

Philip M. Kim, Ph.D.

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Education

Massachusetts Institute of Technology (August 1998- February 2003)

Ph.D., Artificial Intelligence Laboratory and Program in Physical Chemistry

Thesis focuses on the study of biological networks, emergent properties and microarray data mining. GPA 4.8/5.0

University of North Carolina at Chapel Hill (September 1997- May 1998)

Research Exchange Student. Participated in the Graduate Program in Cellular and Molecular Biophysics.

Research on computational structure refinement methodologies.

University of Tuebingen (October 1994- August 1997)

Vordiplom in Physics (German equivalent to B.S.), Perfect GPA. Best Vordiplom in Physics 1997.

Vordiplom in Biochemistry (German equivalent to B.S.), Perfect GPA .

Research Experience

University of Toronto, Terrence Donnelly Center for Cellular and Biomolecular Research (from January 2009)

Assistant Professor, Tenure-stream.

Yale University, Department of Molecular Biophysics & Biochemistry (January 2005- November 2008)

Postdoctoral Associate / Associate Research Scientist. Advisor: Professor Mark B. Gerstein

Pioneered novel structure based and network based approaches to gain further understanding of protein interactions, molecular evolution and network growth.

Building quantitative interaction networks of modular protein domains using the combination of a multi-platform experimental and a computational approach (collaboration with the Boone, Sidhu, Cesareni and Volkmer labs at the University of Toronto, Genentech, the University of Rome and the Charite Berlin).

Mapping the binding specificities of all protein kinases in yeast using peptide library screens and an advanced analysis pipeline that combines structural, evolutionary and genomic information with modern machine learning techniques (collaboration with the Snyder and Turk labs at Yale).

Elucidated mechanisms of formation of Copy Number Variants and Segmental Duplications in the Human Genome. Identified signatures of positive selection and structural genome variation in human protein interaction networks.

Massachusetts Institute of Technology, Artificial Intelligence Laboratory (August 1998- February 2003)

Research Graduate Fellow. Advisor: Professor Bruce Tidor

Developed graph theoretic algorithms to partition gene interaction networks and recognize functional modules of similar topology. Created a mathematical framework to predict the behavior of a type of genetic networks.

Application of machine learning techniques and pattern recognition algorithms. Developed a novel data mining approach of matrix factorizations to be applied to high-throughput gene expression data.

University of North Carolina at Chapel Hill, Dept. of Biochem. and Biophysics (September 1997- May 1998)

Research Assistant. Advisor: Professor Jan Hermans

Developed a new approach for refinement of protein structures determined by x-ray crystallography. Based on a semi-empirical energy function and a novel sampling method developed a program to correctly place the hydrogen atoms in the final structure.

Teaching Experience

Massachusetts Institute of Technology, Department of Chemistry (September 2001- January 2002)
Head Teaching Assistant, Class: "5.60 Thermodynamics and Kinetics"
Supervised 6 teaching assistants, wrote and graded weekly problem sets, taught weekly recitation sections.

Massachusetts Institute of Technology, Department of Chemistry (August 1998- May 1999)
Teaching Assistant, Class: "5.60 Thermodynamics and Kinetics"
Taught weekly recitation sections, graded problem sets and exams.

Yale University, Department of Molecular Biophysics and Biochemistry (January 2005-present)
Mentored a total of 8 graduate/rotation students. Designed research projects and supervised their progress

Work Experience

McKinsey & Company (August 2003- December 2004)
Associate. Management consulting of high-tech and pharmaceutical companies.
Consulting activities focused on highly quantitative analysis of operational and innovation activities. Developed a novel cutting edge approach to optimize tactical pricing. Authored publication about promotional pricing.

