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(and further members yet to be confirmed)

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Isacc Kohane, Harvard Medical School, Boston, USA

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SUPPORTING INSTITUTES AND SOCIETIES

RNBIO Italian Network for Oncology Bioinformatics

National Cancer Research Institute, Genova, Italy

CNR - Bioinformatics Project - ICT Department

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Collegio Ghislieri, Pavia, Italy

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NETTAB

Network Tools and Applications in Biology

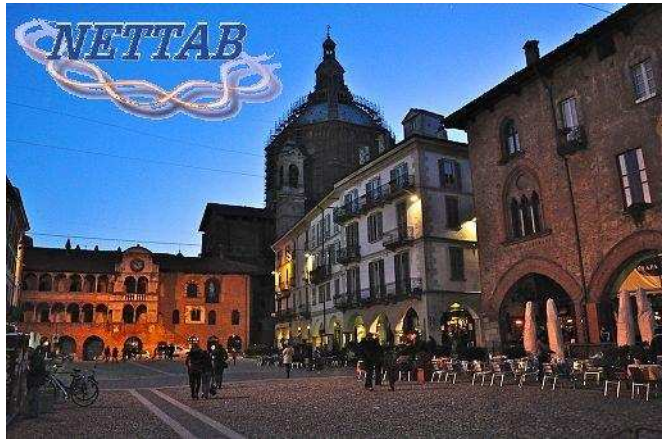
NETTAB 2011

a meeting on

Clinical Bioinformatics

October 12th - 14th, 2011

Pavia, Italy



Call for Papers

http://www.nettab.org/2011/

NETTAB 2011 meeting on Clinical Bioinformatics

RATIONALE

Clinical Bioinformatics, which is focused specifically on applications of bioinformatics innovations within a clinical context, encompasses nearly all areas of biomedical, and clinical research and is characterized by the challenge of integrating molecular and clinical data to accelerate the translation of knowledge discovery to effective treatment as well as customized disease - management and prevention.

Clinical bioinformatics is part of the larger field of translational bioinformatics, which has been defined by the American Medical Informatics Association as the development of storage, analytic, and interpretative methods to optimize the transformation of increasingly voluminous biomedical data - genomic data in particular - into proactive, predictive, preventive, and participatory health management.

In the last few years, new genome sequencing and other high-throughput experimental techniques have generated vast amounts of molecular and clinical data that contain crucial information with the potential of leading to the next major biomedical discoveries. In addition to the scientific challenges, the dimensionality and amount of genomic data sets shows new statistical and technical challenges, like gaining access to the computational power needed to test even simple translational hypotheses using genomic data.

Nowadays, one of the most innovative forces in translational bioinformatics is the public availability of molecular data, which can be used to enable new questions in applied sciences. Public data repositories such as the NCBI Gene Expression Omnibus (GEO), EBI's ArrayExpress enable researchers to face new central translational questions, for example concerning the way to find genes most likely to be up-regulated specifically in cancers rather than in all other human diseases. The high-throughput molecular measurements accessibility brings us closer to fully understand the nature of disease itself and will be able to create novel diagnostics and to discover fundamental causes of disease as targets for therapies.

Moreover, the increasing online availability of the "bibliome", i.e. the biomedical text corpus, made through published manuscripts, abstracts, textual comments and reports, as well as direct-to-web publications, has stimulated the development of new algorithms able to semi-automatically extract knowledge so as to make it available in computable formats. Such algorithms combine the information reported in the text with that contained in biological knowledge repositories and are increasingly used for hypothesis generation or corroboration of clinical findings.

The consistent growth of publicly available data and knowledge sources and the possibility to easily access low-cost, high-throughput molecular technologies has meant that computational technologies and bioinformatics are increasingly central in genomic medicine; cloud computing technology is being recognised as a key technology for the future of genomic research to facilitate large-scale translational research in genomic medicine.

The current major opportunities for clinical bioinformatics are the evolving need to share molecular data and tools and the increasing expectation that clinicians should be able to synthesize and interpret new discoveries in molecular medicine for their patients' benefit; these perspectives require computational advances in order to fill the gaps between genetics discoveries and clinical practice, as well as infrastructures that enable translational bioinformatics research.

NETTAB 2011 is aimed at presenting the methods, tools and infrastructures that are nowadays available in clinical bioinformatics and will also show some of the most interesting applications in this field.

TOPICS

METHODS AND TECHNOLOGIES

- DATA WAREHOUSE
- NATURAL LANGUAGE PROCESSING
- DATA MINING
- ONTOLOGIES, INTEROPERABILITY, STANDARDISATION
- SEARCH COMPUTING
- DECISION SUPPORT

TOOLS

- ICT ARCHITECTURES TO SUPPORT CLINICAL RESEARCH
- BIOBANKS
- SOFTWARE FOR NEXT GENERATION SEQUENCING DATA MANAGEMENT AND STORAGE

APPLICATIONS

- RISK ASSESSMENT
- DIAGNOSIS
- THERAPY PLANNING
- DRUG DESIGN

Dipartimento di Informatica e Sistemistica,
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TUTORIAL AND SPECIAL SESSION

- DATA WAREHOUSE
- NATURAL LANGUAGE PROCESSING
- SEARCH COMPUTING
- INTEROPERABILITY

CALL DEADLINES

Oral presentations due: July 15, 2011

Notification to authors: September 2, 2011

Posters and position papers due: September 5, 2011

Early registration: September 15, 2011

TYPE OF CONTRIBUTIONS

Oral communications/ Posters/ Software demos

INSTRUCTIONS

Submit your contribution through the EasyChair system at:
http://www.easychair.org/conferences/?conf=nettab2011
Contributions format. Font type: Times New Roman; font size: 12 pti; page size: A4; left and right margins: 2.0 cm; upper margin: 2.5 cm; lower margin: 2.0 cm.
The length of *contributions for oral communications* should be between 3 and 5 pages, including tables and figures; they should include: Abstract, Introduction, Methods, Results and Discussion, References. All contributions for oral communications will be evaluated by at least three referees.
The length of *contributions for posters* should be no more then 3 pages, including tables and figures. They should include: Introduction, Methods, Results, References. All posters will be evaluated on the basis of their relevance for the workshop's topics only.

For any further information or clarification, please contact the organization by email at *info@nettab.org* .

PROCEEDINGS - BMC BIOINFORMATICS SUPPLEMENT

All accepted contributions will be published in the proceedings of the workshop. Extended and revised versions of selected contributions will be published in a Supplement of **BMC Bioinformatics**. To this aim, a special Call for papers, limited to contributions submitted to the NETTAB 2011 workshop, will be launched around end of October 2011.

Laboratory for Bio-Medical Informatics, Pavia, Italy