

Class 20: Phylogenetics (1)

Held: Tuesday, 10 November 2009

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

Related Pages:

- EBoard.
- Reading: Chapter 8 .
- Due: Response to Neanderthal and Mitochondrial DNA paper.

Notes:

- Don't forget the Human Rights and the Environment seminar this week.
- Your exams are not yet graded. It's Sam's fault.
- We hope our sick students get better soon.

Overview:

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

Phylogentic 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.

Discussion of Neandertal Paper

- Forthcoming.

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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