

Asa Ben-Hur

Associate Professor

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EDUCATION

- 2004 - 2005 **Postdoc**, *Noble lab*, Department of Genome Sciences, University of Washington.
- 2002 - 2004 **Postdoc**, *Brutlag bioinformatics group*, Dept. of Biochemistry, Stanford University.
- 1996 - 2001 **Ph.D.**, *Information Systems*, Faculty of Industrial Engineering and Management, Technion - Israel Institute of Technology.
- 1993 - 1995 **M.Sc.**, *Physics (cum laude)*, Hebrew University, Jerusalem.
- 1990 - 1993 **B.Sc.**, *Physics and mathematics (cum laude)*, Hebrew University, Jerusalem.

PROFESSIONAL EXPERIENCE

- May 2011 - present **Associate professor**, *Department of Computer Science*, Colorado State University.
- Aug 2005 - 2011 **Assistant professor**, *Department of Computer Science*, Colorado State University.
- Oct 2007 - present **Assistant professor**, *Department of Statistics*, Colorado State University.
- 2003 **Consultant**, *PathWork Informatics*.
Provided guidance on supervised-learning methods for analysis of gene expression data
- Dec 2000 - Feb 2001 **Researcher**, *BIOwulf Technologies*.
Developed data analysis methods for gene expression data, protein expression data, and medical databases
- 2000 **Consultant**, *Camtek*.
Conducted a feasibility study of automatic defect detection in printed circuits using support vector machines
- Oct 1996 - Jun 2000 **Teaching and Research Assistant**, *Faculty of Industrial Engineering and Management*, Technion - Israel Institute of Technology.
- Oct 1993 - Jun 1995 **Teaching Assistant**, *Racach Institute of Physics*, Hebrew University, Jerusalem.

TEACHING

At Colorado State University

- CS646 Machine learning in bioinformatics. An advanced graduate level course focused on applications of kernel methods to bioinformatics problems. Has been taught every other year, alternating with CS/ST548.
- CS/ST548 Bioinformatics algorithms. Developed a graduate level bioinformatics course. Team taught with Hari Iyer in spring 06 at the undergraduate level.
- CS580 Programming for the life sciences. Developed a graduate level programming course for life science students. Students learned to program in Python, with applications to biological data. Taught spring 2010.
- CS440 Artificial intelligence. Taught fall 06, fall 09
- CS320 Algorithms: theory and practice. Taught spring 11, spring 12

CS200 Data structures. Taught spring 08, spring 09

CS161 Object oriented problem solving. Taught fall 09

CS160 Foundations in programming. Taught fall 08

As Teaching Assistant, Technion - Israel Institute of Technology

Neural networks (graduate), Probabilistic modeling with Bayesian networks (graduate), Probability theory (undergraduate), Decision support systems (MBA)

ADVISING

Doctoral students graduated
Todd Iverson. Ph.D. in Statistics June 2008. Co-advisor.

Artem Sokolov. Ph.D. August 2011.

Masters Students Graduated
Adam Labadorf. M.Sc. April 2010.

Michael Hamilton. M.Sc. April 2010.

GRANTS AND RESEARCH FUNDING

NSF - Principal Investigator
PREVALT: Predicting and validating alternative splicing in plants. A collaboration between Asa Ben-Hur and A.S.N. Reddy in the biology department. NSF Division of Biological Infrastructure 0743097, \$1,086,612.00 to Colorado State University, 2008 - 2012.

NSF - Principal Investigator
GOSTRUCT: modeling the structure of the Gene Ontology for accurate protein function prediction. A collaboration between Asa Ben-Hur and Karin Verspoor in University of Colorado at Denver. NSF Advances in biological informatics 0965768, \$523,303 to Colorado State University, 2010 - 2014.

CSU Infectious Disease SuperCluster - co-PI
A pipeline for diagnostic marker identification from next-generation genomic sequence. A collaboration with Jan Leach from the BSPM department. \$30,687, 2010.

