

ANNUAL PROGRESS REPORT: 2003-04

BioInformatics Research Centre (BIRC) Nanyang Technological University, Singapore

I. INTRODUCTION

The BioInformatics Research Centre (BIRC) was established on March 1, 2002, under NTU's partnership with Hewlett-Packard Asia to jointly establish a center of excellence in bioinformatics. The BIRC is the focus of the education, research and development, and human-resource training in bioinformatics at NTU. BIRC is an inter-school research centre hosted by the School of Computer Engineering (SCE). Currently 23 staff members from SCE, SBS, NIE, MPE, and EEE are affiliated and based their research projects at BIRC. It has 7 full-time researchers and 19 Ph.D. students.

Bioinformatics is the field of analyzing biological data, such as sequences, expressions, phenotypes, images, and literature, to discover biological knowledge leading to discover novel drugs and therapeutics. The mission of BIRC is to provide the interdisciplinary environment and training for students and researchers to engage in leading and cutting edge research in bioinformatics at NTU, and thereby become a part of the life sciences workforce in Singapore and elsewhere. BIRC brings together scientists and engineers, who are interested in bioinformatics modeling and computation, and fosters cross-disciplinary interactions among different schools to perform advanced research in bioinformatics. It also facilitates the teaching and research projects of the MSc. (Bioinformatics) offered by SCE.

Mission: The BioInformatics Research Centre (BIRC) has a mission to provide interdisciplinary environment and training for students and researchers to engage in leading and cutting edge research in bioinformatics in NTU, and thereby become a part of the life sciences workforce in Singapore and elsewhere.

Vision: The Centre's vision is to dedicate itself to the advancement of bioinformatics through education, research, and scientific breakthroughs, leading to discoveries of new medical drugs and therapies.

II. RESEARCH INTERESTS

BIRC research interests are currently focussed on the following research areas:

a) GENOMICS

Computational genomics, gene structure prediction, comparative genomics, phylogenetic studies, gene expression analysis

b) STRUCTURAL GENOMICS AND PROTEOMICS

Protein structure prediction, protein-protein interactions, protein classification, modeling, and docking, mass spectroscopy.

c) BIOLOGICAL DATABASES, MINING, AND VISUALIZATION

Biological data integration, storage, and query processing, 3-D visualization.

d) FUNCTIONAL AND MOLECULAR IMAGING

Functional brain imaging, molecular imaging, microarray and electrophoresis image analysis, bioimaging databases.

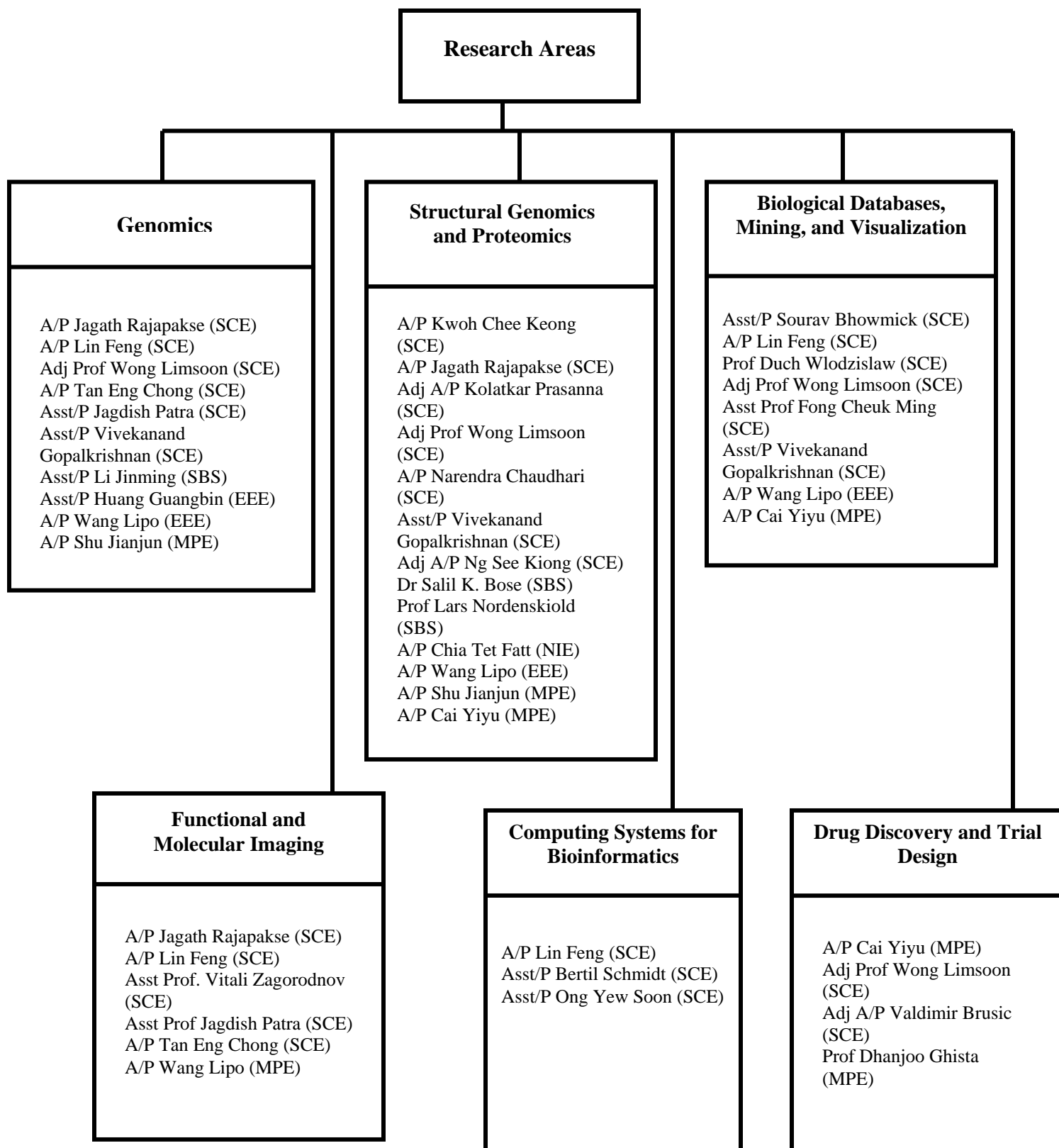
e) COMPUTING SYSTEMS FOR BIOINFORMATICS

Immunoinformatics, modeling human immune system

f) DRUG DISCOVERY AND TRIAL DESIGN

Parallel algorithms and architectures for bioinformatics, grid computing, embedded systems for bioinformatics.

The interests of staff in the center are distributed across its research areas:



III. RESEARCH FUNDING

The research funding for the centre comprises of the following:

List of current research projects					
S/No	Project Title	Source Of Funding	Principle Investigators/ Collaborators	Amount Of Funding S (\$)	Duration (Date)
01	Bio-visualisation	A*Star	A/P Cai Yiyu	\$748,000	2003-2006
02	Elucidation of Expression Profiles of Genes in Alpha-fetoprotein Positive and Alpha-fetoprotein Negative Hepatocellular Carcinoma by cDNA Microarray Analysis	BMRC & NMRC	A/P Lin Feng (collaborator)	\$113,000	2004
03	Design and Simulation of Artificial Bone Implantation	MOE & ARF	A/P Lin Feng	\$17,402	2001-2004
04	Analysis of functional brain images	RGM11/03	A/P Jagath Rajapakse	\$140,000	Oct 2003 – Oct 2006
05	Neural systems modeling using functional MRI	MOE & A*STAR	A/P Jagath Rajapakse	\$658,320	Oct 2002 – May 2006
06	Strategic research initiative at TechnoPlaza	RGM 4/03	A/P Wong Kok Cheong (PI)/ A/P Jagath Rajapakse	\$150,000	Jul 2003 – Dec 2004
07	Markov Random Field based spatial regularization for fMRI detection	CE – SUG 2/04	Asst Prof Vitali Zagorodnov	\$15,625	Oct 2004 – Oct 2005

IV. RESEARCH PROJECTS

Signal Detection in Genomic Sequences

Detection of signals in genomic sequences is important in inferring transcription and translational processes and finding gene annotation. BIRC has developed a Markov/hybrid method to detect three types of signals, namely, splice sites, transcription initiation sites, and transcription start sites. This approach uses a Markov encoding method as inputs to the neural networks, which has given better accuracies over the conventional orthogonal coding.

