

Adam A. Margolin
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EDUCATION

Columbia University, New York, NY

Department of Biomedical Informatics, Ph.D Candidate

January, 2008 (expected)

- Dissertation: "Computational Inference of Genetic Regulatory Networks in Human Cancer Cells"
- GPA: 3.9/4.0
- Honors: Qualifying exam passed with honors, research preparation exam passed with honors

M. Phil. in Biomedical Informatics

2006

University Of Pennsylvania, Philadelphia, PA

School of Engineering and Applied Sciences, M.S. in Computer Information Technology, summa cum laude

December, 2002

Wharton School, B.S. in Economics, Concentration in Information Systems, cum laude

May, 2002

AWARDS

- IBM Ph.D Fellowship (~3 awarded per year) **2006-2008**
- Best Presentation Award, Conference on Intelligent Systems in Molecular Biology (ISMB) & European Conference on Computational Biology (ECCB), Student Council Symposium, Vienna, Austria **July, 2007**
- Two publications rated "must read" by the Faculty of 1000 Biology (see publications list) **2005, 2006**

RESEARCH/PROFESSIONAL EXPERIENCE

Columbia University, New York, NY

Department of Biomedical Informatics, Ph.D Candidate

September 2003 -

Advisor: Prof. Andrea Califano

Present

- Developed ARACNE, a novel, information-theoretic algorithm for the reverse engineering of gene regulatory networks from microarray data.
- Developed computational methods for the analysis of diverse high throughput data sources to infer regulatory programs associated with human transcription factor oncogenes.
- Developed a software platform for the simulation of biochemical networks using massively parallel computation.
- Applied molecular biology techniques to characterize expression patterns of Wnt/beta-catenin target genes in WT1-mutant versus WT1 wild-type Wilms' tumors.

IBM T.J. Watson Research Center, Yorktown Heights, NY

Functional Genomics and Systems Biology Group, Intern

Summers 2005,

Supervisor: Dr. Gustavo Stolovitzky

2006

- Developed the CSA algorithm for inferring binding events from ChIP-on-chip data.

University of Pennsylvania, Philadelphia, PA

Abramson Cancer Research Institute, Bioinformatics Application Developer

September 2001 –

Advisor: Prof. Barbara Weber

August 2003

- Designed and developed CGHAnalyzer, a java application incorporating novel algorithms for analysis of array-based genome copy number data.

National Center for Biotechnology Information, Bethesda, MD

Gene Expression Omnibus, Developer
Supervisor: Dr. Alex Lash

Summer 2002

- Developed software applications for analysis and visualization of microarray data stored in NCBI's Gene Expression Omnibus database.

EGenomics, Inc., New York, NY

Developer

Summer 2001

- Developed bioinformatics tools for global and regional pair-wise DNA sequence alignments, rapid bacterial typing and categorizing based on motif analysis and suffix trees

Bear Stearns & Co., Inc, New York, NY

High Yield Bonds Division, Programmer

**Summers 1999,
2000**

- Developed predictive algorithm and analysis software to model future risk and performance of emerging market bonds.
- Researched, developed, and published a model to estimate fair value of bonds.

New York Mets, Flushing, NY

Marketing Department, Intern

Summer 1998

TEACHING EXPERIENCE

Columbia University, New York, NY

Teaching Assistant – Introduction to Biophysical Modeling.

2005

Teaching Assistant – Computational Biology.

2004

PUBLICATIONS

Margolin, A. A., K. Wang, A. Califano and I. Nemenman (Submitted). "Multivariate dependence and genetic network inference."

Margolin, A. A. and A. Califano (In press). "Theory and limitations of genetic network inference from microarray data." Proceedings of the First Dream Conference, Annals of the New York Academy of Sciences.

Margolin, A. A., T. Palomero, A. Ferrando, A. Califano and G. Stolovitzky (In press). "ChIP-on-chip significance analysis reveals ubiquitous transcription factor binding." [BMC Bioinformatics](#).

