

## **Class 20: Phylogenetics (1)**

**Held:** Tuesday, 10 November 2009

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

## 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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