

Atlantic Symposium on Computational Biology and Genome Information Systems & Technology

Thursday, March 15, 2001

8:30 a.m. - 10:00 a.m.

REGISTRATION

10:05 a.m. - 10:20 a.m.

WELCOME:

Dr. Kristina Johnson

Dean, Pratt School of Engineering, Duke University

Chair: Dr. Howard Clark

10:20 a.m. - 12:00 noon

Morning Sessions (I and II)

TA-I: DATA MINING IN BIOINFORMATICS

Session Chair: Xiong Wang, California State University at Fullerton, USA

A Clustering Method Based On Rough Sets And Its Application To Biochemical Data Analysis

Shoji Hirano, Tomohiro Okuzaki, and Yutaka Hata, Himeji Institute of Technology, Japan; Shusaku Tsumoto, Shimane Medical University, Japan; Kouhei Tsumoto, Tohoku University, Japan

A Lexical Approach to Text Mining for the Integration of Genomic Information

Lauren Harrison and Peter Borgulya, Hoffmann-La Roche, Inc., USA; Olivier Jouve and Brian Simblist, LexiQuest, USA.

Creating Metabolic Network Models using Text Mining and Expert Knowledge

J. A. Dickerson, D. Berleant, Z. Cox, W. Qi, and E. Wurtele, Iowa State University, USA

Analyzing Protein Surface for Classification: A Geometric Hashing Approach

Xiong Wang, California State University at Fullerton, USA; and Jason T. L. Wang, New Jersey Institute of Technology, USA

TA-II (INVITED SESSION)

Session Chair: Cathy Wu, Director of Bioinformatics, National Biomedical Research Foundation

Extracting and Recording Bio-signatures from In vivo Cells using the L-G Graph

Nikolaos Bourbakis, Director of the Information Technology Research Institute, Wright State University

Gene Annotation: Some Nasty Facts from the Pre-mRNA Splicing Field

Stephen M. Mount, Associate Professor, Dept. of Cell Biology and Molecular Genetics, University of Maryland

Physical Mapping of Plant Genomes

Carol Soderlund, Associate Professor, Dept. of Computer Science, Clemson University

Networks of Small, Dispersed, Interrelated Databases: A Viable Complement to Large Stand Alone Databases?

Mark Danielsen, Associate Professor, Dept. of Biochemistry and Molecular Biology, Georgetown University Medical Center

12:00 noon – 1:15 p.m.

LUNCH ON YOUR OWN

1:15 p.m. – 2:00 p.m.

PLENARY SPEECH:

Steven L. Salzberg

Senior Director of Bioinformatics, The Institute for Genomic Research
“Algorithms for Whole Genome Analysis”

Chair: Bruno Sobral, Director, Virginia Bioinformatics Institute, VPI

2:00 p.m. – 3:00 p.m.

KEYNOTE SPEECH:

Jeffrey M. Trent, Ph.D.

Director, Division of Intramural Research, Chief, Cancer Genetics Branch, NIH/National Human Genome Research Institute

“Applying Gene Expression Profiling to the Discovery of Cancer Causing Genes.”

Chair: Alexander Shenderov

3:00 p.m. – 3:20 p.m.

COFFEE BREAK

3:20 p.m. - 5:20 p.m.

Afternoon Sessions (I, II, and III)

TP-I (INVITED SESSION): PLANT GENOMICS: THE HOST-PEST REALM

Session Chair: Dr. Xi Chen, Syngenta (formerly Novartis)

Functional Genomic Study of Plant Fungal Pathogen Interactions.

Xi Chen, Fungal Targets Group, Syngenta

Application of Model System Genetics and Genomics to Target Based Pesticide Development

Kim Kamdar, Invertebrate Targets Group, Syngenta

Herbicide Discovery Via Identification of Essential Genes in Arabidopsis

Joshua Levin, Plant Targets Group, Syngenta

Gene Expression Analysis of a Plant Defense Response; from Profiles to Promoter Elements.

Bob Dietrich, Natural Resistance Groups, Syngenta

Transcriptional Profiling and Gene Function Discovery with Plant Viral Vectors

Yijun Ruan, Sr. Group Leader Of Genomic Technology, Large Scale Biology Corporation

TP-II (INVITED SESSION): ALGORITHMS AND TOOLS FOR MINING BIOLOGICAL DATA, PART I

Session Chairs: Gautam B. Singh, Oakland Univ., Rochester, MI, USA and Cliff Cunningham, Duke Univ.

