

Harvard and Stanford. In addition, SANBI offers formal degrees at PhD and Masters level. SANBI is a founding member of the African Society for Bioinformatics and Computational Biology, and will be a host organisation for the 2011 regional meeting of the International Society for Computational Biology in Cape Town.

Facilities

The Institute has adequate scientific computer infrastructure, and is the site for a pair of high performance 32 CPU IBM P-690 servers and, in the next month, an 8 CPU Xserve cluster, which provide a significant proportion of the research compute infrastructure for bioinformatics in Africa. SANBI scientists have workstations and Internet access, as well as backup and disk storage. In late 2010, SANBI will move its premises to a new building, offering extensive training facilities, a visiting scientist facility and meeting rooms, in addition to the research and service provision currently performed.

Research

- Delivery of an African driven analysis and annotation of *Glossina*, the vector for the tsetse fly.
- Through capacity developed from genome annotation, we apply expertise and technologies developed to other relevant organisms to African health, with a particular emphasis upon integration of HIV clinical, immune and sequence diversity outcomes, and pathways analysis in Malaria.
- We integrate comparison of vector, host and pathogen genomes to deliver unique African knowledge of HIV and Malaria.
- Develop and apply understanding of normal and diseased human gene expression to diseases relevant to South Africans.
- Develop capacity of scientists through tightly defined research projects that have high impact on health in South Africa.

EU Collaborative projects

SANBI faculty and post docs have enjoyed funded collaborations through the EU FP funding programmes and currently we serve on the SYSCO programme, together with Institut Pasteur Tunis and Paris, and Max Planck Berlin.

The Swedish EMBnet Node: AGM 2010 report



Nils-Einar Eriksson

Computing Department of Uppsala Biomedical Centre (BMC), Uppsala, Sweden

People working for EMBnet Sweden are Nils-Einar Eriksson (TM PC), Emil Lundberg, Martin Norling (PR PC) and Erik Bongcam-Rudloff (EMBnet chairman 2003-2009).

Services

EMBnet Sweden has a web-site connected to several unique tools produced by members of EMBnet together with their associated researchers. EMBnet's video conference system (Marratech) is located and managed at the Swedish node. Uppsala University is providing mail-list services for EMBnet. The lists are managed by node personnel. DNS master services for EMBnet are also provided by the Swedish node.

SeqScoring

The tool can be used to up-load your SNP- and indel- files from large re-sequencing projects, and get the data scored by conservation across species: www.seqscoring.net.

EVALLER

EVALLER™ is a web-tool wherein you can electronically test (e-Testing) a protein's potential allergenicity/cross-reactivity based on its amino acid sequence (<http://bioinformatics.bmc.uu.se/evaller.html>).

MolMeth

MolMeth is a structured database that provides free access to methods used in molecular biology and molecular medicine. Submitted methods and contributions are subject to curation. www.molmeth.org.

RetroTector online

A web-based tool for analysis of retroviral elements in small and medium size vertebrate genomic sequences: <http://retrotector.neuro.uu.se/>.

EMBnet Sweden has also been involved in the development of several bioinformatics packages and tools for the MacOSX platform:

- eBiotools: A collection of bioinformatics tools (>200): EMBOSS, Staden, T-coffee, ClustalW, and many others
- BioX: a graphical interface for eBiotools
- eBioKit: a server loaded with bioinformatics tools and databases, a solution for small and medium size research groups. The eBioKit is now used in more than 10 countries worldwide.

The node was one of the main organizers of the Next Generation Sequencing technologies workshop organized in Rome, November 2009, and of part II of the workshop in Bari-Italy, July 2010. (www.nextgensequencing.org).

Selection of Publications (2009-2010)

