

PROGRAM (ISBB 06)
**INTERNATIONAL SYMPOSIUM ON
COMPUTATIONAL BIOLOGY & BIOINFORMATICS**

DEC 15-17, 2006, BHUBANESHWAR, INDIA (in conjunction with CIT)

Venue: Swosti Plaza Conference Center, Bhubaneswar

Symposium URL: isbb06.googlepages.com

Friday, Dec 15

8:00 -8:45 Registration

8:45 -9:00 Opening Remarks

Laxmi Parida,

IBM TJ Watson Research, USA & Courant Institute of Mathematical Sciences, NYU, USA

9:00 -10:00 Gad M Landau, University of Haifa, Israel & Polytechnic University, NY, USA

Indexing Genotypes for Haplotype Search

10:00 -10:30 Ravindra Pushker, UCD Conway Institute, University College Dublin, Ireland

Renu Gautam, Manipal Institute of Technology, India

Alex Mira, Universidad Miguel Hernandez, Alicante, Spain

RNA GeneTracer: a Tool to Trace Evolutionary History of the Ribosomal Genes

10:30 -11:00 Tea/Coffee

11:00 -11:30 Xiao-Dong Yang, Debiprosad Roy Mahapatra* and Roderick V. N. Melnik,

Mathematical Modeling & Computational Sciences,

Wilfrid Laurier University, Waterloo, Ontario Canada

Simulation of RNA Silencing Pathway Based on a Generalized Amplification Model

11:30 -12:00 Ofer Gill, Bud Mishra, New York University, USA

Naren Ramakrishnan, Virginia Tech, USA

PLANAR: RNA Sequence Alignment using Non-Affine Gap Penalty and Secondary Structure

12:00 -1:30 Lunch

1:30 -2:30 See-Kiong Ng, Institute of Infocomm Research, Singapore

Unraveling the Common Denominators of Protein-Protein Interaction Networks

2:30 -3:00 Simone Scalabrin, Alberto Policriti,

Dipartimento di Matematica e Informatica - Universita' di Udine, Italy

Michele Morgante, Dipartimento di Scienze Agrarie ed Ambientali, Italy

Stem-Loop Structure Search for Helitron Discovery

3:00 -3:30 Tea/Coffee

3:30 -4:30 Saugata Basu, Georgia Institute of Technology, USA

Algebraic Geometry and Computational Biology

4:30 -5:00 Samantha Kleinberg, New York University, Bioinformatics Group, USA

Bud Mishra, New York University, USA

CLARITY: Algorithms for Semantic Comparison of Time-course Transcriptomic Data

5:00 -5:30 Saumyadipta Pyne, Broad Institute of MIT and Harvard, USA

Mohammad Sajjad Hossain, SUNY at Stony Brook, USA

Discriminative Meta-Analysis of Microarray Data: Combining Fission Yeast Cell Cycle Studies

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Saturday, Dec 16

- 9:00 -10:00 Gene Myers, Howard Hughes Medical Institute, Janelia Farms Research Campus, USA
Imaging-Based Systems Biology
- 10:00 -10:30 Rahul Siddharthan, The Institute of Mathematical Sciences, Chennai, India
Describing the DNA "background"
- 10:30 -11:00 Tea/Coffee
- 11:00 -11:30 Marco Zantoni, Alberto Policriti, University of Udine, Italy
Emiliano Dalla, Claudio Schneider, LNCIB, Italy
Finding regulatory elements fixing error layouts
- 11:30 -12:00 Preetam Ghosh, Samik Ghosh, Kalyan Basu, Sajal Das
University of Texas at Arlington, USA
Simon Daefer, Mount Sinai School of Medicine, USA
Modeling the Diffusion process in Stochastic Event based Simulation of the PhoPQ system
- 12:00 -1:30 Lunch
- 1:30 -2:30 David Sankoff, University of Ottawa, Canada
Use of phylogenetic context in inferring ancestral tetraploid gene order
- 2:30 -3:00 Gobind Bisht, Indian Institute of Technology, Kharagpur, India
Manju Bansal, Indian Institute of Science, Bangalore, India
A computational investigation of Mg-ADP inhibition of F1-ATPase and its mechanism
- 3:00 -3:30 Tea/Coffee
- 3:30 -4:30 Ramesh Hariharan, Strand Life Sciences, Bangalore, India
Extracting Information from Literature via Language Processing
- 4:30 -5:00 Francois-Joseph Lapointe and Claudine Levasseur,
Universite de Montreal, Canada
An Efficient and Stable Consensus Method for Combining Weighted Trees in Phylogenetic Analysis
- 7:00-10:00 Symposium Banquet

Sunday, Dec 17

- 9:00 -10:00 U.S.N. Murty,
Indian Institute of Chemical Technology (CSIR), Hyderabad, India
Data mining applications for the control of Vector Borne Diseases
- 10:00 -12:00 Poster Sessions 1 & 2 (overleaf)
- 12:00 -12:15 Closing Remarks
Nitai Dhall,
Silicon Institute of Technology, Bhubaneswar, India

