8.xi.

1. trees

2. apomorphy vs. plesiomorphy

3. parsimony

4. summary

Emil Hans WILLI HENNIG

*20.4.1913 †5.11.1976

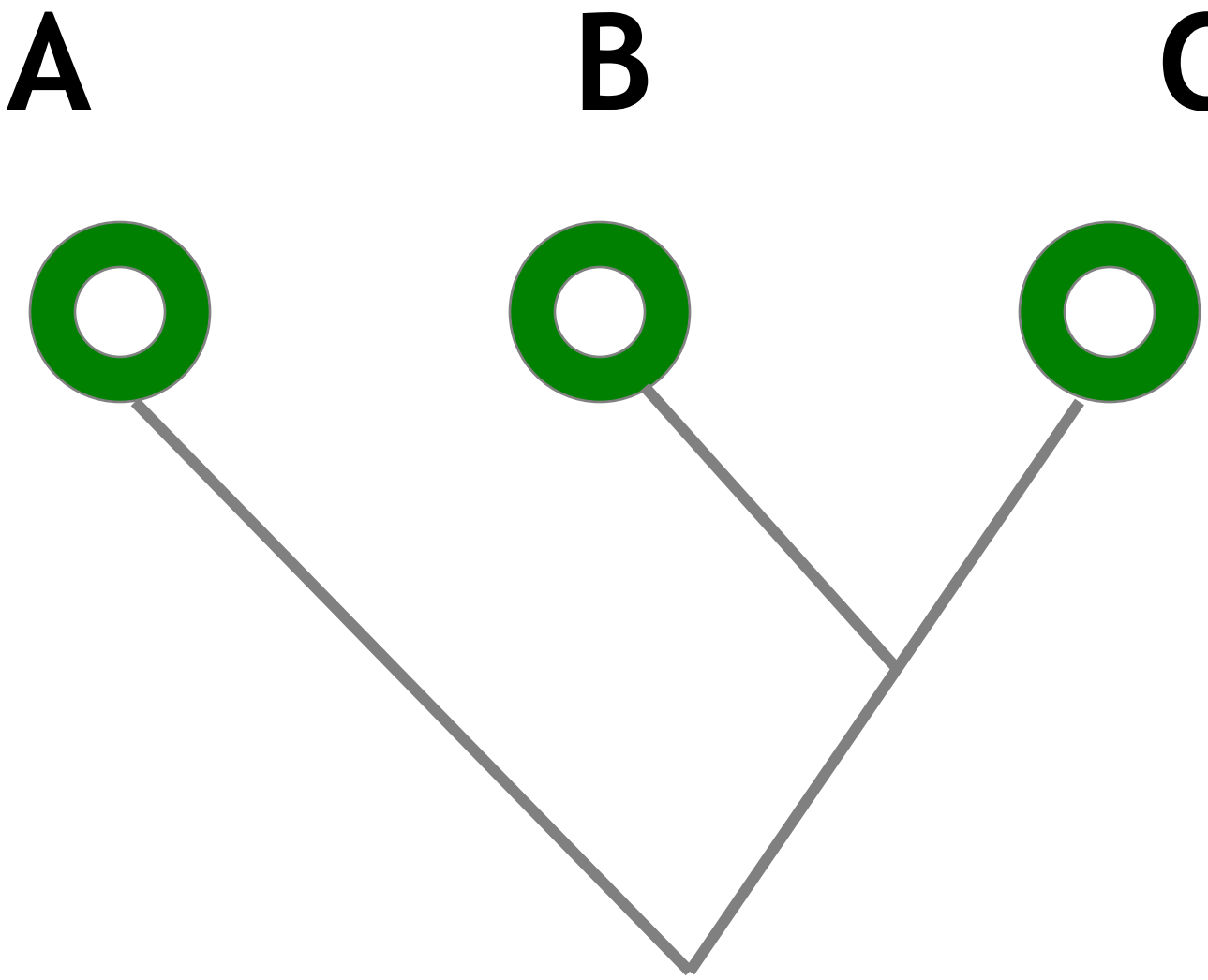
Hennig´s (1965) 3 primary questions:

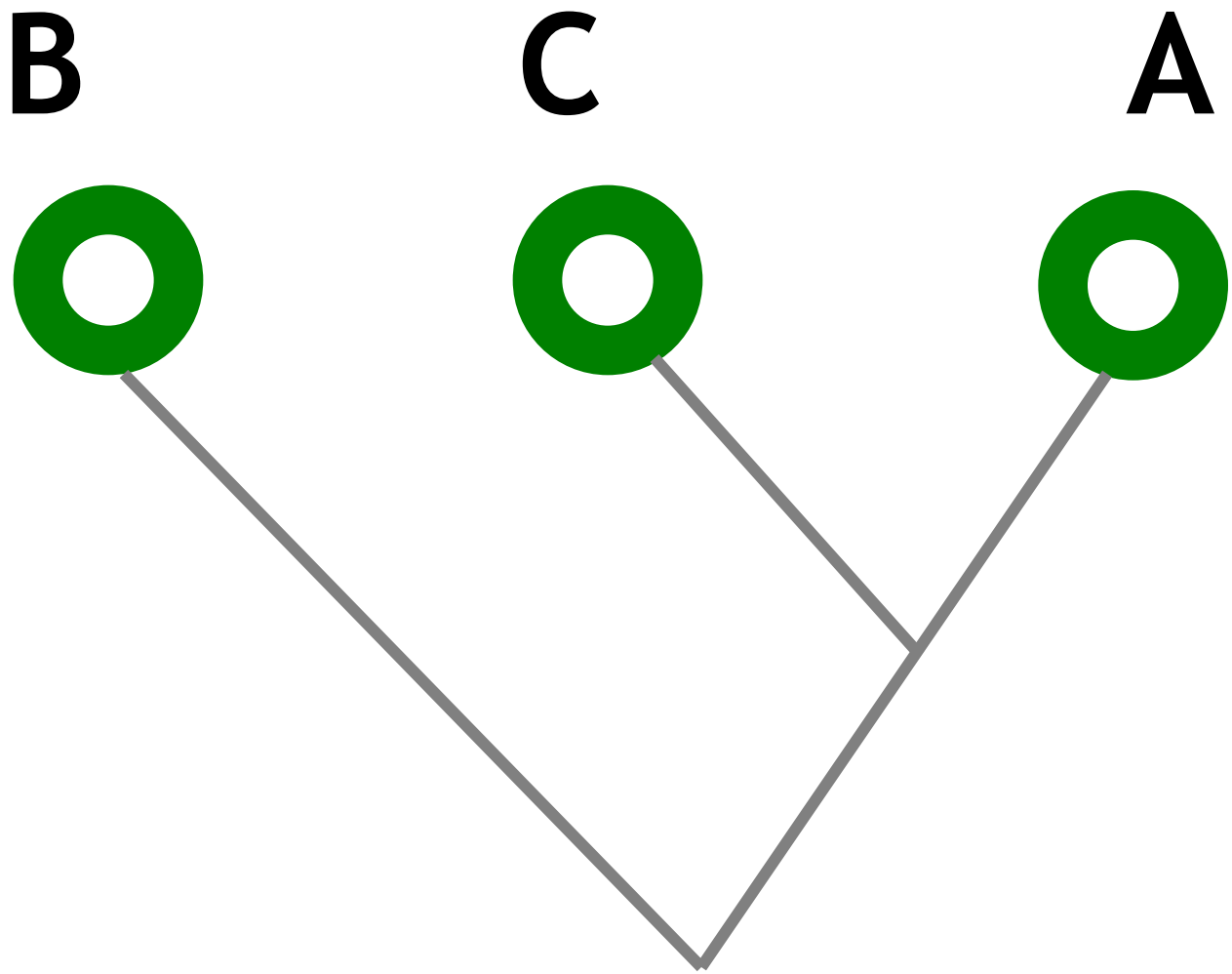
1. What is phylogeny?
2. How is it established?
3. How to describe it explicitly?

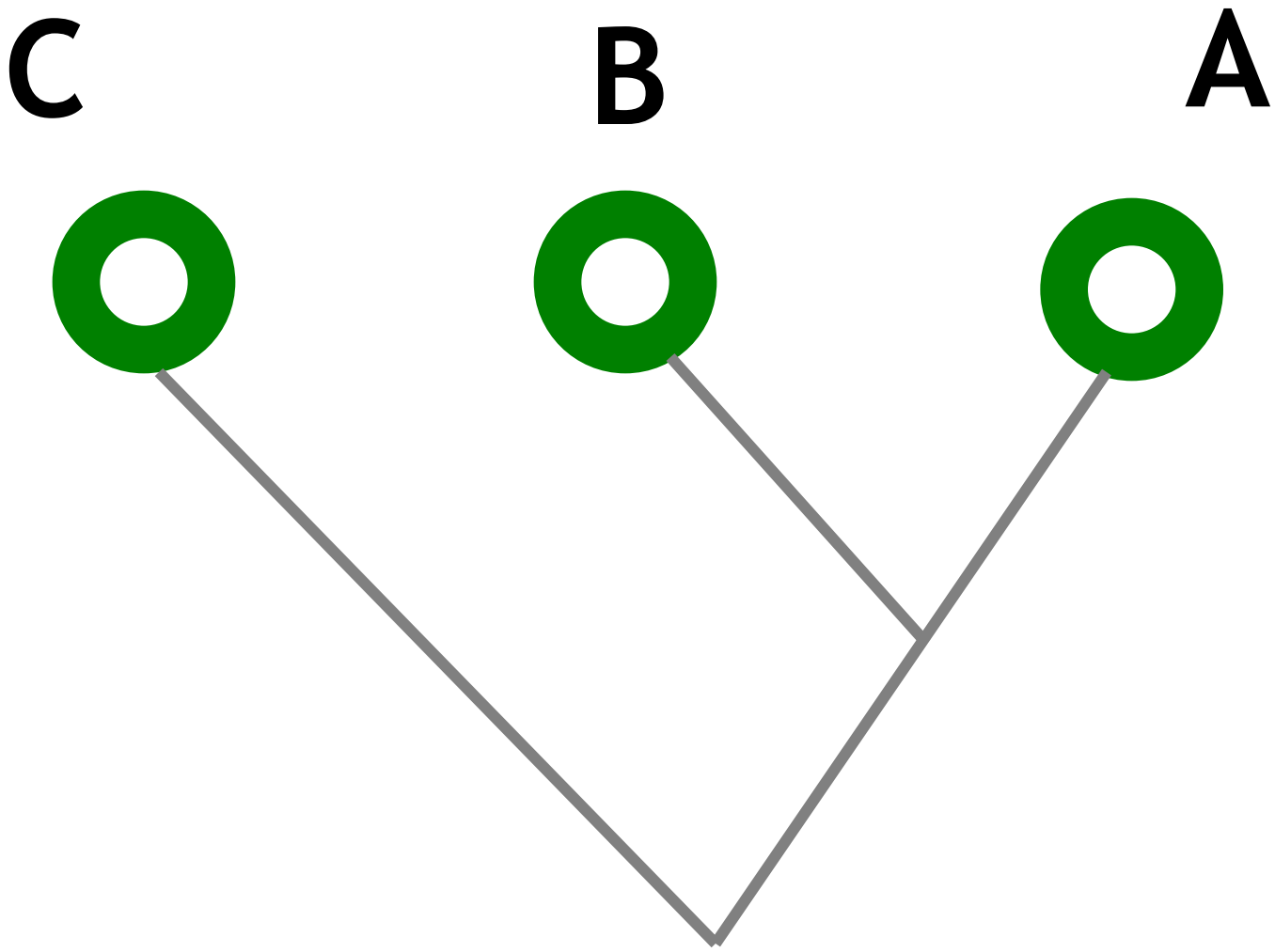
and his 3 precise answers:

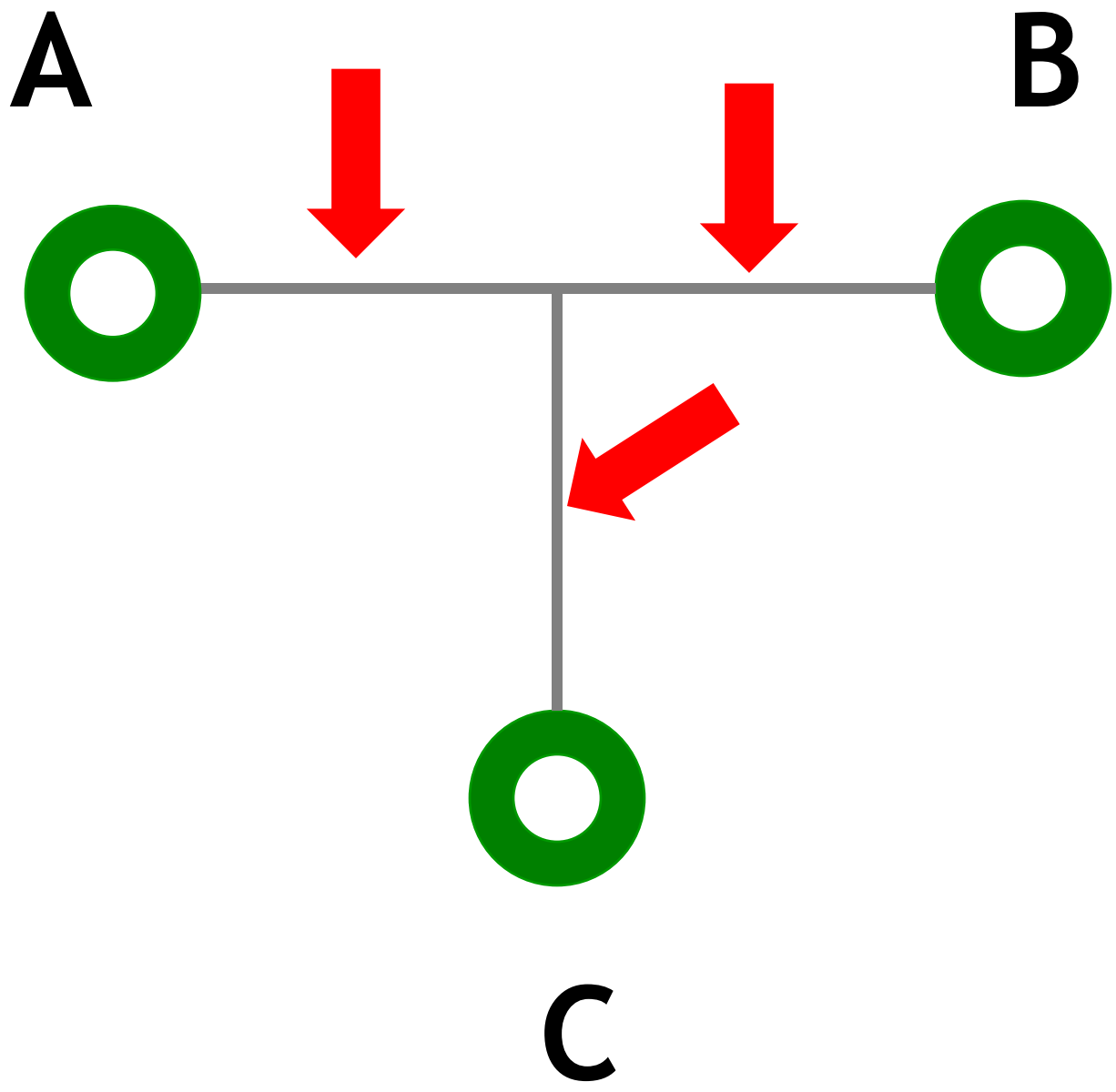
1. Phylogeny is GENEALOGICAL relationship where 2 taxa are more closely related to each other than they are to a 3rd one
2. Relationships are established by SYNAPOMORPHIES
3. **Relationships can be presented using branching diagrams (=cladograms)**

Number of trees?


