

# William Stafford Noble\*

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## Education

- 1991 B.S. with honors and distinction in Symbolic Systems, concentrating in Philosophical Foundations, Stanford University. Prof. Fred Dretske, advisor.
- 1996 M.S. in Computer Science, University of California, San Diego.
- 1998 Ph.D. in Computer Science and Cognitive Science, University of California, San Diego. Prof. Charles Elkan, advisor.

## Employment and Professional Appointments

- 1989 Center for Strategic Technology and Research, Andersen Consulting, Chicago, IL (internship).
- 1990-91 SRI International, Menlo Park, CA.
- 1991-93 United States Peace Corps Volunteer, Lesotho, southern Africa.
- 1994 Entropic Research Laboratory, Palo Alto, CA.
- 1998-99 Postdoctoral fellow, University of California, Santa Cruz. Prof. David Haussler, advisor.
- 1999-02 Assistant Professor, Department of Computer Science, Columbia University, with joint appointment at the Columbia Genome Center.
- 2002-06 Assistant Professor, Department of Genome Sciences, University of Washington
- 2002-06 Adjunct Assistant Professor, Department of Computer Science and Engineering, University of Washington
- 2005-06 Adjunct Assistant Professor, Department of Medicine, University of Washington
- 2006-11 Associate Professor, Department of Genome Sciences, University of Washington
- 2006-11 Adjunct Associate Professor, Department of Computer Science and Engineering, University of Washington
- 2006-11 Adjunct Associate Professor, Department of Medicine, University of Washington
- 2013-2020 Director, Computational Molecular Biology Program, University of Washington
- 2011- Professor, Department of Genome Sciences, University of Washington
- 2011- Adjunct Professor, Department of Computer Science and Engineering, University of Washington
- 2011- Adjunct Professor, Department of Medicine, University of Washington
- 2012- Adjunct Professor, Department of Biomedical Informatics and Medical Education, University of Washington
- 2014- Senior Data Science Fellow, University of Washington eScience Institute

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\*Formerly William Noble Grundy: see <http://noble.gs.washington.edu/~noble/name-change.html>

## Awards

1987	National Merit Scholar
1987	David Starr Jordan Scholar, Stanford University
1991	Phi Beta Kappa, Stanford University
1994–97	Fellow, National Defense Science and Engineering Graduate Fellowship Program
1998–99	Fellow, Alfred P. Sloan Foundation and U.S. Department of Energy Postdoctoral Fellowships in Computational Molecular Biology
2000–02	Pharmaceutical Research and Manufacturers of America Foundation Faculty Development Award in Bioinformatics
2001–06	National Science Foundation CAREER Award
2001–05	Research Fellow, Alfred P. Sloan Foundation
2010	University of Washington Postdoc Mentor of the Year
2013	Fulbright Specialist Grant, African Institute for Mathematical Sciences, Muizenberg, South Africa
2015-6, 18-9	Clarivate Analytics list of “Highly cited researchers”
2017	Fellow, International Society for Computational Biology
2018–19	Chair, BDMA review panel, National Institutes of Health
2019	Innovator Award, International Society for Computational Biology

## Professional Activities

**Board memberships** Member, Board of Directors, International Society for Computational Biology, 2008–2011.

### Editorial boards

- Guest co-editor, Special issue on Machine Learning for Bioinformatics, *IEEE Transactions on Computational Biology and Bioinformatics*, 2004.
- *Journal of Bioinformatics and Computational Biology*, 2004–2020.
- *IEEE Transactions on Computational Biology and Bioinformatics*, 2005–2020.
- *PLOS Computational Biology*, Associate Editor, 2008–2012; Deputy Editor, 2012–present.
- *Quantitative Biology*, 2012–present.
- *Rapid Communications in Mass Spectrometry*, Editorial Advisory Board, 2018–present.
- *BMC Bioinformatics*, Associate Editor, 2018–present.

### Scientific advisory boards

- X-Mine, Inc., Hayward, CA, 2000–2002.
- Bioinformatics of Mammalian Gene Expression project, Canada’s Michael Smith Genome Centre, Vancouver, BC, Canada, 2004–2006.
- Center for Functional Genomics and HCV-Associated Liver Disease, University of Washington, 2006–2007.
- National Center for Systems Biology, Institute for Systems Biology, Seattle, WA, 2006–2009.
- DNAnexus, Mountain View, CA, 2012–present.

**Review panels** National Institutes of Health:

- Special Bioinformatics Study Section, March 12, 2003
- Special Bioinformatics Study Section, June 30, 2004
- Bioengineering Research Partnership Study Section, 13 Dec 2004
- Special Bioinformatics Study Section, March 17–18, 2005
- Bioengineering Sciences and Technologies special emphasis panel on “Microarray data analysis, data integration and data exploration,” August 5, 2005
- National Cancer Institute special emphasis panel on “Advanced proteomic platforms and computation science for the NCI clinical proteomic technologies initiative,” June 26–27, 2006
- National Cancer Institute special emphasis panel on “Advanced Genomic Data Analysis and Visualization Methods for TCGA Data,” April 2, 2008
- Topics in Biomedical Engineering study section, February 14, 2011.
- GCAT special emphasis panel, July 5, 2011.
- HLBP1 Workgroup, January 11, 2012.
- NIDDK—Collaborative Interdisciplinary Team Science Research, February 19, 2013.
- Biodata Management and Analysis study section, Jan 2007, Oct 2008, Feb 2009, Oct 2011, Feb 2012, Oct 2012, Jun 2013
- Member, Biodata Management and Analysis study section, July, 2014–Sep, 2017.
- Chair, Biodata Management and Analysis study section, October, 2017–Jun, 2019.

Panelist, National Science Foundation

- Information Technology Research at the Intersection of Biology and Informatics, 2001.
- Advances in Biological Informatics, Division of Biological Infrastructure, 2015.

**Program committee memberships** Machine learning and artificial intelligence conferences:

- American Association for Artificial Intelligence 1998, 2016–2020 (Senior PC member for 2018).
- Knowledge Discovery in Databases 2000, 2003
- Biological Knowledge Discovery in Databases 2002, 2013
- Conference on Learning Theory 2003
- International Conference on Machine Learning 2004, 2008, 2013–2016, 2019–2020.
- International Joint Conference on Artificial Intelligence 2009
- Neural Information Processing Systems, 2003–2016, 2018–2020
- Neural Information Processing Systems Workshop on Machine Learning Open Source Software 2006, 2008
- Neural Information Processing Systems Workshop on Mining and Learning with Graphs 2008, 2009

- Neural Information Processing Systems Workshop on Machine Learning in Computational Biology 2005–2017, 2019–2020
- Machine Learning in Systems Biology 2009
- Uncertainty in Artificial Intelligence 2013–2016
- AISTATS 2017–2020
- International Conference on Learning Representations 2019–2020

Bioinformatics conferences:

- Intelligent Systems for Molecular Biology 2002–2009, 2011–2016, 2018–2020.
- Research in Computational Biology (RECOMB) 2004, 2007–2015, 2017–2021
- RECOMB Computational Proteomics Satellite 2007, 2010–2012
- RECOMB Massively Parallel Sequencing Satellite, 2012, 2014
- Genome Informatics Workshop 2005–2009
- European Conference on Computational Biology 2005
- Bioinformatics Research and Development (BIRD) 2007
- Computational Systems Biology 2009
- ACM Conference on Bioinformatics, Computational Biology and Biomedicine (ACM-BCB) 2011, 2015, 2016, 2020.
- ASE/IEEE International Conference on BioMedical Computing 2012–2013
- BioKDD 2013, 2016, 2019–2020
- ISCB Africa ASBCB 2013
- High Throughput Sequencing Conference (HitSeq) 2014–2015
- Workshop on Algorithms in Bioinformatics 2015–2016, 2019–2020.
- Workshop on Machine Learning in Systems Biology 2016
- International Conference on Algorithms for Computational Biology 2017–2019
- IEEE International Conference on BioInformatics and BioEngineering (BIBE) 2018
- RECOMB/ISCB Conference on Regulatory and Systems Genomics with DREAM Challenges 2020

Area chair, Bioinformatics and Kernel Methods, Twenty-first Annual Conference on Neural Information Processing Systems, Whistler, BC, Dec 3–8, 2007.

Co-chair, Machine Learning in Computational Biology Workshop, Twentieth Annual Conference on Neural Information Processing Systems, Whistler, BC, 2005–2008.

Member, College of CSR Reviewers, National Institutes of Health. March, 2010–present.

