Evolutionary Thinking 2022 TA session week 2 – Tree building methods

Jilong Ma aujilongm@birc.au.dk





Outline

1. Recap

1. The learning outcome of this today (20 minutes)

Tree building methods

Distance-based phylogeny tree building algorithms

UPGMA, NJ tree

2. Working on MEGA exercises

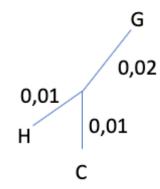




Recap

Sequence Alignemnt Difference matrix (GenBank, BLAST) (MUSCLE, ClustalW) Н >Human ACTCACTGTCTG G 3 3 ACTCACTG TCTG Human >Chimp ACTCACTGAGTG Chimp ACTCACTGAGTG Gorilla AGTGACTGACTG Distance matrix >Gorilla (p-distance, JC, K..) AGTGACTGACTG Substituton Model Test Н C 0,02 G 0,03 0,03

Tree building (UPGMA, Neighbour-Joining...)



Distance based phylogeny tree building



Recap

Sequence (GenBank, BLAST)

>Human ACTCACTGTCTG

>Chimp ACTCACTGAGTG

>Gorilla AGTGACTGACTG Alignemnt (MUSCLE, ClustalW)

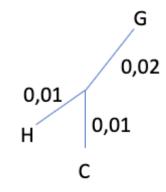
Human ACTCACTG<mark>T</mark>CTG Chimp ACTCACTGA<mark>G</mark>TG Gorilla A<mark>G</mark>T<mark>G</mark>ACTGACTG Difference matrix

Н		
С	2	
G	3	3

Distance matrix (p-distance, JC, K..) Substituton Model Test

Н		
С	0,02	
G	0,03	0,03

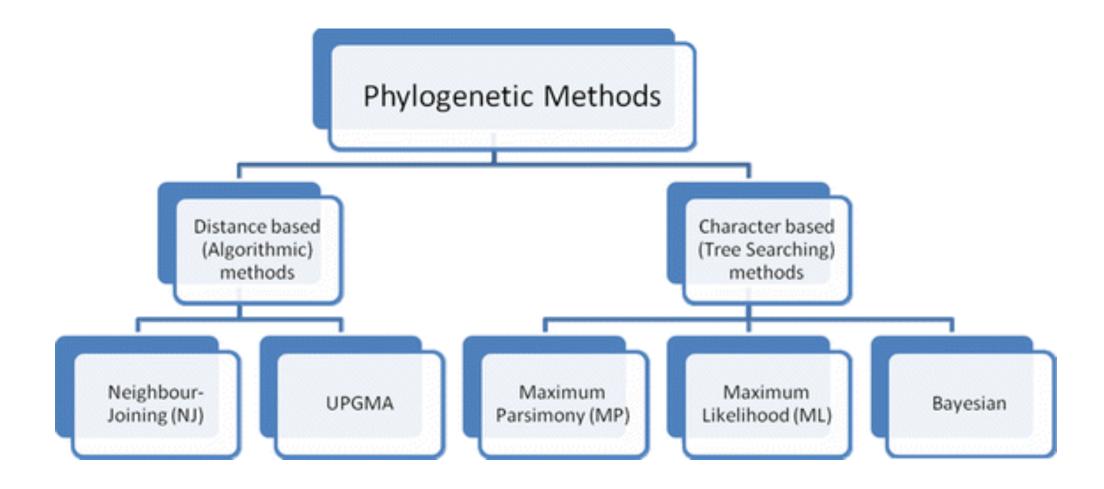
Tree building (UPGMA, Neighbour-Joining...)