A
B
C


B
C
A


C
B
A


A
B
C

n	B(n)
3	1
4	3
5	15
6	105
7	945
8	10 395
9	135 135
10	2 027 025
15	7 905 853 580 625
20	221 643 095 476 699 771 875
50	3×10^{74}

number of undirected trees

$B(n) = (2n-5)!!$

$$B(n) = (2n-5)!!$$

$$(2 \times 9 - 5)!!$$

$$(18 - 5)!!$$

$$13!!$$

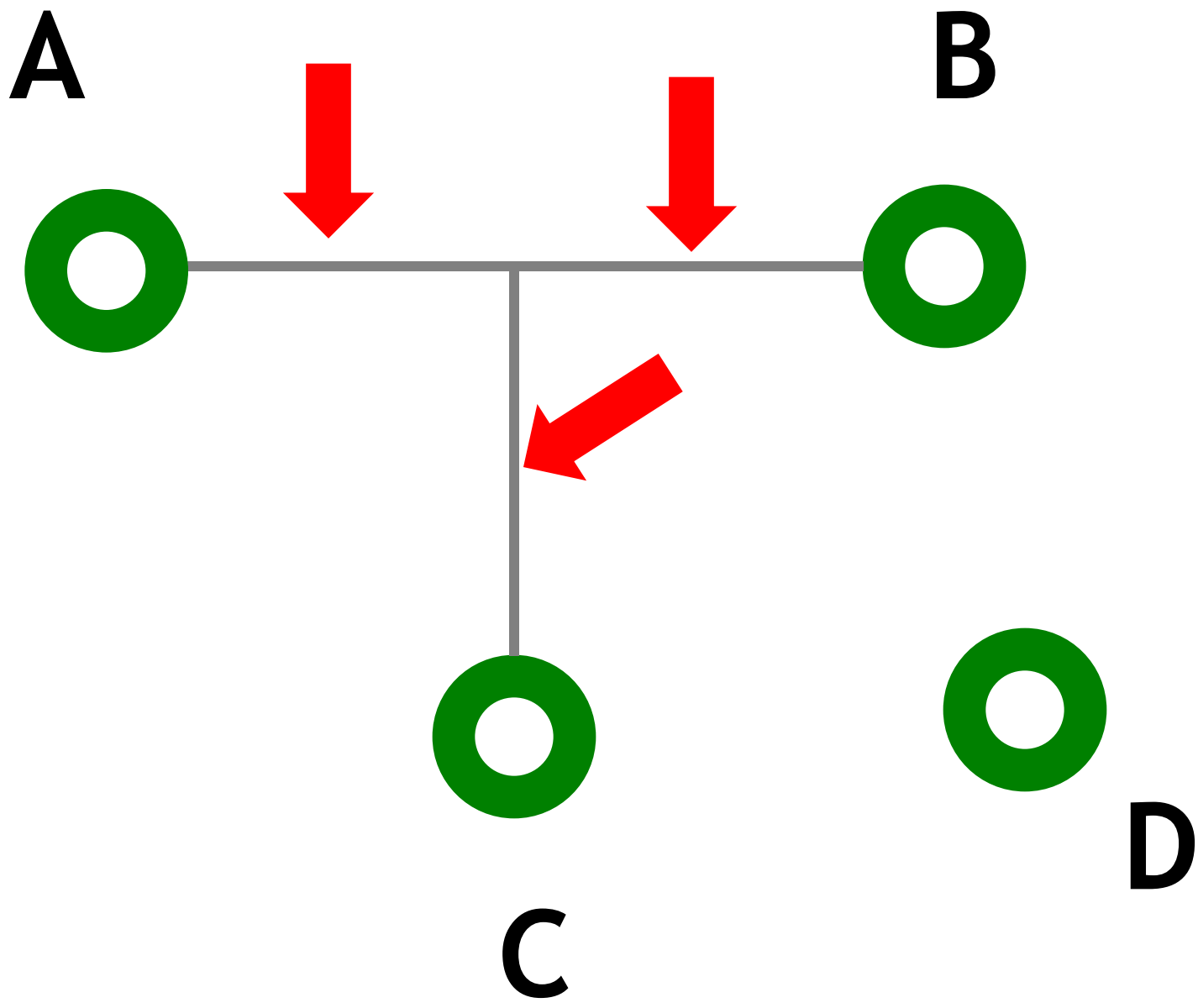
$$13 \times 11 \times 9 \times 7 \times 5 \times 3 \times 1$$

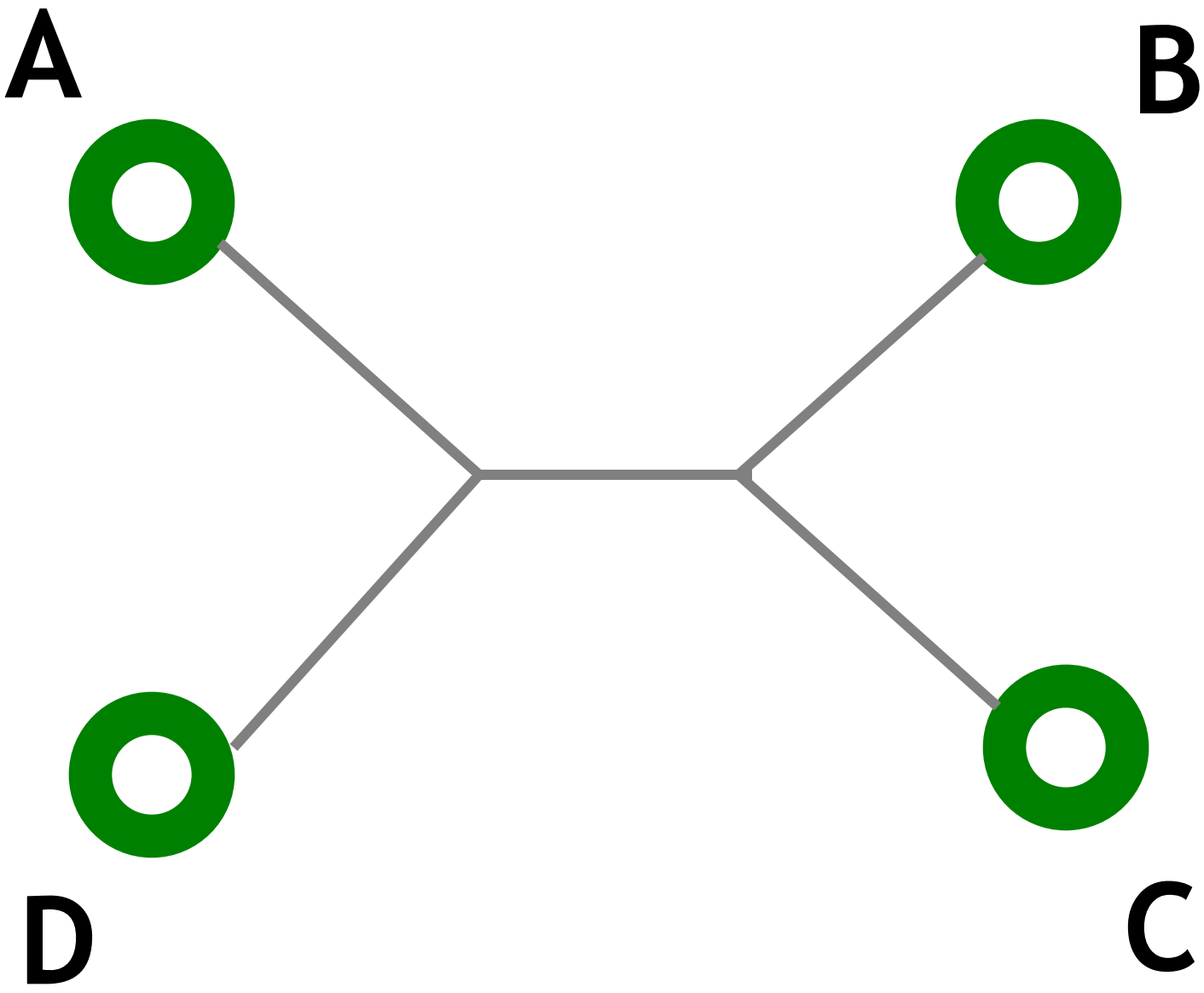
$$135\ 135$$

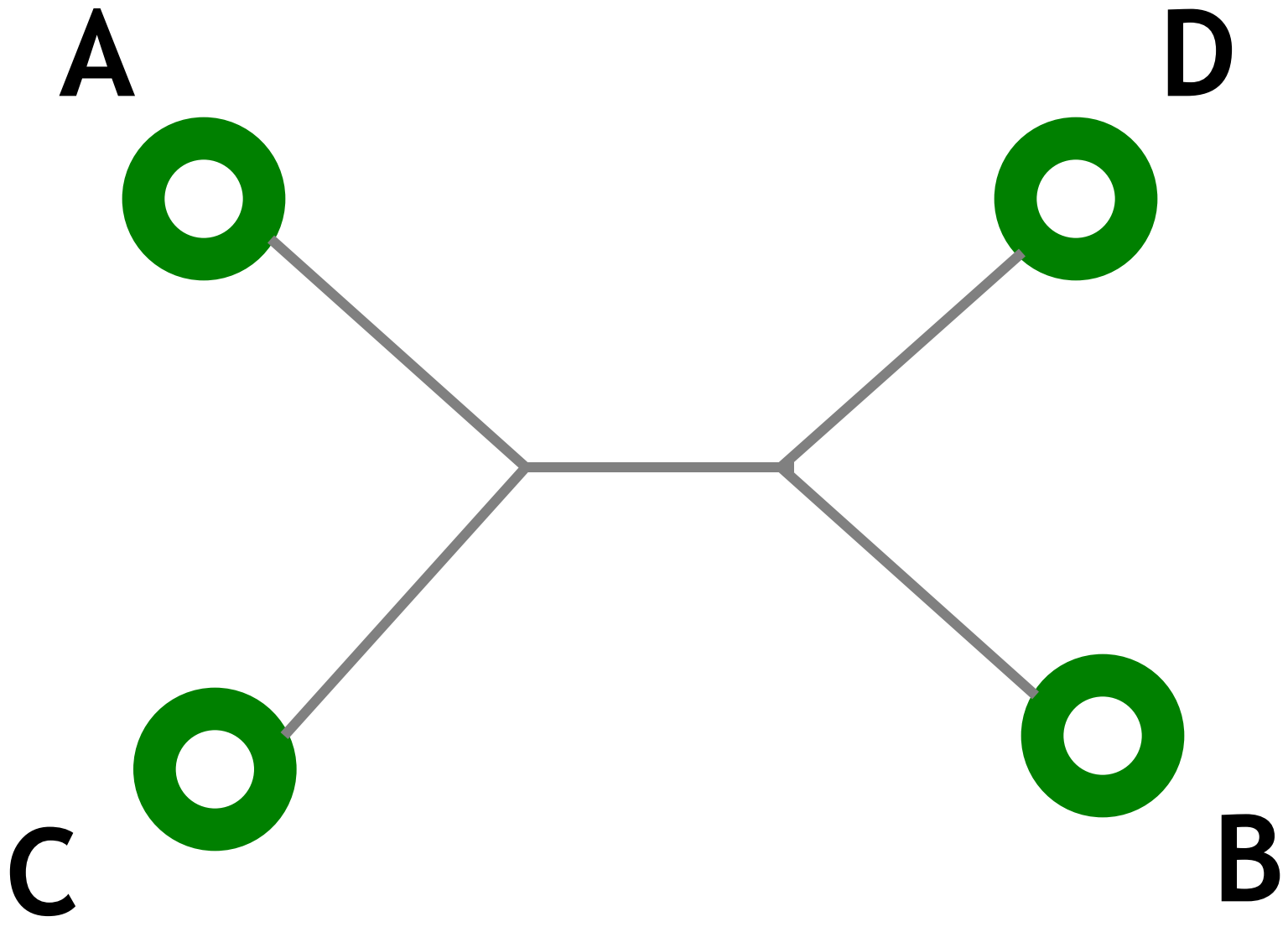
n	B(n)
3	3
4	15
5	105
6	945
7	10 395
8	135 135
9	2 027 025
10	34 459 425
15	213 458 046 676 875
20	8 200 794 532 637 891 559 375