Area chair, Bioinformatics and Kernel Methods, Twenty-fourth Annual Conference on Neural Information Processing Systems, Whistler, BC, Dec 6–11, 2010.

Co-chair, Workshop on the Structure and Function of Chromatin and Chromosomes, Pacific Symposium on Biocomputing, The Big Island of Hawaii, January 3–7, 2012.

Co-chair, Special Session on Computational Methods for Elucidating Nuclear Structure and Dynamics, Intelligent Systems for Molecular Biology Conference, Long Beach, CA, USA, July 15–17, 2012.

Co-chair, Epigenomics session, Pacific Symposium on Biocomputing, The Big Island of Hawaii, January 3–7, 2013.

Co-chair, Mass Spectrometry & Proteomics Track, Intelligent Systems for Molecular Biology Conference, July 11–15, 2014.

Co-chair, Bioinformatics Group, American Society for Mass Spectrometry Annual Conferences, 2019 and 2020.

### Journal referee

	2015	2016	2017	2018	2019
<i>Analytical Chemistry</i>	2				
<i>Bioinformatics</i>	2	1	3	3	1
<i>Chromosome Research</i>		1			
<i>Cell Systems</i>				1	
<i>eLife</i>		1	1		
<i>Epigenomics &amp; Chromatin</i>					1
<i>FEBS Letters</i>	1				
<i>Genome Research</i>	4	4	1	2	2
<i>Genes</i>					1
<i>G3</i>				1	
<i>Journal of Proteome Research</i>	1	2	1	3	1
<i>Molecular &amp; Cellular Proteomics</i>	1				
<i>Nucleic Acids Research</i>		1			
<i>Nature</i>	1	1	4	1	4
<i>Nature Biotechnology</i>	1	1	1	1	1
<i>Nature Communications</i>	1	2	1	2	
<i>Nature Genetics</i>				1	1
<i>Nature Materials</i>				1	
<i>Nature Methods</i>	2	1		1	
<i>Nature Reviews Genetics</i>		1			
<i>Nature Structural Biology</i>	1				
<i>Nature Structural Molecular Biology</i>		1			
<i>PLOS One</i>		1			
<i>PLOS Computational Biology</i>				1	1
<i>PNAS</i>		2	1		
<i>Proteomics</i>		1			
<i>Science</i>			1	5	
<i>Scientific Reports</i>					1
Tenure & promotion review	5	7	4	7	3
Total	22	28	18	28	17

**Committee memberships** Member, Public Affairs and Policies Committee, International Society for Computational Biology, 2003–present.

Audit Committee, International Society for Computational Biology, 2012.

Computational biology search committee, Fred Hutchinson Cancer Research Center, 2010–2011.

Faculty search committee, Department of Biochemistry, computational biology and protein design, 2013–2014, 2014–2015.

### Refereed publications

Underlined names are lab members.

- (1) **WN Grundy**, TL Bailey and CP Elkan. "ParaMEME: a parallel implementation and a web interface for a DNA and protein motif discovery tool." *Computer Applications in the Biosciences*. 12(4):303-310, 1996.
- (2) J Batali and **WN Grundy**. "Modeling the evolution of motivation." *Evolutionary Computation*. 4(3):235-270, 1997.
- (3) **WN Grundy**, TL Bailey, CP Elkan and ME Baker. "Hidden Markov model analysis of motifs in steroid dehydrogenases and their homologs." *Biochemical and Biophysical Research Communications*. 231(3):760-766, 1997.
- (4) **WN Grundy**, TL Bailey, CP Elkan and ME Baker. "Meta-MEME: Motif-based hidden Markov models of protein families." *Computer Applications in the Biosciences*. 13(4):397-406, 1997.
- (5) ME Baker, **WN Grundy** and CP Elkan. "Spinach CSP41, an mRNA-binding protein and ribonuclease, is homologous to nucleotide-sugar epimerases and hydroxysteroid dehydrogenases." *Biochemical and Biophysical Research Communications*. 248(2):250-254, 1998.
- (6) **WN Grundy**. "Homology detection via Family Pairwise Search." *Journal of Computational Biology*. 5(3):479-492, 1998.
- (7) **WN Grundy**. "Family-based homology detection via pairwise sequence comparison." *Proceedings of the Second Annual International Conference on Computational Molecular Biology*, March 22-25, 1998. pp. 94-100.
- (8) ME Baker, **WN Grundy** and CP Elkan. "A common ancestor for a subunit in the mitochondrial proton-translocating NADH:ubiquinone oxidoreductase (complex I) and short-chain dehydrogenases/reductases." *Cellular and Molecular Life Sciences*. 55(3):450-455, 1999.
- (9) **WN Grundy** and TL Bailey. "Family Pairwise Search with embedded motif models." *Bioinformatics*. 15(6):463-470, 1999.
- (10) **WN Grundy** and GJP Naylor. "Phylogenetic inference from conserved sites alignments." *Journal of Experimental Zoology*. 285(2):128-139, 1999.
- (11) TL Bailey and **WN Grundy**. "Classifying proteins by family using the product of correlated p-values." *Proceedings of the Third International Conference on Computational Molecular Biology*, April 11-14, 1999. pp. 10-14.
- (12) MPS Brown, **WN Grundy**, D Lin, N Cristianini, C Sugnet, TS Furey, M Ares, Jr. and D Haussler. "Knowledge-based analysis of microarray gene expression data by using support vector machines." *Proceedings of the National Academy of Science*. 97(1):262-267, 2000.
- (13) E Eskin, **WN Grundy** and Y Singer. "Protein family classification using sparse markov transducers." *Proceedings of the Eighth International Conference on Intelligent Systems for Molecular Biology*, August 20-23, 2000. pp. 134-145.
- (14) P Pavlidis, TS Furey, M Liberto, D Haussler and **WN Grundy**. "Promoter region-based classification of genes." *Proceedings of the Pacific Symposium on Biocomputing*, January 3-7, 2001. pp. 151-163.
- (15) P Pavlidis, J Weston, J Cai and **WN Grundy**. "Gene functional classification from heterogeneous data." *Proceedings of the Fifth International Conference on Computational Molecular Biology*, April 21-24, 2001. pp. 242-248.
- (16) E Eskin, **WN Grundy** and Y Singer. "Using mixtures of common ancestors for estimating the probabilities of discrete events in biological sequences." *Bioinformatics (Proceedings of the ISMB)*. 17(Suppl 1):S64-73, 2001.

- (17) P Pavlidis, C Tang and **WS Noble**. “Classification of genes using probabilistic models of microarray expression profiles.” *Proceedings of BIOKDD 2001: Workshop on Data Mining in Bioinformatics*. August 26, 2001. pp. 15-21.
- (18) RA Muhle, P Pavlidis, **WN Grundy** and E Hirsch. “A high throughput study of gene expression in preterm labor using a subtractive microarray approach.” *American Journal of Obstetrics and Gynecology*. 185(3):716-24, 2001.
- (19) P Pavlidis and **WS Noble**. “Analysis of strain and regional variation in gene expression in mouse brain.” *Genome Biology*. 2(10): research0042.1-0042.15, 2001.
- (20) P Pavlidis, J Weston, J Cai and **WS Noble**. “Learning gene functional classifications from multiple data types.” *Journal of Computational Biology*. 9(2):401-411, 2002.
- (21) C Leslie, E Eskin and **WS Noble**. “The spectrum kernel: An SVM-string kernel for protein classification.” *Proceedings of the Pacific Symposium on Biocomputing*, January 2-7, 2002. pp. 564–575.
- (22) P Pavlidis, DP Lewis and **WS Noble**. “Exploring gene expression data with class scores.” *Proceedings of the Pacific Symposium on Biocomputing*, January 2-7, 2002. pp. 474–485.
- (23) E Eskin, **WS Noble** and Y Singer. “Using substitution matrices to estimate probability distributions for biological sequences.” *Journal of Computational Biology*. 9(6):775-791, 2002.
- (24) L Liao and **WS Noble**. “Combining pairwise sequence similarity and support vector machines for remote protein homology detection.” *Proceedings of the Sixth International Conference on Computational Molecular Biology*, April 18-21, 2002. pp. 225–232.
- (25) B Schölkopf, J Weston, E Eskin, C Leslie and **WS Noble**. “A kernel approach for learning from almost orthogonal patterns.” *Proceedings of the 13th European Conference on Machine Learning*, August 19-23, 2002. pp. 511-528.
- (26) P Pavlidis and **WS Noble**. “Matrix2png: A utility for visualizing matrix data.” *Bioinformatics*. 19(2):295-296, 2003.
- (27) NH Segal, P Pavlidis, **WS Noble**, CR Antonescu, A Viale, UV Wesley, K Busam, H Gallardo, D DeSantis, MF Brennan, C Cordon-Cardo, JD Wolchok and AN Houghton. “Classification of clear cell sarcoma as melanoma of soft parts by genomic profiling.” *Journal of Clinical Oncology*. 21:1775–1781, 2003.
- (28) DC Anderson, W Li, DG Payan and **WS Noble**. “A new algorithm for the evaluation of shotgun peptide sequencing in proteomics: support vector machine classification of peptide MS/MS spectra and SEQUEST scores” *Journal of Proteome Research*. 2(2):137–146, 2003.
- (29) NH Segal, P Pavlidis, CR Antonescu, RG Maki, **WS Noble**, JM Woodruff, JJ Lewis, MF Brennan, AN Houghton and C Cordon-Cardo. “Classification and subtype prediction of soft tissue sarcoma by functional genomics and support vector machine analysis.” *American Journal of Pathology*. 169:691-700, 2003.
- (30) T Gururaja, W Li, **WS Noble**, DG Payan and DC Anderson. “Multiple functional categories of proteins identified in an *in vitro* cellular ubiquitin affinity extract using shotgun peptide sequencing.” *Journal of Proteome Research*. 2:383–393, 2003.
- (31) P Pavlidis, Q Li and **WS Noble**. “The effect of replication on gene expression microarray experiments.” *Bioinformatics*. 19(13):1620-1627, 2003.
- (32) J Qin, DP Lewis and **WS Noble**. “Kernel hierarchical clustering of microarray gene expression data.” *Bioinformatics*. 19:2097-2014, 2003.
- (33) E Eskin, **WS Noble** and Y Singer. “Protein family classification using sparse Markov transducers.” *Journal of Computational Biology*. 10(2):187–213, 2003.

