

Asa Ben-Hur

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 2016 - **Professor**, *Department of Computer Science*, Colorado State University.
present
May 2011 - **Associate professor**, *Department of Computer Science*, Colorado State University.
2016
Aug 2005 - **Assistant professor**, *Department of Computer Science*, Colorado State University.
2011
2003 **Consultant**, *PathWork Informatics*.
Provided guidance on supervised-learning methods for analysis of gene expression data
Dec 2000 - **Researcher**, *BIOwulf Technologies*.
Feb 2001 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 - **Teaching and Research Assistant**, *Faculty of Industrial Engineering and Management*, Technion - Israel Institute of Technology.
Jun 2000
Oct 1993 - **Teaching Assistant**, *Racach Institute of Physics*, Hebrew University, Jerusalem.
Jun 1995

MEMBERSHIPS AND AFFILIATIONS

- 2021 - Senior member of the International Society for Computational Biology ISCB.
2021 - Member, program in Cell and Molecular Biology (CMB).

TEACHING

- DSCI 235 Data wrangling. Designed the course and taught spring 19 - spring 23.
CS 345 Machine learning foundations and practice. Designed the course and taught fall 20, fall 22. Course development was supported by a grant from the Colorado Department of Higher Education's OER Council. Open-access course materials are available at <https://github.com/asabenhur/CS345>.
CS 425 Introduction to bioinformatics algorithms. Taught fall 13, fall 21.
CS 192 Freshman seminar. Fall 2020.
CS 545 Machine Learning. Taught fall 13, fall 15, fall 16, fall 18.
CS 425 Introduction to bioinformatics algorithms. Taught fall 13, fall 21.
CS 440 Artificial intelligence. Taught fall 06, fall 09, fall 14, fall 19.

- CS 320 Algorithms: theory and practice. Taught spring 11, spring 12, fall 12.
- CS 220 Discrete structures and their applications. Taught fall 17 (two sections), fall 21.
- CS 200 Data structures. Taught spring 08, spring 09.
- CS 161 Object oriented problem solving. Taught fall 09, spring 13, spring 14, spring 15, spring 16.
- CS 160 Foundations in programming. Taught fall 08.
- CS 548 Bioinformatics algorithms (developed by Dr. Ben-Hur).
- CS 646 Machine learning in bioinformatics. An advanced graduate level course focused on applications of kernel methods to bioinformatics problems. No longer being offered, as the department has phased out 600 level courses.
- DSCI 510 Linux as a computational platform (1 credit). A one credit course designed to get life science students comfortable with using command-line tools and running jobs on a Linux machine. This is part of a series of modules offered by the GAUSSI program. Taught fall 15.
- DSCI 511 Genomics data analysis in Python (2 credits). A two credit course introducing biologists to Python programming through examples of genomic data analysis tasks. Taught fall 16, fall 17. A precursor to this course was taught spring 10 and spring 13 as CS580:Programming for the life sciences.
- DSCI 512 RNA-seq data analysis. This course is part of the sequence consisting of modules on Linux and Python. Designed in collaboration with Tai Montgomery (biology) and Erin Nishimura (biochemistry), and co-taught by Tai and Erin in fall 2016.

ADVISING

- Current students Michael Hamilton (PhD)
Don Neumann (PhD)
Saira Jabeen (PhD)
Ahmed Daoud (MS)
Soumyadip Roy (MS)
- Doctoral students Fahad Ullah. PhD May 2020.
Indika Kahanda. PhD May 2016.
graduated Fayyaz Minhas. PhD February 2014.
Mark Rogers. PhD August 2013.
Artem Sokolov. PhD August 2011.
Todd Iverson. PhD in Statistics June 2008. Co-advisor.
- Masters students Yashwanth Virupaksha MSc July 2021.
Mridula Bontha. MSc March 2021.
graduated Gareth Haladay. MSc Aug. 2019.
Swapnil Sneham. MSc Sept. 2017.
Alex Fout. MSc Sept 2017.
Kiley Graim. MSc April 2012.
Adam Labadorf. MSc April 2010.
Michael Hamilton. MSc April 2010.
- Project masters Sushant Patankar. MSc December 2021.
students

