ECCB'14 Industrial and Academic Demonstrations

ID01: Bringing the Tools to the Data – Providing Scientists with Personalized and On-Demand Bioinformatics Services on the Cloud of the French Institute of Bioinformatics

Life science researchers, thanks to the continuous improvement of experimental technologies, face a deluge of data whose exploitation requires large computing resources and appropriate software tools. To tackle these issues, the French Institute of Bioinformatics (IFB) developed predefined, personalized bioinformatics cloud services and turnkey appliances encapsulating common bioinformatics tools, workflows and gateways. The size of these appliances, at most a few gigabytes, allows users to move them easily to the data, rather than moving the data (whose size can be three order of magnitude larger - terabytes) to the computing resources. IFB is currently running an academic cloud infrastructure with the appropriate biological data and bioinformatics tools to meet the needs of the life science community.

Presentation Flier
www.eccb14.org/programme/id_track/ID01-summary.pdf

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ID02: A Panel of European Public Galaxy Instances

Galaxy, a web-based platform for data intensive biomedical research, is available as a web server (http://UseGalaxy.org), and as customisable open source software. The first session will introduce the Galaxy project and then the deepTools webserver. The second session will feature the public Galaxy instances "Nebula" and "IFB's cloud".

Presentation Flier
www.eccb14.org/programme/id_track/ID02-summary.pdf

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ID03: Building and Testing Executable Biological Models in the BioModelAnalyzer

Executable models of biological phenomena offer a new set of techniques to address problems arising from biological complexity. Here we present the BioModelAnalyzer, a web-based tool for building and testing executable models, and showcase how it can be used to identify missing protein-protein interactions and understand complex signaling networks.

Presentation Flier
www.eccb14.org/programme/id_track/ID03-summary.pdf

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ID04: EMC Isilon – the Foundation of NGS Data Analysis

NGS usually means PBytes of data. But not only that, the workflow involves different steps, different files with different sizes and bandwidth requirements and different algorithms are used to do the data analysis. And to add another angle different algorithms may even use different protocols to access the data. EMC Isilon takes care of all that in one system. It can be flexibly deployed to your data storage needs and handles all possible requirements. So you end up doing your analysis not solving the data storage problem.

Presentation Flier
www.eccb14.org/programme/id_track/ID04-summary.pdf

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ID05: UniProt: New Website and Latest Developments

The demonstration will cover:

1. A description of UniProt
2. New UniProt beta site, functionalities and design
3. Accessing UniProt using simple query syntax
4. Proteomes querying and retrieval
5. Sequence similarity searches, alignments and ID mapping tools provided

Presentation Flier
www.eccb14.org/programme/id_track/ID05-summary.pdf

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ID06: Enhanced Human NGS Variant and Gene Regulation Analysis

BIOBASE is the leading provider of expert-curated biological databases, software and services for the life sciences. Our products and services identify relations critical to drug and biomarker discovery as well as improve biomedical research by transforming data into scientific concepts.

In the first session (A), you will learn more about the TRANSFAC® database of eukaryotic transcription factors and in the second session (B) more about the NGS analysis tool Genome Trax™.

Presentation Flier
www.eccb14.org/programme/id_track/ID06-summary.pdf

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ID07: A Reputation-Based Web Application (sbv IMPROVER Network Verification Challenge) that Facilitates Collaboration and Applications on Biological Network Models

Part 1. Collaborative crowd-verification approach allows domain experts from various fields of biology to gather robust peer-reviewed information from which relationships are identified and evaluated. The approach is used to investigate smarter solutions to complement classical peer review and expand biological network models suitable for research in respiratory diseases.

Part 2. Using transcriptomics data, we assess the activation of causal network models from sbv IMPROVER BioNet in a quantitative, statistical and interpretable manner. The Biological Impact Factor (BIF) quantifies the response of a cell system to an insult by aggregating the overall network responses.

Presentation Flier
www.eccb14.org/programme/id_track/ID07-summary.pdf

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ID08: KLAST: Fast, Accurate and NGS Scalable Bank-To-Bank Sequence Similarity Search Tool

KLAST is a professional sequence similarity search tool for processing high volumes of genomic sequences. The demo will present the use of the KLAST software on the following application domains: genome annotation, genome comparison and analysis of metagenomic data.