- (34) L Liao and **WS Noble**. “Combining pairwise sequence similarity and support vector machines for detecting remote protein evolutionary and structural relationships.” *Journal of Computational Biology*. 10(6):857–868, 2003.
- (35) C Leslie, E Eskin, J Weston and **WS Noble**. “Mismatch string kernels for SVM protein classification.” *Advances in Neural Information Processing Systems 15*, 2003.
- (36) TL Bailey and **WS Noble**. “Searching for statistically significant regulatory modules.” *Bioinformatics (Proceedings of the European Conference on Computational Biology)*. 19(Suppl. 2):ii16–ii25, 2003.
- (37) SM Gomez, **WS Noble** and A Rzhetsky. “Learning to predict protein-protein interactions from protein sequences.” *Bioinformatics (Proceedings of the Georgia Tech International Conference on Bioinformatics)*. 19:1875–1881, 2003.
- (38) J Weston, A Elisseeff, D Zhou, CS Leslie and **WS Noble**. “Protein ranking: From local to global structure in the protein similarity network.” *Proceedings of the National Academy of Science*. 101(17):6559–6563, 2004.
- (39) C Leslie, E Eskin, A Cohen, J Weston and **WS Noble**. “Mismatch string kernels for discriminative protein classification.” *Bioinformatics*. 20(4):467–476, 2004.
- (40) P Pavlidis, I Wapinski and **WS Noble**. “Support vector machine classification on the web.” *Bioinformatics*. 20(4):586–587, 2004.
- (41) W Wu and **WS Noble**. “Genomic data visualization on the web.” *Bioinformatics*. 20(11):1804–1805, 2004.
- (42) K Tsuda and **WS Noble**. “Learning kernels from biological networks by maximizing entropy.” *Bioinformatics (Proceedings of the Intelligent Systems for Molecular Biology Conference)*. 20(Suppl. 1):i326–i333, 2004.
- (43) J Weston, C Leslie, D Zhou and **WS Noble**. “Semi-supervised protein classification using cluster kernels.” *Advances in Neural Information Processing Systems 16*, 2004. pp. 595–602.
- (44) GRG Lanckriet, M Deng, N Cristianini, MI Jordan and **WS Noble**. “Kernel-based data fusion and its application to protein function prediction in yeast.” *Proceedings of the Pacific Symposium on Biocomputing*, January 3-8, 2004. pp. 300-311.
- (45) GRG Lanckriet, T De Bie, N Cristianini, MI Jordan and **WS Noble**. “A statistical framework for genomic data fusion.” *Bioinformatics*. 20(16):2626-2635, 2004.
- (46) H Lu, W Li, **WS Noble**, DG Payan and DC Anderson. “Riboproteomics of the hepatitis C virus internal ribosomal entry site.” *Journal of Proteome Research* 3(5):949–57, 2004.
- (47) E Feingold, PJ Good, . . . , **WS Noble**, . . . , FS Collins. “The ENCODE (ENCyclopedia Of DNA Elements) Project.” *Science*. 306:636–640, 2004.
- (48) M Tompa, N Li, TL Bailey, GM Church, B De Moor, E Eskin, AV Favorov, MC Frith, Y Fu, WJ Kent, VJ Makeev, AA Mironov, **WS Noble**, G Pavesi, G Pesole, M Régnier, N Simonis, S Sinha, G Thijs, J van Helden, M Vandenbogaert, Z Weng, C Workman, C Ye and Z Zhu. “Assessing computational tools for the discovery of transcription factor binding sites.” *Nature Biotechnology*. 23(1):137–144, 2005.
- (49) A Ben-Hur and **WS Noble**. “Kernel methods for predicting protein-protein interactions.” *Bioinformatics (Proceedings of the Intelligent Systems for Molecular Biology Conference)*. 21(Suppl 1):i38–i46, 2005.
- (50) **WS Noble**, S Kuehn, RE Thurman, R Humbert, JC Wallace, M Yu, M Hawrylycz and JA Stamatoyannopoulos. “Predicting the *in vivo* signature of human gene regulatory sequences.” *Bioinformatics (Proceedings of the Intelligent Systems for Molecular Biology Conference)*. 21(Suppl 1):i338–i343, 2005.



- (51) J Weston, C Leslie, E Ie, D Zhou, A Eliseeff and **WS Noble**. “Semi-supervised protein classification using cluster kernels.” *Bioinformatics*. 21(15):3241–3247, 2005.
- (52) W Sheffler, E Upfal, J Sedivy and **WS Noble**. “A learned comparative expression measure for Affymetrix GeneChip DNA microarrays.” *Proceedings of the Computational Systems Bioinformatics Conference*, August 8-11, 2005, Stanford, CA. pp. 144-154.
- (53) T Mann, R Humbert, JA Stamatoyannopoulos and **WS Noble**. “Automated validation of polymerase chain reactions using amplicon melting curves.” *Proceedings of the Computational Systems Bioinformatics Conference*, August 8-11, 2005, Stanford, CA. pp. 377–385.
- (54) AA Klammer, CW Wu, MJ MacCoss, **WS Noble**. “Peptide charge state determination for low-resolution tandem mass spectra.” *Proceedings of the Computational Systems Bioinformatics Conference*, August 8-11, 2005, Stanford, CA. pp. 175–185.
- (55) E Ie, J Weston, **WS Noble** and C Leslie. “Adaptive codes for multi-class protein classification.” *Proceedings of the International Conference on Machine Learning*, August 7-11, 2005, Bonn, Germany.
- (56) R Kuang, J Weston, **WS Noble** and C Leslie. “Motif-based protein ranking by network propagation.” *Bioinformatics*. 21(19):3711–3718, 2005.
- (57) JP Miller, RS Lo, A Ben-Hur, C Desmarais, I Stagljär, **WS Noble** and S Fields. “Large-scale identification of yeast integral membrane protein interactions.” *Proceedings of the National Academy of Science*. 102(34):12123–12128, 2005.
- (58) J-P Vert, RE Thurman and **WS Noble**. “Kernels for gene regulatory regions.” *Advances in Neural Information Processing Systems 19*. 2006.
- (59) J Weston, R Kuang, C Leslie and **WS Noble**. “Protein ranking by semi-supervised network propagation.” *BMC Bioinformatics*. 7(Suppl 1):S10, 2006.
- (60) A Ben-Hur and **WS Noble**. “Choosing negative examples for the prediction of protein-protein interactions.” *BMC Bioinformatics*. 7(Suppl 1):S2, 2006.
- (61) DP Lewis, T Jebara and **WS Noble**. “Nonstationary kernel combination.” *Proceedings of the International Conference on Machine Learning*, June 25-29, 2006, Pittsburgh, PA.
- (62) T Mann and **WS Noble**. “Efficient identification of DNA binding partners in a sequence database.” *Bioinformatics (Proceedings of the Intelligent Systems for Molecular Biology Conference)*. 22(14):e350–e358, 2006.
- (63) PJ Sabo, MS Kuehn, RE Thurman, B Johnson, EM Johnson, H Cao, M Yu, J Goldy, E Rosenzweig, J Goldy, A Haydock, M Weaver, A Shafer, K Lee, F Neri, R Humbert, MA Singer, TA Richmond, MO Dorschner, M McArthur, M Hawrylycz, RD Green, PA Navas, **WS Noble** and JA Stamatoyannopoulos. “Genome-scale mapping of DNase I sensitivity *in vivo* using tiling DNA microarrays.” *Nature Methods*. 3(7):511–518, 2006.
- (64) BE Frewen, GE Merrihew, **WS Noble** and MJ MacCoss. “Analysis of peptide MS/MS spectra from large-scale proteomics experiments using spectrum libraries.” *Analytical Chemistry*. 78(16):5678–5684, 2006.
- (65) T Pramila, W Wu, **WS Noble** and LL Breeden. “The Forkhead transcription factor Hcm1 regulates chromosome segregation genes and fills the S phase gap in the transcriptional circuitry of the cell cycle.” *Genes and Development*. 20(16):2266–2278, 2006.
- (66) T Mann, R Humbert, JA Stamatoyannopoulos and **WS Noble**. “Automated validation of polymerase chain reactions using amplicon melting curves.” *Journal of Bioinformatics and Computational Biology*. 22(14):350–358, 2006.

