

Curriculum Vitae

Zheng Jie (郑杰)

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Last update: January 6, 2019

Education

Ph.D. in Computer Science & Engineering, University of California, Riverside, USA (2006)

B. Eng (First class honours) in Computer Science & Engineering, Zhejiang University, China (2000)

Work Experience

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|-------------------|---|
| 07/2018 – present | Associate Professor, School of Information Science and Technology, ShanghaiTech University |
| 02/2011 – 07/2018 | Tenure-Track Assistant Professor, School of Computer Science and Engineering, Nanyang Technological University (NTU), Singapore |
| 10/2012 – 07/2018 | Adjunct Senior Research Scientist, Genome Institute of Singapore (GIS), A*STAR, Singapore |
| 05/2016 – 07/2018 | Courtesy Appointment with School of Physical & Mathematical Sciences (SPMS), NTU, Singapore |
| 07/2007 – 02/2011 | Research Scientist, National Center for Biotechnology Information (NCBI), National Institutes of Health (NIH), USA |
| 08/2006 – 07/2007 | Visiting Fellow, NCBI, NIH, USA |
| 02/2002 – 07/2006 | Research Assistant, Department of Computer Science & Engineering, University of California, Riverside, USA |
| 09/2001 – 12/2002 | Teaching Assistant, Department of Computer Science & Engineering, University of California, Riverside, USA |
| 07/2000 – 07/2001 | Research Assistant, State Key Lab of CAD & CG, Zhejiang University, China |

CAREER HIGHLIGHTS

Here is a summary of my strengths, which highlights selected (but not all) achievements and contributions. For details please refer to the rest of the CV.

Research

- High-impact journals: **4** papers with **IF > 10** (5-year IF also considered); **14** papers with **IF > 5**
- Competitive grant applications (completed two MOE Tier 2 grants as the lead PI; **a new MOE Tier 2 grant awarded as the lead PI in January 2018**)
- A paper (with **only two authors**, Dr. Zheng Jie's PhD student as the first author and Dr. Zheng Jie as the corresponding author) accepted by *ISMB/ECCB* 2017 (the flagship conference in Bioinformatics, **acceptance rate = 16.5%**); the first time in history a paper with **authors all from NTU** is accepted by this top conference
- In the past 10 years, **only 3 papers** accepted to the proceedings of ISMB (or ISMB/ECCB) have authors from NTU. Dr. Zheng Jie is in **2 of the 3 papers** (as a co-author in 2015, and as the corresponding author in 2017)
- **Best Paper Award (Gold)** of BMC Track of the 16th International Conference on Bioinformatics (InCoB 2017), Shenzhen, China. 20 – 22 Sept. 2017 (only two authors: my postdoc fellow and myself)
- Gold Medal, International Genetically Engineered Machine (iGEM) competition 2015 (as Coach in computing)
- First-Place Winner, sbv (Systems Biology Verification) IMPROVER Datathon Competition 2016 (as Group leader)

Teaching and Mentoring

- Nominated twice for Nanyang Education Award for Outstanding Lecturer, in 2016 and 2017 (only 5 faculty members of the school nominated)
- High teaching index scores (mostly > 85/100, often > 90/100)
- Teach and coordinate large-cohort classes (350 – 400 students) of CE2001/CZ2001 “Algorithms”, with high student feedback scores (mostly higher than the mean teaching index score for SCSE)
- Graduated 4 Ph.D. students as sole/main supervisor; all of them chose to work in academia (one as a lecturer and 3 as postdoctoral research fellows)
- Mr. Robin, a URECA student I supervised received Lee Kuan Yew Gold Medal 2014
- Ms. Guo Jing, my PhD student, was selected (one of only 6 top students) to represent NTU students to attend the 9th Asia-Oceania Top University League on Engineering Meeting (AOTULE), Melbourne, Australia, 26 – 28 Nov. 2014
- 4 of my Final Year Project (FYP) students published their FYP results in conferences/journals

Service for Nanyang Technological University

- Program Management Committee (PMC) member, SCSE
- Coordinator of “Minor in Computing and Data Analysis” Programme, SCSE
- Coordinator of General Electives, SCSE
- Internal reviewer of CRP grant proposal, in July 2016

Inter-disciplinary effort and industrial impact

- Collaboration with Complexity Institute, NTU (giving seminars, joint grant application)
- Developed 12 software tools for Bioinformatics and Systems Biology
- Manage joint PhD programs of SCSE with BII (Bioinformatics Institute Singapore) and GIS (Genome Institute of Singapore), A*STAR, Singapore
- Joint supervision of PhD students with SBS, NTU and BII, A*STAR
- Adjunct faculty at GIS (Genome Institute of Singapore), A*STAR

RESEARCH

Research Awards

- **Best Paper Award (Gold) of BMC Track of the 16th International Conference on Bioinformatics (InCoB 2017)**
Paper: Lichun Ma (my postdoc fellow), **Jie Zheng**. A polynomial based model for cell fate prediction in human diseases. *BMC Systems Biology* (special issue of the 16th International Conference on Bioinformatics (InCoB 2017)), 2017, in press (**IF** = 2.303)
My role: Corresponding author
Venue: Shenzhen, China
Time: 20 – 22 Sept. 2017
- **Best Oral Presentation Paper Award, The 6th International Conference on Bioinformatics and Biomedical Science (ICBBS 2017)**
Received by Mr. Yin Rui, PhD student of SCSE
My role: Co-author of the paper, TAC member of Mr. Yin Rui
Paper: Rui Yin, Xinrui Zhou (my current PhD student), Fransiskus Xavier Ivan (my former PhD student), Jie Zheng, Vincent T. K. Chow, Chee Keong Kwoh. Identification of potential critical virulent sites based on hemagglutinin of influenza A virus in past pandemic strains. *Proc. 6th International Conference on Bioinformatics and Biomedical Science (ICBBS)*, Singapore, June 22 – 24, 2017.
Venue: NUS, Singapore
Time: 22 – 24 June, 2017
- **First-Place Winner, sbv (Systems Biology Verification) IMPROVER Datathon Competition 2016**
My role: Group leader
Venue: Park Avenue Rochester Hotel, Singapore
Time: 23 – 24 Sept. 2016
- **Gold Medal, International Genetically Engineered Machine (iGEM) competition 2015**
(Collaborated with the SCBE team led by Asst Prof Tan Meng How)
My role: Coach in computational modeling and analysis, supervising SCSE FYP student Mr. Chen Haoting and SPMS undergraduate student Mr. Wong Ming Jie
Project duration: March to September 2015
Dates: 24 - 28 September 2015
Venue: Hynes Convention Center in Boston, MA, USA
Note: This is the first time NTU won a Gold Medal in the prestigious iGEM competition.
- **Nominated candidate, Canada Gairdner Global Health Award 2014**
Nominated by SCSE to NTU
Time: August 2013

Publications

Number of journal papers: **62 (61 in English + 1 in Chinese)**

Number of conference papers: **46**

Number of book chapters: **3**

Citations

	Total times cited	Highest citation of one paper	H-index	As of date
Google Scholar	1123	156	16	16 Oct. 2018
Scopus	667	91	15	20 Jun. 2018
Web of Science (SCI)	495	74	12	19 Jun. 2018

Summary of Journal Papers with Impact Factors ≥ 2

Journal (selected)	Impact Factor	Number of papers
Genome Biology	13.214	1
Nucleic Acids Research	11.561	2
Molecular Biology and Evolution	10.217	1
Oncogene	6.854	1
The Plant Journal	5.775	1
Bioinformatics	5.481	8
Scientific Reports	4.122	1
PLOS Computational Biology	3.955	1
BMC Genomics	3.730	4
BMC Medical Genomics	3.317	3
The Journal of Physical Chemistry B	3.146	1
PLOS ONE	2.766	4
IEEE/ACM Transactions on Computational Biology and Bioinformatics (IEEE/ACM TCBB)	2.428	5
BMC Bioinformatics	2.213	7
BMC Systems Biology	2.050	8

One paper is “highly accessed” in *Genome Biology* 2010 and highlighted on daily news of GenomeWeb.

One paper is “highly accessed” in *BMC Systems Biology* 2009.

Note:

- Marks on authors:
 - “*” means corresponding author (including co-corresponding authors);
 - “#” means joint first authors.
- “IF” stands for “impact factor”.

Note about the importance of corresponding (last) author, which is counted as the “main author”: In the field of Bioinformatics and Computational Biology in which I am working, the corresponding author (also called “last author” or “senior author”) is the most important author, because he is responsible for the idea, design and execution of research in the paper. It is a tradition in the community of Life Sciences that a corresponding authorship carries at least equal (often time more) weight than the first author. The interdisciplinary field of Bioinformatics mostly adopts this tradition (which might be different from conventional fields in Computer Science & Engineering). One purpose for this tradition in Life Sciences (and related areas of informatics) is to reward hard-working students and/or postdoc researchers with the first authorship. Since joining NTU, I have been the corresponding author of most of my journal publications. I hope my contributions to these publications can be fully recognized.

