Scientific Programme

NETTAB 2012
Workshop on "Integrated Bio-Search"

14-16 November 2012, Como, Italy

http://www.nettab.org/2012/

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Wednesday	November 14
9.00 - 10.50	**Tutorial 1**
	Multi-scale data integration and virtual exploration from promoters, through networks to drug targets
	Alexander Kel, GeneXplain GmbH, Wolfenbüttel, Germany, and Biosoft.ru, Skolkovo Center of Bioinformatics, Novosibirsk, Russian Federation
10.50 - 11.10	*Break*
11.10 - 13.00	**Tutorial 2**
	The Taverna Workbench: Integrating and analysing biological and clinical data with computerised workflows
	Katy Wolstencroft, University of Manchester, United Kingdom
13.30 - 14.20	*Registration and poster hang-up*
14.20 - 14.30	*Welcome and Introduction*
14.30 - 15.10	**Invited Lecture**
	Integration and analysis of multi-type high-throughput data for biomolecular knowledge discovery
	Erik Bongcam-Rudloff, Swedish University of Agricultural Sciences, and Uppsala University, Sweden
15.10 - 15.50	**Scientific Session 1**
	Using graph theory to analyze gene network coherence
	Francisco Gómez-Vela, Norberto Díaz-Díaz, Jose Antonio Lagares, Jose Antonio Sánchez and Jesús S. Aguilar-Ruiz
	Network-based gene-disease prioritization using PROPHNET
	Víctor Martínez, Carlos Cano and Armando Blanco
15.50 - 16.20	**Coffee Break**
16.20 - 18.15	**Scientific Session 2**
	Rational design of organelle compartments in cells
	Claudio Angione, Giovanni Carapezza, Jole Costanza, Pietro Lio' and Giuseppe Nicosia
	Filtering with alignment free distances for high throughput DNA reads assembly
	Maria Cristina De Cola, Giovanni Felici, Daniele Santoni and Emanuel Weitschek
	A strategy to reduce technical variability and bias in RNA sequencing data
	Francesca Finotello, Enrico Lavezzo, Luisa Barzon, Paolo Mazzon, Paolo Fontana, Stefano Toppo, Barbara Di Camillo
	Applications of a generic model of genomic variations functional analysis
	Sarah N. Mapelli, Uberto Pozzoli
	The Biovel project: robust phylogenetic workflows running on the Grid
	Saverio Vicario, Bachir Balech, Giacinto Donvito, Pasquale Notarangelo, Graziano Pesole
	Ranking-aware integration and explorative search of distributed bio-data
	Marco Masseroli, Matteo Picozzi and Giorgio Ghisalberti
	Development of a text search engine for medicinal chemistry patents
	Emilie Pasche, Julien Gobeill, Fatma Oezdemir-Zaech, Therese Vachon, Christian Lovis and Patrick Ruch

Thursday	November 15
8.30 - 9.00	*Registration and poster hang-up*
9.00 - 9.40	**Invited Lecture**
	Semantics based biomedical knowledge search, integration and discovery *Barend Mons, Leiden University Medical Center, and Netherlands Bioinformatics Center, The Netherlands*
9.40 - 10.20	**Scientific Session 3**
	Answering Gene Ontology terms to proteomics questions by supervised macro reading in Medline *Julien Gobeill, Emilie Pasche, Douglas Teodoro, Anne-Lise Veuthey and Patrick Ruch*
	IntelliGenWiki: An Intelligent Semantic Wiki for Life Sciences *Bahar Sateli, Marie-Jean Meurs, Gregory Butler, Justin Powlowski, Adrian Tsang and René Witte*
10.20 - 12.00	**Poster and Software Demonstration Session with Coffee Break**
12.00 - 13.00	**Technological - Industrial Session**
	Extracting knowledge from biomedical data through Logic Learning Machines and Rulex *Marco Muselli*
	Data modeling: the key to biological data integration *François Rechenmann*
	GeneGrid: finding disease causing variants in NGS data *Jochen Supper, Claudia Gugenmus, Korbinian Grote and Frederic Eyber*
13.00 - 14.00	**Lunch Break**
14.00 - 15.30	**Panel Discussion**
	Technological and methodological challenges for Integrated Bio-Search *Erik Bongcam-Rudloff, Barend Mons, Eric Neumann, Alexander Kel, François Rechenmann, and Stefano Ceri introduce the topic, then open discussion follows*
15.30 - 19.00	**Guided tour of Como and of the Educational Silk Museum of Como**
20.00 - 23.00	**Social Dinner**

Friday	November 16
9.00 - 9.40	**Invited Lecture**
	Clinical and genomic data integration in support of biomedical research and clinical practice *Eric Neumann, PanGenX and Clinical Semantics Technologies, USA*
9.40 - 10.40	**Scientific Session 4**
	ROCK: a resource for integrative breast cancer data analysis *Marketa Zvelebil, Costas Mitsopoulos and Saif Ur-Rehman*
	QTreds: a flexible LIMS for omics laboratories *Piergiorgio Palla, Gianfranco Frau, Laura Vargiu and Patricia Rodriguez-Tomé*
	The open source ISA software suite and its international user community: knowledge management of experimental data *Alejandra Gonzalez-Beltran, Eamonn Maguire, Philippe Rocca-Serra and Susanna-Assunta Sansone*
10.40 - 11.10	**Coffee Break**
11.10 - 12.30	**Scientific Session 5**
	The ontogene system: an advanced information extraction application for biological literature *Fabio Rinaldi*
	A semantic collaborative system for the management of translational research projects *Matteo Gabetta, Giuseppe Milani, Cristiana Larizza, Valentina Favalli, Eloisa Arbustini and Riccardo Bellazzi*
	BioQuery-ASP: querying biomedical databases and ontologies using Answer Set Programming *Esra Erdem, Umut Oztok*
	DiGSNP: a web tool for Disease-Gene-SNP hierarchical prioritization *Carmen Navarro, Carlos Cano, Armando Blanco, Fernando García*
12.30 - 13.00	**Announcement of NETTAB 2013 and Farewell**