CURRICULUM VITAE

ASA BEN-HUR

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Current Address:
Computer Science Department
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Education

Postdoc, Noble lab, Department of Genome Sciences, University of Washington, 2004 - 2005.

Postdoc, Brutlag bioinformatics group, Dept. of Biochemistry, Stanford University, 2002 - 2004.

Ph.D, information systems, Faculty of Industrial Engineering and Management, Technion - Israel Institute of Technology, 1996 - 2001.

M.Sc., physics (cum laude), Hebrew University, Jerusalem, 1993 - 1995.

B.Sc., physics and mathematics (cum laude), Hebrew University, Jerusalem, 1990 - 1993.

Academic Positions

Aug 2005 - present: Assistant professor, Department of Computer Science, Colorado State University.

Oct 2007 - present: Assistant professor, Department of Statistics, Colorado State University.

Oct 2005 - present: Adjunct assistant professor, Department of Computer Science, University of Colorado at Boulder.

Affiliations

Graduate Program in Molecular Plant Biology (PMPB).

Program in Molecular, Cellular and Integrative Neuroscience (MCIN).

Visiting Appointments

Visiting Researcher, Max-Planck Institute for Biological Cybernetics, Tubingen, Germany, July 2003.

Professional Experience

Consultant, PathWork Informatics, 2003. Provided guidance on supervised-learning methods for analysis of gene expression data.

Researcher, BIOwulf Technologies, 2001-2002. Developed data analysis methods for gene expression data, protein expression data, and medical databases.

Consultant, Camtek, 2000. Supervised the design of a printed circuit defect detection system.

Teaching Experience

Introduction to bioinformatics algorithms (undegraduate/graduate)

Kernel methods in bioinformatics (graduate)

Introduction to artificial intelligence (undergraduate)

Algorithms and data structures (undergraduate)

Invited Talks

Kernel methods for the analysis of proteins: insights and caveats.
    Keynote presentation, Rocky05, December 2005.

Kernel methods for predicting protein-protein interactions.
    University of Colorado, Denver, October 2005.

Inferring motifs that mediate protein-protein interactions.
    Invited presentation, NIPS bioinformatics workshop, December 2003

Protein sequence motifs: Highly predictive features of protein function.
    International Computer Science Institute, Berkeley, April 2004
    Workshop on feature selection, NIPS, December 2003

Remote homology detection: A motif based approach.
    Chemistry department, University of California at Berkeley, April 2004
    Max-Planck Institute for Informatics, Saarbrucken, July 2003
    Max-Planck Institute for Biological Cybernetics, Tubingen, July 2003
    Department of Computer Science, Columbia University, June 2003

A stability-based method for detecting structure in clustered data.
    International Computer Science Institute, Berkeley, March 2003
    Center for the Study of Language and Information, Stanford, January 2003
    EECS Department, University of California at Berkeley, March 2002
    Department of computer science, University of Massachusetts at Amherst, November 2002

Support vector clustering.
    Department of computer science, University of Massachusetts at Amherst, November 2002
    Department of physiology, McGill University, April 1999.

A theory of complexity for continuous time systems.
EECS department, University of California at Berkeley, November 2002
Santa Fe Institute, April 1999

Professional Activities

Reviewing:

Reviewer for: Bioinformatics, BMC Bioinformatics, Journal of Bioinformatics and Computational Biology, PLOS Computational Biology, Nucleic Acids Research, Protein Science, IEEE transactions on Computational Biology and Bioinformatics, Journal of Machine Learning Research.

Conferences: PSB, RECOMB, ECCB, Neural Information Processing Systems (NIPS) 2004-2007.

Program committees: ISMB 2005,2006,2007,2008.

Organizer, Graybill bioinformatics workshop, 2007.

Service to the University

Department of Computer Science committees

- Awards committee 2006
- Research committee 2007

Bioinformatics Center Search Committee 2006

Bioinformatics Center Steering Committee 2006 - present

Graduate Students

Name	Degree	Thesis Topic
Artem Sokolov	PhD, CS	
Mark Rogers	PhD, CS	
Todd Iverson	PhD, statistics	Prediction of type-II diabetes risk (co-advisor with Hari Iyer)
Michael Hamilton	MSc, CS	Prediction of Calmodulin binding proteins
Adam Labadorf	MSc, CS	Prediction of alternative splicing in plants
Mark Ottenberg	MSc, CS	
Kevin Depue	MSc, CS	Kernel methods for composer classification

Publications

Bioinformatics/Machine Learning

H. Wang, E. Segal, A. Ben-Hur, Q. Li, M. Vidal and D. Koller. InSite: a computational method for identifying protein-protein interaction binding sites on a proteome-wide scale. Genome Biology, 8(9): R192, 2007.

J. Qiu, M. Hue, A. Ben-Hur, J-P. Vert and W.S. Noble. An alignment kernel for protein structures. Bioinformatics 23(9): 1090-1098, 2007.

S-Y. Rhee, J. Taylor, G. Wadhera, A. Ben-Hur, D. Brutlag and R.W. Shafer. Genotypic predictors of human immunodeficiency virus type 1 drug resistance. PNAS 103(46): 17355-17360, 2006

A. Ben-Hur and W.S. Noble. Choosing negative examples for the prediction of protein-protein interactions. BMC Bioinformatics 7 (Suppl 1), 2006.

