SIX-MONTHLY PROGRESS REPORT

FOR I^{2}R-SOC JOINT LAB

Section A: To be completed by Principal Investigator

Reporting Period	01 May 2007 – 30 June 2007
Project Vote No. at SOC	R-252-000-172-593
Title of Project	Knowledge Discovery from Biological & Clinical Data
PIs	A/Prof. Wynne Hsu, SOC A/Prof. Ng See Kiong, I^{2}R
Co-PIs	Prof. Wong Limsoon, SOC/I^{2}R Dr. Lee Mong Li, SOC Dr. Ken Sung, SOC A/Prof. Li Jinyan, I^{2}R (Left for NTU, May 06) Prof. Vladimir Bajic, I^{2}R (Left for SANBI, Jan 06) Prof. Vladimir Brusic, I^{2}R (Left for Univ of Queensland, Aug 05)
Project Duration (Start Date – End Date)	1 July 2003 to 30 June 2006, extended to 30 June 2007

1. Expenditure Level – Utilisation Rate

Vote	Original Grant	Received Grant (if applicable)	Actual expenditure to date (exclude commitments)	% Utilization
EOM	$822,000	$770,366.30	$686,967.12	89%
OOE	$45,000	67,994.50	$53,228.83	78%
EQPT	$70,000	57,124.54	$54,189.92	95%
Total	$937,000	895,485.34	$794,385.87	89%

Comments (to include explanation for major variations/virements; use additional pages if necessary)

A project extension to end of June 2007 was requested in Feb 2006.

2. Manpower Development - Project Staffing Status

Manpower Category	Planned Full-time	Actual Full-time
PhD student	10	3
Total	10	3

Comments (to include explanation for major deviations from approved targets and problems encountered; use additional pages if necessary)

Postdoc recruited & funded for this project:

1. **Yang Liang-Huai (till 31 October 2005)**
2. **Liu Gui-Mei (30 June 2005 till 31 May 2006, extended till 30 June 2007)**
3. **Zheng Yun (1 April 2006 till 31 August 2006)**

Research assistant recruited & funded for this project:

1. **Chen Jin (joined 1 Jan 2006 till December 2007)**
2. **Li Ling (joined 1 Jan 2006 till June 2007)**
3. **Chen Ju (joined 1 Sept 2006 till June 2007)**

PhD students recruited & funded for this project:

1. **Chen Jin,**
   - Nationality: China
   - Supervisors: Wynne Hsu, Lee Mong Li, Ng See-Kiong
   - Joined 1st October 2003 (became RA on 1 Jan 2006)
   - Passed qualifying exam in Feb 2003 at SOC
   - PhD Thesis submitted: November 2006
   - PhD awarded: July 2007
   - First job post-PhD: Postdoc at Stanford Univ.
2. **Hugo Willy**
   - Nationality: Indonesian (Singapore PR)
   - Supervisor: Ng See-Kiong, Ken Sung
   - Joined 1st October 2003
   - Passed qualifying exam in May 2004 at SOC
3. **Wong Swee Seong**
   - Nationality: Singapore
   - Supervisor: Ken Sung, Wong Limsoon
   - Joined 1st April 2004
   - Passed qualifying exam January 2004 at SOC
   - PhD Thesis submitted: July 2007
   - First job post-PhD: Lilly Singapore Center for Drug Discovery

PhD students affiliated to this project but funded by other sources:

4. **Kenny Chua**
   - AGA/NUS NGS funded
   - Supervisors: Ken Sung, Wong Limsoon
   - Thesis committee: Lee Mong Li, Ng See-Kiong
   - Joined 1st August 2003
   - Passed qualifying exams in Sept 2005 at SOC
   - PhD Thesis submitted: June 2007
   - First job post-PhD: Research Fellow at I2R

5. **Liu Huiqing (staff)**
    - Self-funded (part-time)
    - Supervisor: Wong Limsoon
    - Thesis committee: Wynne Hsu, Li Jinyan
    - Examiners: Lee Mong Li, Kwoh Chee Keong (NTU), Phil Long (Columbia), Prasanna Kolatkar (GIS)
    - Joined 1st August 2003
    - Passed qualifying exams at SOC
    - Thesis submitted: April 2004
    - PhD awarded: December 2004
    - First job post-PhD: Postdoc at Univ of Georgia
6. **V. S. Sundararajan**
    - I^2R funded
    - Supervisor: Wong Limsoon
    - Joined 1st August 2003
    - Passed qualifiying exams at SOC
    - Passed thesis proposal: April 2006
    - PhD Thesis submitted: June 2007
    - First job post-PhD: Research Fellow at NUS Dentistry
7. **Judice Koh (staff)**
    - Self-funded (part-time)
    - Supervisor: Lee Mong Li ,Vladimir Brusic
    - Thesis committee: Ken Sung, Tan Kian Lee
    - Joined 1st August 2003
    - Passed qualifying exams at SOC
    - PhD Thesis submitted: March 2007
    - PhD awarded: August 2007
    - First job post-PhD: Postdoc at Univ of Toronto
8. **Hou Yuna**
    - SOC funded
    - Supervisor: Wynne Hsu
    - Joined 1st October 2003
    - Passed qualify exam at SOC
    - Withdrawn (new baby) in Jan 2006
9. **Li Haiquan**
    - I^2R funded
    - Thesis submitted: July 2006
    - Supervisor: Wee Sun Lee and Jinyan Li
    - Thesis committee: Limsoon Wong, Ken Sung
    - Joined 1st August 2003
    - PhD awarded: March 2007
    - First job post-PhD: Staff Member, Noble Foundation
10. **Feng Meng Ling**
    - AGA/NTU NGS funded
    - Supervisor: Tan Yap Peng (NTU), Wong Limsoon
    - Joined March 2004
    - Passed confirmation exam at NTU EEE on 27 July 2005
    - PhD Thesis to be submitted: April 2008
11. **Lee Terk Shuen**

- AGA/NUS NGS funded
- Supervisors: Sam Ge, Wong Limsoon
- Thesis committee: Jinyan Li, Wynne Hsu Joined February 2004
- Qualifying exam passed: May 2007

12. Donny Soh

- AIP/IC funded
- Supervisors: Wong Limsoon, Yike Guo (IC)
- Joined December 2004
- PhD transfer/viva to be taken: Autumn 2007

3. Project Progress (use additional pages if necessary)

(a) The extent to which the original project objectives have been achieved.
(b) Significant changes in the research compared with the original proposal.
(c) Scheduled completion rate versus actual completion rate to date with explanation on major variances.
(d) Difficulties, if any, encountered that impeded the progress of the research and actions taken to overcome those difficulties.

