Bri-shur.com

A Site for Bioinformatics Computations

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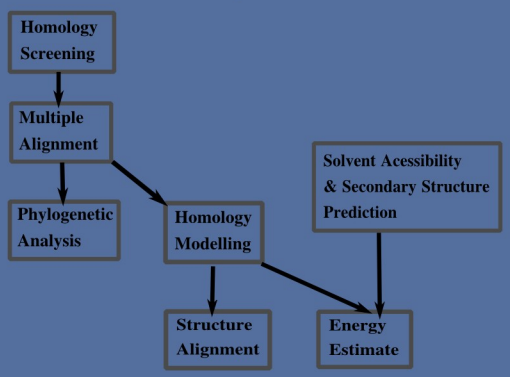
A newly developed web-site with several popular services on bioinformatics is presented. Intended audience is biologists who need an easy access to the tools for the analysis of their data. Typical execution time of one job is from seconds to hours on a single CPU. Services are intended to be provided free of charge.

The popular bioinformatics algorithms including multiple alignment, homology search, homology modeling and others are integrated into one web-interface with a possibility to use pipelines for typical biological problems. The service is designed to be distributed among available hardware platforms to optimize a load to a particular servers where jobs are executed. Web-interface is implemented on ruby while codes of particular algorithms vary from freely available software with closed sources, including GPL and other open-source packages and ending with original and newly developed software. Several databases from ncbi portal are copied to servers to be used locally for the retrieval.

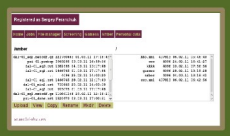
Services and Pipelines on the Site



Web-interface
Virtual Private Server
Ruby on Rails, Bioruby

Servers for Job Processing
Dedicated servers
Php, Bash scripts, C++

Secure Web-interface
Php, Shell Scripts
Grid Client Software



Clusters
Grid Networks

In addition, a web-site with a limited access is developed. The services on resource-consuming biological and chemistry computations are presented there. The computations could be performed on available supercomputer hardware with an access via grid middleware. The interface includes a file manager and a billing system. The price of the computations should be proportional to the consumed resources.

The List of Services:

- Homology Screening
- Quantum Chemistry: Gamess
- Molecular Dynamics: Amber; Gromacs (planned)
- Virtual Screening: Autodock Vina (planned)