GRANTS AND RESEARCH FUNDING

- National Institute of Justice Expanding and validating microbiome database for estimating the postmortem interval. PI: Jessica L Metcalf. 15PNIJ-22-GG-04402-MUMU. \$834,503.
- NSF (PI) Deep learning tools for the identification of RNA modifications from direct RNA sequencing data. coPI: ASN Reddy. NSF-EAGER 1949036, \$300,000 to Colorado State University, 04/1/2020-03/31/2023.

- NSF (PI) DeepStruct: learning representations of protein 3-d structures and their interfaces using deep architectures. coPI: Charles Anderson (CS). NSF ABI, \$570,295 to Colorado State University, 2016 - 2020.
- NIH T-32 Pre-Doctoral Training in Quantitative Cell Molecular Biology at Colorado State University. PI: (co-PI) Carol Wilusz (Colorado State University). 07/01/19 – 06/30/24
- NSF-NRT GAUSSI: Generating, Analyzing, and Understanding Sensory and Sequencing Information—A (co-PI) Trans-Disciplinary Graduate Training Program in Biosensing and Computational Biology (award number 1450032). CSU was awarded a 2.9M grant from NSF to start a new interdisciplinary program on the interface of biology and computer science/engineering/statistics/math. This award comes from the NRT program which replaces the IGERT program. For more details on our GAUSSI program see <http://gaussi.colostate.edu>. The program awards 8 one-year NSF fellowships a year, and includes 0.5 month of summer salary for the co-PIs. PI is Tom Chen in ECE. Co-PIs are Drs. Ben-Hur and Willusz.
- DOE (co-PI) Global analysis of epigenetic regulation of gene expression in response to drought stress in sorghum. PI is A.S.N. Reddy in the biology department. DOE Plant Feedstock Genomics for Bioenergy program, \$1,385,763 to Colorado State University, 2013 - 2016.
- NIH (co-PI) The Determinants of Aggregation and Toxicity of Prion-like Domains PI is Eric Ross in the biochemistry department. NIH R01.
- NSF (PI) 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 - 2015.
- NSF (PI) 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 - 2013.
- Internal grants An accessible and interactive machine learning text. Asa Ben-Hur and Ross Beveridge were awarded \$4,000 from the Colorado OER Council to support the development of an Open Education Resource (OER) for our 300-level machine learning course (see <https://github.com/asabenhur/CS345>), 2020.
- Dean's Faculty Support Program. Seed grant for purchasing an Oxford Nanopore sequencing device. ASN Reddy and Asa Ben-Hur. \$6,000, 2018.
- course Asa Ben-Hur and Christina Boucher were awarded a provost course redesign grant to convert the department's graduate level bioinformatics course as an undergraduate course. \$5,000, 2013.
- redesign competition
- 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

- Workshops/ symposia Co-organizer with ASN Reddy of the workshop “Post-transcriptional Gene Regulation”, for the Plant and Animal Genome conference, 2015, 2016.
- Organized the Front Range Computational and Systems Biology 2015 symposium. See <http://combi.cs.colostate.edu/csb2015/>.
- Organizer of a bioinformatics workshop as part of the yearly Graybill conference, 2007. See <http://www.stat.colostate.edu/graybillconference2007/Workshop.htm>.
- Editorial boards Guest editor, Genome Biology special issue on deep learning in genomics, 2021. Editor, Frontier in Plant Science (2010-2017); PeerJ (2017-)

