



BioinfoGRID Symposium 2007

Bioinformatics Grid Application for life science



10-13 December 2007, Milano, Italy

Monday
10 Dec 07

09:00-09:30

Registration

LITA, CNR-ITB, Via Fratelli Cervi 93
20090 Segrate, Milano, Italy

09.15-09.30

Welcome

Alberto Albertini, Director CNR-ITB, Italy

09:30-12:30

LITBIO – Laboratory for Interdisciplinary Technology in Bioinformatics - project

09:30-09:50

Overview of the LITBIO Project

Luciano Milanese, CNR-ITB, Italy

09:50-10:10

Development of prognostic signatures using large data sets

Ulrich Pfeffer, IST Genova, Italy

10:10-10:30

Hardware development for biotech applications

Pierfrancesco Zuccato, Exadron Eurotech

10:30-10:50

Orion Framework for systems biology applications

Emanuela Merelli, Ezio Bartocci, Nicola Cannata, Flavio Corradini, Luca Tesei, Università di Camerino, Italy

10:50-11:10

Coffee Break

11:10-11:30

HPC infrastructure for life science applications

Claudio Arlandini, CILEA, Italy

11:30-11:50

A methodology for the automation of in-silico data analysis processes

Paolo Romano, IST, Genova, Italy

11:50-12:10

Workflow applications in Bioinformatics

Ivan Porro, Francesco Beltrame, DIST, Genova, Italy

12:10-12:30

A web based image processing tool for the study cell movement and other applications running in a parallel environment,

Giovanni Paoletta, Università di Napoli, Italy

12:30-14:00

Lunch *

14:00-17:00

Bioinformatics Related Projects: applications for Life Science

14:00-14:20

Welcome

14:20-14:40

Bioinformatics strategies for functional annotation of deep sequencing data.

Alessandro Guffanti, Michele Iacono, Giorgio Corti, Raoul Bonnal, Ermanno Rizzi, Ivan Merelli, Lizeta Gjanci, Luciano Milanese, Gianluca de Bellis, ITB-CNR, Milano, Marco Pirola, CILEA, Segrate, Milano, Italy

14:40-15:00

Bioinformatics applications for promoter regions and transcription start site detection

Chanchal Mitra, University of Hyderabad, India

15:00-15:20

Grid-based Data Mining: Services for Data Analysis Applications

Domenico Talia, DEIS-University of Calabria, Italy

15:20-15:40

Coffee Break

15:40-16:00

An Agent-Based Environment for Web Service Enabled E-Science

MariaGrazia Fugini, Francesco Amigoni, Politecnico di Milano, Italy

16:00-16:20

Cardioworkbench EU Project

Carmelina Ruggero, DIST- Università di Genova, Italy

16:20-16:40

Pattern discovery in discrete structures, with applications to Bioinformatics

Raffaele Giancarlo, Università di Palermo, Italy

16:40-17:00

Neuroweb: Integration and sharing of information and knowledge in neurology and neurosciences

G. Mauri, Università di Milano-Bicocca, F. Sicurello, AITIM e Regione Lombardia, Italy

17:00-17:20

A Grid Portal Framework for e-Science Grid Infrastructures

Livia Torterolo, NICE srl, DIST UniGe, Maurizio Melato, Nicola Venuti, NICE srl

17:20-17:40

Multi-Relational Data Mining for pattern discovery in mitochondrial UTRs

Antonio Turi, Università di Bari, Giorgio Grillo, CNR-ITB, Donato Malerba, Università di Bari, Domenica D'Elia, CNR-ITB, Bari, Italy



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Bioinformatics Grid Applications for Life Science

09:30-09:50

BioinfoGRID project introduction

Luciano Milanesi, CNR-ITB, Italy

09:50-10:10

Multiple sequence alignments in a grid environment

Sandor Suhai, DKFZ, Martin Senger, STC, Germany

10:10-10:30

Transcriptomics and phylogenetics applications in grid

Pietro Liò, University of Cambridge, UK

10:30-10:50

D-Chip performance evaluation in grid

Ivan Porro, DIST- Università di Genova, Italy

10:50-11:10

Coffee Break

11:10-11:30

Database and applications in grid

Gabriele Trombetti, Ivan Merelli, Alessandro Orro, Luciano Milanesi, CNR-ITB, Italy