EXTERNAL SERVICE

Program committee
ISMB 2005 - 2012
IJCNN 2011
ECCB 2010
ACMBCB 2011
22nd IEEE International Conference on Tools with Artificial Intelligence 2010.
AISTATS 2009
NIPS workshop on open source software 2008
ICML workshop on open source software 2010
NIPS workshop: Machine Learning in Computational Biology (MLCB) 2009
AAAI bioinformatics track 2010
22nd IEEE International Conference on Tools with Artificial Intelligence 2010

Conference reviewing
NIPS 2004 - 2010
RECOMB 2009,2011
Pacific Symposium on Biocomputing (PSB)

Journal reviewing
Reviewer for: Bioinformatics, Journal of Bioinformatics and Computational Biology, PLoS Computational Biology, BMC Bioinformatics, Genome Biology, Nucleic Acids Research, Proteins, Protein Science, Journal of Biomedical Informatics, Molecular Systems Biology, IEEE transactions on Computational Biology and Bioinformatics, Journal of Machine Learning Research.

- Grant reviewing NSF panels 2010, 2011.
Ad-hoc reviewer for NSF, ISF (Israeli Science Foundation), Canda Foundation for Innovation.
- Invited workshop participant Participated in NSF's iPlant cyberinfrastructure collaborative organizational conferences, March 2009, July 2009.

UNIVERSITY SERVICE

- Workshops Organized a session on human-computer interaction as part of The bi-annual Future Visions symposium in 2010.
Organized a CSU bioinformatics retreat bringing together researchers on campus interested in bioinformatics, 2008.
Organizer of a bioinformatics workshop as part of the yearly Graybill conference, 2007. See <http://www.stat.colostate.edu/graybillconference2007/Workshop.htm>.
- Department committees Awards committee 2006/7, 2009/10, Research committee 2007/8, Undergraduate committee 2008-10, Search committee 2012.
- University committees Bioinformatics Center Search Committee 2006, Bioinformatics Center Steering Committee 2006 - 2010, ISTeC Education Advisory Committee 2009/10.

PUBLICATIONS

- Journals M.F. Rogers, J. Thomas, A.S.N. Reddy and A. Ben-Hur. SpliceGrapher: detecting patterns of alternative splicing from RNA-Seq data in the context of gene models and EST data. *Genome Biology* 13:R4, 2012.
- A.S.N. Reddy, Mark F. Rogers, Dale N. Richardson, Michael Hamilton, and Asa Ben-Hur. Deciphering the plant splicing code: Experimental and computational approaches for predicting alternative splicing and splicing regulatory elements *Frontiers in Plant Genetics and Genomics* 3, 2012.
- D.N. Richardson, M.F. Rogers, A. Labadorf, A. Ben-Hur, H. Guo, A.H. Paterson, and A.S.N. Reddy. Comparative analysis of Serine/Arginine-rich proteins across 27 eukaryotes: Insights into subfamily classification and extent of alternative splicing. *PLoS ONE* 6(9): e24542, 2011.
- A.S.N. Reddy, A. Ben-Hur, and I.S. Day. Experimental and computational approaches for the study of calmodulin interactions. *Phytochemistry* 72(11): 1007-1019, 2011.
- A. Sokolov and A. Ben-Hur. Hierarchical classification of Gene Ontology terms using the GOstruct method. *Journal of Bioinformatics and Computational Biology* 8(2): 357-376, 2010.
- Adam Labadorf, Alicia Link, Mark F Rogers, Julie Thomas, Anireddy SN Reddy and Asa Ben-Hur. Genome-wide analysis of alternative splicing in *Chlamydomonas reinhardtii*. *BMC Genomics* 11:114, 2010.
- C.D. Ross, B. McCarty, M. Hamilton, A. Ben-Hur, and E.D. Ross. A promiscuous prion: Efficient induction of [URE3] prion formation by heterologous prion domains. *Genetics* 183: 929-940, 2009.
- M. Rogers and A. Ben-Hur. The Use of Gene Ontology evidence codes in preventing classifier assessment bias. *Bioinformatics* 25(9):1173-1177, 2009.
- A. Ben-Hur, C-S. Ong, S. Sonnenburg, B. Schoelkopf, and G. Raetsch. Support vector machines and kernels for computational biology. *PLoS Computational Biology* 4(10): e1000173, 2008.
- 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. Wadhwa, 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. Special issue for the NIPS workshop on bioinformatics.

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.

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 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.

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

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, 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.