Journal Papers

1. Yong Liu, Min Wu*, Chenghao Liu, Xiao-Li Li, **Jie Zheng***. SL2MF: Predicting synthetic lethality in human cancers via logistic matrix factorization. *IEEE/ACM Transactions on Computational Biology and Bioinformatics* (TCBB) (special issue of GIW 2018), accepted, 2019 (**IF** = 2.428).
2. Ket Hing Chong, Sandhya Samarasinghe, Don Kulasiri*, **Jie Zheng**. Mathematical modelling of core regulatory mechanism in p53 protein that activates apoptotic switch. *Journal of Theoretical Biology*, Vol. 462 (7 Feb.), pp. 134-147, 2019 (**IF** = 1.833).
3. Lichun Ma, **Jie Zheng***. Single-cell gene expression data analysis reveals beta-cell dysfunction and deficit mechanisms in type 2 diabetes. *BMC Bioinformatics*, 19(Suppl 19):515, 2018 (special issue of GIW 2018) (**IF** = 2.213).
4. Xinrui Zhou, Rui Yin, Chee Keong Kwoh*, **Jie Zheng***. A context-free encoding scheme of protein sequences for predicting antigenicity of diverse influenza A viruses. *BMC Genomics*, 19(Suppl 10):936, 2018 (special issue of GIW 2018) (**IF** = 3.730).
5. Rui Yin, Xinrui Zhou, **Jie Zheng**, Chee Keong Kwoh*. Computational identification of physiochemical signatures for host tropism of influenza A virus. *Journal of Bioinformatics and Computational Biology* (JBCB), Vol. 16, No. 6, 1840023, 2018 (special issue of GIW 2018) (**IF** = 0.991).
6. Haifen Chen, Devamuni A.K. Maduranga, Piyushkumar Mundra, **Jie Zheng***. Bayesian data fusion of gene expression and histone modification profiles for inference of gene regulatory network. *IEEE/ACM Transactions on Computational Biology and Bioinformatics* (TCBB), Early Access, 2018 (**IF** = 2.428).
7. Hongfei Liu, Paolo A Lorenzini, Fan Zhang, Shaohai Xu, Mei Su M Wong, **Jie Zheng**, Xavier Roca*. Alternative splicing analysis in human monocytes and macrophages reveals MBNL1 as major regulator. *Nucleic Acids Research*, 46 (12), pp. 6069 – 6086, 2018 (**IF** = 11.561).
8. Ket Hing Chong, Xiaomeng Zhang, **Jie Zheng***. Dynamical analysis of cellular ageing by modeling of gene regulatory network based attractor landscape. *PLOS ONE*, 13(6), e0197838, 2018 (**IF** = 2.766).

9. Xiaomeng Zhang[#], Ket Hing Chong[#] (joint first authors), **Jie Zheng***. A Monte Carlo method for in silico modeling and visualization of Waddington's epigenetic landscape with intermediate details. *bioRxiv* 310771, 2018.
10. Xinrui Zhou, **Jie Zheng**, Xaverius Ivan Fransiskus, Rui Yin, Shoba Ranganathan, Vincent T. K. Chow, Chee Keong, Kowh. Computational analysis of the receptor binding specificity of novel influenza A/H7N9 viruses. *BMC Genomics* (special issue of APBC 2018) 19 (Suppl 2):88, 2018 (**IF** = 3.730).
11. Bobby Ranjan, Ket Hing Chong, **Jie Zheng***. Composite mathematical modeling of calcium signaling behind neuronal cell death in Alzheimer's disease. *BMC Systems Biology* (special issue of APBC 2018) 12(Suppl 1):10, 2018 (**IF** = 2.050).
12. Jing Guo, Hao Chen, Peng Yang, Yew Ti Lee, Min Wu, Teresa M. Przytycka, Chee Keong Kwoh, **Jie Zheng***. LDSplitDB: A database for studies of meiotic recombination hotspots in MHC using human genomic data. *BMC Medical Genomics* 11(Suppl 2): 27, special issue of the 28th International Conference on Genome Informatics (GIW/BIOINFO 2017), 2018 (**IF** = 3.317).
13. Huey Eng Chua, Sourav S. Bhowmick*, **Jie Zheng**. TROVE: A User-friendly Tool for Visualizing and Analyzing Cancer Hallmarks in Signaling Networks. *Bioinformatics*, 34(2):314-316, 2018 (**IF** = 5.481).
14. Hui Liu, Libo Luo, Zhazhan Cheng, Jianjiang Sun, Jihong Guan, **Jie Zheng***, Shuigeng Zhou* (co-corresponding authors). Group-sparse modeling drug-kinase networks for predicting combinatorial drug sensitivity in cancer cells. *Current Bioinformatics*, Vol. 13 (E-pub ahead of print), 2018 (**IF** = 0.540, **5-year IF** = 0.777).
15. Lichun Ma, **Jie Zheng***. A polynomial based model for cell fate prediction in human diseases. *BMC Systems Biology* (special issue of the 16th International Conference on Bioinformatics (InCoB 2017)), 11(Suppl 7):126, 2017, (**IF** = 2.050). (**Best Paper Award, Gold Medal**)
16. M Pek, SMJM Yatim, Y Chen, J Li, M Gong, X Jiang, F Zhang, **J Zheng**, X Wu, Q Yu, Oncogenic KRAS-associate gene signature defines co-targeting of CDK4/6 and MEK as a viable therapeutic strategy in colorectal cancer. *Oncogene*, 36, pp. 4975 – 4986, 2017 (**IF** = 6.854).
17. Jing Guo, **Jie Zheng***. HopLand: Single-cell pseudotime recovery using continuous Hopfield network based modeling of Waddington's epigenetic landscape, *Bioinformatics*, 33(14): i102 – i109 (special issue of conference ISMB/ECCB 2017, acceptance rate 16.5%), 2017 (**IF** = 5.481).
18. Jing Guo, Feng Lin, Xiaomeng Zhang[^], Vivek Tanavde, **Jie Zheng***. NetLand: quantitative modeling and visualization of Waddington's epigenetic landscape using probabilistic potential. *Bioinformatics*, 33(10), pp. 1583 – 1585, 2017 (**IF** = 5.481).
19. Jing Guo, Hui Liu*, **Jie Zheng***. SynLethDB: synthetic lethality database toward discovery of selective and sensitive anticancer drug targets. *Nucleic Acids Research*, 44 (D1): D1011 – D1017, 2016 (**IF** = 11.561).
20. Hui Liu, Fan Zhang, Shital Kumar Mishra, Shuigeng Zhou, **Jie Zheng***. Knowledge-guided fuzzy logic modeling to infer cellular signaling networks from proteomic data. *Scientific Reports*, 6:35652, 2016 (**IF** = 4.122).

21. Fan Zhang, Min Wu, Chee Keong Kwoh, **Jie Zheng***. Power-law modeling of cancer cell fates driven by signaling data to reveal drug effects. *PLOS ONE*, 11(10):e0165049, 2016 (**IF** = 2.766).
22. Haifen Chen, Xinrui Zhou, **Jie Zheng**, Chee Keong Kwoh. Rules of co-occurring mutations characterize the antigenic evolution of human influenza A/H3N2, A/H1N1 and B viruses. *BMC Medical Genomics*, 9 (Suppl 3):69, 2016 (**IF** = 3.317).
23. Fan Zhang, Runsheng Liu, **Jie Zheng***. Sig2GRN: a software tool linking signaling pathway with gene regulatory network for dynamic simulation. *BMC Systems Biology*, 10(4), 541, 2016 (**IF** = 2.050).
24. Yifeng Li[#], Haifen Chen[#] ([#]joint first authors), **Jie Zheng**, Alioune Ngom. The Max-Min High-Order Dynamic Bayesian Network for Learning Gene Regulatory Networks with Time-Delayed Regulations. *IEEE/ACM Transactions on Computational Biology and Bioinformatics* (TCBB), 13(4):792-803, 2016 (**IF** = 2.428).
25. Fan Zhang, Haoting Chen, Li Na Zhao, Hui Liu, Teresa M. Przytycka and **Jie Zheng***. Generalized logical model based on network topology to capture the dynamical trends of cellular signaling pathways. *BMC Systems Biology*, 10(Suppl 1):7, 2016 (**IF** = 2.050).
26. Hui Liu, Jianjiang Sun, Jihong Guan, **Jie Zheng** and Shuigeng Zhou*. Improving compound-protein interaction prediction by building up highly credible negative samples. *Bioinformatics*, 31(12), i221 – i229, 2015. (**IF** = 5.481).
27. Haifen Chen, Jing Guo, Shital K Mishra, Paul Robson, Mahesan Niranjan, **Jie Zheng***. Single-cell transcriptional analysis to uncover regulatory circuits driving cell fate decisions in early mouse development. *Bioinformatics*, 31(7), pp. 1060 – 1066, 2015 (**IF** = 5.481).
28. Li Na Zhao, **Jie Zheng**, Lock Yue Chew, Yuguang Mu. An Investigation on the Fundamental Interaction between Abeta Peptides and the AT-Rich DNA. *The Journal of Physical Chemistry B*, Volume 119, Issue 26, Pages 8247 – 8259, 2015 (**IF** = 3.146).
29. Hao Chen, Peng Yang, Jing Guo, Chee Keong Kwoh, Teresa M. Przytycka, **Jie Zheng***. ARG-walker: Inference of Individual Specific Strengths of Meiotic Recombination Hotspots by Population Genomics Analysis. *BMC Genomics*, 16(Suppl 12):S1, 2015 (**IF** = 3.730).
30. María Muñoz-Amatriaín, Stefano Lonardi, ..., **Jie Zheng**, ..., Timothy J Close*. Sequencing of 15 622 gene-bearing BACs clarifies the gene-dense regions of the barley genome. *The Plant Journal*, Volume 84, Issue 1, pages 216 – 227, 2015 (**IF** = 5.775).
31. Shital K Mishra, Sourav S Bhowmick, Huey Eng Chua, Fan Zhang[^], **Jie Zheng***. Computational cell fate modelling for discovery of rewiring in apoptotic network for enhanced cancer drug sensitivity. *BMC Systems Biology*, 9 (Suppl. 1):S4, 2015 (**IF** = 2.050).
32. Fan Zhang, Min Wu, Xuejuan Li, Xiaoli Li, Chee Keong Kwoh, **Jie Zheng***. Predicting essential genes and synthetic lethality via influence propagation in signaling pathways of cancer cell fates. *Journal of Bioinformatics and Computational Biology*, 13(03), 1541002, 2015 (**IF** = 0.991).
33. Biaoru Li, George Liu, Hongliang Hu, Jianqing Ding, **Jie Zheng**, Alex Tong. Biomarkers Analysis for Heterogeneous Immune Responses of Quiescent CD8⁺ cells-A Clue for Personalized Immunotherapy. *Biomarkers Journal*, Vol. 1, No. 1:3, pp. 1 – 11, 2015.