Summary:

As this is the final report of the project, we provide here an overall summary of the notable outcomes of the project:

- **Deepened understanding of molecular biology through computational analysis of clinical and biological data.** We have successfully employed our analysis methods and tools on clinical and biological data to discover new biological insights. For example, we were the first to discover that that a large percentage of proteins shared functions w/ 2nd level neighbours. Based on this, we have developed a novel method for predicting protein functions that outperformed existing methods by a large margin. We have also developed the first algorithms that can discover and label meso-scale network motifs from large PPI networks with biological functional annotations, and showed, for the first time, that the complex topological motifs can be associated and preserved with underlying biological functional patterns. We also pioneer in methods for discovering interacting motif pairs which contribute to protein-protein interaction. The results generated from our methods deepen our understanding of the mechanism of protein-protein interaction.
- **Deepened understanding of data mining methods through the analysis of clinical and biological data.** The analysis of clinical and biological data places high demands on data mining methods, requiring efficiency, accuracy, as well as explainability. For example, two high performance classification methods, PCL and CS4, were developed to give performance matching that of the best classifiers available, and at the same time, to provide rules that are easily to understand and explain. The analytical challenges of the clinical and biological domain have become a main driver for our theoretical research on emerging pattern and ensemble-based classification methods, resulting in our deepened understanding on frequent pattern space and equivalence classes.
- **Inspired new research directions in advanced bioinformatics and data mining topics**. As biology moves beyond simple sequence-level analyses into complex system-level dissections of bio-molecular interaction networks, it has provided many new opportunities for developing novel computational approaches for key biological problems. For example, our "Pathway Informatics" research has inspired our foray in the "network mining" domain for which we have developed sophisticated graph mining

methods to mine the biological networks for novel motifs and subgraphs which may correspond to such new biological entities as protein complexes and functional modules, which are generally hard to discover experimentally. The various practical data challenges that biologists are currently facing (namely, poor coverage, high data noise, disparate and heterogeneous online data sources) have also inspired our many innovative approaches in false positive/negative detection, text mining, data integration, and cleansing.

- **Published extensively in both bioinformatics and data mining.** Our work has been published in leading journals and premier conferences of computational biology (Bioinformatics, RECOMB, etc) as well as data mining (e.g. KDD, ICDE, etc). A total of 130 publications have been generated by the joint lab, including 10 books, 1 conference best paper, and 1 keynote paper. The investigators have also further established themselves as leaders in this field, with more than 80 invited seminars (including 8 keynotes) and also serving on the technical programme committees of international conferences.
- **Contributed world-class human capital for the emerging bioinformatics domain**. The joint-lab has also provided an excellent platform for the professors at NUS and the researchers at I^{2}R to jointly contribute to the postgraduate training for this emerging domain. In addition to the three PhD students who were fully supported by this project, the PIs also co-supervised nine other additional post-graduate students through the joint-lab. Upon graduation, the graduates either joined the A*STAR RI's to contribute to further research in related domains in Singapore, or were accepted by leading universities (e.g. Stanford, U. of Toronto) worldwide for doctoral and post-doctoral training.

Upon the successful completion of this joint lab, the PIs will be seeking further opportunities to continue the bioinformatics research and fruitful collaborative relationships that have resulted from this joint-lab.

Objectives:

Develop methods for analysis suitable for clinical and biological data.

Milestones (Past Period):

A. Data mining technologies **(completed)**

- Meng Ling has continued his investigation of how the frequent pattern space and equivalence classes evolve when updates are made to the underlying transaction database. The work on maintaining equivalence classes when transactions were removed has been accepted at *PAKDD07*. For this reporting period, he has worked out exactly how the equivalence classes are changed when the support threshold is changed. He has also devised a practical algorithm for maintaining equivalence classes when support threshold is changed. He has also worked on maintaining equivalence classes when transactions are added to the database. However, some bugs remain to be ironed out in this case. Other than this minor issue, we have dealt with maintaining equivalence classes under all the main ways of updating the transaction database. We expect Meng Ling to complete the final implementation and integration in the next 6 months and submit his PhD thesis in Q1 2008.

- Terk Shuen has demonstrated that the following during this evaluation period. (a) Emerging patterns that are generators form a more effective basis for training the PCL classifier than jumping emerging patterns and emerging patterns that are closed patterns. (b) PCL trained with emerging patterns that are generators are much more resistant to missing values and noise in the training data than a large variety of other classifiers such as SVM, C4.5, Naïve Bayes, KNN, etc. We have thus reached a good point to complete the project by packaging up the generator-based PCL classifier. We expect Terk Shuen to write up these results and complete his qualifiers in Q2 2007.

- Jinyan and his team completed their study of mining maximal cliques and bicliques. The results have been summarized, written up, and submitted to *TKDE*.

B. Gene feature recognition **(completed)**

- Kenny Chua, Ken Sung, and Limsoon continued their work on protein function prediction. The work on function prediction based on protein interactions was published in both *Bioinformatics* (yeast) and *BMC Bioinformatics* (other species). They have further validated their method for information fusion to predict protein function by combining information from protein interaction, literature co-ocurrence, sequence similarity, etc. The results have been written up and submitted to *Bioinformatics*. We have thus reached a good point to wrap up the project by packaging up the information fusion technique and the protein-interaction-based prediction into an integrated extensible protein function prediction system. We expect Kenny Chua to complete and submit his PhD thesis in Q2 2007.

- An undergraduate student Koh Chuan Hock joined the lab for the last 6 months for his UROP. He worked with Limsoon to predict Arabidopsis poly-A sites. This served as a nice second substantial validation of the “feature generation, feature selection, feature integration” developed earlier in the joint lab by Huiqing and Limsoon. Chuan Hock tested our model on public datasets and achieved more than 97.5% sensitivity and specificity. We also directly compared with another Arabidopsis prediction model, PASS 1.0, and achieved better results. The results have been written up and submitted to *GIW2007*. With this, the poly-A recognition project reached full completion.

E. Pathway informatics **(completed)**

- With the publication of the LeMoFinder at ICDE-2007, Chen Jin has completed the protein interaction network motif project. He is currently a postdoc at Sue Rhee’s Lab in Stanford University.

- With the publication of the D-STAR algorithm in BMC Bioinformatics, Soon-Heng Tan has completed the interaction linear motif project for his MSc degree at SOC. He is now a doctoral student at Gary Bader’s Lab in University of Toronto. Hugo Willy continues to develop better algorithms for this problem. A paper in collaboration with Soon-Heng Tan, under supervision of Wing-Kin Sung and See-Kiong, is in preparation.