- (67) DP Lewis, T Jebara and **WS Noble**. “Support vector machine learning from heterogeneous data: an empirical analysis using protein sequence and structure.” *Bioinformatics*. 22(22):2753–2760, 2006.
- (68) S Gupta, JA Stamatoyannopoulos, TL Bailey and **WS Noble**. “Quantifying similarity between motifs.” *Genome Biology*. 8:R24, 2007.
- (69) AA Klammer, X Yi, MJ MacCoss, and **WS Noble**. “Improving tandem mass spectrum identification using peptide retention time prediction across diverse chromatography conditions.” *Analytical Chemistry*. 79(160):6111–6118, 2007.
- (70) J Qiu, M Hue, A Ben-Hur, J-P Vert and **WS Noble**. “A structural alignment kernel for protein structures.” *Bioinformatics*. 23(9):1090–1098, 2007.
- (71) AA Klammer, X Yi, MJ MacCoss and **WS Noble**. “Peptide retention time prediction yields improved tandem mass spectrum identification for diverse chromatography conditions.” *Proceedings of the International on Research in Computational Biology (RECOMB)*. April 21–25, 2007. pp. 459–472.
- (72) The ENCODE Project Consortium. “Identification and analysis of functional elements in 1% of the human genome by the ENCODE project.” *Nature*. 447:779–816, 2007.
- (73) RE Thurman, N Day, **WS Noble** and JA Stamatoyannopoulos. “Identification of higher-order functional domains in the human ENCODE regions.” *Genome Research*. 17(6):917–927, 2007.
- (74) JH Dennis, H-Y Fan, SM Reynolds, G Yuan, J Meldrim, DJ Richter, DG Peterson, OJ Rando, **WS Noble** and RE Kingston. “Independent and complementary methods for large-scale structural analysis of mammalian chromatin.” *Genome Research*. 17(6):928–939, 2007.
- (75) I Melvin, E Ie, J Weston, **WS Noble** and C Leslie. “Multi-class protein classification using adaptive codes.” *Journal of Machine Learning Research*. 8:1557–1581, 2007.
- (76) N Day, A Hemmaplardh, RE Thurman, JA Stamatoyannopoulos and **WS Noble**. “Unsupervised segmentation of continuous genomic data.” *Bioinformatics*. 23(11):1424–1426, 2007.
- (77) S Asthana, **WS Noble**, G Kryukov, CE Grant, S Sunyaev and JA Stamatoyannopoulos. “Widely distributed non-coding selection in the human genome.” *Proceedings of the National Academy of Science*. 104(30):12410–12415, 2007.
- (78) H Peckham, RE Thurman, Y Fu, JA Stamatoyannopoulos, **WS Noble**, K Struhl and Z Weng. “Nucleosome positioning signals in genomic DNA.” *Genome Research*. 17(8):1170–1177, 2007.
- (79) AA Klammer, X Yi, MJ MacCoss and **WS Noble**. “Peptide retention time prediction yields improved tandem mass spectrum identification for diverse chromatography conditions.” *Analytical Chemistry*. 79(16):6111–6118, 2007.
- (80) L Käll, J Canterbury, J Weston, **WS Noble** and MJ MacCoss. “Semi-supervised learning for peptide identification from shotgun proteomics datasets.” *Nature Methods*. 4(11):923–925, 2007.
- (81) I Melvin, E Ie, R Kuang, J Weston, **WS Noble** and C Leslie. “SVM-fold: a tool for discriminative multi-class protein fold and superfamily recognition.” *BMC Bioinformatics*. 8(Suppl 4):S2, 2007.
- (82) JP Vert, J Qiu and **WS Noble**. “A new pairwise kernel for biological network inference with support vector machines.” *BMC Bioinformatics*. 8(Suppl. 10):S8, 2007.
- (83) J Qiu, W Sheffler, D Baker and **WS Noble**. “Ranking predicted protein structures with support vector regression.” *Proteins: Structure, Function, and Bioinformatics*. 71(3):1175–1182, 2007.
- (84) RE Thurman, **WS Noble** and JA Stamatoyannopoulos. “Multi-scale correlations in continuous genomic data.” *Proceedings of the Pacific Symposium on Biocomputing*. January 4–8, 2008, pp. 201–215.
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### Software

All of the software listed below is available with source code at the URLs specified. When indicated, some of the software is augmented with a free web server. Dates indicate release dates of the software, with multiple years indicating multiple released versions.

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- (16) A Klammer, C Park, B Frewen, J Eng, MJ MacCoss and **WS Noble**. CRUX analyzes shotgun proteomics tandem mass spectra, associating peptides with observed spectra. <http://crux.ms>. 2008–present.
- (17) SM Reynolds, L Käll, ME Riffle, JA Bilmes and **WS Noble**. PHILIUS predicts protein transmembrane topology and signal peptides. Source code is available at <http://noble.gs.washington.edu/proj/philius>, and predictions and a web server are available via the Yeast Resource Center (<http://www.yeastrc.org/philius>). 2008.
- (18) L Käll, J Storey and **WS Noble**. QUALITY performs nonparametric estimation of posterior error probabilities. <http://noble.gs.washington.edu/proj/qvality>. 2008.
- (19) M Hoffman, O Buske and **WS Noble**. GENOMEDATA provides efficient storage of multiple tracks of numeric data anchored to a genome. <https://hoffmanlab.org/proj/genomedata>. 2010–present.
- (20) M Hoffman, O Buske, J Bilmes and **WS Noble**. SEGWAY performs simultaneous segmentation and clustering of genomic signal data such as those from CHIP-seq and DNase-seq, finding recurring patterns in these data. <https://segway.hoffmanlab.org>. 2010–present.
- (21) O Buske, M Hoffman and **WS Noble**. SEGTOOLS provides exploratory data analysis on genomic segmentations. <https://hoffmanlab.org/proj/segtools>. 2010–present.
- (22) O Serang and **WS Noble**. FIDO uses a probability model to rank proteins according to the posterior probability of their presence in a complex mixture, based on evidence derived from a shotgun proteomics experiment. Available as a stand-alone tool and also as part of Percolator and Crux. <http://noble.gs.washington.edu/proj/fido>. 2010.