Presentation Flier
www.eccb14.org/programme/id_track/ID08-summary.pdf

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ID09: Protein Model Portal and SWISS-MODEL Workspace: Giving the Proteome a Third Dimension

The three-dimensional structure of a protein provides valuable information for understanding its molecular function and guides the rational design of experiments. In this tutorial, we will illustrate how protein structure homology modelling can be used to study proteins still lacking experimental characterization.

Presentation Flier
www.eccb14.org/programme/id_track/ID09-summary.pdf

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www.proteinmodelportal.org
www.swissmodel.expasy.org

ID10: BioMercator 4.0: A Complete Framework to Integrate QTL, Meta-QTL and Genome Annotation

Compilation of genetic maps combined to QTL meta-analysis has proven to be a powerful approach for identification of candidate genes underlying quantitative traits. BioMercator is the first software covering all steps required to perform QTL meta-analysis and mine genome functional annotation related to QTL and meta-QTL. BioMercator V4 is freely available: http://moulon.inra.fr/biomercator

Presentation Flier
www.eccb14.org/programme/id_track/ID10-summary.pdf

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ID11: iPlant Collaborative^{TM} A Scalable Cyberinfrastructure for Life Science

The iPlant Collaborative develops cyberinfrastructure to solve data-intensive problems of biology - those involving genome, phenotype, and environmental data. iPlant provides free access to cyberinfrastructure through web-based platforms and services, many of which are accessible to biologists without extensive computational backgrounds. This demo surveys these tools and their applications.

Presentation Flier
www.eccb14.org/programme/id_track/ID11-summary.pdf

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ID12: Garuda : Fly to the Future of Biology

With the ever-increasing diversity of omics-scale experimental data, a key challenge is the ability to discover the right tools for a specific analysis and navigate through their specific formats. Garuda is an open, community-driven, platform that provides a framework to discover, connect & navigate through different applications in bio-medical research.

Presentation Flier
http://www.eccb14.org/programme/id_track/ID12-summary.pdf

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ID13: Totalinux

Created in 2004, TotaLinuX is a french compagny providing IT solutions and specialized in HPC and Big Data. Totalinux main skills are focused on designing and building IT infrastructure dedicated to computing (HPC), storage (Scale-out, Big Data) and graphical simulation (VDI).

Presentation Flier
http://www.eccb14.org/programme/id_track/ID13-summary.pdf

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ID14: Sushi: An Exquisite Recipe for Fully Documented, Reproducible and Reusable NGS Data Analysis

We present Sushi, an agile framework for web- and commandline-based data analysis that lets users build fully reproducible analysis workflows. All results and associated meta-information are fully defined on the file system in tabular clear text format that is independent of Sushi and ready for sharing and distribution.

Presentation Flier
www.eccb14.org/programme/id_track/ID14-summary.pdf

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ID15: JAMM: A Peak Finder for Joint Analysis of NGS Replicates

We introduce JAMM: a peak finder that can integrate biological replicates and determine enrichment site widths accurately. JAMM is a universal peak finder that is applicable to different types of datasets. It is available for free and can run on Linux machines through the command line: http://code.google.com/p/jammpeak-finder

Presentation Flier
www.eccb14.org/programme/id_track/ID15-summary.pdf

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ID16: POPS: Predicting and Enhancing Protein Solubility

Protein solubility is a prerequisite for many biophysical and biochemical applications. However, it remains challenging to produce soluble proteins by using heterologous expression systems. In this regard, computational approaches to correctly predict the solubility level of a protein and enhancing the solubility level by modifying the protein sequences are highly valuable.

Presentation Flier
www.eccb14.org/programme/id_track/ID16-summary.pdf

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ID17: Computational Tools for the Taxonomic Analysis of Shotgun Metagenome Samples

Metagenomics characterizes microbial communities by shotgun sequencing of environmental DNA. We present software (taxator-tk, PhyloPythiaS+) to facilitate the taxonomic analysis of large NGS datasets. The taxonomic assignment of individual (sub)sequences allows estimating the abundances of community members and to reconstruct taxonomic bins with sequence data for the individual taxa.

Presentation Flier
www.eccb14.org/programme/id_track/ID17-summary.pdf

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ID18: Goes Open: publish with *Genomics, Proteomics & Bioinformatics*

Genomics, Proteomics and Bioinformatics (GPB) is a peer-reviewed and fast-track open access journal that focuses on disseminating the newest discoveries in the -omics and bioinformatics studies. A through introduce on the GPB would facilitate your publishing with this fast-processing journal and help increasing the impacts of your study.

Presentation Flier
www.eccb14.org/programme/id_track/ID18-summary.pdf

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