- See-Kiong, together with Xiaoli and Chuan-Sheng, completed their protein complex discovery project by developing a better algorithm called DeCAFF to discover protein complexes in dense reliable neighborhoods of PPI network. The new method is both more accurate and more efficient than current methods. A paper on DECAFF has been accepted by CSB-2007 as a full paper.

- See-Kiong, together with Zeyar Aung, Soon-Heng Tan, and Kian-Lee Tan, also investigated on uncovering the structural basis of protein interactions with efficient clustering of 3-D interaction interfaces. Analysis of the resulting interface clusters revealed groups of structurally diverse proteins having similar interface patterns. Most interestingly, we also found, in some of the interface clusters, the presence of well-known linear binding motifs which were non-contiguous in the primary sequence. A paper on this work has also been accepted by CSB-2007 as a full paper, as well as being invited to *JBCB*.

- Kenny Chua, under supervision of Ken Sung and Limsoon, showed that the CD distance measure and the FSWeight measure (developed originally for protein function prediction using protein interaction information) could be used for ranking the reliability of protein interactions. This result was published as a keynote paper in GIW2006. During this reporting report, we investigated the possibility of using CD distance/FSWeight to identify false negatives in protein interactions and to identify protein complexes. We showed that the use of FSWeight to augment protein-protein interactions could improve the precision of clusters predicted by various existing clustering algorithms. Our complex finding algorithm performed very well on interaction networks modified in this way. This work has been accepted by *CSB2007*, and has been invited to *JBCB.*

F. Intelligent Data Warehousing with application to Bioinformatics (**completed**)

- Judice, under the supervision of Mong Li and Wynne, has completed the design of two methods, ODDS and XODDS, to detect attribute outliers in relational and XML data respectively. These methods have been implemented and evaluated on both synthetic and real world datasets, including UniProt. A paper on ODDS has been published in DASFAA 2007 while a paper on XODDS is currently under review. Judice has also submitted her thesis for examination.

- During this reporting period, an undergraduate student Chen Ju joined the lab under Limsoon's supervision to develop the GIORG Data Collection System. GIORG is a cross-hospitals study on gastro and intestinal cancer lead by NUS. There are 6 hospitals involved in the project. They are: National University Hospital (NUH), Singapore General Hospital (SGH), John Hopkins Hospital, Tan Tock Seng Hospital (TTSH), National Cancer Centre (NCC), and Alexandra Hospital. This project aims to manage all their patient information in a way that cross-hospital/-department web-based data mining queries can be implemented easily and securely across the heterogeneous data from the 6 hospitals. The completed prototype is now being tested.

<u>Milestones (Reporting Period 01/05/07-30/06/07)</u>:

There are no further research updates for this 2-month period.

4. Milestones / Deliverables				
(a) Performance Indicators				
Economic Impact Indicators				
		Actual for reporting period - incremental	Cum actual for project	Cum target for project
Attracting investments	Total value of investments attracted to Singapore for which the project plays a significant role	0	0	
Improving the competitiveness of local industry	Cash contribution from industry	0	0	
	In-kind contribution from industry	0	0	
	Royalties and licensing fees from IP	0	0	
	No. of joint projects with industry	0	0	
	Value (total project cost) of joint projects with industry	0	0	
Creating new industries	No. of spin-off companies or joint ventures (please provide listing)	0	0	
	No. of licensing agreements	0	0	
	No. of new products or processes developed	0	0	
	No. of new products or processes commercialized	0	0	
Capability Building Indicators				
Carrying out world class research	No. of patents filed (please provide listing)	0	1	
	No. of patents granted (please provide listing)	0	0	
	No. of papers published in prestigious journals or conferences (please provide listing)	12 (include: 1 book and 1 keynote paper)	130 (include: 10 books, 14 book chapters, 1 best paper and 1 keynote paper)	
	No. of joint programmes with prestigious international research organizations	0	0	
Developing manpower	No. of undergraduate/polytechnic students attached to the project for more than 3 months	2 (Chen Ju, Koh Chuan Hock)	2	
	No. of postgraduate students attached to the projects for more than 3 months	0	11	
	No. of RSEs trained through formal post-graduate studies	0	1	
	No. of RSEs trained through joint projects	0	1	
	No. of conferences & seminars organised (please provide listing)	1	10	

(b) Additional milestones/deliverables not captured in 4(a) above (use additional pages if necessary)

Conferences & seminars organized

New: None for the current reporting period 01/05/07-30/06/07.

Cumulative:

1. 12/02/07. 6th Korea-Singapore Workshop on Bioinformatics and NLP. The workshop was well-attended with Korean participants from KAIST and ICU, as local participants from the universities (both NUS and NTU) and I^{2}R (KDD and Media Semantics). A total of 2 keynote and 11 student talks were presented. (The meeting also facilitated the organizational discussion on the international symposium LBM-2007 to be co-located with GIW-07 in December.)
2. 27/7/06. Internal seminar: “Dissecting Genome-Wide Protein-Protein Interactions with Meso-scale networks Motifs” by Chen Jin. I^{2}R Postgraduate Student Research Seminar Series.
3. 22/2/06. 5th Korea-Singapore Workshop on Bioinformatics and NLP. The workshop was attended by participants from NUS, NTU, I^{2}R, KAIST, and ICU. A total of 13 talks presented.
4. 09/04/06, the first BioDM 2006 workshop was organized in conjunction with PAKDD 2006. The proceedings was published as a volume of LNBI by Springer-Verlag.
5. 16/8/05. Internal seminars: “Function Prediction from Protein Interactions” by Kenny Chua, and “Accurate Identification of MicroRNA Precursors” by Yang Lianghuai.
6. 17-21/1/05. 3rd Asia-Pacific Bioinformatics Conference, held at I^{2}R, with Vladimir Brusic as organizing chair. The conference attracted 118 full paper submissions, with 35 selected for plenary presentations, and attracted over 200 participants from 22 countries.
7. 24/1/05. I2R-SOC Joint Meeting with Yuan Ze Univ Taiwan, held at I^{2}R, with Ng See-Kiong as organizing chair. Students in our joint lab made 8 short presentations on our work to our Taiwanese visitors lead by Prof. Shu-Yuan Chen.
8. 28/11/03. Internal seminar: “On Combining Multiple Microarray Studies for Improved Functional Classification by Whole-Dataset Feature Selection” by V. S. Sundararajan.
9. 28/11/03. Internal seminar: “Efficient Remote Homolog Detection Using Local Structure” by Hou Yuna
10. 30/9/03. Internal seminar: “Belief Propagation with Dynamic Arc Removal for Systematic Assessment of High-Throughput Protein Interaction Data” by Chen Jin.