1. Pettifer S, Ison J, Kalas M, Thorne D, McDermott P, Jonassen I, Liaquat A, Fernández JM, Rodriguez JM, Partners I, Pisano DG, Blanchet C, Uludag M, Rice P, Bartaseviciute E, Rapacki K, Hekkelman M, Sand O, Stockinger H, Clegg AB, Bongcam-Rudloff E, Salzemann J, Breton V, Attwood TK, Cameron G, Vriend G. The EMBRACE web service collection. *Nucleic Acids Res.* 2010 May 12. [Epub ahead of print] PMID: 20462862.
2. Markus Klint , Mikael Tholleson , Erik Bongcam-Rudloff , Svend Birkelund , Anders Nilsson and Bjorn Herrmann. Mosaic structure of intragenic repetitive elements in histone H1-like protein Hc2 varies within serovars of *Chlamydia trachomatis*. *BMC Microbiology* 2010, 10:81doi: 10.1186/1471-2180-10-81 17 March 2010
3. Danika Bannasch, Amy Young, Jeffrey Myers, Katarina Truvé, Peter Dickinson, Jeffrey Gregg, Ryan Davis, Erik Bongcam-Rudloff, Matthew T. Webster, Kerstin Lindblad-Toh, and Niels Pedersen. Localization of Canine Brachycephaly Using an Across Breed Mapping Approach. *PLoS One.* 2010; 5(3): e9632. Published online 2010 March 10. doi: 10.1371/journal.pone.0009632
4. Heli Salminen-Mankonen, Jan-Eric Litton, Erik Bongcam-Rudloff, Kurt Zatloukal and Eero Vuorio. The Pan-European research infrastructure for Biobanking and Biomolecular Resources: managing resources for the future of biomedical research. *EMBnet.News.* 15.2. pp. 3-8. July 2009.
5. Álvaro Martínez Barrio, Erik Lagercrantz, Göran O Sperber, Jonas Blomberg, Erik Bongcam-Rudloff. Annotation and visualization of endogenous retroviral sequences using the Distributed Annotation System (DAS) and eBioX. *BMC Bioinformatics.* BMC Bioinformatics 2009, 10(Suppl 6):S18doi:10.1186/1471-2105-10-S6-S18
6. Domenica D'Elia , Andreas Gisel , Nils-Einar Eriksson , Sophia Kossida , Kimmo Mattila , Lubos Klucar and Erik Bongcam-Rudloff. The 20th anniversary of EMBnet: 20 years of bioinformatics for the Life Sciences community. *BMC Bioinformatics.* BMC Bioinformatics 2009, 10 (Suppl 6):S1doi:10.1186/1471-2105-10-S6-S1
7. R. P. Joosten, J. Salzemann, V. Bloch, H. Stockinger, A.-C. Berglund, C. Blanchet, E. Bongcam-Rudloff, C. Combet, A. L. Da Costa, G. Deleage, M. Diarena, R. Fabbretti, G. Fettahi, V. Flegel, A. Gisel, V. Kasam, T. Kervinen, E. Korpelainen, K. Mattila, M. Pagni, M. Reichstadt, V. Breton, I. J. Tickle and G. Vriend. PDB_REDO: automated re-refinement of X-ray structure models in the PDB. *J. Appl. Cryst.* (2009). 42 [doi:10.1107/S0021889809008784]
8. Sperber G, Lövgren A, Eriksson NE, Benachenhou F, Blomberg J. RetroTector online, a rational tool for analysis of retroviral elements in small and medium size vertebrate genomic sequences. *BMC Bioinformatics.* 2009 Jun 16;10 Suppl 6:S4
9. Álvaro Martínez Barrio, Marie Ekjerlund, Göran O Sperber, Jonas Blomberg, Erik Bongcam-Rudloff and Göran Andersson. In silico analysis of the dog genome identifies Canine Endogenous Retroviruses (CfERVs). *Frontiers of Retrovirology: Complex retroviruses, retroelements and their hosts* Montpellier, France. 21-23 September 2009. *Retrovirology* 2009, 6(Suppl 2):P7doi:10.1186/1742-4690-6-S2-P7
10. David E. Gloriam, Sandra Orchard, Daniela Bertinetti, Erik Bjorling, Erik Bongcam-Rudloff, Julie Bourbeillon, Andrew R. Bradbury, Antoine

de Daruvar, Stefan Dubel, Roanld Frank, Toby J. Gibson, Niall Haslam, Friedrich W. Herberg, Tara Hiltke, Jorg D. Hoheisel, Samuel Kerrien, Manfred Koegl, Zoltan Konthur, Bernhard Korn, Ulf Landegren, Silvere van der Maarel, Luisa Montecchi-Palazzi, Sandrine Palcy, Henry Rodriguez, Sonja Schweinsberg, Volker Sievert, Oda Stoevesandt, Michael J. Taussig, Mathias Uhlen, and Christer Wingren. A community standard format for the representation of protein affinity reagents. *Molecular and Cellular Proteomics*. August 2009.

The contribution of the eBioKit to Bioinformatics Education in Southern Africa



Yasmina Jaufferally-Fakim¹, Hans-Henrik Fuxelius², Erik Bongcam²

¹Faculty of Agriculture, University of Mauritius, Mauritius, ²Swedish University for Agricultural Sciences, Uppsala, Sweden

As bioinformatics has been making major progress and contributing to the development in the rest of the world, it has still not yet fully integrated the tertiary education and research sector in the countries of Southern Africa. In this context SANBio (Southern African Network for Biosciences)



Figure 1. Students of the University of Mauritius attending the eBioKit Education.

launched a project in 2009, on capacity building in this area so as to address the immediate needs of the scientific community within the region. This project is funded under the BIOFISA program from Finland. The main challenge is to bring to the scientists the knowledge and skills required to fully tap the resources available in the public domain. With an already established network of researchers, a series of workshops were initiated so as to train those in specific fields to become familiar with some of the commonly