



The International Association for
Pattern Recognition
Technical Committee 20

Pattern Recognition for Bioinformatics

Progress Report

July 2007 - June 2008

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1 TC-20 Aims and Scope

1.1 Background

Pattern recognition techniques and tools to tackle associated bioinformatics problems are not evolving fast enough at a comparable rate to the emergence of life sciences data. In view of this, during ICPR meeting in Cambridge, UK, November 2004, a proposal to form the TC-20, put forward by the Founding Co-Chairs, Raj Acharya and Jagath C. Rajapakse, was accepted by the IAPR Executive Committee.

1.2 Aim

The aim of TC-20 is to investigate how pattern recognition techniques can be effectively used to resolve specific bioinformatics problems and handle high throughput life sciences data.

Statistical, structural, and syntactic pattern recognition, neural networks, computational intelligence, graphical and data mining techniques, and their hybrids have found many applications in computational biology and bioinformatics. Such applications include:

- Analyses of bio-sequences
- Gene expression analysis and functional genomics
- Phylogenetic analysis of species, sequences, structures
- Structural genomics and proteomics
- Information fusion such as combining sequences, expressions, texts, and images, etc.
- Systems biology: pathway analysis, gene regulatory networks, etc.
- Disease modeling
- Medical informatics
- Biological imaging: functional, molecular, and cellular imaging

1.3 Goal

The goal of TC-20 is to bring together pattern recognition scientists and life scientists to find solutions to problems in bioinformatics and to foster multidisciplinary research in pattern recognition community.

One of the goals is to facilitate interactions between pattern recognition and life sciences communities to interact through its memberships and associate memberships, thereby to match-make pattern recognition techniques and bioinformatics applications. An example of the benefits of proliferation of pattern recognition techniques in bioinformatics applications could be the discovery of new drugs.

The committee has a membership list and maintains a website for the exchange and dissemination of ideas among its members. The membership is currently for two years and offered by the invitation of TC-20 Chairs. The core membership is limited to 20 members who are expected to actively engage in TC-20 activities. TC-20 also maintains a PRIB membership list which comprises of participants in PRIB conferences. Who are interested in participating in TC-20 and PRIB conferences can be PRIB members. It plans its website as source for education and research in pattern recognition for bioinformatics. The TC-20 will organize and support related workshops and seminars to bring its members and interested researchers together and disseminate information on latest research in the field.

3. TC-20 Structure and Organization

3.1 Chairs

TC-20 is led by the Chair assisted by the Vice Chair. At ICPR 2006 meeting, Prof Jagath Rajapakse was appointed as the Chair of TC-20 for a two-year term. Prof Rajapakse invited Prof Acharya to act as Vice-Chair for his experience with IAPR and vast exposure in the area of pattern recognition and bioinformatics.

Chair: Jagath C. Rajapakse, Nanyang Technological University, Singapore

Vice Chair: Raj Acharya, The Pennsylvania State University, University Park, USA

3.2 Membership

The membership of TC-20 is by invitation of the TC-20 Chairs. Presently, TC-20 has 25 members worldwide (*expiring in July, 2007*).

- Raj Acharya, The Pennsylvania State University, USA, (acharya@cse.psu.edu) (Vice-Chair)
- Shandar Ahamad, National Institute of Biomedical Innovation, Japan
- Vladimir Brusic, Dana-Farber Cancer Institute, USA (vladimir_brusic@dfci.harvard.edu)
- Phoebe Chen, Deakin University, Australia, (phoebe.chen@deakin.edu.au)
- [Madhu Chetty, Monash University, Australia](#)
- Marchiori Elena, Vrije Universiteit Amsterdam, The Netherlands, (elena@cs.vu.nl)
- Mariofanna Milanova, University of Arkansas at Little Rock, USA, (mgmilanova@ualr.edu)
- Gary Fogel, Natural Selection, Inc., USA, (gfogel@natural-selection.com)
- Saman Halgamuge, University of Melbourne, Australia, (saman@unimelb.edu.au)
- Visakan Kadiramanathan, The University of Sheffield, United Kingdom, (visakan@sheffield.ac.uk)
- Nik Kasabov, Auckland University of Technology, New Zealand, (nkasabov@aut.ac.nz)
- Alexey V. Kochetov, Russian Academy of Sciences, Russia, (ak@bionet.nsc.ru)
- Nikhil R. Pal, Indian Statistical Institute, India, (nikhil@isical.ac.in)
- Jagath C. Rajapakse, Nanyang Technological University, Singapore (asjagath@ntu.edu.sg) (Chair)
- Gwenn Volkert, Kent State University, USA, (volkert@cs.kent.edu)
- Roy E. Welsch, Massachusetts Institute of Technology, USA, (rwelsch@mit.edu)
- Kay C. Wiese, Simon Fraser University, Canada, (wiese@sfu.ca)
- Limsoon Wong, National University of Singapore, Singapore, (limsoon@nus.edu.sg)
- Jerry Wu, Wellcome Trust Sanger Institute, United Kingdom (jerry.wu@sanger.ac.uk)
- Yanqing Zhang, Georgia State University, USA, (yzhang@cs.gsu.edu)