34. Hongliang Hu, Qinghua Zhang, Shen Li, Xiaona Zhang, Junsong Han, Huasheng Xiao, David Yan, **Jie Zheng**, Biaoru Li. A Therapeutic Targeting Identification from Microarray Data and Quantitative Network Analysis. *The Open Access Journal of Science & Technology*, Volume 3, Article ID 101114, Pages 10, 2015.
35. Jing Guo, Ritika Jain, Peng Yang, Rui Fan, Chee-Keong Kwoh, **Jie Zheng***. Reliable and Fast Estimation of Recombination Rates by Convergence Diagnosis and Parallel Markov Chain Monte Carlo. *ACM/IEEE Transactions on Computational Biology and Bioinformatics (TCBB)*, 11(1), Article No. 6646172, pp. 63-72, 2014 (**IF** = 2.428).
36. Min Wu, Chee-Keong Kwoh, Xiaoli Li, **Jie Zheng***. Finding trans-regulatory genes and protein complexes modulating meiotic recombination hotspots of human, mouse and yeast. *BMC Systems Biology*, 8:107, 2014 (**IF** = 2.050).
37. Haifen Chen, Piyushkumar A Mundra, Li Na Zhao, Feng Lin, **Jie Zheng***. Highly sensitive inference of time-delayed gene regulation by network deconvolution. *BMC Systems Biology*, 8 (Suppl. 4), S6, 2014 (**IF** = 2.050).
38. Peng Yang, Min Wu, Jing Guo, Chee Keong Kwoh, Teresa M Przytycka, **Jie Zheng***. LDsplit: screening for cis-regulatory motifs stimulating meiotic recombination hotspots by analysis of DNA sequence polymorphisms. *BMC Bioinformatics*, **15**:48, 2014 (**IF** = 2.213).
39. Wenting Liu, Kui Miao, Guangxia Li, Kuiyu Chang, **Jie Zheng**, Jagath C Rajapakse. Extracting rate changes in transcriptional regulation from MEDLINE abstracts. *BMC Bioinformatics*, **15**(Suppl 2):S4, 2014 (**IF** = 2.213).
40. Chinh Tran-To Su, Thuy-Diem Nguyen, **Jie Zheng**, Chee Keong Kwoh. IFACEwat: the interfacial water-implemented re-ranking algorithm to improve the discrimination of near native structures for protein rigid docking. *BMC Bioinformatics*, 15 (Suppl. 16), S9, 2014. (**IF** = 2.213).
41. Ragini Rai, Lei Zhu, Haifen Chen[^], Archana Patkar Gupta, Siu Kwan Sze, **Jie Zheng**, Christiane Ruedl, Zbynek Bozdech, Mark Featherstone. Genome-wide analysis in *Plasmodium falciparum* reveals early and late phases of RNA polymerase II occupancy during the infectious cycle. *BMC Genomics*, 15:959, 2014 (**IF** = 3.730).
42. Xue-juan Li, Shital K Mishra, Min Wu, Fan Zhang, **Jie Zheng***. Syn-Lethality: An Integrative Knowledge Base of Synthetic Lethality towards Discovery of Selective Anticancer Therapies. *BioMed Research International*, Vol. 2014, Article ID 196034, 7 pages, 2014 (**IF** = 3.169).
43. Haifen Chen, Stefano Lonardi, **Jie Zheng***. Deciphering Histone Code of Transcriptional Regulation in Malaria Parasites by Large-scale Data Mining. *Computational Biology and Chemistry*, Vol. 50, pp. 3-10, 2014 (**IF** = 1.595).
44. Min Wu, Xuejuan Li, Fan Zhang, Xiaoli Li, Chee-Keong Kwoh, **Jie Zheng***. In Silico Prediction of Synthetic Lethality by Meta-Analysis of Genetic Interactions, Functions, and Pathways in Yeast and Human Cancer. *Cancer Informatics*, 13(Suppl. 3), pp. 71-80, 2014.

45. Pamela Thompson, Kevin Urayama, **Jie Zheng**, Peng Yang, Matt Ford, Patricia Buffler, Anand Chokkalingam, Tracy Lightfoot, Malcolm Taylor. Differences in meiotic recombination rates in childhood acute lymphoblastic leukemia at an MHC class II hotspot close to disease associated haplotypes. *PLoS ONE*, 9(6):e100480, 2014 (**IF** = 2.766).
46. Yunbo Xu, Hongliang Hu, **Jie Zheng***, Biaoru Li* (co-corresponding author). Feasibility of Whole RNA Sequencing from Single-Cell mRNA Amplification, *Genetics Research International*, Vol. 2013, No. 724124, 2013.
47. Daniel Lin-Kit Wong, Xiao-Li Li, Min Wu, **Jie Zheng**, See-Kiong Ng. PLW: Probabilistic Local Walks for detecting protein complexes from protein interaction networks. *BMC Genomics*, **14**(Suppl 5): S15, 2013 (**IF** = 3.730).
48. Chinh Tran-To Su, Xuchang Ouyang, **Jie Zheng**, Chee-Keong Kwoh. Structural analysis of the novel influenza A (H7N9) viral Neuraminidase interactions with current approved neuraminidase inhibitors Oseltamivir, Zanamivir, and Peramivir in the presence of mutation R289K. *BMC Bioinformatics*, **14** (Suppl 16), S7, 2013 (**IF** = 2.213).
49. Min Wu, Zhipeng Xie, Xiaoli Li, Chee-Keong Kwoh, **Jie Zheng***. Identifying protein complexes from heterogeneous biological data. *Proteins: Structure, Function, and Bioinformatics*, 81(11), 2023-2033, 2013 (**IF** = 2.289).
50. M. Wu, Q. Yu, X-L, Li, **J. Zheng**, J-F Huang, C-K Kwoh. Benchmarking Human Protein Complexes to Investigate Drug-Related Systems and Evaluate Predicted Protein Complexes. *PLOS ONE*, 8(2): e53197, 2013 (**IF** = 2.766).
51. J. Mei*, C-K Kwoh, P. Yang, X-L Li, **J. Zheng**. Drug-Target Interaction Prediction by Learning from Local Information and Neighbors. *Bioinformatics*, 29(2): 238-245, 2013 (**IF** = 5.481).
52. R. Salari[#], D. Wojtowicz[#], **J. Zheng[#]** (joint first authors in alphabetical order), D. Levens. Y. Pilpel, TM Przytycka*. Teasing Apart Translational and Transcriptional Components of Stochastic Variations in Eukaryotic Gene Expression. *PLOS Computational Biology*, 8(8):e1002644, 2012 (**IF** = 3.955).
53. Min Wu, Chee-Keong Kwoh, Teresa M. Przytycka, Jing Li, and **Jie Zheng***. Epigenetic Functions Enriched in Transcription Factors Binding to Mouse Recombination Hotspots. *Proteome Science*, 10(Suppl 1):S11, 2012 (**IF** = 1.769).
54. **J. Zheng**, PP Khil, RD Camerini-Otero, TM Przytycka. Detecting sequence polymorphisms associated with meiotic recombination hotspots in the human genome. *Genome Biology*, 11:R103. 2010 (Highly accessed, highlighted on daily news of GenomeWeb) (**IF** = 13.214).
55. **J. Zheng***, D. Zhang, PF Przytycki, R. Zielinski, J. Capala, TM Przytycka* (co-corresponding author). SimBoolNet - A Cytoscape plugin for dynamic simulation of signaling networks. *Bioinformatics*, 26(1): 141-142, 2010 (**IF** = 5.481).
56. R. Zielinski, PF Przytycki, **J. Zheng**, D. Zhang, TM Przytycka, J. Capala. The crosstalk between EGF, IGF, and Insulin cell signaling pathways – computational and experimental analysis. *BMC Systems Biology*, 3(88), 2009 (Highly accessed) (**IF** = 2.050).
57. **J. Zheng**, IB Rogozin, EV Koonin, TM Przytycka. Support for the Coelomata Clade of animals from a rigorous analysis of the pattern of intron conservation. *Molecular Biology and Evolution*, 24(11):2583-92, 2007 (**IF** = 10.217).

