- 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

- familiarizing the students with the command line interfaces to the tools, and the possibilities that they open up with regards to creating pipelines.

This course has been offered at the Mexican EMBnet node in March 2010, and will be offered at the University of Oslo later this summer. Feedback from the course in Mexico has been very favorable. The course material has been made available online, as has video recordings of the course.

In the past 3 years, we have also offered courses on the following subjects:
- Bioperl (July 2008)
- R (January 2009)
- EMBOSS/GCG (June 2009)

In terms of new areas of research, we believe that GPU computing is an exciting new field, and will provide significant improvements over CPU-based systems in terms of computational power for the price. Certain types of bioinformatics algorithms can be run in massively parallel mode using GPU cores and thus benefit from this technology.

To enable us to work in this new field, we have applied for, and received, funding to purchase a small GPU cluster. We have acquired a server equipped with 4 NVIDIA Tesla c1060 GPU cards, for a total of 960 processing cores. Two of these cards will be replaced by the next generation Fermi c2050 cards as soon as these are available on the market, bringing the total up to 1376 cores. The current configuration gives a processing power of approximately 3600GFLOPs. After the upgrade, this will be increased to approximately 4400GFLOPs. This system will enable us to both build competence in this important field, and allow our members to run their algorithms in an adequately powerful system. Our plan is to port various bioinformatics algorithms to the GPU processors and make them available to the node members by the end of 2010. We also plan to share our expertise with the EMBnet community.

The Norwegian EMBnet node wishes to acknowledge its user base and the Molecular Life Science committee of the University of Oslo for providing funding to achieve these goals. (http://www.uio.no/forskning/tverrfak/mls/kjernefasiliteter/miniplattformer/).

The South African EMBnet Node: AGM 2010 report

Winston Hide, Alan Christoffels

The South African National Bioinformatics Institute (SANBI), University of the Western Cape, Bellville

The South African National Bioinformatics Institute[1] (SANBI) conducts high-quality scientific research focused upon delivery of translatable biomedical discoveries, primarily through local and international collaboration with partner organisations. SANBI is part of the University of the Western Cape, situated outside Bellville near Cape Town. The Institute is headed by a Director, who reports through the Faculty of Natural Sciences, and provides overall leadership to the organization. The Institute consists of a group of faculty supported by technical and administration staff, guiding research of a group of Masters and PhD students and Post-Doctoral scientists.

SANBI became a member of the European Molecular Biology Network[2] in 1997. It developed close relationships with faculty at the University of Witwatersrand and University of Pretoria, supporting training and research there and at other sites around the country.

SANBI is well recognised in the areas of gene expression and host-pathogen disease research, including HIV, Trypanosomes and Malaria; and in the provision of bioinformatics and biomedical informatics training. This recognised expertise and proven capacity development has enabled the Institute to secure additional funding from a number of high-profile international agencies, e.g., National Institutes of Health, to expand its training programmes with the aim of developing faculty capable of producing NIH-funded research.

1   http://www.sanbi.ac.za/
2   http://www.embnet.org/