3.4 Website

The IAPR website is currently has the following URL:
<http://www.ntu.edu.sg/home/asjagath/iapr-tc20/>

It is hosted by Nanyang Technological University, Singapore.

The website still needs a lot of improvements, with links to major information sources, data sources, software tools, literature, etc.

3.6 IAPR TC-20 Secretariat

IAPR secretariat is maintained at the BioInformatics Research Centre (BIRC), Nanyang Technological University, Singapore. Ms. Norhana Ahmad will serve as the secretary for IAPR TC-20. Norhana has served as the secretary for PRIB 2006 and PRIB 2007 workshops.

IAPR TC-20 Secretariat
c/o BioInformatics Research Centre
Nanyang Technological University,
Research TechnoPlaza, 3rd Storey, XFrontiers Block
50 Nanyang Drive
Singapore 639798
Tel: (65) 67906609 Fax: (65) 63162780
Email: prib@ntu.edu.sg

3.5 Mailing List

The current mailing list consists of the members and associate members. In addition, it maintains email lists for publicity of PRIB workshops, which is owned exclusively by IAPR TC-20

4. Events

TC-20 will support and organize events pertaining to bioinformatics and pattern recognition. As a regular event, TC-20 initiated the Workshop on Pattern Recognition in Bioinformatics (PRIB) to be held in conjunction with the biennial International Conference on Pattern Recognition (ICPR), a major event of IAPR or as an isolated event, and as a standalone event in the alternate years.

2nd IAPR Workshop on Pattern Recognition in Bioinformatics (PRIB 2007)

Grand Plaza Park Royal, Singapore

Oct 1 - 2, 2007

www.ntu.edu.sg/sce/prib/prib07

The arrangements are under way to hold from Oct 1 - 2, 2007 at Grand Plaza Park Royal, Singapore. The two-day workshop is jointly organized by TC-20 and the School of Computer Engineering, Nanyang Technological University, Singapore, and sponsored by IAPR.

PRIB 2007 Organizing Committee

General Chair: Jagath C. Rajapakse, Nanyang Technological University, Singapore
General Co-Chair: Raj Acharya, Pennsylvania State University, USA
Program Chairs: Bertil Schmidt, University of New South Wales Asia, Singapore
Gwenn Volkert, Kent State University, USA
Special Session Chairs: Shandar Ahmad, National Institute of Biomedical Innovation, Japan
Madhu Chetty, Monash University, Australia
Elena Marchiori, Vrije University of Amsterdam, the Netherlands
Publicity Chairs: Saman K. Halgamuge, University of Melbourne, Australia
Roberto Tagliaferri, Università Di Salerno, Italy
Wei Wang, Fudan University, China
Yanqing Zhang, Georgia State University, USA
Publication Chairs: Sy Loi Ho, Nanyang Technological University, Singapore
Feng Lin, Nanyang Technological University, Singapore
Local Chair: Graham Leedham, University of New South Wales Asia, Singapore
Local Organizing: Byron Koon Kau Choi, Nanyang Technological University, Singapore
Yulan He, Nanyang Technological University, Singapore
Hwee Kuan Lee, Bioinformatics Institute, Singapore
Jinming Li, Nanyang Technological University, Singapore
Secretary: Norhana Ahmad, Nanyang Technological University, Singapore
Technical Executive: Sing Yau Tan, Nanyang Technological University, Singapore
Webmaster: Linda Ang, Nanyang Technological University, Singapore
Program Committee: Tatsuya Akutsu, Kyoto University, Japan
Guillaume BOURQUE, Genome Institute of Singapore, Singapore
Timo Rolf Bretschneider, Nanyang Technological University, Singapore
Zehra Cataltepe, Istanbul Technical University, Turkey
Phoebe Chen, Deakin University, Australia
Francis Y.L. Chin, University of Hong Kong, Hong Kong
Peter Clote, Boston College, USA
David Corne, Heriot-Watt University, UK
Carlos Cotta, University of Malaga, Spain
Antoine Danchin, Institut Pasteur, France
Joaquín Dopazo, Centro de Investigación Príncipe Felipe, Spain
James G. Evans, Massachusetts Institute of Technology, USA
Alexandru Floares, Oncological Institute Cluj-Napoca, Romania
Mikhail S. Gelfand, Institute for Information Transmission Problems, Russia

