EMBnet at ISCB Latin America 2012 Conference on Bioinformatics

Andreas Gisel, Jose Ramon Valverde, Erik Bongcam-Rudloff

CNR - Institute for Biomedical Technologies, Bari, Italy,
Centro Nacional de Biotecnología (CSIC), Madrid, Spain
Institutionen för husdjursgenetik, Uppsala, Sweden

The second Latin American regional meeting of the International Society for Computational Biology (ISCB-Latin America) took place 17-21 March 2012, in Santiago, Chile. More than 250 people attended, primarily from countries in Latin America. The major aim of ISCB-Latin America 2012[1] was to motivate and inspire young Latin American students and post-docs to conduct the best possible research in the areas of Bioinformatics and Computational Biology.

The first two days of the meeting (17-18 March) were dedicated to hands-on practical tutorials and workshops[2] covering different topics of interest: analysis, comparison and classification of protein structures; genome browsers, with special emphasis in the ENSEMBL system; protein resources and tools; sequence, architecture and protein interactions; algorithms and tools for transcriptomics, and multiple-gene profiling using the open-source platforms R and Bioconductor; immunoinformatics; an introduction to next generation sequencing (NGS) for bioinformaticians; functional genomics and computer-based drug design. EMBnet[3] sponsored two tutorial sessions by financing travel and accommodation for two teachers.

Figure 1. Participants of the ENSEMBL tutorial.

On the first day, Dr. Erik Bongcam-Rudloff (from the Swedish EMBnet node) gave the course, 'Genome browsers, with special emphasis on the ENSEMBL system', offering a broad introduction to biological databases and the ENSEMBL genome browser[4]. More than 15 participants followed this tutorial, using it mainly as an introduction to basic bioinformatics. On the second day, Dr. Andreas Gisel (from the Italian EMBnet node) gave the course 'Next generation sequencing: an introduction for bioinformaticians', a tutorial for more advanced bioinformaticians.

Figure 2. Some of the participants of the NGS tutorial.

With the help of the local administrator, a virtual machine, created by the Italian EMBnet node, including all data for the hands-on, was installed on each classroom computer. In this way, the 35 participants had the same platform, with

1   http://www.iscb.org/iscb-latinamerica2012
2   http://www.iscb.org/iscb-latinamerica2012-program/tutorials
3   http://www.embnet.org
4   http://www.ensembl.org

all the basic NGS-data analysis and visualisation tools. The tutorial included an introduction, NGS-data mapping, and visualisation of mapping data with the Web-based GBrowse tool from the GMOD project[5].

the open source platforms R and Bioconductor'. This session, jointly orga-nised by EMBnet with the Free Software for Life and Health (FreeBIT[6], (CYTED 510RT0391) and the Iberoamerican Society of Bioinformatics (SolBio[7]), aimed to demonstrate to

Figure 3: Dr. Andreas Gisel explaining NGS-data formats.

In a third session, Dr. José Ramón Valverde (manager of the EMBnet node in Spain) and Dr. J. de las Rivas (from the University of Salamanca, Spain), gave a course entitled, `Algorithms and tools for transcriptomics, and multiple-gene profiling using

and teach 45 students the power and ease-of-use of R and Bioconductor for processing micro-array and transcriptomics data, such as RNA-seq data-sets.

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5   http://gmod.org/wiki/GBrowse

6   http://www.free-bit.org) Network of Excellence
7   http://www.soibio.org