Russian EMBnet node: AGM2011 report

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The Russian EMBnet node is based on the Belozersky Institute of Physical-Chemical Biology, which is a scientific department of Moscow State University (MSU) and is closely connected with the Faculty of Bioengineering and Bioinformatics of MSU.

People

Department of Mathematical Methods in Biology of Belozersky Institute

- Andrei Alexeevski (head)
- Sergei Spirin
- Olga Zanegina
- Eugeny Aksianov

Computing group of Belozersky Institute (former "GeneBee")

- Vladimir Nikolaev (head)
- Alexander Kravchenko
- Andrei Leontovich
- Lidia Smirenina

Hardware

- Server Prime Power 850 (16 processors SPARC64 IV GP 810 MHz, 2 TB disks, Sun Solaris);
- a number of servers under Linux;
- a number of workstations under Windows XP and Windows 7.

Activity

Education and training

The 95% of the energies were spent to the Faculty of Bioengineering and Bioinformatics of MSU (undergraduate courses: "Practical bioinformatics" for the first and second year of the degree course and "Structural bioinformatics" for the third one). Other educational activity:

a. annual three-day courses in practical bioinformatics for students of MSU specialised in virology;
b. consultations for students of Russian-Armenian (Slavonic) University in Yerevan;
c. annual public lectures (mainly for high school students) in bioinformatics (in frames of so-called "Day of Science");
d. consultations in bioinformatics for "Wet Lab" researchers;
e. consultations and seminars for mathematicians and computer scientists. For example, in Spring of 2010 and of 2011, Sergei Spirin held a special course in bioinformatics for students of Faculty of Computational Mathematics and Cybernetics of MSU.

Software development and support

In 2008-2011 a number of publicly available bioinformatics software was developed.
Among them:

f. Geometrical Core[1] for a family of aligned 3D structures;
g. SheeP[2], an automatic description of beta- and alpha/beta-structural proteins;
h. ConClus[3], conserved hydrophobic clusters in aligned 3D structures of proteins;
i. Malakite:[4] searching for reliable blocks in a given protein sequence alignment;
j. Blocks3D[5]: this service searches for blocks that are supported by 3D superimposition in aligned sequences of PDB proteins;
k. wLake[6]: a tool which allows to identify clusters of a structural water molecules in given superimposed 3D structures.

Also, previously developed software remains supported, in particular:

a. NPIDB[7]: a database of structures of DNA-protein and RNA-protein complexes. A new interface is available at http://npidb.belozersky.msu.ru.
b. AliBee[8]: an original program for multiple alignment;
c. TreeTop[9]: a tool for phylogenetic tree prediction;
d. DotHelix[10]: local similarity map for two biological sequences;
e. SVETKA[11]: simultaneous analysis of a multiple alignment and the phylogenetic tree of the same sequences; search for classifying positions in the alignment;
f. CluD[12]: hydrophobic clusters in 3D structures;
g. GEA[13]: a system for Gene Expression Analysis.

See also http://www.genebee.msu.ru/bioinformatics.html and http://mouse.belozersky.msu.ru/.

Research

Some directions of research in bioinformatics provided in our Institute (those that are not reflected in the above list of new software) are as follows:

a. comparative structural description of several families of proteins[14];
b. drug design;
c. development of algorithms for next generation sequencing data;
d. comparative analysis of performance of phylogeny reconstruction methods.

Funding

The grant of the Russian Foundation of Basic Research No. 10-07-00685 supports software development and installation but not education and training activities. The grant is for 2010–2012, the grant amount for 2010 was 400,000 roubles (~10 000 euro), the grant for 2011 amounts to 350,000 roubles.

Perspective

EMBnet membership

The governing body of the Institute has definitely expressed the intention to maintain the status of Russian EMBnet node. The member fee for 4 years will be paid at the first opportunity.

1 http://mouse.genebee.msu.ru/tools/gc.html
2 http://mouse.belozersky.msu.ru/~evgeniy/cgi-bin/sheep/sheep.php
3 http://mouse.genebee.msu.ru/~bennigsen/conclus.html
4 http://mouse.belozersky.msu.ru/tools/malakite.html
5 http://kodomo.fbb.msu.ru/blocks3d/
6 http://mouse.belozersky.msu.ru/~evgeniy/cgi-bin/wLake/wLake.php
7 http://mouse.genebee.msu.ru/NPIDB/index.html
8 http://www.belozersky.msu.ru/services/malign_reduced.html
9 http://www.belozersky.msu.ru/services/phtree_reduced.html
10 http://www.belozersky.msu.ru/services/dhm/advanced.html
11 http://monkey.belozersky.msu.ru/~dian/cgi-bin/austerlitz.pl?type=index
12 http://mouse.belozersky.msu.ru/npidb/cgi-bin/hftri.pl
13 http://www.genebee.msu.ru/~nikonov/GEA/
14 http://mouse.genebee.msu.ru/families.html

Education

The teaching of undergraduate students will remain the main part of our training activity. We will do our best to increase the number of consultations and possibly to organise bioinformatics courses for "Wet Lab" biologists. Publishing a Russian textbook in bioinformatics is in our plans.

Software development

Hopefully, the intensity of software development (including creation of new public available programs and improvement of old ones) will, at least, not decreased.