58. **J. Zheng**, J. Svensson, K. Madishetty, T. Close, T. Jiang, S. Lonardi. OligoSpawn: a software tool for the design of overgo probes from large unigene databases. *BMC Bioinformatics*, 7:7, 2006 (**IF** = 2.213).
59. X. Chen, **J. Zheng**, Z. Fu, P. Nan, Y. Zhong, S. Lonardi and T. Jiang. Assignment of orthologous genes via genome rearrangement. *IEEE/ACM Transactions on Computational Biology and Bioinformatics (TCBB)*, 2(4), 302-315, 2005 (**IF** = 2.428).
60. A. Goldstein[#], P. Kolman[#], **J. Zheng[#]** (joint first author, alphabetized in authors' last names). Minimum common string partition problem: hardness and approximation. *Electronic Journal of Combinatorics*, 12(1), 2005.
61. **J. Zheng**, T. Close, T. Jiang, S. Lonardi. Efficient Selection of Unique and Popular Oligos for Large EST Databases. *Bioinformatics*, 20(13), 2101-2112, 2004 (**IF** = 5.481).

Non-English journal paper (in Chinese)

62. **Jie Zheng**, Tao Jiang. International Conference on Research in Computational Molecular Biology. *Communications of China Computer Federation (CCCF)*, vol. 59, 2011 (in Chinese)

Conference Papers

1. Xinrui Zhou, **Jie Zheng**, Xaverius Ivan Fransiskus, Rui Yin, Shoba Ranganathan, Vincent T. K. Chow, Chee Keong, Kowh. Computational analysis of the receptor binding specificity of novel influenza A/H7N9 viruses. The 16th Asia Pacific Bioinformatics Conference (APBC), Yokohama, Japan, 15 – 17 Jan. 2018.
2. Bobby Ranjan, Ket Hing Chong, **Jie Zheng***. Composite mathematical modeling of calcium signaling behind neuronal cell death in Alzheimer's disease. The 16th Asia Pacific Bioinformatics Conference (APBC), Yokohama, Japan, 15 – 17 Jan. 2018.
3. Jing Guo, Hao Chen, Peng Yang, Yew Ti Lee, Min Wu, Teresa M. Przytycka, Chee Keong Kwoh, **Jie Zheng***. LDSplitDB: A database for studies of meiotic recombination hotspots in MHC using human genomic data. *The 28th International Conference on Genome Informatics (GIW/BIOINFO 2017)*, Seoul, Korea, 31 Oct. – 3 Nov. 2017.
4. Lichun Ma, **Jie Zheng***. A polynomial based model for cell fate prediction in human diseases. *The 16th International Conference on Bioinformatics (InCoB 2017)*, Shenzhen, China, 20 – 22 Sept. 2017.
5. Fransiskus Xavier Ivan, Xinrui Zhou[^], Akhila Deshpande, Rui Ying, **Jie Zheng**, Chee Keong Kwoh. Phylogenetic tree based method for uncovering co-mutational site-pairs in influenza viruses. *Proc. of 8th ACM Conference on Bioinformatics, Computational Biology, and Health Informatics (ACM-BCB)*, pages 21 – 26, Boston, MA, USA, 20 – 23 Aug. 2017.
6. Jing Guo, **Jie Zheng***. HopLand: Single-cell pseudotime recovery using continuous Hopfield network based modeling of Waddington's epigenetic landscape. *Proc. Intelligent Systems for Molecular Biology*

and European Conference on Computational Biology (ISMB/ECCB) 2017, Prague, Czech Republic, 21 – 25 July, 2017. [acceptance rate 16.5%].

7. Rui Yin, Xinrui Zhou, Fransiskus Xavier Ivan, **Jie Zheng**, Vincent T. K. Chow, Chee Keong Kwoh. Identification of potential critical virulent sites based on hemagglutinin of influenza A virus in past pandemic strains. *Proc. 6th International Conference on Bioinformatics and Biomedical Science (ICBBS)*, Singapore, June 22 – 24, 2017.
8. Shital Kumar Mishra, Sourav S Bhowmick, Huey Eng Chua and **Jie Zheng**. Predictive Modeling of Drug Effects on Signaling Pathways in Diverse Cancer Cell Lines. *The 7th ACM Conference on Bioinformatics, Computational Biology, and Health Informatics (ACM-BCB 2016)*, pp. 200 – 209, Seattle, WA, USA, 2 – 5 Oct. 2016.
9. Huey Eng Chua, Sourav S Bhowmick, **Jie Zheng** and Lisa Tucker-Kellogg. TAPESTRY: Network-centric Target Prioritization in Disease-related Signaling Networks. *The 7th ACM Conference on Bioinformatics, Computational Biology, and Health Informatics (ACM-BCB 2016)*, pp. 108 – 117, Seattle, WA, USA, 2 – 5 Oct. 2016.
10. Hui Liu, Zhanzhan Cheng, Jiangjiang Sun, Jihong Guan, **Jie Zheng***, Shuigeng Zhou*. Sparse linear modeling kinase inhibition network for predicting combinatorial drug sensitivity in cancer cells. *The first CCF Bioinformatics Conference (CBC 2016)*, Chongqing, China, 10 – 13 Nov. 2016.
11. Haifen Chen, Xinrui Zhou, **Jie Zheng**, Chee Keong Kwoh. Rules of co-occurring mutations characterize the antigenic evolution of human influenza A/H3N2, A/H1N1 and B viruses. *Proc. 15th International Conference on Bioinformatics (INCOB 2016)*, Biopolis, Singapore, 21st – 23rd Sept. 2016.
12. Fan Zhang, Runsheng Liu, **Jie Zheng***. Sig2GRN: a software tool linking signaling pathway with gene regulatory network for dynamic simulation. *The 27th International Conference on Genome Informatics (GIW 2016)*, Shanghai, China, 3 – 5 Oct. 2016.
13. Fan Zhang, Haoting Chen, Li Na Zhao, Hui Liu, Teresa M. Przytycka and **Jie Zheng***. Generalized logical model based on network topology to capture the dynamical trends of cellular signaling pathways. *Proc. 14th Asia Pacific Bioinformatics Conference (APBC 2016)*, San Francisco, California, USA, 11 – 13 January, 2016.
14. Hui Liu, Jianjiang Sun, Jihong Guan, **Jie Zheng** and Shuigeng Zhou. Improving compound-protein interaction prediction by building up highly credible negative samples. *Proc. 23rd Annual International Conference on Intelligent Systems for Molecular Biology and 14th European Conference on Computational Biology (ISMB/ECCB 2015)*, Dublin, Ireland, 10 – 14 July, 2015.
15. Ket Hing Chong, S. Samarasinghe, D. Kulasiri, **Jie Zheng**. Computational techniques in mathematical modelling of biological switches. *Proc. 21st International Congress on Modelling and Simulation (MODSIM 2015)*, pp. 578 – 584, Gold Coast, Australia, 29 Nov to 4 Dec. 2015.
16. Hao Chen, Peng Yang, Jing Guo, Chee Keong Kwoh, Teresa M. Przytycka, **Jie Zheng***. ARG-walker: Inference of Individual Specific Strengths of Meiotic Recombination Hotspots by Population Genomics Analysis. *The 26th Genome Informatics Workshop and 14th International Conference on Bioinformatics (GIW/InCoB 2015)*, Odaiba, Tokyo, Japan, 9 – 11 Sept. 2015.