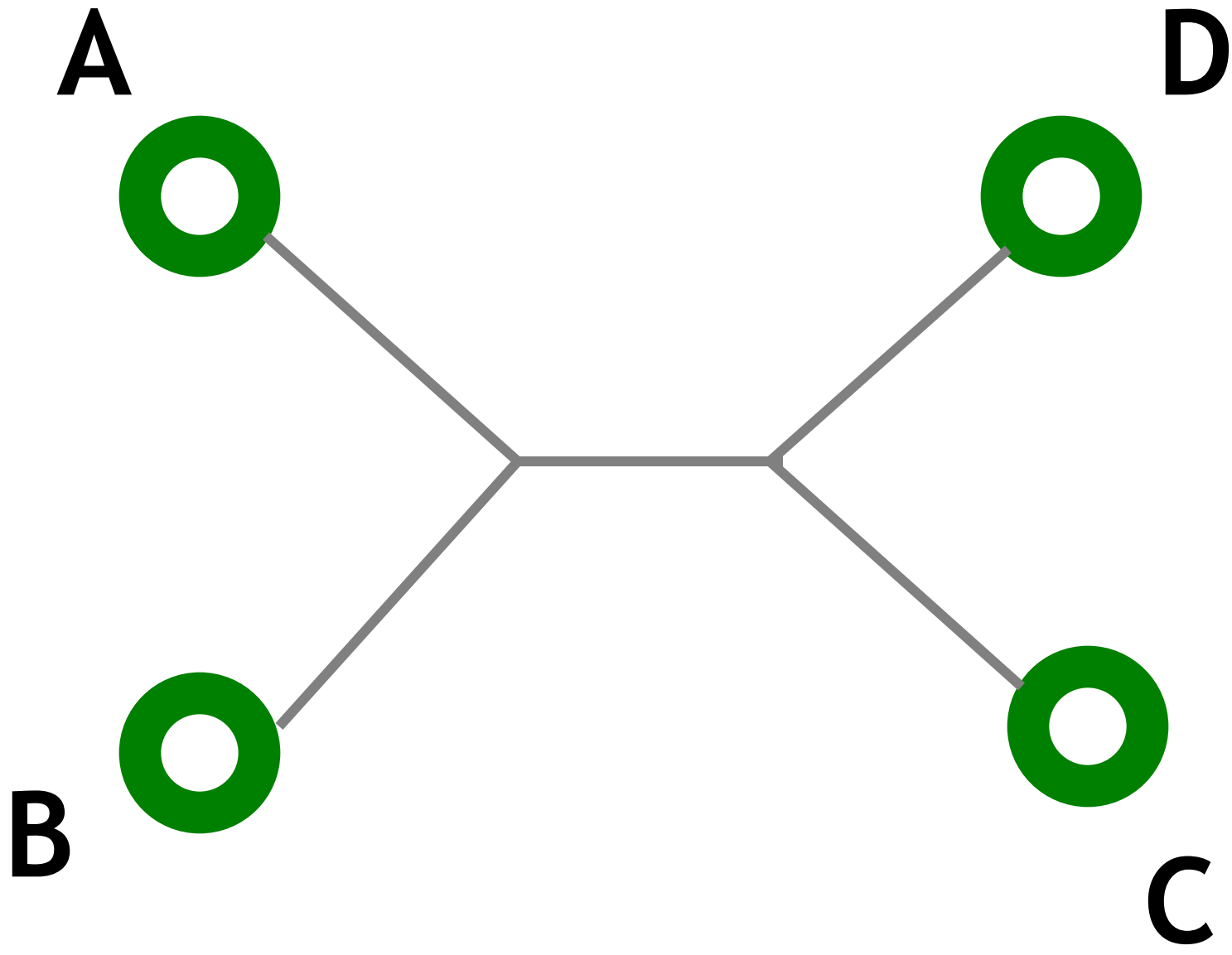
number of directed trees

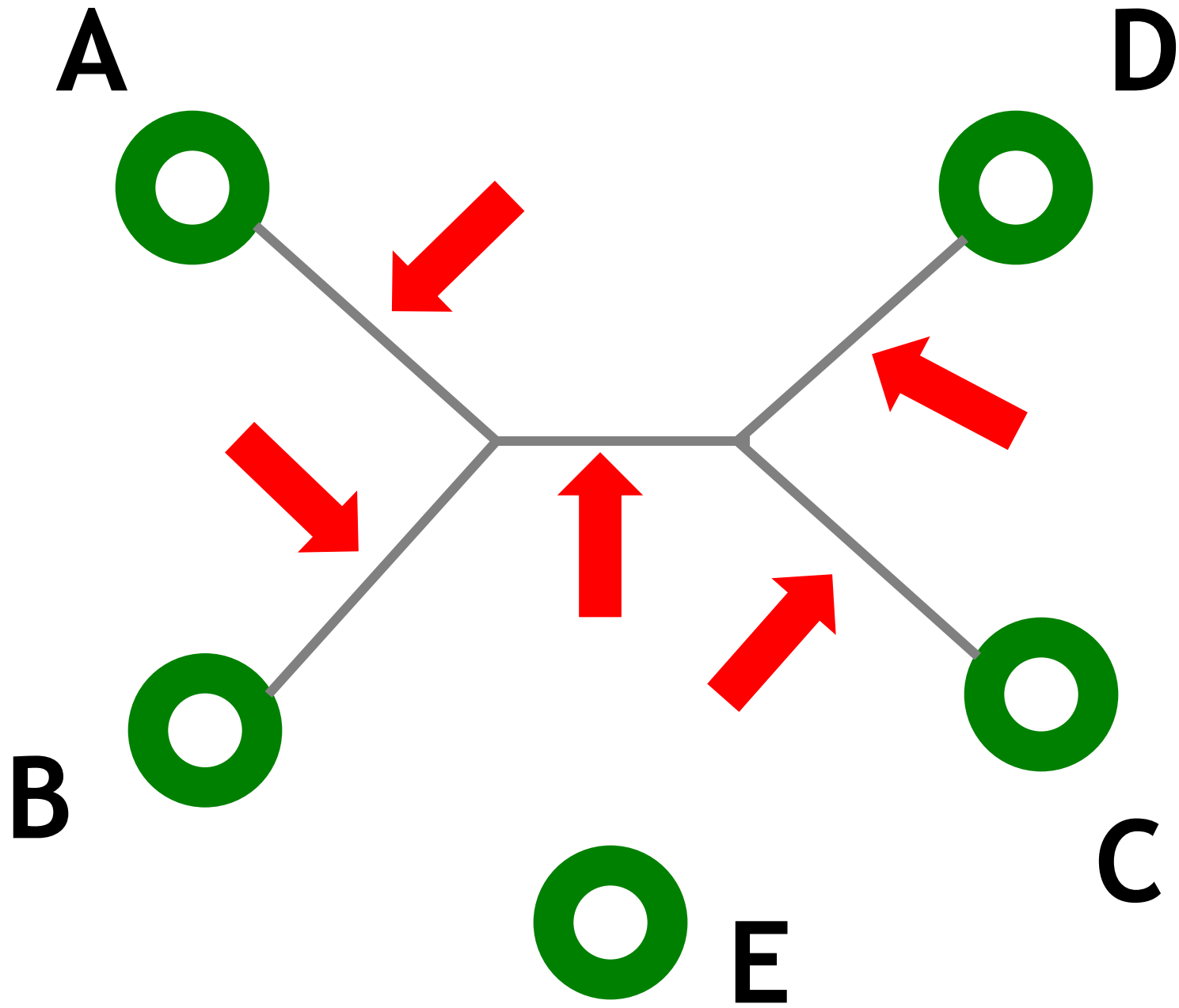
$B(n) = (2n-3)!!$

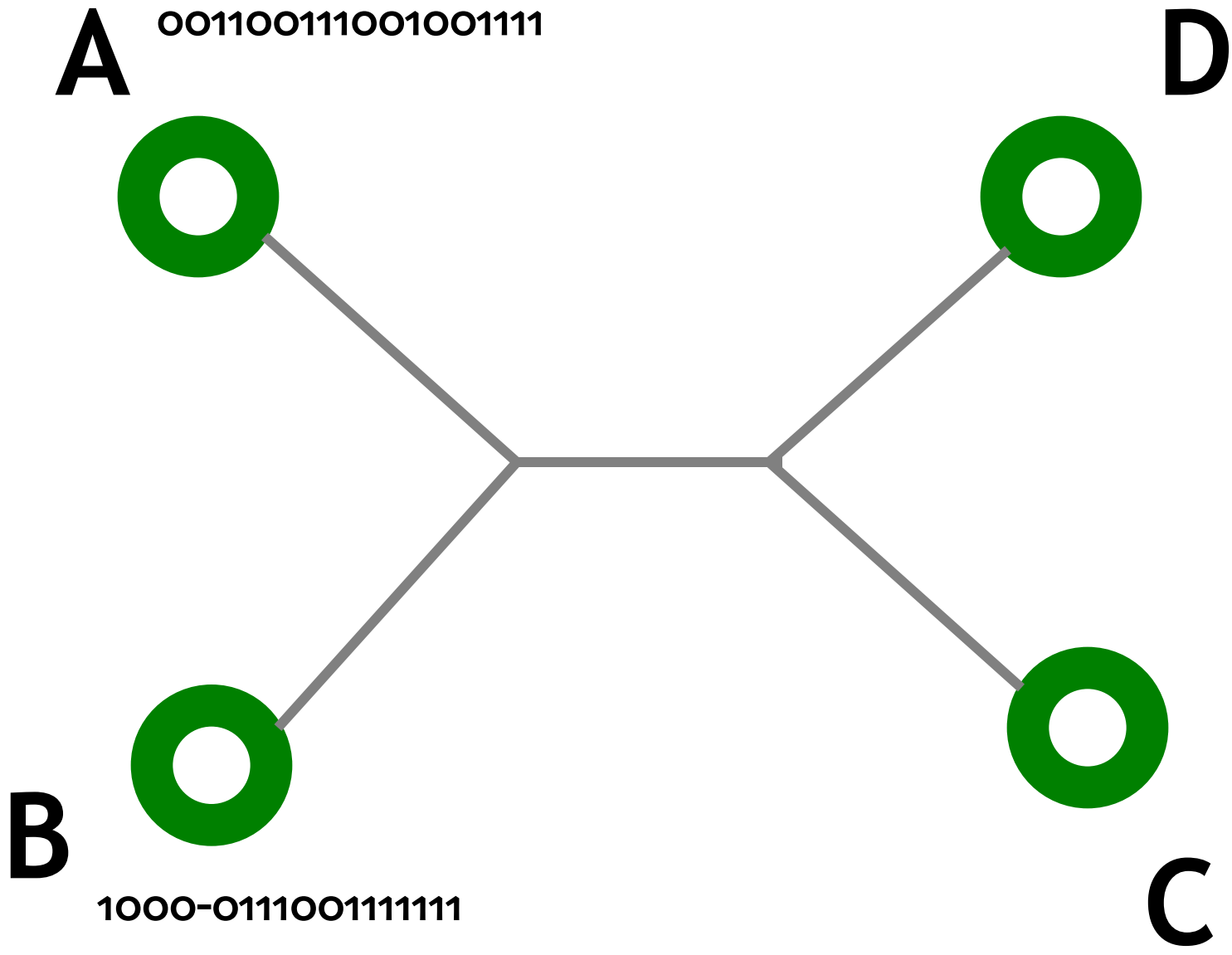

A
B
C
D


A
B
D
C


A
D
C
B


A
D
B
C


A
D
B
C
E


A
0011001110010001111
D
B
1000-01110011111111
C

characters coded as a simple matrix

characters		1.	2.	3.	4.	5.	6.	7.	8.	9.	10.
taxa	A	1	0	0	0	0	1	0	0	0	0
	B	1	0	1	1	1	1	1	1	1	1
	C	0	1	1	0	0	1	1	1	1	0
	D	1	0	0	0	0	1	1	0	0	0
	E	1	0	1	0	1	1	1	1	1	0

Construction of phylogenetic trees

our GOAL is hypothesis about evolutionary history

how is this done?

COMPARATIVE study of organisms

traces about evolutionary history can be found in ALL LIVING ORGANISMS

living fossils

Construction of phylogenetic trees

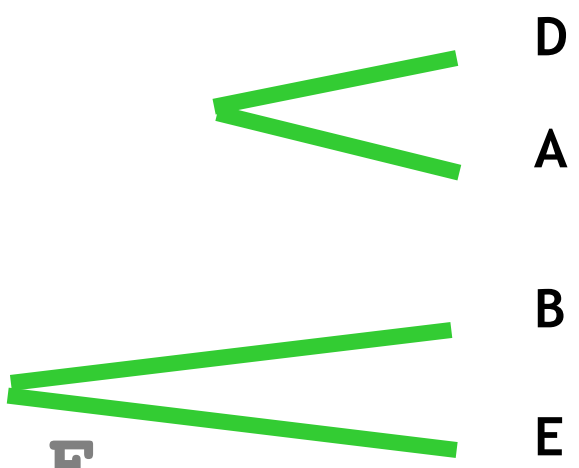
organisms sharing largest number of characters with each other are also each other´s closest relatives

	1.	2.	3.	4.	5.	6.	7.	8.	9.	10.
A	1	0	0	0	0	1	0	0	0	0

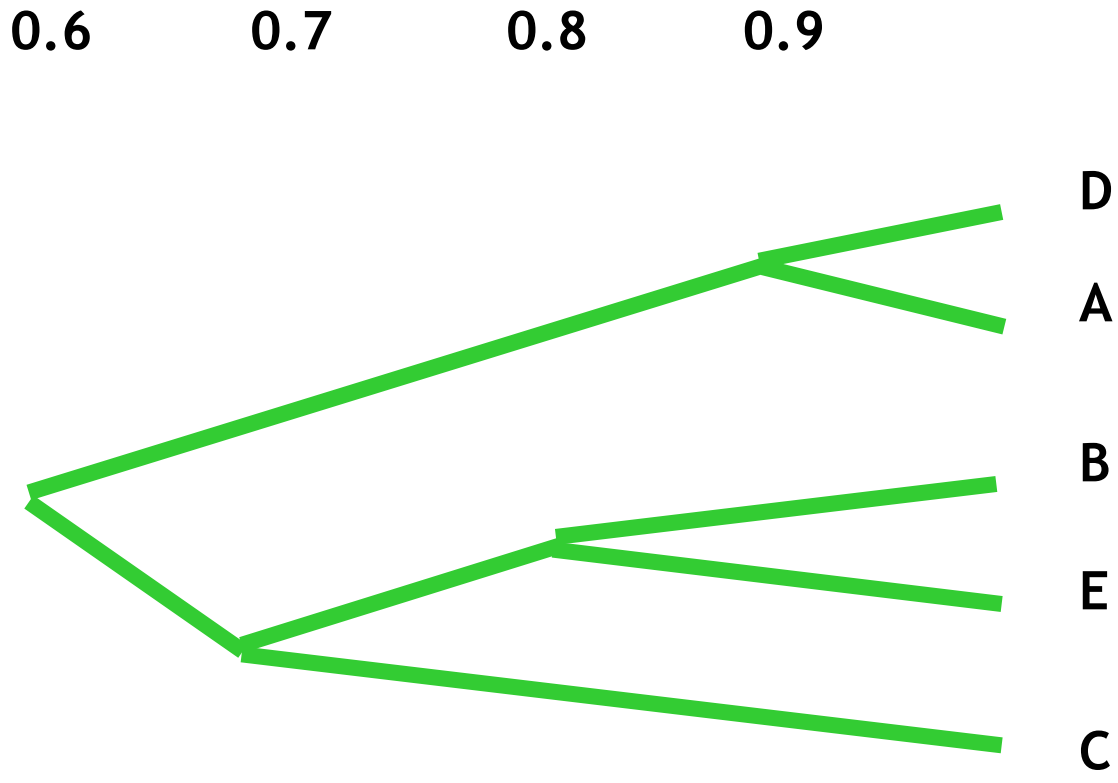
E	1	0	1	0	1	1	1	1	1	0

	A	B	C	D	E
A	10	3	4	9	5
B		10	5	4	8
C			10	5	7
D				10	6
E					10

0.6 0.7 0.8 0.9



	A	B	C	D	E
A	10	3	4	9	5
B		10	5	4	8
C			10	5	7
D				10	6
E					10


0.6
0.7
0.8
0.9
D
A
B
E
C

Construction of phylogenetic trees

organisms that resemble each other most are also most closely related to each other

WHY?

Emil Hans WILLI HENNIG

*20.4.1913 †5.11.1976

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Construction of phylogenetic trees

organisms that resemble each other most are also most closely related to each other

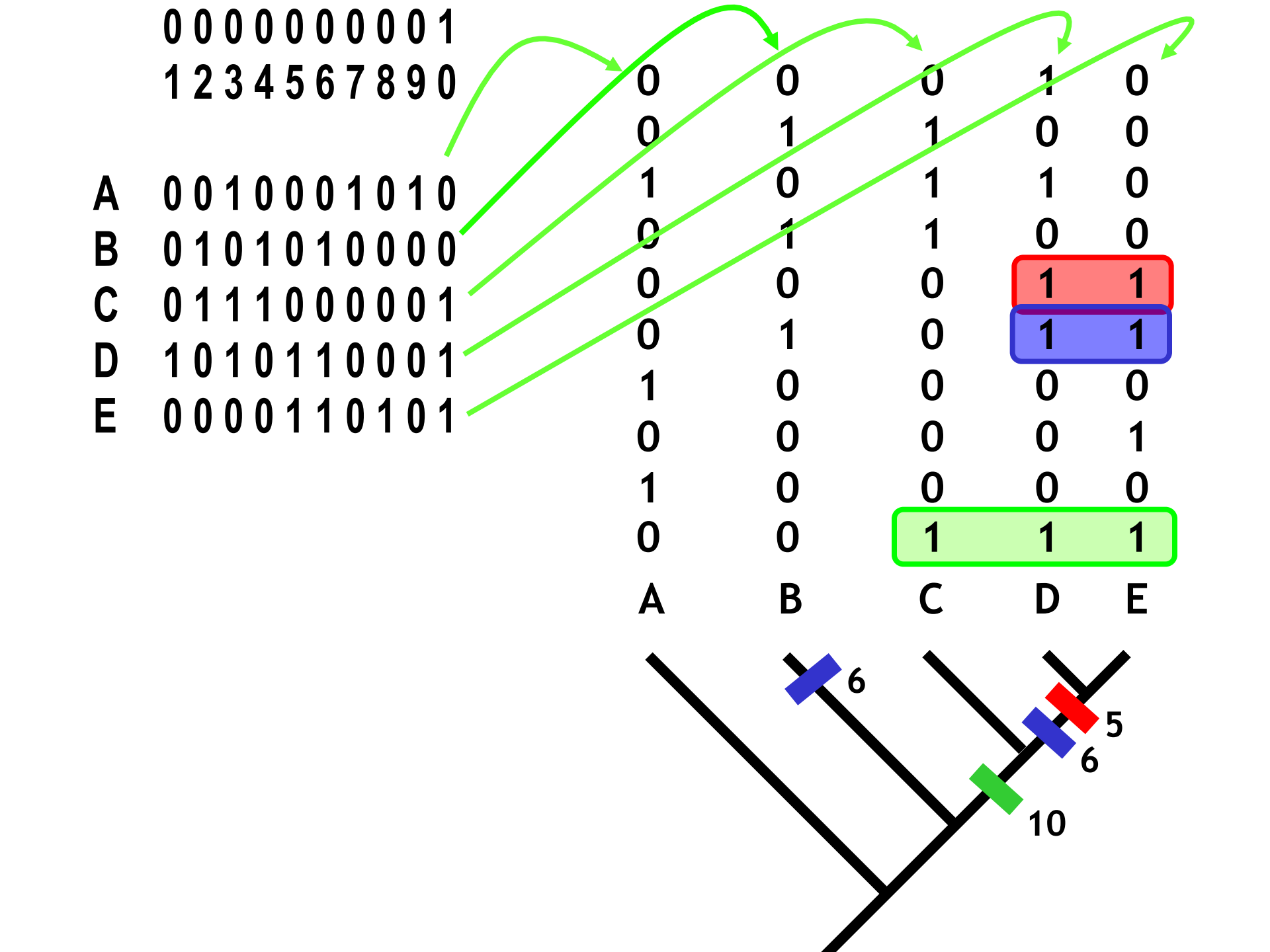
NO

WHY? apomorphies should be distinguished from plesiomorphies

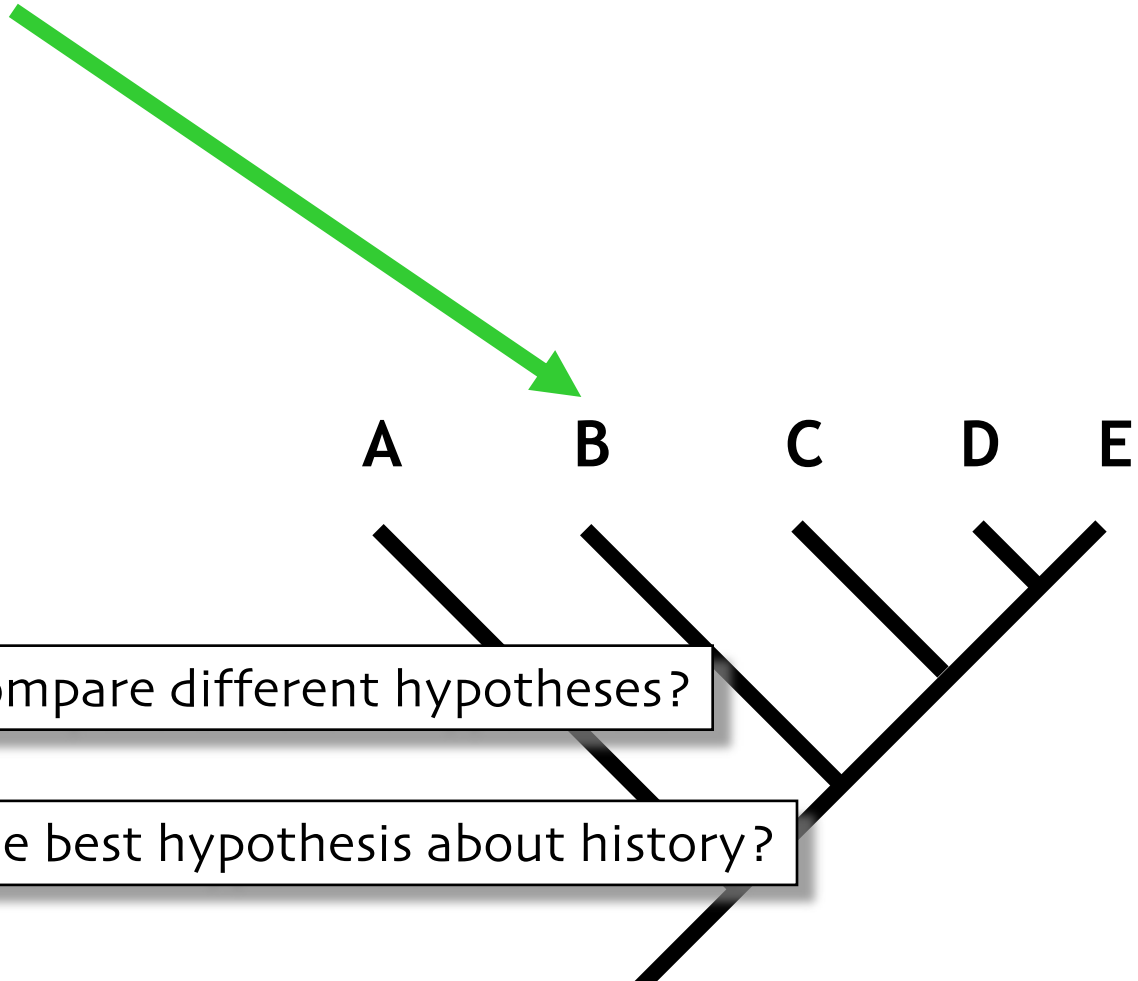
how is this performed?

how do we recognize apo- & plesiomorphies?

