

Porting HMMER to Science Gateway

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Agenda

- HMMER.
- What is the problem?
- Our aims
- Questions

HMMER

- Searching sequence databases for homologs of protein sequences.
- Making protein sequence alignments.
- Implements methods using probabilistic models called profile Hidden Markov Models (profile HMMs).

In other words, HMMER compares a sequence with a probabilistic model that describes a family or pattern of sequences.

Problem

- Bioinformatics applications integrated in the Grid are quite difficult to use for people that are not use to write either commands or scripts in it. One of them is HMMER which is used for searching protein sequences.
- For this reason, students have to spend time learning shell scripting and other Linux things that they do not need for their research.

OUR AIM

- Our aim is to integrate HMMER in GISELA Science Gateway as a first step of our support policy.
- To Migrate other applications used with difficult by our students in our infrastructure.
- To improve our support in Grid to students and professors that either belong or not to the Universidad de Los Andes.

Questions