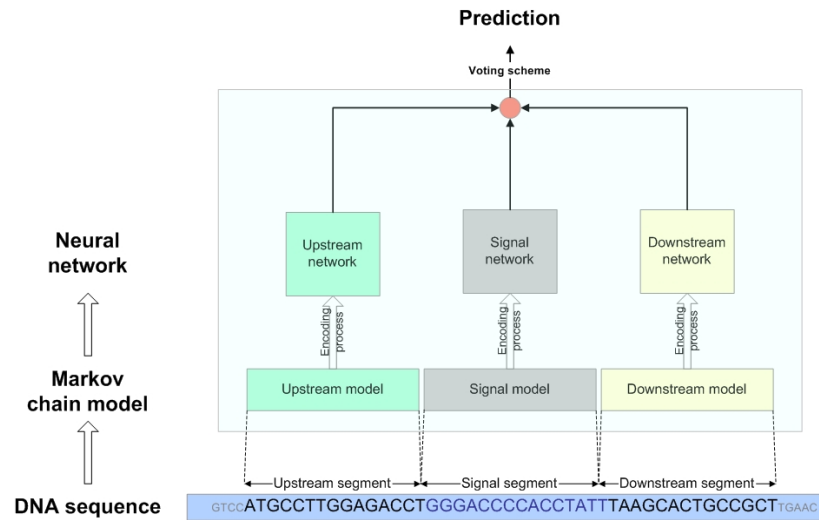


Figure 1: Markov/neural hybrid model for the detection of signals in genomic sequences

Inferring Molecular Evolution of PD and AD Genes with Comparative Genomics

BIRC has taken a comparative genomic approach to infer the evolution of the genes affecting Parkinson's Disease (PD) and Alzheimer's Disease (AD), including the variants of PARK genes. The study used relative rate tests to determine synonymous and nonsynonymous substitutions. Comparative genomics of human, chimp, mouse, chicken, and fugu revealed most of the genes did not provide evidence of rate heterogeneity, thereby inferring most of them are undergoing neutral or nearly neutral mutation.

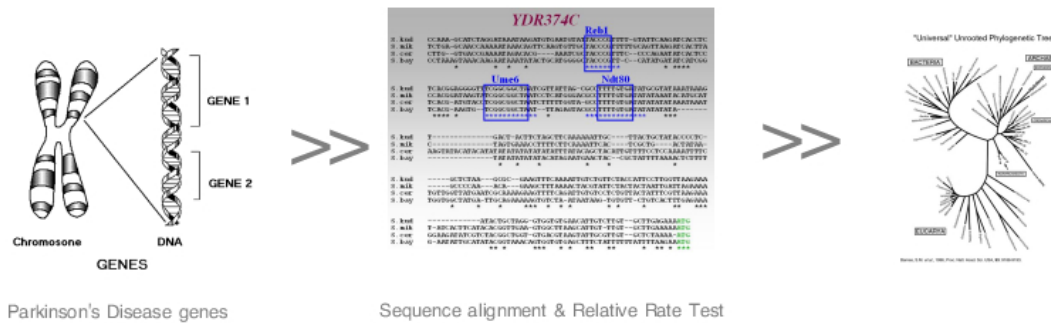


Figure 2: The framework for phylogenetic studies on Parkinson's and Alzheimer's Disease genes.

Neural Network Based Analysis of DNA Microarray Gene Expression Data

DNA microarray technologies provide gene expression data on a massive scale involving thousands of genes. Exploratory data analyses in the form of clustering analysis with a goal to group the genes into meaningful sets are investigated using neural networks and machine learning approaches: Kohonen's self-organizing map (SOM), PCA and ICA algorithms, and SVMs. Our development leads to identify the genes whose transcript profiles response to specific stimuli such as timing, cell type, temperature, or drug dosage. The objective is to estimate pertinent parameters for individual transcripts, with a goal of testing specific hypotheses concerning transcript response to the stimulus.

Computational Approaches for Reconstructing Gene Regulatory Networks

The rapid accumulation of complete genome sequences and the application of microarray technology to genome-wide gene expression profiling have made computational approaches to the regulatory motif discovery and the study of transcriptional regulatory networks feasible. DNA-binding transcription factors (TFs) are one of the important components of transcription regulatory network. TFs usually bind to specific, short DNA sequence motifs in the cis-regulatory region of a gene to activate or repress its expression in response to changes in the environment. This project looks in to the development of novel methods or the improvement of the current methods for identifying transcription factor binding sites by analyzing time course microarray data. We also use expression profiling to identify sets of co-regulated genes and correlate these to regulatory motif search. The underlying assumption of using microarray data in regulatory region analysis is that a set of co-regulated genes usually share a similar set of regulatory motifs.

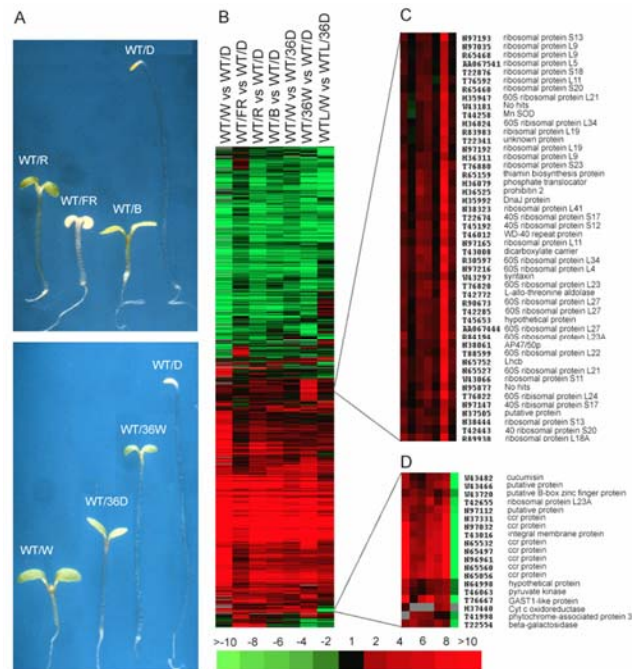


Figure 3: Gene expression profile data was used to identifying coordinate regulated genes in Arabidopsis genome

Predicting Protein-Protein Interfaces Directly from Amino-acid Sequences

Protein-protein interactions are fundamental biochemical reactions in the organisms and play an important role in determining the biological processes. A novel information theory based algorithm is being developed for predicting protein-protein interfaces directly from amino-acid sequences. Each type of interface corresponds to a different functional or structural association between residues. With this method and using amino acid composition alone, we expect to predict statistically which of the six different types of interfaces a pool of 1000 residues at a better accuracy. The six types of interfaces include intra-domain, domain-domain, homo-obligomer, homo-complex, hetero-obligomer, and hetero-complex.

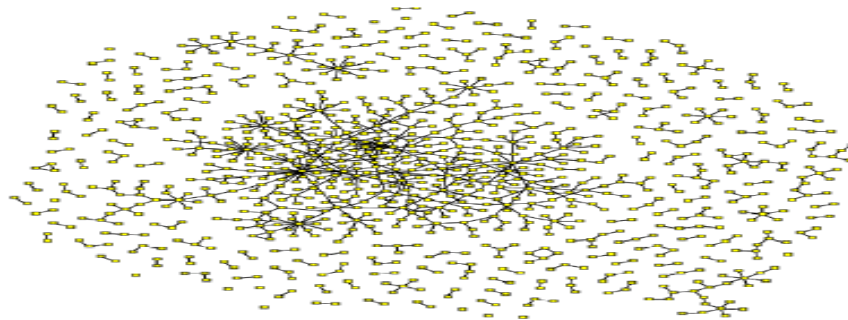


Figure 4: Illustration of a protein-to-protein interaction network

Cancer Classification with Mass Spectra Data

BIRC has addressed the problem of cancer classification with mass spectra data and used Support Vector Machine Recursive Feature Elimination (SVM-RFE) to select a small subset of peaks as input variables for classification. We found that SVM-RFE always selects the best peak subset which has the top ranked peaks detected by T-statistics. Our finding supports that selecting a small subset of peaks not only improves the efficiency of the algorithm, but also improves the cancer classification accuracy.

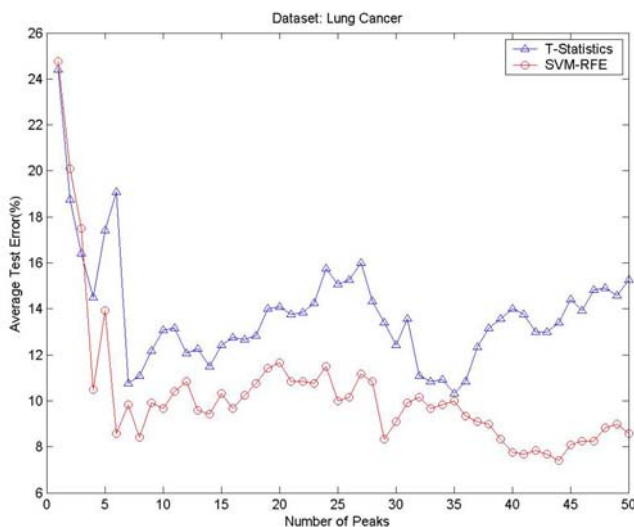


Figure 5: Average test error rates at different sizes of peak subsets, selected by T-statistics and SVM-RFE, on Lung Cancer dataset

Computer Simulations Modeling Electrostatic Attraction of Nucleosomal DNA Mediated by Charged Histone Tails

The fundamental unit of DNA packed in chromatin in eukaryotic cells is the nucleosome core particle (NCP), composed of a histone protein octamer core with DNA wrapped around it and flexible positively charged histone tails protruding out. The net negatively charged NCPs also show counterion induced aggregation *in vitro*. DNA-histone tail interactions are important for the mechanisms which are responsible for transcription and replication. Molecular dynamics (MD) computer simulations of charged tail – DNA interactions in systems mimicking NCPs are performed modeling simplified systems of the NCP as flexible polycationic histone tails attached to the negatively charged spherical particle, with a dielectric model of the aqueous solvent. The size, charge and distribution of the tails relative to the core were built mimicking real NCP. Results are in good agreement with experimental data. More detailed mechanisms of the histone tail – DNA binding and dynamics have been obtained from all-atom MD simulations (including water) comprising three parallel DNA oligomers and fragments of the H4 histone tail. We found correlation of the DNA-DNA distance with the presence and binding of the histone

tail between the DNA molecules. Future comparison of the results for unmodified and modified (reduced positive charge on the tails corresponding to transcriptionally active states of chromatin) could help to understand molecular mechanisms behind epigenetic control of transcriptional regulation.