Ilkka Havukkala, Auckland University of Technology, New Zealand
Jaap Heringa, Vrije Universiteit, the Netherlands
Lisa Holm, University of Helsinki, Finland
Ming-Jing Hwang, Academia Sinica, Taiwan
Visakan Kadirkamanathan, University of Sheffield, UK
Nikola Kasabov, Auckland University of Technology, New Zealand
Irwin King, The Chinese University of Hong Kong, Hong Kong
Alex V. Kochetov, Russian Academy of Sciences, Russia
Vladimir A. Kuznetsov, Genome Institute of Singapore, Singapore
Chee Keong Kwoh, Nanyang Technological University, Singapore
Wing-Ning Li, University of Arkansas, USA
Alan Wee-Chung Liew, Chinese University of Hong Kong, Hong Kong
Frederique Lisacek, Swiss Institute of Bioinformatics, Switzerland
Hiroshi Matsuno, Yamaguchi University, Japan
Martin Middendorf, Universität Leipzig, Germany
Mariofanna Milanova, University of Arkansas at Little Rock, USA
Aleksandar Milosavljevi, Baylor College of Medicine, USA
Satoru Miyano, University of Tokyo, Japan
Jason H. Moore, Dartmouth Medical School, USA
Parvin Mousavi, Queen's University, Canada
See-Kiong Ng, Institute for Infocomm Research, Singapore
Yanay Ofran, Columbia University, USA
Christos Ouzounis, European Bioinformatics Institute, UK
Zoran Obradovic, Temple University, USA
Nikhil R. Pal, Indian Statistical Institute, India
Laxmi Parida, IBM T.J. Watson Research Center, USA
Mihail Popescu, University of Missouri, USA
Predrag Radivojac, Indiana University, USA
Nikolaus Rajewsky, Max Delbrück Center for Molecular Medicine, Germany
Jem Rowland, University of Wales Aberystwyth, UK
Meena Kishore Sakharkar, Nanyang Technological University, Singapore
Akinori Sarai, Kyushu Institute of Technology, Japan
Alexander Schliep, Max Planck Institute for Molecular Genetics, Germany
Christian Schoenbach, Nanyang Technological University, Singapore
N.Srinivasan, Indian Institute of Science, India
P. N. Suganthan, Nanyang Technological University, Singapore
Wing Kin Sung, National University of Singapore, Singapore
Anna Tramontano, University of Rome "La Sapienza", Italy
Michael Wagner, Cincinnati Children's Hospital Research Foundation, USA
Haiying Wang, University of Ulster at Jordanstown, N. Ireland
Lusheng Wang, City University of Hong Kong, Hong Kong
Michael Q. Zhang, Cold Spring Harbor Laboratory, USA

PRIB 2007 has received a total number of 128 papers and 46 papers were accepted (36%) for oral presentations. The papers presented at the oral sessions will be published as a volume in the *Lecture Notes in Bioinformatics* (a sub-series of *Lecture Notes in Computer Science*) by Springer. The best papers have been invited for consideration of publication in a *Special Issue of IEEE Engineering in Medicine and Biology Magazine* on "Pattern discovery from bioinformatics data".

Poster presentations are published in a Supplementary Proceedings of PRIB 2007.

The workshop will feature talks by the following keynote speakers:

Gary Fogel, Natural Selection Inc., San Diego, USA
Nikhil R. Pal, Indian Statistical Institute, India
Raj Acharya, The Pennsylvania State University, USA
Glenn Tesler, University of California, San Diego, USA

There will be two parallel sessions of oral presentations and one poster session on each day of the workshop.

