Overview

BITS 2010 aims at:

- presenting some of the most recent and interesting bioinformatics achievements at international level
- presenting a landscape of Italian bioinformatics research
- allowing young researchers to present their work in a collaborative and supporting atmosphere
- training young researchers on the most innovative tools, technologies and methods in the field
- allowing for as much discussion as possible

The conference includes:

- 4 keynote lectures
- 21 oral communications
- 3 Poster Sessions (77 posters presentations). Instructions for poster presentation.
- 2 tutorials

The conference is also meant to build a friendly atmosphere among participants, enabling a better reciprocal knowledge. It will therefore also include the following social events:

- welcome party
- guided tour & gala dinner

The gala dinner will take place at conclusion of the guided tour guided tour in Trani, one of the most beautiful town of the Apulia region with many typical examples of roman-apulian architecture. More information about the guided tour will be soon available in this page.
Scientific sessions and the BITS General Assembly will be hosted at Centro Congressi Domina Hotel & Conference Bari – Palace (see Conference venue).

Tutorials will be held at the Department of Computer Science, University Campus, Bari.

Program
Wednesday, April 14, 2010

Satellite event – Tutorials

Location: Department of Computer Science, University Campus, Bari
08:00 - 08:45  Registration

08:45 - 10:30  **Tutorial 1, Saverio Vicario**, Phylogenetic analysis based on mixed models performed on the LIBI platform powered by HPC facilities (Lecture and hands-on session)

10:30 - 10:45  Break (free)

10:45 - 12:30  **Tutorial 2, Monica Santamaria**, Metagenomics and metadata analysis (Lecture and hands-on session)

**BITS Conference**

**Location:** Domina Hotel & Conference Bari - Palace
13:30 - 14:00  Registration

Opening Lectures

14:00 - 14:30  Commemoration of Prof. Giuliano Preparata 10 years after he passed away
Dott.ssa Emilia Campochiaro, Fondazione "Giuliano Preparata
Prof. Luigi Nitti, Dipartimento di Biochimica Medica, Biologia Medica e Fisica Medica, Università degli Studi di Bari

14:30 - 15:15  Preparata Lecture, Prof. Cecilia Saccone “The mitochondrial genome: an evolutionary puzzle”

15:15 - 16:15  Scientific Session 1
Chair Prof. Cecilia Saccone

MOLECULAR EVOLUTION AND COMPARATIVE GENOMICS
15:15 - 15:35  Evolution of protein interaction network properties of cancer genes  
*D’Antonio M, Ciccarelli FD*

15:35 - 15:55  Genes involved in vitamin D pathway and schizophrenia show signature of latitude-dependent adaptation  
*Amato R, Pinelli M, Monticelli A, Miele G, Cocozza S*

15:55 - 16:15  Exploring the evolution of coding sequences in metazoan mtDNAs: effects of mutation and selection in Insects and Vertebrates  
*Castellana S, Vicario S, Donvito G, Saccone C*

16:15 - 17:15  Coffee break & **Poster Session 1**

17:15 - 20.15  BITS General Assembly

20:15 - 20.30  “BITS 2011” proposals - candidates’ presentation
20:30 - 22.30  Welcome Party

Thursday, April 15, 2010

09:00 - 10:00  Invited Lecture, *Prof. Edward N. Trifonov* “The chromatin code is cracked. Sequence pattern recognized by histone octamers”

10:00 - 11:00  **Scientific Session 2**  
*Chair: Prof. Graziano Pesole*  
**GENOMICS**

10:00 - 10:20  Enhanced Reference Guided Assembly  
*Vezzi F, Policriti A, Cattonaro F*

10:20 - 10:40  Finding new genes for non-syndromic hearing loss through an in silico prioritization study  
10:40 - 11:00  Inter and intra species comparative analyses of RHNumtS sequences  

11:00 - 12:00  Coffee Break & Poster Session 2

12:00 - 13:00  Scientific Session 3  
Chair: Prof. Giorgio Valle

GENOMICS

12:00 - 12:20  Functional and structural annotation of human protein variants originated from alternative splicing in human  

TRANSCRIPTOMICS

12:20 - 12:40  Large scale detection and analysis of RNA editing in grape mtDNA by RNA deep-sequencing  
Picardi E, Horner DS, Chiara M, Schiavon R, Valle G, Pesole G