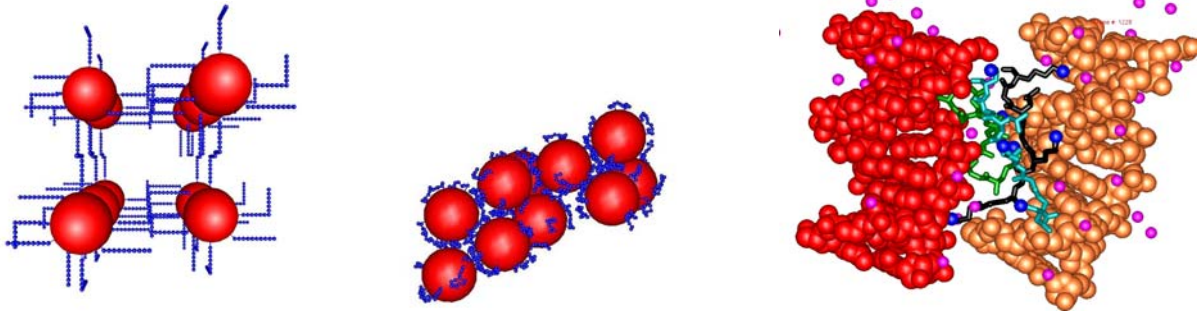


Figure 6: Initial configuration of NCPs in dielectric continuum MD simulations (left); aggregation in the presence of Mg^{2+} (middle); DNA - DNA interaction mediated by positively charged peptide histone tails from all atom MD (water not shown) (right).

BioWare: A Warehouse of Biological Data

We build a biological data integration system, BioWare, that is build on XML data model and supports novel query optimization techniques. We first generate a relational schema. Second, we transform data from various sources to XML format by creating valid XML documents of the corresponding data. Third, we parse XML documents created from the previous step and load them into tuples of relational tables in a standard commercial DBMS (in our case, SQL Server). We support a visual XML-based query interface. Through the interface, DTD/schema of stored XML documents are displayed, and users can formulate queries by clicking the relevant data elements and entering conditions. Such queries are transformed into SQL queries over the corresponding relational data. The results are formatted as XML documents and returned back to the user or passed to another application for further processing. The novelties of our system are as follows: it creates an illusion of a fully XML-based data management system as the underlying relational system remains hidden from the users; the storage structure does not need to be maintained when the structure of remote sources evolve; it allows bioinformatics researchers to concentrate on gathering and analysis of data and relieving them of the burden of learning new query languages; it expedites query processing greatly; our approach provides us with the flexibility to ``plug" it on top of any existing optimization technique for processing biological data in relational environment; there does not exist any additional cognitive overhead to the users while they formulate their queries using the GUI; Finally, our optimization techniques noticeably improve the performance of XML query execution.

Neural Systems Modeling with functional MRI

The project seeks to find a general framework for modeling interactions among neural populations involved in sensory or cognitive tasks and thus studying brain disorders by mimicking lesion studies. BIRC has developed techniques to analyze brain connectivity using Independent Component Analysis and Graphical Models. These techniques have applied to analyze data obtained from language and memory experiments and from normal as well as patients.

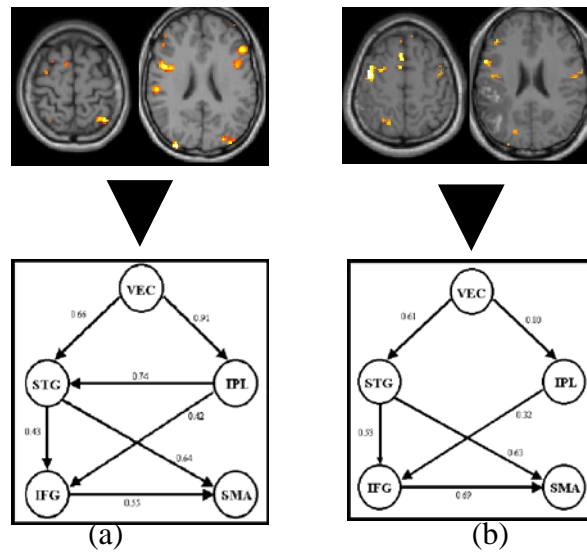


Figure 7: Neural systems derived from (a) normal subject and (b) stroke patient.

High Performance Computing Technologies for Computational Biology

A High Performance Computing (HPC) system for analysis and visualization of biological and clinical data has been developed. Various parallel algorithms for computational biology have been studied and implemented on a cluster of multiple compute nodes, using an industrial standard message passing package, MPI; for examples, BLAST for searching similar sequences, dynamic programming for local alignment, ClustalW for multiple sequence alignment, hierarchical clustering and supervised machine learning algorithms for gene expression analysis, and homology modelling for protein secondary structure prediction. The execution of these parallelised programs on centre's Alpha SC-45 Supercomputer has shown a great improvement of speed and accuracy, due to the methods used in maximizing the utilisation of the computing resources.



Figure 8: BIRC has developed a parallel algorithm for protein structure prediction on its Alpha supercomputer.

Toolkit for First Phase Clinical Trial Design

In collaboration with the National Cancer Center (NCC), Singapore, and University of Sheffield, we have been developing novel techniques for 1st phase clinical trial design. A window-based software system called CDT explorer is developed as well and is currently under NCC's evaluation.

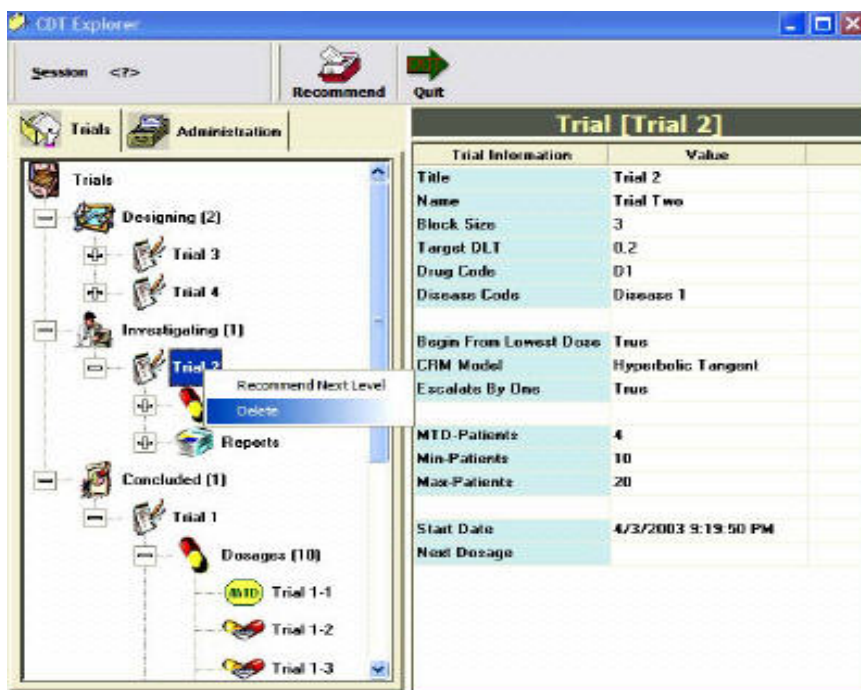


Figure 9: A toolkit for first phase clinical trial design

Feature Selection in Gene Expression Data

Gene expression data from DNA microarrays is a great source for scientists to understand the simultaneous activities of thousands of genes. One of the characteristics of gene expression data is that the number of genes (often more than 1000) far exceeds the number of samples (often less than 100). Furthermore, it has been shown that the large proportion of the genes in a microarray are not relevant to the discrimination of disease types. Hence the identification of those important genes that have the most discriminate power is of considerable interest to both biologists and medical professionals, where the research can be concentrated on small set of those important genes. In BIRC, we implemented a algorithm inspired by wrapper approach and LS-SVM to our feature selection problem. We implemented a fast Leave-One-Out (LOO) Guided Feature Selection (LGFS) implementation address this problem. The classification accuracies were notably increased while the number of genes required was drastically decreased to just a few and the timely improved as compare to other implementations.