Patents

New: None for the current reporting period 01/05/07-30/06/07

*Cumulati*ve:

1. Jinyan Li, Haiquan Li, Limsoon Wong. **System and Method for Identifying Sets of Attributes in a Database, System and Method for Constructing a Tree Structure for a Database and Computer Program Elements**, I^{2}R Invention Disclosure P2004054. PCT/SG2005/000386, 10 November 2005.

Papers

New:

As this is the final progress report, we include here also accepted publications that will be published at a later date after the conclusion of the project:

1. X.-L. Li, J. Lee, B. Veeravalli, and S.-K. Ng (2007) “An HV-SVM Classifier to Infer TF-TF Interactions using Protein Domains and GO Annotations”, accepted by the *IEEE 7th International Symposium on Bioinformatics and Bioengineering (BIBE 2007),* Boston, USA, October 14-17, 2007.
2. Z. Aung, S.-H. Tan, S.-K. Ng and K. L. Tan (2007) "Uncovering the Structural Basis of Protein Interactions with Efficient Clustering of 3-D Interaction Interfaces", accepted by the 6*th* *International Conference on Computational Systems Bioinformatics (CSB 2007),* San Diego, California, August 13-17, 2007.
3. X.-L. Li, C.-S. Foo, and S.-K. Ng (2007) "Discovering Protein Complexes in Dense Reliable Neighborhoods of Protein Interaction Networks", accepted by the 6*th* *International Conference on Computational Systems Bioinformatics (CSB 2007),* San Diego, California, August 13-17, 2007.
4. Nguyen Bao Nguyen, Cam Thach Nguyen and Wing-Kin Sung. Fast Algorithms for computing the Tripartition-based Distance between Phylogenetic Networks. **Journal of Combinatorial Optimization**, 13(3):223-242, 2007.
5. Nguyen Bao Nguyen, Cam Thach Nguyen, Wing-Kin Sung and Louxin Zhang. Reconstructing Recombination Network from Sequence Data: The Small Parsimony Problem. **IEEE IEEE/ACM Transactions on Computational Biology and Bioinformatics (TCBB)**, 4(3):394-402, 2007.
6. Francis Y.L. Chin, Henry C.M. Leung, W.K. Sung and S.M. Yiu. The Point Placement Problem on a Line – Improved Bounds for Pairwise Distance Queries. **WABI**, 2007.
7. Hon Nian Chua, Kang Ning, Wing-Kin Sung, Hon Wai Leong and Limsoon Wong. Using Indirect Protein-Protein Interactions for Protein Complex Prediction. **CSB**, 2007.
8. Huiqing Liu, Limsoon Wong, Ying Xu. **Patient Survival Prediction from Gene Expression Data**. *Knowledge Discovery in Bioinformatics: Techniques, Methods, and Applications*, edited by Xiaohua Hu, Yi Pan, chapter 6, pages 89--111, Wiley, July 2007.
9. Donny Soh, Difeng Dong, Yike Guo, Limsoon Wong. **Enabling More Sophisticated Gene Expression Analysis for Understanding Diseases and Optimizing Treatments**. *ACM SIGKDD Explorations*, 9(1):3--14, June 2007. (Invited reviewed paper.)
10. Limsoon Wong. **Manifestation and Exploitation of Invariants in Bioinformatics**, *Proceedings of 2nd International Conference on Algebraic Biology (AB2007)*, pages 365--377, Castle of Hagenberg, Austria, 2-4 July 2007.
11. Jinyan Li, Guimei Liu, Limsoon Wong. **Mining Statistically Important Equivalence Classes and Delta-Discriminative Emerging Patterns**. *Proceedings of 13th International Conference on Knowledge Discovery and Data Mining*, pages 430--439, San Jose, California, 12-15 August 2007.

Cumulative:

12. Wah-Heng Lee and Wing-Kin Sung. **RB-Finder: An Improved Distance-based Sliding Window Method to Detect Recombination Breakpoints**, pages 518-532, in Proceedings of the 11th RECOMB, Oakland, USA, April 2007.

13. Jin Chen, Hon Nian Chua, Wynne Hsu, Mong-Li Lee, See-Kiong Ng, Rintaro Saito, Wing-Kin Sung, Limsoon Wong. **Increasing Confidence of Protein-Protein Inteactomes**. *Proceedings of 17th International Conference on Genome Informatics (GIW)*, pages 284--297, Yokohama, Japan, 18-20 December 2006. (invited keynote paper)

14. J. Chen, W. Hsu, M.L. Lee, and S.-K. Ng (2007) “**Labeling Network Motifs in Protein Interactomes for Protein Function Prediction**”, in Proceedings of the *23rd International Conference on Data Engineering (ICDE 2007),* pp 546-555, Istanbul, Turkey, April 16-20, 2007.

15. Hon Nian Chua, Wing-Kin Sung, Limsoon Wong. **Using Indirect Protein Interactions for the Prediction of Gene Ontology Functions**. *BMC Bioinformatics*, 8(Suppl 4):S8, May 2007.

16. Judice Koh, Mong Li Lee, Wynne Hsu, Kai Tak Lam. **Correlation-based Detection of Attribute Outliers**. *Proceedings of 12th International Conference on Database Systems for Advanced Applications (DASFAA)*, Thailand, April 2007.

17. X. Li, Y.C. Tan, and S.-K. Ng (2006) "**Systematic gene function prediction from gene expression data by using a fuzzy nearest-cluster method**", *BMC Bioinformatics* vol 7 (Suppl 4): S23.

18. Guimei Liu, Jinyan Li, Kelvin Sin, Limsoon Wong. **Distance-Based Subspace Clustering with Flexible Dimension Partitioning**, *Proceedings of 23rd IEEE International Conference on Data Engineering (ICDE)*, pages 1250--1254, Istanbul, Turkey, April 2007.

19. Scott Mann, Jinyan Li, and Yi-Ping Phoebe Chen. **A pHMM-ANN based discriminative approach to promoter identification in prokaryote genomic contexts**. Nucleic Acids Research, Vol 35 (2), e12, pages 1-7, January, 2007.

20. S.-K. Ng, S.-H. Tan (2006) "**Challenges in Biological Literature Mining for Online Discovery of Molecular Interaction Pathways**", in *International Journal of Computer Applications in Technology (IJCAT)*, vol 27, No 4, pages 259-269

21. Jagath C. Rajapakse, Limsoon Wong, Raj Acharya, editors. *Pattern Recognition in Bioinformatics*, Springer-Verlag, Berlin, 25 September 2006. (186 pages)

22. S.-H. Tan, H. Willy, W.-K. Sung and S.-K. Ng (2006) "**A Correlated Motif Approach for Finding Short Linear Motifs from Protein-Protein Interaction Data**", *BMC Bioinformatics* vol 7:502.