Program committees	ISMB 2005 - 2016, 2018-present RECOMB 2014; ECCB 2010, 2012, 2014, 2020; ACMBCB 2011-2016; IJCNN 2011, 2013; MLOSS 2013, 2015; 22nd IEEE International Conference on Tools with Artificial Intelligence 2010; AISTATS 2009; Automated Function Prediction (AFP) SIG at ISMB 2011,2012, 2013; Bio-KDD 2016,2019-2020; NIPS workshop on open source software 2008, 2013; 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	NeurIPS 2004 - 2010, 2019 - 2020; ICML 2019; RECOMB 2009,2011; Pacific Symposium on Biocomputing (PSB) 2016.
Journal reviewing	Reviewer for: Oxford Bioinformatics, PLoS Computational Biology, Journal of Bioinformatics and Computational Biology, BMC Bioinformatics, BMC Genomics, Genome Biology, Scientific Reports, The Plant Journal, 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.
Proposal reviewing and panels	NSF panels: 2010 (1), 2011 (2), 2012 (2), 2013 (1), 2014 (1), 2015 (1), 2016 (1), 2017 (1), 2018 (2), 2019 (1). Ad-hoc reviewer for NSF, ISF (Israeli Science Foundation), Canada Foundation for Innovation, Austrian Science Fund.
Invited workshop participant	Participated in NSF's iPlant cyberinfrastructure collaborative organizational conferences, March 2009, July 2009.

AWARDS

- 2019 CSU Interdisciplinary Scholarship Award. Jointly with Dr. ASN Reddy (Department of Biology) for our on-going work to understand the process of alternative splicing in plants.
- 2016 Graduate Student Council Advising and Mentorship Award.
- 2013-2014 College of Natural Sciences award for Faculty Excellence in Graduate Education and Mentoring.

UNIVERSITY SERVICE

Department committees	Undergraduate director 2017 - present. Awards committee 2006/7, 2009/10, Research committee 2007/8, Undergraduate committee 2008-14, faculty search committee 2012, 2013, 2017, 2018, Chair-search committee 2017, Graduate recruiting 2014 - 2017, GTA assignment committee 2015 - present, Executive committee 2016 - present. Research coordinator search committee, 2019. Chair, data science search committee, 2018-2019.
University committees	College Curriculum Committee 2018 - present. OVPR awards rating, 2021. College of Natural Sciences undergraduate fellowship rater, 2020-2021. Bioinformatics Center Search Committee 2006, Bioinformatics Center Steering Committee 2006 - 2010, ISTeC Education Advisory Committee 2009/10, Biology search committee 2012, MIP search committee 2013.
Workshops/symposia	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.

PUBLICATIONS

- Journals 2022 Don Neumann, ASN Reddy, and Asa Ben-Hur. RODAN: a fully convolutional architecture for basecalling nanopore RNA sequencing data. *BMC Bioinformatics* 23, 142, 2022.
- Don Neumann, Soumyadip Roy, Fayyaz Ul Amir Afsar Minhas, and Asa Ben-Hur. On the choice of negative examples for prediction of host-pathogen protein interactions. *Frontiers in Bioinformatics*, 2, 2022.
- Runxuan Zhang et al. A high-resolution single-molecule sequencing-based Arabidopsis transcriptome using novel methods of Iso-seq analysis. *Genome biology* 23(1), 1-37, 2022.

