

HSIN-TA WU, PhD

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Education

Brown University, USA

Ph.D. in Computational biology and Computer science, GPA: 4.0/4.0 2010-2016
Thesis Title: Computational detection of driver mutations in cancer genomes. Advisor: Benjamin J. Raphael
M.S. in Computer science, GPA: 3.83/4.0 2008-2010

National Yang-Ming University, Taiwan

M.S. in Bioinformatics, GPA: 4.0/4.0 2004-2006

National Cheng Chi University, Taiwan

B.S. in Computer science, GPA: 3.38/4.0 2000-2004

Research experience

Graduate Research Assistant, Brown University

2010-present

Advisor: Benjamin J Raphael. Developed algorithms for identifying structural variants in cancer: GASVPro and a statistical model for 10X Genomics linked-read technology. Developed algorithms for distinguishing driver mutations/pathways causing cancer: RAIG, HotNet2 and CoMEt. Participated in several projects in The Cancer Genome Atlas (TCGA) analysis working group. Developed visualization tool MAGI (<http://magi.brown.edu/>) that enables dissemination of these datasets to the cancer research community.

Research Assistant, IIS, Academia Sinica, Taiwan

2008

Advisor: Wen-Lian Hsu. Developed a multi-stage gene normalization algorithm: uses a dictionary-based matching algorithm to assign correct gene ID in biological literature and a rule-based voting algorithm classifier.

Graduate Research Assistant, National Yang Ming Univ.

2004-2006

Advisor: Ueng-Cheng Yang. Developed an integrated method effectively capture disease-associated genes using the statistic approach and natural language processing technologies.

Undergraduate Research Project, National Cheng Chi Univ.

2003-2004

Advisor: Man-Kwan Shen. Developed an *Apriori* approach to discover sequence signals associated with different types of alternative splicing.

Professional experience

PhD-level Intern, Pfizer, Cambridge, MA USA

2015 Summer

Advisor: Austin Huang. Set up an interface to perform comparative analysis between varied drug targets on transcriptomics, phospho-proteomics and proteomics data. Investigated and performed network algorithms on omics data for different drug targets, and created an R package for visualizing and interacting with the results of network propagation algorithms.

Intern, Protein Information Resource, Washington DC USA

2005 Summer

Advisor: Cathy Wu. Developed a rule-based literature mining system and website for protein phosphorylation. Propose a new mapping algorithm for iProLINK literature mining resource.

Computational skills

[Expert level] Python, R

[Proficient level] Perl, C/C++/Java, Javascript, D3.js, Bash script, Illustrator

[Knowledgeable level] SQL, MATLAB

Awards

Travel fellowship award for RECOMB 2015, Warsaw, Poland	2015
Travel fellowship award for ISMB 2014, Boston, USA	2014
Winner in BioCreAtIvE II.5 Interactor Normalization Task	2009
Hsun-Ruo Yin Scholarship for the Best Thesis Award of National Yang Ming Univ.	2006
Medical Scholarship Foundation in Memory of Prof. Ly-Young Shen	2005
Research Creativity Award for undergraduate offered by National Science Council	2004

Selected publications

- Comprehensive Pan-Genomic Characterization of Adrenocortical Carcinoma. The Cancer Genome Atlas Research Network. **Cancer Cell**. (2016)
- Reply: Co-occurrence of *MYC* amplification and *TP53* mutations in human cancer. Leiserson, M.D.M., Vandin, F., **Wu, H.**, Raphael, B.J. **Nature Genetics**. (2016)
- CoMEt: A Statistical Approach to Identify Combinations of Mutually Exclusive Alterations in Cancer. Leiserson, M.D.M.*, **Wu, H.*+**, Vandin, F., Raphael, B.J. **Genome Biology / 19th Annual International Conference on Research in Computational Molecular Biology (RECOMB)**. (2015) *Equal contribution. +Presenting author at **RECOMB** and **TCGA symposium 2015** at NIH.
- MAGI: visualization and collaborative annotation of genomic aberrations. Leiserson, M.D.M., Gramazio, C.C., Hu J., **Wu, H.**, Laidlaw, D.H., Raphael, B.J. **Nature Methods**. (2015)
- Pan-Cancer Network Analysis Identifies Combination of Rare Somatic Mutations across Pathways and Protein Complexes. Leiserson, M.D.M., Vandin, F., **Wu, H.**, Dobson, J.R., Papoutsaki, A., Eldridge, J.V., Nui, B., McLellan, M, Lawrence, M.S., Gonzalez-Perez, A., Tamborero, D., Ryslik, G.A., Cheng, Y., Lopez-Bigas, N., Getz, G., Ding, L., Raphael, B.J. **Nature Genetics**. (2014)
- Comprehensive molecular characterization of gastric adenocarcinoma. The Cancer Genome Atlas Research Network. **Nature**. (2014)
- Multiplatform Analysis of 12 Cancer Types Reveals Molecular Classification within and across Tissues of Origin. The Cancer Genome Atlas Research Network. **Cell**. (2014)
- Detecting Independent and Recurrent Copy Number Aberrations using Interval Graphs. **Wu, H.**, Hajirasouliha, I., Raphael, B.J. **Bioinformatics / 22nd Annual International Conference on Intelligent Systems for Molecular Biology (ISMB)**. (2014)
- Expression Profiling of Primary and Metastatic Ovarian Tumors Reveals Differences Indicative of Aggressive Disease Brodsky, A.S., Fischer, A., Miller, D.H., Vang, S., MacLaughlan, S., **Wu, H.**, Yu, J., Collins, C., Steinhoff, M., Smith, P.J.S., Raphael, B.J., Brard, L. **PLOS One**. (2014)
- The Cancer Genome Atlas Pan-Cancer analysis project. The Cancer Genome Atlas Research Network. **Nature Genetics**. (2013)
- Comprehensive Molecular Characterization of Clear Renal Cell Carcinoma. The Cancer Genome Atlas Research Network. **Nature**. (2013)
- Genomic and Epigenomic Landscapes of Adult De Novo Acute Myeloid Leukemia The Cancer Genome Atlas Research Network. **The New England Journal of Medicine**. (2013)
- Identification of Ovarian Cancer Metastatic miRNAs Vang, S., **Wu, H.**, Fischer, A., Miller, D.H., MacLaughlan, S., Douglass, E., Steinhoff, M., Collins, C., Smith, P.J.S., Brard, L., Brodsky, A.S. **PLOS One**. (2013)
- An Integrative Probabilistic Model for Identification of Structural Variation in Sequencing Data Sindi, S.S., Önal, S., Peng, L.C., **Wu, H.**, Raphael, B.J. **Genome Biology**. (2012)
- An Online Literature Mining Tool for Protein Phosphorylation Yuan, X., Hu Z., **Wu, H.**, Torii, M., Narayanaswamy, M., Ravikumar, K.E., Vijay-Shanker, K., Wu, C.H. **Bioinformatics**. (2009)