23. Swee-Seong Wong, Wing-Kin Sung, Limsoon Wong. **CPS-tree: A Compact Partitioned Suffix Tree for Disk-Based Indexing on Large Genome Sequences**. *Proceedings of 23rd IEEE International Conference on Data Engineering*, pages 1350--1354, Istanbul, Turkey, April 2007.

24. Guimei Liu, Kelvin S.H. Sim, Jinyan Li. **Efficient Mining of Large Maximal Bicliques**. In the Proceedings of the 8th International Conference on Data Warehousing and Knowledge Discovery (DaWaK 2006), pages 437-448, Krakow, Poland, 4 - 8 September 2006.

25. Kuralmani Vellaisamy and Jinyan Li. **Bayesian Approaches to Sequential Patterns Interestingness**. In the Proceedings of the Ninth Pacific Rim International Conference on Artificial Intelligence (PRICAI 2006), pages 241-250, August 2006, Guilin, China.

26. Jinyan Li, Haiquan Li, Limsoon Wong, Jian Pei, Guozhu Dong. **Minimum Description Length Principle: Generators Are Preferable to Closed Patterns**. In the Proceedings of the Twenty-First National Conference on Artificial Intelligence (AAAI-06), pages 409-414, July 16 - 20, 2006 in Boston, Massachusetts.

27. Jagath C. Rajapakse, Limsoon Wong, Raj Acharya, editors. *Pattern Recognition in Bioinformatics*, Springer-Verlag, Berlin, 25 September 2006. (186 pages)

28. Rajesh Chowdhary, Limsoon Wong, Vladimir Bajic. **Finding Functional Promoter Motifs By Computational Methods: A Word of Caution**. *International Journal of Bioinformatics Research and Applications*, 2(3):282--288, 2006.

29. Rajesh Chowdhary, Sin Lam Tan, R. Ayesha Ali, Brent Boerlage, Limsoon Wong, and Vladimir B Bajic. **Dragon Promoter Mapper (DPM): A Bayesian Framework for Modeling Promoter Structures**. *Bioinformatics*, 22:2310--2312, 2006.

30. Hon Nian Chua, Wing-Kin Sung, Limsoon Wong. **Exploiting Indirect Neighbours and Topological Weight to Predict Protein Function from Protein-Protein Interactions**. *Bioinformatics*, 22:1623--1630, 2006.

31. Yun Zheng, Wynne Hsu, Mong Li Lee, Limsoon Wong. **Exploring Essential Attributes for Detecting MicroRNA Precursors from Background Sequences**. *Proceedings of 2006 VLDB Workshop on Data Mining in Bioinformatics*, pages 131--145, Seoul, Korea, September 2006.

32. Ho-Leung Chan, Tak Wah Lam, Wing-Kin Sung, Siu-Lung Tam, Swee-Seong Wong. **A Linear Size Index for Approximate Pattern Matching**. *Proc. 17th Annual Symposium on Combinatorial Pattern Matching (CPM 2006)*, pages 49--59, July 2006.

33. Ho-Leung Chan, Tak-Wah Lam, Wing-Kin Sung, Siu-Lung Tam, Swee-Seong Wong. **Compressed Indexes for Approximate String Matching**. *Proc. 16th Annual European Symposium on Algorithms (ESA 2006)*, pages 208-219, September 2006.

34. J. Chen, W. Hsu, M.L. Lee, and S.-K. Ng. **Increasing Confidence of Protein Interactomes using Network Topological Metrics**, *Bioinformatic* vol 22, no 16, pages 1998-2004. 2006.

35. X.-L. Li, S.-H. Tan, and S.-K. Ng. **Improving Domain-Based Protein Interaction Prediction Using Biologically-Significant Negative Dataset.** *International Journal of Data Mining and Bioinformatics (IJDMB)* vol 1, no. 2, pages 138-149. 2006.

36. J. Jansson, S.-K. Ng, W.-K. Sung, H. Willy. **A Faster and More Space-Efficient Algorithm for Infering Arc-Annotations of RNA Sequences through Alignment.** *Algorithmica* vol 46, no 2, pages 223-245. 2006.

37. J. Chen, W. Hsu, M.L. Lee, and S.-K. Ng. **NeMoFinder: Dissecting genome wide protein-protein interactions with repeated and unique network motifs.** In Proceedings of the *Twelfth ACM SIGKDD International Conference on Knowledge Discovery and Data Mining (KDD 2006)*, pp 106-115, Philadelphia, USA, August 20-23, 2006.

38. Z. Zhang, M. Veronika, S.-K. Ng, and V.B. Bajic. **Intelligent Extraction versus Advanced Query: Recognize Transcription Factors from Databases.** In Proceedings of the *International Workshop on Pattern Recognition in Bioinformatics (PRIB 2006)*, pp 133-139, Hong Kong, August 20, 2006.

39. Tao Jiang, Ueng-Cheng Yang, Phoebe Chen, Limsoon Wong, editors. *Proceedings of the 4th Asia-Pacific Bioinformatics Conference,* Imperial College Press, London, February 2006. (book)

40. Jinyan Li, Qiang Yang and Ah Hwee Tan (Editors). **Data Mining for Biomedical Applications: Proceedings of PAKDD 2006 Workshop, BioDM 2006, Singapore**. Lecture Notes in Bioinformatics, volume 3916 (LNBI 3916), April, 2006, Springer-Verlag (book).

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127. Wei Chen , W.-K. Sung, **On Half Gapped Seeds**. *Proceedings of 14th International Conference on Genome Informatics,* Yokohama, December 2003.

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Invited talks
New:

1. Limsoon Wong. **Increasing Confidence of Protein-Protein Interactomes**. *Invited tutorial at Computational Methods in Biomolecular Structures and Interaction Networks Program*, Institute for Mathematical Sciences, Singapore, 13 July 2007.

2. Limsoon Wong. **Manifestation and Exploitation of Invariants in Bioinformatics**. *Invited tutorial at 2nd International Conference on Algebraic Biology (AB2007)*, Castle of Hagenberg, Austria, 2-4 July 2007.

Cumulative:

3. Wing-Kin Sung. **Detecting viruses using Pathogen chip**, *invited talk at Bioinformatics for Biologists* seminar series, Office of Life Sciences, National University of Singapore, 5 January, 2007.