11:30-11:50

Comparative evaluation of tools providing access to different types of data resources exposed on the grid

Giacinto Donvito, Giorgio Maggi, INFN, Italy

11:50-12:10

Gene Analogue Finder

Andreas Gisel, Giulia Di Sario CNR-ITB; Angelica Tulipano, Giacinto Donvito, Giorgio Maggi, INFN, Italy

12:10-12:30

Systems Biology applications in grid

Roberta Alfieri, Ettore Mosca, Ivan Merelli, Luciano Milanesi, CNR-ITB, Italy

12:30-14:00

Lunch *

14:00-17:00

Grid-enabled Drug Discovery

14:00-14:20

Database federation for epidemiological data collection

Vincent Breton, CNRS-IN2P3, France

14:20-14:40

Joint deployments on desktop grids and e-infrastructures

Nicolas Jacq, CNRS-IN2P3, France

14:40-15:00

WISDOM new production environment

Vincent Bloch, CNRS-IN2P3, France

15:00-15:20

Molecular Dynamics in WISDOM

Giulio Rastelli, Gianluca Degliesposti, Università di Modena, Italy

15:20-15:40

Coffee Break

15:40-16:00

WISDOM-I data challenge on malaria: status of biochemical analysis

Ana Da Costa, CNRS-IN2P3, France

16:00-16:20

WISDOM-II Data challenges on malaria: status of biochemical analysis

Vinod Kasam, SCAI Fraunhofer, Germany

16:20-16:40

Grid docking simulations for comparative ligand binding of neuraminidase

P. D'Ursi, F. Chiappori, P. Cozzi, E. Salvi, I. Merelli, E. Roviada, L. Milanesi, CNR-ITB, Italy

16:40-17:00

e-Science for e-Scientists: the OMII-Europe model for sharing resources

Steve Brewer, University of Southampton UK, OMII-Europe

17:00-17:20

Data challenges on Avian Flu: status

Hung-Chun Lee, Academia Sinica, Taiwan

17:20-17:40

Discussion:

New deployments

How to join WISDOM

* Please note that meals are not provided, but there is a bar/canteen on the 1st Floor



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Enabling Grids for E-science

EGEE Bioinformatics Meeting #6

Christophe Blanchet and Luciano Milanese

09:30-10:10

The EGEE Bioinformatics activity

Christophe Blanchet, CNRS-IBCP, France

10:10-10:30

Grid methods for stability analysis of biomarkers

Cesare Furlanello, Fondazione Bruno Kessler, Italy

10:30-10:50

Genome Wide Association Studies of human complex diseases with EGEE

Alexandru Ionut Munteanu Inserm, France

10:50-11:10

Coffee Break

11:10-11:30

Protein structure prediction within the EUChinaGRID framework

Fabio Politicelli, Università Roma3, Italy

11:30-11:50

Bioinformatics Experiences at University Magna Graecia of Catanzaro

Mario Cannataro, Pietro H. Guzzi, Giuseppe Tradigo, Pierangelo Veltri, Università Magna Graecia di Catanzaro, Italy

11:50-12:10

The LIBI Problem Solving Environment

Maria Mirto Università di Salento, Italy

12:10-12:30

Mapping "conserved sequence tags" among human genome and a number of vertebrate genome assemblies

Tiziana Castrignanò, CASPUR, Italy

12:30-14:00

Lunch *

14:00-17:00

EGEE Bioinformatics Meeting #6

14:00-14:40

Large scale genome comparison in a GRID infrastructure

Rita Casadio, Università di Bologna, Italy

14:40-15:00

Grid Solving a Bioinformatics Challenge : a First Step to Anchoring the Nucleosome

Christophe Blanchet, CNRS-IBCP, France

15:00-15:20

Metagenomic experiment in EGEE

Ignacio Blanquer Universidad Politecnica de Valencia, Spain

15:20-15:40

Coffee Break

15:40-15:55

Bioinformatic Research in the PI2S2 Project of the Consorzio COMETA

Santo Motta, Università di Catania, Italy

15:55-16:10

The ImmunoGrid Project: Simulating Immune response on the Grid.

