Final points:

- Distance Methods are **fast**.

- NJ constructs an unrooted tree that joins neighbors and avoids mistake of assuming closest texa are also neighbors

- Theorem: If a dissimilarity map on X comes from a tree metric (T, w), the NJ reconstructs the tree and branch lengths correctly.

Parting thoughts:

The only distance we have seen is the Hamming distance

- this measures only visible differences between pairs of sequences i.e. it does not account for multiple mutations or back substitutions

- It is unclear if a Hamming distance table (or any distance table) is close to a tree metric.