12:40 - 13:00  Analysis of transcriptional and post-transcriptional regulatory networks
13:00 - 14:30  Lunch

14:30 - 15:30  Scientific Session 4  
Chair: Prof. Uberto Pozzoli

TRANSCRIPTOMICS

14:30 - 14:50  AMDA 2.10, an automated cross-platform pipeline for Affymetrix and illumina data analysis  

PROTEOMICS

14:50 - 15:10  An Optimized Data Structure For High-Throughput 3D Proteomics Data: mzRTree  
*Nasso S, Silvestri F, Tisiot F, Di Camillo B, Pietracaprina A, Toffolo GM*

PROTEIN STRUCTURE AND FUNCTION
15:10 - 15:30  Ranking C alpha traces with Neural Network Pairwise Interaction Fields
Martin AJM, Pollastri G, Tosatto S

16:00  Guided tour & Social Dinner

Friday, April 16, 2010

09:00 - 10:00  Invited Lecture, Paula F. Campos “Hunting the molecular past”

10:00 - 10:40  Scientific Session 5
Chair: Prof. Manuela Helmer-Citterich

PROTEIN STRUCTURE AND FUNCTION
10:00 - 10:20 Phosphate-binding sites identification in unbound protein structures
Parca L, Gherardini PF, Helmer-Citterich M, Ausiello G

10:20 - 10:40 A novel indicator for distinguishing biologically relevant interfaces from crystal contacts
Capitani G., Schaerer MA, Gruetter MG

10:40 - 11:40 Coffee Break & Poster Session 3

12:40 - 13:40 Scientific Session 6
Chair: Prof. Alberto Policriti

NEW TOOLS FOR NEXT GENERATION SEQUENCING

11:40 - 12:40 Invited Lecture, Prof. Erik Bongcam-Rudloff “The impact of Next Generation Sequencing technology on Bioinformatics”

12:40 - 13:00 De novo assembly combining SOLiD mate-pair and 454 data

13:00 - 13:20 Complete and comparative analysis of algorithms for whole genome shotgun assembly
Finotello F, Peruzzo D, Lavezzo E, Di Camillo B, Toffolo GM, Cobelli C, Toppo S
13:20 - 13:40  Sequence analysis of deep sequencing data of viroid-derived small RNAs in plants
Tulipano A, Navarro B, Di Serio F, Flores R, Gisel A

13:40 - 15:00  Lunch

15:00 - 16:20  Scientific Session 7
Chair: Prof. Marcella Attimonelli

SYSTEMS BIOLOGY

15:00 - 15:20  The role of incoherent microRNA-mediated feedforward loops in noise buffering
Osella M, Bosia C, Corà D, Caselle M

BIOLOGICAL DATABASES AND BIOBANKS

15:20 - 15:40  Quality checking of data in biomolecular databases
Ghisalberti G, Masseroli M, Tettamanti L

15:40 - 16:00  The miRò project: towards a unified resource for miRNA research
16:00 - 16:20  Social Database for Biodiversity  

16:20 - 16:30  Concluding remarks

**Poster Sessions**  
Wednesday, April 14, 2010

16:15 - 17:15  **Poster Session 1**
MOLECULAR EVOLUTION AND COMPARATIVE GENOMICS

Code

Title

Authors

PS1_1

A Bioinformatic Workflow for Grapevine Viral Diseases Analysis with Reference to Grapevine Leafroll

Balech B et al.

PS1_2

Efficient computation of a geodesic distance approximation in phylogenetic tree space
Battagliero S

et al.

PS1_3

Molecular Biodiversity of the ferritin protein family

Di Micco P et al.

PS1_4

COSRaptor: a software for large-scale COS identification and polymorphic microsatellite in several plant species

Grillo G et al.

PS1_5

Towards Mobilome Inference in Yeast Genomes

Mencon G et al.
PS1_6

An effective Workflow for automated comparative analysis

Miele M et al.

PS1_7

Utility of Citochrome Oxidase I (COI) DNA Barcode in generating robust molecular criteria for fish species identification

Pappalardo AM et al.

PS1_8

Prospects of barcoding the Italian wild dendroflora: lights and shadows

Piredda R et al.

PS1_9
Pathogen-driven selection and human genetic variability: the case of protozoa

Pozzoli U et al.

