

The First Frontier

Welcome to the first newsletter of the ESF Frontiers of Functional Genomics research network programme or FFG. This programme aims to connect the most promising developments in functional genomics technologies with the expanding concept of systems biology, focusing particularly on applications in biomedicine, as well as the environment and implications for society at large, through a series of events and grants. The 5 year programme is supported by scientific research councils and academies from 17 European countries.

This programme began in 2006 and its first full year of events is coming to a close. Some highlights of this year are described below: Oda Stoevesandt tells us of ligand binders on the ski slopes and Daniel Berrar tells of the workshop discussing how to mine gems out of the mountain of high-throughput data. Finally we are pleased to bring you news of the 3rd Functional Genomics & Disease Conference to be held in the heart of the Austrian Alps in Innsbruck – so put 1-4 October 2008 in your diaries now!

Apply for science meetings and travel grants

FFG invites proposals from organisers of science meetings to be held in 2008 on topics with a clear connection to the programme. Priority is given to events taking place in countries that financially support the programme.

FFG is also offering a number of **Short Visits** and **Exchange Grants** (up to 6 months). Projects must be within the scope of the programme and start during 2008. Priority is given to applicants coming from and intending to visit labs in countries that support the programme.

Countries currently supporting the programme are Austria, Belgium, Czech Republic, Denmark, Estonia, Finland, France, Germany, Luxembourg, Netherlands, Norway, Poland, Spain, Sweden, Switzerland, Turkey & UK.

Deadline for submission of proposals is Friday 2 May 2008 17:00 CET. There will be a second call for proposals later in the year. For further information and to apply online go to www.esf.org/ffg or for regular (but not too regular!) updates on events and funding opportunities join our email list at www.functionalgenomics.org.uk/sections/contact/join.htm or contact cheryl.smythe@bbsrc.ac.uk.

Events 2008

Hot Topics in Molecular Imaging: Imaging of Nano-objects, Les Houches, France 4-8 February

Advanced Large-Scale Expression Profiling – Focus on mRNA, ChIP-chip and Whole Genome Associations, Turku, Finland 19-22 March

Antiviral Applications of RNA Interference, St Feliu de Guixols, Spain 5-10 April

3rd Conference on Animal Functional Genomics, Edinburgh, 7-9 April

Non-Coding RNAs: Computational Challenges & Applications, Antalya, Turkey 28-30 April

Systems Biology in Medicine, Barcelona, Spain 21-23 May

Gene Forum 2008 – Functional Genomics, Tartu, Estonia 12-14 June

Governing Biobanks – What are the Challenges?, Oxford, UK 23-26 June

Integrated Mechanisms of Cellular Identity and Homeostasis, Cambridge, UK 26-27 June

Dynamics of Cell Signal Systems, Oslo, Finland 25-29 Sept

Functional Genomics & Disease, Innsbruck, Austria 1-4 Oct

For scientific reports from all our events, please go to our website www.functionalgenomics.org.uk.

3rd Functional Genomics & Disease Conference

Innsbruck, Austria, 1-4 October 2008



Following on from two stimulating conferences in Prague and Oslo, we are delighted to announce that the 3rd Functional Genomics and Disease Conference will be held in

Innsbruck. Areas that will be covered include whole genome associations, comparative genomics, RNA-omics and miRNA, proteomics, epigenetics, regulatory networks, systems biology, single molecule/cell technologies, personalised medicine, oncogenomics, inflammatory diseases, immune system, metabolomics, neurogenomics, ageing, lipidomics, angiogenomics, bioinformatics, high-throughput technologies, and affinity proteomics. Travel bursaries will be available for young researchers. For further information and to pre-register, please go to www.esffg2008.org.

Non-protein-coding RNAs come into the light

Juergen Brosius

The dark ages for non-protein-coding RNAs (npcRNAs) are over. These macromolecules not only constitute important players in gene and genome evolution but also are vital for an astounding variety of cellular functions and key regulatory pathways in modern organisms.