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Poster Session-1 (Sunday, Dec 17, 10:00-12:00)

SHRISHAIL PATIL, BVDUCE, Pune, India
DATTATRAYA BORMANE, BVCOEW, Pune, India
SANDEEP NAROTE, SINHGAD ENGG COLLEGE, Pune, India
Electroencephalograph Signal Analysis During Basarika Using wavelet

Bishnu Mukhopadhyay, Bratati Ghosh and Hridoy Bairagya
National Institute Of Technology, Durgapur, India
Invariant water molecular interaction in the acidophilic redox protein Rysticyanin of Thiobacillus ferrooxidans

Sumeet Dua, Pradeep Chowriappa and Ramakrishnan Rajagopalan
College of Engineering and Science, Louisiana Tech University, USA
Computational Prediction of Protein Structure Using Supervised Classification

Dharmendra Kumar, RV College of Engineering, Bangalore, India
Shweta Gupta, IOB, Bangalore, India
Sushil Middha, MACW, Bangalore, India
Pushpa Agrawal, RVCE, Bangalore, India
SEQUENCE ANALYSIS AND EVOLUTIONARY STUDIES OF AQUAPORINS

Poongavanam Sardar Maran, Vinita Vishwakarma and Manoharan N
Sathyabama Institute of Science and Technology, Chennai, India
Development of Asthma Drug Database ? A Nanotechnology approach

Gadi Gayatri and SWASTIK CHOUDHURY
National Institute of Science and Technology, BPUT, Behrampur, India
Use of Artificial Neural Network in Protein Structure Prediction

Rajan Mishra, Yogesh Joshi and Sujay singh
IMGENEX INDIA Pvt. Ltd., Bhubaneswar, India
BIOINFORMATICS STRATEGIES FOR BETTER UNDERSTANDING OF ANTIBODY DEVELOPMENT

Syamal Kumar Dana, Indian Institute of Chemical Biology, Kolkata, India
Chin -Kun Hu, Academia Sinia, Taipei, Taiwan
Neuron-like Spiking and Bursting in Josephson junction

Madhumita Patra and Chhabinath Mandal
Indian Institute of Chemical Biology, Kolkata, India
Search for binding site using different computational tools

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Poster Session-2 (Sunday, Dec 17, 10:00-12:00)

Bishnu Mukhopadhyay, Bratati Ghosh and Hridoy Bairagya
National Institute of Technology, Durgapur, India
Modeling Studies of the Rysticyanin Cytochrome C₄ Complex Involving in the Thiobacillus ferrooxidans During the Electron Transfer Reaction

Dharmendra Kumar, RV College of Engineering, Bangalore, India
Sushil Middha, MACW, Bangalore, India
Biplab Bhattacharjee, Kavita Iyer, BTM, Bangalore, India
Shweta Gupta, IOB, Bangalore, India
Pushpa Agrawal, RVCE Banaglore, India
SEQUENCE ANALYSIS OF H5N1 & H1N1 FOR ASCERTAINING TEST SYSTEMS

Virendra Gomase and Karbhari Kale
Dr. Babasaheb Ambedkar Marathwada University, Aurangabad, India
In silico sequence analysis of coat protein from garlic mosaic virus

Sainty C . Thomas, Raunak Guha, Anand Poddar and Ankit Sehgal
Sathyabama Institute of Science and Technology, Chennai, India
A comprehensive web portal on bioinformatics

Pallavi Somvanshi, Biotech Park, Lucknow, India
Genome Wide Identification of Vaccine Candidates in Antigenically Distinct Variants of Dengue virus: A Bioinformatics Approach

Kinshuk Nayak and Subrata Kumar Das
Institute of Life Sciences, Dept of Biotechnology, Bhubaneswar, India
Analysis of codon usage variation in a hyperthermophilic bacterium Nanoarchaeum equitans

Santhosh Srinivasan and Venkatakrisnan A.J.
Vellore institute of technology, Vellore, India
PERLPRED - A NOVEL APPROACH FOR PROTEIN STRUCTURE IDENTIFICATION

Anjali Mohapatra, ITER, Bhubaneswar, India
P M Mishra, OMC Ltd., India
S Padhy, Utkal University, Bhubaneswar, India
Motif Search using Dynamic Hybrid Tree

Kaouther NOUIRA and Abdelwahed Trabelsi
Business & Economic Statistics Modelling Laboratory, Tunis University, Tunisia
Temporal Multi-Agent System in Intensive care Monitoring

Virendra Gomase, Karbhari Kale,
Dr. Babasaheb Ambedkar Marathwada University, Aurangabad, India
Satish Hatture, Department of Biotechnology, SCB, Solapur, India
Bioinformatics based antigenic prediction of viral capsid protein