- 2021 Fahad Ullah and Asa Ben-Hur. A self-attention model for inferring cooperativity between regulatory features. *Nucleic Acids Research*, 2021. <https://doi.org/10.1093/nar/gkab349>
- Travis J Sanders, Fahad Ullah, Alexandra M Gehring, Brett W Burkhart, Robert L Vickerman, Sudili Fernando, Andrew F. Gardner, Asa Ben-Hur, and Thomas J Santangelo. Extended archaeal histone-based chromatin structure regulates global gene expression in *Thermococcus kodakarensis*. *Frontiers in microbiology* 12, 2021: 1071.
- 2020 Bryce C Asay, Blake Blue Edwards, Jenna Andrews, Michelle E Ramey, Jameson D Richard, Brendan K Podell, Juan F Muñoz Gutiérrez, Chad B Frank, Forgivemore Magunda, Gregory T Robertson, Michael Lyons, Asa Ben-Hur, and Anne J Lenaerts. Digital image analysis of heterogeneous tuberculosis pulmonary pathology in non-clinical animal models using deep convolutional neural networks. *Scientific Reports*, 10(1), 1-14, 2020.
- Salah E Abdel-Ghany, Fahad Ullah, Asa Ben-Hur, and A.S.N. Reddy Transcriptome analysis of drought-resistant and drought-sensitive sorghum (*Sorghum bicolor*) genotypes in response to PEG-induced drought stress. *International journal of molecular sciences*, 21(3), 772, 2020.
- A.S.N. Reddy, Jie Huang, Naeem H Syed, Asa Ben-Hur, Suomeng Dong, and Lianfeng Gu. Decoding co-/post-transcriptional complexities of plant transcriptomes and epitranscriptome using next-generation sequencing technologies. *Biochemical Society Transactions*, 48(6), 2399-2414, 2020.
- Mercedes Bentata, Guy Morgenstern, Yuval Nevo, Gillian Kay, Avital Granit Mizrahi, Mark Temper, Ofra Maimon, Liza Monas, Reham Basheer, Asa Ben-Hur, Tamar Peretz, and Maayan Salton. Splicing factor transcript abundance in saliva as a diagnostic tool for breast cancer. *Genes*, 11(8), 880, 2020.
- 2019 Naihui Zhou et al. The CAFA challenge reports improved protein function prediction and new functional annotations for hundreds of genes through experimental screens. *Genome Biology*, 20:244, 2019.
- 2018 Wajid Arshad Abbasi, Amina Asif, Asa Ben-Hur, and Fayyaz ul Amir Afsar Minhas. Learning protein binding affinity using privileged information. *BMC Bioinformatics*, 19:425, 2018.
- Fahad Ullah, Michael Hamilton, Anireddy SN Reddy, and Asa Ben-Hur Exploring the relationship between intron retention and chromatin accessibility in plants *BMC Genomics*, 19:21, 2018.
- Sergei A Filichkin, Mike Hamilton, Palitha D Dharmawardhana, Sunil K Singh, Christopher Sullivan, Asa Ben-Hur, Anireddy SN Reddy, and Pankaj Jaiswal. Abiotic stresses modulate landscape of poplar transcriptome via alternative splicing, differential intron retention, and isoform ratio switching. *Frontiers in Plant Science*, 9, 2018.
- 2017 Fayyaz ul Amir Afsar Minhas, Eric D. Ross and Asa Ben-Hur. Amino acid composition predicts prion activity. *PLoS Computational Biology* 13(4), e1005465, 2017.
- 2016 Salah E. Abdel-Ghany*, Michael Hamilton*, Jennifer L. Jacobi, Peter Ngam, Nicholas Devitt, Faye Schilkey, Asa Ben-Hur, and Anireddy SN Reddy. A survey of the sorghum transcriptome using single-molecule long reads. *Nature Communications* 7, 2016. (*Joint first authors).
- Yuxiang Jiang et al. An expanded evaluation of protein function prediction methods shows an improvement in accuracy. *Genome Biology* 17:184, 2016.
- Thomas Harrison, Dan Sloan, Jaime Ruiz, Asa Ben-Hur, and Christina Boucher. aPPRove: an HMM-based method for accurate prediction of RNA-pentatricopeptide repeat protein binding events. *PLOS ONE*, 11(8), 2016.
- 2015 Indika Kahanda, Chris Funk, Fahad Ullah, Karin Verspoor and Asa Ben-Hur. A close look at automated protein function prediction evaluation protocols. *GigaScience* 4:41, 2015.
- Indika Kahanda, Christopher Funk, Karin Verspoor, and Asa Ben-Hur. PHENOstruct: Prediction of human phenotype ontology terms using heterogeneous data sources. *F1000Research* 4(259), 2015.
- Christopher Funk, Indika Kahanda, Asa Ben-Hur and Karin Verspoor. Evaluating a variety of text-mined features for automatic protein function prediction with GOstruct. *Journal of Biomedical Semantics* 6:1, 2015.

