Hands-on Session 2: Obtaining Data from On-line Sources

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Session Organization

- Goal: To be comfortable building trees from real data
- Lecture:
  - Standard Software Packages
  - Details on Web-based Software
  - Motivating Problem
- Lab:
  - Organized so you can use the DIMACS lab, or your own laptop
  - Welcome to work singly or in groups

Lecture Outline

- Motivating Problem

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- Building Trees Overview

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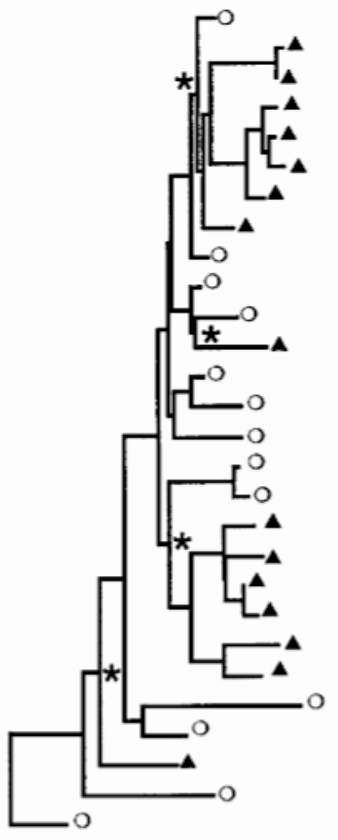
- Using Sequence Databases
- Aligning Sequences

Motivating Problem: Building Trees with Serial Data?

Rodrigo *et al.*,
"Coalescent estimates of
HIV-1 generation time in vivo."
PNAS '99



Motivating Problem: Using Serial Data

- Rodrigo *et al.* includes 55 HIV-env partial sequences, all from the same patient

Table 1. Summary statistics for each sequence sample set

Sample	Days from first sample	No. of sequences	Average pairwise diversity, %	θ	N
1	0	13	3.6	0.088	1100
2	214	15	3.9	0.106	1325
3	671	15	5.0	0.074	925
4	699	9	4.2	0.144	1800
5	1005	8	4.1	0.092	1150

- Starting question: what is the genealogy samples (from the same patient) taken at different times?

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5. Analyze Results.

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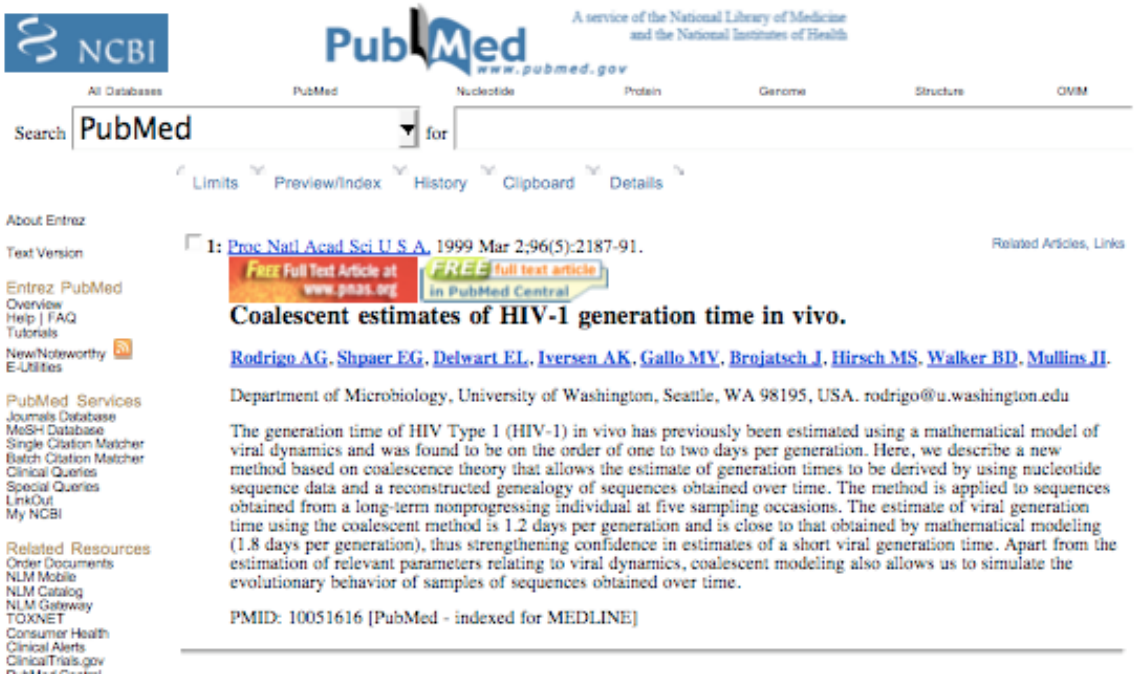
We'll focus on the first two today.

Using PubMed

An on-line index of scientific papers:



Can search by all standard methods...

Sequence Databases

- GenBank: repository of sequences from NCBI (NIH).
- As of August 2005, GenBank had 100 gigabases of sequences.
- Almost all sequences from published articles are there, and can be located by their unique accession number or PubMed ID.

LANL HIV Databases

- Los Alamos National Laboratory maintains databases of sequences, resistance, immunology, and vaccine trials.
- Can be searched in numerous ways including accession number or PubMed ID.

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- One of the most common alignment programs is ClustalW:
  - Available via multiple servers including EBI & the Pasteur Institute
  - Does a global multiple sequence alignment

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- Use the PMID to find the sequences in the HIV Sequence Database.
- Use ClustalW to align the sequences.
- Using your favorite phylogenetic reconstruction method, build a tree from the sequences.
- Analyze resulting trees

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  For example, after returning the distance matrix, you have the option of applying a method to the matrix.

Helpful Websites

- Dataset for this tutorial:

  `http://comet.lehman.cuny.edu/stjohn/dimacsTutorial`

- PubMed & Genbank:

  `http://www.ncbi.nlm.nih.gov/entrez`

- HIV Sequence Database:

  `http://hiv-web.lanl.gov/content/index`

- The Pasteur Institute:

  `http://bioweb.pasteur.fr/intro-uk.html`