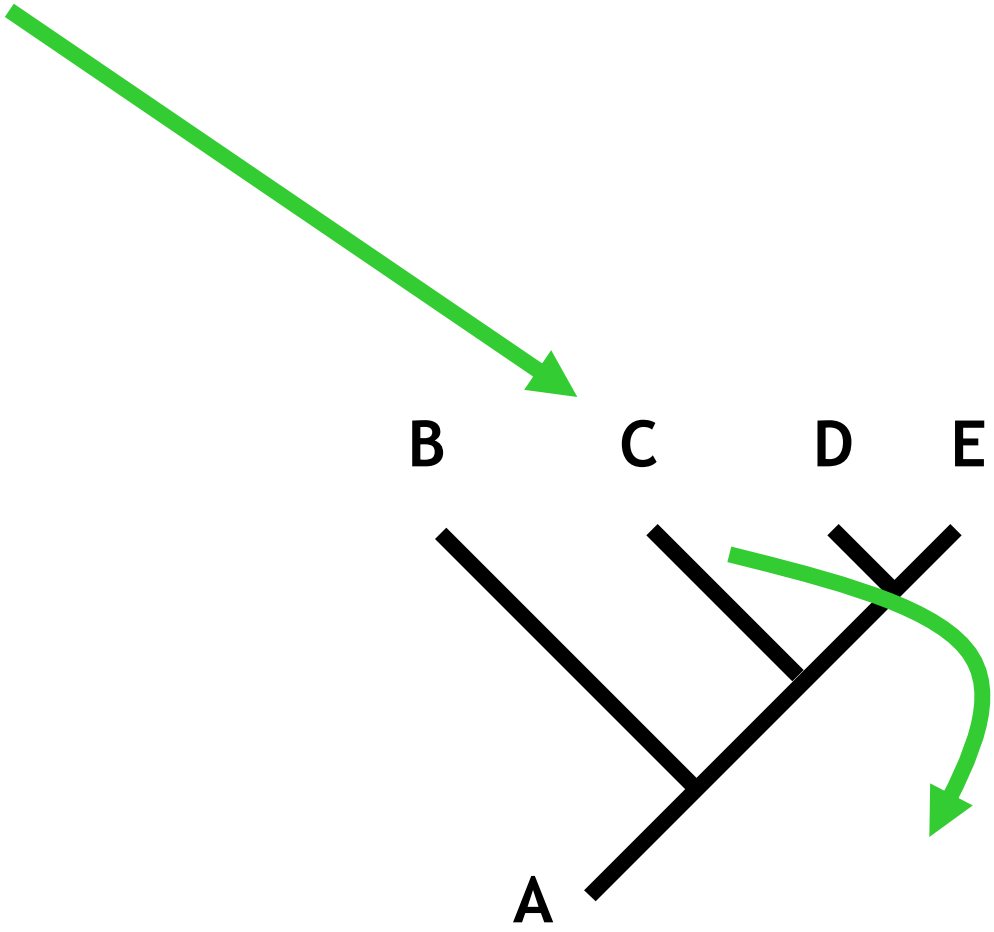
How recognize apo- & plesiomorphies?


0 0 0 0 0 0 0 0 0 1
1 2 3 4 5 6 7 8 9 0
A 0 0 1 0 0 0 1 0 1 0
B 0 1 0 1 0 1 0 0 0 0
C 0 1 1 1 0 0 0 0 0 1
D 1 0 1 0 1 1 0 0 0 1
E 0 0 0 0 1 1 0 1 0 1
0 0 0 1 0
0 1 1 0 0
1 0 1 1 0
0 1 1 0 0
0 0 0 1 1
0 1 0 1 1
1 0 0 0 0
0 0 0 0 1
1 0 0 0 0
0 0 1 1 1
A B C D E
6
5
6
10

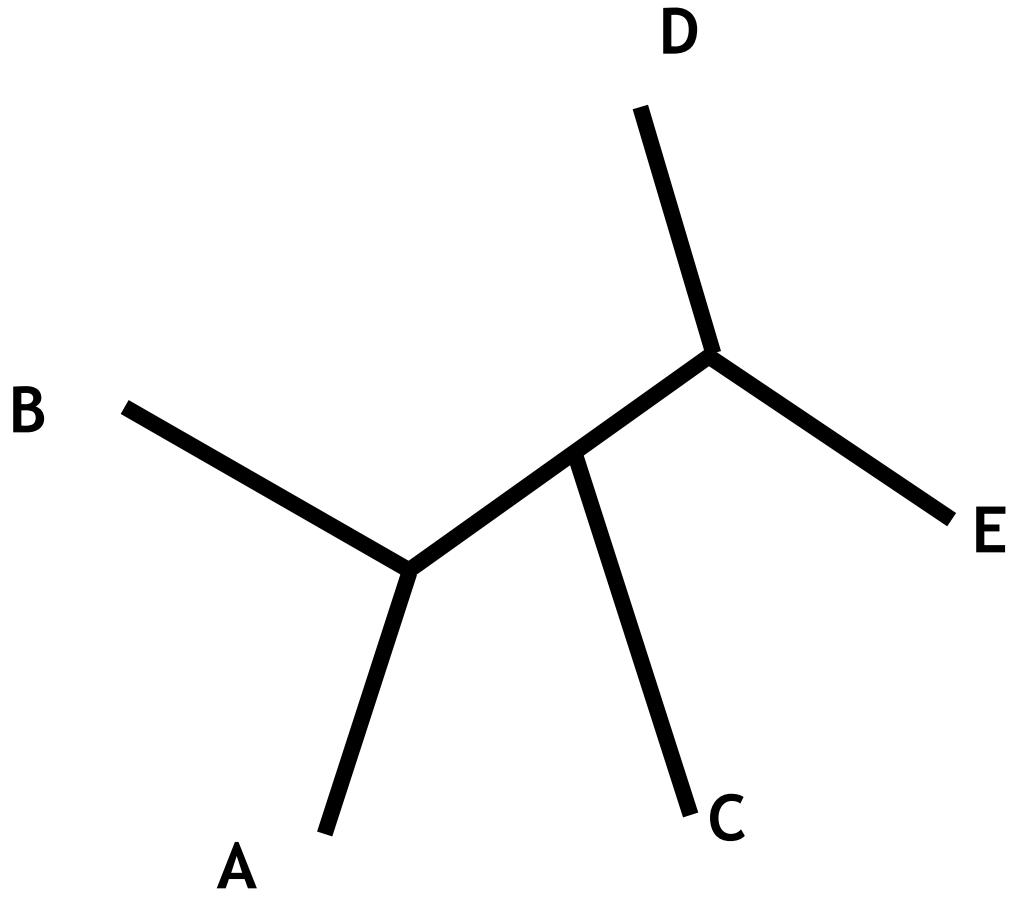
```
          0 0 0 0 0 0 0 0 0 1
          1 2 3 4 5 6 7 8 9 0

A         0 0 1 0 0 0 1 0 1 0
B         0 1 0 1 0 1 0 0 0 0
C         0 1 1 1 0 0 0 0 0 1
D         1 0 1 0 1 1 0 0 0 1
E         0 0 0 0 1 1 0 1 0 1
```



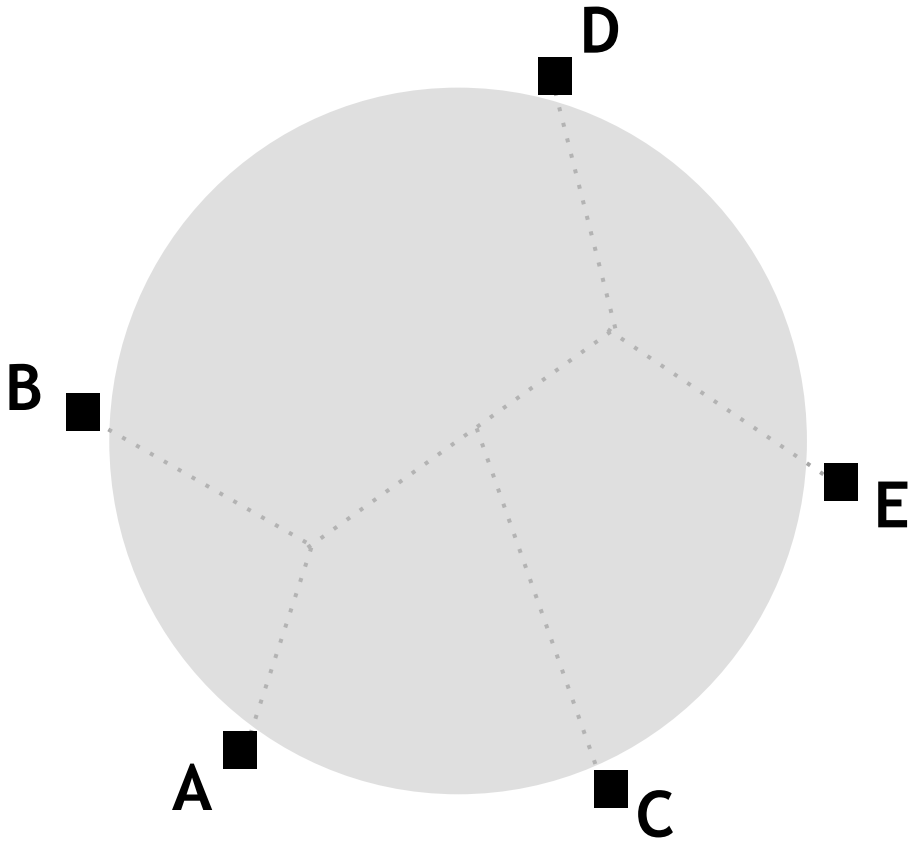
	0 0 0 0 0 0 0 0 0 1
	1 2 3 4 5 6 7 8 9 0
A	0 0 1 0 0 0 1 0 1 0
B	0 1 0 1 0 1 0 0 0 0
C	0 1 1 1 0 0 0 0 1
D	1 0 1 0 1 1 0 0 0 1
E	0 0 0 0 1 1 0 1 0 1

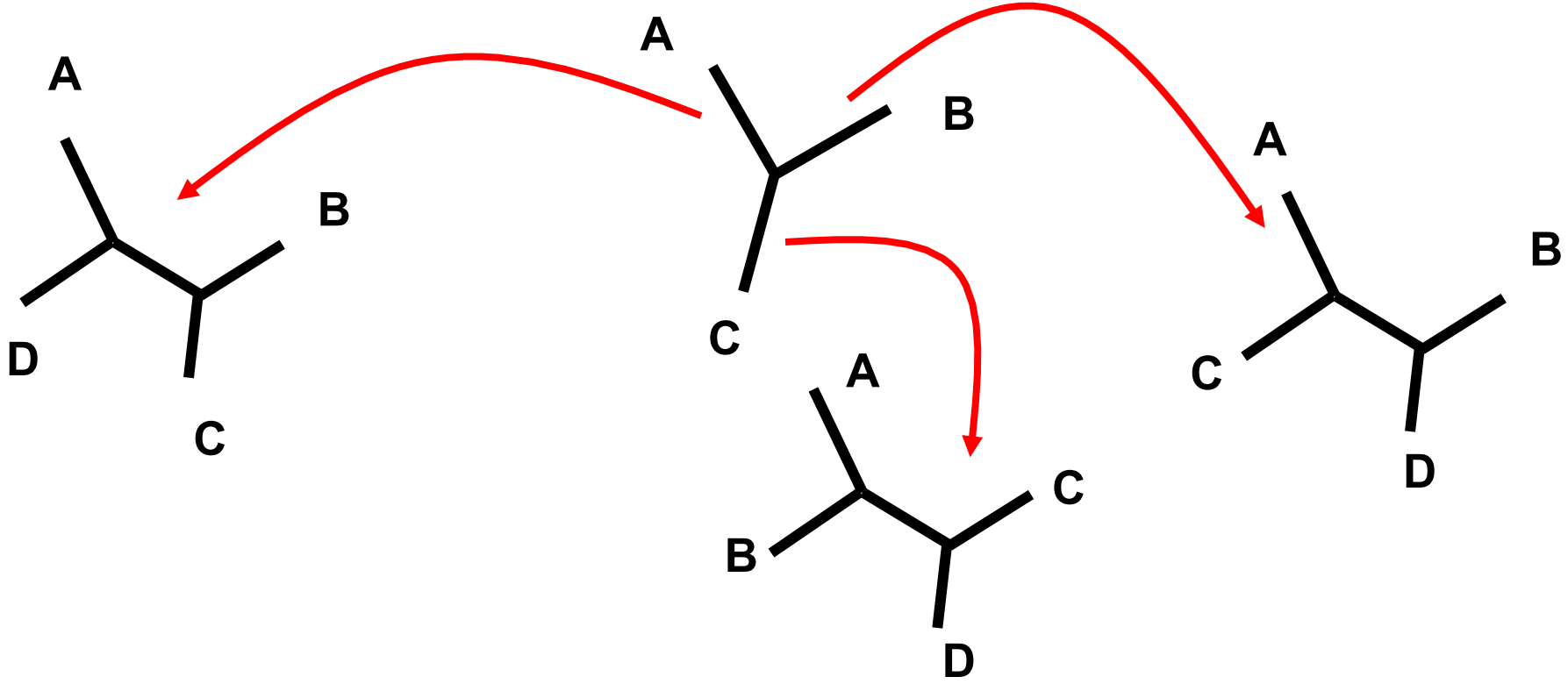


	0 0 0 0 0 0 0 0 0 1
	1 2 3 4 5 6 7 8 9 0
A	0 0 1 0 0 0 1 0 1 0
B	0 1 0 1 0 1 0 0 0 0
C	0 1 1 1 0 0 0 0 0 1
D	1 0 1 0 1 1 0 0 0 1
E	0 0 0 0 1 1 0 1 0 1