In silico Modelling of Hormone-regulated Gene Expression Network

The molecular effect of estrogen and progesterone are reflected by their receptor regulated gene expression. It is, therefore, important to identify the direct target genes of estrogen and progesterone receptors and the down-stream targets of these genes. A list of potential progesterone-regulated human genes consists of about 200 (microarray data), but not all of them are regulated by progesterone receptor directly. If a particular gene is progesterone-regulated, its product may, in turn, regulate expression of another gene, and so on. This project is aimed at reconstruction of such “progesterone-regulated” gene expression network for clinical trial and cancer counteraction. Existing information on progesterone receptor DNA-specificity allows us to define potential PRE target genes using complete human genome sequence and different methods for statistical prediction of gene regulatory elements (promoters, PRE binding sites). Then, using gene description databases (OMIM, GeneOntology), it would be possible to establish entire pathway of hormone-induced effect on gene expression. This project is to define direct target genes for progesterone receptor on basis of experimental microarray data, to develop a method and the corresponding software for prediction of new potential progesterone-regulated human genes, to create progesterone-regulated gene expression network, and finally to extend described results over the whole family of steroid hormones.

V. STAFF PUBLICATIONS AND IMPACT FACTOR

Books

No.	Books
1	Limsoon Wong, editor, "The Practical Bioinformatician", <i>Imperial College Press</i> , London, December 2003. (In press.)
2	Louxin Zhang, Limsoon Wong, editors, "Selected Topics in Post-Genome Knowledge Discovery", <i>Singapore University Press</i> , Singapore, September 2003. (In press.)
3	J. C. Rajapakse and L. Wang, (eds.) "Neural Information Processing: Research and Development", <i>Springer - Verlag</i> , March 2004, ISSN 1434-9922, pp. 478.
4	Feng Chu and Lipo Wang, "Bio-medical data mining using neural networks", in <i>Encyclopedia of Data Warehousing and Mining</i> , John Wang (Editor), Information Sciences Publishing, 2005.

Journals

No.	Journals
1	Corona, T., Bao, Q., Christ, N., Schwartz, T., Jinming Li and Droge, P., "Activation of site-specific integration in human cells by a single chain integration host factor", <i>Nucleic Acid Research</i> , Vol 31, No 17 (2003).
2	Xiuju Fu and Lipo Wang, "Data dimensionality reduction with application to simplifying RBF network structure and improving classification performance", <i>IEEE Trans. System, Man, Cybern, Part B - Cybernetics</i> , vol.33, no.3, pp. 399-409, 2003.
3	Korolev, N.; Lyubartsev, A. P.; Laaksonen, A.; & Nordenskiöld, L. "A Molecular Dynamics Simulation Study of Oriented DNA with Polyamine and Sodium Counterions. Diffusion and Averaged Binding of Water and Cations", <i>Nucl. Acid Res.</i> , 31 (20) 5971-5981, 2003.
4	Korolev, N., Lyubartsev, A., and Nordenskiöld, L. "Application of the Poisson Boltzmann Polyelectrolyte Model for Analysis of Thermal Denaturation of DNA in the Presence of Na ⁺ and Polyamine Cations", <i>Biophys. Chem.</i> , 104, 55-66, 2003.
5	R. G. N. Meegama and J. C. Rajapakse, "NURBS-based segmentation of the brain in medical images," <i>International Journal of Pattern Recognition and Artificial Intelligence</i> , vol. 17, no. 6, pp 995-1009, 2003.
6	R.G. N. Meegama and J. C. Rajapakse, "NURBS snakes," <i>Image and Vision Computing</i> , 21 (2003) pp. 551-562.
7	W. Lu and J. C. Rajapakse, "Eliminating indeterminacy in ICA", <i>Neurocomputing</i> , 50, (2003), pp. 271 – 290.
8	M. N. Nguyen and J. C. Rajapakse, "Two-stage support vector machines for protein secondary structure prediction", <i>Neural, Parallel, and Scientific Computing</i> , Vol. 11, Issue 1 & 2, 2003.

No.	Journals
9	J. C. Rajapakse and M. N. Nguyen, "General framework for two-stage approaches to protein secondary structure prediction", <i>Asia Pacific Biotech News</i> , vol. 7, no.3, 2003, pp. 122 – 128.
10	J. C. Rajapakse, "Book review: adaptive blind signal and image processing," <i>IEEE Transactions on Neural Networks</i> , vol. 14, no. 6, Nov. 2003, pp. 1580-1580.
11	Guang-Bin Huang, "Learning Capability and Storage Capacity of Two-Hidden-Layer Feedforward Networks", <i>IEEE Transactions on Neural Networks</i> , vol. 14, no. 2, pp. 274--281, 2003.
12	Wu, Z. K., Lin, F. and Seah, H. S., "Topology Preserving Voxelisation of Rational Bezier and NURBS Curves", <i>Computers & Graphics</i> , Vol. 27, No. 1, 2003.
13	Wu, Z. K., Lin, F. and Seah, H. S., "Tunnel-free Voxelisation of Rational Bezier Surfaces", accepted for publication in <i>The Visual Computer</i> journal, 2003.
14	Qi, Y. T., Lin, F. and Wong, K. K., "High Performance Computing in PSSP", <i>WSEAS Transactions on Circuits and Systems</i> , No. 3, Vol. 2, July 2003, ISSN 1109-2734, pp616-618.
15	B. Schmidt, H. Schroder, M. Schimmler, "A hybrid Architecture for Bioinformatics", <i>Future Generation Computer Systems</i> , Vol. 18, 855-862.
16	Guozhu Dong, Leonid Libkin, Limsoon Wong, "Incremental Recomputation in Local Languages", <i>Information and Computation</i> , 181:88--98, 2003.
17	Jinyan Li, Huiqing Liu, James R. Downing, Allen Eng-Juh Yeoh, Limsoon Wong, "Simple Rules Underlying Gene Expression Profiles of More than Six Subtypes of Acute Lymphoblastic Leukemia (ALL) Patients", <i>Bioinformatics</i> . 19:71--78, 2003.
18	Huiqing Liu, Limsoon Wong, "Data Mining Tools for Biological Sequences", <i>Journal of Bioinformatics & Computational Biology</i> , 1(1): 139--168, April 2003.
19	Jinyan Li, Huiqing Liu, See-Kiong Ng, Limsoon Wong, "Discovery of Significant Rules for Classifying Cancer Diagnosis Data", <i>Bioinformatics</i> , 19(suppl. 2): ii93--ii102, September 2003.
20	Ho LV, Hui SC and Fong ACM, "Monitoring scientific publications over the WWW", <i>The Electronic Library</i> , Vol. 21/2, pp. 110-116, 2003.
21	Lee PY, Hui SC and Fong ACM, "A structural and content-based analysis for web filtering", <i>Internet Research</i> , Vol. 13/1, pp. 27-37, 2003.
22	He Y, Hui SC and Fong ACM, "Citation-based retrieval for Web publications using KSOM neural network", <i>IEEE Intelligent Systems</i> , Vol. 18/2, pp. 58-65, 2003.
23	Fong B, Hong GY, Rapajic PB, and Fong ACM, "A continuous phase modulation scheme for telemedicine systems", <i>WSEAS Transactions on Communications</i> , Vol. 2/4, pp. 382-386, Oct 2003.
24	Di Wang, and Narendra S. Chaudhari, "Binary neural network training algorithms based on linear sequential learning", <i>International Journal of Neural Systems</i> , Vol. 13, No. 5, pp. 333-351 (2003).

No.	Journals
25	Chen Chunxi*, B.Schmidt, "Computing Large-Scale Alignments on a Multi-Cluster", <i>IEEE Cluster Computing</i> , 2003.
26	Liu Weiguo*, B.Schmidt, "Parallel Design Pattern for Computational Biology and Scientific Computing", <i>IEEE Cluster Computing</i> , 2003.
27	Bose, S., S. French, F.J. Evans, F. Joubert, and R.S. Balaban, "Metabolic network control of oxidative phosphorylation: multiple role of inorganic phosphate", <i>J. Biol. Chem</i> 278: 39155-65, 2003.
28	Hendler, R.W. and S. Bose, "Interconversions among four M-intermediates in the bacteriorhodopsin photocycle", <i>Eur. J. Biochem</i> 270: 3518-24, 2003.
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30	Balaban, R.S., S.Bose, S. French, and P. R. Territo, "Role of calcium in metabolic signaling between cardiac sarcoplasmic reticulum and mitochondria in vitro", <i>Am. J. Physiol. Cell Physiol</i> 284:C285-C293, 2003.
31	Ying Gao, Jinming Li, Sujun Hua, Hongyu Zhao, Zhangliang Chen, Lijia Qu, and Xing Wang Deng, "An Arabidopsis Promoter Microarray and Its Initial Usage in the Identification of HY5 Binding Targets in vitro", <i>Plant Molecular Biology</i> , 2004, in publish.
32	R. G. N. Meegama and J. C. Rajapakse, "Fully Automated Peeling Technique for T1-Weighted High Quality MR Head Scans", <i>International Journal of Image and Graphics</i> , World Scientific, vol 4, no. 2, pp. 141-156, 2004.
33	W. Lu and J. C. Rajapakse, "Approach and applications of constrained ICA", <i>IEEE Transactions on Neural Networks</i> , (in press).
34	Y. Kanyan and J. C. Rajapakse, "ICA gives higher-order connectivity of the brain", <i>Neural Information Processing: letters and reviews</i> vol. 2, no. 2, February 2004.
35	S. L. Ho, and J. C. Rajapakse, "Input encoding method for identifying transcription start sites in RNA polymerase II promoters by neural networks," <i>Soft Computing</i> , (accepted).
36	Bramachary M., Krishnan S.P.T., Koh J.L.Y., Seah S.H., Tan T.W., Brusica V., Bajic V.B., "ANTIMIC: a database of antimicrobial sequences", <i>Nucleic Acids Research</i> 32, D586-589.
37	Brusica V. and Flower D.R., "Bioinformatics tools for identifying T-cell epitopes", <i>Drug Discovery Today: Biosilico</i> 2, 18-23.
38	Brusica V., Takagi Y. and Nakamura H., "Bioinformatics in Asia (<i>in Japanese</i>)", <i>Tanpakushitsu kakusan koso</i> (Protein, nucleic acid, enzyme) 49, 74-83.
39	Tan P.T.J., Srinivasan K.N., Seah S.H., Koh J.L.Y., Tan T.W., Shoba Ranganathan S. and Brusica V., "Accurate prediction of scorpion toxin functional properties from primary sequences", <i>Journal of Molecular Graphics and Modelling</i> . (In press)
40	Srinivasan K.N., Zhang G., Khan A.M., August T.J. and Brusica V., "Prediction of class I T-cell epitopes: evidence of presence of immunological hot spots inside antigens", <i>Bioinformatics</i> (ISMB/ECCB 2004 issue). (In press).

