

Preface

NETTAB 2013

Workshop on “Semantic, Social, and Mobile Applications for Bioinformatics and Biomedical Laboratories”



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Due to the distributed nature of biomedical information resources, and to their heterogeneity and size, it is now clear that bioinformatics plays an essential role in every domain of biomedical research, from experimental to clinical studies. In this context, network tools, platforms and applications are one of the most relevant research and development domain for bioinformatics, because they may indeed allow an efficient and effective integration of information, that is the basis for any further data analysis.

Since 2001, a series of workshops has been devoted to this topic and held annually in Italy, under the name of “Network Tools and Applications in Biology” (NETTAB). These workshops have been aimed at presenting and discussing some of the most innovative Information and Communication Technologies (ICTs) and their application in the biomedical domain.

Each workshop has been focused on a different topic. Since 2001, many different focus themes have been explored, including Standardization for data integration (Genoa, 2001), Multi Agent Systems (Bologna, 2002), Scientific workflows (Naples, 2005), Grid and Web Services (Santa Margherita di Pula, 2006), Semantic Web (Pisa, 2007), Collaborative research and development (Catania, 2009), and Biological Wikis (Naples, 2010).

The NETTAB 2013 workshop, the thirteenth in the series, is held in Lido of Venice, Italy, on October 16-18, 2013. It is focused on “Semantic, Social,

and Mobile Applications for Bioinformatics and Biomedical Laboratories”.

Human beings are social animals and ICT have recently permeated human society of newer forms and ways of participation in social activities. In the Internet, the hype has shifted from Web2.0 to Social Media; in science too, this development is evident. Beside facilitating communication and making easier the sharing of information, social platforms and technologies are enhancing learning, problem solving and crowdsourcing. In biology, and especially in the “-omic” disciplines, we already rely on a wide diffusion of social tools and applications, e.g. for distributed annotations, Wiki knowledge bases, documentation and productivity.

On the other hand, access to the Internet is nowadays increasingly happening through mobile devices. Mobile Internet access is expected to soon overtake access from standard PCs and workstations. Moreover, mobile phones are expected to become the main personal computing devices. Smartphones and tablets represent the most practical computing devices in biomedical laboratories and they actually are the ideal companions for “always on the move” scientists. While we can observe a widespread diffusion of health and lifestyle mobile applications and a rapid adoption of mobile solutions in medicine and healthcare we cannot say the same for life sciences and bioinformatics.

Semantic methodologies and technologies are instead well established in “-omic” projects. It can even be proudly observed that the bioinformatics community was an early adopter of Semantic Web technologies.

In the NETTAB 2013 workshop, mobile and/or social and/or semantic solutions for bioinformatics and laboratory informatics problems will be explored. It is our opinion that a savvy combination of these three technologies could greatly enhance the research outcome of life scientists and markedly simplify the workflows in biomedical laboratories.

The workshop is open to all aspects of the focus theme, including issues, methods, algorithms, and technologies for the design and development of tools and platforms able to provide semantic, social, and mobile applications supporting bioinformatics and the activities carried out in a biomedical laboratory.

The Call for abstracts was able to attract 20 quality submissions that are after peer review and revision included in these proceedings, grouped by submission type. Oral communication abstracts are listed according to the presentation in the programme, while poster abstracts are ordered by first author name.

The Chairs of the NETTAB 2013 workshop hope that this is a great meeting for all participants. Ideas, and doubts, on the perspectives of the widespread application of these new technologies will be discussed with outstanding scientists such as Antony Williams, Ross King, Barend Mons, Andrea Splendiani, Christine Chichester, Dominique Hazaël-Massieux, and Alex Clark, who present invited keynotes and tutorials, and many others who enthusiastically join the workshop and actively participate in it.

We wish to thank all participants, but also all Supporting Institutes and companies that made this workshop possible and successful.

Speakers

Keynote Speakers

Antony Williams

Royal Society of Chemistry

Ross D. King

School of Computer Science, University of Manchester, Manchester, United Kingdom

Barend Mons

Leiden University Medical Center, Leiden, and Netherlands Bioinformatics Center, The Netherlands

Tutorials

Andrea Splendiani

IntelLeaf, United Kingdom, and Digital Enterprise Research Institute, Ireland

Christine Chichester

Swiss Institute of Bioinformatics, CALIPHO group, Geneva, Switzerland

Dominique Hazaël-Massieux

W3C/ERCIM, Sophia Antipolis, Biot, France

Alex Clark

Molecular Materials Informatics, Inc

Oral presentations

Christine Chichester

René Witte

Ismael Navas-Delgado

Fabio Rinaldi

Rebecca Lawrence

Tim P. Eyres

Steffen Möller

Stian Soiland-Reyes

Alejandra Gonzalez-Beltran

Martijn Devisscher

Larisa N. Soldatova

Mario Cannataro