Expressed Sequence Tag Data Mining: The Reality of Virtual Gene Expression.

Sorin Draghici, Rui P. Martins, Richard E. Leach, and Stephen A. Krawetz, Wayne State University, School of Medicine, Detroit, MI, USA

Text Mining and Genomic Database Retrieval: Is there a Connection?

Donglin Liu and Gautam Singh, Oakland University, Rochester, MI, USA

Large-Scale Promoter Prediction: Results On The Human Genome And Consequences For Large-Scale SNP Analysis.

Tom Werner, Genomatix, Germany

Stochastic Modeling of Protein Sequence and Structure

Scott Schmidler, Duke University

TP-III: PROTEIN MOTIF ANALYSIS AND PATTERN DISCOVERY

Session Chair: TBA

Data-Driven Generation of Decision Trees for Motif-Based Assignment of Protein Sequences to Functional Families

Dake Wang, Xiangyun Wang, Vasant Honavar and Drena L. Dobbs, Iowa State University, USA

Towards a Comprehensive Collection of Diagnostic Patterns for Protein Sequence Classification

Bjorn Olsson and Kim Laurio, University of Skövde, Sweden

Association between Statistical and Functional Patterns in Biomolecules

David K.Y. Chiu, Xin Chen, University of Guelph, Canada; and Andrew K.C. Wong, University of Waterloo, Canada

Molecular Modeling of Human DNA Repair Protein and Helicase, XPD (Xeroderma Pigmentosum Group D)

Rachelle Bienstock and Bennett Van Houten, National Institute of Environmental Health Sciences, USA

Consigned Interdependency for Pattern Discovery from Biomolecular Sequences

David K.Y Chiu and Thomas W.H. Lui, University of Guelph, Canada

5:30 p.m. – 6:15 p.m.

PLENARY SPEECH:

Bruce Shapiro, Ph.D.

Principal Investigator, Laboratory of Experimental and Computational Biology, National Cancer Institute, NIH, USA

“Computational Insights into RNA Folding Pathways: Getting from Here to There”

(Additional Authors: David Bengali, Wojciech Kasprzak, Jin Chu Wu)

Chair: Ratko Orlandic, Illinois Institute of Technology

6:30 p.m. - 7:15 p.m.

CASH BAR

7:15 p.m. - 9:15 p.m.

DINNER BANQUET

Speaker:

Kenneth R. Tindall, Ph.D.

Senior Executive Vice President, North Carolina Biotechnology Center

Chair: Howard Clark, Duke University

Friday, March 16, 2001

8:15 a.m. - 9:00 a.m.

PLENARY SPEECH:

Stephen Altschul

Senior Investigator, National Center for Biotechnology Information, National Library of Medicine, National Institutes of Health

“Iterated Profile Searches with PSI-BLAST”

Chair: Simon Lin, DUMC

9:00 a.m. – 10:00 a.m.

KEYNOTE SPEECH:

Joseph Nevins, Ph.D.

James B. Duke Professor, Duke University

Chair: Ron Yager, Iona College

10:00 a.m. – 10:20 a.m.

COFFEE BREAK

10:20 a.m. - 12:00 noon

Morning Sessions (I and II)

FA-I: FUZZY COMPUTING IN BIOMEDICAL APPLICATIONS

Session Chair: H. D. Cheng, Utah State University, USA

Two-layer Fuzzy Relational Networks: Some Preliminary Results

A. Ciaramella, University of Salerno, Italy

W. Pedrycz, University of Edmonton, Canada

R. Tagliaferri, University of Salerno, Italy

Fuzzy Similarity Measures and Tree Comparison

R. De Sutter, Ghent University, Belgium

H. De Meyer, Ghent University, Belgium

B. De Baets, Ghent University, Belgium

H. Naessens, Hogeschool Gent, Belgium

Towards the Use of Nearest Neighbor Rules in Bioinformatics

Ronald R. Yager, Iona College, USA

Mammogram Contrast Enhancement Using a Novel Fuzzy Homogeneity Measure

H. D. Cheng, Utah State University, USA

M. Xue, Utah State University, USA

R. Freimanis, Bowman Gray School of Medicine, USA

FA-II (INVITED SESSION): BIOINSPIRED SYSTEMS

Session Chair: Dr. Liam P. Maguire, Intelligent Systems Engineering Laboratory, Magee College, UK

