Characters and distances

- Two types of input for phylogeny problems
- Characters:
  - matrix species vs. characters
- Distances:
  - square matrix of distances between species

Character data

- Multiple state, unordered characters
- Small phylogeny
  - Given species & tree, find ancestors minimizing changes
  - Fitch algorithm (Sankoff algorithm)
- Big phylogeny
  - Given species, find most parsimonious tree
  - Perfect phylogeny

Perfect phylogeny

- Perfect phylogeny is NP-hard
- Fixed # of states: polynomial time
  - Example: binary phylogeny
- Fixed # of characters: polynomial time
  - Example: two characters
- Fixed # of species: constant time

Distance data

- Big parsimony
- Additive trees
  - Exact: easy, but infinitely rare
  - Approximate: NP-hard
- Ultrametric trees
  - Exact: easy, but even rarer
  - Approximate: polynomial time