The awards will be given to the Best Paper, Best Student Paper, and Best Poster at the workshop. About twenty five PRIB 2007 Student Awards towards their registration will be awarded. Three travel awards will be offered to overseas students.

Third IAPR International Conference on Pattern Recognition in Bioinformatics (PRIB 2008)

Novotel St Kilda, Melbourne VIC- 3182, Australia

Oct 15 – 17, 2008

<http://www.infotech.monash.edu.au/prib08>

The arrangements are under way to hold from Oct 15 – 17, 2008 at Novotel St Kilda Melbourne Australia. The three-day conference is jointly organized by and TC-20 and the Faculty of IT, Monash University Australia and is sponsored by IAPR. This year PRIB was upgraded to a conference.

PRIB 2008 Organization

| | |
|--------------------------|---|
| General Chair | Madhu Chetty Monash University, Australia |
| General Co-Chair | Raj Acharya Pennsylvania State University, USA |
| Program Co-Chairs | Alioune Ngom, University of Windsor, Canada Jagath C. Rajapakse, Nanyang Technological University, Singapore |
| Technical Co-Chairs | Elena Marchiori Vrije Universiteit, The Netherlands Bertil Schmidt NICTA, Australia |
| Short Paper Co-Chairs | Shandar Ahmad National Institute of Biomedical Innovation, Japan Ponraj Prabhakaran Duke University, USA Michael Grominha Computational Biology Research Centre, Japan |
| Special Session Chair | Alioune Ngom University of Windsor, Canada |
| Local Organization Chair | Shyh Wei Teng Monash University, Australia |
| Publicity Co-Chairs | Shandar Ahmad National Institute of Biomedical Innovation, Japan Phoebe Chen Deakin University, Australia Mariofanna Milanova University of Arkansas at Little Rock, USA Md. Tamjidul Hoque Gri_th University, Australia |
| Publication Co-Chairs | Sy Loi Ho Nanyang Technological University, Singapore Girija Chetty University of Canberra, Australia |
| Sponsorship Chair | Dieter Bulach CSIRO, Australia |
| Finance Manager | Narelle Wilkins Monash University, Australia |
| Secretariat | Tina Bradshaw Monash University, Australia |
| Webmaster | Margot Schuhmacher Monash University, Australia |
| Technical Manager | Glen Pringle Monash University, Australia |
| Program Committee | Raj Acharya Pennsylvania State University, USA Shandar Ahmad Nat Inst Biomedical Innovation, Japan Tatsuya Akutsu Kyoto University, Japan |

James Bailey University of Melbourne, Australia
Tim Bailey University of Queensland, Australia
Sanghamitra Bandyopadhyay Indian Statistical Institute, India
Wolfgang Banzhaf Memorial University of Newfoundland, Canada
Justin Bedo The Australian National University, Australia
Nitin Bhardwaj University of Illinois at Chicago, USA
Mikael Boden University of Queensland, Australia
Sebastian Boecker Friedrich-Schiller-Universitaet Jena, Germany
Guillaume Bourque Genome Institute of Singapore, Singapore
Roelof Brouwer University of Stellenbosch, South-Africa
Vladimir Brusic Dana-Farber Cancer Institute
Shakuntala Bulusu DNA Research Centre, India
Conrad Burden Australian National University, Australia
Yu-Dong Cai Shanghai Institutes for Biological Science, China
Frederic Cazals INRIA Sophia, France
Francis Chin The University of Hong Kong, China
Peter Clote Boston College, USA
Michael Cohen Gri_th University, Australia
Yun Cui Nanyang Technological University, Singapore
Antoine Danchin Institut Pasteur, France
Suash Deb National Institute of Science and Technology
Omid Dehzangi Nanyang Technological University, Singapore
Yong-Sheng Ding Donghua University, China
M. Michael Gromiha Computational Biology Research Center
Nadia El-Mabrouk University of Montreal, Canada
Alexandru Floares Oncological Institute Cluj-Napoca
Gary B. Fogel Natural Selection Inc., USA
Mehdi Ghayoumi Azad University, Iran
Prashant Goley University Nanded Maharashtra, India
Iqbal Gondal Monash University, Australia
Robin Gras University of Windsor, Canada
Saman K. Halgamuge University of Melbourne, Australia
Xiaoxu Han Eastern Michigan University, USA
Jin-Kao Hao University of Angers, France
Jaap Heringa Vrije Universiteit, Belgium
Sy Loi Ho Nanyang Technological University, Singapore
Md Tamjidul Hoque Gri_th University, Australia
Seiya Imoto University of Tokyo, Japan
Shunsuke Inenaga Kyushu University, Japan
R. Krishna Murthy Karuturi Genome Institute of Singapore, Singapore
Nawaz Khan Middlesex University, UK
Amit Kumar DNA Research Centre, India
Lukasz Kurgan University of Alberta, Canada
Adam Kowalczyk NICTA, Australia
Vlad Kuznetsov Genome Institute of Singapore, Singapore
Zoe Lacroix Arizona State University, USA
Hon Wai Leong National University of Singapore, Singapore
Jinyan Li Nanyang Technological University