- (23) B Diament and **WS Noble**. TIDE is an ultra-fast implementation of the SEQUEST algorithm for identifying fragmentation mass spectra. Originally is distributed in binary format only, the software was subsequently released open source as part of the Crux toolkit. <http://noble.gs.washington.edu/proj/tide>. 2011.
- (24) F Ay, TL Bailey and **WS Noble**. FIT-Hi-C is a tool for assigning statistical confidence estimates to intra-chromosomal contact maps produced by genome-wide genome architecture assays such as Hi-C. <https://github.com/ay-lab/fithic>. 2014–present.
- (25) N Varoquaux, F Ay, JP Vert, and **WS Noble**. PASTIS infers the three-dimensional structure of the genome on the basis of Hi-C data. <http://cbio.ensmp.fr/~nvaroquaux/pastis>. 2015.
- (26) J Halloran, J Bilmes and **WS Noble**. DRIP TOOLKIT is a tandem mass spectrometry search engine that uses a dynamic Bayesian network model. <http://melodi-lab.github.io/dripToolkit>. 2016.
- (27) J Liu, J Bilmes and **WS Noble**. THEMIS infers the genotypes and relative frequencies of cancer clones from deep DNA sequence of multiple biopsies from a single cancer. <https://github.com/jieliu6/THEMIS>. 2017.
- (28) J Schreiber, MW Libbrecht, J Bilmes, and **WS Noble**. RAMBUTAN uses a deep neural network to predict Hi-C contacts on the basis of DNA sequence and DNA-seq accessibility data. <https://github.com/jmschrei/rambutan>. 2017.
- (29) TJ Durham, MW Libbrecht, J Bilmes, and **WS Noble**. PREDICTD imputes complete, genomic data sets on the basis of related data sets from other cell types and other assay types. <https://github.com/tdurham86/PREDICTD>. 2018.

#### Invited lectures (since 2015)

“Learning embeddings of bulk and single-cell genomic data for imputation and multi-omic integration.” Keynote, Omics Research Day, Simon Fraser University, Feb 8, 2020.

“Machine learning methods for making sense of big genomic and proteomic data.” Keynote, Machine Learning for Computational Biology Workshop, Vancouver, BC, Dec 14, 2019.

“Imputing and prioritizing epigenomics experiments.” Cancer Epigenetics Affinity Group, Fred Hutch, Sep 3, 2019.

“NOT all the things: submodular representative set selection for when big data is too big.” Keynote, Machine Learning in Computational and Systems Biology subgroup, Intelligent Systems for Molecular Biology Conference, Basel, Switzerland, Jul 25, 2019.

“Traveling across spaces: the power of embedding genomic and proteomic data into a latent space.” Keynote, Intelligent Systems for Molecular Biology Conference, Basel, Switzerland, Jul 22, 2019.

“Learning latent embeddings of genomic and proteomic data.” Genetics, Bioinformatics and Systems Biology Colloquium, UC San Diego, Mar 8, 2019.

“Learning latent embeddings of genomic and proteomic data.” DCMB Seminar, University of Michigan, Feb 27, 2019.

“Unsupervised embedding of single-cell Hi-C data.” Joint Statistical Meetings, Vancouver, BC. Jul 20, 2018.

“Modeling and predicting the 3D genome.” Keynote, 3D Genomics Special Interest Group, Intelligent Systems for Molecular Biology, Chicago, IL. Jul 7, 2018.

“Modeling the 3D architecture of the genome.” Keystone Symposium on Chromatin Architecture and Chromosome Organization, Whistler, BC, Canada. Mar 27, 2018.

“Machine learning methods for making sense of big genomic data.” Computational Genomics Winter Institute, UCLA, March 1, 2018.

“Machine learning applications in genetics and genomics.” Data Science Seminar, Fred Hutch, Jan 16, 2018.

“Machine learning and statistical challenges in protein mass spectrometry.” Huck Institute Distinguished Lecture Series, Penn State University, Nov 7, 2017.

“Machine learning and statistical challenges in protein mass spectrometry.” Penn Bioinformatics Forum, University of Pennsylvania, Nov 8, 2017.

“Machine learning and statistical challenges in protein mass spectrometry.” Keynote speaker, X-Meeting (13th International Conference of the Brazilian Bioinformatics and Computational Biology Association), Sao Paulo, Brazil, Oct 4-6, 2017.

“Machine learning methods for annotating and extending big, heterogeneous genomic data.” Distinguished Lecture Series, Department of Computer Science, University of Illinois at Urbana-Champaign, Nov 14, 2016.

“Chromosome organization and chromatin dynamics during the transmission stages of Plasmodium parasites.” Monday Seminar Series, Center for Infectious Disease Research, Seattle, WA. Nov 7, 2016.

“Machine learning methods for annotating and extending big, heterogeneous genomic data.” Genomics Seminar Series, University of Wisconsin, Madison, WA. Oct 27, 2016.

“Machine learning analysis of big, heterogeneous genomic data.” Machine Learning Seminar, University of Washington. Oct. 18, 2016.

“Joint imputation of epigenomics data by three dimensional tensor factorization.” BigLS 2016 ACM International Workshop on Big Data in Life Sciences, Oct 2, 2016.

“Selecting genomics assays.” Workshop on Regulatory Genomics and Epigenomics, Simons Institute, UC Berkeley, Berkeley, CA. Mar. 10, 2016.

“Selecting genomics assays and making sense of the resulting data.” Genomics@JHU seminar series. Johns Hopkins University, Baltimore, MD. Feb 23, 2016.

“Gene regulation in 3D.” Keynote speaker, RECOMB ISCB Regulatory and Systems Genomics Conference, Philadelphia, PA. Nov 17, 2015.

“How to fit 6 billion nucleotides into a 6 micron nucleus.” RECOMB Satellite Conference on Bioinformatics Education, Chevy Chase, MD. Nov 15, 2015.

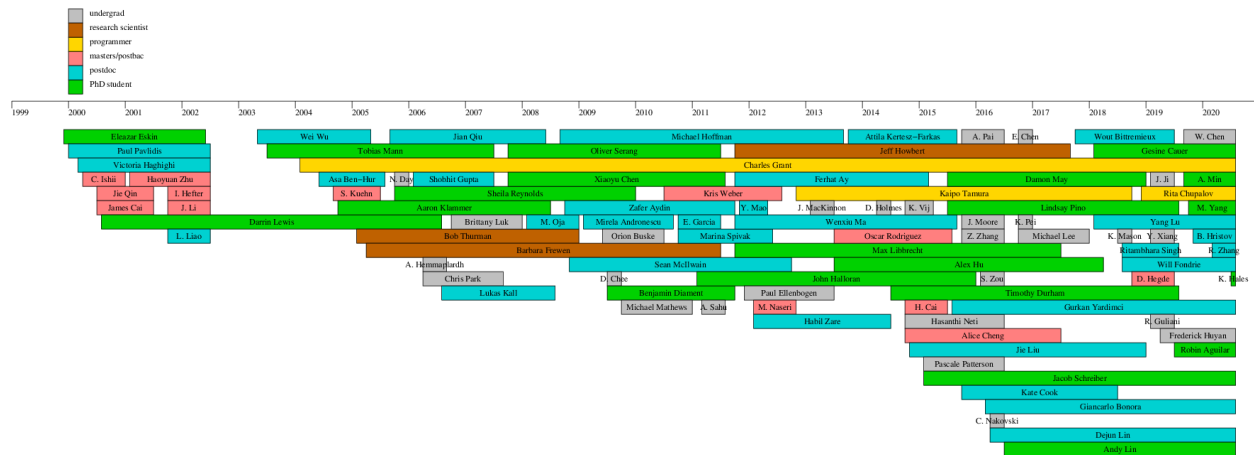
“Joint annotation of chromatin state and chromatin conformation.” Session on “Computational/statistical methods for integrative -omics” at the Joint Statistical Meeting, Seattle, WA. Aug 9, 2015.

“Modeling the 4D nucleome.” Workshop on “Interdisciplinary Approaches to Biomedical Data Science Challenges : SAMSI Innovations Lab”, Statistical and Applied Mathematical Sciences Institute, Research Triangle Park, NC. July 21, 2015.

“Gene regulation in 3D.” CMO/BIRS workshop on “Rules of Protein-DNA Recognition: Computational and Experimental Advances,” Oaxaca, Mexico. June 25, 2015.

“Linear and three-dimensional genome architecture.” cBio Seminar, Memorial Sloan-Kettering Cancer Center. April 16, 2015.

“Three-dimensional genome architecture.” Biostatistics Seminar, University of North Carolina, March 26, 2015.



### Current graduate students and postdoctoral associates

**Ran Zhang**, Postdoctoral Associate, Genome Sciences, University of Washington

Dates: 02/20–present

Prior Degree: Ph.D., Department of Computer Science, Princeton University, 2019

Project: “Integration of multiple single-cell 3D genome architecture data sets”

Funding: NIH U54 DK107979

**Borislav Hristov**, Postdoctoral Associate, Genome Sciences, University of Washington

Dates: 10/19–present

Prior Degree: Ph.D., Department of Computer Science, Princeton University, 2019

Project: “Analysis methods for deciphering lncRNA-DNA binding in *Plasmodium falciparum*”

Funding: NIH R01 AI136511

**Yang Lu**, Postdoctoral Associate, Genome Sciences, University of Washington

Dates: 01/18–present

Prior Degree: Ph.D., Department of Computer Science, University of Southern California, 2017

Project: “Detecting linked peptide pairs in data-independent acquisition tandem mass spectrometry data.”