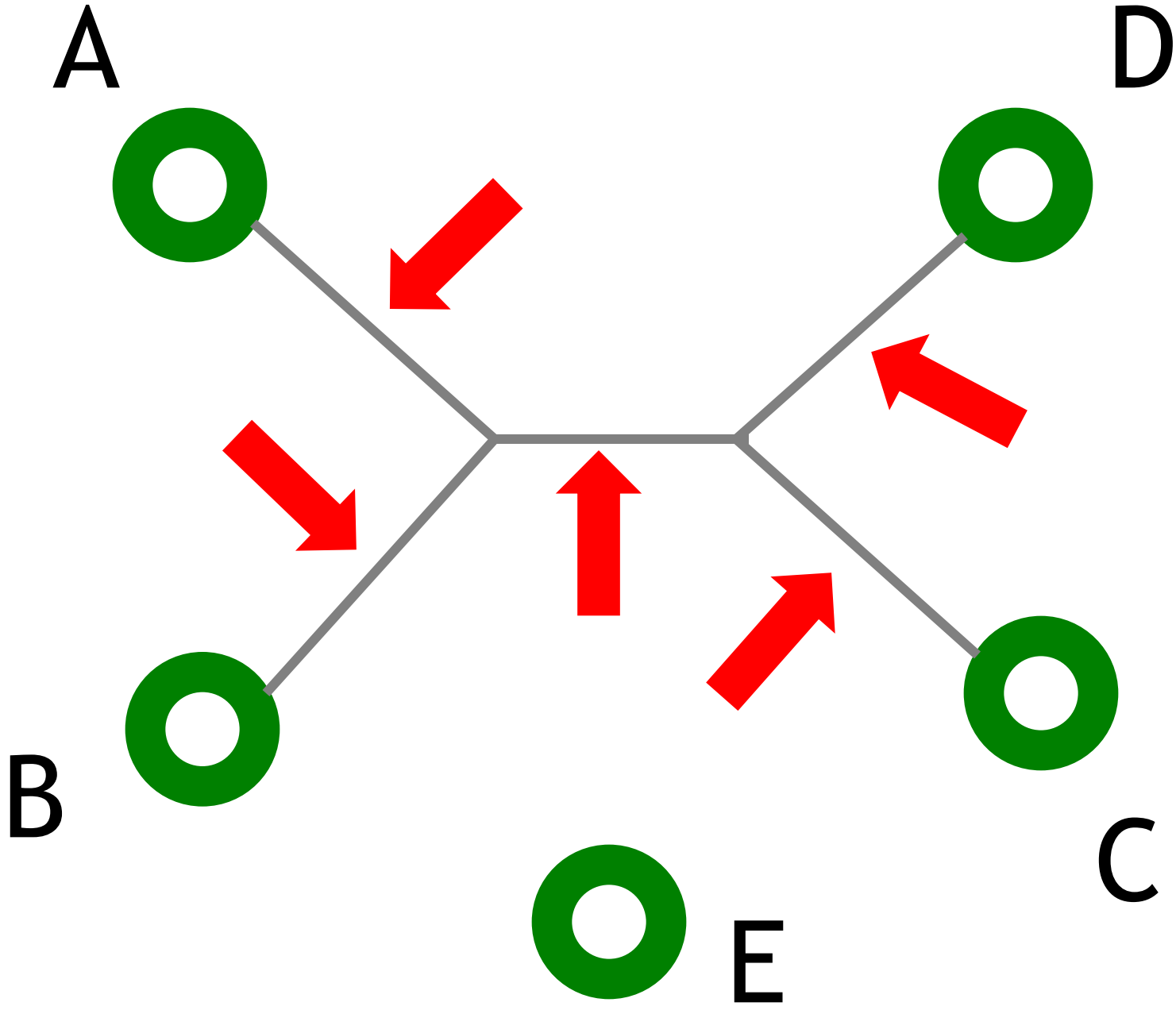
	0 0 0 0 0 0 0 0 0 1
	1 2 3 4 5 6 7 8 9 0
A	0 0 1 0 0 0 1 0 1 0
B	0 1 0 1 0 1 0 0 0 0
C	0 1 1 1 0 0 0 0 0 1
D	1 0 1 0 1 1 0 0 0 1
E	0 0 0 0 1 1 0 1 0 1

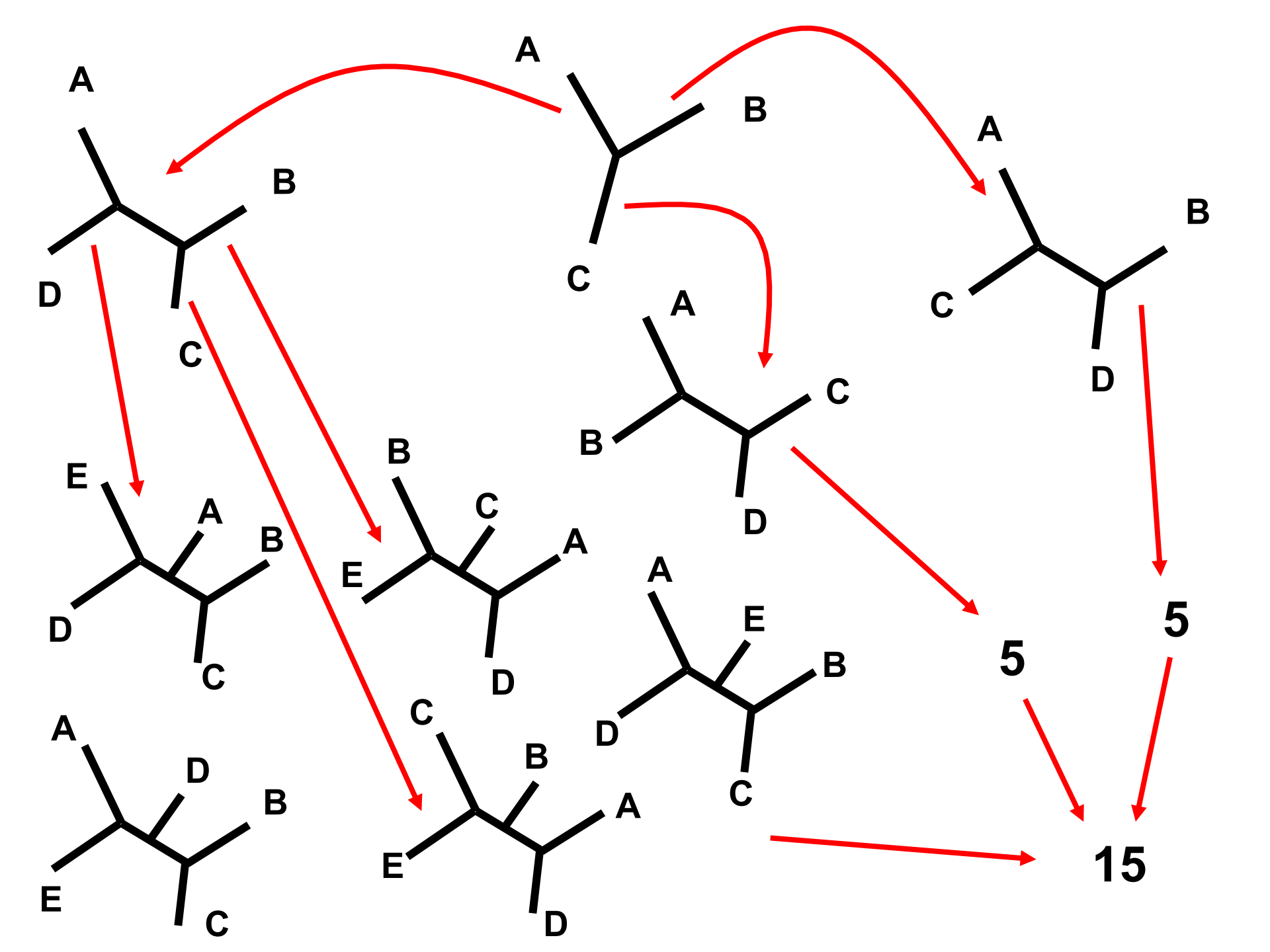




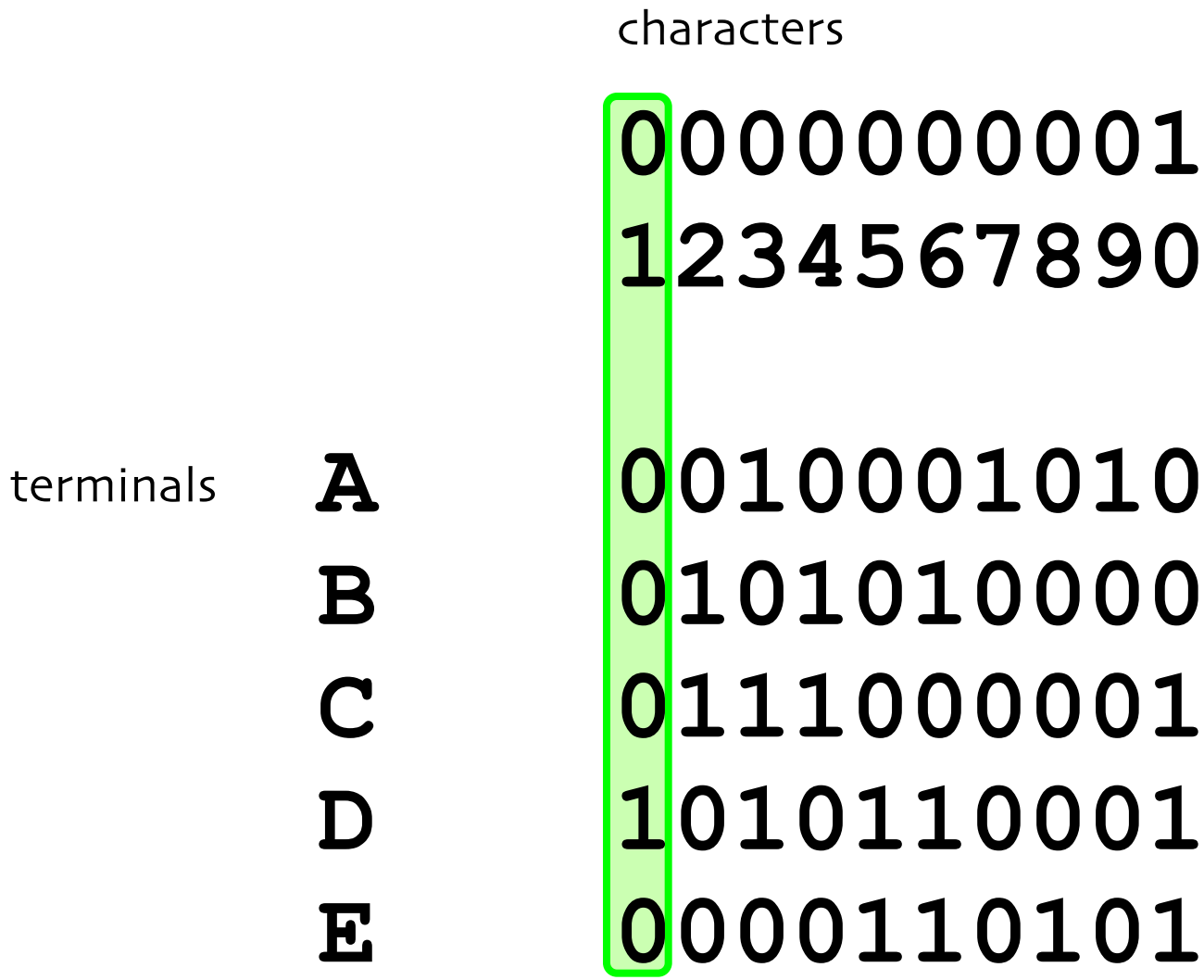
3 BRANCHES > 3 DIFFERENT PLACES TO ADD 4TH TERMINAL

5 BRANCHES > 5 DIFFERENT PLACES TO ADD 5TH TERMINAL



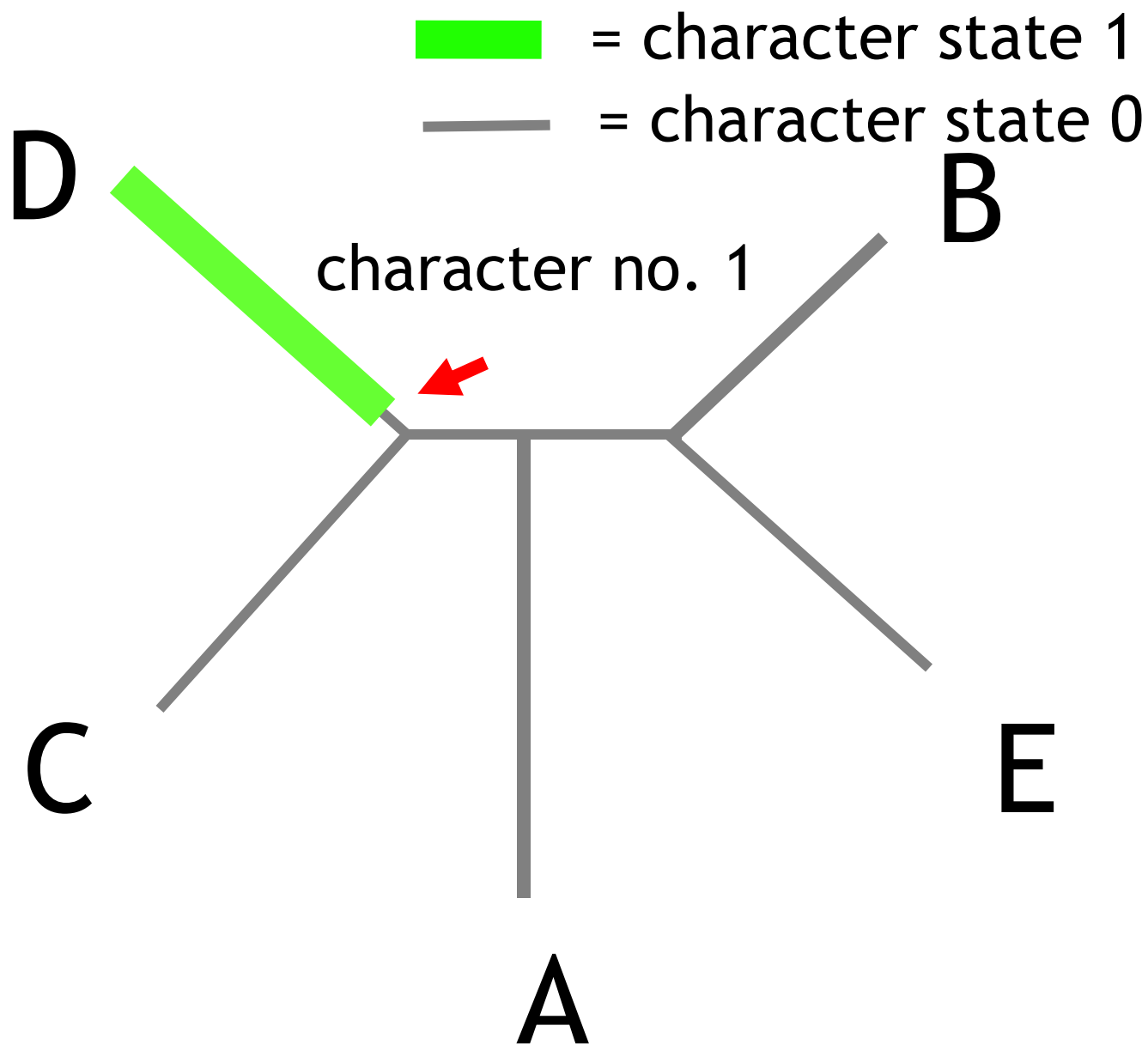

A
B
C
D
E
5
15

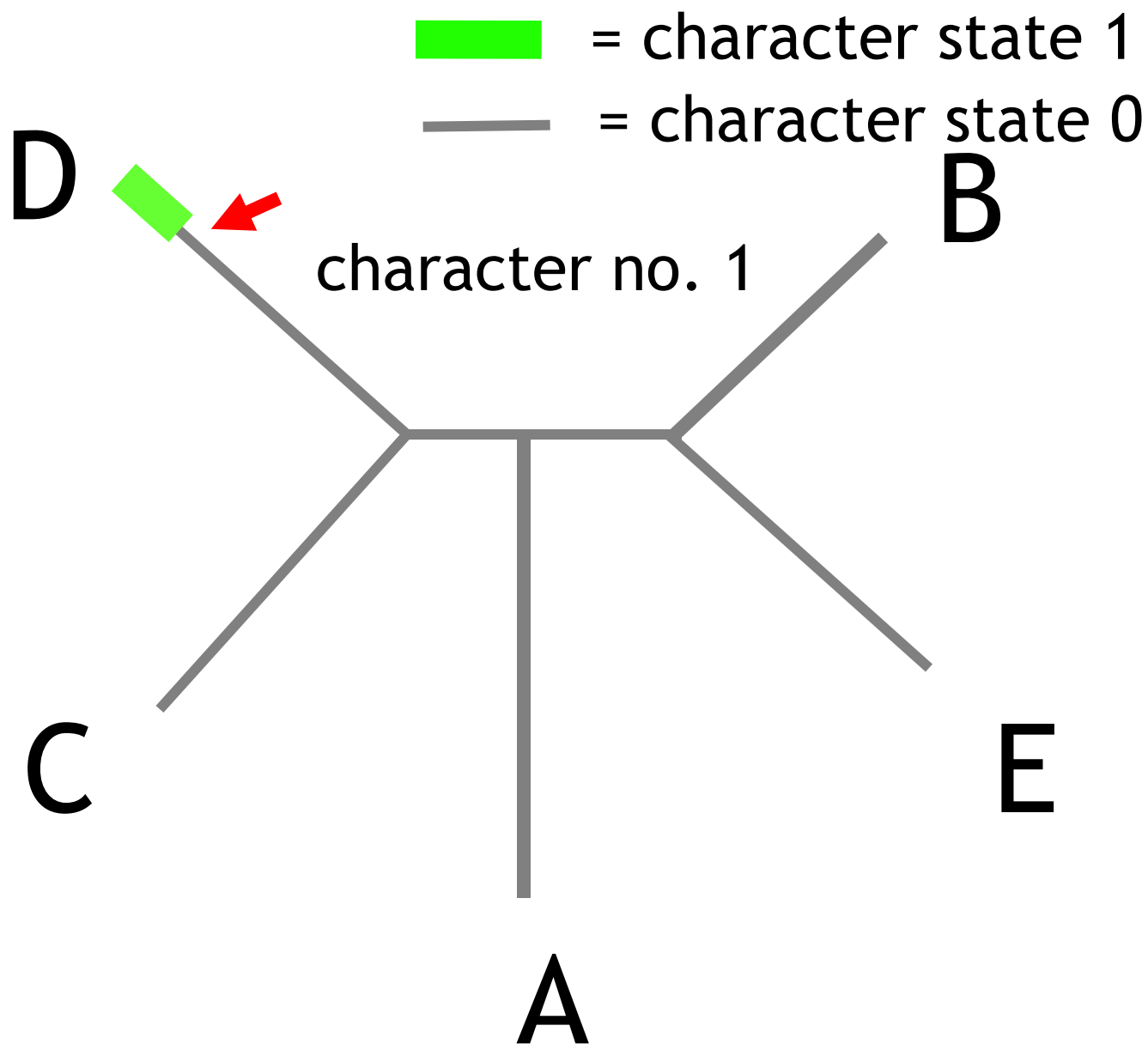
n	branches	B(n)
3	3	x 1
4	5	x 3
5	7	x 15
6	9	x 105
7	11	x 945
8	13	x 10 395
9	15	x 135 135
10		~2 x 10^6
15		~8 x 10^{12}
20		~2 x 10^{20}
50		~3 x 10^{74}