- Upulee Kanewala, James Bieman, and Asa Ben-Hur. Predicting Metamorphic Relations for Testing Scientific Software: A Machine Learning Approach Using Graph Kernels. *Software Testing, Verification and Reliability*, 2015.
- Denghui Xing, Yajun Wang, Michael Hamilton, Asa Ben-Hur and Anireddy S.N. Reddy. Transcriptome-wide identification of RNA targets of Arabidopsis Serine/Arginine-Rich45 uncovers the unexpected roles of this RNA binding protein in RNA processing. *The Plant Cell*, 2015.
- 2014 Corey Broeckling, Fayyaz Afsar Minhas, Steffen Neumann, Asa Ben-Hur, and Jessica Prenni. RAMClust: a novel feature clustering method enables spectral-matching based annotation for metabolomics data. *Analytical Chemistry*, 86(14):6812-6817, 2014.
- F.A. Minhas, B. Geiss, and A. Ben-Hur. PAIRpred: Partner-specific prediction of interacting residues from sequence and structure, *PROTEINS: Structure, Function, and Bioinformatics*, 82:7, 2014.
- 2013 P. Radivojac et al. A large-scale evaluation of computational protein function prediction. *Nature Methods*, 10:221-227, 2013.
- A. Sokolov, C. Funk, K. Graim, K. Verspoor, and A. Ben-Hur. Combining heterogeneous data sources for accurate functional annotation of proteins. Automated Function Prediction Meeting Proceedings (ISMB 2011). *BMC Bioinformatics*, 14(Suppl 3), 2013.
- 2012 J. Thomas, S.G. Palusa, K.V. Prasad, G.S. Ali, G.K. Surabhi, A. Ben-Hur A, S.E. Abdel-Ghany, and A.S.N. Reddy. Identification of an intronic splicing regulatory element involved in autoregulation of alternative splicing of the SCL33 pre-mRNA. *Plant J.* 72(6): 935-946, 2012.
- Milana Frenkel-Morgenstern, Alessandro Gorohovski, Vincent Lacroix, Mark Rogers, Kristina Ibanez, Cesar Boullosa, Eduardo Andres Leon, Asa Ben-Hur and Alfonso Valencia. ChiTaRS: a database of human, mouse and fruit fly chimeric transcripts and RNA-sequencing data. *Nucleic Acids Research*, 2012.
- James A. Toombs, Michelina Petri, Kacy R. Paul, Grace Y. Kan, Asa Ben-Hur, and Eric D. Ross. De novo design of synthetic prion domains. *PNAS*, 2012.
- 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.
- 2011 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.
- 2010 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.
- 2009 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.
- 2008 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.

- 2007 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.
- 2006 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. Special issue for the NIPS workshop on bioinformatics.
- 2005 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.
- 2004 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.
- 2003 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.
- 2002 A. Ben-Hur, H.T. Siegelmann and S. Fishman. Complexity for continuous time systems. *Journal of Complexity* 18(1):51-86, 2002.
- 2001 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
- 2022 Adiba Yaseen, Imran Amin, Naeem Akhter, Asa Ben-Hur, Fayyaz Minhas. Insights into performance evaluation of compound-protein interaction prediction methods. *Bioinformatics* 38(Supplement₂), ii75-ii81, 2022. Special issue of ECCB 2022.
- 2019 Ameni Trabelsi, Mohamed Chaabane, Asa Ben-Hur. Comprehensive evaluation of deep learning architectures for prediction of DNA/RNA sequence binding specificities. *Bioinformatics*, 35:14, i269-i277, 2019 (ISMB 2019 special issue).
- 2018 Basir Shariat, Don Neumann, and Asa Ben-Hur. BLRM: A Basic Linear Ranking Model for protein interface prediction. In: *IEEE International Conference on Bioinformatics and Biomedicine (BIBM)*, 2018.
- 2017 Alex Fout, Jonathon Byrd, Basir Shariat, and Asa Ben-Hur. Protein interface prediction using graph convolutional networks. In: *Advances in Neural Information Processing Systems (NIPS)**, 2017.
- Indika Kahanda and Asa Ben-Hur. GOstruct 2.0: Automated protein function prediction for annotated proteins. In: *ACM Conference on Bioinformatics, Computational Biology and Biomedicine*, 2017.
- 2016 Cameron Tolooee, Asa Ben-Hur, and Sangmi Pallickara. Mendel: A Distributed Storage Framework for Similarity Searching over Sequencing Data. In: *The 30th IEEE International Parallel & Distributed Processing Symposium, 2016*.

