

CURRICULUM VITAE
Carnegie Mellon University
School of Computer Science

BIOGRAPHICAL

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Lane Center for Computational Biology
School of Computer Science
Carnegie Mellon University
Pittsburgh, PA 15213

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Education

Undergraduate:

- 09/1988 – 07/1992; Fudan University (Shanghai, P. R. China); B.S., 1992;
Major: Genetics and Genetic Engineering.

Graduate:

- 09/2001 – 07/2002; University of California, Santa Cruz, CA; M.S., 2002;
Research advisor: Prof. David Haussler;
Major: Computer Science.
- 09/1995 – 12/2000; Joint Graduate Program of Rutgers University and University
of Medicine and Dentistry of New Jersey; Ph.D., 2000;
Research advisor: Prof. Sidney Pestka;
Major: Computational Molecular Biology.

Postgraduate:

- 08/2002 - 09/2004; Life Sciences Division, Lawrence Berkeley National Lab,
Berkeley, CA;
Research advisor: Dr. Mina Bissell;
Discipline: Bioinformatics.

Appointments and Positions

Academic:

Carnegie Mellon University
Associate Research Professor
Lane Center for Computational Biology
School of Computer Science

Pittsburgh, PA, USA
2012 – present

University of Pittsburgh
Research Assistant Professor
Division of Pulmonary, Allergy
and Critical Care Medicine

Pittsburgh, PA, USA
2004 – 2011

Lawrence Berkeley National Laboratory
Guest Scientist
Life Sciences Division

Berkeley, CA, USA
2004 – 2011

Honors and Awards

- Best Paper Award, International Conference on Intelligence Systems for Molecular Biology, 2011.

Publications

Refereed journal papers:

1. Zhou, X.¹, **Wu, W.**¹, Hu, H., Milosevic, J., Konishi, K., Kaminski, N., Wenzel, S. E. (2011) "Genomic differences and functional pathway analysis of human airway and distal lung fibroblasts" (2011) *Am J Respir Cell Mol Biol* (PMID: 21757679).
(¹ co-first authors)
2. Parikh, A. P. ¹, **Wu, W.** ¹, Curtis, R. E. and Xing, E. P. (2011) "TREEGL: Reverse engineering tree-evolving gene networks underlying developing biological lineages" *the Nineteenth International Conference on Intelligence Systems for Molecular Biology (ISMB 2011)*. *Bioinformatics* 27(13): i196-i204. **Recipient of the ISMB BEST PAPER Award.**
(¹ co-first authors)
3. **Wu, W.**, Kaminski, N. "Systems biology and medicine: chronic lung diseases" (2009) John Wiley & Sons, Inc. *WIREs Syst Biol Med* 1: 298-308.
4. **Wu, W.***, Dave, N. B., Yu, G., Stollo, P. J., Kovkarova-Naumovski, E., Ryter, S. W., Reeves, S. R., Dayyat, E., Wang, Y., Choi, A. M. K., Gozal, D., Kaminski, N.* (2008) "Network Analysis of Temporal Effects of Intermittent- and Sustained Hypoxia on Rat Lungs." *Physiological Genomics* 36:24-34.
5. Dolinay, T., **Wu, W.**, Kaminski, N., Ifedigbo, E., Kaynar, A.M., Szilasi, M., Watkins, S.C., Ryter, S.W., Hoetzel, A., Choi, A.M.K. (2008) "Mitogen-activated protein kinases regulate susceptibility to ventilator-induced lung injury." *PLoS ONE* 3(2):e1601.
6. **Wu, W.***, Dave, N., Tseng, G., Richards, T., Xing, E.P., and Kaminski, N. (2005) "Comparison of normalization methods for CodeLink Bioarray data." *BMC Bioinformatics* 6(1):309.
(“Highly accessed” article designated by *BMC Bioinformatics*).