Funding: Keck Foundation

**Dejun Lin**, Postdoctoral Associate, Genome Sciences, University of Washington

Dates: 03/16–present

Prior Degree: Ph.D., Biophysics, University of Rochester, 2015

Project: “Molecular dynamics modeling of 3D genome architecture”

Funding: U54 DK107979

**Giancarlo Bonora**, Postdoctoral Associate, Genome Sciences, University of Washington

Dates: 02/16–present

Prior Degree: Ph.D., Computer Science, University of California, Los Angeles, 2015

Project: “Computational methods for analysis of 3D nucleome data”

Funding: U54 DK107979

**Gesine Cauer**, Ph.D. student, Genome Sciences, University of Washington

Dates: 01/18–present

Prior degree: B.S., Biology, Haverford College, 2012

Project: “Inference of 3D structure of diploid genomes from Hi-C data”

Funding: NIH F31 GM134642

**Andy Lin**, Ph.D. student, Genome Sciences, University of Washington

Dates: 06/16–present

Prior degree: B.S., Cellular and Molecular Biology and Bioinformatics, University of Michigan, 2012

Project: “Unsupervised ranking of mass spectrometry runs”

Funding: DARPA

**Robin Aguilar**, Ph.D. student, Genome Sciences, University of Washington

Dates: 06/19–present

Prior degree: B.S., Biochemistry, De Pauw University, 2018

Project: Oligo probe design for high-throughput fluorescence microscopy

Funding: NSF Graduate Fellowship Program

**Alan Min**, Ph.D. student, Statistics, University of Washington

Dates: 08/19–present

Prior degree: B.S., Computer science, math, and statistics, Purdue University, 2018

Project: Latent Dirichlet allocation modeling of single-cell expression and chromatin accessibility data

Funding: NSF Graduate Fellowship Program

**Mu Yang**, Ph.D. student, Biomedical Informatics and Medical Education, University of Washington

Dates: 09/19–present

Prior degree: B.S., Public Health, National Taiwan University, 2015

Project: Cross-species analysis of single-cell RNA-seq data

Funding: Government scholarship for overseas Ph. D. study from the Ministry of Education, Taiwan

**Kianna Hales**, Ph.D. student, Department of Genome Sciences

Dates: 06/20–present

Prior degree: B.S., Molecular, Cellular & Developmental Biology / Data Science, University of Washington, 2019

Project: Deep neural network de-noising of tandem mass spectrometry data

Funding: NIH R01 AI136511

#### **Former graduate students and postdoctoral associates**

**Jacob Schreiber**, Ph.D. student, Computer Science and Engineering, University of Washington

Dates: 01/15–09/20

Prior degree: B.S., Biomolecular Engineering, University of California, Santa Cruz, 2013

Project: “Deep tensor factorization for large-scale imputation of epigenomic data”

Current position: Postdoctoral Fellow with Prof. Anshul Kundaje, Department of Genetics, Stanford University

**Gürkan Yardımcı**, Postdoctoral Associate, Genome Sciences, University of Washington

Dates: 07/15–08/20

Prior Degree: Ph.D., Computational Biology and Bioinformatics, Duke University, 2014

Project: “Computational methods for analysis of 3D nucleome data”

Current position: Assistant Professor, Oncological Sciences Division, Oregon Health Sciences University

**Timothy Durham**, Ph.D. student, Genome Sciences, University of Washington

Dates: 06/14–08/19

Prior degree: B.S., Biology and Computer Science, Williams College, 2009

Project: “Machine learning methods to impute epigenomic maps”

Current position: Scientist, Broad Institute

**Ritambhara Singh**, Postdoctoral Associate, Genome Sciences, University of Washington

Date: 07/18–07/19

Prior Degree: Ph.D., Department of Computer Science, University of Virginia, 2018

Project: “A deep neural network approach to improving resolution of single-cell Hi-C data.”

Current position: Assistant Professor, Department of Computer Science, Brown University

**Lindsay Pino**, Ph.D. student, Genome Sciences, University of Washington

Dates: 06/15–06/19

Prior degree: B.S., Biochemistry and Molecular Biology, Pennsylvania State University, 2009

Project: “Proteomics technologies to uncover the molecular phenotypes of aging”

Current position: Postdoctoral fellow, Ben Garcia lab, University of Pennsylvania.

**Wout Bittremieux**, Postdoctoral Associate, Genome Sciences, University of Washington

Dates: 09/17–06/19

Prior Degree: Ph.D., Computer Science, University of Antwerp, 2017

Project: “Generating theoretical peptide mass spectra using a generative adversarial network.”

Current position: Postdoctoral fellow with Prof. Pieter Dorrestein, Skaggs School of Pharmacy and Pharmaceutical Sciences, UC San Diego

**Jie Liu**, Postdoctoral Associate, Genome Sciences, University of Washington

Dates: 10/14–12/18

Prior Degree: Ph.D., Computer Science, University of Wisconsin–Madison, 2014

Project: “Summarization of big cancer data”

Current position: Assistant Professor, Department of Computational Medicine and Bioinformatics, University of Michigan

**Damon May**, Ph.D. student, Genome Sciences, University of Washington

Dates: 06/15–12/18

Prior degree: M.S., Computer Science and Engineering, University of Washington, 2005

Project: “A learned embedding for efficient joint analysis of millions of mass spectra”

Current position: Computational Immunologist, Adaptive Biotechnologies

**Kate Cook**, Postdoctoral Associate, Genome Sciences, University of Washington

Dates: 09/15–06/18

Prior Degree: Ph.D., Molecular Genetics, University of Toronto, 2015

Project: “Relating gene expression to genome architecture in *Plasmodium falciparum*”

Current position: Research Associate, Ottawa Hospital Research Institute, University of Ottawa

**Alex Hu**, Ph.D. student, Genome Sciences, University of Washington

Dates: 06/13–03/18

Prior degree: B.S., Biomedical Engineering and B.S., Biology, UT Austin, 2012

Project: “Computational methods for the analysis of data-independent acquisition shotgun proteomics data.”

Current position: Research scientist, Benaroya Research Institute

**Max Libbrecht**, Ph.D. student, Computer Science and Engineering, University of Washington

Dates: 09/11–06/17

Prior degree: B.S., Computer Science, Stanford University, 2011

Project: “Understanding human genome regulation through entropic graph-based regularization and sub-modular optimization”

Current position: Assistant Professor, Department of Computer Science, Simon Fraser University.

**John Halloran**, Ph.D. student, Electrical Engineering, University of Washington

Dates: 01/11–12/15

Prior degree: M.S., Electrical Engineering, University of Hawaii at Manoa, 2010

Project: “Graphical Models for Peptide Identification of Tandem Mass Spectra.”

Current position: Postdoctoral Fellow, Division of Biostatistics, UC Davis

**Attila Kertesz-Farkas**, Postdoctoral Associate, Genome Sciences, University of Washington

Dates: 09/13–08/15

Prior degree: Ph.D., Computer Science, University of Szeged, Hungary, 2010

Project: “Accurate and rapid identification of post-translationally modified peptides from shotgun proteomics data.”

Current position: Assistant Professor, School of Data Analysis and Artificial Intelligence, the Faculty of Informatics, National Research University Higher School of Economics in Moscow, Russian Federation.

**Wenxiu Ma**, Postdoctoral Associate, Genome Sciences, University of Washington

Dates: 09/11–08/15

Prior Degree: Ph.D., Computer Science, Stanford University, 2012

Project: “Analysis of ChIP-seq and chromatin architecture data”  
Current position: Assistant Professor, Department of Statistics, University of California, Riverside.

**Ferhat Ay**, Postdoctoral Associate, Genome Sciences, University of Washington

Dates: 09/11–02/15

Prior Degree: Ph.D., Computer Science, University of Florida, 2011

Project: “Inference of genome architecture from DNA-DNA interaction data.”

Current position: Institute Leadership Assistant Professor of Computational Biology, La Jolla Institute for Allergy and Immunology

**Habil Zare**, Postdoctoral Associate, Genome Sciences, University of Washington

Dates: 01/12–06/14

Prior Degree: Ph.D., Computer Science, University of British Columbia, 2011

Project: “Inferring clonal composition from multiple sections of a breast cancer”

Current position: Assistant Professor, Department of Cell Systems & Anatomy, University of Texas Health Science Center at San Antonio

**Michael Hoffman**, Postdoctoral Associate, Genome Sciences, University of Washington

Dates: 08/08–08/13

Prior degree: Ph.D., Biology, Trinity College, University of Cambridge, 2008

Project: “Unsupervised dynamic Bayesian networks for segmentation of heterogeneous genomic data sets.”