Neural Networks on “Cultured Probe” Micro-Electrode Arrays: Network Confinement and Activity Patterns

Wim L.C. Rutten, Institute for Biomedical technology, University of Twente, Enschede, Netherlands

J. van Pelt, Netherlands Institute for Brain Research, Amsterdam, Netherlands

Selection of Behaviors by Their Consequences in the Human Baby, Software Agents, and Robots

Philippe Preux, Laboratoire d'Informatique du Littoral Calais, France; Samuel Delepouille, URECA & LIL, France; Jean-Claude Darcheville, Unité de Recherche sur l'Évolution du Comportement et des Apprentissages (URECA), Villeneuve d'Ascq, France

Networks of Real Neurons with an Artificial Body

Massimo Grattarola, Marco Bove, Michele Giugliano, Sergio Martinoia, Neural and Bioelectronic Technologies Group Department of Biophysical and Electronic Engineering, University of Genoa, Italy

An Approach for the Realisation of Bio-Inspired Systems on Programmable Logic Devices

B.P. Glackin, L.P. Maguire, T.M. McGinnity, Intelligent Systems Engineering Laboratory, University of Ulster, UK

12:00 noon – 1:15 p.m.

LUNCH ON YOUR OWN

1:15 p.m. - 2:00 p.m.

PLENARY SPEECH:

Mike West

Duke University

“Statistical Analysis for Clinical Discriminant Using DNA Micro-array Data.”

Chair: Nik Kasabov, University of Otago

2:00 p.m. - 3:00 p.m.

KEYNOTE SPEECH:

Russell F. Doolittle

Center for Molecular Genetics, University of California, San Diego, La Jolla, CA

“Sequences and Computers: A Personal Reflection on the Digital Age”

Chair: Howard Clark

3:00 p.m. - 3:20 p.m.

COFFEE BREAK

3:20 p.m. - 5:20 p.m.

Afternoon Sessions (I, II, III)

FP-I: ADVANCES IN BIOCOMPUTING

Session Chair: Jason T. L. Wang, New Jersey Institute of Technology, USA

Complementary Retrieval for Distorted Images

Chun-Jiun Liao, Yuan Ze University, Taiwan

Shu-Yuan Chen, Yuan Ze University, Taiwan

An Algorithm for the Approximate String-Matching Problem

Mourad Elloumi, Faculty of Sciences of Tunis, Tunisia

DNA Word Optimization

Horatio Voicu, Duke University, USA

Influence of Linear Gene Regulatory Model—Reverse Engineering by Genetic Algorithms

Shin Ando, University of Tokyo, Japan

Hitoshi Iba, University of Tokyo, Japan

Approximate Searching in Phylogenetic Databases

Katherine G. Herbert, New Jersey Institute of Technology, USA

Huiyuan Shan, New Jersey Institute of Technology, USA

Jason T. L. Wang, New Jersey Institute of Technology, USA

FP-II (INVITED SESSION): UNCERTAINTY ANALYSIS AND FUSION METHODOLOGY: THEORY AND APPLICATIONS, PART I

Session Chair: Da Ruan, SCK-CEN, Belgium

Fusing Nonmonotonic Knowledge: Preliminary Results

E. Grégoire, Université d'Artois, France

Evidential Analysis in Bioinformatics

D.A. Bell and J.W. Guan, University of Ulster at Jordanstown, UK

A New Method for Time Series Prediction Combining Neural Networks, Fuzzy Logic, and Fractal Theory

Oscar Castillo and Patricia Melin, Tijuana Institute of Technology, USA

Controlling Electrochemical Processes Using a New Neuro-Fuzzy-Genetic Approach

Patricia Melin and Oscar Castillo, Tijuana Institute of Technology, USA

FP-III: SEQUENCE SEARCH OPTIMIZATION AND MOLECULAR EVOLUTION

Chair: Nikolaos Bourbakis, Director of the Information Technology Research Institute, Wright State University

An Optimization Approach to Multiple Sequence Alignment: A Preliminary Report

Fern Y. Hunt and Anthony J. Kearsley, National Institute of Standards and Technology;

Honghui Wan, National Library of Medicine, USA

A Learning Algorithm for the Shortest Superstring Problem

Mark K. Goldberg and Darren T. Lim, Rensselaer Polytechnic Institute

Statistical Testing for Protein Functional Divergence after Major Evolutionary Events

Jianying Gu, Yufeng Wang, Xun Gu, Iowa State University, USA

Patterns of Functional Divergence after Gene Duplications in Vertebrate Gene Families: Altered Functional Constraints

Yufeng Wang, Jianying Gu, and Xun Gu, Iowa State University, USA

Information Theory, Evolution and the Origin of Life

Hubert P. Yockey, USA

5:20 p.m. – 6:20 p.m.