No.	Journals
41	Jinyan Li, Guozhu Dong, Kotagiri Ramamohanarao, Limsoon Wong, "DeEPs: A New Instance-based Discovery and Classification System", <i>Machine Learning</i> , 54(2): 99--124, 2004.
42	Shao-Wu Meng, Zhuo Zhang, Jinyan Li and Limsoon Wong, "A +1 programmed ribosomal frameshifting in a human C2H2 zinc finger gene", <i>Bioinformatics</i> , 2004, accepted.
43	See-Kiong Ng, Limsoon Wong, "Accomplishments and Challenges in Bioinformatics", <i>IEEE IT Professional Magazine</i> , 6(1): 44-50, January/February 2004. (Reviewed invited paper)
44	Huiqing Liu, Hao Han, jinyan Li, Limsoon Wong, "Using Amino Acid Patterns to Accurately Predict Translation Initiation Sites", <i>In silico Biology</i> , 4:0022, 2004. Draft.
45	Xiaolei Li, Lu Zheng, Chunguang Kong, Prasanna R. Kolatkar and Maxey C.M. Chung, "Purpureotin: a novel didimeric C-type lectin like protein (CLP) from <i>Trimeresurus purpureomaculatus</i> venom is stabilized by noncovalent interactions", <i>Archives of Biochemistry and Biophysics</i> , 2004. 424:53-62.
46	Yang Song, S S Bhowmick, S K Madria, "Bio2X: A Rule-based Approach to Semi-automatic Transformation of Semistructured Biological Data to XML", to appear in <i>Data and Knowledge Engineering Journal (DKE)</i> , Elsevier Science, 2004.
47	Xiangrui Wang, and Narendra S. Chaudhari, "Recurrent Neural Networks for recognition of sequence patterns", <i>International Journal of System Modeling and Simulation</i> (special issue on advancement in algorithms), Vol. 2, No. 1 pp. 1-6 (Jan. 2004).
48	Di Wang, and Narendra S. Chaudhari, "An Approach for construction of Boolean Neural Networks based on Geometrical expansion", <i>Neurocomputing</i> , Vol. 57C, pp. 455-461 (2004).
49	SHU Jian Jun, L. S. Ouw, 2004, "Pairwise alignment of the DNA sequence using hypercomplex number representation", <i>Bulletin of Mathematical Biology</i> , Vol. 66, pp 1423-1438.
50	Wu, Z. K., Lin, F., Seah, H. S. and Chan, K. Y., "Evaluation of Difference Bounds for Computing Rational Bezier Curves and Surfaces", <i>Computers & Graphics</i> , Vol. 28, No. 4, 2004, pp551-558.
51	Schmidt, B., Lin F., Amey Laud, Yusdi Santoso, "Development of Distributed Bioinformatics Applications with gMP", <i>Concurrency and Computation: Practice and Experience</i> , Vol. 16, 2004, pp945-959.
52	J. Liu, L. Chen, L. Li, X. Hu and Y. Cai, "Steady-state fluorescence study on release of camptothecin from agar hydrogel", <i>Accepted for publication in International Journal of Pharmaceutics</i> , 2004.
53	YY Cai, CK Chui, XZ Ye, et al, "Simulation-based Virtual Prototyping of Customized Catheterization Devices", <i>ASME Transaction Journal of Computing and Information Science in Engineering</i> , Vol. 4, No. 2, pp. 132-139, 2004.
54	Fong B, Ansari N, Fong ACM, Hong GY and Rapajic PB, "On the scalability of fixed broadband wireless access network deployment", accepted by <i>IEEE Communications Magazine</i> .

No.	Journals
55	Jagdish C. Patra, Vivekanand Goplakrishnan, Ee Luang Ang, Amitabha Das, "Neural Network-Based Self-Calibration/ Compensation of Sensors Operating in Harsh Environments", <i>IEEE Sensors 2004</i> , Vienna.
56	Zonglin Zhou, Chee Keong Kwoh, Stan Z. Li, "The Nearest Feature Midpoints - a Novel Approach for Pattern Classification", Accepted to be published in <i>International Journal of Information Technology</i> .
57	S.-H. Tan, Z. Zhang, S.-K. Ng, "ADVICE: Web Service for Automated Detection and Validation of Interaction by Co-Evolution", to appear in <i>Nucleic Acids Research</i> .
58	Z. Zhang, S.-K. Ng, "InterWeaver: Interaction Reports for Discovering Potential Interaction Partners with Online Evidence", to appear in <i>Nucleic Acids Research</i> .

Book Chapters

No.	Book Chapters
1	Feng Chu and Lipo Wang, "Gene expression data analysis using support vector machine", in <i>Bioinformatics using Computational Intelligence Paradigms</i> , Udo Seiffert and Lakhmi C. Jain (Editors), Springer-Verlag, 2003.
2	M. N. Nguyen and J. C. Rajapakse, "Multi-class Support Vector Machines for Protein Secondary Structure Prediction", <i>Genome Informatics 14</i> , M. Gribskov, et al. (Eds.), Universal Academic Press Inc., Japan, pp. 218-227, 2003.
3	S. L. Ho and J. C. Rajapakse, "Splice site detection with a higher-order Markov model implemented on a neural network", <i>Genome Informatics 14</i> , M. Gribskov, et al. (Eds.), Universal Academic Press Inc., Japan, pp. 64-72, 2003.
4	Jing Chen, Su-Yun Chung, Limsoon Wong, "The Kleisli Query System as a Backbone for Bioinformatics Data Integration and Analysis", <i>Bioinformatics: Managing Scientific Data</i> , edited by Zoe Lacroix and Terence Critchlow, chapter 6, pages 147--187, Morgan Kaufmann, San Francisco, CA, 2003.
5	Susan Davidson, Limsoon Wong, "The Kleisli Approach to Data Transformation and Integration", <i>The Functional Approach to Data Management: Modeling, Analyzing, and Integrating Heterogeneous Data</i> , edited by Peter Gray, Larry Kerschberg, Peter King, Alex Poulouvasilis, chapter 6, pages 135--165. Springer-Verlag, September 2003.
6	Jinmiao Chen, and Narendra S. Chaudhari "Protein Family classification using second order recurrent neural networks", <i>Genome Informatics</i> , Vol. 14, pp. 520-521 (2003).
7	Xiuju Fu and Lipo Wang, "Class-dependent feature selection using genetic algorithms", in <i>Evolutionary Computing in Data Mining</i> , Ashish Ghosh and Lakhmi C. Jain, Editors, Springer-Verlag, 2004.

No.	Book Chapters
8	Fong ACM and Hui SC, Book Chapter: ‘Networking Support for Neural Network-Based Intelligent Web Monitoring and Filtering’, Eds. Y.Q. Zhang, A. Kandel, T.Y. Lin and Y.Y. Yao, World Scientific. <Forthcoming in 2004>
9	J. C. Rajapakse and S. L. Ho, “Markov/neural model for eukaryotic promoter recognition,” <i>Advanced Methods for Knowledge Discovery from Complex Data</i> , S. Bandyopadhyay, U. Maulik, L. Holder, and D. Cook, (Eds.), Springer Verlag, London. (Accepted)