17. Shital K Mishra, Sourav S Bhowmick, Huey Eng Chua, Fan Zhang, **Jie Zheng***. Computational cell fate modelling for discovery of rewiring in apoptotic network for enhanced cancer drug sensitivity. *Proc. 13th Asia Pacific Bioinformatics Conference (APBC 2015)*, HsinChu, Taiwan, 21 – 23 Jan. 2015.
18. Fan Zhang, Min Wu, Xuejuan Li, Xiaoli Li, Chee Keong Kwoh, **Jie Zheng***. Predicting essential genes and synthetic lethality via influence propagation in signaling pathways of cancer cell fates. *Proc. 5th International Conference on Computational Systems-Biology and Bioinformatics (CSBio2014)*, Singapore, 10 – 12 Nov. 2014.
19. Fan Zhang, Chee-Keong Kwoh, Min Wu, **Jie Zheng***. Data-driven prediction of cancer cell fates with a nonlinear model of signaling pathways. *Proc. 5th ACM Conference on Bioinformatics, Computational Biology, and Health Informatics (ACM-BCB2014)*, pp. 436 – 444, Newport Beach, California, USA, 20 – 23 Sept. 2014.
20. Haifen Chen, Piyushkumar A Mundra, Li Na Zhao, Feng Lin, **Jie Zheng***. Highly sensitive inference of time-delayed gene regulation by network deconvolution. *Proc. 13th International Conference on Bioinformatics (InCoB2014)*, Sydney, Australia, 31st July – 2nd Aug. 2014.
21. Chinh Tran-To Su, Thuy-Diem Nguyen, **Jie Zheng**, Chee Keong Kwoh. IFACEwat: the interfacial water-implemented re-ranking algorithm to improve the discrimination of near native structures for protein rigid docking. *Proc. 13th International Conference on Bioinformatics (InCoB2014)*, Sydney, Australia, 31st July – 2nd August, 2014.
22. Seyed Ziaeddin Alborzi, DAK Maduranga, Rui Fan, Jagath C Rajapakse, **Jie Zheng***. CUDAGRN: Parallel Speedup of Inferring Large Gene Regulatory Networks from Expression Data Using Random Forest. *Proc. 9th IAPR International Conference of Pattern Recognition in Bioinformatics (PRIB2014)*, LNCS 8626, pp. 85 – 97, Stockholm, Sweden, 21 – 23 Aug. 2014.
23. Haifen Chen, Stefano Lonardi, **Jie Zheng***. Deciphering Histone Code of Transcriptional Regulation in Malaria Parasites by Large-scale Data Mining. *Proc. Asia Pacific Bioinformatics Conference (APBC2014)*, Shanghai, China, 17 – 19 Jan. 2014.
24. Wenting Liu, Kui Miao, Guangxia Li, Kuiyu Chang, **Jie Zheng**, Jagath C Rajapakse. Extracting rate changes in transcriptional regulation from MEDLINE abstracts. *Proc. Asia Pacific Bioinformatics Conference (APBC2014)*, Shanghai, China, 17 – 19 Jan. 2014.
25. Sourav S Bhowmick, Huey-Eng Chua, **Jie Zheng**. INGOT: Towards Network-driven In Silico Combination Therapy. *Proc. of 1st International Conference on Big Data and Smart Computing (BigComp 2014)*, Bangkok, Thailand, 15 – 17 Jan. 2014.
26. Jing Guo, Ritika Jain, Peng Yang, Rui Fan, Chee-Keong Kwoh, **Jie Zheng***. Reliable and Fast Estimation of Recombination Rates by Convergence Diagnosis and Parallel Markov Chain Monte Carlo. *Proc. Genome Informatics Workshop (GIW2013)*, Singapore, Dec. 2013.
27. Xue-juan Li[#], Shital Kumar Mishra[#] ([#]joint first authors), Min Wu, Fan Zhang, **Jie Zheng***. Syn-Lethality: An Integrative Knowledge Base of Synthetic Lethality towards Discovery of Selective Anticancer Therapies. *Proc. IEEE International Conference on Bioinformatics and Biomedicine (BIBM2013)*, in workshop "Biomolecular Networks and Human Diseases", Shanghai, China, Dec. 2013.

28. Min Wu, Xuejuan Li, Fan Zhang, Xiaoli Li, Chee-Keong Kwoh, **Jie Zheng***. Meta-analysis of Genomic and Proteomic Features to Predict Synthetic Lethality of Yeast and Human Cancer. *Proc. the International Conference on Bioinformatics, Computational Biology and Biomedical Informatics (ACM-BCB2013)*, pp. 384- 391, Washington DC, USA, Sept. 22-25, 2013.
29. Daniel Lin-Kit Wong, Xiao-Li Li, Min Wu, **Jie Zheng**, See-Kiong Ng. PLW: Probabilistic Local Walks for detecting protein complexes from protein interaction networks. *Proc. 12th International Conference on Bioinformatics (InCoB2013)*, Taicang, China, Sept. 20-22, 2013.
30. Chinh Tran-To Su, Xuchang Ouyang, **Jie Zheng**, Chee-Keong Kwoh. Structural analysis of the novel influenza A (H7N9) viral Neuraminidase interactions with current approved neuraminidase inhibitors Oseltamivir, Zanamivir, and Peramivir in the presence of mutation R289K. *Proc. 12th International Conference on Bioinformatics (InCoB2013)*, Taicang, China, Sept. 20-22, 2013.
31. D.A.K. Maduranga, **Jie Zheng**, Piyushkumar A. Mundra, Jagath C. Rajapakse. Inferring gene regulatory networks from time-series expressions using random forests ensemble. *Proc. Pattern Recognition in Bioinformatics (PRIB2013)*. LNBI 7986, pp. 13-22, Nice, France, June 17-20, 2013.
32. Piyushkumar A. Mundra, **Jie Zheng**, Mahesan Niranjan, Roy E. Welsch, Jagath C. Rajapakse. Inferring Time-Delayed Gene Regulatory Networks Using Cross-Correlation and Sparse Regression. *Proc. Bioinformatics Research and Applications (ISBRA)*, LNCS 7875, pp. 64-75, Charlotte, USA, May 20-23, 2013.
33. Wenting Liu, Kuiyu Chang, **Jie Zheng**, Jain Divya, Jung-Jae Kim, Jagath C. Rajapakse. Gene Regulatory Networks from Gene Ontology. *Proc. Bioinformatics Research and Applications (ISBRA)*, LNCS 7875, pp. 87-98, Charlotte, USA, May 20-23, 2013.
34. Haifen Chen[#], D.A.K. Maduranga[#](joint first authors), Piyushkumar A. Mundra, **Jie Zheng***. Integrating Epigenetic Prior in Dynamic Bayesian Network for Gene Regulatory Network Inference. *Proc. IEEE Symposium on Computational Intelligence in Bioinformatics and Computational Biology (CIBCB2013)*, pp. 76-82, as part of *IEEE Symposium Series on Computational Intelligence (SSCI)*, Singapore, April 2013.
35. M. Wu, C-K Kwoh, X-L Li, **J. Zheng***. NetPipe: A Network-based Pipeline for Discovery of Genes and Protein Complexes Regulating Meiotic Recombination Hotspots. *Proc. ACM Conference on Bioinformatics, Computational Biology and Biomedicine (ACM-BCB2012)*, pp. 20-27, Orlando, FL, USA, Oct. 2012.
36. M. Wu, C-K Kwoh, TM Przytycka, J. Li, **J. Zheng***. Integration of Genomic and Epigenomic Features to Predict Meiotic Recombination Hotspots in Human and Mouse. *Proc. ACM Conference on Bioinformatics, Computational Biology and Biomedicine (ACM-BCB2012)*, pp. 297-304, Orlando, FL, USA, Oct. 2012.
37. J. Mei, C-K Kwoh, P. Yang, X-L Li, **J. Zheng**. Globalized Bipartite Local Learning Model for Drug-Target Interaction Prediction. *International Workshop on Data Mining in Bioinformatics (BIOKDD)*, Beijing, China, Aug. 2012.
38. Peng Yang, Min Wu, Chee Keong Kwoh, Pavel P. Khil, R. Daniel Camerini-Otero, Teresa M. Przytycka, and **Jie Zheng***. Predicting DNA Sequence Motifs of Recombination Hotspots by Integrative Visualization and Analysis. *Proc. International Symposium on Integrative Bioinformatics*, pp. 52-58, Hangzhou, China, April 2-4, 2012.

39. **Jie Zheng**, Iti Chaturvedi and Jagath Rajapakse. Integration of Epigenetic Data in Bayesian Network Modeling of Gene Regulatory Network. *IAPR International Conference on Pattern Recognition in Bioinformatics* (PRIB2011), LNCS 7036, pp. 87-96, Delft, Netherlands, Nov. 2011.
40. Min Wu, Chee Keong Kwoh, Teresa Przytycka, Jing Li, and **Jie Zheng***. Prediction of Trans-regulators of Recombination Hotspots in Mouse Genome. *Proc. IEEE International Conference on Bioinformatics & Biomedicine* (BIBM2011), pp. 57-62, Atlanta, USA, Nov. 12-15, 2011.
41. Z. Wang, H. Hu, **J. Zheng*** and B. Li*(co-corresponding author). Gene expression and pathway analysis of quiescent CD8+ T Cells from liver cancer, liver sinusoid and peripheral blood -- study on toxicogenomics and prevention targeting. *Proc. IEEE International Symposium on Bioinformatics and BioEngineering* (BIBE2011), pp. 72-77, 2011.
42. **J. Zheng**, IB Rogozin, EV Koonin, TM Przytycka. A rigorous analysis of the pattern of intron conservation supports the Coelomata clade of animals. *RECOMB Comparative Genomics*, LNCS 4751, pp. 177-192, 2007.
43. X. Chen, **J. Zheng**, Z. Fu, P. Nan, Y. Zhong, S. Lonardi and T. Jiang. Computing the assignment of orthologous genes via genome rearrangement. *Proc. of Asia-Pacific Bioinformatics Conference* (APBC2005), pp. 363-378, 2005.
44. **J. Zheng**, S. Lonardi. Discovery of repetitive patterns in DNA with accurate boundaries. *Proc. of IEEE International Symposium on Bioinformatics and BioEngineering* (BIBE2005), pp. 105-112, 2005.
45. A. Goldstein[#], P. Kolman[#], **J. Zheng[#]** ([#]co-first authors in alphabetic order). Minimum common string partition problem: hardness and approximation. *Proc. of International Symposium on Algorithms and Computation* (ISAAC), pp. 484-495, LNCS 3341, 2004.
46. **J. Zheng**, T. Close, T. Jiang, S. Lonardi. Efficient Selection of Unique and Popular Oligos for Large EST Databases. *Proc. of Symposium on Combinatorial Pattern Matching* (CPM), pp. 384-401, LNCS 2676, 2003.

