

Focus on:

**Technologies, Tools and Applications for
Collaborative and Social
Bioinformatics Research and Development**

Special session on:

**Methods and Tools for
RNA Structure and Functional Analysis**

10 - 13 June 2009

**Computer Science Department
University of Catania, Sicily, Italy**

Presentation of the NETTAB 2009 Workshop



Motivations

Advent of Wide Area Networks (WAN) allowed the availability of **distributed information** (Network Information Retrieval tools, NIR) and the development of unprecedented communications between users (**Computer Mediated Communication tools, CMC**).

Initially, CMC was **asynchronous** and based on electronic **mail** and newsgroups. From email, mailing lists and newsletter were soon derived, while newsgroups generated, shortly after, electronic **fora**.

Synchronous communication were introduced through the set up of **chat services**. On this line, current multimedia **teleconference** systems were then set up.

Virtual reality was first introduced for educational purposes by MUD (Multi-users Domain) systems, and especially by MOO (MUD Object-oriented). This line produced current virtual reality environment, like the emerging Second Life system.

Motivations

Life Sciences researchers largely took profit from CMC tools.

The [bionet newsgroups hierarchy](#) remains one of the most famous and useful CMC system supporting life science research. Many mailing lists that were born in that context are still used.

The development of [open source software](#) was largely made possible by the possibility of exchanging, in an effective way, knowledge, practices and skills.

[Web sites of communities of scientistis](#) were set up and often constituted the base for a real collaborative development and research.

Motivations

The most recent developments of collaborative development tools are impressive.

Researchers can now collaboratively develop software (open source systems), discuss and compare development strategies (social networks), write documents (google docs), build knowledge bases.

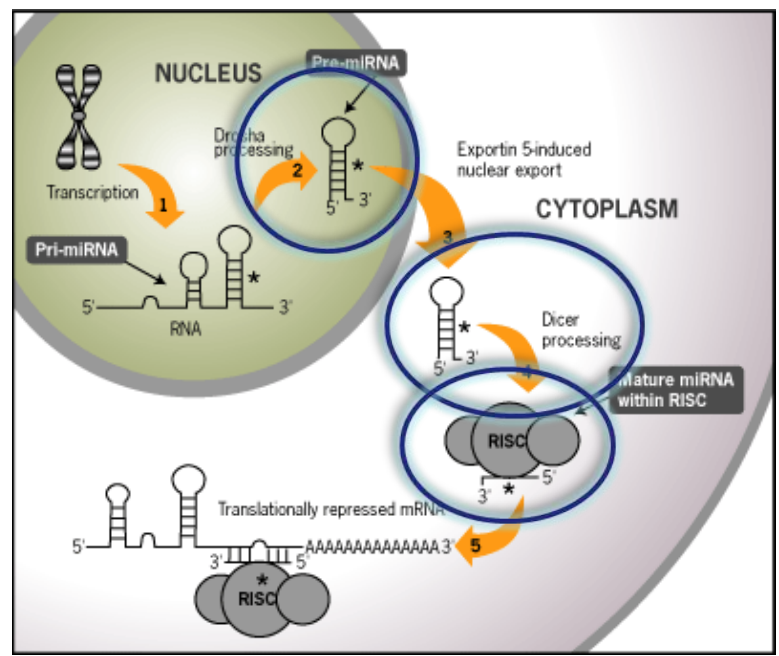
So, it may now be the time for presenting technologies, tools and applications for collaborative work and for discussing perspectives of their utilization in support of Bioinformatics.

For these reasons, NETTAB 2009 will be devoted to

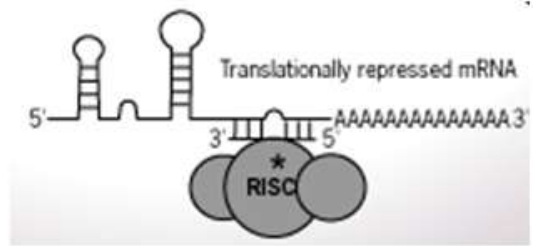
"Technologies, Tools and Applications for Collaborative and Social Bioinformatics Research and Development".

Moreover, there will be a special session on **"Methods and Tools for RNA Structure and Functional Analysis"**

microRNAs (miRNAs)



- Small non-coding RNAs.
- Derived from longer dsRNAs called pre-miRNAs.
- Processed by Dicer in the cytoplasm.
- Mature miRNA on one strand of pre-miRNA.
- Mature miRNA is incorporated into RISC.
- They act as regulators of gene expression through degradation of specific mRNAs and/or repression of their translation.



microRNA

miRNAs are small non coding RNAs responsible of post transcriptional gene silencing

They are involved in both physiological and pathological processes (Development Apoptosis, Cell differentiation, Cancer, Cardiac pathologies, Neurodegeneration)

Computational tools:

- **Databases of miRNAs and targets:** miRBase, miRNAmap, TarBase, ..
- **Identification of miRNA genes:** MiRScan, ProMir, RNAMicro, MiMatcher, ..
- **miRNA target prediction:** TargetScan, PicTar, miRanda, RNAhybrid, miTarget, ..
- **Synthetic siRNA design:** siDirect, SiRNA at Whitehead, BLOCK-iT RNAi Designer, RNAi design, ..