DINNER

Attendees are invited to purchase a buffet dinner at the Regal Hotel and join us for conversation and socializing followed by an after-dinner speech in the general meeting room.

6:30 p.m. - 7:15 p.m.

DINNER SPEAKER:

Thomas LaBean

Duke University

“Meanderings in Sequence Space: Random Evolution and Rational Engineering of Bio-polymers”

Chair: Jane Richardson, Duke University

7:15 p.m. - 9:15 p.m.

PANEL DISCUSSION:

“The Future of Genomics Research”

Panelists:

Russell Doolittle, University of California, San Diego, La Jolla

Jim Siedow, Duke University

Bruce Shapiro, NCI

Jacob Maizel, NCI

Panel Chair: Jeff Dangl, University of North Carolina

Saturday, March 17, 2001

8:15 - 9:00 a.m.

PLENARY SPEECH:

Cathy Wu, Ph.D.

Director of Bioinformatics, National Biomedical Research Foundation, Georgetown University Medical Center

“Integrated Protein Family Classification for Functional Genomics”

Chair: Nik Kasabov, University of Otago

9:00 - 10:00 a.m.

KEYNOTE SPEECH:

Mark Adams, Ph.D.

Vice President, Genome Programs, Celera Genomics, Maryland

“Sequencing and Analysis of the Human Genome”

Chair: Stanley Burt, Director, Advanced Biomedical Computing Center, SAIC

10:00 a.m. – 10:20 a.m.

COFFEE BREAK

10:20 a.m. - 12:00 noon

Morning Sessions (I and II)

SA-I (INVITED SESSION): COMPUTATIONAL BIOLOGY AT THE NATIONAL CANCER INSTITUTE, NATIONAL INSTITUTES OF HEALTH, FREDERICK, MARYLAND

Session Chair: Bruce A. Shapiro, National Cancer Institute, NIH, USA

The Role of High Performance Computing in Exploring Structure-Function Relationships

Stanley Burt, Director, Advanced Biomedical Computing Center, SAIC, USA

Application of Sequence Analysis Pipelining Tools for High-Throughput Sample Processing at the Biomedical Computing Center

Robert M. Stephens and Gary W. Smythers, Advanced Biomedical Computing Center, SAIC, USA

Computational Methods in the Analysis of Ligand-Macromolecule Contacts

Nagarajan Pattiraman, Advanced Biomedical Computing Center, SAIC, USA

Dynamic Models of Virus/Cell Turnover in HIV Infections

D.S. Dimitrov, I.A. Sidorov, Laboratory of Experimental and Computational Biology; Y. Endo, T. Igarashi, M.A. Martin, Laboratory of Molecular Microbiology; R.A. Lempicki, J. Lifson, SAIC; J. Kovacs, Critical Care Medicine Department; R.T. Davey and H.C. Lane, Laboratory of Immunoregulation

SA-II (INVITED SESSION): UNCERTAINTY ANALYSIS AND FUSION METHODOLOGY: THEORY AND APPLICATIONS, PART II

Session Chair: Da Ruan, SCK-CEN, Belgium

Soft Computing Techniques For Speech Recognition

Mike Nachtegael, Martine De Cock, and Etienne E. Kerre, Ghent University, Belgium

On the Fusion of Nuclear Safeguards Relevant Information Based on Weighted Linguistic Aggregation Operators

Da Ruan, Jun Liu, and Roland Carchon, Nuclear Research Center, Belgium

Predicting Regulatory Elements in Repetitive Sequences Using Transcription Factor Binding Sites

Jorng-Tzong Horng, Wen-Fu Cho, and Cheng-Yan Kao National Central University, Taiwan, ROC