PS1_10

Linking the tomato and the potato genomes: the comparative season is now opened

Traini A et al.
GENOMICS

Code

Title

Authors

PS1_11
Generation of SNPs in eggplant (Solanum melongena L.)

Barchi L et al.

PS1_12

SNP array data and quantitative determination of cell fraction bearing Copy Neutral-LOH regions in tumoral samples

Capizzi C et al.

PS1_13

Renewing bioinformatics workflow system by using a Web 2.0 approach

Colella R et al.

PS1_14

Challenging an ensemble approach (GENTES) with the Gene-Environment iNteraction Simulator (GENS)

D’Andrea D
et al.

PS1_15

Revealing the chromosome organization of the emerging tomato genome

Di Filippo M

et al.

PS1_16

Polyketide and non-ribosomal peptide synthetases in Aspergillus carbonarius genome: a strategy for identification of secondary metabolite clusters

Gallo A et al.

PS1_17

aCGH Segmentation: analysis of a male breast cancer dataset

Iannelli G
PS1_18

The repetitive landscape of Wheat Chromosome 5A. A preliminary study based on low-coverage NGS technologies

Lamontanara A et al.

PS1_19

Enabling a Multivariate Strategy for Genotyping Quality Control as a Grid Service

Malovini A et al.

PS1_20

Gene functional clustering for improved prediction of Gene Ontology annotations

Masseroli M

et al.
PS1_21

An optimized web server for metagenomics data analysis

Paoletti D et al.

PS1_22

Microsatellites mined in Globe Artichoke EST database: linkage analysis and relation to gene function

Scaglione D

et al.

PS1_23

The human NumtS revised compilation, RHNumtS.2: custom tracks, polymorphisms and validation by amplification and sequencing

Simone D et al.
Thursday, April 15, 2010

11:00 - 12:00 Poster Session 2
TRANSCRIPTOMICS

Code

Title

Authors

PS2_1

Meta-analysis of microarray raw data using a virtual integrated platform

Bisognin A et al.

PS2_2
In-silico microRNAs analysis from Cartamus and Cynara spp. EST datasets

Catalano D et al.

PS2_3

Mining spatial association rules of multiple co-occurring motifs to discover cis-regulatory modules

Ceci M et al.

PS2_4

Expressed Sequence Tags versus RNA-Seq. Methods and services for large-scale transcriptome analysis

D’Agostino N et al.

PS2_5
MulCom: a multiple comparison statistical test for microarray data in Bioconductor

Isella C et al.

PS2_6

A bioinformatics workflow for the analysis of transcriptome data generated by deep-sequencing

Licciulli F et al.

PS2_7

Predictive transcriptomic analysis identified specific deregulated pathways before and after renal transplantation

Maglietta R et al.

PS2_8

Prediction of cellular developmental stage from whole-transcriptome expression profiles
Mulas F et al.

PS2_9

Definition plant microRNA primary transcripts and their splicing patterns using RNAseq

Piccolo V et al.

PS2_10

Mining microarray data for inflammatory stimuli probes selection and classification

Tuana G et al.

PROTEOMICS
Code

Title

Authors

PS2_11

Identifying Structure Transitions for Protein Secondary Structure Prediction

Armano G et al.

PS2_12

Classification of serum proteome data in familial and sporadic breast cancer

d’Acierno A

et al.
PS2_13

Use of powered supervised learning statistics for the uninvasive diagnosis of Renal Cell Carcinoma through urine proteome analysis

Maglietta R et al.

PS2_14

Using Support Vector Machines to predict expression-purification success of recombinant integral membrane proteins in Escherichia coli

Punta M et al.

PS2_15

A Perl procedure for the analysis of phosphopeptide tandem mass spectra

Tiengo A et al.
PROTEIN STRUCTURE AND FUNCTION

Code

Title
Authors

PS2_16

Fast elaboration of motion and intuitive visualization of surface properties of moving proteins

Andrei RM et al.

PS2_17

PDBinders: a new method for binding site prediction in protein structures

Bianchi V et al.

PS2_18

A parallel implementation of Genetic Algorithms for parameters estimation of Molecular Surfaces similarity analysis

Cozzi P et al.

PS2_19
SCOP protein families fingerprints

Fabris F

PS2_20

Alloxan derivatives as inhibitors of matrix metalloproteinase-2: theoretical calculations and experimental results

Lattanzi G et al.