Vladimir Likic University of Melbourne, Australia
Feng Lin Nanyang Technological University, Singapore
Tsun-Chen Lin Dahan Institute of Technology, Taiwan
Frederique Lisacek Swiss Institute of Bioinformatics, Switzerland
Feng Liu Vrije Universiteit, Belgium
Lifang Liu Xi'an University, China
Weiguo Liu National Technological University, Singapore
Geo_Macintyre Victorian Research Lab, Australia
Niranjan Mahesan University of Shefeld, UK
Veli Makinen University of Helsinki, Finland
Elena Marchiori Vrije Universiteit, The Netherlands
Hiroshi Matsuno Yamaguchi University, Japan
Geo_McLachlan University of Queensland, Australia
Aleksandar Milosavljevic Baylor College of Medicine
Martin Middendorf University of Leipzig, Germany
Mariofanna Milanova Uni of Arkansas at Little Rock, USA
Satoru Miyano University of Tokyo, Japan
Krishna Mohan NIBIO, Japan
Sukanta Mondal NIBIO, Japan
Bernard Moret Swiss Federal Institute of Technology, Switzerland
Narayana Nagesh Centre for Cellular and Molecular Biology, India
See-Kiong Ng Institute for Infocomm Research
Alioune Ngom University of Windsor, Ontario, Canada, Canada
Bing Niu Shanghai University, China
Diana Oliveira Universidade Estadual do Ceara, Brazil
Nikhil R. Pal Indian Statistical Institute, India
Kuldip Paliwal Griffith University, Australia
Mihail Popescu University of Missouri-Columbia, USA
Jagath Rajapakse Nanyang Technological University, Singapore
Ramesh Ram Monash University, Australia
Alice Richardson University of Canberra, Australia
Luis Rueda Universidad de Concepcion, Chile
Marie-France Sagot INRIA, France
Meena Kishore Sakharkar Nanyang Technological University, Singapore
Alexander Schliep Max Planck Institute for Molecular Genetic, Germany
Bertil Schmidt NICTA, Australia
Christian Schoenbach Nanyang Technological University, Singapore
Jan Schröder Christian-Albrechts-University of Kiel, Germany
Heiko Schroeder RMIT University
Muhammad Shoaib Sehgal University of Queensland, Australia
Mona Singh Princeton, USA
Ingolf Sommer Max-Planck-Institute for Informatics, Germany
Alexandros Stamatakis Ludwig-Maximilians-University Munich, Germany
Gregor Stiglic University of Maribor, Slovenia
Wing Kin Sung National University of Singapore, Singapore
Roberto Tagliaferri Universiti di Salerno
Y-H. Taguchi Chuo University, Japan

Shyh Wei Teng Monash University, Australia
Qi-Chuan Tian Taiyuan University of Science and Technology, China
Lokesh Tripathi NIBIO, Japan
Lusheng Wang City University of Hong Kong, China
Alan Wee-Chung Liew Griffith University, Australia
Yanqing Zhang Georgia State University, USA
Xingming Zhao Shanghai University, China
Justin Zobel NICTA