RSDB—A Database of Repetitive Elements in Complete Genomes

Jorng-Tzong Horng, Jia-Hwang Lin, and Cheng-Yan Kao, National Central University, Taiwan, ROC

SA-III (INVITED SESSION): ALGORITHMS AND TOOLS FOR MINING BIOLOGICAL DATA, PART II

Session Chair: Gautam B. Singh, Oakland Univ. Rochester, MI, USA

Native Structure and Structure-based design of Phospholipase A2 inhibitors

Punit Kaur, Vikas Chandra, Jayasankar Jasti and Tej P. Singh, All India Institute of Medical Sciences, New Delhi, India

Design and Implementation of an Introductory Course for Computer Applications in Molecular Genetics: A Case Study

Stephen A. Krawetz and David D. Womble, Wayne State University, School of Medicine, Detroit, MI, USA

The Genomics Drug Discovery Connection: Evolutionary Chemistry

Bruce Eaton, Invenux, Inc., Denver, CO

Statistical Mining of S/MAR Database

Swami Ganapathy and Gautam Singh, Oakland University, Rochester, MI, USA

12:00 noon - 1:15 p.m.

LUNCH ON YOUR OWN

1:15 p.m. – 2:15 p.m.

PLENARY SPEECH:

Jacob V. Maizel, Jr.

Chief, Laboratory of Experimental and Computational Biology, National Cancer Institute, NIH, USA

“Computational Discovery of Important Functional and Structural Features in mRNA Sequences”

(Additional Author: Shu-Yun Le)

Chair: TBA

2:15 p.m. – 3:15 p.m.

PLENARY SPEECH:

Erich Jarvis

Department of Neurobiology, Duke University Medical Center, USA
“The Importance of Anatomical Substrates”

Chair: Li Chen, North Dakota State University

3:15 – 3:30 p.m.

COFFEE BREAK

3:30 p.m. - 5:30 p.m.

Afternoon Sessions (I and II)

SP-I (INVITED SESSION): CLASSIFICATION AND PATTERN RECOGNITION OF GENE EXPRESSION DATA

Session Chair: Etienne E. Kerre, University Gent

Knowledge Based Neural Networks for On-line and Off-line Modeling and Rule Extraction

Nikola Kasabov, Melanie Middlemiss, Matthias Futschik

Department of Information Science, University of Otago

Class Prediction and Discovery based on Gene Expression Data

Leping Li, National Institute of Environmental Health Sciences; Lee G. Pedersen, National Institute of Environmental Health Sciences, University of North Carolina; Thomas A. Darden, National Institute of Environmental Health Sciences; and Clarice R. Weinberg, University of North Carolina

Data Mining in High Dimensionality

Dr. George Karypis, University Minnesota

Who Needs Genomes?

Barry McMullin, Axel von Kamp, Dublin City University, Ireland

Tim Taylor, University of Abertay Dundee, UK

SP-II: GENE EXPRESSION ANALYSIS

Session Chair: Mark Danielsen, Associate Professor of Biochemistry and Molecular Biology, Georgetown University Medical Center

Constructing Bayesian Network Models of Gene Expression Networks from Microarray Data

Peter Spirtes, Richard Scheines, Department of Philosophy, Carnegie Mellon University;

Clark Glymour, Institute for Human and Machine Cognition; Stuart Kauffman, Valerio Aimale,

Frank Wimberly, Bios Group, USA

Temporal Boolean Network Models of Genetic Networks and Their Inference from Gene Expression Time Series

Adrian Silvescu and Vasant Honavar, Iowa State University, USA

Mining Association Rules in Analysis of Transcription Factors Essential to Gene Expressions

Ruzhu Chen, Qiyu Jiang, Honglin Yuan and Le Gruenwald, University of Oklahoma

Telomerase Expression in Exfoliated Cervical Cells Correlates with Known Cervical Cancer Risk Factors: A Genetic Perspective

John F. Boggers, Lesly R. Lamarque, Thomas P. Morrissey, Jean A. Roayaei, and Bruce A. Lessey, University of North Carolina, USA

5:30 p.m. – 6:30 p.m.

PLENARY SPEECH:

Jane Richardson

James B. Duke Professor of Biochemistry, Duke University, USA

“High-Grade Ore for Data Mining—Improving 3D Structural Genomics Data”

Chair: John C. Rockett, EPA, USA

END OF CONFERENCE