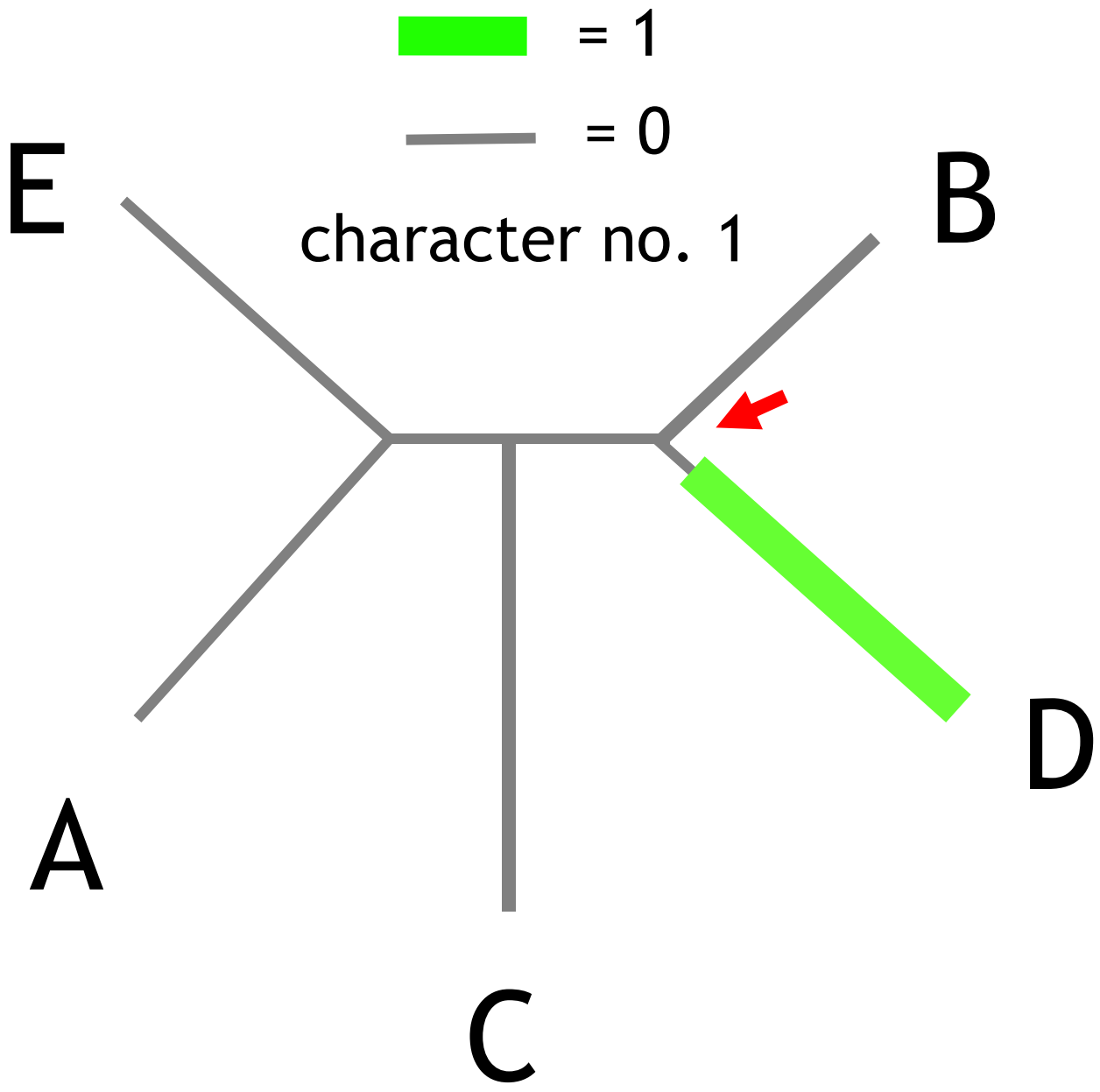

characters
0000000001
1234567890
terminals
A 0010001010
B 0101010000
C 0111000001
D 1010110001
E 0000110101

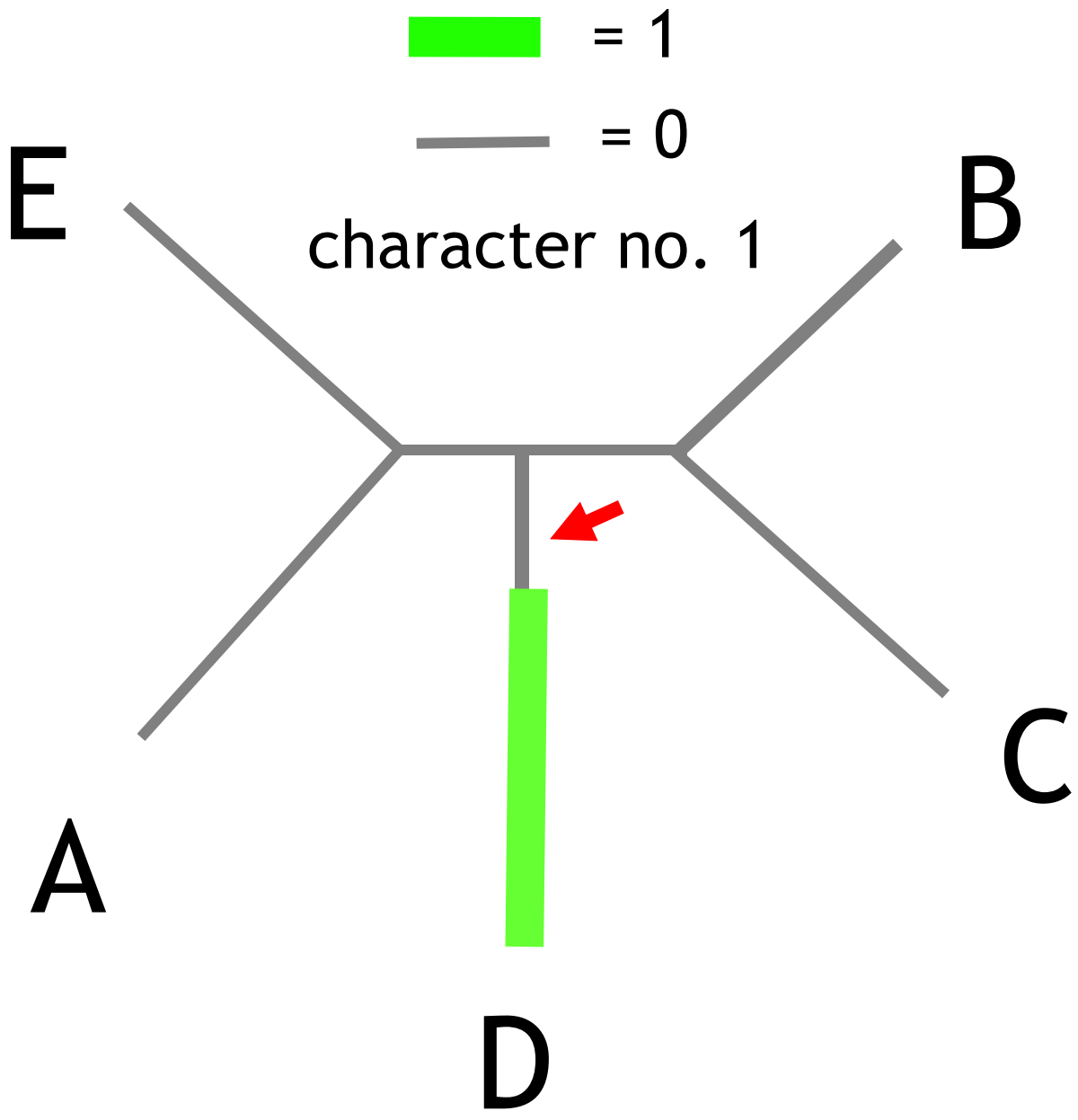
characters

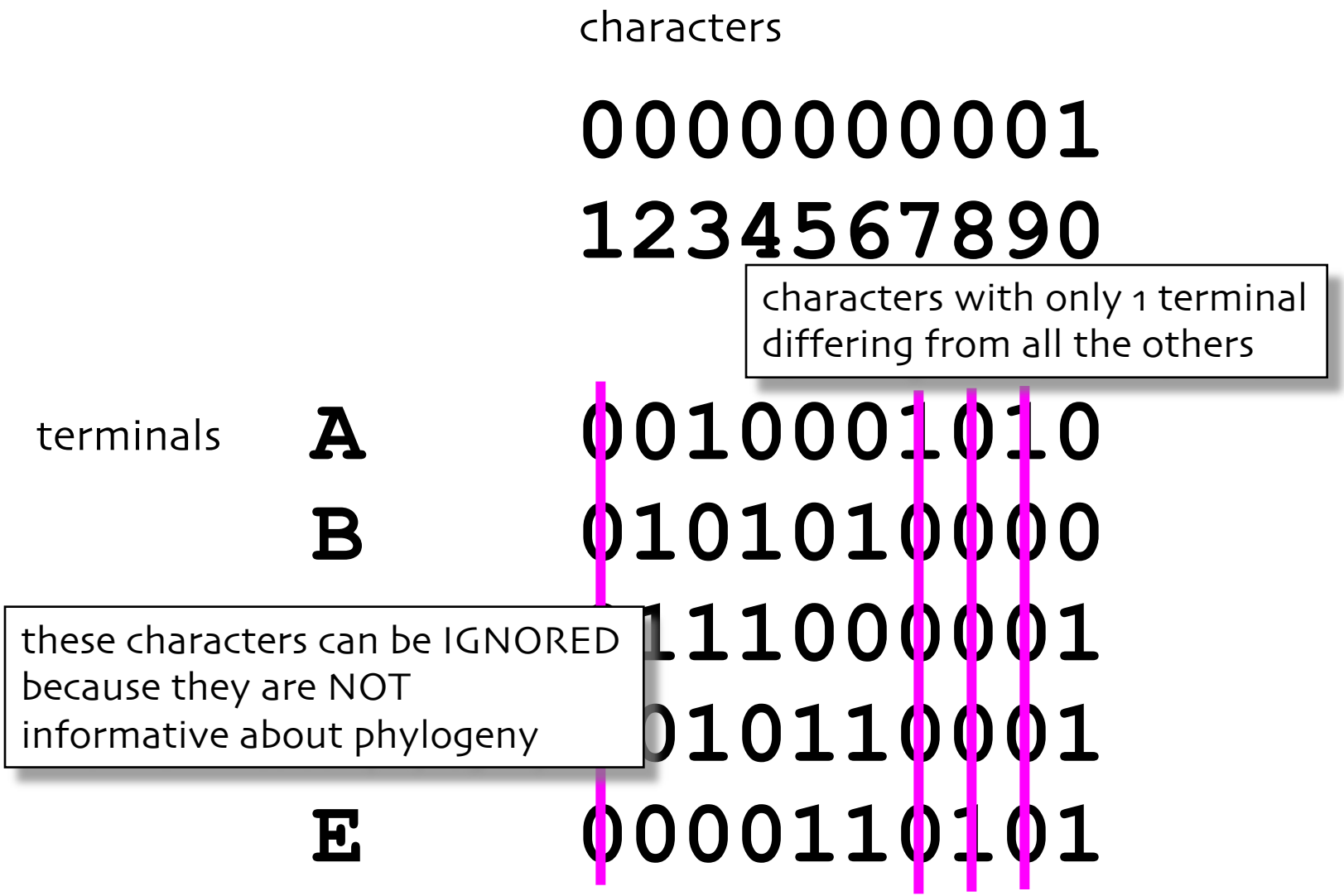
		0000000001
		1234567890
terminals	A	0010001010
	B	0101010000
	C	0111000001
	D	1010110001
	E	0000110101