PRIB 2008 has received a total number of 121 papers and 39 papers were accepted (32%) for inclusion in the volume in the *Lecture Notes in Bioinformatics* (a sub-series of Lecture Notes in Computer Science) published by Springer. A supplementary proceedings published by PRIB 2008 was also published to include 12 Short papers and the remaining regular papers. Authors of top selected papers presented at PRIB 2008 will be invited to extend their work for consideration for publication in following special issues of reputed journals:

a) Elsevier's Pattern Recognition Letters (PRL) journal: Special Issue on "Pattern recognition in bioinformatics"

b) Elsevier's Neurocomputing journal: Special Issue on "Neurocomputing in bioinformatics and computational biology"

The Conference will feature talks by the following keynote speakers:

1. Professor Haruki Nakamura (Osaka University, Japan)
2. Associate Professor Ram Samudrala, (University of Washington , USA)
3. Professor David Sankoff (University of Ottawa , Canada)
4. Professor Geoff McLachlan (The University of Queensland , Australia)

There will be two parallel sessions of oral presentations for the three days of the conference. The conference dinner is organized on the second day of the conference. On the final day, a panel discussion on the theme, "Microarrays" has also been scheduled involving three experienced panelists from bioinformatics community.

The awards will be given to the Best Paper, Best Student Paper, and Best Short Paper at the conference. About seventeen PRIB 2008 student registration awards towards their will be given. Seven student travel awards will be offered to overseas students.

Special Sessions at WCCI-2008

Two special sessions were conducted at WCCI-2008 by TC-20.

NN10 - Analysis of Gene and Protein Expression Data

Organizers:

Vladimir Kuznetsov, Genome Institute of Singapore, kuznetsov@gis.a-star.edu.sg
Jagath Rajapakse, Nanyang Technological University, Singapore, jagath@ieee.org

Paper submission deadline: December 1, 2007

For instruction on paper submission, visit WCCI website: <http://www.wcci2008.org/>

Advances in high throughput technologies, such as microarrays, sequences-based DNA-protein complexes, and mass spectrometry methods, and the availability of human and other complex genome sequences now allow scientists to identify gene expression profiles, gene copy numbers, transcription factor binding sites (TFBS), regulatory pathways, macromolecular interaction networks at genome scale. Furthermore, computational approaches are combined to make inferences on complex pictures of basic biological phenomena such as cancer progression, stem cell differentiation, etc.

To infer such phenomena, researchers have widely used computing paradigms such as feed-forward neural networks, self-organizing feature maps, SVM, independent component analysis, genetic algorithms, etc., to predict essential gene expression patterns, gene and protein modules, DNA-protein, protein-protein, RNA-protein networks. This had led to a numerous approaches for data analysis and data mining, and web servers providing useful classifications and predictions tools for gene and protein expression analysis. However, novel neural network based algorithms and their hybrids with computer simulations and statistic-based approaches, which are capable of handling diverse high throughput expression data for feature detection, feature selection, pattern recognition, and evolutionary analysis, effectively are urgently required. The subsequent challenge is quantitative and integrative analyses, and adequate interpretation of voluminous data having potentially low signal to noise ratio, high dimension and essential incompleteness of genome-scale datasets.

We invite papers dealing with all aspects of computational analysis and modeling of gene expression, transcription control (genome, transcriptome, and proteome complexity), mass spectra, prediction and modeling of different types of macromolecular interaction networks:

Areas of interests are but not limited to as follows:

- Preprocessing and de-noising of data
- Techniques for feature extraction and gene selection
- Clustering and identifying co-expressed genes
- Identification gene signatures and co-regulatory gene patterns
- Prediction of binding sites and regulatory modules at genome scale level
- Predication and analysis microRNAs, their targets, and antisense interactions
- Identification and prediction direct gene targets for TF and their combinations
- Analysis of spatio-temporal gene expression patterns and finding gene regulatory networks.
- Analysis of normal and disease pathways
- Optimization and automation of pattern recognition protocols and methods for complex data visualization

This specials session is organized by IAPR Technical Committee on Pattern Recognition for Bioinformatics ([TC-20](#)).

