

Class 09: Protein Alignments (2)

Held: Thursday, 22 September 2011

Summary: We continue our exploration of protein alignment by exploring some code that can be used for such alignment.

Related Pages:

- EBoard.
- Reading: Markham et al. al. 1998..
- Due: Reading Response: Markham et al.; Exploration of HIV Data.

Notes:

Overview:

- Exploring Markham's data.
- Lab: Project 4.5.

The HIV env. sequence

- We'd like to hear a short report from each group.
 - What question were you asking?
 - What data set (which sequences) did you choose for the exploration?
 - What did you learn or discover?
- We'd also like to hear about your experiences with alignment
 - What were the strengths and weaknesses of Clustal-W?
 - In what ways was it helpful that you'd written your own alignment program?
- What do you anticipate being the difficulties as you go from a program that aligns two sequences to one that aligns multiple sequences

Lab

- Do Project 4.5.

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