Santo Motta, Università di Catania, Italy

16:10-16:30

Enhanced sampling algorithms for protein folding on the EU-IndiaGrid infrastructure

Riccardo di Meo, EU-IndiaGrid/ICTP, **Fabio Pietrucci**, Sissa, **Stefano Cozzini**, EU-IndiaGrid, Italy

16:30-16:50

Blood flow and thrombosis modeling in large arteries

Nenad Filipovic, Milos Kojic, University of Kragujevac, SERBIA, (SEE-GRID-2 Project) and Harvard University, USA, Milos Ivanovic, University of Kragujevac, SERBIA, (SEE-GRID-2 Project) and Akira Tsuda, Harvard University, USA

16:50-17:20

Discussion

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CNR-Bioinformatics: ICT applications for Bioinformatics

09:30-09:50

BATS: A Bayesian User-Friendly software for analyzing time series microarray data

Claudia Angelini, CNR-IAC, Luisa Cutillo, TIGEM, Daniela De Canditiis, CNR-IAC, Margherita Mutarelli, Seconda Università di Napoli, Marianna Pensky, University of Central Florida.

09:50-10:10

Soft topographic maps for clustering and classifying bacteria using housekeeping genes

M. La Rosa, **G. Di Fatta**, **S. Gaglio**, **R. Rizzo**, **A. Urso**, CNR-ICAR, Italy

10:10-10:30

Feature selection techniques for gene expression data analysis

Mario Guarracino, Davide Feminiano, Salvatore Cuciniello, ICAR-CNR, Italy, Francesca Del Vecchio Blanco, Università Federico II di Napoli, Italy

10:30-10:50

Grid-based imaging processing and visualisation for biomedical applications

Andrea Clematis, Daniele D'Agostino, CNR-IMATI, Italy

10:50-11:10

Coffee Break

11:10-11:30

Electronic patient record: distributed clinical data

Fabrizio L. Ricci, Mariangela Contenti, Luca D. Serbanati, CNR-ITB, Italy

11:30-11:50

Gene selection in microarray experiments through unproper ROC curves

Marco Muselli, CNR-IEIIT, Italy, Stefano Parodi, Vito Pistoia

11:50-12:10

Virtual screening based on molecular dynamics

Giorgio Colombo, CNR-ICRM, Italy

12:10-12:30

Dynamics of gene regulatory networks: towards a computational framework for qualitative simulation

Liliana Ironi, Luigi Panzeri, CNR-IMATI, Italy

12:30-14:00

Lunch *

14:00-17:00

CNR-Bioinformatics: ICT applications for Bioinformatics

14:00-14:20

Mathematical methods for the analysis of the barcode of life

Paola Bertolazzi, Giovanni Felici CNR-IASI, Italy

14:20-14:40

FPF-SB: a Scalable Algorithm for Microarray Gene Expression Data Clustering

Mauro Leoncini, Manuela Montangero, University of Modena and Reggio Emilia, Italy

14:40-15:00

The application of Blind Source Separation techniques to some bioinformatics problems

Anna Tonnazzini, CNR-ISTI, Italy

15:00-15:20

Mathematical models for intracellular signal transduction

E. Bersani, **A. Cangiani**, CNR-IAC & CNR-ISMAL, **R. Natalini**, **A. Serafini** CNR-IAC, Italy

15:20-15:40

Coffee Break

15:40-16:00

Bioinformatics and computational studies on protein structure for the investigation of pathological states.

Angelo Facchiano, CNR-ISA, Italy

16:00-16:20

Web Based Applications for creating, handling and integrating biological data bases: Some Results

Antonio d'Acierno, CNR-ISA, Italy

16:20-16:40

Modelling, analysis and classification of 3D shapes derived from molecular structures

M. Spagnuolo, **F. Giannini**, **M. Attene**, **S. Biasotti**, **C. Catalano**, **G. Patané**, **S. Marini**, **D. Giorgi**, **F. Robbiano**, **M. Mortara**, **R. Albertoni**, **B. Falcidieno**, CNR-IMATI, Italy

16:40-17:00

Integrated architectural solutions for Bioinformatics and Computational Biology: an innovative proposal

Roberto Vaccaro, CNR-ICAR, Italy

17:00-17:20

Supporting the Bioinformatics Community in the OpenAdap.net framework
Francesco Masulli, University of Genova, **Alessandro E.P. Villa** and **Javier Iglesias**, Inserm, University Joseph Fourier, Grenoble, France and University of Lausanne, Switzerland

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