PS2_21

Computational and experimental approaches to characterize the molecular organization and structural stability of an Arginine-binding protein from Thermotoga maritima

Marabotti A et al.

PS2_22

Modelling of human adiponectin trimer and its complex with ADIPOR1 receptor: possible therapeutic targets

Miele M et al.
PS2_23

Development of a Leishmania-specific phosphorylation sites predictor

Palmeri A et al.

PS2_24

A Structural Alphabet to study Protein Dynamics

Pandini A et al.

PS2_25

Hepatitis C virus envelope glycoprotein E2: critical analysis of two proposed models

Piano MA et al.

PS2_26
PiSQRD: a novel variational scheme to identify dynamical domains in proteins

Potestio R et al.

PS2_27

Prediction and cleaning of ten residue-residue distance thresholds using machine learning

Walsh I et al.

Friday, April 16, 2010

10:40 - 11:40 Poster Session 3
NEW TOOLS FOR NEXT GENERATION SEQUENCING

Code

Title

Authors

PS3_1

DSgen: a tool to generate SOLiD and ILLUMINA synthetic NGS datasets to test mapping tools behavior

Beccuti M et al.

PS3_2

PolySite: A tool for searching polymorphic sites within sequences from RNA-Seq and Sanger technology
Cassandra R et al.

PS3_3

Towards a novel method for small indels detection using Illumina/Solexa data

Chiara M et al.

PS3_4

A web-based service for ChIP-Seq data analysis
D’Onorio

De Meo P et al.

PS3_5

GAMES: a new tool for genomic annotation of next generation sequencing data

Sana ME et al.
PS3_6

Table of Periodic Properties of Human Immunodeficiency Virus Inhibitors

Torrens F et al.

PS3_7

Algorithms for tagging and recognizing a large set of samples in highly parallel 454 sequencing

Vicario S et al.

PS3_7bis

Scaffolder, a tool to detect and manage contig and scaffold relations in de novo high-throughput sequencing

Petrillo M et al.
SYSTEMS BIOLOGY

Code

Title

Authors

PS3_8

Exact and inexact subgraph matching in large networks

Di Natale R

et al.
PS3_9

A curated database of miRNA mediated Feed Forward Loops involving the MYC Transcription Factor as Master Regulator

El Baroudi M et al.

PS3_10

Reprogramming of miRNA networks in cancer and leukemia

Galasso M et al.

PS3_11

Gene autoregulation via intronic microRNAs and its functions

Bosia C et al.

PS3_12

Reconstruction and analysis of the NF-kB pathway interactome
Tieri P et al.

BIOLOGICAL DATABASES AND BIOBANKS
Code

Title

Authors

PS3_13

An ontological probabilistic approach to the breast cancer problem in semantic medicine

Bevilacqua V

et al.

PS3_14

Integrated computational strategies for annotating microRNA target genes over genome-wide dataset

Corrada D et al.
PS3_15

Viral-KB: an integrated Knowledge-Base to support Viral molecular biodiversity studies

Di Tota F et al.

PS3_16

CDDM: Clinical database for data mining

Evangelista D

et al.

PS3_17

Non syndromic Hereditary Hearing Loss (HHL) bioinformatic workbench

Leo P et al.
PS3_18

A combined approach for successful reannotation of animal mitochondrial tRNAs based on pattern-matching and tRNA-predictor programs

Lupi R et al.

PS3_19

Investigating the gene order variability and non-coding sequences of metazoan mitochondrial genomes: design and construction of a mitogenomics database

Lupi R et al.

PS3_20

Towards NERVE 2.0: creation and integration of the NERVE database

Mazzocco G et al.

PS3_21
Recent activities of the Italian Network for Oncology Bioinformatics

Parodi S et al.

PS3_22

Scholar Search: A global assessment of the productivity of Italian Universities

Peluso D et al.

PS3_23

REDIdb: an upgraded bioinformatics resource for organellar RNA editing

Picardi E et al.

PS3_24

Standard protocol definition for human oocytes selection based on morphological and structural data analysis

Vaccina A et al.
PS3_25

A system for barcode primer retrieval and evaluation

Pappadà G et al.

PS3_26

Bioinformatics infrastructure for the analysis of the relationships between particulate matter and human health

Moscatelli M et al.