- 2013 Mark F. Rogers, Christina Boucher, and Asa Ben-Hur. SpliceGrapherXT: From Splice Graphs to Transcripts Using RNA-Seq. In: *ACM Conference on Bioinformatics, Computational Biology and Biomedical Informatics (ACM-BCB)*, 2013.
- 2012 F.A. Minhas and A. Ben-Hur. Multiple instance learning of Calmodulin binding sites. *Bioinformatics* 28(18): i416-i422, 2012. Special issue for European Conference on Computational Biology 2012.
- 2011 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*.
- 2009 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.
- 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.
- 2003 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.
- 2002 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.
- 2001 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.
- 2000 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: *Data Mining Techniques for the Life Sciences*. Oliviero Carugo and Frank Eisenhaber (eds.), 2009.
- 2007 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.
- 2006 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.
- 2003 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.

- Preprints Fayyaz Minhas, Dimitris Grammatopoulos, Lawrence Young, Imran Amin, David Snead, Neil Anderson, Asa Ben-Hur, and Nasir Rajpoot. Improving COVID-19 Testing Efficiency using Guided Agglomerative Sampling. bioRxiv preprint, 2020.
- Fayyaz Minhas, Amina Asif, and Asa Ben-Hur. Ten ways to fool the masses with machine learning. arXiv preprint arXiv:1901.01686, 2019.
- Amina Asif, Wajid Arshad Abbasi, Farzeen Munir, Asa Ben-Hur, and Fayyaz ul Amir Afsar Minhas. pyLEMMINGS: Large margin multiple instance classification and ranking for bioinformatics applications. arXiv:1711.04913 [cs.LG], 2018.
- Other A. Ben-Hur. Support vector clustering. Scholarpedia, 3(6):5187. http://www.scholarpedia.org/article/Support_vector_clustering.

