

User manual

AlignMiner

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September 22, 2009

1 Introduction

This document is only a quick guide to AlignMiner, if you need an in-depth explanation you should read the article "XXXXX".

1.1 Login in the system

The first action you need to do in order to use Alignminer is to do a login in the system. Enter any valid email in the form of the main page, as seen in the following picture:

Once logged in, you can choose between submitting new jobs, or browse already sent ones.

1.2 Submit a new job

To submit a new job for execution, you need to upload a file that contains a valid alignment. AlignMiner supports a wide variety of formats (fasta, clustal, msf, ...), so you can try to upload your alignment files without any conversion. Select the alignment to upload using the file field.

You may also provide a name for the job. If not a automatically generated number is assigned.

Click send button to submit the file.

When the file has been successfully uploaded to our servers, you will see a new form where you can select some parameters:

- Master sequence: you can select a master sequence from the popup to be used by scoring methods. If you don't select a Master sequence, then a consensus of the whole alignment is calculated.
- Alignment subset: with this parameters you can force AlignMiner to use only a portion of the alignment. If you leave both fields with zero, then an automatic range will be calculated, and weak ends (those with little information) of the alignment will be cropped.

Click Run when you are done to send the job.

The job will appear in the job list:

Actually, the job is run in our supercomputers using a batch queue system, because of that you can view different status of execution in the job list:

- Waiting run: the job has just been uploaded and is waiting you to click the RUN button.
- Queued: the job has been sent to the batch system and is waiting for resources to be available for execution.
- Running: the job is running. In the STEP column you can see the completed phases.
- Done: the job is done and available for browsing.
- Error: there has been an error that prevents the job from executing correctly. Check the small info icon for more information.

Once a job is submitted you can close the system and come later to see its status, or wait it to finish.

1.3 Browse existing jobs

Jobs are saved for later browsing, so you can access the system at any time and choose a job from the job list to browse its results.

If you click on a job name, you get a list of available scoring methods:

When a scoring method is selected, a graph is shown with the visual representation of the results. You can drag, zoom or click the graph to your desire:

Below the graph, the interesting regions that have been found are presented in tables. You can sort the results by clicking on the column titles. When you click on a row (a region of interest), its corresponding alignment is shown at the right of the page. In DNA alignments, characteristics of a putative oligo that uses this region are also calculated. You can change the oligo's width by clicking on the arrows, and its characteristics will be calculated again for you.