Needs to Understand Tools

Briefings in Bioinformatics is an international forum for researchers and educators in the life sciences. The journal publishes reviews for the users of databases and analytical tools of contemporary genetics and molecular biology and is unique in providing practical help and guidance to the non-specialist

A screenshot of the Oxford Journals website for Briefings in Bioinformatics. The top navigation bar includes "OXFORD JOURNALS", "CONTACT US", "MY BASKET", and "MY ACCOUNT". The main header area features the journal title "Briefings in Bioinformatics" in white text on a blue background, with a smaller version of the title below it. Below the header is a secondary navigation bar with links for "ABOUT THIS JOURNAL", "CONTACT THIS JOURNAL", "SUBSCRIPTIONS", "CURRENT ISSUE", "ARCHIVE", and "SEARCH". A user login section shows "Institution: Universita' degli Studi di Catania" and "Sign In as Personal Subscriber".

[Oxford Journals](#) > [Life Sciences & Mathematics & Physical Sciences](#) > [Briefings in Bioinformatics](#) > [Search](#) > Results

**Briefings in Bioinformatics Special Issue:
COMPUTATIONAL PROTEOMICS**

Impact Factor 24,370

June 11-13, 2009 - Catania, Italy



ADDITIONAL PAPER:

Peter Bengert and Thomas Dandekar

Current efforts in the analysis of RNAi and RNAi target genes

Brief Bioinform, 2005; 6: 72 - 85.

▶UTR (untranslated region) of the mRNA. **microRNAs** (miRNAs) are short RNAs acting as natural...UTR (untranslated region) of the mRNA. **microRNAs** (miRNAs) are short RNAs acting as natural...Support, Non-U.S. Gov't | Review | 0 **MicroRNAs** | Animals | Gene Expression Profiling.....

Irmtraud M. Meyer

A practical guide to the art of RNA gene prediction

Brief Bioinform, November 2007; 8: 396 - 414.

▶degraded or prevented from being translated. **MicroRNAs** were first detected in the nematode *Caenorhabditis...* BJ, Weinstein EG, Rhoades MW, et al. **MicroRNAs** in plants. *Gene Dev* (2002) 13:1616-26...Jones-Rhoades MW, Bartel DP, Bartel B. **MicroRNAs** and their regulatory roles in plants.....

Alain Laederach

Informatics challenges in structured RNA

Brief Bioinform, September 2007; 8: 294 - 303.

▶and down-regulate the associated gene. **MicroRNAs** (miRNAs) are naturally occurring hairpin...Detection of the argonaute protein Ago2 and **microRNAs** in the RNA induced silencing complex...et al. Computational identification of **microRNAs** and their targets. *Comput Biol Chem*.....

Edgar Wingender

The TRANSFAC project as an example of framework technology that supports the analysis of genomic regulation

Brief Bioinform, Advance Access published on April 24, 2008; doi:

doi:10.1093/bib/bbn016

▶was more recently included into the TRANSFAC concept were **microRNAs** (since release 10.4, December 2006). These data are required...*Nucleic Acids Res* (2006) 34:D108-10. 17 Mendell JT. **MicroRNAs**: critical regulators of development, cellular physiology and.....

Ravi Sachidanandam

RNAi as a bioinformatics consumer

Brief Bioinform, 2005; 6: 146 - 162.

▶Harbor Laboratory, NY 11724, USA. sachidan@cshl.org | Journal Article | Review | 0 **MicroRNAs** | Computational Biology methods | Gene Targeting methods | **MicroRNAs** chemistry genetics | Oligonucleotide Array Sequence Analysis methods | RNA Interference.....

Gary B. Fogel

Computational intelligence approaches for pattern discovery in biological systems

Brief Bioinform, Advance Access published on May 5, 2008; doi:

doi:10.1093/bib/bbn021

▶Connect tools) and a history of expertise for problem solving in bioinformatics, including pattern recognition for novel **microRNAs** and biomarkers for cancer diagnosis. Other application areas CI is being used in a wide variety of other bioinformatics.....



Topics (preliminary)

Collaborative Web sites (bioinformatics.org, biojava, bioperl, ...)