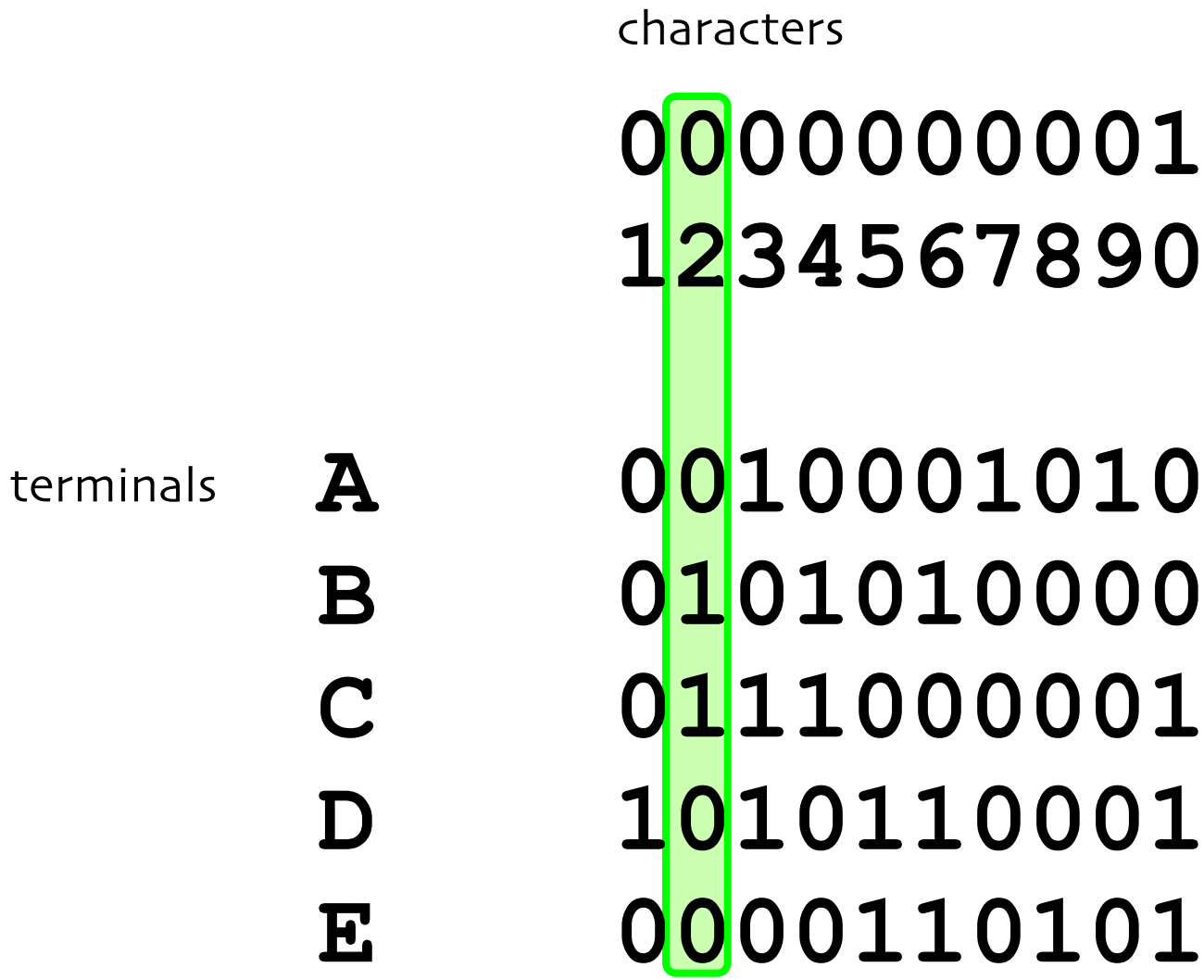

= character state 1
= character state 0
D
B
character no. 1
C
E
A

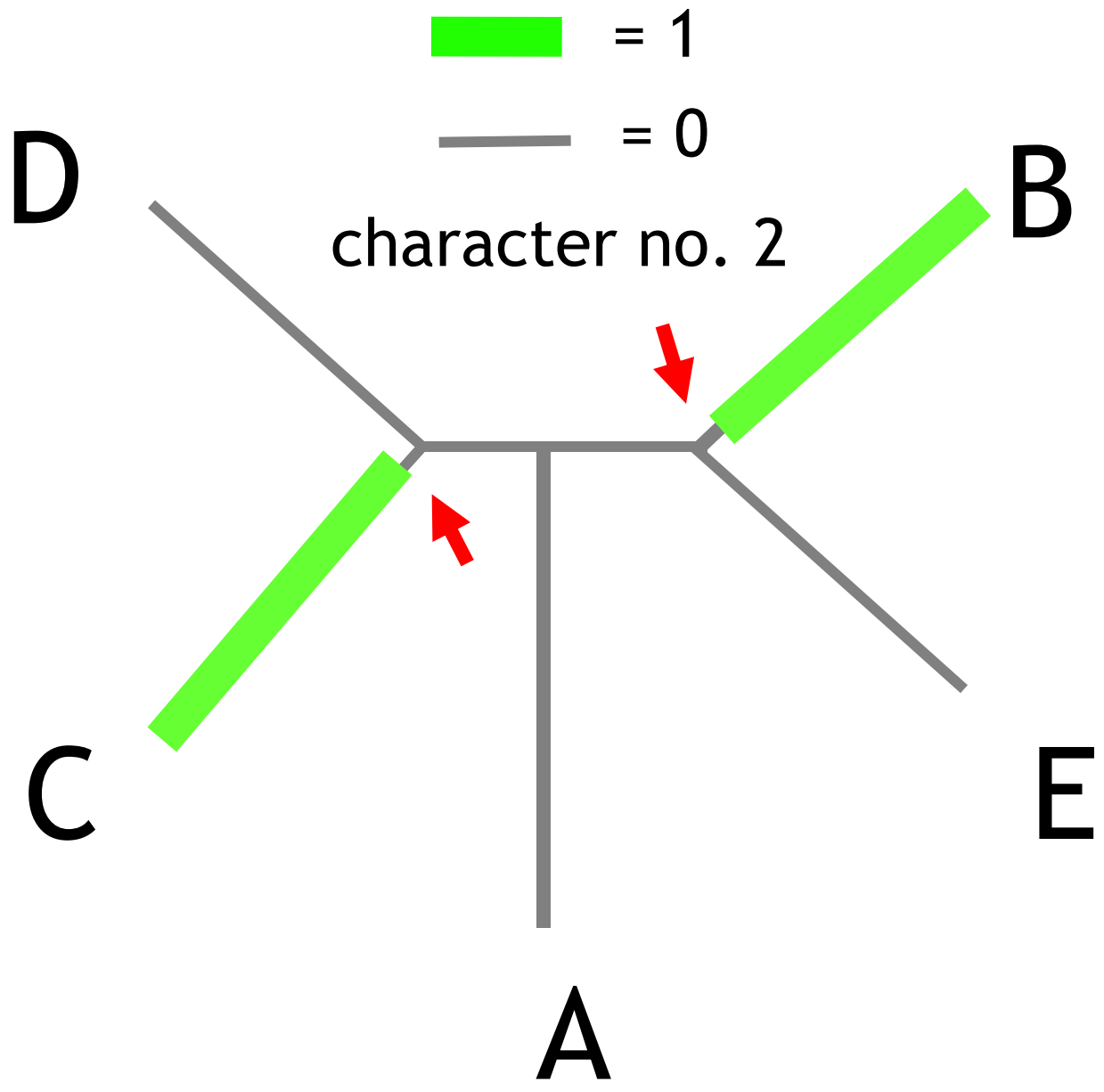

= character state 1
= character state 0
D
B
character no. 1
C
E
A

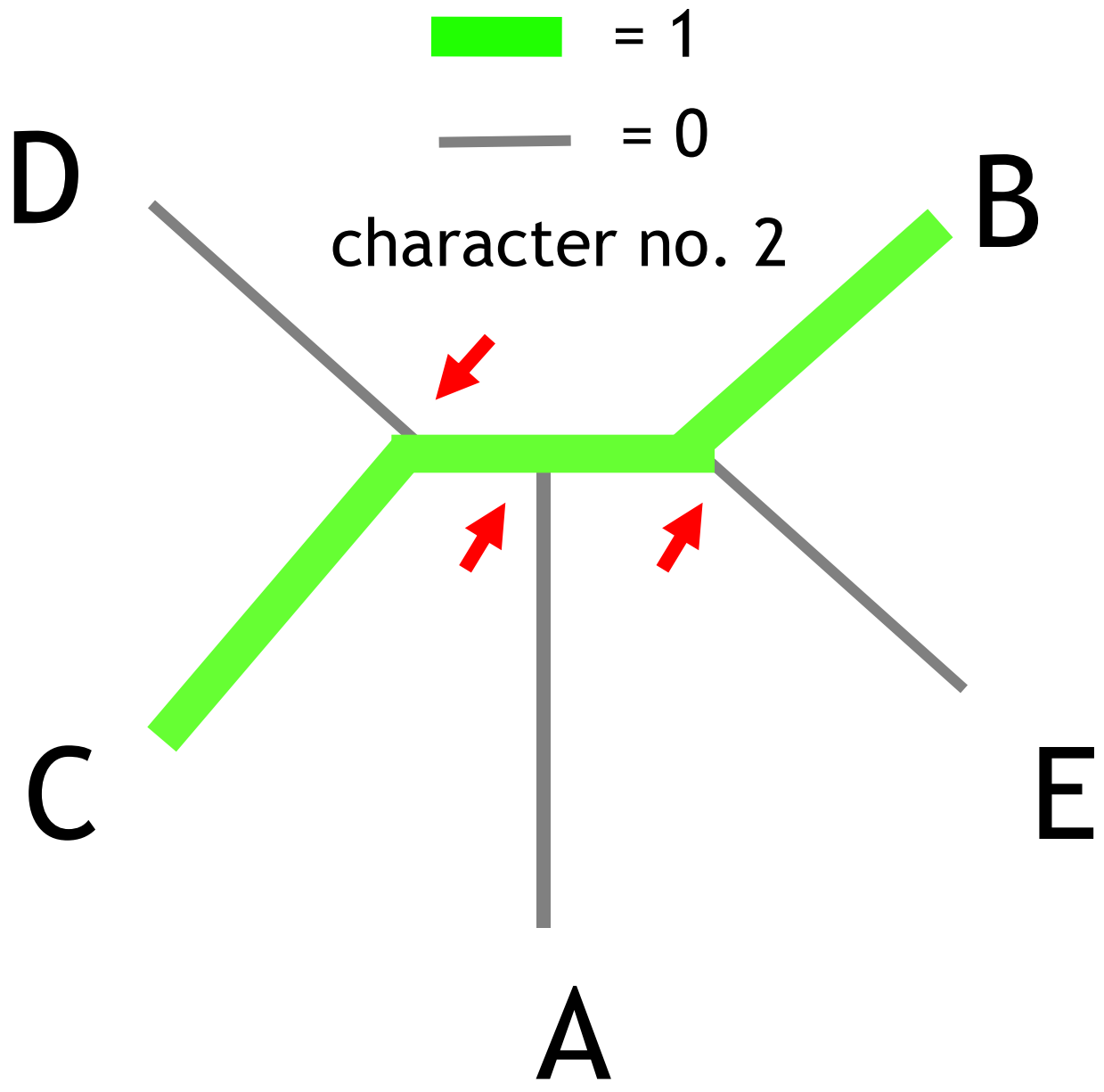

= 1
= 0
character no. 1
E
B
A
C
D


= 1
= 0
character no. 1
E
B
A
C
D


characters
0000000001
1234567890
characters with only 1 terminal differing from all the others
terminals
A 0010001010
B 0101010000
1110000001
0101110001
E 0000110101
these characters can be IGNORED because they are NOT informative about phylogeny


characters
0000000001
1234567890
terminals
A 0010001010
B 0101010000
C 0111000001
D 1010110001
E 0000110101


= 1
= 0
character no. 2
D
B
C
E
A


= 1
= 0
character no. 2
D
B
C
E
A

PARSIMONY

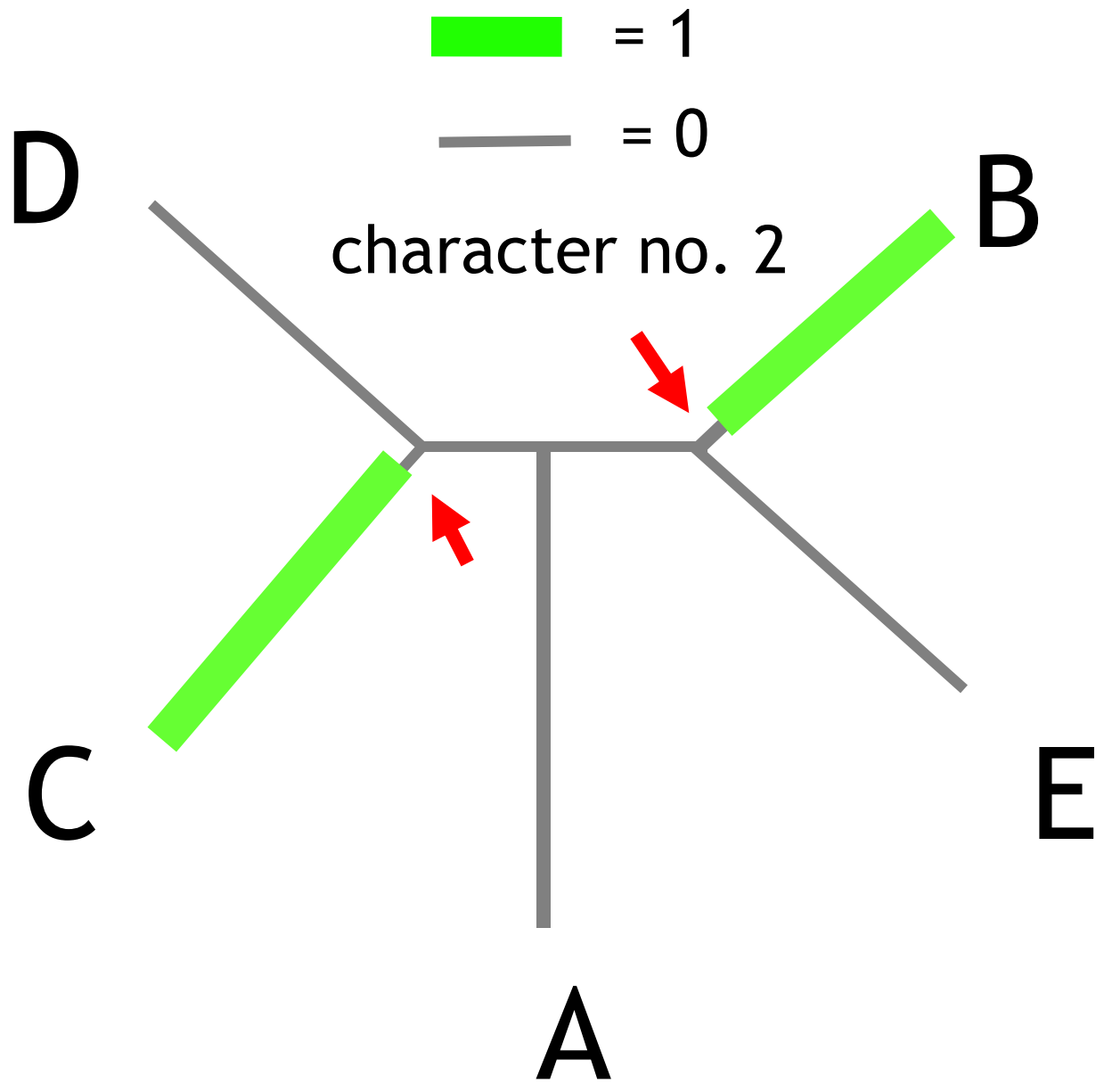
PLURALITAS NON EST PONENDA
SINE NECESSITATE