During all periods including the recent soaring of the field, European scientists have made important contributions. The *Non-Protein-Coding RNA* meeting brought established scientists that participated in several EU sponsored RNA-based STREPs together and, importantly, also mixed junior scientists including graduate students. About 60 participants from all corners of Europe exchanged their findings on various aspects of RNA Biology: from large npcRNAs to the tiniest (miRNAs), from systems as diverse as plants, fungi, invertebrates, vertebrates including mammals, bacteria, in normal development and cellular function as well as disease using computational and wet-lab approaches. Several posters were presented and accessible for discussion during the entire meeting. The pleasant setting at the Mediterranean coast in Carry-Le-Rouet near Marseille and secluded location led to vivid and prolonged discussion among all participants. I am certain that all participants greatly benefited from these exciting interactions in an exploding field.

Of binders & bindings

Oda Stoevesandt



Three sunny early spring days in a green alpine valley provided the setting for the *Affinity Proteomics* workshop, co-organised by the ESF FFG programme and the EC FP6 projects ProteomeBinders and Moltools (March 13-15

2007, Alpbach, Austria).

Affinity Proteomics designates the area of proteomic research based on affinity reagents and methods. As the specific reagents available to date only cover a fraction of the human proteome, Affinity Proteomics also comprises systematic approaches to extend the set of specific affinity reagents to a proteome-wide range of target proteins. Attended by 119 academic and industrial participants from Europe and the US, conference sessions reviewed the human proteome in overview, bioinformatics infrastructures for proteomics, classical and recombinant antibodies and alternative binders, affinity tools and methods, intrabodies as tools for therapeutics and research, applications and quality control of binding reagents, biomolecular resources in the context of biobanks, and future directions for large binder resource projects.

Surrounded by the green valley, global warming seemed to be taking its toll, however at closer inspection the peaks of the Alpbach ski resort were still snow-capped under an immaculately blue sky. Consequently, the meeting programme took proteomics research and researchers beyond the doors of the conference centre, a meeting layout which proved very popular with all participants. Future issues of a similarly structured meeting can not be excluded – watch this space at www.proteomebinders.org.

At the coal-face

Daniel Berrar

The ESF workshop *Mining High-Throughput Data in Functional Genomics* was held in Coleraine, Northern Ireland, in May 2007, and brought together 35 academic researchers and industrial practitioners from eight different countries. The scientific background of the attendees covered a wide range of fields, including (molecular) biology, biomedicine, statistics, and computer science. This reflected the modern research practice in functional genomics, which is characterised by a truly multidisciplinary effort.

The workshop represented a platform for an exchange of ideas, discussions of the state of the art in analysing data from functional genomics, and critical assessment of the limitations of current approaches. A particular focus was on systems biology, which takes into account complex interactions of genes, transcripts, proteins, and other cell elements, and pays particular attention to the dynamic behavior of these interactions. As a result of the underlying biological complexity and technologies involved, genomic, transcriptomic and proteomic data structures vary largely. They include temporally and spatially resolved data (e.g., from various imaging instruments), data from spectral analyses, encodings for the sequential and spatial representation of biological macromolecules and smaller chemical and biochemical compounds, time-variant or time-series information, graph structures, and natural language text.

Twelve invited speakers presented an arsenal of modern tools and methodologies to tackle these challenges. Of particular importance are methods for generating, visualising, analysing, and understanding large graphs and networks, for example, gene regulatory networks.

Steering committee spotlight

Mike Taussig is the chair of the FFG steering committee. He graduated from Cambridge, a little while ago now, with a BA in Biochemistry and PhD in Immunology. His love of travel took him to Israel and Switzerland for post-docs, and he returned to Cambridge where he is head of the Technology Research Group at the Babraham Institute. He is also a Fellow at Selwyn College, Cambridge, where he teaches general pathology, but between lectures he travels Europe co-ordinating the EU ProteomeBinders project. His few moments of spare time he fills with Italian operas and eating chocolate biscuits.

Compiled and created by Cheryl Smythe, FFG Co-ordinator