

Class 09: Gene Alignments (4)

Held: Thursday, 24 September 2009

Summary: We continue our exploration of alignment with a practical pattern: Given a collection of related mutants, what patterns do we see in the mutation?

Related Pages:

- EBoard.
- Due: On your own project (2.6) [extended deadline].

Notes:

- Did anyone attend convo today? What did you think?
- For Monday, read through Chapter 4 of St. Clair and Visick.
- You have a new assignment for next Thursday which replaces the “on your own” part of Chapter 3.
- Tomorrow’s CS Table is on Software and Intellectual Property. For those who have thought about patenting of genes, it provides an another domain to think about appropriateness of patent.

Overview:

- Lab, continued.
- Exploring the HIV env gene.

Lab

- Continue Project 3.5
 - Note: When you implement the “length-independent deletion cost” part, you’ll need a new algorithm for listing all alignments. (Sorry.)
 - The base code has also been updated in other ways. (You need not make a new copy.)

Exploring the HIV env Gene

- The full instructions are in the P’Web site.
- We’re going to look at data from Markham et al. 1998.
- Grab about a dozen related sequences from that experiment from NCBI.
 - Search like Markham AND HIV AND env.
 - For example, you might see AF089401
 - Form of description: S#V#-#
- Align using multiple tools
 - ClustalW
 - The thing you just wrote

- ...
 - Make some hypotheses about what you see
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