J.P. Miller, R.S. Lo, A. Ben-Hur, C. Desmarais, I. Stagljar, W.S. Noble and S. Fields. Large-scale identification of yeast integral membrane protein interactions. PNAS 102(34): 12123-12128, 2005.

A. Ben-Hur and W.S. Noble. Kernel methods for predicting protein-protein interactions. In: *Proceedings, thirteenth international conference on intelligent systems for molecular biology*. Bioinformatics 21 Suppl. 1: i38-i46, 2005.

I. Guyon, S.R. Gunn, A. Ben-Hur and G. Dror. Results analysis of the NIPS 2003 feature selection challenge. In: *Advances in Neural Information Processing Systems*, 545-552, 2005.

H. Wang, E. Segal, A. Ben-Hur, D. Brutlag and D. Koller. Identifying protein-protein interaction sites on a genome-wide scale. In: *Advances in Neural Information Processing Systems*, 1465-1472, 2005.

R. Sharan, A. Ben-Hur, G. Loots and I. Ovcharenko. CREME: cis-regulatory module explorer for the human genome. *Nucleic Acids Research* 32: W83-W88, 2004.

A. Ben-Hur and D. Brutlag. Remote homology detection: A motif based approach. In: *Proceedings, eleventh international conference on intelligent systems for molecular biology*. Bioinformatics 19 Suppl. 1: i26-i33, 2003.

R. Sharan, I. Ovcharenko, A. Ben-Hur and R.M. Karp. CREME: A framework for identifying cis-regulatory modules in human-mouse conserved segments. In: *Proceedings, eleventh international conference on intelligent systems for molecular biology*. Bioinformatics 19 Suppl. 1: i283-i291, 2003.

A. Ben-Hur, D. Horn, H.T. Siegelmann and V. Vapnik. Support vector clustering. *Journal of Machine Learning Research* 2:125-137, 2001.

A. Ben-Hur, A. Elisseeff and I. Guyon. A stability-based method for discovering structure in clustered data. *Pacific Symposium on Biocomputing 7*, 6-17, 2002.

A. Ben-Hur, D. Horn, H.T. Siegelmann and V. Vapnik. A support vector method for hierarchical clustering. *Advances in Neural Information Processing Systems 13*, 367-373, 2001.

A. Ben-Hur, D. Horn, H.T. Siegelmann and V. Vapnik. A kernel clustering method. In: *15th International Conference on Pattern Recognition*, 728-731, 2000.

Book Chapters

W.S. Noble and A. Ben-Hur. Integrating information for protein function prediction. In: *Bioinformatics - From Genomes to Therapies Vol. 3*. Thomas Lengauer (ed.) Wiley, 2007 pp. 1297-1314.

A. Ben-Hur and D. Brutlag. Protein sequence motifs: Highly predictive features of protein function. In: *Feature extraction, foundations and applications*. I. Guyon, S. Gunn, M. Nikravesh, and L. Zadeh (eds.) Springer Verlag, 2006.

I. Guyon, S. Gunn, A. Ben-Hur, G. Dror. Design and analysis of the NIPS2003 challenge. In: *Feature extraction, foundations and applications*. I. Guyon, S. Gunn, M. Nikravesh, and L. Zadeh (eds.) Springer Verlag, 2006.

A. Ben-Hur and I. Guyon. Detecting stable clusters using principal component analysis. In *Methods in Molecular Biology*, M.J. Brownstein and A. Khodursky (eds.) Humana press, 2003 pp. 159-182.

Analog Computation

A. Ben-Hur and H.T. Siegelmann. Computation in gene networks. *Chaos: An Interdisciplinary Journal of Nonlinear Science* 14(1):145-151, 2004.

A. Roitershtein, A. Ben-Hur and H.T. Siegelmann. On probabilistic analog automata. *Theoretical Computer Science*, 320(2-3):449-464, 2004.

A. Ben-Hur, J. Feinberg, S. Fishman and H.T. Siegelmann. Random matrix theory for the analysis of the performance of an analog computer: a scaling theory. *Physics Letters A* 323(3-4):204-209, 2004.

A. Ben-Hur, J. Feinberg, S. Fishman and H.T. Siegelmann. Probabilistic analysis of a differential equation for linear programming. *Journal of Complexity* 19(4):474-510, 2003.

A. Ben-Hur, H.T. Siegelmann and S. Fishman. Complexity for continuous time systems. *Journal of Complexity* 18(1):51-86, 2002.

H.T. Siegelmann, A. Ben-Hur, and S. Fishman. Computational complexity for continuous time dynamics. *Physical Review Letters*, 83(7):1463–1466, 1999.

A. Ben-Hur and H.T. Siegelmann Computation in gene networks. *in:* M. Margenstern and Y. Rogozhin (Eds.): MCU 2001, LNCS 2055, pp. 11-24, 2001.

H.T. Siegelmann, A. Roitershtein, and A. Ben-Hur. Noisy neural networks and generalizations. In *Advances in Neural Information Processing Systems 12*, Cambridge, MA, 2000. MIT Press.

Physics

A. Ben-Hur, R. Hallgass, and V. Loreto. A renormalization procedure for directed self-organized critical models. *Physical Review E*, 54:1426–1432, 1997.

A. Ben-Hur and O. Biham. Universality in sandpile models. *Physical Review E*, 53:1317–1321, 1996.

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5