4. Jinyan Li. **Research on subgraph mining and biomedical applications**. *Keynote for Korean Information Processing Society Fall Conference*, Chungbuk National University, Korea, 10 Nov. 2006.
5. S.-K. Ng. **Mining the Protein-Protein Interaction Networks**, *invited talk at Bioinformatics for Biologists* seminar series, Office of Life Sciences, National University of Singapore, 30 January, 2007.
6. S.-K. Ng. **Unraveling the Common Denominators in Protein Interaction Networks**, *invited keynote at International Symposium on Computational Biology and Bioinformatics*, India, 15-17 December 2006.

7. S.-K. Ng. **Uncovering the Biological Building Blocks of Protein Interaction Networks**, *invited plenary at 8th National Symposium on Biology*, Malaysia, 5-7 December 2006.

8. Limsoon Wong. **Exciting the Reluctant Bioinformatician**. *Invited talk at International Symposium on Bioinformatics Education and Research*, Yokohama, Japan, 17 December 2006.

9. Limsoon Wong. **Increasing Confidence of Protein-Protein Inteactomes**. *Keynote talk at 17th International Conference on Genome Informatics*, Yokohama, Japan, 18-20 December 2006.

10. Limsoon Wong. **Guilt by Association: A Tutorial on Protein Function Inference**. *Tutorial at 5th Asia-Pacific Bioinformatics Conference (APBC2007)*, Hong Kong, 15-17 January 2007.

11. Limsoon Wong. **Protein Function Inference Enhanced by Text Mining**. *Invited talk at Forum on Advanced NLP and Text Mining (T-FaNT)*, Tokyo, Japan, 11-13 March 2007.

12. Limsoon Wong. **An Introduction to Knowledge Discovery Applications and Challenges in Life Sciences**. *Advanced Seminar at IEEE 23rd International Conference on Data Engineering (ICDE2007)*, Istanbul, Turkey, 16-20 April 2007.

13. Limsoon Wong. **Guilt by Association: A Tutorial on Data Mining Techniques for Protein Function Inference**. *Tutorial at 11th Pacific-Asia Conference on Knowledge Discovery and Data Mining (PAKDD 2007)*, Nanjing, China, 22-25 May 2007.
14. Hon Nian Chua, Wing-Kin Sung, Limsoon Wong. **Exploiting Indirect Neighbours and**

Topological Weight to Predict Protein Function from Protein-Protein Interactions. *Invited talk at Academia Sinica*, Taipei, Taiwan, 1 June 2006.

15. Limsoon Wong. **Building Gene Networks by Information Extraction, Cleansing, & Integration**. *Invited talk at National Taiwan University*, Taipei, Taiwan, 1 June 2006.

16. Hon Nian Chua, Wing-Kin Sung, Limsoon Wong. **Exploiting Indirect Neighbours and Topological Weight to Predict Protein Function from Protein-Protein Interactions**. *Invited talk at Bioinformatics Minisymposium---from Sequences, Structures, to Systems*, National Chiao Tung University, Hsinchu, Taiwan, 2 June 2006.

17. Limsoon Wong. **Building Gene Networks by Information Extraction, Cleansing, & Integration**. *Invited talk at Bioinformatics Minisymposium---from Sequences, Structures, to Systems*, National Chiao Tung University, Hsinchu, Taiwan, 2 June 2006.

18. Hon Nian Chua, Wing-Kin Sung, Limsoon Wong. **Exploiting Indirect Neighbours and Topological Weight to Predict Protein Function from Protein-Protein Interactions**. *Invited talk at Yang Ming National University*, Taiwan, 5 June 2006.

19. Limsoon Wong. **Building Gene Networks by Information Extraction, Cleansing, & Integration**. *Invited talk at Yang Ming National University*, Taiwan, 6 June 2006.

20. Limsoon Wong. **Discovering Motif Pairs at Interaction Sites from Protein Sequences on a Proteome-Wide Scale**. *Invited talk at Yang Ming National University*, Taiwan, 7 June 2006.

21. Limsoon Wong. **An Introduction to Knowledge Discovery Applications in Biomedical Sciences**. *Invited talk at Taipei Medical University*, Taiwan, 8 June 2006.

22. Hon Nian Chua, Wing-Kin Sung, Limsoon Wong. **Exploiting Indirect Neighbours and Topological Weight to Predict Protein Function from Protein-Protein Interactions**. *Invited talk at Taipei Medical University*, Taiwan, 8 June 2006.

23. Limsoon Wong. **Guilt by Association of Common Interaction Partners**. *Invited talk at IMS Workshop on BioAlgorithmics*, Institute for Mathematical Sciences, Singapore, 12-14 July 2006.

24. Limsoon Wong. **Exciting Media**. *Invited talk at ICAAS-UIAAS Innovation Symposium*, NLB @ Victoria Street, Singapore, 26 August 2006.

25. Limsoon Wong. **Increasing Confidence of Protein-Protein Inteactomes**. *Invited talk at Hong Kong Baptist University*, Kowloon Tong, Hong Kong, 4 September 2006.

26. Limsoon Wong. **Adventures of a Logician-Engineer: A Journey Through Logic, Engineering, Medicine, Biology, and Statistics**. *Invited talk at 8th International Symposium on Symbolic and Numeric Algorithms for Scientific Computing (SYNASC 2006)*, Timisoara, Romania, 26-29 September 2006.

27. Limsoon Wong. **Discovering Motif Pairs at Interaction Sites from Protein Sequences on a Proteome-Wide Scale**. *Invited talk at Renyi Institute of Mathematics*, Budapest, Hungary, 2 October 2006.

28. Limsoon Wong. **Guilt by Association of Common Interaction Partners**. *Talk at Xi'an Jiaotong University*, Xi'an, China, 23 October 2006.

29. Limsoon Wong. **Adventures of a Logician-Engineer: A Journey Through Logic, Engineering, Medicine, Biology, and Statistics**. *Talk at Northwestern Polytechnical University*, Xi'an, China, 23 October 2006.

30. Limsoon Wong. **Increasing Confidence of Protein-Protein Inteactomes**. *Talk at Southeast University*, Nanjing, China, 25 October 2006.

31. Limsoon Wong. **Guts of Dragon Promoter Finder and Mapper**. *Invited talk at 5th East Asian Biophysics Symposium & 44th Annual Meeting of the Biophysical Society of Japan*, Okinawa, Japan, 14 November 2006.

32. Limsoon Wong. **An Introduction to Knowledge Discovery Applications and Challenges in Life Sciences**. *Invited tutorial at EII PhD Winter School in Data Mining & Bioinformatics*, ARC Research Network in Enterprise Information Infrastructure, Lorne, Victoria, Australia, 13-17 August 2006.

