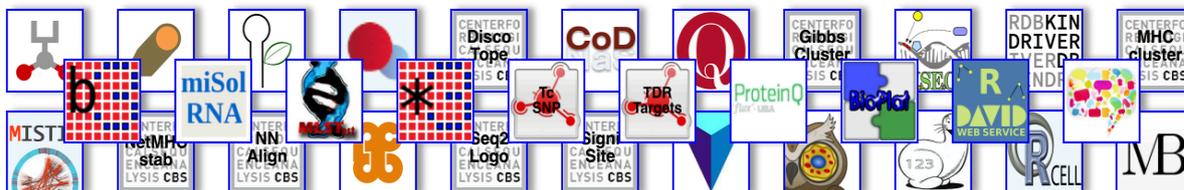


Bioinformática Federal (BiFe) 2015 Activities

by Ignacio Enrique Sánchez, EMBnet Argentina



Bioinformática Federal, [BiFe](#), is the [Argentine Node of EMBnet](#). The site groups bioinformatics and genomics resources (fully or partially) developed in Argentina. BiFe was devised to contribute to the accessibility of research results, and strengthen Argentine bioinformatics and genomics communities.

BiFe hosts, or links to, 32 bioinformatics resources, whose logos are shown above. Of these servers and databases, [18](#) are dedicated to the analysis of protein and nucleic acid sequence and structure, [10](#) to genomics and drug design, [three](#) to image analysis, while [one](#) is a database of biological databases.

Two application servers hosted by BiFe have been developed using our **open-source toolkit**, which is [publicly available](#) on our website, under “*Build your own server*”, together with a tutorial.

The general-purpose toolkit can help to build an application server by providing easy implementation of fully customisable input and output forms, file uploading, automatic FTP file retrieval, dynamic application loading, tables, graphics and protein structure representation.

Moreover, our [database of 30 genomes](#) showcases the results of genome projects dealing with Argentine organisms and carried out (totally or partially) in Argentina. Of these genome projects, 15 deal with bacteria relevant to human health, the food industry and agriculture, nine with bacteria from extreme environments - such as Antarctica and high-altitude Andean lakes - and six with eukaryotes.

BiFe is currently located at the Protein Physiology Laboratory, Departamento de Química Biológica and IQUBICEN-CONICET, Facultad de Ciencias Exactas y Naturales, Universidad de Buenos Aires, Argentina.

The current EMBnet staff include Dr. Adrián G. Turjanski and M.Sc. Leandro G. Radusky. We acknowledge funding from Ministerio Argentino de Ciencia, Tecnología e Innovación Productiva (MINCYT) and Consejo Nacional de Investigaciones Científicas y Técnicas (CONICET).



IMGT®: Past, Present, Future

by Marie-Paule Lefranc & Sofia Kossida, IMGT, Montpellier, France.



IMGT®, the international ImMunoGeneTics information system®, was created in 1989 by Marie-Paule Lefranc at Montpellier, France. The founding of IMGT® marked the advent of immunoinformatics, a new science, which emerged at the interface between immunogenetics and bioinformatics.

For the first time, ImmunoGlobulin (IG) or antibody and T cell Receptor (TR) Variable (V), Diversity (D), Joining (J) and Constant (C) genes were officially recognised as 'genes' alongside conventional genes. This major breakthrough allowed genes and data of complex and highly diversified adaptive immune responses to be managed in genomic databases and tools.

IMGT® comprises seven databases, 15,000 pages of Web resources and 17 tools, and provides a high-quality and integrated system for the analysis of genomic and expressed IG and TR repertoires of adaptive immune responses. These tools and databases are used in basic, veterinary and medical research, in clinical applications and in therapeutic antibody engineering and humanisation.

IMGT® has been built on the IMGT-ONTOLOGY axioms and concepts, which bridges the gap between genes, sequences and three-dimensional (3D) structures.

The IMGT® standards are used in clinical applications and in therapeutic antibody engineering. Thus, IMGT/V-QUEST is frequently used by clinicians for the analysis of IG somatic hypermutations in leukemia, lymphoma and myeloma, and, more particularly, in Chronic Lymphocytic Leukemia (CLL), in which a low percentage of mutations of the rearranged IGHV gene in the VH domain of the leukemic clone have a poor prognostic value for patients.

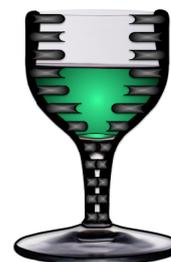
A new era is opening with the use of Next Generation Sequencing (NGS), and the IMGT/HighV-QUEST Web portal has become the paradigm for the analysis of the adaptive immune repertoire in normal (vaccination) and pathological situations (infectious disease, ...).

IMGT® standards use is also more needed than ever before in therapeutic antibody humanisation and engineering, as demonstrated by the IMGT/DomainGapAlign tool and the IMGT/2Dstructure-DB, IMGT/3Dstructure-DB and IMGT/mAb-DB databases.



GOBLET : Major Achievements from 2012 to 2015

By Teresa K. Attwood



Under the auspices of its 24th AGM, held in Uppsala (SE) in June 2012, EMBnet invited leaders of nine bioinformatics, biocuration and computational biology societies and networks to a workshop to discuss global bioinformatics training initiatives.

Like EMBnet, each of these organisations included some kind of education and training committee or programme, each with similar aims, and each with the same problem: how to deliver tangible benefits to their communities with limited funds and a mere handful of time-pressed volunteers.

The participants concluded that it would be useful to establish an umbrella organisation to coordinate bioinformatics training activities world-wide: to share, not duplicate, effort; to share, not duplicate, cost; to work together towards common solutions and a sustainable future. Thus was born GOBLET, the Global Organisation for Bioinformatics Learning, Education and Training.

GOBLET was subsequently established, in November 2012, as a legal foundation: its mission, to provide a global, sustainable support structure for bioinformatics trainers and trainees; to facilitate bioinformatics capacity development in all countries; to develop standards and guidelines for bioinformatics education and training; to act as a hub for fund gathering; to reach out, amongst others, to high-school teachers, to bridge the gap to the next generation of bioinformaticians; and to foster international communities of bioinformatics trainers.

With membership having grown more than threefold, GOBLET is going from strength to strength.

Notable highlights include:

- Three publications (in [Bioinformatics](#), [EMBnet journal](#) & [PLoS CB](#)),
- Development of a [joint training strategy](#) with ELIXIR,
- Holding education & training workshops (in Manchester, Boston & Toronto),
- Running global surveys of bioinformatics training needs,
- With the ISCB, establishing an education track for posters at ISMB conferences,
- Again working with the ISCB, launching the Computational Biology Education (CoBE) Community of Special Interest (COSI), to harmonise the ISCB education & GOBLET training communities,
- Winning a grant from the Canadian Institutes of Health Research to support the [2014 AGM](#),
- Planning the fourth AGM in Cape Town (ZA), November 18-20.

EMBnet can be proud to have spearheaded this highly successful initiative. To get involved, please contact us at www.mygoblet.org.



EMBnet.digest

EMBnet.Spotlight is a quarterly release of InFocus sections published in EMBnet.digest (www.embnet.org/embnet-digest), EMBnet's monthly publication that provides a round-up of news from the community. The InFocus section features member activities, projects, initiatives, etc., especially from new members, that may be of interest both to the network and to EMBnet's associated communities, societies and projects.