

EMBnet.news

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July 2008



- ChemGPS-NP_{web}
- ASPicDB: A database resource for alternative splicing analysis
- Grid tutorials and more ...

Editorial

Here is another issue of EMBnet.news with plenty to read. We start with a report on the third course in Kenya, followed with a sum-up of the activities of the ASBCB, that shows their activity in Africa and their connections with the rest of the world. Then we have an article on a very interesting tool that allows one to navigate in biologically relevant chemical space. A report on the new FP7 funded LUPA project reveals how interesting it can be to study human genetic disorders using the dog as a model system. The ASPicDB, a database of alternative splice patterns in human and mouse genes, with monthly updates. A series of papers is actually a tutorial on GRID usage for newcomers, topped by an article on effective large scale multitasking on a GRID environment. The next issue is already in preparation but will only be out after our AGM and 20th anniversary celebrations in Bari, Italy, in September. As usual we invite our readers to contribute to EMBnet.news and to encourage an even greater number of colleagues to do so.

The editorial board: Erik Bongcam-Rudloff, Domenica D'Elia, Pedro Fernandes, Kimmo Mattila and Lubos Klucar.



Protein Spotlight (ISSN 1424-4721) is a periodical electronic review from the SWISS-PROT group of the Swiss Institute of Bioinformatics (SIB). It is published on a monthly basis and consists of articles focused on particular proteins of interest. Each issue is available, free of charge, in HTML or PDF format at

<http://www.expasy.org/spotlight>

We provide the EMBnet community with a printed version of issue 94. Please let us know if you like this inclusion.

Cover picture: *Kniphofia uvari*, 'Red hot poker'.
Nairobi, 2008 [© Erik Bongcam-Rudloff]

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New tools for bioinformatics teaching.



The course team: Erik Lagercrantz, Maria Wilbe, Erik Bongcam-Rudloff, Alvaro Martinez Barrio, Etienne de Villiers and Saidimu Apale (not all in the picture)

For the third year the ILRI/Beca EMBNet node organized an introductory course in Bioinformatics at the International Livestock Research Institute (ILRI) campus in Nairobi, Kenya. The objective was to introduce young scientists from east and central Africa to use bioinformatics/computational biology in their research and to present some of the biological resources available on the ILRI-BECA bioinformatics platform.

The course is organized in collaboration with the Swedish University of Agricultural Sciences (SLU), Uppsala University (UU) and Linnaeus Centre for Bioinformatics (LCB) funded by SIDA.

The course was 9 days long, from May 5 to 15, 2008. 24 participants from Uganda, Sudan, Tanzania, Burundi, Somalia, Cameroon, Ethiopia and Kenya attended the course. Furthermore the lectures were recorded on DVD and will be used at the University of Buea, Cameroon and Maseno University in Kenya.



The course participants at ILRI, Kenya, May 9, 2008.

Topics covered during the course were: sequence analysis and alignments, EMBOSS/wEMBOSS, Staden package, Unix/Perl basics, genomics and comparative genomics, Artemis and Artemis Comparison Tool and Ensembl.

Many course participants are learning new tools and techniques that will be useful for them when returning to their own laboratories. Last year each student received a Bioinformatics Live-CD with all programs used during the course, but it was not possible for them to easily save their work. The course team came therefore up with a new idea that resulted on an "Bioinformatics workbench on a USB memory stick", **eBioUSB**. Each student received one USB-stick to use during the course and bring back home for continuous work. By using an USB the students were also able to save all their work directly on the stick.



Saidimu Apale filming the lectures

The eBioUSB stick is based on a Linux environment: the African UBUNTU system. The USB solution has the advantage that it can be used in any computer without changing any settings. It has a complete Desktop environment (e.g. office package, text editor and mail client).

The programs that were necessary for the course and installed on eBioUSB were:

- ClustalW
- ClustalX
- NCBI BLAST
- NCBI Tools
- EMBOSS
- wEMBOSS
- Staden
- PHYLIP
- Artemis
- Artemis comparison Tool
- JalView
- BioPerl

We have created 2 different USB sticks: one that can be ran on old computers and the one used for the course can be used on newer machines resulting on a higher speed system.

Future improvements of the eBioUSB include incorporating the SwissProt database for running most common analysis locally.

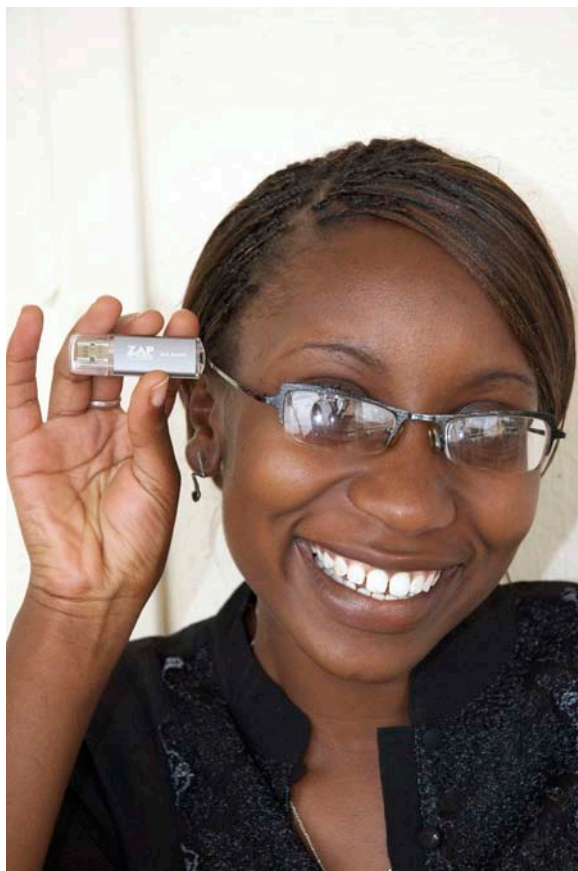
The “**BioMacKit**” a Bioinformatics Portable Teaching Kit that was created last year was used this time to access a complete mirror of various programs and databases used during the course (More information: EMBnet.news, Vol 13 Nr 2:7, 2007).

The course evaluation resulted on an average 4.9 of maximum 5 points encouraging the teachers to organize a new course next year.

Student comments of the course:

“Interesting and highly applicable to our work though not so easy for beginners”

“I enjoy working with the emboss software because it has many programs and each has a manual, thus quite user friendly”



The eBioUSB used for the course.

“I look forward to applying the knowledge I have acquired in the training in my research work and to assist others”

“The USB stick enables me to reproduce exactly what I have learned”

“I learned a lot about databases that were available to me and programs I could use to analyze protein and DNA sequences”

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RMC Gunn Building B19,
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of Vienna, Vienna

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Italy

ILRI/BECA

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Dear reader,

If you have any comments or suggestions regarding this newsletter we would be very glad to hear from you. If you have a tip you feel we can print then please let us know. Please send your contributions to one of the editors. You may also submit material by e-mail.

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