Honors/Awards

Boehringer Ingelheim Fonds Ph.D. Fellow 2001-2003
Merck Graduate Fellow in Bioinformatics 1999-2001
Howard Hughes Medical Institute Predoctoral Fellowship (Honorable Mention) 1999
Recipient of a study abroad fellowship from the University of Tuebingen 1997-1998
Award for the best Chemistry Student from the German Chemical Industry 1993
3rd West German Champion in Judo 1993, Competitor in the National Judo League 1993-1994

Professional Activities

Referee for *PLoS Comp. Biol.*, *Mol. Sys. Biol.*, *BMC Bioinformatics*, *Annu. Rev. of Biochem.*, *Pattern Recognition*, *Bioinformatics*, *Gene*
Member of the Program Committee for ISMB 2008, ISMB/ECCB 2007
Treasurer, the European Professional and Academic Network, 2002-2003
Co-Chair, IT-Chair and Organizer, the European Career Fair at MIT, 2000-2003
Organizer and IT-coordinator, Euro-US Biotechnology Summit at MIT 2001

References

Prof. Mark Gerstein
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Biological Engineering Division and Dept. of EECS
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Prof. Michael Snyder
Dept. of Mol. Cell. and Devel. Biology
266 Whitney Ave., KBT 926, Yale University
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Prof. Ben Turk
Dept. of Pharmacol. Sciences and Mol. Medicine
333 Cedar St., PO Box 208066, Yale University
New Haven, CT 06520, USA
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Languages, IT-Skills and Interests

Languages: German (native), English (near-native fluency) and Korean (conversant)
IT-Skills: Matlab (expert), Perl (expert), Java (advanced), C (basic), R (basic), Linux and Mac OS X (expert)
Interests: Rock climbing, running, weight lifting, hiking, skiing, cycling, surfing, judo and history.

Papers submitted for publication and in preparation

R. Tonikian*, **P.M. Kim***, X. Xin*, C. Landgraf, R. Volkmer, M.B. Gerstein, G. Cesareni, C. Boone and S.S. Sidhu “Multi-platform high-accuracy mapping of SH3 domain binding targets” (in preparation) [*joint first author]

J. Mok, **P.M. Kim**, M.B. Gerstein, M. Snyder and B. Turk “Genome-wide analysis of kinase binding targets using oriented peptide library screens” (in preparation)

P.M. Kim*, H.Y.K. Lam*, and M.B. Gerstein “MAPLES, a motif analysis pipeline for accurately predicting binding sites of modular protein domains” (in preparation) [*joint first author]

K.Y. Yip, **P.M. Kim**, D. McDermott and M.B. Gerstein “Multi-Layer Modeling: A Method for Simultaneous Prediction of Protein, Domain and Residue Interactions” (submitted)

P.M. Kim, J.O. Korbel, X. Chen and M.B. Gerstein, “Different patterns of formation of segmental duplications and copy number variants in the human genome” (submitted)

Publications (in press and published)

J.O. Korbel*, **P.M. Kim***, X. Chen, A.E. Urban, M. Snyder and M.B. Gerstein (2008) “The current excitement about copy-number variation: how does it relate to gene duplication and protein families?” *Curr. Op. Struct. Biol.* 18(3):366-74 [*joint first author]

P.M. Kim*[#], A. Sboner*, Y. Xia and M.B. Gerstein[#] (2008) “The Role of Disordered Proteins in Interaction Networks: A Structural Analysis” *Nature Molecular Systems Biology* 4:179 [*joint first author, [#]corresponding author]

K.Y. Yip*, P. Patel*, **P.M. Kim**, D.M. Engelman, D. McDermott and M.B. Gerstein (2008) “An Integrated System for Studying Protein Residue Coevolution”, *Bioinformatics* 24: 290-292

P.M. Kim*[#], J.O. Korbel[#] and M.B. Gerstein[#] (2007), “Positively Selected Nucleotide Changes and Segmental Duplications at the Protein Network Periphery: Mechanisms for Adaptation”, *PNAS* 104:20274-9 [*joint first author, [#]corresponding author]

J.O. Korbel*, A.E. Urban*, J.P. Affourtit*, B. Godwin, F. Grubert, J.F. Simons, **P.M. Kim**, ..., M.E. Hurles, S.M. Weissman, T.T. Harkins, M.B. Gerstein, M. Egholm, M. Snyder (2007) “Paired-End Mapping Reveals Structural Variation in the Human Genome”, *Science* 318: 420-6

L.J. Lu, A. Sboner, Y.J. Huang, D.X. Lu, T.A. Gianoulis, K.Y. Yip, **P.M. Kim**, G.T. Montelione and M.B. Gerstein (2007) “Comparing Biochemical Pathways and Networks: Towards Developing an Edge Ontology” *Trends in Biochem. Sci.* 32(7):320-31