Distance based phylogeny tree building









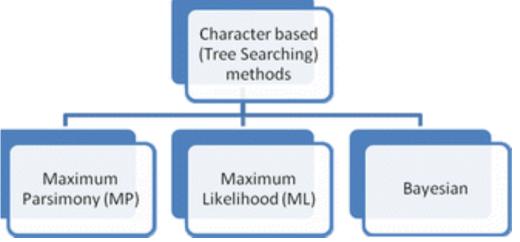








Conceptually, what are MP, ML and Bayesian doing? (3 minutes)





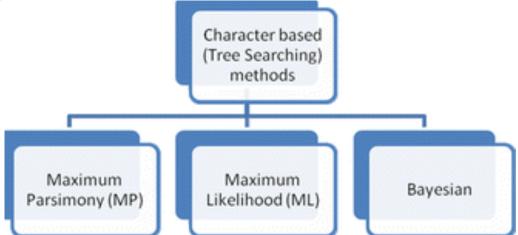


Conceptually, what are MP, ML, and Bayesian doing?

MP: Finding the topology requires the smallest evolutionary changes (substitutions)

ML: Finding the phylogeny maximize P(Data | Phylogeny)

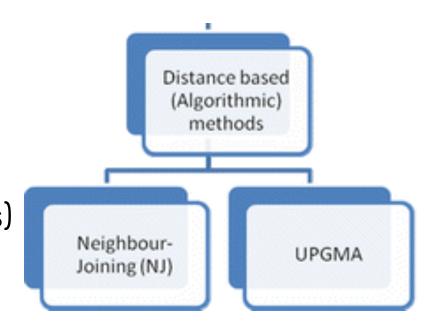
Bayesian: Finding the Phylogeny has the highest P(Phylogeny | Data)







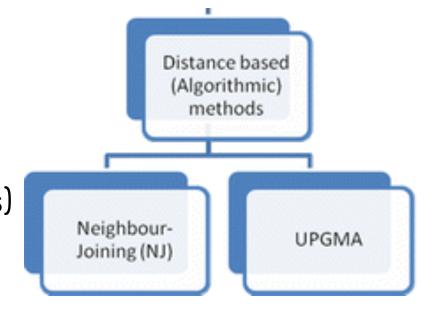
	A	В	С	D
A				
В	5			
C	2	3		
D	1	4	6	



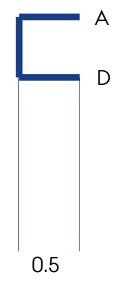




	A	В	C	D
A				
В	5			
C	2	3		
D	1	4	6	



$$Min d = d_AD = 1$$



AD B C
AD
B
4.5
C
3 5

UPGMA	
(unweighted pair-group method with arithmetic me	ans)

