

NETTAB 2013 Scientific Programme

Wednesday	October 16, 2013 TUTORIAL DAY
10.30 - 17.30	<i>Registration and poster hang-up</i>
11.00 - 13.00	Tutorial 1
	<p><i>Semantic Web for Life Sciences: vision, aims, tools, platforms</i> <i>Andrea Splendiani,</i> <i>IntelLeaf, United Kingdom, and Digital Enterprise Research Institute, Ireland</i></p>
	<i>Demonstration on Tutorial 1</i>
13.00 - 13.30	<i>Brunch Break</i>
13.30 - 15.30	Tutorial 2
	<p><i>Open PHACTS and NanoPublications</i> <i>Christine Chichester,</i> <i>Swiss Institute of Bioinformatics, CALIPHO group, Geneva, Switzerland</i></p>
	<i>Demonstration on Tutorial 2</i>
15.30 - 17.30	Tutorial 3
	<p><i>Standards for Web Applications on Mobile: current state and roadmap</i> <i>Dominique Hazaël-Massieux,</i> <i>W3C/ERCIM, Sophia Antipolis, Biot, France</i></p>
	<i>Demonstration on Tutorial 3</i>
17.30 - 19.30	Tutorial 4
	<p><i>Mobile applications for life sciences: perspectives, limitations, and real examples</i> <i>Alex Clark,</i> <i>Molecular Materials Informatics, Inc</i></p>
	<i>Demonstration on Tutorial 4</i>

Thursday	October 17, 2013 WORKSHOP DAY 1
8.30 - 18.30	<i>Registration and poster hang-up</i>
9.15 - 9.30	<i>Welcome and Introduction</i>
9.30 - 10.10	Scientific Session 1
	<i>Mobile applications driven by Open PHACTS semantic web technology,</i> <i><u>Christine Chichester</u></i>
	<i>TagCurate: Crowdsourcing the verification of biomedical annotations to mobile users,</i> <i><u>Bahar Sateli</u>, <u>Sebastien Luong</u>, <u>René Witte</u></i>
10.10 - 11.00	Invited Lecture
	<i>Facilitating Scientific Discovery through Crowdsourcing and Distributed Participation</i> <i><u>Antony Williams</u>, Royal Society of Chemistry</i>
11.00 - 11.30	Coffee Break
11.30 - 12.10	Scientific Session 2
	<i>Genome interpretation and annotation,</i> <i><u>Ismael Navas-Delgado</u>, <u>Maria Jesús García Godoy</u>, <u>Fátima Arjona-Pulido</u>, <u>Trinidad Castillo-Castillo</u>, <u>Ana Isabel Ramos-Ostio</u>, <u>José F. Aldana-Montes</u></i>
	<i>The OntoGene literature mining web service,</i> <i><u>Fabio Rinaldi</u></i>
12.10 - 13.10	Poster Session
13.10 - 14.30	Lunch Break
14.30 - 15.10	Industrial - Technological Session
	<i>New publishing opportunities for digital life science,</i> <i><u>Rebecca Lawrence</u>, <u>Michael Markie</u></i>
	<i>Extracting more value from data silos: Using the semantic web to link chemistry and biology for innovation,</i> <i><u>Tim P Eyres</u></i>
15.10 - 15.30	Introduction to open group discussions
	<i>Semantic, social & mobile technologies at the forefront of bioinformatics research</i> <i>Speakers and Chairs propose the topics to be discussed by groups</i>
15.30 - 16.30	Open group discussions
	<i>Semantic, social & mobile technologies at the forefront of bioinformatics research: selected topics</i> <i>All participants discussing in the topic group of their greatest interest</i>
16.30 - 17.00	Coffee Break
17.00 - 17.50	Invited Lecture
	<i>Semantic technologies for the automation of research in biomedicine</i> <i><u>Ross D. King</u>, School of Computer Science, University of Manchester, Manchester, United Kingdom</i>
17.50 - 18.30	Plenary reports of group discussions
20.00 - 23.00	Social Dinner at Nicelli Airport Restaurant, Lido of Venice

Friday	October 18, 2013 WORKSHOP DAY 2
8.30 - 9.30	<i>Registration</i>
9.00 - 9.40	Scientific Session 3
	<i>Sprints, Hackathons and Codefests as community gluons in computational biology,</i> <i>Steffen Möller, Enis Afgan, Michael Banck, Peter J. A. Cock, Matus Kalas, Laszlo Kajan, Pjotr Prins, Jacqueline Quinn, Olivier Sallou, Francesco Strozzi, Torsten Seemann, Andreas Tille, Roman Valls Guimera, Toshiaki Katayama, Brad Chapman</i>
	<i>Taverna Mobile: Taverna workflows on Android,</i> <i>Hyde Zhang, Stian Soiland-Reyes, Carole Goble</i>
9.40 - 10.30	Invited Lecture
	<i>SCIMOBIS; the million minds approach revisited in mobile context</i> <i>Barend Mons, Leiden University Medical Center, Leiden, and Netherlands Bioinformatics Center, The Netherlands</i>
10.30 - 11.00	Coffee Break
11.00 - 12.20	Scientific Session 4
	<i>Bio-GraphIn: a graph-based, integrative and semantically-enabled repository for life science experimental data,</i> <i>Alejandra Gonzalez-Beltran, Eamonn Maguire, Pavlos Georgiou, Susanna Sansone, Philippe Rocca-Serra</i>
	<i>An ontology based query engine for querying biological sequences,</i> <i>Martijn Devisscher, Tim De Meyer, Wim Van Criekinge, Peter Dawyndt</i>
	<i>The representation of biomedical protocols,</i> <i>Larisa N. Soldatova, Ross D. King</i>
	<i>The role of parallelism, web services, and ontologies in bioinformatics and omics data management and analysis,</i> <i>Mario Cannataro, Pietro Hiram Guzzi</i>
12.20 - 13.00	Closing session
	Assignment of Best Poster Awards
	Announcement of NETTAB 2014
	Farewell