Current position: Assistant Professor, Department of Medical Biophysics and the Department of Computer Science, University of Toronto. Scientist (Principal Investigator), Princess Margaret Cancer Center, Toronto, CA.

**Sean McIlwain**, Postdoctoral Associate, Genome Sciences, University of Washington

Dates: 10/08–09/12

Prior degree: Ph.D., Department of Computer Science, University of Wisconsin, Madison, 2008

Project: “Analysis of tandem mass spectra from cross-linked peptides”

Current position: Bioinformatics Researcher, Greater Lakes Bioenergy Research Center, University of Wisconsin

**Kris Weber**, Masters student, Computer Science and Engineering, University of Washington

Dates: 06/10–07/12

Prior degree: B.S., Computer Science and Engineering, University of Washington, 2010

Project: “Characterizing the clonal population of a single cancer using high-throughput sequencing.”

Current position: Amazon.com.

**Marina Spivak**, Postdoctoral Associate, Genome Sciences, University of Washington

Dates: 09/10–05/12

Prior Degree: Ph.D., Computer Science, New York University, 2010

Project: “Joint peptide and protein identification from shotgun proteomics data.”

Current position: Data Scientist, Center for Computational Biology, Simons Foundation.

**Yi Mao**, Postdoctoral Associate, Genome Sciences, University of Washington

Dates: 10/11–04/12

Prior Degree: Ph.D., Physical Chemistry, Northwestern University, 2000

Project: “Modeling mammalian genomes.”

Current position: Unknown

**Benjamin Diament**, Ph.D. student, Computer Science and Engineering, University of Washington

Dates: 06/09–09/11

Prior degree: M.S., Computer Science, UC Berkeley

Project: “Ultrafast peptide identification from tandem mass spectra: method and applications.”

Current position: Mass spectrometry software start-up

**Zafer Aydin**, Postdoctoral Associate, Genome Sciences, University of Washington

Dates: 09/08–09/11

Prior degree: Ph.D., Electrical and Computer Engineering, Georgia Institute of Technology, 2008  
Project: “Supervised learning for analysis of *C. elegans* single cell expression images”; “Dynamic Bayesian networks for predicting protein secondary structure”  
Current position: Assistant Professor, Computer Engineering Department, Abdullah Gul University, Kayseri, Turkey.

**Xiaoyu Chen**, Ph.D. student, Computer Science and Engineering, University of Washington  
Dates: 09/07–07/11

Prior degree: M.S., Computer Science, McGill University, 2006  
Project: “Discovering and characterizing tissue-specific regulatory motifs in the human genome.”  
Current position: Illumina, San Diego, CA.

**Eric Garcia**, Postdoctoral Associate, Genome Sciences, University of Washington  
Dates: 09/10–06/11

Prior degree: Ph.D., Electrical Engineering, University of Washington, 2010  
Project: “The relationship between structure and function of the human genome.”  
Current position: Machine Learning Engineer, Spotify.

**Oliver Serang**, Ph.D. student, Genome Sciences, University of Washington  
Dates: 09/07–06/11

Prior degree: B.S., Computer Science, University of North Carolina, 2006  
Project: “Accurate and efficient characterization of complex protein mixtures.”  
Current position: Assistant Professor, Department of Computer Science, University of Montana

**Mirela Andronescu**, Postdoctoral Associate, Genome Sciences, University of Washington  
Dates: 01/09–08/10

Prior degree: Ph.D., Computer Science, University of British Columbia  
Project: “Characterizing the 3D structure of the yeast and human genomes.”  
Current position: Bioinformatics Scientist, Shah Lab, University of British Columbia

**Sheila Reynolds**, Ph.D. student, Electrical Engineering, University of Washington  
Dates: 09/05–12/09

Prior degree: M.S, Electrical Engineering, George Washington University, 1990.  
Project: “Classification and labeling of biological sequences using dynamic Bayesian networks.”  
Current position: Senior Research Scientist, Ilya Shmulevich lab, Institute for Systems Biology.

**Merja Oja**, Postdoctoral Associate, Genome Sciences, University of Washington  
Dates: 01/08–12/08

Prior degree: Ph.D., Department of Computer Science, University of Helsinki, 2007  
Project: “Multitask learning for predicting protein properties from sequence.”  
Current position: Researcher, Protein Production Lab, VTT Technical Research Centre of Finland.

**Lukas Käll**, Postdoctoral Associate, Genome Sciences, University of Washington  
Dates: 07/06–07/08

Prior degree: Ph.D., Bioinformatics, Karolinska Institute, 2006  
Project: “Machine learning and statistical tools for enhanced peptide identification from shotgun proteomics data.”  
Current position: Professor, Applied Systems Biology, KTH—Royal Institute of Technology

**Aaron Klammer**, Ph.D. student, Genome Sciences, University of Washington  
Dates: 09/04–06/08

Prior degree: B.A., Biology and Biochemistry, University of California, Santa Barbara, 1999  
Project: “A machine learning approach to peptide identification with tandem mass spectrometry”  
Current position: Pacific Biosciences, Menlo Park, CA.

**Jian Qiu**, Postdoctoral Associate, Genome Sciences, University of Washington  
Dates: 08/05–05/08

Prior degree: Ph.D., Computer Science, Cornell University, 2005



Project: “Combining sequence and structure information to characterize yeast protein complexes.”  
Current position: Hedge fund.

**Shobhit Gupta**, Postdoctoral Associate, Genome Sciences, University of Washington

Dates: 01/06–06/07

Prior degree: Ph.D., Bioinformatics, Max-Planck Institute for Molecular Genetics, Berlin, Germany

Project: “Discovery and characterization of regulatory motifs in DNaseI hypersensitive sites.”

Current position: MBA program, Cornell University

**Tobias Mann**, Ph.D. student, Genome Sciences, University of Washington

Dates: 06/03–06/07

Prior degree: M.S., Electrical Engineering, University of Washington, 2002

Project: “A thermodynamic approach to PCR primer design.”

Current position: Director of Bioinformatics, Progenity

**Darrin Lewis**, Ph.D. student, Computer Science, Columbia University

Dates: 07/00–07/06.

Prior degree: M.S., Computer Science, Hofstra University, 1993

Project: “Combining kernels for classification.”

Current position: Postdoctoral Associate, Michael Zhang lab, Cold Spring Harbor Laboratory.

**Asa Ben-Hur**, Postdoctoral Associate, Genome Sciences, University of Washington

Dates: 05/04–07/05

Prior degree: Ph.D., Information Systems, Technion, Israel, 2001

Project: “SVM prediction of protein-protein interactions.”

Current position: Associate Professor, Department of Computer Science, Colorado State University, Ft. Collins, CO.

**Wei Wu**, Postdoctoral Associate, Genome Sciences, University of Washington

Dates: 04/03–04/05

Prior degree: Ph.D., Biomedical Sciences, SUNY Albany, 2003, and M.S., Computer Sciences, SUNY Albany, 2002

Project: “Data fusion for cell cycle gene recognition in yeast.”

Current position: Microsoft, Redmond, CA.

**Paul Pavlidis**, Associate Research Scientist, Columbia Genome Center

Dates: 12/99–6/02

Prior degree: Ph.D., Molecular and Cell biology, UC Berkeley, 1994, and five years of postdoctoral experience in neuroscience at Stanford (Daniel V. Madison) and Columbia (Eric R. Kandel)

Project: “Statistical and machine learning tools for microarray analysis.”

Current position: Professor, Department of Psychiatry, University of British Columbia.

**Victoria Haghghi**, Postdoctoral Associate, Columbia Genome Center

Dates: 02/00–6/02

Prior degree: B.A., computer science, UC Berkeley, 1993, and Ph.D., genetics and development, Columbia, 2000.

Project: “Gene finding and genetic network modeling.”

Current position: Assistant Professor, Department of Psychiatry, Columbia University.

**Li Liao**, Masters student, Computer Science, Columbia University

Prior degree: Ph.D., physics, Peking University, 2002. Dates: 9/01–6/02

Project: “Combining pairwise sequence similarity and support vector machines for remote protein homology detection.”

Current position: Associate Professor, Department of Computer Science, University of Delaware.

**Haoyuan Zhu**, Masters student, Computer Science, Columbia University

Dates: 01/01–06/02

Project: “Software tools for the analysis of promoter regions.”

Current position: Rosetta Inpharmatics, Kirkland, WA.