NN09 - Prediction of protein structures and features

Organizers:

Shandar Ahmad, National Institute of Biomedical Innovation, Osaka, Japan

(shandarahmad@yahoo.com)

Michael Gromiha, Computational Biology Research Center, AIST, Tokyo, Japan (michael-gromiha@aist.go.jp)

Paper submission deadline: December 1, 2007

For instruction on paper submission, visit WCCI website: <http://www.wcci2008.org/>

Synopsis

Biological experiments to determine structure and function of proteins are far behind those generating sequences. Computational methods to determine structure and function of a protein from its amino acid sequence have a challenging task despite the widely held view that all structural information is available from the amino acid sequence of a protein. At a local level, structure and function of a protein have been computationally defined in the form of features such as secondary structure, solvent accessibility, disorder and dihedral angles. Also, function has been typically the residue-wise characterization of protein-protein, protein-DNA and protein-ligand interaction sites. On a full sequence scale, such characterization is aimed at identifying structure class, fold, and topology of the protein and protein-protein interaction pairs.

Researchers have widely used neural networks related paradigms such as MLP, recurrent networks, SVM, evolutionary algorithms, etc., to predict protein structure and functional features. This has led to a number of models, algorithms and web servers providing useful predictions. We invite papers dealing with all aspects of prediction and modeling of protein structure and function by computational approaches. The areas of interests are but not limited to as follows:

- Prediction of protein secondary and 3-D structure
- Prediction of binding sites
- Prediction of protein-protein interaction pairs
- Prediction of solvent exposure, trans-membrane and disordered regions.
- Prediction of domains, domain boundaries, class, fold and architecture.
- Computational theories and intelligent models of proteins
- Knowledge representation and feature selection
- Protocol optimization and automation for protein structure and function prediction

This special session is organized by IAPR Technical Committee on Pattern Recognition on Bioinformatics ([TC-20](#))

Technical Committee:

Shandar Ahmad, National Institute of Biomedical Innovation, Japan

Zulfiqar Ahmad, East Tennessee State University, USA

Samuel Selvaraj, Bhartidasan University, India

Dongbo Bu, Chinese Academy of Sciences, China

Xin Gao, Univ. of Waterloo, Canada

Michael Gromiha, Computational Biology Research Center, AIST, Japan

A.Y. Istomin, University of North Carolina Charlotte, USA

S. C. Li, Univ. of Waterloo, Canada

Chioko Nagao, National Institute of Biomedical Innovation, Japan

Ponraj Prabhakaran, Duke University, USA

Shaikh Abdul Rajjak, Kyoto University, Japan

Y. H. Taguchi, Chuo University, Japan

5. Member Activities

5.1 Conferences

Several TC-20 members are actively engaged as Chairs of related conferences:

- Limsoon Wong: conference chairs of *RECOMB 2008*, Singapore, from 30 March – 2 April, 2008; *GIW 2007*, Singapore from 3 - 5 Dec 2007; *BioDM 2007* in May 2007, China.
- Gwenn Volkert: general co-chairs for the *2007 IEEE Symposium on Computational Intelligence in Bioinformatics and Computational Biology* in Honolulu, Hawaii from April 1-5, 2007.
- Phoebe Chen: conference co-chair of the *CMLSA2007*, November 05-09, 2007, Auckland, New Zealand.
- Elena Marchiori: conference co-chair and program co-chair for the *5th European conference On Evolutionary Computation Machine Learning And Data Mining In Bioinformatics (EvoBIO 2007)* in Valencia, Spain, 11-13 April 2007..
- Saman Halgamuge: program vice-chair of *IEEE Vehicular Technology Conference* from 25 to 28 September 2006 in Montréal, Québec, Canada; general co-chair of *IEEE International Conference on Information Acquisition* from August 20 - 23, 2006 in Shandong University, China.
- Visakan Kadirkamanathan: co-chair, *IEEE UK&RI Control Systems Chapter Colloquium on 'Control in Systems Biology'*, Sheffield, 2007
- Irwin King: workshop chair, *World Congress on Computational Intelligence (WCCI2008)* in Hong Kong from June 1-6, 2008; technical track chair, *Pacific-Rim Conference on Multimedia* in Hong Kong from 11-14 December 2007 and as Technical Co-Chair, *International Joint Conference on Neural Networks (IJCNN2007)* in Orlando, Florida from August 12 -17, 2007.
- Yanqing Zhang: program co-chair: *IEEE 7th International Symposium on Bioinformatics & Bioengineering (BIBE07)*, Cambridge - Boston, Massachusetts, USA, October 15-17, 2007; as vice chair of the *2007 International Conference on Bioinformatics & Computational Biology (BIOCOMP'07)*, Las Vegas, June 25-28, 2007; vice chair of the *2007 International Conference on Artificial Intelligence*, Las Vegas, June 25-28, 2007; and organizing co-chair: *2007 International Symposium on Bioinformatics Research and Applications (ISBRA2007)*, Atlanta, May 7-10, 2007.
- Jagath C. Rajapakse: general co-chair of *2007 IEEE Symposium on Computational Intelligence in Bioinformatics and Computational Biology* in Honolulu, Hawaii from April 1-5, 2007; program co-chair for the *5th European conference On Evolutionary Computation Machine Learning And Data Mining In Bioinformatics (EvoBIO 2007)* in Valencia, Spain, 11-13 April 2007.
- Vladimir Brusica: Congress Co-chair for the *International Congress of Immunogenomics and Immunomics (BCII 2006)*, Oct 8-12, 2006, Budapest, Hungary.