Conferences

No.	Conference
1	R. G. N. Meegama and J.C.Rajapakse, "Curvature-based rational surface model for the detection of age and gender-related diversity in cortical morphology", <i>3rd International Symposium on Image and Signal Processing and Analysis (ISPA'03)</i> , September 2003, Rome, pp. 411-416.
2	K. Yang and J. C. Rajapakse, “Denoising of functional MRI using ICA,” <i>Proceedings of 3rd International Symposium on Image and Signal Processing and Analysis, (ISPA'03)</i> , September 2003, Rome, pp. 561-566.
3	L.Wei*, J.C.Rajapakse, "Eliminating indeterminacy in ICA", <i>Neurocomputing</i> , 2003, vol. 50, pp. 271-290.
4	C. L. Tan and J. C. Rajapakse, “Tissue segmentation of multi-channel brain images with inhomogeneity correction,” <i>Proceedings of 3rd International Symposium on Image and Signal Processing and Analysis, (ISPA'03)</i> , September 2003, Rome, pp. 571-576.
5	R. Yu*, E.C.Tan, "Comparison of different time-frequency distribution in pitch detection", <i>Fourth International Conference on Information, Communications & Signal Processing and Fourth Pacific-Rim Conference on Multimedia (ICICS-PCM 2003)</i> , 2003.
6	S.B.Sourav, D T Singh*, A Laud*, "Data Management Issues in Metaboloinformatics – Issues and Challenges", <i>14th International Conference on Database and Expert Systems Applications (DEXA 2003)</i> , 2003.
7	S S Bhowmick, Vivek Vedagiri, Amey Laud, “HyperThesis: The gRNA Spell on the Curse of Bioinformatics Applications Integration”, <i>In the Proceedings of the 12th ACM International Conference on Information and Knowledge Management (ACM CIKM 2003)</i> , ACM Press, New Orleans, USA, Nov 2003.
8	Y.T.Qi*, F.Lin, "Parallelisation of BLAST Algorithm", <i>International Conference on Bioinformatics 2003 (InCoB2003)</i> , Malaysia, 8 – 10 September 2003.
9	Z.H.Du*, F.Lin, "pClustalW: A Deployment of Parallel ClustalW", <i>International Conference on Bioinformatics 2003 (InCoB2003)</i> , Malaysia, 8 – 10 September 2003.

No.	Conference
10	P. Cheang*, H. Chandra*, R. A. Yan*, F.Lin, R. Kumar*, K. A. Khor*, "Three Dimensional Printing for Fabrication of Near Net Shape Bioceramic Implants", <i>8th IUMRS International Conference on Advanced Materials (IUMRS-ICAM)</i> , Japan, 11 – 13 October 2003.
11	Qi Yutao*, F.Lin, "CyberparaBLAST: A Parallelized BLAST Web Server," <i>Cyberworlds 2003</i> , Singapore, 3 – 5 December 2003.
12	Z.H.Du*, F.Lin, "Parallel Computation for Multiple Sequence Alignments", <i>IEEE Fourth International Conference on Information, Communications & Signal Processing and Fourth Pacific-Rim Conference on Multimedia (ICICS-PCM 2003)</i> , Singapore, 15 - 18 December 2003.
13	B. Schmidt, F. Lin, A. Laud, Y. Santoso: "Parallel Detection of Regulatory Elements with gMP", <i>International Parallel and Distributed Processing Symposium 2003</i> .
14	Schmidt, B., Lin, F., Amey Laud, Yusdi Santoso, "Parallel Detection of Regulatory Elements with gMP", <i>IEEE International Workshop on High Performance Computational Biology</i> , France, 22 April 2003.
15	M. Schimmler*, B.Schmidt, H.W. Lang*, "Design of a bit-serial floating point unit for a fine grained parallel processor array," <i>PDPTA'03</i> , 2003
16	M. Schimmler*, B.Schmidt, S. Heithecker*, "A area-efficient bit-serial integer multiplier," <i>VLSI'03</i> , 2003
17	J. Chen*, C.Narendra, "Improvement of the Inside-Outside Algorithm using Prediction and application to RNA modeling", <i>The Second International Conference on Machine Learning and Cybernetics</i> , 2003
18	J. Chen*, C.Narendra, "Protein family classification using second-order recurrent neural networks", <i>The 14th International Conference on Genome Informatics - GIW 2003</i> , 2003.
19	Yiyu Jia*, C.K.Kwoh, Meena K. Sakharkar*, Pandjassarame Kanguane*, "Statistical analysis of symmetric exon sets in eukaryotic genes", <i>GIW2003</i> , 2003
20	Jinyan Li, See-Kiong Ng, Limsoon Wong, "Bioinformatics Adventures in Database Research", <i>Proceedings of 9th International Conference on Database Theory</i> , pages 31--46, Siena, Italy, January 2003. (Keynote paper.)
21	Jinyan Li, Limsoon Wong, "Using Rules to Analyse Bio-medical Data: A Comparison between C4.5 and PCL", <i>Proceedings of 4th International Conference on Web-Age Information Management</i> , pages 254--265, Chengdu, PRC, August 2003.
22	Jinyan Li, Huiqing Liu, Limsoon Wong, "Mean-entropy discretized features are effective for classifying high-dimensional biomedical data", <i>Proceedings of 3rd ACM SIGKDD Workshop on Data Mining in Bioinformatics</i> , pages 17--24, Washington, DC, August 2003.
23	Huiqing Liu, Hao Han, Jinyan Li, Limsoon Wong, "An in silico method for prediction of polyadenylation signals in human sequences", <i>Proceedings of 14th International Conference on Genome Informatics</i> , pages 84--93, Yokohama, December 2003.

No.	Conference
24	YY Cai, YT Lee and Tony Woo, "Knot Invariance and Protein Characterization", <i>1st International Symposium on Geometric Representation and Processing in the Nano-Bio Scale</i> , Hangzhou, China, Sept 2003.
25	Vladimir Bajic, Vladimir Brusic, Jinyan Li, See-Kiong Ng, Limsoon Wong. "From Informatics to Bioinformatics", <i>Proceedings of 1st Asia Pacific Bioinformatics Conference</i> , pages 3--14, Adelaide, Australia, February 2003. (Keynote paper.)
26	X.F.Liu, Z.H.Man, S. Kumar*, Y Cai*, "Video Analysis and Knowledge based Fire Detection," 3rd IASTED International Conference- Visualization, Imaging, and Image Processing, 2003, vol. 2, pp. 698-703
27	Z.H.Man, X.F.Liu, X. Yu*, X. Zhang*, "A new dynamical fuzzy modeling and eigenstructure assignment control for SISO complex systems", <i>The IASTED International Conference on Artificial Intelligence and Applications</i> , 2003
28	Z Zhou*, J Li*, K M Liew*, C.K.Kwoh, T F Chia*, "The SVM classification of light regulated Arabidopsis genome expression profiles," <i>Joint Singapore-Canada Workshop on The Interface of Biology with Information Technology</i> , 2003.
29	Y. M. Cheong and J. C. Tay, "Approximate String Matching for Multi-attribute, Large-scale Customer Address Databases," In LNCS 2911 Springer Verlag, Proceedings of the Sixth International Conference on Asian Digital Libraries, pp. 168-172, ICADL 2003.
30	L. Adianto and J. C. Tay, "On the Implementation of Temporal Constraints in CSL," In Proceedings of the Third IASTED International Conference on Artificial Intelligence and Applications, p157-162, 2003.
31	L. Y. Tan and J. C. Tay, "A Graph-Oriented Measure of Rule Adaptivity and Flexibility," In Proceedings of the Third IASTED International Conference on Artificial Intelligence and Applications, p178-185, 2003.
32	S. K. Ng, S. P. Khadayate and Y. S. Ong, "Whole-Genome Functional Classification of Genes by Latent Semantic Analysis on Microarray Data", <i>2nd Asia-Pacific Bioinformatics Conference (APBC2004)</i> , Dunedin, New Zealand, 18 - 22 Jan 2004.
33	M. P. Rajapakse, J. Tan, and J. C. Rajapakse, "Color channel encoding with NMF for face recognition," <i>IEEE International Conference on Image Processing</i> , (ICIP04), Singapore, October 2004 (accepted).
34	M. N. Nguyen and J. C. Rajapakse, "Two-stage support vector machines to protein relative accessibility prediction," <i>IEEE Symposium on Computational Intelligence in Bioinformatics and Computational Biology</i> , San Diego, 2004 (accepted)
35	X. Yang, and J. C. Rajapakse, "Graphical approach for motif recognition in DNA sequences," <i>IEEE Symposium on Computational Intelligence in Bioinformatics and Computational Biology</i> , San Diego, 2004 (accepted)
36	K. Duan and J. C. Rajapakse, "A variant of SVM-RFE for gene selection in cancer classification with expression data," <i>IEEE Symposium on Computational Intelligence in Bioinformatics and Computational Biology</i> , San Diego, 2004 (accepted)

