SCIENTIFIC COMMITTEE

- **Claudia Angelini**, IAC, National Research Council, Napoli, Italy
- **Roland Barriot**, Laboratoire de Microbiologie et Génétique Moléculaires, Université Paul Sabatier - CNRS, Toulouse, France
- **Alex Bateman**, Wellcome Trust Sanger Institute, Hinxton, United Kingdom
- **Dan Bolser**, University of Dundee, Scotland, United kingdom
- **Philip E. Bourne**, University of California, San Diego UCSD, La Jolla, USA
- **Mike Carasio**, Keygene N.V., Wageningen, The Netherlands
- **Maria Luisa Chiusano**, University of Napoli "Federico II", Napoli, Italy
- **Antonio d'Acierno**, ISA, National Research Council, Avellino, Italy
- **Italia De Feis**, IAC, National Research Council, Napoli, Italy
- **Angelo Facchiano**, ISA, National Research Council, Avellino, Italy
- **Carl Herrmann**, Université de la Méditerranée, Marseille, France
- **Pascal Hingamp**, Université de la Méditerranée, Marseille, France
- **Eran Hodis**, Weizmann Institute of Science, Rehovot, Israel
- **Robert Hoehndorf**, Department of Genetics, University of Cambridge, United Kingdom
- **Robert Hoffmann**, Computational Biology Center, Memorial Sloan-Kettering Cancer Center, New York, USA
- **Thomas Kelder**, BiGCaT Bioinformatics, University of Maastricht, The Netherlands
- **Roderic Page**, Ecology and Evolutionary Biology, University of Glasgow, Scotland, United Kingdom
- **Alexander Pico**, The Gladstone Institutes, University of California, San Francisco, USA
- **Jaime Prilusky**, Bioinformatics, Weizmann Institute of Science, Rehovot, Israel
- **Paolo Romano**, Bioinformatics, National Cancer Research Institute, Italy
- **Katharina Siorpaes**, Semantic Technology Institute (STI), University of Innsbruck, Austria
- **Andrew Su**, Bioinformatics, Genomics Institute of the Novartis Research Foundation, San Diego, USA
- **Joel Sussman**, Weizmann Institute of Science, Rehovot, Israel
- **Tim Vickers**, Department of Molecular Microbiology, Washington University in St. Louis, St. Louis, USA
- **Wyeth Wasserman**, Department of Medical Genetics, University of British Columbia, Vancouver, Canada

SUPPORTING INSTITUTES AND SOCIETIES

National Cancer Research Institute, Italy

RNBIO Italian Network for Oncology Bioinformatics

Istituto di Scienze dell'Alimentazione, ISA-CNR, Italy

Istituto per le Applicazioni del Calcolo, IAC-CNR, Italy

Istituto di Tecnologie Biomediche, ITB-CNR, Italy

Bioinformatics Italian Society - Italy

CALL DEADLINES

Oral presentations due: **September 24, 2010**

Notification to authors: **October 24, 2010**

Posters and position papers due: **October 17, 2010**

Early registration: **October 29, 2010**

ORGANIZING COMMITTEE

- Claudia Angelini, IAC-CNR, Napoli, Italy
- Maria Luisa Chiusano, University of Napoli "Federico II", Napoli, Italy
- Italia De Feis, IAC-CNR, Napoli, Italy
- Angelo Facchiano, ISA–CNR, Avellino, Italy
- Paolo Romano, Bioinformatics, National Cancer Research Institute, Genoa, Italy

NETTAB

Network Tools and Applications in Biology
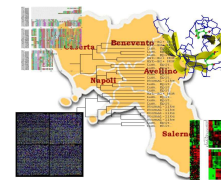
Bioinformatica e Biologia Computazionale in Campania

NETTAB 2010   and   BBCC 2010

joint meeting on

Biological Wikis

November 29th - December 1st, 2010
Naples, Italy

Call for Papers

http://www.nettab.org/2010/

NETTAB 2010 and BBCC 2010 joint meeting on BioWikis

RATIONALE

It is now clear that wiki systems offer a variety of advantages for the management of biological data and information. Some of the specific aims of wikis for biology (biowikis) include:

- Collaborative development and sharing of knowledge
- Collaborative annotation of database contents
- Collaborative creation of database contents

The **collaborative development and sharing of documentation and knowledge** allows communities to promote, exploit, discuss and reach consensus on information, procedures, data, experiences, news, and other varied information. This aim is motivated by the awareness that valuable expertise and interests in special topics are usually distributed, and are rarely concentrated in a unique site or research group. The objective is the implementation of high quality compendia on specialist biological topics.