33. Hon Nian Chua. **A Graph-Based Approach to Inferring Protein Function from Heterogeneous Data Sources**. *Invited talk at IMS Workshop on BioAlgorithmics*, Institute for Mathematical Sciences, Singapore, 12-14 July 2006.

34. Hon Nian Chua. **Guilt by Indirect Functional Association**. Plenary talk at Annual Meeting on Automated Function Prediction (AFP2006), San Diego, 30 August - 1 September 2006.

35. Hugo Willy. **On Simultaneous Knowledge Extraction from Protein-Protein Interaction Data**. *Invited talk at IMS Workshop on BioAlgorithmics*, Institute for Mathematical Sciences, Singapore, 12-14 July 2006.

36. Wing-Kin Sung. **Annotating the Genome Using Paired-End diTag**. *Invited talk at Symposium on Bioinformatics in Taiwan (BIT2006)*, National Chung-Hsing University, Taichung, Taiwan, 12-15 September 2006.

37. Wing-Kin Sung. **Gene and Transcription Factor Binding Sites Finding Methods**. *Invited tutorial at Symposium on Bioinformatics in Taiwan (BIT2006)*, National Chung-Hsing University, Taichung, Taiwan, 12-15 September 2006.

38. See-Kiong Ng. **Dissecting Protein Interaction Networks with Meso-scale Network Motifs.** Invited talk for the *Fifth Korea-Singapore Workshop on Bioinformatics and NLP*, KAIST, Korea, 17 Nov 2006.

39. See-Kiong Ng. **Unraveling Multi-Domain Dependencies in Protein-Protein Interactions**. Invited keynote for the First International Conferences on Computational Systems Biology, Shanghai, 20-23 July 2006.

40. Wing-Kin Sung. **Phylogenetic Network Construction and Comparison**. *Invited talk at 3rd Association of Asian Societies for Bioinformatics Symposum (AASBi 2006),* National Taiwan University, 12 February 2006.

41. Limsoon Wong. **Some Data Mining Challenges Learned From Bioinformatics & Actions Taken**. *Invited talk at 1st Bertinoro Workshop on Data Mining*, University of Bologna Residential Center, Bertinoro, Italy, 24-27 October 2005.

42. Limsoon Wong. **Protein Function Prediction From Protein Interactions**. *Invited talk at 1st International Symposium on Languages in Biology and Medicine*, KAIST, Daejon, Korea, 24-26 November 2005.

43. Limsoon Wong. **Protein Function Prediction From Protein Interactions**. *Invited talk at "Figuring Out Life: NUS-Karolinska Joint Symposium on Application of Mathematics in Biomedicine"*, Institute for Mathematical Sciences, Singapore, 28-29 November 2005.

44. Limsoon Wong. **Exciting Bioinformatics Adventures.** *Invited keynote at 12th International Conference on Biomedical Engineering*, Suntec Singapore International Convention and Exhibition Centre, Singapore, 7-10 December 2005.

45. Limsoon Wong. **Protein Function Prediction From Protein Interactions**. *Invited talk at University of Hong Kong* , Hong Kong, 6 March 2006.

46. Hon Nian Chua, Wing-Kin Sung, Limsoon Wong. **Exploiting Indirect Neighbours and Topological Weight to Predict Protein Function from Protein-Protein Interactions** *Invited keynote at BioDM2006*, Singapore, 9 April 2006. *Proc. PAKDD 2006 Workshop on Data Mining for Biomedical Applications (BioDM2006)*, Singapore, 9 April 2006, page 1.

47. Limsoon Wong. **The Bright and Dark Side of Data Mining Research**. *Invited panel discussion at PAKDD 2006*, Hilton Hotel, Singapore, 11 April 2006.Jinyan Li, Limsoon Wong. **Bioinformatics and Machine Learning**. *Tutorial talk at 20th National Conference on Artificial Intelligence (AAAI-05)*, Pittsburgh, 9-13 July 2005.

48. Ken Sung, Limsoon Wong. **Bioinformatics in Practice**. *Invited tutorial at 8th International Conference on Discovery Science*, Marina Mandarin Hotel, Singapore, 8 October 2005.

49. Limsoon Wong. **Selection of Patient Samples and Genes for Disease Prognosis**. *Invited talk at "Informatics Inspired Biology" Symposium*, BioPolis, Singapore, 16 January 2005.

50. Limsoon Wong. **Assessing Reliability of Protein-Protein Interaction Experiments.** *Invited keynote at 3rd Korea-Singapore Joint Workshop on Bioinformatics and Natural Language Processing*, Muju Resort, 20-22 February 2005.

51. Limsoon Wong. **Building gene networks by information extraction, cleansing, and integration**. *Invited plenary lecture at 3rd International Symposium on e-Biology Initiative: Towards New Frontiers of Biology*, Takeda Hall, University of Tokyo, Tokyo, Japan, 11 March 2005.

52. Limsoon Wong. **Some interesting issues in constructing gene/protein networks**, *Invited round-table presentation at 3rd International Symposium on e-Biology Initiative: Towards New Frontiers of Biology*, National Institute of Informatics, Tokyo, Japan, 10 March 2005.
53. Haiquan Li, Jinyan Li, Limsoon Wong. **Binding Motif Pairs from Interacting Protein Groups**. *Invited talk at Workshop on Data Analysis and Data Mining in Proteomics*, Institute for Mathematical Sciences, NUS, Singapore, 12 May 2005.

54. Limsoon Wong. **Building Gene Networks by Information Extraction, Cleansing, & Integration.** *Invited talk at Tamkang University*, Taiwan, 31 May 2005.

55. Limsoon Wong. **Discovering Binding Motif Pairs from Interacting Protein Groups.** *Invited talk at Tamkang University*, Taiwan, 31 May 2005.

56. Limsoon Wong. **Assessing Reliability of Protein-Protein Interaction Experiments.** *Invited talk at Tamkang University*, Taiwan, 1 June 2005.

57. Limsoon Wong. **Assessing Reliability of Protein-Protein Interaction Experiments.** *Invited talk at Changchun International Bioinformatics Workshop,* Changchun, Jilin, China, 5-7 July 2005.

58. Hon-Nian Chua, Wing-Kin Sung, Limsoon Wong. **Protein Function Prediction from Protein Interactions.** *Invited talk at Singapore-Bangalore Biomedical Symposium,* Biopolis, Singapore, 8-9 September 2005.

