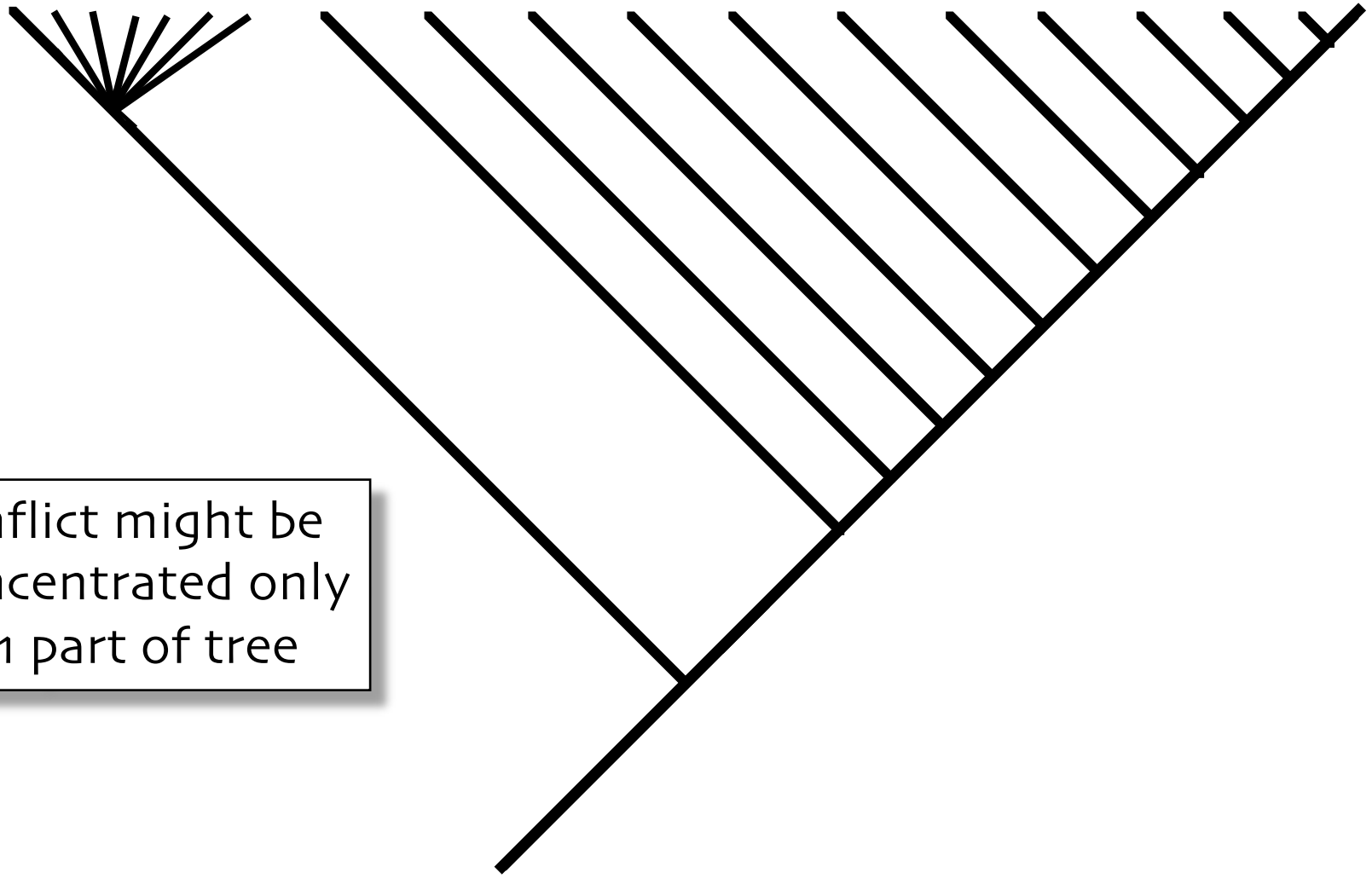
groups shared by ALL trees are presented on 1 tree

LARGE number of trees a problem ?

NOT necessary because ….

n	B(n)
3	3
4	15
5	105
6	945
7	10 395
8	135 135
9	2 027 025
10	34 459 425
15	213 458 046 676 875
20	8 200 794 532 637 891 559 375

despite of the fact that number of trees > 10 000


conflict might be
concentrated only
on 1 part of tree

COMPROMISE TREES

often referred to as consensus trees

Majority rule compromise

Adams

Combinable component (semistrict)

Nixon, K. C. & Carpenter, J. 1996. On consensus, collabsibility, and clade concordance. *Cladistics* 12: 305-321.

COMPROMISE TREES

Majority rule compromise

Margush, T. & McMorris, F. R. 1981. Consensus n-trees. *Bull. Math. Biol.* 43: 239-244.

Adams

Combinable component (semistrict)

COMPROMISE TREES

commonly used for presentation of support values

mostly those groups present on $\geq$ 50% of original trees presented

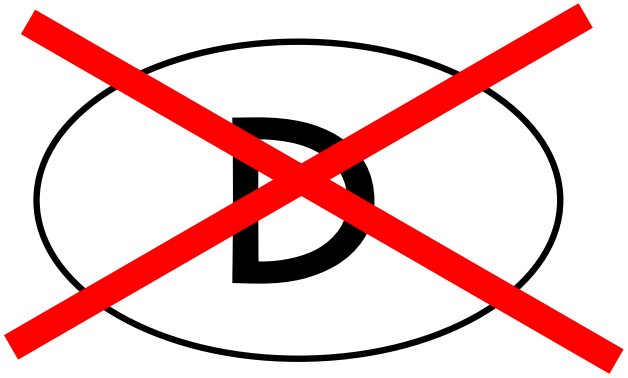
percentage describing the presence of groups on original trees marked on compromise tree (50-100)

COMPROMISE TREES

majority rule compromise

when used as summary of optimal trees it should be noticd that part of the original trees are in **CONFLICT** with this summary!!

this kind of usage **IS NOT RECOMMENDED**



SUMMARY

different equally parsimonious optimizations might posit character state changes VERY DISTANT in time from each other

also correlation with ***other*** characters might be different

also DIRECTION of changes might differ in alternate optimizations

monophyly is one of the CENTRAL PRINCIPLES of cladistics

ONLY MONOPHYLETIC groups (=clades) provide precise information about relationships

trees can be presented as parenthetical notations

consensus tree is ONLY SUMMARY of numerous trees

all trees are **NOT** equal

both consensus- & compromise trees can be useful but only if used properly