Book Chapters

1. Biao Li, Xiaomeng Zhang and **Jie Zheng**. Single-cell Next Generation Sequencing and Its Applications in Cancer Biology. *Next Generation Sequencing in Cancer Research: From Basepairs to Bedsides* (Volume 2), pp. 1 – 18, Edited by Wei Wu and Hani Choudhry, Springer International Publishing, 2015.
2. Teresa M. Przytycka and **Jie Zheng**. Hidden Markov Models. *eLS (Encyclopedia of Life Sciences)*. John Wiley & Sons Ltd, Chichester, May 2011.
3. Yang Huang[#], **Jie Zheng[#]** (co-first author), Teresa M. Przytycka. Discovery of Regulatory Mechanisms from Gene Expression Variation by eQTL Analysis. *Biological Data Mining*, Chapman and Hall/CRC Press, 2009.

Research Grants

Sum of grants:

Total value awarded:	S\$8,157,055.19
Total value as PI:	S\$2,841,972.00
Total external as PI:	S\$2,299,937.00

Current Awarded Projects (as PI S\$793,652.00):

- Project Title:** “Virtual stem cell: A digital platform for regenerative medicine”
Funding: MOE AcRF Tier 2 (**S\$593,652.00**)
Duration: 1 Jun. 2018 – 31 May 2021
Role: PI (Co-PI: Peter M. Slood, Complexity Institute, NTU)
- Project Title:** “Computational modelling of cell death dysregulation in ageing-related diseases”
Funding: MOE AcRF Tier 1, 2015-T1-002-094 (**S\$200,000**)
WBS: M4011549.020
Duration: 1 Mar. 2016 – 28 Feb. 2018
Role: PI (Co-PI: Chew Lock Yue, SPMS, NTU; Peter M. A. Slood, Complexity Institute, NTU; Collaborator: Su Haibin, MSE, NTU; Yusuf Ali, LKC School of Medicine, NTU)
- Project Title:** “Predicting missing and spurious links and labels of protein interaction networks”
Funding: MOE AcRF Tier 2 (**S\$579,536.87**)
WBS: M4020321.020
Duration: 9 Jan. 2017 – 8 Jan. 2020
Role: Co-PI (PI: Jagath C. Rajapakse, SCSE, NTU; Co-PI: Cong Gao, SCSE, NTU)
- Project Title:** “Research Center of Excellence in Active Living for the Elderly (LILY)”
Funding: Media Development Authority (MDA), MDA/IDM/2012/8/8-2 VOL 01 (total **\$9,985,000**; allocated **S\$295,000**)
WBS: M4061074.D70.601001
Duration: 01 Aug. 2012 – 31 Jul. 2018
Role: Co-PI (PI: Miao Chun Yan, SCSE, NTU)
- Project Title:** “Alternative splicing events and regulators important for human myeloid immunity”
Funding: MOE AcRF Tier 2 (**S\$792,900**)
Duration: 01 Jul. 2017 – 30 Jun. 2020
Role: Co-PI (PI: Francesc Xavier Roca Castella, SBS, NTU)
- Project Title:** “Characterization of the splicing functions of the two pseudouridines in U1 small nuclear RNA”
Funding: MOE AcRF Tier 1 (2015-T1-001-033) (**S\$150,000**)
Duration: 02 Nov. 2015 - 01 Nov. 2018
Role: Collaborator (PI: Francesc Xavier Roca Castella, SBS, NTU)
- Project Title:** “Computational virulence model with functional information for influenza viruses”
Funding: MOE AcRF Tier 2, MOE2014-T2-2-023 (**S\$747,169.00**)
WBS: M4020242.020
Duration: 2 Aug. 2015 – 1 Aug. 2018
Role: Collaborator (PI: Kwoh Chee Keong, SCSE, NTU)

Completed Projects (in total S\$4,798,797.32; as PI S\$2,048,320.00):

- Project Title:** “Computational Systems Biology of Synthetic Lethality towards New Cancer Medicine”

- Funding:** MOE AcRF Tier 2, ARC39/13 (**S\$514,665.00**)
WBS: M4020175.020
Duration: 1 Feb. 2014 – 31 Jan. 2017
Role: PI (Co-PI: Kwoh Chee Keong, SCSE, NTU; Collaborators: Sourav S. Bhowmick, SCSE, NTU, and Yu Qiang, GIS, A*STAR)
2. **Project title:** “Modeling, Validation, and Analysis of Gene Regulatory Network including Delays”
Funding level: MOE AcRF Tier 2, ARC9/10, (**S\$1,191,000.00**)
WBS: M4020007.020
Duration: 15 Dec. 2010 – 14 Jun. 2014
Role: PI (convert from co-PI to PI in Jan. 2013; former PI: Jagath C. Rajapakse, SCSE, NTU)
 3. **Project Title:** “In silico modelling of ageing and stem cell based rejuvenation on Waddington’s epigenetic landscape”
Funding: MOE AcRF Tier 1 Seed Funding on Complexity, RGC2/13 (**S\$92,655.00**)
WBS: M4011101.020
Duration: 1 Oct. 2013 – 30 Sept. 2016
Role: PI (Co-PI: Lin Feng, SCSE, NTU; Collaborator: Huck-Hui Ng, Genome Institute of Singapore (GIS), A*STAR)
 4. **Project title:** “Bioinformatics Algorithms for Detecting Genetic and Epigenetic Determinants of Meiotic Recombination Hotspots from Genomic Data”
Funding level: MOE AcRF Tier 1, RG32/11 (**S\$150,000.00**)
WBS: M4010977.020
Duration: 01/03/2012 – 31/08/2014
Role: PI (Co-PI: Kwoh Chee Kong, SCSE, NTU; Collaborator: Teresa M. Przytycka, NCBI/NLM/NIH; Jing Li, Case Western Reserve University, USA)
 5. **Project title:** “Bioinformatics Research in Genomics and Systems Biology with Applications in Human Disease Study”
Funding level: NTU Startup Grant (**S\$100,000.00**)
WBS: M4080108.020
Duration: 21/02/2011 – 20/02/2014
Role: PI
 6. **Project Title:** “INGOT: Towards systems biology-driven in silico combination therapy with application to cancer”
Funding level: AcRF Tier 1 Seed Funding on Complexity (**S\$197,000.00**)
WBS: M4011100.020
Duration: 01 Nov. 2013 - 31 Dec. 2016
Role: Co-PI (PI: Sourav S. Bhowmick, SCSE, NTU)
 7. **Project Title:** “Global analysis of alternative splicing upon differentiation of human monocytes”
Funding level: MOE AcRF Tier 2, MOE2013-T2-1-101 (**S\$675,142.00**)
Duration: 01 Feb. 2014 – 30 Apr. 2017
Role: Co-PI (PI: Francesc Xavier Roca Castella, SBS, NTU)
 8. **Project Title:** “Algorithmic analysis for high-throughput next-generation genomic sequencing data”
Funding level: MOE AcRF Tier 2, MOE2012-T2-1-055 (**S\$302,500.00**)
Duration: 01 Jan. 2013 – 31 Dec. 2015
Role: Co-PI (PI: Chen Xin, SPMS, NTU)
 9. **Project Title:** “The control of gene expression in the protozoan parasite *Plasmodium falciparum*”
Funding: NMRC Cooperative Basic Research Grant (CBRG12nov104) (**S\$1,425,835.32**)
Duration: 1 July 2013 – 31 Dec. 2016
Role: Collaborator (PI: Mark Featherstone, SBS, NTU)

- 10. Project Title:** “The mixed lineage leukemia gene in eye development”
Funding: MOE AcRF Tier 1 (**S\$150,000.00**)
Duration: Nov. 2016 – 24 Jun. 2017
Role: Collaborator (PI: Mark Featherstone, SBS, NTU)

TEACHING

Teaching Award

- Nominated for Nanyang Education Award 2016, under school category (only 5 faculty members nominated). This award is given to outstanding lecturers
- Nominated for Nanyang Education Award 2017, under school category (only 5 faculty members nominated). This award is given to outstanding lecturers

Awards and Achievements of Students Supervised

- Ms. Zhou Xinrui, my PhD student, was shortlisted for the Excellence in Teaching Assistantship Award 2018 (top 3 candidates interviewed) for the course in which I supervised her TA work
- Mr. Bobby Ranjan, undergraduate research (URECA) student under my supervision published a top-tier journal paper in *BMC Systems Biology* (IF = 2.050) as the first author, and presented at the conference of APBC 2018, based on his URECA project under my supervision
- Mr. Robin, a URECA student I supervised received Lee Kuan Yew Gold Medal 2014
- Ms. Guo Jing, my PhD student, was selected (one of only 6 students) to represent NTU research students to attend 9th Asia-Oceania Top University League on Engineering Meeting (AOTULE), Melbourne, Australia, 26 – 28 Nov. 2014
- 4 of my FYP students have published their projects in conferences and journals
- Mr. Gupta Aakash, my FYP student, had his project titled “LD Cluster View – A Visualization for Genomics Data” featured as one of SCSE’s “Interesting and Good Student FYP’s” in June 2017

Text-books, book chapters, monograph, software

3 Book chapters:

- Biaoru Li, Xiaomeng Zhang and **Jie Zheng**. Single-cell Next Generation Sequencing and Its Applications in Cancer Biology. *Next Generation Sequencing in Cancer Research: From Basepairs to Bedsides* (Volume 2), pp. 1 – 18, Edited by Wei Wu and Hani Choudhry, Springer, 2015.
- Teresa M. Przytycka and **Jie Zheng**. Hidden Markov Models. *eLS (Encyclopedia of Life Sciences)*. John Wiley & Sons Ltd, Chichester, May 2011.
- Yang Huang*, **Jie Zheng*** and Teresa M. Przytycka (*co-first author). Discovery of regulatory mechanisms from gene expression variation by eQTL analysis. *Biological Data Mining*, Chapman and Hall/CRC Press, 2009.