Communities of Practices (CoPs)

- Scientific practices in scientific communities

- Automatic detection / gathering / modelling of scientific practices

- Implementations of CoPs

Social networking (myExperiment, Annotea, myScience)

- Social Bookmarking

- Semantic Document Markup

- Relationships mining from literature

Open Source development

- Sharing of data models, libraries, interfaces



Topics (preliminary)

Social software for collaborative documentation development

Wikis, blogs, google docs

Knowledge Wikis

Social-software-mediated collaborative scientific research

Social-software-mediated collaborative tools' development

Knowledge base collaborative development

Ontologies collaborative development

Education and training tools

E-learning

Virtual environments



Topics (preliminary)

Methods and Tools for RNA Structure and Functional Analysis

Databases of miRNAs and targets

Identification of miRNA genes

miRNA target prediction

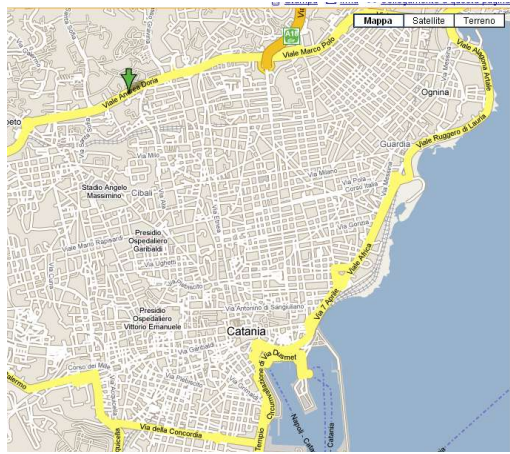
Synthetic siRNA design

Department of Computer Science, Catania,



Research Groups

- 2. Data Mining and Bioinformatics
- 3. Cryptography and Security
- 4. Imaging and Multimedia
- 5. Distributed Systems
- 6. Artificial Intelligence
- 7. Logic and Algorithms



- **Workshop Chairs**

- Paolo Romano, IST - Genoa, Italy
- Alfredo Ferro, University of Catania, Italy
- Rosalba Giugno, University of Catania, Italy
- Alfredo Pulvirenti, University of Catania, Italy
-

- **Organizing Chairs**

- Paolo Romano, IST - Genoa, Italy
- Alfredo Ferro, University of Catania, Italy
- Rosalba Giugno, University of Catania, Italy
- Alfredo Pulvirenti, University of Catania, Italy
- Alessandro Lagana', University of Catania, Italy

- **Scientific Committee**

- Under definition
(if interested, propose your name!)


Foreseen deadlines

- November 10, 2008: Call for papers launched
- March 27, 2009: Oral communication submission
+ Acceptation communication: April 20, 2009
+ Final version available: May 8, 2009
- April 23, 2009: Posters submission
- May 8, 2009: Early registration
- June 10-13, 2009: Tutorials and Workshop



Summer School


Lipari International School 2008 Edition - Microsoft Internet Explorer

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Lipari International School

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Computer Science **Bioinformatics and Computational Biology**

<http://lipari.cs.unict.it/LipariSchool/>

Operazione completata Internet

Summer School 13-20 June, 2009:

RNA: Structure, Function and Therapy

SPEAKERS

Dr. Oliver Hobert, Howard Hughes Medical Institute Department of Biochemistry and Molecular Biophysics, Columbia University Medical Center, New York, USA

Chris Sander, Computational Biology Center, Sander Research Lab Memorial Sloan-Kettering Cancer Center, New York, USA

Peter Stadler, Institut für Informatik, Universität Leipzig Germany

TUTORIALS:

M. Levitt: Methods for Structural Alignment, Stanford University, USA

Matteo Comin: RNA-protein interaction, University of Padova, Italy

A. Pulvirenti: Algorithms for Sequence Alignment, University of Catania, Italy

R. Giancarlo: Alignment-free distances, University of Palermo, Italy

Knut Reinert: SeqAn: An efficient, generic C++ library for sequence analysis, Institut für Informatik, Fachbereich Mathematik und Informatik, Freie Universität Berlin

Christine Heitsch: RNA structure prediction Berkeley University, School of Mathematics Georgia Institute of Technology, Atlanta, USA

Doron Betel: Non coding RNAs, Memorial Sloan-Kettering Cancer Center, New York, USA

Alessandro Laganà: Tools for miRNA genes and target prediction, University of Catania, Italy

Summer School 2008: Biological Networks: Evolution, Interaction and Computation --June 14 - June 21, Lipari Island, 2008

Lectures

Making Viruses, in Vivo and in Vitro
Bill Gelbart, UCLA, Los Angeles, California, USA

Biomolecular Network Evolution
Sarah Teichmann, MRC Laboratory of Molecular Biology, Cambridge, UK

Phylogenetic Networks
Gabriel Valiente, Technical University of Catalonia, Barcelona, Spain

Comparative Analysis of Protein Networks
Roded Sharan, Tel Aviv University, Tel Aviv, Israel

Tutorials by

Michael Levitt, Jon Widom, Concettina Guerra, Alfredo Pulvirenti, Raffaele Giancarlo, Rosalba Giugno

Summer School 2008: Algorithms: Science and Engineering July 13 - 26, 2008, Lipari Island

Lectures by

Catherine McGeoch, Kurth Melhorn, Giovanni Manzini, Susanne Albers, Silvio Micali, Giuseppe F. Italiano, Martin Tompa, Anna Tramontano, Luca Trevisan, Cliff Stein

<http://lipari.cs.unict.it/LipariSchool/Bio>

We are looking forward to meeting you at NETTAB 2009 in Catania!

Paolo Romano, Alfredo Ferro,
Rosalba Giugno, Alfredo Pulvirenti

<http://www.nettab.org/2009/>
info2009@nettab.org