59. Wing-Kin Sung. **DTSeq: Decision Tree Based De Novo Peptide Sequencing**. *Invited talk at Workshop on Data Analysis and Data Mining in Proteomics*, Institute for Mathematical Sciences, NUS, Singapore, 12 May 2005.

60. See-Kiong Ng. **Mining Motifs from Protein Interaction Data**. *Invited talk at Workshop on Data Analysis and Data Mining in Proteomics*, Institute for Mathematical Sciences, NUS, Singapore, 12 May 2005.

61. See-Kiong Ng. **Computational Purification of Protein Interactomes Using Network Topology.** Invited talk at *3rd Symposium of Association of Asian Societies for Bioinformatics* (AASBi 2005), September 23 2005, Busan, Korea.

62. Limsoon Wong**. Imagination to Reality: Life as a Researcher**. *Invited talk at Hwa Chong Junior College Annual Student Research Symposium*, Hwa Chong Junior College, 3 April 2004.

63. Limsoon Wong**. Exciting Media.** *Invited talk at World Scientific*, 6 April 2004.

64. Limsoon Wong. **A Practical Introduction to Bioinformatics**. *Invited short course at National Yang Ming University*, Taipei, Taiwan, 22 May 2004.

65. Limsoon Wong. **Assessing Reliability of Protein-Protein Interaction Experiments**. *Invited talk at National Yang Ming University,* Taipei, Taiwan, 26 May 2004.

66. Limsoon Wong. **Convexity of Itemset Spaces**. *Invited talk at Academia Sinica*, Taipei, Taiwan, 28 May 2004.

67. Limsoon Wong. **Diagnosis of Childhood Acute Lymphoblastic Leukaemia and Optimization of Risk-Benefit Ratio of Therapy.** *Invited talk at National Cheng Kung University*, Tainan, Taiwan, 21 May 2004.

68. Limsoon Wong. **Assessing Reliability of Protein-Protein Interaction Experiments**. *Invited talk at Genome Institute of Singapore*, 4 June 2004.

69. Limsoon Wong. **Assessing Reliability of Protein-Protein Interaction Experiments.** *Invited talk at 3rd International Conference on Bioinformatics*, Auckland, New Zealand, 4-8 September 2004.

70. Jinyan Li, Limsoon Wong. **Rule-Based Data Mining Methods for Classification Problems in Biomedical Domains.** *Tutorial given at 8th European Conference on Principles and Practice of Knowledge Discovery in Databases*, Pisa, Italy, 20-24 September 2004.

71. Limsoon Wong. **Assessing Reliability of Protein-Protein Interaction Experiments.** *Invited talk at 5th HUGO Pacific Meeting and 6th Asia-Pacific Meeting on Human Genetics,* BioPolis, Singapore, 17-20 November 2004.

72. Limsoon Wong. **Gene Finding and Gene Feature Recognition by Computational Analysis**. *Invited tutorial at Beijing Normal University,* Beijing, 21-25 November 2004.

73. Limsoon Wong. **Assessing Reliability of Protein-Protein Interaction Experiments.** *Invited talk at Tsing Hua University,* Beijing, 25 November 2004.

74. Limsoon Wong. **Assessing Reliability of Protein-Protein Interaction Experiments.** *Invited talk at Edinburgh University,* Edinburgh, 1 October 2004.

75. Limsoon Wong. **Diagnosis of Childhood Acute Lymphoblastic Leukaemia and Optimization of Risk-Benefit Ratio of Therapy**. *Invited talk at Edinburgh University,* Edinburgh, 1 October 2004.

76. Limsoon Wong. **Knowledge Discovery in Biomedicine**. *Invited talk at National Healthcare Group Annual Scientific Congress*, Raffles Convention Centre, Singapore, October 2004.

77. Limsoon Wong**. Research & Discovery: Technologies Today for Solving Problems Tomorrow .** *Talk at Pre-Horizon Seminar, Infocomm Horizon 2004*, I^{2}R, Singapore, 1 November 2004.

78. Limsoon Wong**. Selection of Patient Samples and Genes for Disease Prognosis.** *Invited talk at "Informatics Inspired Biology" Symposium*, BioPolis, Singapore, 16 January 2005.

79. Vladimir Brusic**. Databases and Warehouses for Bioinformatics**. *Invited lecturer at "New Zealand Summer School of Bioinformatics"*, Knowledge Engineering and Discovery Research institute, Auckland, New Zealand, February 2004.

80. Sin Lam Tan, Vidhu Choudhary, Alan Christoffels, Byrappa Venkatesh, Vladimir B. Bajic. **Comparison of core promoters in Fugu rubripes and human**. *Invited keynote at 3rd Asia-Pacific Bioinformatics Conference*, Singapore, January 2005. (Talk given by Vladimir Bajic)

81. Limsoon Wong. **Assessing Reliability of Protein-Protein Interaction Experiments.** *Invited talk at Lilly Systems Biology Symposium*, BioPolis, Singapore, 4 February 2004.

82. See-Kiong Ng. **Whole-Genome Functional Classification of Genes by Latent Semantic Analysis on Microarray Data.** Invited talk at *2nd Korea-Singapore Joint Workshop on NLP and Bioinformatics,* KAIST, Korea, 19 February 2004.

83. See-Kiong Ng. **Combining Multiple Microarray Studies for Improved Functional Classification by Whole-Dataset Feature Selection.** Invited talk at *2nd Korea-Singapore Joint Workshop on NLP and Bioinformatics,* KAIST, Korea, 19 February 2004.

Awards

New: None for this reporting period.

Cumulative:

1. Ken Sung. National Science Award 2006, for contributions to paired-end ditag sequencing technology in GIS
2. Limsoon Wong. Singapore Youth Award Medal of Commendation 2006, for sustained contributions to science and technology.
3. See-Kiong Ng *et al.* Best Paper Award at GIW 2005.
4. Haiquan Li. SOC Dean's Graduate Award, January 2005
5. Haiquan Li, NUS President's Graduate Fellowship, August 2005.

MILESTONES AND STATUS

A. Data mining technologies (completed)
B. Gene feature recognition (completed)
C. Gene expression analysis (completed)
D. Venom informatics (abandoned, as Vladimir Brusic has left Singapore)
E. Pathway informatics (completed)
F. Intelligent Data Warehousing with application to Bioinformatics (completed)

Principal Investigator:

Name: _Wynne Hsu_________ (SOC)

Signature: ____________________________________ Date: __________

Name: __Ng See Kiong_____ (I^2R)

Signature: ____________________________________ Date: ______________________

Section B: To be completed by I^2R Reviewing Officer:

Comments:

Name:

Signature: ____________________________________ Date: ________________________