The **collaborative annotation of biological databases** leverages the fact that an extended and accurate curation of an ever increasing volume of data is extremely costly and time consuming. The aim is to improve and extend databases curation beyond that which is possible with, typically, a small number of curation staff. It allows users to contribute their expertise, experiences, observations and results independently of the database organization and staff. Users can control this extended curation, correcting and updating the archives in a timely manner. Although contents of the database are collaboratively annotated, databases themselves are left unchanged.

The **collaborative creation of community database** captures emerging structure in rapidly developing fields. These database-wikis are indexes of biologically relevant data that emerge from focused and rapidly developing communities. They form a stopgap between unstructured discussion in fora and on mailing lists and the 'mature' databases that emerge subsequently. They can be useful for discerning trends and promoting best practices, but often, by their nature, collect unique and important information.

TOPICS

The following list is not meant to be exclusive of any further topics as stated above. Submitted contributions should address one or more of the following topics:

Wiki development tools

- Wikimedia
- Wikimedia extensions
- Semantic Wikis
- Wiki-coupled CMSs
- Other wikis

Arising issues for the biomedical domain:

- Authoritativeness of contributions and sites
- Quality assessment
- Users acknowledgement
- Stimulatation of quality contributions
- Authorships management and reward
- 'Scientific production' value for contributions
- Management of bioinformatics data types

Wikis and collaborative systems for:

- Genomics, proteomics, metabolomics, any -omics
- Proteins analysis and visualization
- Gene and proteins interactions
- Metabolic pathways
- Oncology research

Issues to be tackled by wiki and collaborative research for:

- Genomics, proteomics, metabolomics, any -omics
- Proteins analysis and visualization
- Gene and proteins interactions
- Metabolic pathways

INVITED SPEAKERS

- *The Pros and Cons of Wikipedia for Scientists.*
  Alex Bateman, Wellcome Trust Sanger Institute, Hinxton, Cambridge, United Kingdom
- *WikiPathways, community-based curation for biological pathways.*
  Alexander Pico, Gladstone Institute of Cardiovascular Disease, San Francisco, USA
- *The Gene Wiki: Achieving critical mass and mining for novel annotations.*
  Andrew Su, Bioinformatics and Computational Biology, Genomics Institute of the Novartis Research Foundation (GNF), San Diego, USA
- *PDBWiki: success or failure?*
  Dan Bolser, College of Life Sciences, University of Dundee, Scotland, United Kingdom
- *Collaborative publishing with authorship tracking and reputation system - WikiGenes.*
  Robert Hoffmann, Computational Biology Center, cBIO, Memorial Sloan-Kettering Cancer Center, MSKCC, New York, USA

TUTORIALS

- *Everything you wanted to know about Wikipedia but were too afraid to ask.*
  Alex Bateman, Wellcome Trust Sanger Institute, Hinxton, Cambridge, United Kingdom
  Andrew Su, Bioinformatics and Computational Biology, Genomics Institute of the Novartis Research Foundation (GNF), San Diego, USA
- *Semantic MediaWiki: a community database and more.*
  Dan Bolser, College of Life Sciences, University of Dundee, Scotland, United Kingdom
- *Mining biological pathways using WikiPathways web services and more...*
  Thomas Kelder, Department of Bioinformatics (BiGCaT), Maastricht University, the Netherlands
- *How to create your own collaborative publishing project with WikiGenes.*
  Robert Hoffmann, Computational Biology Center, cBIO, Memorial Sloan-Kettering Cancer Center, MSKCC, New York, USA