

Unweighted Pair-Group Method with Arithmetic Mean

Reminder: \uparrow UPGMA Algo

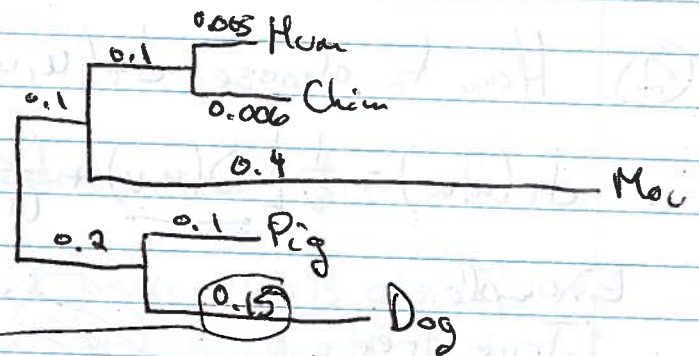
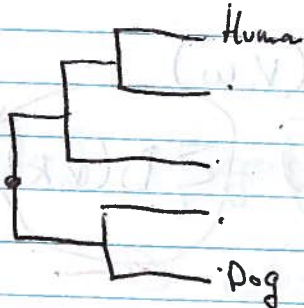
Input: S_1, \dots, S_n

Output: Tree T with branch lengths

- ① Estimate distance matrix D from pairwise alignments
- ② Repeat
 - 2.1. Choose two nodes (u, v) to pair up
 - 2.2. Remove (u, v) from D
 - 2.3. Create new node w as ancestor of u, v
 - 2.4. Add new row/column for w in D .

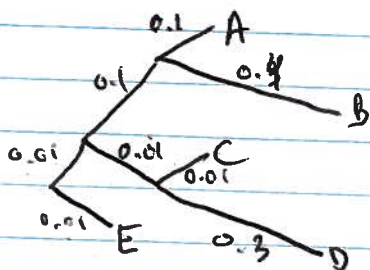
UPGMA produces correct output if

- ① Distances are estimated perfectly accurately
- ② Mutation rate is constant

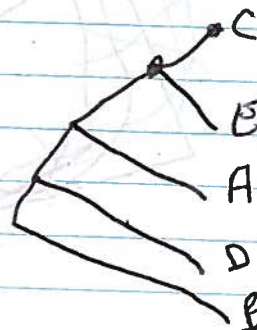


Expected number of subst. per site

Suppose true tree



UPGMA



Wrong Tree

Neighbor-joining Algo (Nei, Saitou)

Same as UPGMA, but different ^{node} pair selection rule

Calculate $Q_{n \times n}$, where $Q(i,j) = \sum_{k=1}^n D(i,k) + \sum_{k=1}^n D(j,k) - (n-2)D_{ij}$

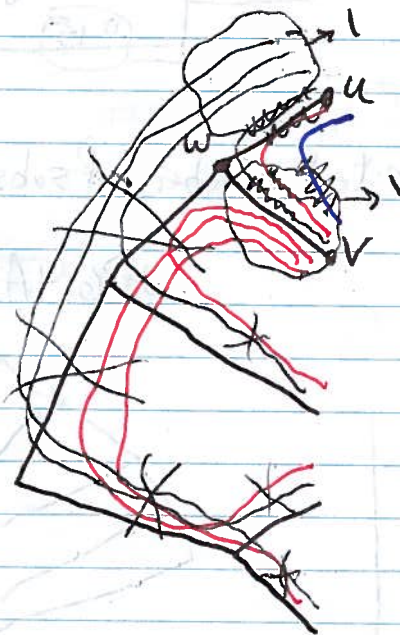
- ① Theorem: $u, v \leftarrow \underset{i,j}{\operatorname{argmax}} \{Q(i,j)\}$, then nodes u and v must be a cherry