Li, C. M., A. A. Margolin, M. Salas, L. Memeo, M. Mansukhani, H. Hibshoosh, M. Szabolcs, A. Klinakis and B. Tycko (2006). "PEG10 is a c-MYC target gene in cancer cells." [Cancer Res](#) **66**(2): 665-72.

Margolin, A. A., I. Nemenman, K. Basso, C. Wiggins, G. Stolovitzky, R. Dalla Favera and A. Califano (2006). "ARACNE: an algorithm for the reconstruction of gene regulatory networks in a mammalian cellular context." [BMC Bioinformatics](#) **7 Suppl 1**: S7.

- Selected as "must read" by the Faculty of 1000 Biology (*F1000 factor 6.0*)

Margolin, A. A., K. Wang, W. K. Lim, M. Kustagi, I. Nemenman and A. Califano (2006). "Reverse Engineering Cellular Networks." [Nature Protocols](#) **1**(2): 662-671.

Palomero, T., W. Lim, D. Odom, M. Sulis, P. Real, J. O'Neal, D. Neuberg, A. Margolin, A. Weng, J. Aster, F. Sigaux, J. Soulier, A. Look, R. Young, A. Califano and A. Ferrando (2006). "NOTCH1 directly regulates MYC and activates a feed-forward-loop transcriptional network promoting leukemic cell growth." [Proc Natl Acad Sci](#) **103**(48).

Palomero, T., D. T. Odom, J. O'Neil, A. A. Ferrando, A. Margolin, D. S. Neuberg, S. S. Winter, R. S. Larson, W. Li, X. S. Liu, R. A. Young and A. T. Look (2006). "Transcriptional regulatory networks downstream of TAL1/SCL in T-cell acute lymphoblastic leukemia." Blood **108**(3): 986-92.

Wang, K., I. Nemenman, K. Basso, A. Margolin, N. Banerjee, R. Dalla-Favera and A. Califano (2006). Genome-wide identification of modulators of cellular networks in human B lymphocytes. Proceedings of the 10th Annual International Conference on Research in Computational Molecular Biology (RECOMB).

Basso, K., A. A. Margolin, G. Stolovitzky, U. Klein, R. Dalla-Favera and A. Califano (2005). "Reverse engineering of regulatory networks in human B cells." Nat Genet **37**(4): 382-90.

- *Comment in Nature Biotechnology, May, 2005*
- *Selected as "must read" by the Faculty of 1000 Biology (F1000 factor 4.8)*

Margolin, A. A., J. Greshock, T. L. Naylor, Y. Mosse, J. M. Maris, G. Bignell, A. I. Saeed, J. Quackenbush and B. L. Weber (2005). "CGHAnalyzer: a stand-alone software package for cancer genome analysis using array-based DNA copy number data." Bioinformatics **21**(15): 3308-11.

Margolin, A. A., J. Greshock and B. L. Weber (2005). CGH data analysis. Encyclopedia of Genetics, Genomics, Proteomics and Bioinformatics. L. B. Jorde, P. F. R. Little, M. J. Dunn and S. Subramaniam. Chichester, Wiley & Sons Ltd: 3193-3201.

Margolin, A. A. and M. N. Stojanovic (2005). "Boolean calculations made easy (for ribozymes)." Nat Biotechnol **23**(11): 1374-6.

Mosse, Y. P., J. Greshock, A. Margolin, T. Naylor, K. Cole, D. Khazi, G. Hii, C. Winter, S. Shahzad, M. U. Asziz, J. A. Biegel, B. L. Weber and J. M. Maris (2005). "High-resolution detection and mapping of genomic DNA alterations in neuroblastoma." Genes Chromosomes Cancer **43**(4): 390-403.

Greshock, J., T. L. Naylor, A. Margolin, S. Diskin, S. H. Cleaver, P. A. Futreal, P. J. deJong, S. Zhao, M. Liebman and B. L. Weber (2004). "1-Mb resolution array-based comparative genomic hybridization using a BAC clone set optimized for cancer gene analysis." Genome Res **14**(1): 179-87.