Development of teaching materials at NTU

- Video recording and course materials, Technology-Enabled Learning (TEL), CE/CZ2001 (Algorithms), Dec. 2015 – Sept. 2016
- hour video for e-learning tutorial of CE/CZ2001 (Algorithms), September 2015
- hour video for e-learning tutorial of CE/CZ1007 (Data Structures), February 2015
- hour video for e-learning tutorial of CE/CZ 2001 (Algorithms), September 2013
- General information, scoring scheme, and problems for Example class in CE/CZ2001 (Algorithms), Aug. 2013
- hour video for e-learning tutorial of CE/CZ 1007 (Data Structures), February 2013
- hour video for e-learning lectures of CE/CZ 2001 (Algorithms), September 2012
- hour video for e-learning tutorial of CE/CZ 2001 (Algorithms), September 2012
- hour video for e-learning tutorial of CE/CZ 1007 (Data Structures), February 2012
- Lecture notes for a 3-hour lecture for BI6103 (Computational Biology), April 2012
- Lecture notes on Algorithms for CPE 204 (Discrete Mathematics and Algorithms), Oct – Nov. 2011

Teaching Index Scores for the past 3 years at NTU

Weighted Scores Combined of multiple class codes by response sizes

AY, Semester	Course, PG/UG – L/T	Class size / Response	Score (%)
16/17, S2	*CE/CZ2001, UG-L	45 / 9	94.92
16/17, S2	CZ2001, UG-T	16 / 5	86.86
16/17, S1	*CE/CZ2001, UG-L	361 / 122	88.33
16/17, S1	CZ2001, UG-T	37 / 15	88.77
15/16, S2	*CE/CZ2001, UG-L	63 / 14	92.00
15/16, S2	*CE/CZ2001, UG-T	28 / 9	89.18
15/16, S1	*CE/CZ2001, UG-L	363 / 113	89.95
15/16, S1	CZ2001, UG-T	35 / 12	95.23
14/15, S2	*CE/CZ2001, UG-L	64 / 14	84.53
14/15, S2	CZ1007, UG-T	40 / 21	90.06
14/15, S1	*CE/CZ2001, UG-L	329 / 84	87.12
14/15, S1	CZ2001, UG-T	25 / 11	84.63

Breakdown scores of multiple course codes

AY, Semester	Course code	Class size / Response	Score (%)
16/17, S2	CE2001, UG-L	15 / 4	100

	CZ2001, UG-L	30 / 5	90.86
16/17, S1	CE2001, UG-L	76 / 27	83.63
	CZ2001, UG-L	285 / 95	89.66
15/16, S2	CE2001, UG-L	20 / 7	92.6
	CZ2001, UG-L	43 / 7	91.4
15/16, S2	CE2001, UG-T	20 / 7	91.8
	CZ2001, UG-T	8 / 2	80
15/16, S1	CE2001, UG-L	71 / 21	88.6
	CZ2001, UG-L	292 / 92	90.26
14/15, S2	CE2001, UG-L	22 / 8	88.29
	CZ2001, UG-L	42 / 6	79.51
14/15, S1	CE2001, UG-L	75 / 17	86.03
	CZ2001, UG-L	254 / 67	87.4

Supervision of Postgraduate Students

MSc Students at ShanghaiTech University

- Mr. Wang Ke (Sept. 2018 – present)
- Mr. Wang Xin (Sept. 2018 – present)

MSc Students at NTU, Singapore

Sole/Main Sup: 3

- Ms. Vijayaraghavan Aadhitthya (Aug. 2011 - July 2012, MSc student), **MSc Thesis:** Detecting codon usage bias selected against protein misfolding (currently PhD student at Cambridge University)
- Mr. Devamuni Adhikaramge Kasun Maduranga (Jan. 2012 – Jan. 2013, MSc student), **MSc Thesis:** Performance comparison of dynamic Bayesian networks and Random forests ensemble on gene network inference
- Mr. CHEN Hao (Aug. 2012 – July 2013, MSc student), **MSc Thesis:** Genome-wide discovery of DNA sequence motifs stimulating meiotic recombination hotspots

PhD Supervising at NTU, Singapore

Sole/Main Sup: 3

Full Name	Academic Status	Status of Students	Co-supervisor
GUO JING	Current	All but defense	Vivek Tanavde (BII, A*STAR)
ZHOU XINRUI	Current	Passed Qualifying Exam	Kwoh Chee-Keong (SCSE, NTU)

PRITHA DUTTA	Current	Start from Aug. 2017	Peter M. Sloom (Complexity Institute, NTU)
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PhD / Graduated at NTU, Singapore

As Sole/Main Supervisor: 4

Full Name	Oral Defense Date	Current Employment
FRANSISKUS Xaverius Ivan	July, 2013	Lecturer, Surya University, Indonesia
CHEN Haifen	May, 2016	Postdoctoral Research Fellow, McGill University, Canada
ZHANG Fan	October, 2016	Postdoctoral Research Fellow, Genome Institute of Singapore, A*STAR, Singapore
MISHRA Shital Kumar	31 March, 2017	Postdoctoral Research Fellow, Guangzhou Medical University, China

Co-Sup: 1

Full Name	Oral Defense Date	Status of Students	Main-supervisor	Funding source
LORENZINI PAOLO	May, 2018	Graduated	FRANCESC XAVIER ROCA CASTELLA (SBS, NTU)	Interdisciplinary Graduate School (NITHM)

Supervision of Research Undergraduate Students

- Number of FYP (Final Year Project) students: **32**
- Number of URECA students: **3**
- Number of CN Yang Scholars Programme student: **1**
- Number of Industry Orientation (IO) / Industry Attachment (IA) students: **37**

Supervision of Research Staff:

- Number of Post-doctoral Research Fellows: **7**
- Number of Pre-doctoral Research Associates: **3**
- Number of Project Officers: **6**

SERVICES

Services to School and University

Member of Programme Management Committee (PMC): Feb. 2014 – present

Elective Coordinator (SAG Lead): Feb. 2014 – present

Coordinator of “Minor in Computing and Data Analysis” Programme: Feb. 2014 – present

Responsibilities:

- Curriculum management
- Examination paper management
- Course matching of exchange students
- Evaluation of SAEs' teaching performance
- Consultation for students about course registration, etc.

Review Committee of SCE-BII joint Ph.D. programme: July 2011 – present

Responsibilities:

- Interview and recruit Ph.D. applicants to this programme
- Monitor progress of PhD students towards graduation

Help NTU Library to set up, test and showcase the “**NTU data repository**” project: Jun. 2017 – present

Review CRP grant proposal: invited by NTU RSO, July 2016

Interview SINGA (Singapore International Graduate Award) candidates for PhD study: Matrix Building, Biopolis, A*STAR, 09 Sept. 2014

Internal examiner (or oral panel member):

- **14** Ph.D. (internal examiner or panel member): Wu Min, Liu Qian, Li Zhenhua, Sun He Quan, Seah Boon Siew (panel member), Thidathip Wongsurawat, Sun Ruimin (SPMS), Jaydeep De, Liu Yong (panel member), Pan Hong, Han Xu (panel member), Luay Aswad (substitute A/P Lin Feng as panel member), Shamima Babu, Aly Mohamed Aly Ezzat
- **12** Ph.D. Qualifying Exam
- **4** TAC (Thesis Advisory Committee) of Ph.D. students not under my supervision
- **8** M.Sc dissertations
- **1** M.Eng dissertation (Liu Hui, Oct. 2014)

External PhD thesis examiner

- Department of Pharmacy, National University of Singapore (Jul. 2016 – Jun. 2017)

Judge for GreenTECH Video & Invitational Presentation Competition 2016: invited by Institution of Engineering and Technology NTU on Compus (Mar. 2016)

Academic Service for Journals and Conferences

Associate editor:

- IET (The Institution of Engineering and Technology) Journal of Engineering Biology (7 July 2016 – 6 July 2022)

Editorial board member:

- Journal of Computational Systems Biology (Annex Publishers), Dec. 2013 – present
- Frontiers in Genetics (session of Bioinformatics & Computational Biology), Dec. 2013 - present

Guest editor:

- Journal of Bioinformatics and Computational Biology (JBCB), special issue on the 5th International Conference on Computational Systems-Biology and Bioinformatics (CSBio) 2014
- Journal of Medical Imaging and Health Informatics (JMIHI), special issue on CSBio 2014

Organization of Conferences

- Program co-chair, GIW (International Conference on Genome Informatics) 2018

- Panel Discussion, 4th Annual Single Cell Analysis Asia Congress, Singapore, 11 – 12 Oct. 2016
- Facilitator of Roundtable Discussion, Bioinformatics Strategic Meeting APAC 2016, Shangri-La Hotel, Singapore, 19th Oct. 2016
- Program Co-Chair of the 5th International Conference on Computational Systems-Biology and Bioinformatics (CSBio2014), Singapore, 10 – 12 Nov. 2014
- Session Chair, “Silent Transformation”, Para Limes Annual Conference, NTU, Singapore, March 7 – 9, 2016
- Session Chair, 2nd Symposium on Complex Biodynamics & Networks (cBio 2015), Tsuruoka, Japan, May 11 – 13th, 2015
- Session Chair, 12th Asia-Pacific Bioinformatics Conference (APBC 2014), Shanghai, China, January 17 – 19, 2014