- ② How to choose $d_T(u,w)$ and $d_T(v,w)$

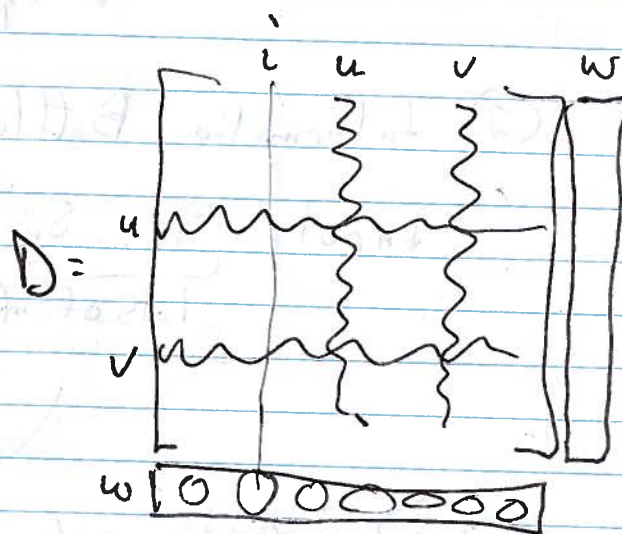
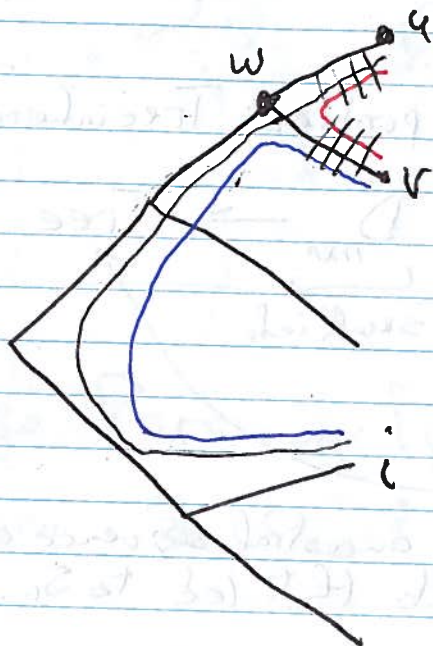
$$d_T(u,w) = \frac{1}{2} \left[\underline{D(u,v)} + \frac{1}{(n-2)} \left(\underbrace{\sum_k D(u,k)}_{\text{circled}} - \underbrace{\sum_k D(v,k)}_{\text{circled}} \right) \right]$$

Example:
True tree



Adding row/col for w in D

$$D(w, i) = \frac{1}{2} (\underbrace{D(u, i)}_{\text{blue}} + \underbrace{D(r, i)}_{\text{purple}} - \underbrace{D(u, r)}_{\text{red}})$$



$N-J$ is guaranteed to produce correct tree if

D is ultrametric \rightarrow There exists a tree with branch length such that

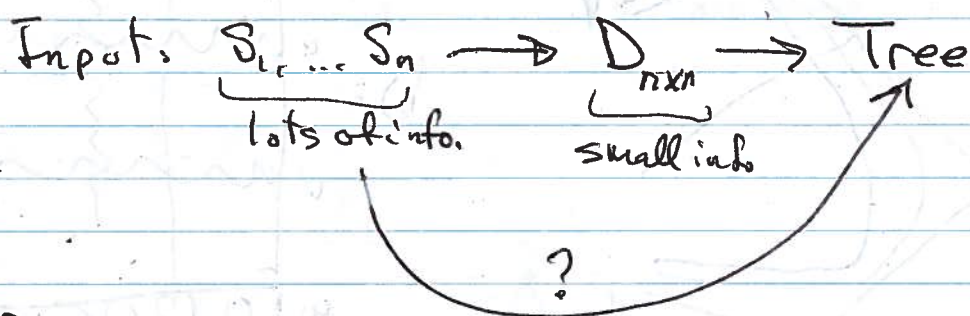
$$d_T(i, j) = D(i, j)$$

Running time: $O(n^4)$, but can be reduced to $O(n^3)$

Problems with N-J algo

① If D is not ultrametric (D is not estimated ~~with~~ perfectly)
 \Rightarrow N-J comes with guarantees about optimality
NO \rightarrow

② Information Bottleneck problem: Tree inferred may be inaccurate



③ Provide no info about ancestral sequence or about evolutionary events that led to S_1, \dots, S_n