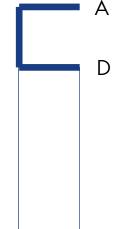
	A	В	С	D
A				
В	5			
C	2	5		
D	1	4	6	

$$d(AD)B = (dAB + dBD) / 2$$

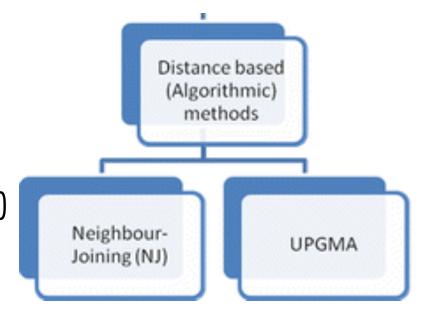
= $(5 + 4) / 2 = 4.5$

$$d(AD)C = (dAC + dCD) / 2$$

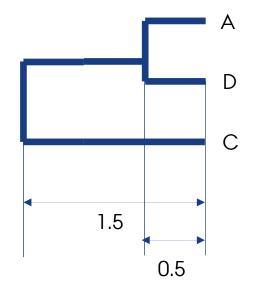
= $(2 + 6) / 2 = 3$



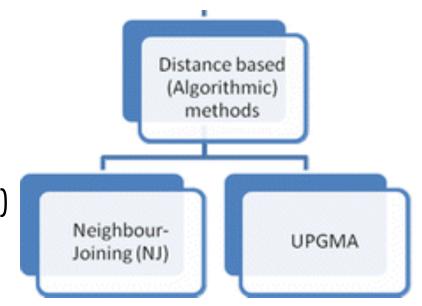




	AD	В	С
AD			
В	4.5		
C	3	5	

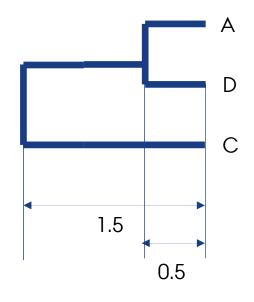






	AD	В	C
AD			
В	4.5		
C	3	5	

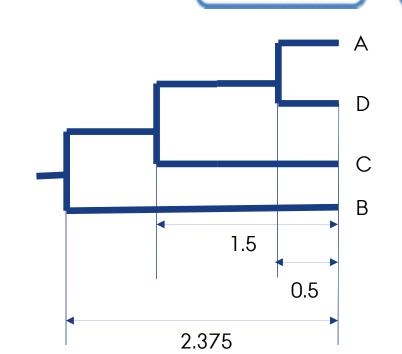
	ADC	В
ADC		
В	4.75	





UPGMA (unweighted pair-group method with arithmetic means)

	ADC	В
ADC		
В	4.75	



Neighbour-

Joining (NJ)

(Algorithmic) methods

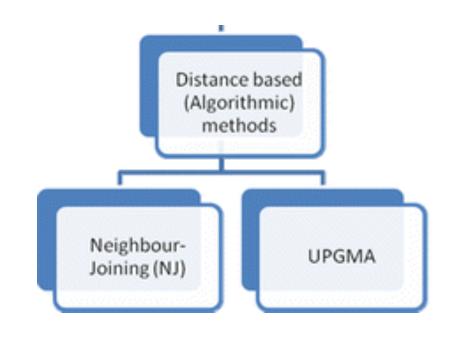




UPGMA

Neighbor-joining

Understand the formula (5.11) and (5.12). Dan Graur P107 With drawing examples



Total tree length

$$S_0 = \frac{1}{N-1} \sum_{i < j} d_{ij}$$

Total tree length after connecting 1 and 2

$$S_{12} = \frac{1}{2(N-2)} \sum_{k=3}^{N} (d_{1k} + d_{2k}) + \frac{1}{2} d_{12} + \frac{1}{N-2} \sum_{3 \le i < j \le N}^{N} d_{ij}$$





Difference between UPGMA and NJ (5 min)

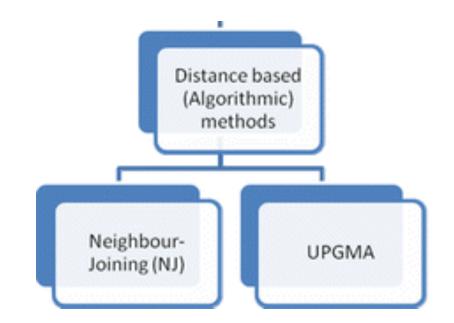
UPGMA

- 1. Rooted Tree
- 2. Branch tips come out equal (equal distance from the root, equal rates of evolution)

NJ

- 1. Unrooted Tree
- 2. Branch length varies and proportional to the amount of change (Allow unequal rates of evolution)







Difference between UPGMA and NJ (5 min)

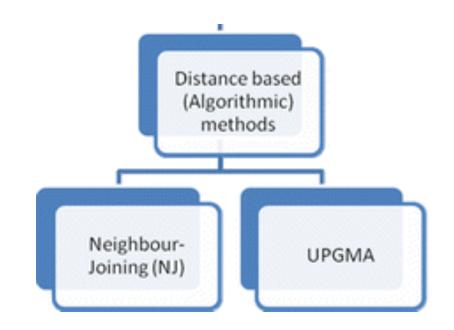
UPGMA

- 1. Rooted Tree
- 2. Branch tips come out equal (equal distance from the root, equal rates of evolution)

NJ

- 1. Unrooted Tree
- 2. Branch length varies and proportional to the amount of change (Allow unequal rates of evolution)







MEGA exercises

- 1. Finding the best-fitted substitution models
- 2. Building phylogeny trees with different methods





