

# Dr. Hailong Zhu

## Academic Qualifications

<i>Year</i>	<i>Degree</i>	<i>Field of Study</i>	<i>Institution</i>
2002	Ph.D	Mechanical Engineering <i>Doctoral Dissertation: Statistical Learning Theory and Its Engineering Applications</i>	Xi'an Jiaotong University, Xi'an, China
1996	BEng	Mechanical Engineering	Xi'an Jiaotong University, Xi'an, China

## Present Academic Position

2015.9- Assistant Professor School of Chinese Medicine, Hong Kong Baptist University

## Previous Positions Held

<i>Year</i>	<i>Position/Title</i>	<i>Institution</i>
2010.9-2015.8	Research Assistant Professor	Department of Computer Science, Hong Kong Baptist University
2006.5-2010.7	Research Engineer	Research Institute of Innovative Products and Technologies The Hong Kong Polytechnic University
2003.1-2006.4	Research Engineer	Global Research of General Electronic

## Research Interests

- Bioinformatics
- Computational Biology
- Systems Biology
- Big Data Analytics

## Research Grants

### Recent:

- GRF (PI), 2013-2016, "Development of an Integrative Model for Reconstructing Dynamic Transcriptional Regulatory Networks from High Throughput Data", Project No.: 212613. Funding: HK\$500,000.
- GRF (PI), 2011-2014, "A Stage-varying Methodology That Can Reconstruct the Dynamic Gene Regulations during the Process of Cancer Progression from Stage-course Transcriptional Data", Project No.: 212111, Funding: HK\$922,500.
- FRG (PI), 2013-2014, "A pilot study of modelling the dynamic gene regulation during the developmental cycle of human malaria parasite", Funding: HK\$135,000.
- FRG (PI), 2014-2015, "A Computational Framework of Modeling the Transcriptional Regulation in Single Cells", Funding: HK\$127,000.

### Completed:

- FRG (PI), 2012-2013, "A simulation Study of Identifying the Transcriptional Regulatory Network", Funding: HK\$65,000.
- 2007-2010, PI, Competitive Niche Area Funding, "Clinical Decision Support System for Cancer Diagnosis & Treatment", Project No: 1-BB56. Funding: HK\$3,899,000.
- 2008-2009, PI, Internal Competitive Grant, "Recurrence Prediction for Osteosarcoma Treatment", Project No: A-PD0E. Funding: HK\$150,000.

## Publications

### \*Corresponding author

1. Yu GX, **Zhu HL\***, Domeniconi C, Liu JM. Predicting protein function via downward random walks on a gene ontology. (2015) BMC Bioinformatics 16: 271. doi:10.1186/s12859-015-0713-y.