TALKS AND POSTERS

- Refereed Predicting differential intron retention with iDiffIR. Presented by Michael Hamilton at the Plant posters and and Animal Genome Conference, 2016.
- presentations
- GOstruct 2.0: Automated Protein Function Prediction for Annotated Proteins. Presented at Function SIG 2016, part of Intelligent Systems for Molecular Biology (ISMB) 2016.
- Alternative and differential polyadenylation detection from single molecule long sequencing reads. Presented by Michael Hamilton at the Integrative RNA Biology SIG 2016, part of Intelligent Systems for Molecular Biology (ISMB) 2016.
- Exploring the relationship between intron retention and DNase I hypersensitivity in plants. Poster presentation by Fahad Ullah at the Integrative RNA Biology SIG 2016, part of Intelligent Systems for Molecular Biology (ISMB) 2016.
- 2014 Corey Broeckling, Fayyaz-ul-Amir Afsar Minhas, Steffen Neumann, Asa Ben-Hur, and Jessica Prenni. ramclustR: post-XCMS feature clustering for data reduction and spectral matching-based annotation. In: ASMS2014 (American Association for Mass Spectrometry), 2014.
- Indika Kahanda, Christopher Funk, Fahad Ullah, Karin Verspoor and Asa Ben-Hur. PHENOS-struct: Prediction of human phenotype ontology using heterogeneous data sources. In AFP 2014 (workshop of ISMB).
- 2013 Fayyaz Minhas, Brian Geiss, and Asa Ben-Hur. PAIRpred: A large margin method for partner-specific prediction of protein interfaces. in: 11th Annual Rocky Mountain Bioinformatics Conference, 2013.
- RAMClust: an unsupervised feature clustering method for non-targeted metabolomics datasets", Corey Broeckling, Fayyaz A. Afsar, Asa Ben-Hur, Jessica Prenni, accepted for oral presentation in 61st American Society for Mass Spectrometry (ASMS) Conference, June 9 - 13, 2013, Minneapolis, USA.
- PAIRpred: Prediction of partner-specific interacting residues from sequence and structure, Fayyaz A. Afsar, Brian Geiss and Asa Ben-Hur, oral presentation in Seventh International Workshop on Machine Learning in Systems Biology (MLSB13), July 19-20, 2013, Berlin, Germany.
- Indika Kahanda and Asa Ben-Hur. Impact of Critical Edges on SVM-based Automated Function Prediction methods. In: Automated Function Prediction SIG Meeting July 20th 2013, Berlin, Germany ISMB/ECCB 2013.
- Michael Hamilton, ASN Reddy, and Asa Ben-Hur. Detection of Putative Splicing Regulatory Elements from the Analysis of Discriminative Motifs Across Plants. Post-transcriptional Gene reGulation in Plants July 25-26 Providence, Rhode island. A satellite meeting of Plant Biology 2013.
- Albaqami Mohammed, Hamilton Michael, Rogers Mark, Palusa Saiprasad G, Xing D, Ali Gul Shad, Ben-Hur Asa, and Reddy Anireddy S.N. .Global Analysis of Gene Expression and Alternative Splicing in a Splicing Regulator Mutant: Role of SR45 in Thermotolerance. Post-transcriptional Gene regulation in Plants. July 25-26 Providence, Rhode island. A satellite meeting of Plant Biology 2013.

- 2012 M. Hamilton, A.S.N. Reddy and A. Ben-Hur. Towards a plant splicing code: conserved splicing regulatory elements from SVM-weighted features. Alternative Splicing Special Interest Group, ISMB, Long Beach, CA, 2012.
- 2011 M.F. Rogers, ASN Reddy and A. Ben-Hur. SpliceGrapher: Predicting Splice Graphs from Diverse Evidence. ISMB 2011 Late Breaking Research, Vienna Austria, Jul 2011.
- 2010 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.
- 2008 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).

INVITED TALKS

- 2021 Graph Convolutional Networks for Analyzing Protein 3D Structures, 2nd Summer School on Machine Learning in Bioinformatics.
- 2019 Convolutional networks for sequence and structure. Machine Learning and Data Science Seminar, Icahn School of Medicine at Mount Sinai, 2019.
- 2015 Multiple instance learning for the detection of imprecisely defined protein sub-structures. CSU Department of Statistics, 2015.
Differential splicing and long read transcriptome assembly using iDiffIR and TAPIS. Presented at: Computational Biology: Data Analysis and Modeling in the Genomic Sciences. DOE PI meeting Tysons, Virginia, 2015.
Biology in the era of big data. RMACC High Performance Computing Symposium, 2015.
Partner-specific prediction of protein interfaces from sequence and structure: it takes two to tango. University of Indiana Bloomington computer science department colloquium. January 2015.
- 2013 Intron retention: tools and insights from RNA-seq data. Computational Bioscience Program, University of Colorado-Denver October 2013.
- 2011 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.
- 2010 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 Dolorado 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 Supergroup, 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.

Corey Broeckling, Jessica Prenni, Asa Ben-Hur, and Fayyaz Minhas. RAMClust - Clustering of Mass Spectrometry Features for Identification. U.S. Provisional Patent Application.