No.	Conference
37	G. Pang and J. C. Rajapakse, "Inferring neutral evolution from Parkinson's disease genes," <i>IEEE Symposium on Computational Intelligence in Bioinformatics and Computational Biology</i> , San Diego, 2004 (accepted)
38	S. L. Ho and J. C. Rajapakse, "High sensitive technique for translation initiation site detection," <i>IEEE Symposium on Computational Intelligence in Bioinformatics and Computational Biology</i> , San Diego, 2004 (accepted)
39	J. C. Rajapakse, D. Srinivasan, M. J. Er., G.-B. Huang, and L. Wang, "Excerpts of research in brain sciences and neural networks in Singapore," <i>International Joint Conference on Neural Networks (IJCNN2004)</i> , Budapest 2004, pp. 369-375
40	X. Zheng and J. C. Rajapakse, "Graphical models for brain connectivity from functional imaging data," <i>International Joint Conference on Neural Networks (IJCNN2004)</i> , Budapest 2004, pp. 531-536.
41	K. Yang and J. C. Rajapakse, "An exploratory approach to modeling effective connectivity," <i>IEEE International Symposium on Biomedical Imaging</i> , Arlington, Virginia, April 2004, pp. 844-847
42	Jinyan Li, Huiqing Liu, Limsoon Wong, "Use of Built-in Features in the Interpretation of High-dimensional Cancer Diagnosis Data", <i>Proceedings of 2nd Asia Pacific Bioinformatics Conference</i> , pages 67--74, Dunedin, New Zealand, January 18-22, 2004.
43	SHU Jian Jun, Ouw Li Shan, 2004, "Pairwise alignment of DNA sequence using hypercomplex number representation", <i>The 1st International Conference From Scientific Computing to Computational Engineering</i> , Athens, Greece, 8-10 September 2004, Greece.
44	Du, Z. H. and Lin, F., "Using Blocks+ Database in Needleman-Wunsch Algorithm", <i>The 23rd International Conference of the North American Fuzzy Information Processing Society (NAFIPS 2004)</i> , Canada, June 2004.
45	Du, Z. H. and Lin, F., "Improvement of the Needleman-Wunsch Algorithm", <i>Fourth International Conference on Rough Sets and Current Trends in Computing 2004 (RSCTC 2004)</i> , Sweden, June 2004.
46	Du, Z. H. and Lin, F., "Using Prior Knowledge for Sequence Alignment, The 8th World Multiconference on Systemics", <i>Cybernetics and Informatics (SCI 2004)</i> , USA, Accepted for Publication in 2004
47	Qi, Y. T. and Lin, F., "mpiPSSP: Parallelized Protein Secondary Structure Prediction", <i>IASTED International Conference on Biomedical Engineering (BioMED 2004)</i> , Canada, Accepted for publication in 2004
48	Yan, R. A., Cheang, P. and Lin, F., "Spline-based Volumetric Modeling and Printing for Bioceramic Implants", (<i>VRCAI 2004</i>), Singapore, 16 - 18 June 2004.
49	Lin, F., Du, Z. H. and Qi, Y. T., "HPTC for Sequence Analyses in Bioinformatics", <i>HP-CAST 2004</i> , Australia, 28-31 March 2004
50	Qi, Y. T. and Lin, F., "Parallelized Protein Secondary Structure Prediction", <i>The 3rd International Conference on Machine Learning and Cybernetics (ICMLC 2004)</i> , China, 26-29 August 2004

No.	Conference
51	Yan, R. A., Cheang, P. and Lin, F., "Customized Body Parts: Computerized and Printing of Bioceramic Based Porous Scaffold for Clinical Implants", <i>The 6th Asia Symposium on Biomedical Materials (ASBM 2004)</i> , China, 19-22 July 2004.
52	Narendra S. Chaudhari, and Nirmal Dagdee, "Turing Machine Simulation using Hard-limiter Neurons", <i>International Joint Conference on Neural Networks (IJCNN 2004)</i> , Budapest, Hungary (26-29 July 2004).
53	Jinmiao Chen, and Narendra S. Chaudhari, "Improvement of Bidirectional Recurrent Neural Network for Learning Long Term Dependencies", <i>International Conference on Pattern Recognition (ICPR-2004)</i> , Cambridge, U.K. (23-26 Aug. 2004).
54	Weiguo Liu, B. Schmidt, "A Generic Parallel Pattern-based System for Bioinformatics", <i>Proceedings of Euro-Par'04, 2004</i> , to appear.
55	Tong Liu, B.Schmidt, "Parallel RNA Sequence-Structure Alignment", <i>Proceedings of IPDPS'04</i> , IEEE, 2004
56	Chen Chunxi, B. Schmidt, "Performance Analysis of Computational Biology Applications on Hierarchical Grid Systems", <i>Proceedings of CCGrid'04</i> , IEEE, 2004
57	SCH Wong, Y Cai, et al, "Knowledge enhanced cellular visualization using 3D confocal images", <i>Focus on Microscopy 2004</i> , Philadelphia, USA, 2004.
58	Huiqing Liu, Jinyan Li, Limsoon Wong, "Selection of Patient Samples and Genes for Outcome Prediction", <i>IEEE Bioinformatics Proceedings (CSB2004)</i> , Stanford, CA, August 2004.
59	Rickard Liow S. J., Tham W, Lim W.E.H, Ng S.E.S, Ho G. L., Tan K., "Neurolinguistic Correlates in Chinese-English Bilingual Biscrptals: An fMRI Study", <i>American Association for Applied Linguistics (AAAL)</i> , Portland, Oregon, 1-4 May 2004.
60	Su Li, B Lu, and Y Cai, "VR-enhanced Modeling and Visualization of Cystine Knot Proteins", <i>ACM SIGGRAPH International Conference on Virtual Reality Continuum and its Applications in industry, VRCAI 2004</i> , 15-18 Jun 2004.
61	Jianhui Zhao*, Ling Li*, C.K.Kwoh, "A Model-based Approach for Human Motion Reconstruction from Monocular Images", <i>2nd International Conference on Information Technology for Application (ICITA 2004)</i> .
62	Zhang Yan*, Jia Yiyu*, C.K.Kwoh, Liu Jianjun*, "Comparison of four algorithms for haplotype inference problem", <i>2nd RECOMB satellite workshop on computational methods for SNPs and Haplotypes</i> , 2004, pp. 113-123
63	YY Jia*, Y Zhang*, C.K.Kwoh, V Gopalan*, "Length Distributions Of Exons And Introns Imply The Evolutionary Constraints For Exon/Intron Length", <i>Conference on Research in Computational Molecular Biology (RECOMB 2004)</i> .
64	ZL Zhou*, C.K.Kwoh, "The SVM Classification of Light Regulated Arabidopsis Genome Expression Profiles," <i>Biotech China 2004</i> .

No.	Conference
65	YY Jia*, Y Zhang*, C.K.Kwoh, M K Sundaram*, "Intron/exon: which one tells us more about coding of life? – evidence from statistical analysis of length distribution", <i>Genomic Signal Processing and Statistics (GENSIPS 2004)</i> .
66	Y Zhang*, JJ Liu*, C.K.Kwoh, YY Jia*, "The sensitivity and rationality of pairwise linkage disequilibrium measures - a practical analysis," <i>Genomic Signal Processing and Statistics (GENSIPS 2004)</i> .
67	ZL Zhou*, C.K.Kwoh, "An evolutionary lineage for intron loss/gain in five eukayotic genomes," <i>The Fourth International Conference on Bioinformatics of Genome Regulation and Structure (BGRS'2004)</i> .
68	Y Zheng*, C.K.Kwoh, "Dynamic Algorithm For Inferring Qualitative Models of Gene Regulatory Networks," <i>IEEE Computer Society Bioinformatics Conference, CSB2004</i> .
69	Zhao Ying*, C.K.Kwoh, "Fast Leave-one-out Evaluation and Improvement on Inference for LS-SVMs," <i>International Conference on Pattern Recognition (ICPR), 2004</i>
70	Zhou Zonglin*, C.K.Kwoh, "The Pattern Classification Based on the Nearest Feature Midpoints," <i>International Conference on Pattern Recognition (ICPR), 2004</i>
71	Yun Zheng *, C.K.Kwoh, "Reconstructing Boolean Networks from Noisy Gene Expression Data," <i>Eighth International Conference on Control, Automation, Robotics and Vision (ICARCV 2004)</i> .
72	Yang Song*, S.B.Sourav, "BioDiff: An Effective Fast Change Detection Algorithm for Genomic and Proteomic Data," <i>Proceedings of the 13th ACM International Conference on Information and Knowledge Management (ACM CIKM 2004)</i> .
73	L. Shen and E. C. Tan, "Gene Selection for Cancer Classification from Microarray Data using PLS-RLSC", <i>1st International BioEngineering Conference 2004 (IBEC 2004)</i> , 8-10 Sep 2004, Singapore.
74	Shen L. and Tan E.C., "PLS and SVD based Penalized Logistic Regression for Cancer Classification using Microarray Data", <i>APBC 2004</i> , in press.
75	Shen L. and Tan E.C., "Nonlinear Kernel MSE Methods for Cancer Classification", <i>ICARCV 2004</i> , accepted.
76	Shen L. and Tan E.C., "Kernel PLS-SVM and Kernel SVD-SVM for Cancer Classification using Microarray Data", <i>ICMLC 2004</i> , accepted.
77	Shen L. and Tan E.C., "Efficient Algorithm for Gene Selection using PLS-RLSC", <i>BGRS 2004</i> , accepted.
78	R. Yu and E. C. Tan, "Application of Time-Frequency Analysis in Exon Classification". <i>10th International Symposium On Integrated Circuits, Devices & Systems (ISIC 2004)</i> , 8-10 Sep 2004, Singapore.
79	Bing Liu, Chunru Wan and Lipo Wang, "Unsupervised gene selection via spectral biclustering," <i>International Joint Conference on Neural Networks, Budapest, July, 2004</i> .
80	C. W. Ong and J. C. Tay, "A Robust Rule-based Event Management Architecture for Call-Data Records," accepted for publication in the Eighth International Conference on Knowledge-Based Intelligent Information and Engineering Systems 2004.