7. **Wu, W.***, Xing, E.P., Myers, C., Mian, I.S., and Bissell, M.J. (2005) "Evaluation of normalization methods for cDNA microarray data by k-NN classification." *BMC Bioinformatics* 6: 191.
("Highly accessed" article designated by *BMC Bioinformatics*).
8. **Wu, W.**, Kerrigan, J., Yadav, P., Schwartz, B., Izotova, L., and Pestka, S. (2004) "Design and Construction of a Phosphorylatable Chimeric Monoclonal Antibody with a Highly Stable Phosphate." *Oncology Research* 14(11-12):541-558.
9. Xing, E.P., **Wu, W.**, Jordan, M.I., and Karp, R.M. (2004) "LOGOS: A modular Bayesian model for *de novo* motif detection." *Journal of Bioinformatics and Computational biology*. 2(1): 127-154.
10. Clark, W.A., Izotova, L., Philipova, D., **Wu, W.**, Lin, L., Pestka, S. (2002) "Site-specific ³²P-labeling of cytokines, monoclonal antibodies, and other protein substrates for quantitative assays and therapeutic application." *Biotechniques*. Suppl:76-8, 80-87.
11. Pestka, S., Lin, L., **Wu, W.**, and Izotova, L. (2000) "Use of Phosphorylation Site Tags in Protein." *Methods Enzymol.* 327:594-613.
12. Pestka, S., Lin, L., **Wu, W.**, and Izotova, L. (1999) "Introduction of Protein Kinase Recognition Sites into Proteins: A Review of Their Preparation, Advantages and Applications", *Protein Expr Purif.* 17(2):203-14.
13. Lin, L., Gillies, S.D., Lan, Y., Izotova, L., **Wu, W.**, Schlom, J., and Pestka, S. (1998) "Construction of Phosphorylatable Chimeric Monoclonal Antibody CC49." *Intl. J. Oncology* 13, 115-120.
14. Kotenko, S.V., Krause, C.D., Izotova, L.S., Pollack, B.P., **Wu, W.**, and Pestka, S. (1997) "Identification and Functional Characterization of a Second Chain of the Interleukin-10 Receptor Complex." *EMBO J.* 16, 5894-5903.

(* corresponding or contact author)

Refereed conference papers:

15. Shi, Y., Guo, F., **Wu, W.** and Xing, E.P. (2007) "GIMscan: A New Statistical Method for Analyzing Whole-Genome Array CGH Data." The Eleventh Annual International Conference on Research in Computational Molecular Biology (RECOMB, full paper).
16. Xing, E.P., **Wu, W.**, Jordan, M.I. and Karp, R.M. (2003) "LOGOS: A modular Bayesian model for *de novo* motif detection." In *IEEE Computer Society Bioinformatics Conference (CSB'03)*: Stanford, California.

Book Chapters:

17. **Wu, W.**, and Xing, E.P. (2008) "A Survey of cDNA Microarray Normalization and a Comparison by k-NN Classification" in P. Stafford ed., *Methods in Microarray Normalization*, p81-120, CRC Press.

Selected published abstracts:

18. **Wu, W.**, J. Chamberlin, D. Curran-Everett, and S. E. Wenzel. "Clinical subphenotyping of severe asthma patients in the Severe Asthma Research Program (SARP) using an unsupervised learning approach." ATS 2011 International Conference (Abstract, oral presentation).
19. **Wu, W.**, Dave, N. B., Strollo, P. J., Kovkarova-Naumovski, E., Ryter, S. W., Reeves, S. R., Dayyat, E., Wang, Y., Choi, A. M. K., Gozal, D., Kaminski, N. "Study of Temporal Effects of Intermittent- and Sustained Hypoxia on Gene Expression Patterns in Rat Lungs using a Systems Biology Approach." *RECOMB Regulatory Genomics* 2007.
20. **Wu, W.**, Dave, N., Strollo, P.F., Choi, A.M.K., Row, B.W., Gozal, D., Kaminski, N. "LRSA Analysis of Temporal Effects of Hypoxia on Gene Expression Patterns in Rat Lung." *Am J Respir Crit Care Med* 2007; 175: A387 Abstracts Issue April 2007.

Other publications:

21. Shi, Y., Guo, F., **Wu, W.** and Xing, E.P. (2006) "GIMscan: A New Statistical Method for Analyzing Whole-Genome Array CGH Data", CMU-MLD Technical Report 06-115.
22. **Wu, W.**, Tatarsky, P. and Haussler, D. (2002) "Procedure for creating a mirror site for Human Genome Browser." <http://genome.ucsc.edu/admin/mirror.html>.

Professional activities

Teaching:

Courses:

1. Laboratory Methods for Computational Biologists (3 lectures, 2008): the CMU-Pitt joint computational biology program.
2. Laboratory Methods for Computational Biologists (a 1-hour class, 2007): the CMU-Pitt joint computational biology program.
3. Bioinformatics (a 3-hour class, 2006): Fundamentals in Basic Research, PACCM Research Training Program.
4. Bioinformatics (a 3-hour class, 2005): Fundamentals in Basic Research, PACCM Research Training Program.
5. Introduction to Computer Science (a quarter: about 3 months, 2001): Computer Science Department, University of California, Santa Cruz.

Presentations and Invited Lectures:

1. *Clinical subphenotyping of severe asthma patients in the Severe Asthma Research Program (SARP) using unsupervised and supervised learning approaches*, PACCM Grand Rounds, School of Medicine, Stanford University, Dec 16, 2011.