H. Yu*, **P.M. Kim***, V. Trifonov and M.B. Gerstein (2007) “Network Topologies Determine Protein Function and Expression: The Importance of Bottlenecks”, *PLoS Comp. Biol.* 3(4): e59 [*joint first author]
Highlight in *Science* (“Editors choice”), *Faculty of 1000* (“recommended”) and *Science STKE*

P.M. Kim, L.J. Lu, Y. Xia and M.B. Gerstein (2006) “Redefining Nodes and Edges: Analyses of 3D Structures in Interaction Networks gives Evolutionary Insight”, *Science* 314: 1938-41
Highlight in *Science* (“News and views”), *Faculty of 1000* (“exceptional paper”), *Nature Genetics* (“Research highlight”) and *C&E News*

K.Y. Yip, H. Yu, **P.M. Kim**, and M. Gerstein (2006) “tYNA, an integrated web-based tool for network analysis and visualization”, *Bioinformatics* 22: 2968-70

P.M. Kim and B. Tidor (2003), “Limitations of Quantitative Gene Regulation Models: A Case Study”, *Genome Research* 13: 2391-5

P.M. Kim and B. Tidor (2003), “Subsystem Identification through Dimensionality Reduction of Large-scale Gene Expression Data”, *Genome Research* 13:1706-18

Invited and Refereed Talks

University of Cambridge, Department of Biochemistry, Cambridge, UK, July 2008
National University of Singapore, Department of Biochemistry, Singapore, May 2008
University of Toronto, Terrence Donnelly Centre for Cellular and Biomolecular Research, Toronto, ON, May 2008
University of California Davis, Department of Computer Science, Davis, CA, May 2008
Spanish National Cancer Research Center (CNIO), Madrid, Spain, April 2008
Scripps Research Institute, San Diego, CA, April 2008
Fred Hutchinson Cancer Research Center, Seattle, WA, March 2008
Carnegie-Mellon University, Lane Center for Computational Biology, Pittsburgh, PA, March 2008
University of California Irvine, Department of Computer Science, Irvine, CA, March 2008
University of Maryland, Department of Bioengineering, College Park, MD, February 2008
Universitaet Duesseldorf, Fakultae fuer Informatik, Duesseldorf, Germany, February 2008
Wellcome Trust Sanger Institute, Hinxton, Cambridge, UK, February 2008
EMBL-EBI, Hinxton, Cambridge, UK, February 2008
Max Planck Institutes Selection Symposium, Berlin, Germany, February 2008
University of California Davis, Genome Center, Davis, CA, January 2008
Georgia Institute of Technology, School of Biology, Atlanta, GA, January 2008
EMBL/CRG, Systems Biology Unit, Barcelona, Spain, January 2008
University of Pennsylvania, Department of Biology, Philadelphia, PA, January 2008
Institute for Molecular Bioscience, University of Queensland, Brisbane, Australia, December 2007
Munich Information Center for Protein Sequences (MIPS), Munich, Germany, November 2007
University of Munich, Fakultae fuer Informatik, Mathematik und Statistik, Munich, Germany, November 2007
Memorial Sloan-Kettering Cancer Center, Computational Biology Seminar, New York, NY, November 2007
FEBS Workshop on Modular Protein Domains, Seefeld, Austria, September 2007
ISMB/ECCB 2007 Highlight Talk, Vienna Austria, July 2007
Biopathways SiG (ISMB 2007), Vienna, Austria, July 2007
ZBSA Research Seminar, Freiburg, Germany, July 2007
Boehringer Ingelheim Fonds Meeting, Woods Hole, MA, September 2006
German Conference on Bioinformatics, Tuebingen, Germany, September 2006
NSF Workshop on Mechanisms of Cellular Networks, Telluride, CO, August 2006
Yeast Genetics and Molecular Biology Meeting, Princeton, NJ, July 2006
Yale Center for Structural Biology Seminar, New Haven, CT, February 2006
EAROTO Kitano Center for Systems Biology, Tokyo, Japan, August 2004
SONY Computer Science Laboratories, Tokyo, Japan, August 2004
Institute Pasteur, Paris, France, August 2004