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October 2015

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Up-coming courses

- **Human & Vertebrate Genomics: Bioinformatics Tools & Resources Course**, 7-12 Feb 2016, Bangkok (TH). **Registration deadline:** 13 Nov 2015
- **EMBO Practical Course: Metabolomics Bioinformatics for Life Scientists**, 14-19 Feb 2016, Hinxton (UK). **Application deadline:** 13 Nov 2015
- **BioSB Course:Managing & Integrating Life Science Information (4th edition)**, 30 Nov-4 Dec 2015, Utrecht (NL).
- **Intermediate R**, 7-9 Dec 2015, SIB, Lausanne (CH). **Deadline:** 27 Nov 2015
- **EMBL Course: Genome Engineering: CRISPR/Cas**, 8-12 Feb 2016, Heidelberg (DE). **Application deadline:** 1 Dec 2015

Job opportunities

- **3 Postdoc positions for the Crossover Research Project**, Norwegian University of Science & Technology, Trondheim (NO).
- **ELIXIR-Estonia seeks a developer. Application deadline:** 13 Nov 2015.

News

- Help the **Gene Ontology Consortium** to improve their service by completing their Assessing User Needs survey; complete this before 15 Nov 2015 to enter the prize draw!

Events

- **BILS Annual Symposium & User Meeting 2015**, 12 Nov 2015, Stockholm (SE). **Register here**.
- **6th Annual PhD Symposium in Computational Biology & Innovation 2015**, 3-4 Dec 2015, Dublin (IR). **Registration deadline:** 30 Oct 2015
- **10th Benelux Bioinformatics Conference**: 7-8 Dec 2015, Antwerp (BE). **Registration deadline:** 30 Nov 2015
- **International Plant & Animal Genome XXIV (PAG ASIA 2016)**, 9-13 Jan 2016, San Diego (US). **Registration deadline:** 7 Jan
- **ABRF 2016 Annual Meeting**, 20-23 Feb 2016, Lauderdale (US). **Registration deadline:** 11 Jan 2016
- **EMBL Conference: Visualizing Biological Data Conference (VIZBI)**, 9-11 Mar 2016, Heidelberg (DE). **Registration deadline:** 31 Jan 2016
- **SAVE-SD 2016 Workshop**, co-located with the **25th International W3C Conference**, 11 or 12 Apr 2016, Montreal (CA). **More info**.

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Bioinformatics in Action

Best wishes,
The EMBnet Operational Board

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InFocus
October 2015

NETTAB & IB 2015
“Two-Day Hands-on Tutorial”

by Domenica D’Elia, EMBnet Italy

The NETTAB & Integrative Bioinformatics *Two-Day Hands-on Tutorial: Bioinformatics Analysis of Omics Data* was held 12-13 October 2015, in Bari (IT) as a satellite event of the NETTAB & IB 2015 Joint Symposium. Organised by Domenica D’Elia (EMBnet Italy) and Paolo Romano (IRCCS San Martino IST, Genoa (IT)), it received generous support from EMBnet (which granted 10 free tutorial registrations), from the InterOmics project and from the IT resources of the ReCaS project (Programma Operativo Nazionale Ricerca e Competitività 2007-2013 – 4).

The tutorials (four in total) were held at the University of Bari’s Department of Computer Science and organised in full- and half-day parallel sessions, the last replicated on both days. The aim of the programme was to provide researchers and students opportunities to learn about best practices in challenging bioinformatics tasks. Specifically, a full-day tutorial was dedicated to the analysis of re-sequencing data for detecting genomic variants in human diseases, such as somatic single nucleotide variants (SNVs) in cancer (run by Fabio Iannelli, IFOM, Milan, IT) and germline SNVs in rare Mendelian disorders (run by Anna De Grassi, Professor at the University of Bari). The other full-day tutorial, run by Ioannis Vlachos (from the DIANA-Lab, Pasteur Institute of Athens and the Department of Computer & Communication Engineering of the University of Thessaly (GR)), covered the design and analysis of small-RNA-Seq experiments, methods for genome alignment and/or microRNA expression estimation, and the state-of-the-art of online tools for microRNA functional analysis. Emek Demir, from the Sloan Kettering Institute, New York (USA), ran a half-day tutorial on the use of the Pathway Commons Web service and BioPAX, a standard, community-developed language for the description of biological pathways. Pasqualina D’Ursi, from the CNR-ITB in Milan (IT), focused her tutorial on applications of fast and inexpensive docking protocols, combined with accurate molecular dynamics techniques to predict protein-ligand complexes.

I would like to thank first of all EMBnet, InterOmics, the ReCaS project and the Department of Computer Science for their precious support, and all the teachers and students both for their dedication and for the enthusiasm they expressed for this initiative.