2. Narasundaram N, Liu JM, Karthick V, Doss GP, Chakraborty C, Chen LN, **Zhu HL\***. (2015) Analysing the effect of mutation on protein function and discovering potential inhibitors of CDK4: Molecular modelling and dynamics studies. *PLoS ONE* 10(8): e0133969. doi:10.1371/journal.pone.0133969. (Impact Factor: 3.53)
3. Yu GX, **Zhu HL\***, Domeniconi C, and Guo MZ. (2015) Integrating Multiple Networks for Protein Function Prediction, *BMC Systems Biology*, 2015, 9(S1): S4. (Impact Factor: 2.85)
4. Yu GX, **Zhu HL\***, Domeniconi C. (2015) Predicting Protein Function using Incomplete Hierarchical Labels, *BMC Bioinformatics*, 16:1. (Impact Factor: 2.67)
5. Doss GP, C, Rajith B, Chakraborty C, NagaSundaram N, Ali SK, **Zhu HL\***. (2014) Structural signature of the G719S-T790M double mutation in the EGFR kinase domain and its response to inhibitors. *Scientific Reports*, 4, Article number: 5868, doi:10.1038/srep05868. (Impact Factor: 5.078)
6. Doss GP, Chakraborty C, Chen LN and **Zhu HL\***. (2014) Integrating In Silico Prediction Methods, Molecular Docking, and Molecular Dynamics Simulation to Predict the Impact of ALK Missense Mutations in Structural Perspective. *BioMed Research International*. Volume 2014, Article ID 895831, 14 pages, (Impact Factor: 2.880)
7. Doss GP, Chakraborty C, Syed SA, NagaSundaram N, Chen LN, **Zhu HL\***. (2014) Evolution- and Structure-Based Computational Strategy Reveals the Impact of Deleterious Missense Mutations on MODY 2 (Maturity-Onset Diabetes of the Young, Type 2). *Theranostics*, 4(4):366-385. doi:10.7150/thno.7473. (Impact Factor: 7.806)
8. Chakraborty C, C GPD, C, Chen LN, **Zhu HL\***. (2014) Evaluating protein-protein interaction networks for diseases, pathway, target discovery, and drug-design using in silico pharmacology. *Curr Protein Pept Sci*. 2014;15(6):561-71. (Impact Factor: 2.33)
9. Zeng T, Sun SY, Wang Y, **Zhu HL**, Chen LN. (2013) Network biomarkers reveal dysfunctional gene regulations during disease progression. *FEBS Journal*, 2013 Sep 20. doi: 10.1111/febs.12536. (Impact Factor: 4.25)
10. Doss CGP, Nagasundaram N, Chakraborty C, Chen LN, **Zhu HL\***. (2013) Extrapolating the effect of deleterious nonsynonymous single nucleotide polymorphisms in the binding adaptability of flavopiridol with CDK7 protein: a molecular dynamics approach, *Human Genomics*, 7:10, doi:10.1186/1479-7364-7-10. (Impact Factor: 2.69)
11. **Zhu HL\***, Rao RSP, Zeng T, Chen LN. (2012) Reconstructing dynamic gene regulatory networks from sample-based transcriptional data. *Nucleic Acids Research*, 40(21):10657-10667; doi: 10.1093/nar/gks860. (Impact Factor: 8.278)
12. **Zhu HL\***, Rao RSP, Chen LN. (2012) Reconstructing Dynamic Gene Regulatory Network for the Development Process of Hepatocellular Carcinoma. 2012 Workshop on Pharmaco-Informatics for Drug Discovery in Conjunction with 2012 IEEE International Conference on Bioinformatics and Biomedicine (BIBM 2012), Philadelphia, Oct. 2012.
13. Zhang Lin, Zhang Lei, Zhang D, **Zhu HL**. (2011) Ensemble of local and global information for finger-knuckle-print recognition, *Pattern Recognition*. 44(9):1990-1998. (IF: 3.219)
14. Zhang Lin, Zhang Lei, Zhang D and **Zhu HL**. (2010) Online finger-knuckle-print verification for personal authentication, *Pattern Recognition*, 43(7):2560-71. (IF: 3.219)
15. Chow CK, **Zhu HL\***, Kuo WP. (2010) Error margin analysis for feature gene extraction, *BMC Bioinformatics*, 11:241, (11 May 2010). (IF: 3.02)
16. Wang HQ, **Zhu HL\***, Cho CS, Yip TC, Ngan KC, Law CK. (2010) Method of regulatory network that can explore protein regulations for disease classification, *Artificial Intelligence in Medicine*, 48(2-3):119-127. (IF: 1.767)
17. Lau HY, Tong KY, **Zhu HL**, (2009). Support vector machine for classification of walking conditions of persons after stroke with dropped foot. *Human Movement Science*, 28(4):504-514. (IF: 2.602)
18. Wang HQ, Wong HS, **Zhu HL**, Yip TC. (2009) A neural network-based biomarker association information extraction approach for cancer classification. *Journal of Biomedical Informatics*. 42:654-666. (IF: 2.434)
19. Wang HQ, **Zhu HL\***, Zheng CH, Yip TC, Cho CS, Law CK. (2009) Mining protein regulatory relationships using neural network methods for early prediction of SARS, *Journal of Circuits, Systems, and Computers*, 18(8): 1397-1407.
20. Lau HY, Tong KY, **Zhu HL**. (2008) Support Vector Machine for Classification of Walking Conditions Using Miniature Kinematic Sensors, *Medical & Biological Engineering & Computing*, 46(6): 563-573. (IF: 1.790)
21. Au SK, Cho CS, Yip TT, Yip C, **Zhu HL**, Leung WF, Tsui YB, Kwok LP, Kwan SM, Cheng WW, Tzang CH, Yang M, Law CK. (2007) Deep Proteome profiling of sera from never-smoked lung cancer patients, *Biomedicine & Pharmacotherapy*, 61(9):570-577. (IF: 2.231)

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22. **Zhu HL\***, Rao RSP, Chen LN. (2012) Reconstructing Dynamic Gene Regulatory Network for the Development Process of Hepatocellular Carcinoma. 2012 Workshop on Pharmaco-Informatics for Drug Discovery in Conjunction with 2012 IEEE International Conference on Bioinformatics and Biomedicine (BIBM 2012), Philadelphia, Oct. 2012.
  23. **Zhu HL\***, Wang HQ. (2010) Feature relation network that can identify underlying data structure for effective pattern classification, pp 531 – 534, 2010 IEEE International Conference on Bioinformatics and Biomedicine (BIBM), 18-21 Dec. 2010, Hong Kong.
  24. Chan KY, **Zhu HL**, Lau CC, Dillon TS, Ling SH. (2010) Determination of chemo-response for osteosarcoma using a hybrid evolutionary algorithm, IEEE CEC 2010, July, Barcelona, Spain.
  25. Chow CK, **Zhu HL\***, Lacy J, Lingen MW, Kuo WP, Chan K. (2009) A cooperative feature gene extraction algorithm that combines classification and clustering. International conference of bioinformatics and biomedicine (BIBM) 2009, Nov.1-4. Washington DC, USA.
  26. Wang HQ, **Zhu HL\***, Yip TC, Cho CS, Ngan KC, Law CK. (2008) Mining protein regulation relationships using neural network methods for early prediction of SARS, International Conference of Intelligent Computing 2008, Sep.15-18, Shanghai.
  27. Chan KY, **Zhu HL\***, Aydin ME, Lau CC. (2008) An Integrated Approach of Support Vector Machine and Variable Neighborhood Search for Discovering Combinational Gene Signatures in Predicting Chemo-response of Osteosarcoma. IEEE World Congress on Computational Intelligence 2008 (IEEE WCCI 2008), Jun.1-6, Hong Kong.
  28. Wang HQ, **Zhu HL\***, Yip TC, Cho CS, Ngan KC, Law CK. (2008) Exploring protein regulations with regulatory network for cancer classification. Proceedings of the 2008 International Conference on BioMedical Engineering and Informatics, 133-137, BMEI 2008, May 28-30, Sanya, Hainan.
  29. Wang HQ, Wong HS, **Zhu HL**. (2008) Constructing the histogram representation for automatic gridding of cDNA microarray images. Medical Biometrics, First International Conference, ICMB 2008, Hong Kong, China, January 4-5, 2008, Proceedings, 248-255. Lecture Notes in Computer Science 4901 Springer 2008.