No.	Conference
81	Ho Nhu Binh and Tay Joc Cing, "GENACE: An Efficient Cultural Algorithm for solving the Flexible Job-Shop Problem", <i>In Proceedings of the IEEE Congress on Evolutionary Computation 2004</i> , pp1759-1766.
82	Tay Joc Cing and Djoko Wibowo, "An Effective Chromosome Representation for Evolving Flexible Job Shop Schedules", <i>In Proceedings of AAAI Genetic and Evolutionary Computation 2004</i> , pp210-221.
83	Duch W, Blachnik M, "Fuzzy rule-based systems derived from similarity to prototypes", <i>Lecture Notes in Computer Science, ICONIP 2004</i> , submitted 5/04, (in print).

Impact Factors

Impact factors for Years 2003-2004 (years with available data):

	2003 - 2004
Total impact	114.385
Number of papers	40
Number of Staff*	23
Number of Academic Staff	23
Impact factor per paper	2.86
Impact factor per Staff*	4.97
Impact factor per Academic Staff	4.97

*Staff includes both academic and research staff except research students.
Research staff includes RF, RA and PO, regardless of the funding source.

VI. POSTGRADUATE STUDENTS COMPLETED

PhD Students

No	Name	Supervisor	Previous degree	Year Graduated	Placement
1	Dr Tan Choong Leong	A/P Jagath Rajapakse	PhD Eng, NTU	2003	Research Fellow, BioInformatics Research Center Nanyang Technological University, Singapore
2	Dr. R. G. N. Meegama	A/P Jagath Rajapakse	PhD Eng, NTU	2004	Senior Lecturer, Department of Computer Science University of Sabaragamuwa, Sri Lanka

MSc Students

No	Name	Supervisor	Previous degree	Year Graduated	Project Title
1	Yang Kanyan	A/P Jagath Rajapakse	MSc	2004	Brain connectivity with ICA
2	Jia Yiyu	A/P Kwoh Chee Keong	MSc	2004	Statistical analysis of intron phases at the splice sites of eukaryotic genes
3	Zhao Ying	A/P Kwoh Chee Keong	MSc	2004	Probalitistic based algorithm to analyse gene expression data

VII. PRESTIGE

Professional Activities

No.	Title	Staff Name	Activity
1	Senior Member	A/P Jagath Rajapakse	Institute of Electrical and Electronic Engineers (IEEE)
2	Governing Board Member	A/P Jagath Rajapakse	Asia-Pacific Neural Network Assembly (APNNA)
3	Governing Board Member	A/P Jagath Rajapakse	Asia Pacific Neural Network Assembly (APNNA): Promote research and organize activities in neural information processing; organization of International Conference on Neural Information Processing (ICONIP)
4	Member, Technical Committee on Neural Networks	A/P Jagath Rajapakse	The International Association of Science and Technology for Development (IASTED) (2003 - 2006): Responsible for advisement on the planning and the organization of IASTED activities such as conferences, meetings, and publications.
5	Member, International Advisory Board	A/P Jagath Rajapakse	Knowledge Engineering and Discovery Research Institute, Auckland University of Technology, Sept 2002 - present: Make recommendations to the Institute and the Institutions in New Zealand in terms of directions of research, links with industry, integrating international research groups from different countries, sharing information and developing joint research projects.
6	Member, ICA Steering Committee	A/P Jagath Rajapakse	Organization of annual conference on Independent Component Analysis (ICA)
7	Committee Member	A/P Wong Lim Soon	Tan Kah Kee-DSTA Defense Science Award Committee (2003)
8	Management Committee	A/P Wong Lim Soon	National University of Singapore Institute of Engineering Science (2004-2005)
9	Board of Directors	A/P Wong Lim Soon	Association of Asian Societies for Bioinformatics (2003)
10	Board of directors	A/P Wong Lim Soon	Molecular Connections, Bangalore, India
11	SAB	A/P Wong Lim Soon	geneticXchange inc, California, USA
12	Chairman	A/P Wong Lim Soon	A*STAR Tech Scan Panel on Information Management
13	Member	Dr Salil K Bose	New York Academy of Sciences

Conference Activities

No.	Title	Staff Name	Activity
1	Member, Technical Program Committee	A/P Jagath Rajapakse	<i>First IEEE Symposium on Computational Intelligence in Bioinformatics and Computational Biology</i> , San Diego, October, 2004
2	Member, International Program Committee	A/P Jagath Rajapakse	<i>4th Symposium of Independent Component Analysis and Blind Signal Separation (ICA2004)</i> , Granada, Spain, 2004.
3	Member, International Program Committee	A/P Jagath Rajapakse	<i>3rd Symposium of Independent Component Analysis and Blind Signal Separation (ICA2003)</i> , Japan, 2003.
4	Member, Program Committee Member	A/P Jagath Rajapakse	<i>7th IASTED International Conference on Computers, Graphics, and Imaging, CGIM 2004</i> , August 2004, Hawaii, USA.
5	Member, Program Committee Member	A/P Jagath Rajapakse	<i>6th IASTED International Conference on Computers, Graphics, and Imaging, CGIM 2003</i> , August 2003, Hawaii.
6	Program Committee	Asst/P Vivekanand Gopalkrishnan	<i>5th International Conference on Web-Age Information Management (WAIM'2004)</i>

Journal Activities

No.	Title	Staff Name	Activity
1	Guest Editor	A/P Jagath Rajapakse	Special Issue on “Softcomputing in Bioinformatics”, Softcomputing, March 2004 issue
2	Editorial Board Member	A/P Jagath Rajapakse	International Journal of Computational Intelligence
3	Editorial Board Member	A/P Jagath Rajapakse	Neural Information Processing - Letters and Reviews: Review at least four letters and reviews per year and advise Editor-in-Chief on their publication in the journal
4	Guest Editor	Ast/P Sourav Bhowmick	Special Issue, Data and Knowledge Engineering Journal, Elsevier Science
5	Associate Editor	A/P Wang Lipo	IEEE Transactions on Neural Networks, 2002 -
6	Associate Editor	A/P Wang Lipo	IEEE Transactions on Evolutionary Computation, 2003
7	Editorial Board Member	A/P Wang Lipo	Soft Computing, 2002
8	Editorial Board Member	A/P Wang Lipo	Neural Information Processing – Letters and Reviews, 2003

Editorial Services

No.	Title	Staff Name	Activity
1	Series Editor	A/P Wong Lim Soon	Advances in Bioinformatics & Computational Biology (book series) (2004)
2	Editor	A/P Wong Lim Soon	International Journal of Information Technology
3	Managing Editor	A/P Wong Lim Soon	Journal of Bioinformatics & Computational Biology
4	Advisor	Dr Salil K. Bose	Editorial Board of Journal of Biology Education, UK

Staff Awards

No.	Staff	Awards
1	A/P Wong Lim Soon	2003 FEER Asian Innovation Gold Award

Student Awards

No.	Student / Supervisor	Awards
1	Ho Sy Loi / A/P Jagath Rajapakse	50,000 yen by Japanese Bioinformatics Society for the work presented at GIW2003 Splice site detection with a higher-order Markov model implemented on a neural network.
2	Minh Nguyen Ngoc / A/P Jagath Rajapakse	50,000 yen by Japanese Bioinformatics Society for the work presented at GIW2003: Multi-class Support Vector Machines for Protein Secondary Structure Prediction.

VIII. PATENTS AND COMMERCIAL PRODUCTS

No.	Staff Name	Patents
1	Ast/P Fong Cheuk Ming	International patents filed by the Motorola IP Law Department in 1999-2000 for innovations incorporated into our Mobilepad™ range of handheld wireless communication products.
2	A/P Prasanna Kolatkar	The use of a fungal immunomodulatory protein, Fve, for immunotherapy, against allergy, virus infection and cancer.

No.	Staff Name	Commercial Products
1	Ast/P Sourav Bhowmick	Research in biological data integration has been adopted and implemented in the commercial product gRNA now marketed by Genvea BioSciences, Singapore (previously marketed by HeliXense Pte Ltd, Singapore)

IX. COLLABORATORS

The centre brings together scientists and engineers, who are interested in bioinformatics modeling and computation, and fosters cross-disciplinary interactions among different schools at NTU to perform advanced research in bioinformatics. It also makes the necessary partnerships with other research and educational institutions, locally and abroad, to achieve its objectives.

No.	International Collaborators
1	Brain Science Institute, RIKEN, Japan
2	Knowledge Engineering and Discovery Research Institute (KEDRI), Auckland University of Technology
3	Bioimaging Centre, Whitehead Institute, Massachusetts Institute of Technology (MIT), USA
4	Signal & Image Processing Group, Max-Planck-Institute of Cognitive Neuroscience, Germany
5	RMIT University, Melbourne, Australia
6	Stockholm University, Sweden
7	The Children's Hospital Research Foundation, Cincinnati Children's Hospital Medical Centre, USA
8	Department of Neurology, University of Freiburg, Germany

No.	Local Collaborators
1	Bioinformatics Institute (BII)
2	Genomic Institute of Singapore (GIS)
3	Institute for Infocomm Research (I2R)
4	National Neuroscience Institute (NNI)
5	Singapore General Hospital (SGH)
6	National Cancer Centre (NCC)