



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 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
- 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



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	09:30-12:30	Bioinformatics Grid Applications for Life Science
	09:30-09:50	BioinfoGRID project introduction Luciano Milanese, 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 Milanese, 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 Milanese, 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. Milanese, 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 Hurng-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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Thursday
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09:00-09:30 **Registration**

09:30-12:30 **CNR-Bioinformatics: ICT applications for Bioinformatics**

09:30-09:50 Bioinformatics and computational studies on protein structure for the investigation of pathological states.

Angelo Facchiano, CNR-ISA, Italy

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

Marco Pellegrini, M. Elena Renda, CNR-IIT, Italy

14:40-15:00 Application and automation of molecular docking protocols for ligand-receptor studies

Ermanna Rovida, Pasqualina D'Ursi, Erika Salvi, Jacopo Negrone, Luciano Milanese, CNR-ITB, Italy

15:00-15:20 Partial differential models of Ran cycle

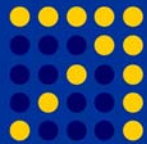
E. Bersani, A. Cangiani, CNR-IAC & CNR-ISMAL, R. Natalini, A. Serafini CNR-IAC, Italy

15:20-15:40 **Coffee Break***

15:40-16:00 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.

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- 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 The application of Blind Source Separation techniques to some bioinformatics problems
Anna Tonnazzini, CNR-ISTI, Italy