Li, C. M., C. E. Kim, A. A. Margolin, M. Guo, J. Zhu, J. M. Mason, T. W. Hensle, V. V. Murty, P. E. Grundy, E. R. Fearon, V. D'Agati, J. D. Licht and B. Tycko (2004). "CTNNB1 mutations and overexpression of Wnt/beta-catenin target genes in WT1-mutant Wilms' tumors." Am J Pathol **165**(6): 1943-53.

Margolin, A. A., I. Nemenman, C. Wiggins, G. Stolovitzky and A. Califano (2004). On the reconstruction of interaction networks with applications to transcriptional regulation. Neural Information Processing Systems, Whistler, BC, Canada.

SELECTED INVITED PRESENTATIONS

2007 – Intelligent Systems in Molecular Biology / European Conference on Molecular Biology, Student Council Symposium, Vienna, Austria

2007 – Princeton University Program in Integrative Information, Computer and Application Sciences (PICASso), Princeton, NJ

2007 – Cold Spring Harbor Laboratories Computational Biology and Bioinformatics Seminar Series, Cold Spring Harbor, NY

2006 – DIMACS Workshop on Computational Tumor Modeling, Rutgers University, Piscataway, NJ

2006 – National Library of Medicine Informatics Training Conference, Vanderbilt University, Nashville, TN

POSTERS

Margolin, A.A., T. Palomero, A.A. Ferrando, A. Califano and G. Stolovitzky (2007). *ChIP-on-chip significance analysis reveals large scale transcription factor activity*. Intelligent Systems in Molecular Biology / European Conference on Computational Biology, Vienna, Austria.

Margolin, A. A., I. Nemenman, K. Basso, C. Wiggins, G. Stolovitzky, R. Dalla Favera and A. Califano (2005). *ARACNE: An Algorithm for the Reconstruction of Accurate Cellular Networks*. Keystone Symposium in Systems Biology, Keystone, CO.

Wang, K., I. Nemenman, K. Basso, A. A. Margolin, N. Banerjee, R. Dalla-Favera and A. Califano (2005). *Conditional network analysis: exploring network dynamics and identifying key modulator genes from gene expression data*. Intelligent Systems in Molecular Biology, Detroit, MI.

T.L. Naylor, J.D. Greshock, S.H. Cleaver, B.J. Baxter, A. Margolin, M.L. Liebman, R. Wooster, P.A. Futreal, M.R. Stratton, B.L. Weber. (2002) *Novel Approaches to Visualizing and Analyzing Array-Based Comparative Genomic Hybridization Data*. Annual Meeting of the American Society of Human Genetics, Baltimore, MD.

J. Greshock, T.L. Naylor, S.H. Cleaver, M.R. Gererro, A. Margolin, M.L. Liebman, B.L. Weber. (2002) *Genomic Profiling of Primary Breast Cancers and Cell Lines Using Array CGH*. Annual Meeting of the American Society of Human Genetics, Baltimore, MD.

REVIEWER ACTIVITY

Journals

- Bioinformatics, BMC Bioinformatics, Genomics, IEEE Signal Processing, Molecular Systems Biology

Conference Proceedings

- Intelligent Systems in Molecular Biology, Pacific Symposium on Biocomputing, Research in Computational Molecular Biology

PROFESSIONAL AFFILIATIONS

- Dialogue on Reverse Engineering Assessment and Methods (DREAM), Program Committee
- International Society of Computational Biology
- New York Academy of Sciences
- Center for Development of a Virtual Tumor

SKILLS

Computational skills

- ASP, C, C++, EJB, HTML, Java, JSP, LISP, Matlab, Microsoft Access, Microsoft Office, Oracle, Perl, Python, SQL, SQL Server, Sybase, UNIX, Visual Basic, XML

Experimental techniques

- Experience in basic molecular biology techniques including: Cell culture, FACS, PCR, sub-cloning, transfection, Western blotting
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