Invited presentations at scientific meetings/workshops

- Invited talk, China Conference of Developmental Biology (CCDB), Nanjing, China, 21 – 24 May 2017
- Invited talk, International Conference on Bioinformatics and Biomedical Engineering (iCBBE), Hangzhou, China, 18 – 20 May 2017
- Invited talk, Joint Korea-Singapore Workshop on Discrete Mathematics, SPMS, NTU, Singapore, 17 – 19 Feb. 2017
- Invited talk, 4th Single Cell Analysis Asia Congress, Singapore, 11 – 12 Oct. 2016
- Invited talk, 12th Korea-Singapore Joint Workshop on Bioinformatics and Natural Language Processing, KAIST, Daejeon, Korea, 22nd Sept. 2016
- Highlight talk, Intelligent Systems for Molecular Biology (ISMB), Orlando, Florida, USA, 11 July 2016
- Oral poster talk, Intelligent Systems for Molecular Biology (ISMB), Orlando, Florida, USA, 10 July 2016
- Invited presentation, Free Webinar, 4th Single Cell Analysis Asia Congress, Singapore, 8 June 2016
- Invited talk, Multidisciplinary Bio-informatics Workshop, NITHM, NTU, 25 Jan. 2016
- Invited talk, Next Generation Sequencing (NGS) Asia and Single Cell Asia Congress, Singapore, 14 Oct. 2015
- Invited talk, The Protein Network Workshop, Institute for Mathematical Science (IMS), NUS, Singapore, 12 June, 2015
- Seminar on Ageing and Stem Cell (Seed Grant), Complexity Institute, NTU, 8 Dec. 2014
- Invited talk, Systems Biology @ Systems Medicine Workshop, LKC School of Medicine, NTU, 26 Nov. 2014
- Invited talk, School of Biological Science & Medical Engineering, Southeast University, China, 5 June 2014
- Seminar on Ageing and Stem Cell (Seed Grant), Complexity Institute, NTU, Jan. 2014
- Invited talk, Dept. of Computer Science, Fudan University, China, Dec. 2013
- Invited talk, Workshop with NHG (National Healthcare Group) Ageing Research, Tan Tock Seng Hospital, April 2013
- Highlights talk, RECOMB (International Conference on Research in Computational Molecular Biology), Beijing, 8 April 2013
- Invited talk, Genome Institute of Singapore, July 2012
- Invited talk, Department of Bioinformatics, Tongji University, China, June 2012
- Invited talk, School of Biological Science & Medical Engineering, Southeast University, China, June 2012
- Invited talk, Dept. of Computer Science, Fudan University, China, June 2012
- Invited talk, National Cancer Centre Singapore, April 2012
- Invited talk at American Mathematical Society (AMS) Spring Southeastern Meeting, Baton Rouge, LA, USA 2008

Review Service

Invited to review grant proposal

- CRP proposal, invited by RSO, NTU (Jul. 2016)
- Skills Development Fellowship Proposal, Medical Research Council, UK (Aug. 2015)
- UK “Breast Cancer Now” Grant (Oct. 2015)
- USA NSF (National Science Foundation), Plant Genome Research Program, grant merit assessor (Oct. 2010)

Review for Journals

2018

Bioinformatics
IET Systems Biology
PLOS Computational Biology
Molecular Omics
IEEE/ACM TCBB
Scientific Reports

2017

Bioinformatics
Cancer Informatics
IET Systems Biology
Interdisciplinary Science: Computational Life Sciences
Molecular BioSystems
Advances in Genomics and Genetics (Dove Medical Press)
The EuroBiotech Journal

2016

Nucleic Acids Research
Scientific Reports
IEEE/ACM TCBB
PLOS Computational Biology (2 papers)
BioSystems
Cancer Informatics
Bioinformatics (2 papers)
BMC Bioinformatics
IET Systems Biology
Apoptosis
Computer Methods and Programs in Biomedicine (CMPB)
Progress in Biophysics and Molecular Biology (PBMB)

Number of journal papers reviewed in 2016: 14

2015

Briefings in Bioinformatics
Cancer Biology & Research
Cancer Informatics (2 papers)
EURASIP Journal on Bioinformatics and Systems Biology
FEBS Letters
International Journal of Bioinformatics Research and Applications (IJBRA)
Journal of Bioinformatics and Computational Biology (JBCB)
Journal of Biomedical and Health Informatics (JBHI)
Metabolites
Molecular BioSystems (4 papers)
PLOS Computational Biology (2 papers)
IEEE/ACM Transactions on Computational Biology and Bioinformatics (TCBB) (2 papers)

Number of journal papers reviewed in 2015: 18

2014

PLoS Computational Biology
Briefings in Bioinformatics
BioMed Research International (2 papers)
IEEE/ACM Transactions on Computational Biology and Bioinformatics (ACM-BCB special issue) (2 papers)
British Journal of Applied Science & Technology
Evolutionary Bioinformatics
Combinatorial Chemistry & High Throughput Screening (CCHTS)
Number of journal papers reviewed in 2014: 9

2013:

BMC Bioinformatics (3 papers)
Bioinformatics
Ageing Cell
Epigenetics
Journal of Bioinformatics and Computational Biology (JBCB)
IEEE/ACM Transactions on Computational Biology and Bioinformatics
Number of journal papers reviewed in 2013: 8

2012:

IEEE/ACM Transactions on Computational Biology and Bioinformatics
Bioinformatics
Human Molecular Genetics

2011:

IEEE/ACM Transactions on Computational Biology and Bioinformatics
BMC Bioinformatics
Bioinformatics

Before 2011:

Journal of Combinatorial Optimization, 2010
Bioinformatics, 2008
PLoS ONE, 2008
Theoretical Computer Science, 2007
Information Processing Letters, 2005
Special Series of Discrete Applied Mathematics on Computational Molecular Biology, 2004
Journal of Computational Biology, 2002

Review for Conferences

2017 (ongoing)

APBC 2018 (PC member, reviewer)
ISMB/ECCB 2017 (PC member, review 3 papers)
ACM-BCB 2017 (PC member, review 6 papers)
RECOMB Comparative Genomics 2017 (PC member, review 3 papers)
ICBBS 2017 (review 2 papers)
BIOKDD 2017 (PC member, review 1 paper)
The 11th International Conference on Systems Biology (ISB) 2017 (PC member, review 1 paper)

2016

APBC 2017 (PC member, review 5 papers)
GIW 2016 (PC member, review 5 papers)
RECOMB Comparative Genomics 2016 (PC member, review 4 papers)
BIOKDD 2016 (PC member, review 1 paper)
ISMB 2016 (PC member, review 1 paper)

Number of conference papers reviewed in 2016: 16

2015

APBC 2016 (PC member, review 7 papers)
RECOMB Comparative Genomics 2015 (PC member, review 3 papers)
RECOMB 2015 (sub-reviewer, review 1 paper)
ACM-BCB 2015 (TPC member, review 10 papers)
ICDM 2015, Workshop on Biological Data Mining & Its Applications in Healthcare (PC member, review 1 paper)
BioKDD 2015 (review 1 paper)
MODSIM 2015 (review 1 paper)
Number of conference papers reviewed in 2015: 24

2014:

APBC 2015 (PC member, review 5 papers)
CSBio 2014 (Program co-chair, review 2 papers)
APBC 2014 (PC member and session chair, review 6 papers)
GIW 2014 (PC member, review 8 papers)

2013:

GIW 2013 (PC member, review 5 papers)
BIOKDD 2013 (PC member, review 2 papers)
ACM-BCB 2013 (PC member, review 4 papers)
BIOINFORMATICS (PC member, review 1 paper)
RECOMB 2013 (sub-reviewer, review 1 paper)

2012:

ISMB
SIGKDD
BIOKDD
SDM

Before 2012:

ISMB/ECCB, 2011
RECOMB Comparative Genomics, 2010
IEEE International Symposium on Bioinformatics and BioEngineering (BIBE), 2010
International Symposium on Mathematical Foundations of Computer Science (MFCS), 2007, 2010
Brazilian Symposium on Bioinformatics (BSB), 2009, 2010
International Symposium on Bioinformatics Research and Applications (ISBRA), 2009
Pacific Symposium on Biocomputing (PSB), 2009
BIOKDD, 2007, 2008
Combinatorial Pattern Matching (CPM), 2004, 2007, 2008
String Processing and Information Retrieval (SPIRE), 2005
IEEE International Conference on Tools with Artificial Intelligence, 2005
ACM Conference on Research in Computational Molecular Biology (RECOMB), 2004
International Colloquium on Automata, Languages and Programming, 2004
IEEE Computational Systems Bioinformatics Conference (CSB), 2003

Review of book chapter or proposal

2017:

Book proposal review
Book title: “Computational Non-coding RNA Biology”
Publisher: Elsevier

2013:

Book chapter: “Microarray Image and Data Analysis: Theory and Practice”
Book series: Digital Imaging and Computer Vision
Publisher: CRC Press/Taylor & Francis