

## Colombian EMBnet node: progress report



### Emiliano Barreto Hernández

Bioinformatics Center, Biotechnology Institute, National University of Colombia.

The Bioinformatics Center of the Biotechnology Institute at the National University of Colombia (CBIB) provides Bioinformatics tools, databases, training and support to the Colombian research community.

CBIB maintains the public access to updated versions of all the major genomics databanks (EMBL, PDB, UNIREF, UNIPROT, TAXONOMY, PROSITE and PATHWAY ), through our SRS (sequence Retrieval System) service.

CBIB provides access to several known Bioinformatics tools such as EMBOSS (through EMBOSS:GUI, wEMBOSS and jEMBOSS), BLAST, SMS, SRS, DOTLET, PHRAP, PHRED , Consed), and also provides access to some tools developed "in-house", listed in the next table:

Tool	Details
SINCO	Pharmaceutical colorant database
BLA.id	Information system that allows the molecular and clinical data cross, and $\beta$ -lactamases identification from resistant organisms at intra-hospital level
ENKI	Database of molecular and taxonomy information of Colombian biodiversity
BLEE	Extended spectrum $\beta$ -lactamases (ESBL) molecular identification information

In the training area, the CBIB runs 6 Bioinformatics courses to Colombian scientists (during the academic semester), which were attended by more

than 120 students. Besides this activity, the CBIB runs others training courses and workshops on Sequence Analysis, General Bioinformatics and Microarrays.

We have also continued supporting and advising the researchers involved in the following projects:

- Phylogenetic approach for a Colombia's Andes amphibian distribution hypothesis;
- ENKIdb, molecular and taxonomic linking system for Colombian species;
- the functional biodiversity and the edaphic metabolism of agricultural soils associated with potato crop;
- development of a bioinformatics tool for the identification of BLEEs genes;
- machine learning approach for the identification of protein binding sites;
- correlation with diagnostic categories a successful approach for selecting SNPs predictors of chronic fatigue syndrome.

In 2008, the node's hardware was upgraded with a DELL HPC machine, with 10 nodes (dual processor Xeon quad core 2.83 Ghz, 8Mb RAM) and storage with 6 Tb space. These machines represent a considerable improvement in our computing capacity, and that had immediate impact on our users' perception of our work.



Figure 1. Biotechnology Institute of the National University of Colombia.