Conferences A. Sokolov and A. Ben-Hur. Multi-view prediction of protein function. In: *ACM Conference on Bioinformatics, Computational Biology and Biomedicine 2011*.

M. Hamilton, A.S.N. Reddy, and A. Ben-Hur. Kernel methods for Calmodulin binding and binding site prediction. In: *ACM Conference on Bioinformatics, Computational Biology and Biomedicine 2011*.

A. Sokolov and A. Ben-Hur. GOstruct: utilizing the structure of the Gene Ontology for accurate prediction of protein function. In: *8th Annual International Conference on Computational System Bioinformatics (CSB2009)*, 2009. Acceptance rate: 20/86.

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. Acceptance rate: 56/426.

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. Acceptance rate: 207/822.

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. Acceptance rate: 207/822.

- 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. Acceptance rate: 13%.
- 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. Acceptance rate: 13%.
- 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.
- 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.
- Book chapters A. Ben-Hur and J. Weston. A User's Guide to Support Vector Machines. In *Biological Data Mining*. Oliviero Carugo and Frank Eisenhaber (eds.) Springer Protocols, 2009.
- 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.
- Refereed posters and extended abstracts T. Iverson, H. Iyer, and A. Ben-Hur. Predicting the Risk of Type 2 Diabetes Using Insurance Claims Data. NIPS 2010 workshop on predictive models in personalized medicine.
- Mark F. Rogers, Anireddy S.N. Reddy, and Asa Ben-Hur. SpliceGrapher: Predicting Splice Graphs from Diverse Evidence. Presented at the Rocky 2010 bioinformatics conference.
- Betty Eskow, Asa Ben-Hur, Hubert Yin, Debra Goldberg, and Deanne Sammond. Predicting flexible regions in protein structures. Poster presented at RosettaCon 2010 and the Rocky 2010 bioinformatics conference.
- M. Hamilton, A.S.N. Reddy and A. Ben-Hur. SVM methods for prediction of Calmodulin binders and binding sites. ISMB 2010.
- M. Hamilton and A. Ben-Hur. A structured outputs method for predicting protein binding sites. In: MLG-2008: 6th International Workshop on Mining and Learning with Graphs (ICML workshop).
- A. Sokolov and A. Ben-Hur. A structured outputs method for predicting protein function. In: MLG-2008: 6th International Workshop on Mining and Learning with Graphs (ICML workshop).

Other A. Ben-Hur. Support vector clustering. Scholarpedia, 3(6):5187.
http://www.scholarpedia.org/article/Support_vector_clustering.

INVITED TALKS

SpliceGrapher: detecting patterns of alternative splicing from RNA-seq data in the context of gene models and EST data. University of Wisconsin-Madison, October 2011, University of Colorado-Boulder, October 2011.

Prediction of Calmodulin binding and binding sites. Hebrew University, June 2010.

GOstruct: utilizing the structure of the Gene Ontology for accurate protein function prediction. Tel-Aviv University, June 2010; Technion, Israel Institute of Technology, June 2010; Iowa State University summer bioinformatics program, August 2009; Computational bioscience program, school of medicine at the University of Colorado Denver, July 2009.

A structured outputs method for predicting protein function. Machine learning in systems biology (MLSB) 2008 (presented by Artem Sokolov).

Machine learning for the analysis of DNA and proteins. Integrated systems biology seminar series. Colorado State University, October 2007.

Predicting Calmodulin-binding proteins. University of Wyoming, July 2007; Plant Super-group, Colorado State University, April 2007.

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

Kernel methods for predicting protein-protein interactions. University of Colorado, Denver, October 2005; Colorado State University: Department of Statistics, MCIN, Biochemistry Department, Department of Microbiology, Immunology, Pathology (2005/6).

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, Saarbrücken, July 2003
Max-Planck Institute for Biological Cybernetics, Tübingen, 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

Introduction to machine learning and support vector machines. Bay Area Python Interest Group, April 2003

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

PATENTS

A. Ben Hur, A. Elisseeff, O. Chapelle and J. Weston. Kernels and kernel methods for spectral data. US Patent Application 20050228591.

A. Ben Hur, A. Elisseeff and I. Guyon. Model selection for cluster data analysis. US Patent Application 20080140592.