

<u>Protein tools</u>	
Sbase ¹	Support vector machines, domain prediction system
Fthom ²	Predict domains in your sequence
P450 ³	A directory of p450-containing systems
CX ⁴	This server calculates the atomic Protrusion Index from a three-dimensional protein structure.
Pride ⁵	This server calculates the PRobability of IDentity between three-dimensional domains (or whole structures)
DPX ⁶	This server calculates the atom depth from a three-dimensional protein structure.
Benchmark ⁷	A protein classification benchmark collection for testing machine-learning algorithms
prideNMR ⁸	NMR Protein fold similarity server
theGPM ²	This is an in-house modified version of the Gpm global proteome machine, a tandem mass spectrometry data analysis server.

1 <http://hydra.icgeb.trieste.it/sbase/>

2 <http://hydra.icgeb.trieste.it/sbase/sbase.php?sec=analyse&sub=predict>

3 <http://www.icgeb.org/~p450srv/>

4 <http://hydra.icgeb.trieste.it/cx/>

5 <http://hydra.icgeb.trieste.it/pride/>

6 <http://hydra.icgeb.trieste.it/dpx/>

7 <http://net.icgeb.org/benchmark/>

8 <http://net.icgeb.org/pridenmr/>

9 http://proteome.icgeb.trieste.it/tandem/thegpm_tandem.html

The French EMBnet node: AGM 2010 report



Guy Perrière

Laboratoire de Biométrie et Biologie Évolutive, Université Claude Bernard, Lyon, Villeurbanne Cedex - France

The ReNaBi (*Réseau National des plates-formes en Bioinformatique*) is the French EMBnet node since 2008. Present head of ReNaBi is Claudine Médigue (Génoscope, 2 rue Gaston Crémieux, 91057 Evry Cedex) and its delegate for EMBnet is Guy Perrière. This structure is a national network of 13 bioinformatics platforms officially commissioned by IBISA a national French agency. IBISA individually evaluates each platform every four years in order to determine if it still can be labelled as such. Among the requirements for a labelling are:

- self-funding of the platform
- dedicated personnel
- regular formation and teaching activities
- public on-line services offered

At this date, all the ReNaBi platforms met those requirements. Those platforms are also affiliated with many research laboratories and universities all around France (in Bordeaux, Lyon, Marseille, Montpellier, Paris, etc.) and are routinely used to assist research, mainly at academic level.

Due to the fact ReNaBi gathers many sites having a broad range of activities, the computing services offered cover the whole spectrum of bioinformatics:

- access to general or specialized sequence databases
- alignment and similarity search programs
- general sequence analysis package
- biostatistics packages
- molecular phylogeny programs
- tools for proteomics and transcriptomics data analysis

- tools for protein structure prediction and modelling
- Next Generation Sequencing (NGS) specific programs and pipelines

As all the platforms are independent, it is not possible to give a global financial assessment. The ReNaBi itself receives a recurring funding of 50,000€ from IBiSA in order to support scientific animations such as workshops, conferences or thematic networks. As for the conferences supported, the main one is the French national conference in bioinformatics: JOBIM (*Journées Ouvertes en Biologie Informatique et Mathématique*). Among the different thematic networks, one is devoted to the use of grid computing and one to NGS users.

Again, due to its very own structure, it is difficult to give the complete list of machines available through ReNaBi. Standard equipment for a ReNaBi platform consist usually in a small computing cluster with about 100-500 cores, a mail server, one or two databases server(s), and a set (of variable size) of micro-computers. If we take the example of the PRABI (*Pôle Rhône- Alpes de Bioinformatique*), we have:

- one Dell PowerEdge 2950 (2×quadcore CPU@2.66 GHz, 8 Gb RAM, 146 Gb disk)
- one Dell PowerEdge 2950 (2×quadcore CPU@2.66 GHz, 8 Gb RAM, 600 Gb disk)
- one Dell PowerEdge 2950 (2×quadcore CPU@2.66 GHz, 32 Gb RAM, 900 Gb disk)
- three Sun Fire X4500 M2 (8×quadcore CPU@2.3 GHz, 64 Gb RAM, 3×145 Gb disk)
- two Sun Fire X4500 M2 (8×bicore CPU@2.8 GHz, 64 Gb RAM, 3×145 Gb disk)
- one Sun Fire V490 (4×bicore CPU@1.5 GHz, 16 Gb RAM, 2×146 Gb disk)
- one Sun Fire 880 (8 CPU@900 MHz, 28 Gb RAM, 6×36 Gb disk)

This, for the sole genomic aspects covered by this platform. Indeed, all aspects related to protein structure prediction and biostatistics have also their own sets of dedicated computers.

Lastly, the ReNaBi is involved in the Elixir European initiative. Particularly, we plan to modify its legal status in order to apply for being a node in the forthcoming Elixir infrastructure.

The Norwegian EMBnet node: AGM 2010 report



George Magklaras

Biotek - UiO, Oslo, Norway

The Norwegian EMBnet node has 65 members, and offers a range of life science computing services:

- official mirror of the EMBL, UniProt and Genbank databases
- MRS 4 install (command line and web)
- EMBOSS (command line and web)
- GCG (holders of license for legacy users)
- R tool
- dedicated application hosting (provision of relational databases and web services for science groups)

We have our own dedicated machine room, with nightly incremental backup, offering a variety of systems to our members:

- several memory intense systems (up to 64 GB RAM)
- total of 40 CPU cores
- Multi-Tbyte capable filesystem
- GPU cluster (work in progress, not yet operational)

At present, the node employs two staff members and is active with the EMBnet TM PC, specifically with:

- technical issues
- HTS IT (published HTS IT draft report, as well as articles on EMBnet News)

Our users are affiliated with Universities all over Norway, as well as private companies working in the field of Life Sciences. As such, our services assist both in the research at the University level as well as the development of commercial products.

At present, we are offering a course on sequence mining using MRS and EMBOSS, with the aim of:

- introducing students to some commonly used sequence databases
- introducing students to sequence mining tools, primarily MRS and EMBOSS