5.2 Editorial activities

Several TC-20 members serve as either Editors or Associate Editors of related journals:

- Nikhil Pal: the Editor-in-Chief of *IEEE Transactions on Fuzzy Systems*
- Limsoon Wong: Managing Editor of *Journal of Bioinformatics and Computational Biology* and in the editorial boards of *Bioinformatics* and *Drug Discovery Today*.
- Raj Acharya: Associate Editors of *IEEE/ACM Transactions on Bioinformatics and Computational Biology*.
- Vladimir Brusic: the Deputy Editor of the *Immunome Research*, and an Editorial Board Member of *Briefings in Bioinformatics*.
- Phoebe Chen: Associate Editor for the *IEEE Transactions on Multimedia*, an Associate Editor for the *Journal of Research and Practice in Information Technology*, an Associate Editor for the *International Journal of Intelligent Computing in Medical Sciences and Image Processing*
- Dave W. Corne: Editorial Boards for *IEEE Computational Intelligence Magazine (IEEE)*, *IEEE Transactions on Evolutionary Computation*, of *Evolutionary Computation (MIT Press)*, of *Applied Soft Computing (Elsevier)*, *International Journal of Bioinformatics Research and Applications (Inderscience)*, *International Journal of Hybrid Intelligent Systems (IOS Press)*, *Applied Intelligence (Elsevier)*, the Editorial Board for *Journal of Computational Intelligence in Bioinformatics*
- Gary Fogel: an associate editor for the journals *BioSystems*, *IEEE Transactions on Evolutionary Computation*, *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, *IEEE Computational Intelligence Magazine*, and *Ecological Information*
- Visakan Kadirkamanathan: Co-Editor of the *International Journal of Systems Science*.
- Irwin King is the Special Issue Guest Editor, *Neurocomputing*, *International Journal of Computational Intelligent Research (IJCIR)*, 2006
- Jagath C. Rajapakse: Associate Editor of *IEEE/ACM Transactions on Bioinformatics and Computational Biology*; Associate Editor, *IEEE Transactions on Medical Imaging*, Editorial Board member, *Neural Information Processing -- Letters and Reviews* and Guest Editor for *IEEE Engineering in Medicine and Biology Magazine*.
- Qiang Yang is the Associate Editor of *Journal of Computational Intelligence in Bioinformatics*, *International Journal of Data Mining and Bioinformatics*; Guest Editor of *IEEE/ACM Transactions on Computational Intelligence Approaches in Computational Biology and Bioinformatics*.
- Gwenn Volkert: Associated Editor for the new *IEEE Computational Intelligence Magazine*.

6. Summary and Future Plans

- Due to increased interest in PRIB, the workshop was upgraded to and held as a three day conference PRIB 2008.
- PRIB 2009 will be organized by University of Sheffield (General Chairs: Visakan Kadirkamanathan and Guido Sanguinetti) in August, 2009.
- Invite TC-20 members for July 2007 – July 2009 period
- Open PRIB membership of TC-20 via the website.
- Three journal special issues are in progress
- As recommended by IAPR VP (Technical Committees), TC-20 website has been upgraded and some of the activities of TC-20 has been made available:
 - Education: through the website. The educational materials such as lecture notes, tutorials, etc., are yet to be made available.
 - Research: activities of TC-20 have been made available. A database of bioinformatics applications, bioinformatics software and benchmark datasets to be constructed and maintained.
 - Events: annual conference of TC-20, PRIB, is evolving well. Two special sessions were organized by TC-20 at WCCI 2008. 3 journal special issues.