Class 20: Phylogenetics (1)

Held: Tuesday, 8 November 2011

Summary: We begin to consider why and how one builds phylogenetic trees.

Related Pages:
- EBoard.
- Reading: Chapter 8.

Notes:
- Don’t forget: Project proposals and Paper responses due Thursday.
- Does anyone lack a project group?
- Thursday extra: Summer opportunities in CS.
- EC for BioFriday: ???

Overview:
- Why build phylogenetic trees?
- Bioinformatic approaches.
- Some challenges.
- Primary literature discussion: Neandertals.

Phylogenetic Trees
- What are phylogenetic trees?
- Why are they useful?
- What kinds of data can we use to create them?

Algorithms for Generating Phylogenetic Trees
- Most algorithms are fairly similar
  - Find the distance between pairs of sequences.
  - “Merge the closest pair”
  - Repeat
- You may want to align everything first
- There are different metrics for finding the distance between two sequences
- There are different metrics for finding the distance between two merged sets of sequences.
Some Obstacles in Generating Phylogenetic Trees

- Basically: Insufficient knowledge!
- Don’t know precursor species
- Don’t know amount of time
- Don’t know mutation rate
- Mutation rate is inconsistent
- Etc.

Web Exploration

- For those who don’t have the patience to come up with ten homologs, here are some sequences our authors suggest as interesting.
  - YP_026263
  - YP_002174466
  - ZP_02621494
  - NP_000048
  - XP_510594
  - NP_075529
  - NP_445977
  - CAC00282
  - ABA95537

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