PLURALITY should NOT be assumed BEYOND NECESSITY

William of Ockham

Ockham chooses a razor

SIMPLE hypotheses are desirable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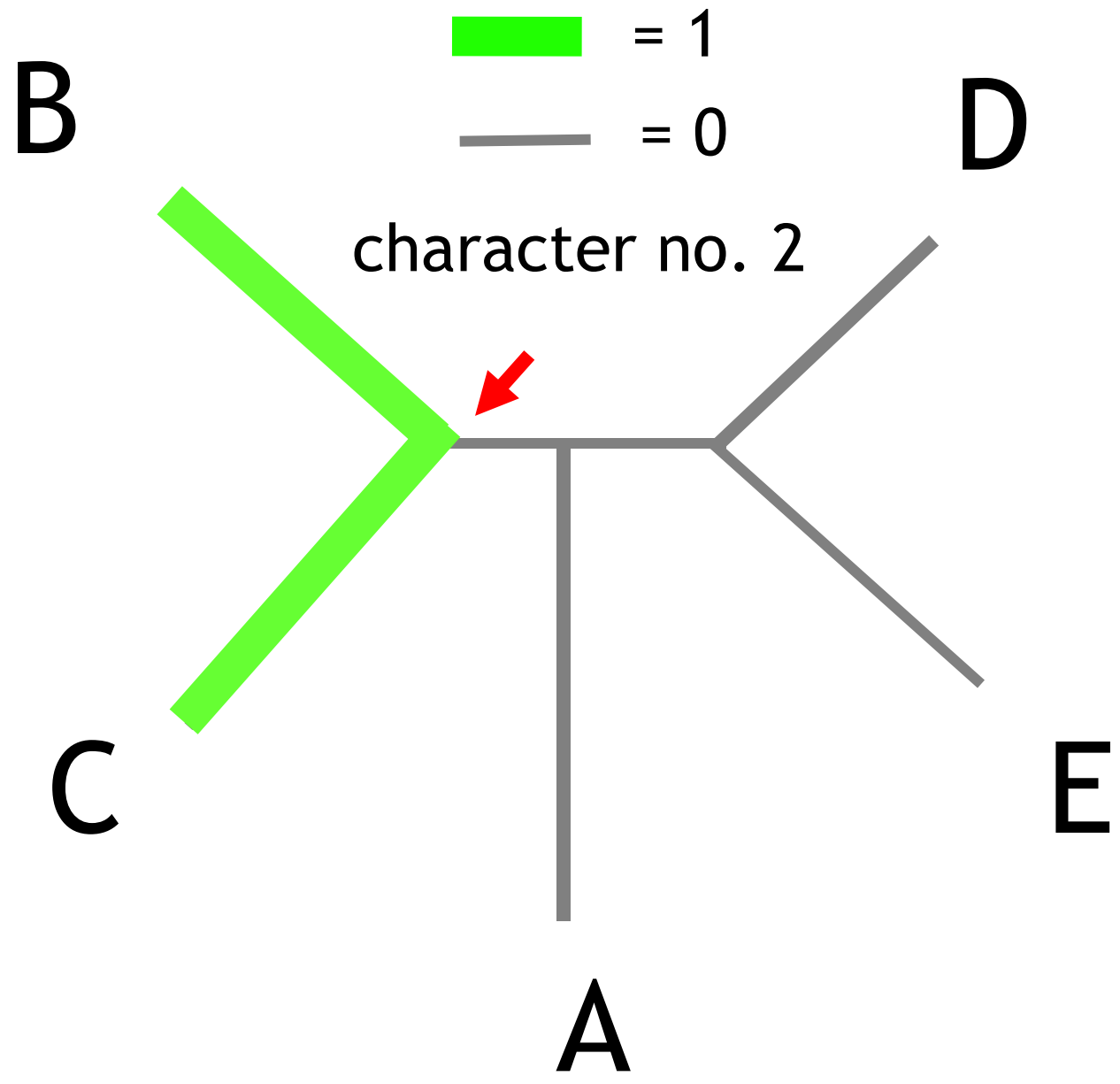
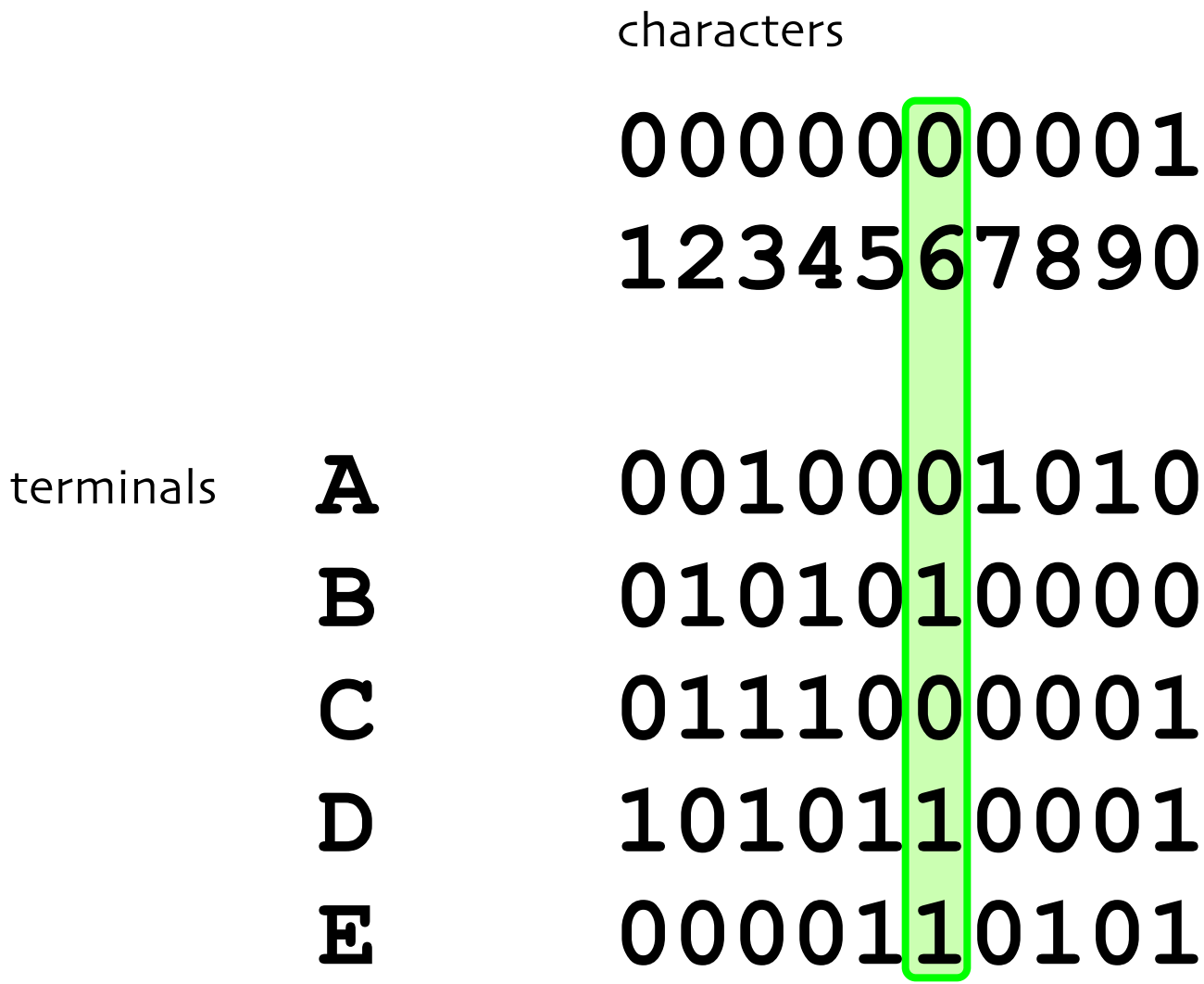
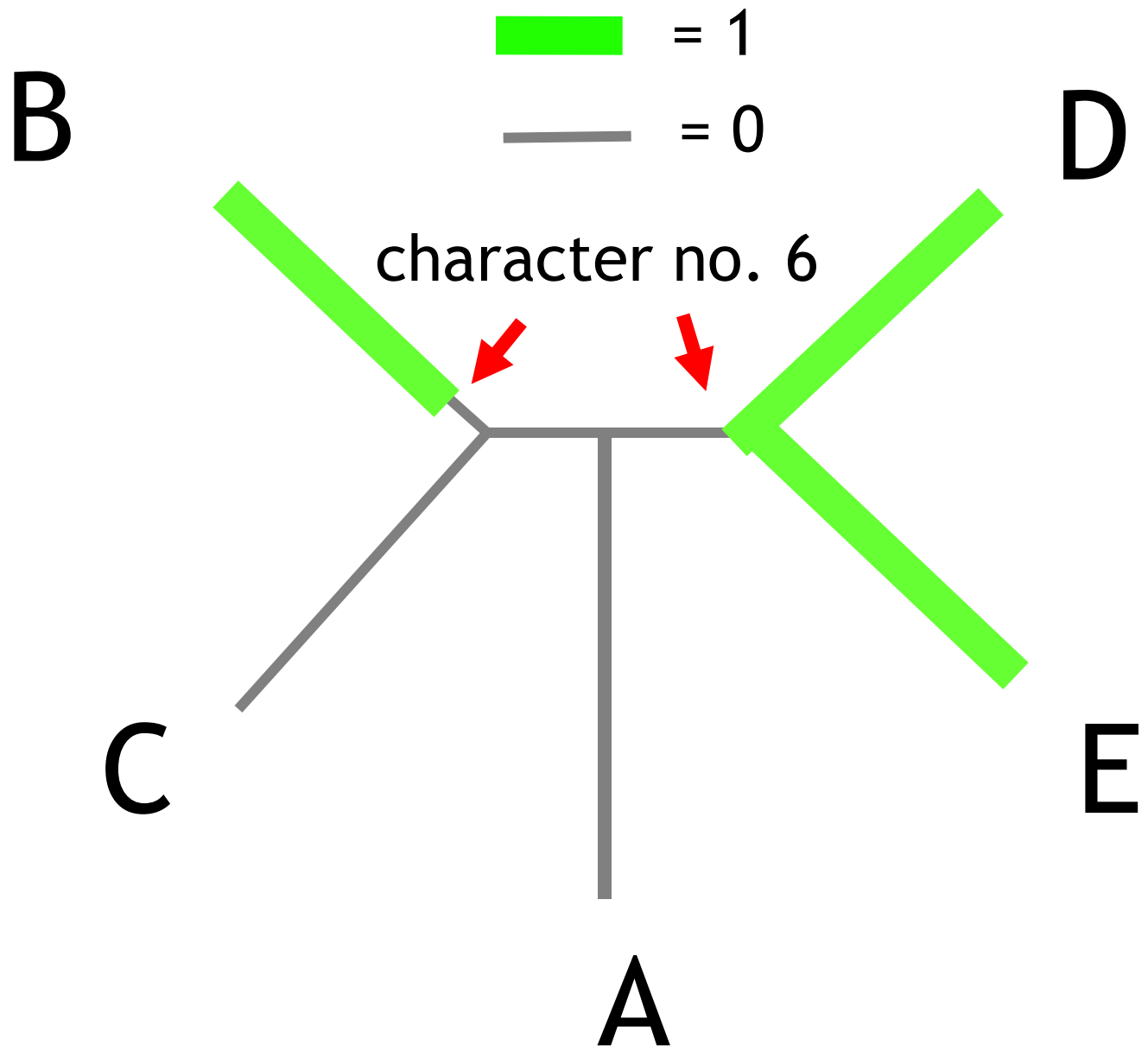
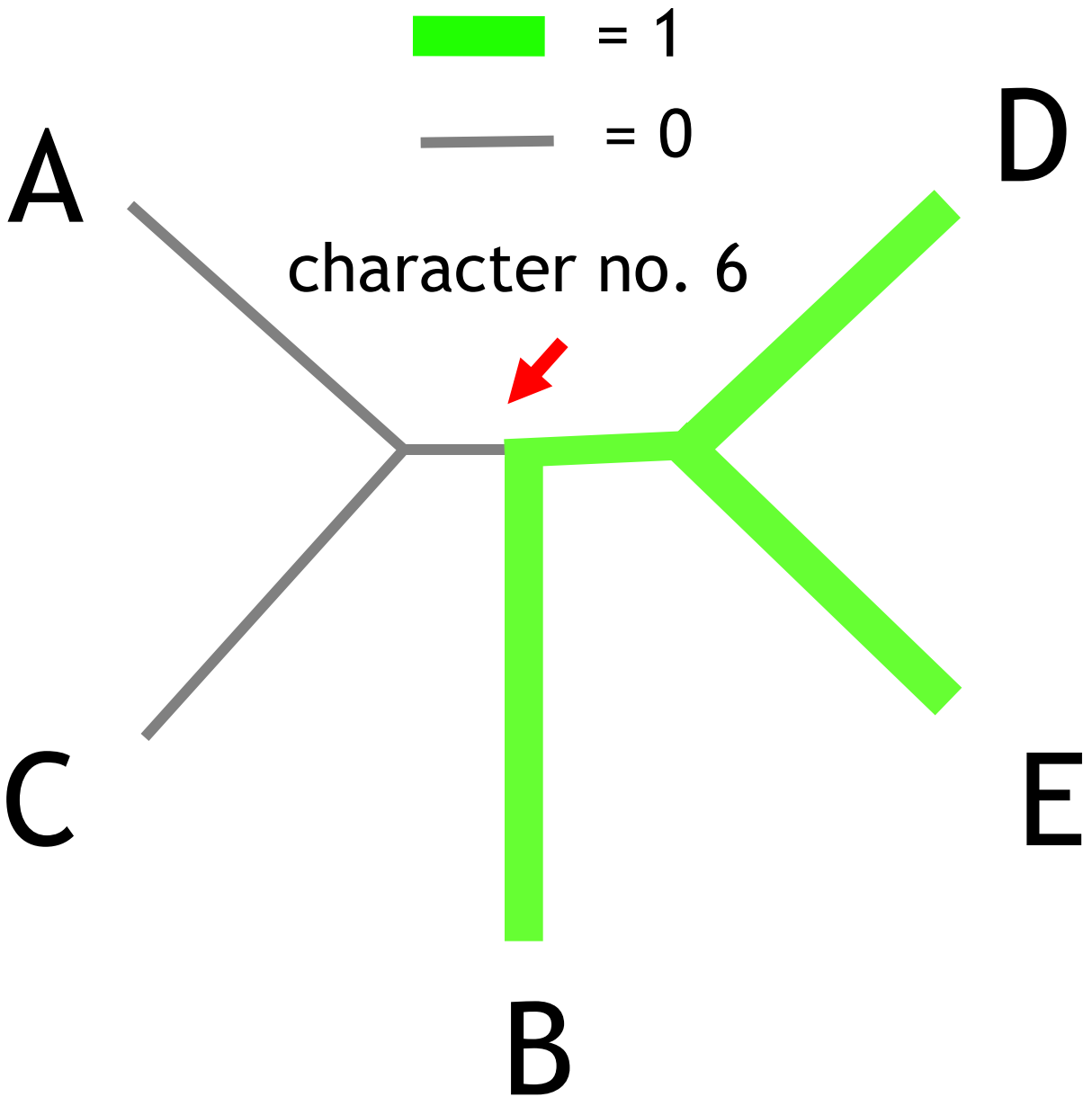
= 0
character no. 2
D
B
C
E
A


= 1
= 0
B
D
character no. 2
C
E
A


characters
0000000001
1234567890
terminals
A
0010001010
B
0101010000
C
0111000001
D
1010110001
E
0000110101


= 1
= 0
B
D
character no. 6
C
E
A


= 1
= 0
A
D
character no. 6
C
E
B

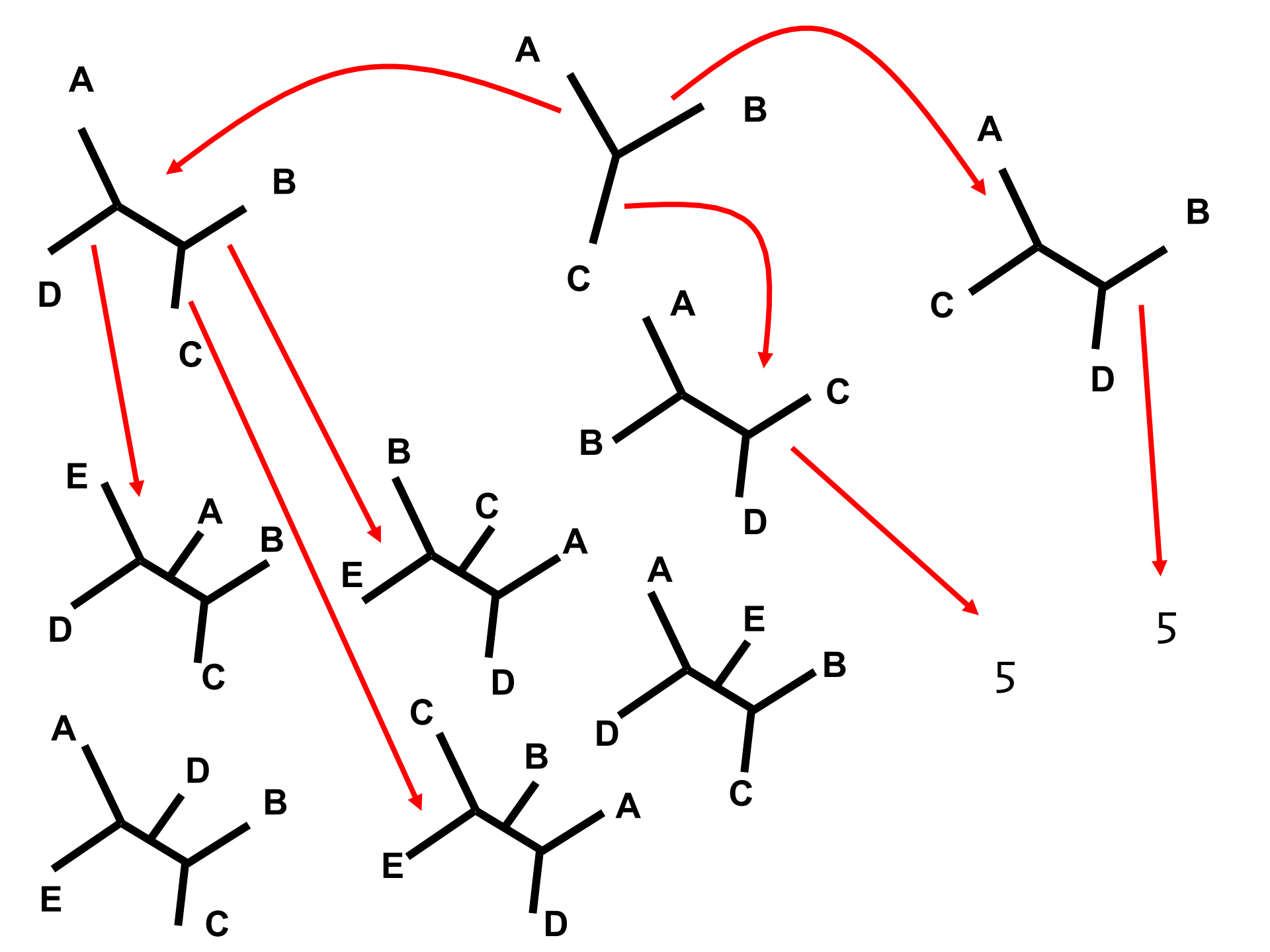
BEST HYPOTHESIS ?

PARSIMONY

PLURALITAS NON EST PONENDA
SINE NECESSITATE

William of Ockham

SIMPLE hypotheses are desirable


A
B
C
D
E
5

characters		0 0 0 0 0 0 0 0 0 1 1 2 3 4 5 6 7 8 9 0	Σ
Tree	1	1 1 2 1 2 2 1 1 1 2	14
	2	1 1 2 1 1 2 1 1 1 2	13
	3		
	4		
	5		
	6		
	7		
	8		
	9		
	10		
	11		
	12		
	13		
	14		
	15		

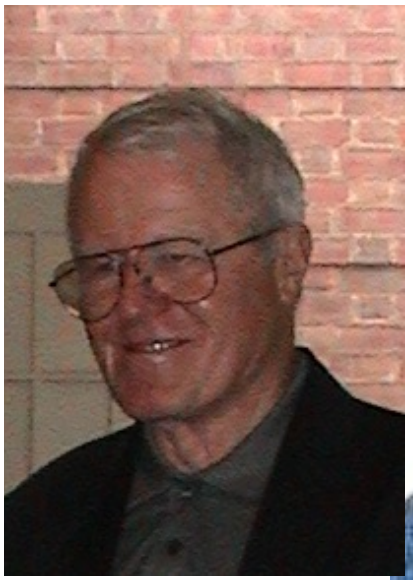
SUM of ch. state changes

EVALUATION of all possible trees feasible only for a SMALL number of trees and thus……

Wagner algorithm

Kluge, A. G. & Farris, J. S. 1969. Quantitative phyletics and the evolution of anurans. *Systematic Zoology* 18:1-32.

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



SUMMARY

number of trees grows EXPONENTIALLY when number of studied organisms increase

by comparing ALL possible trees for certain number of terminals we will find a tree requiring smallest number of changes in ALL characters

most of the resemblance between terminals is explained by shared evolutionary history

descent with modification

maximizing **explanatory power** of the hypothesis

if we use parsimony as our optimality criterion this tree is the best hypothesis of phylogeny