2. *Reverse Engineering Dynamic Gene Networks Underlying Breast Cancer Cell Lineages and Yeast Cell Cycle Transcription*, Center for Cancer Systems Biology, Stanford University, August 19, 2011.
3. Wu, W., J. Chamberlin, D. Curran-Everett, and S. E. Wenzel. "Clinical subphenotyping of severe asthma patients in the Severe Asthma Research Program (SARP) using an unsupervised learning approach." ATS International Conference (Oral presentation), 2011.
4. *Applying Microarrays to Complex Diseases*, American Academy of Allergy Asthma and Immunology (AAAAI) conference. San Diego, USA, 2007.
5. Organized a seminar series discussing the "*MicroArray Quality Control (MAQC) Project*", Pittsburgh, 2006.
6. *Diagnosis and Outcome Prediction: Can High-throughput Approaches Improve Over Clinical Diagnosis?*, PACCM Grand Rounds, University of Pittsburgh, 2006.
7. *Do Normalization Methods for Microarray Data Affect Results?*, PACCM Joint Collaborative Conference, University of Pittsburgh, 2005.

Supervised students:

- Co-supervised
 1. three post-doctoral medical fellows: Drs. Tamas Dolinay and Judie Howrylak (with Dr. Augustine Choi at Harvard Medical School) and Dr. Zhihong Zhou (with Dr. Danielle Morse at Harvard Medical School).
 2. two post-doctoral fellows: Drs. Andrew Wei Xu and Le Song (with Dr. Eric Xing at CMU).
 3. four graduate students, Kusum Pandit (with Dr. Naftali Kaminski at UPMC), Ankur Parikh, Kyung-Ah Sohn and Jing Xiang (with Dr. Eric Xing at CMU).
 4. a research associate, Melissa Paglia (with Dr. Prabir Ray at UPMC).

Manuscript Reviewers for:

- Bioinformatics
- BMC-Bioinformatics
- BMC-Genomics
- American Journal of Respiratory Cell and Molecular Biology
- Journal of Applied Physiology
- Computer Methods and Programs in Biomedicine

Program Committee Members for:

- 19th Annual International Conference on Intelligent Systems for Molecular Biology (ISMB 2011)
- 18th Annual International Conference on Intelligent Systems for Molecular Biology (ISMB 2010)

Grant Panelist for:

- National Science Foundation, 2008

Memberships:

2003- International Society for Computational Biology
2010- American Statistical Association
2010- the American Thoracic Society (ATS)

Research:

Current Grant Support:

1. Project number: NIH R01 (co-PI) 03/01/10 - 02/28/15

Agency: National Institutes of Health

Title of project: Time/Space-Varying Networks of Molecular Interactions: A New Paradigm for Studying Dynamic Biological Regulation and Pathways

The central theme of our proposed work emphasizes modeling and analyzing temporally and spatially varying molecular interactions between genes (or gene products), and systematically integrating multiple sources of information to understand these spatial and temporal biological processes.

Role: Co-PI

2. Project number: NIH R01 (co-PI) 03/01/09 - 02/28/14

Agency: National Institutes of Health

Title of project: Genome-Transcriptome-Phenome-Wide Association: A New Paradigm for Association Studies of Complex Diseases

Our aim is to develop a mathematically rigorous and computationally efficient machine learning platform and software to address the methodological challenges involved with unraveling the interplay between disease-relevant elements in the genome, transcriptome, and phenome.

Role: Co-PI

Past Research Grants:

1. CCF-0523757 (co-PI) 11/1/05 - 7/31/08

Agency: Carnegie Mellon University/National Science Foundation

Title of project: Non-Parametric Bayesian Models for Genetic Variations and its Association with Disease and Population Demography

The overall goal of this project is to associate the SNP data obtained from IFP patients and gene expression profiles from the same patients using the computational models we propose to develop. We will use these data to obtain cross-confirmation of the individual SNP-gene associations.

Curriculum Vitae
03/01/2012

Wei Wu, Associate Research Professor
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Research Interests:

My research focuses on understanding complex human diseases by undertaking integrative approaches, which combine biology, computational and statistical learning, bioinformatics, and genomics. In particular, I am interested in developing computational algorithms, software and tools i) to help identify genetic and regulatory mechanisms underlying human diseases, so that we can better understand why different genetic and gene expression changes in patients can lead to different disease phenotypes; ii) to identify biomarkers, and classify and diagnose various human diseases using metadata (e.g., genetic, gene expression and phenotypic data); and iii) to predict outcomes of patients with human diseases using metadata.