**Johnny Li**, Masters student, Computer Science, Columbia University

Dates: 09/01–06/02

Prior degree: Ph.D., Molecular Genetics, UT Austin, 1998

Project: “Statistics of replicated microarray experiments.”

Current position: Scientist—Bioinformatics & Biostatistics, Nestlé Research Center, St. Louis, MO.

**Ilana Hefter**, Masters student, Computer Science, Columbia University

Dates: 09/01–06/02

Project: “Computational methods to differentiate spliced exons from pseudoexons.”

Subsequent position: medical school.

**Eleazar Eskin**, Ph.D. student, Computer Science, Columbia University

Dates: 11/99–05/02

Project: “Sparse sequence modeling with applications to computational biology and intrusion detection.”

Current position: Associate Professor, Department of Computer Science and Engineering, University of California, Los Angeles.

**Jie Qin**, Masters student, Computer Science, Columbia University

Dates: 06/00–06/01

Prior degree: Ph.D

Project: “Web-based microarray analysis tools and kernel hierarchical clustering for microarray analysis.”

Current position: Associate Research Scientist, Columbia Genome Center.

**James Cai**, Masters student, Medical Informatics, Columbia University

Dates: 06/00–6/01

Prior degree: Ph.D., Biochemistry, University of Vermont

Project: “Cancer classification from microarray data.”

Current position: Roche Pharmaceuticals.

**Chihiro Ishii**, Masters student, Computer Science, Columbia University

Dates: 3/00–12/00

Project: “Meta-MEME modeling of promoters and proteins.”

Current position: NEC Tokyo.

### Thesis committee membership

Adam Wilcox. “Automated classification of medical text reports.” Department of Medical Informatics, Columbia University, 2000.

Regina Barzilay. “Multidocument summarization by information fusion.” Department of Computer Science, Columbia University, 2001.

Heather McCune. “Better late than never: microarray-based analysis of DNA replication dynamics in a yeast mutant with inefficient late origin activation.” Department of Genetics, University of Washington, 2004.

Amol Prakash. “Algorithms for comparative sequence analysis and comparative proteomics.” Department of Computer Science and Engineering, University of Washington, 2006.

Nick Norberg. “Giant Zeeman effects in colloidal diluted magnetic semiconductor quantum dots with homogeneous dopant speciation.” Department of Chemistry, University of Washington, 2006.

Rui Kuang. “Inferring protein structure with discriminative learning and network diffusion.” Department of Computer Science, Columbia University, 2006.

Luca Cazzanti. “Generative models for similarity-based classification.” Department of Electrical Engineering, University of Washington, 2007.

Cristi Stoick-Cooper. “The role of Wnt signaling in fin and heart regeneration of the zebrafish.” Program in Neurobiology and Behaviour, University of Washington, 2007.

Chris Bartels. “Graphical models for large vocabulary speech recognition.” Department of Electrical Engineering, University of Washington, 2008.

Paul Murphy. Program in Molecular and Cellular Biology, University of Washington, 2008.

Chua Hon Nian. “Graph-based Methods for Protein Function Prediction.” Graduate School for Integrative Sciences and Engineering, National University of Singapore, 2008.

Zizhen Yao. “Genome scale search of noncoding RNAs: bacteria to vertebrates.” Department of Computer Science and Engineering, University of Washington, 2008.

Michael Hoopman. “Identification of unusual isotope distributions to facilitate rapid, high-throughput analysis using mass spectrometry.” Department of Genome Sciences, University of Washington, 2009.

Kevin Duh. “Semi-supervised ranking: algorithms & applications.” Department of Electrical Engineering, University of Washington, 2009.

Will Sheffler. “A volumetric score function for computational protein structure modeling and protein structure validation.” Department of Genome Sciences, University of Washington, 2009.

Eithon Cadag. “Statistical learning and data integration across heterogeneous sources for virulence factor recognition.” Department of Biomedical and Health Informatics, University of Washington, 2009.

Jon Malkin. “Smoothing class transitions with hard labels.” Department of Electrical Engineering, University of Washington, 2009.

Youyi Fong. “Modeling protein subfamilies; finding the number of mixture components from sequences of generalized Bernoulli random variables.” Department of Biostatistics, University of Washington, 2009.

Yihua Chen. “Strategies for Similarity-based Learning.” Department of Electrical Engineering, University of Washington, 2010.

Richard Schaeffer. “Detecting conservation of folding pathway by family: Three-helix bundles, SH3 domains and  $\beta$ -graph domains.” Department of Biochemistry, University of Washington, 2010.

Alex Scouras. Department of Biochemistry, University of Washington. 2010.

Sangsoon Woo. “A computationally efficient modular optimal discovery procedure.” Department of Biostatistics, University of Washington, 2010.

Troy Zerr. “Genotyping Human Genomic Structural Variation.” Department of Genome Sciences, University of Washington, 2010.

Pragya Singh. “Structural and Functional Characterization of Bacterial Secretion Systems Using Mass Spectrometry.” Department of Medicinal Chemistry, University of Washington, 2011.

James Thompson. “Comparative Modeling of Protein Structures.” Department of Genome Sciences, University of Washington, 2011.

Claire Ryu. “Statistical Approaches to Analyze Mass Spectrometry Data.” Department of Statistics, University of Washington, 2011.

Albert Huang. “Integrated systems approach to the study of dendritic cell differentiation.” Program in Molecular and Cellular Biology, University of Washington, 2011.

Jarrett Egertson. “Development of Data Independent Acquisition Techniques for the Analysis of High-Complexity Samples by Tandem Mass Spectrometry.” Department of Genome Sciences, University of Washington, 2013.

Sharon Greenblum. “Metagenomic systems biology: frameworks for modeling and characterizing the gut microbiome.” Department of Genome Sciences, University of Washington, 2014.

Jeff Staples. “PRIMUS: Pedigree Reconstruction and Identification of a Maximum Unrelated Set.” Department of Genome Sciences, University of Washington, 2014.

Marea Cobb (masters). “NGSdb: A NGS Data Management and Analysis Platform for Comparative Genomics.” Department of Biomedical and Health Informatics, University of Washington, 2015.

Alexander Rosenberg. “Learning Models of Gene Expression from Synthetic DNA Sequences.” Department of Electrical Engineering, University of Washington, 2016.

Kai Wei. “Submodular Optimization and Data Processing.” Department of Electrical Engineering, University of Washington, 2016.

Ying Sonia Ting. “Shifting the Paradigm: Peptide-Centric Analysis of Systematically Sampled Mass Spectrometry Data.” Department of Genome Sciences, University of Washington, 2016.

Jean Morrison. “Statistical Methods for Spatially Structured Genomic Data and High Dimensional Studies.” Department of Biostatistics, University of Washington, 2016.

Sergey Ovchinnikov. “Protein Structure Determination Using Metagenomic Sequencing Data.” Program in Molecular and Cellular Biology, University of Washington, 2017.

Rodrigo Goya. “Bioinformatics Approaches for Identifying Single Nucleotide Variants and Profiling Alternative Expression in Cancer Transcriptomes.” Program in Bioinformatics, University of British Columbia, 2017.

Han-Yin Yang. “Development Of Amyloidosis Typing Method and Data Acquisition Strategy Using Tandem Mass Spectrometry.” Department of Genome Sciences, University of Washington, 2018.

Brian Searle. “Development Of Data Independent Acquisition Methods to Systematically Analyze the human proteome.” Department of Genome Sciences, University of Washington, 2018.

Xiaojie Qiu. “A Computational Framework to Resolve Complex Developmental Trajectories and Regulatory Networks from scRNA-seq.” Department of Genome Sciences, University of Washington, 2018.

Seungsoo Kim. “Maps And Mechanisms Of Three-dimensional Genome Organization.” Department of Genome Sciences, University of Washington, 2019.

Cecilia Noecker. “Metabolic Modeling-based Tools For Integrative Microbiome Data Analysis.” Department of Genome Sciences, University of Washington, 2019.

Alex Eng. “Model-based Computational Methods to Aid the Design of Synthetic Microbial Communities.” Department of Genome Sciences, University of Washington, 2019.

Hannah Pliner. “Algorithms for Modeling Gene Regulation and Determining Cell Type Using Single-cell Molecular Profiles.” Department of Genome Sciences, University of Washington, 2019.

Sen Zhao. Department of Biostatistics, University of Washington.

Sumit Mukherjee. Department of Electrical Engineering, University of Washington.

Ken Jean-Baptiste. Department of Genome Sciences, University of Washington.

Elijah Overbey. Department of Genome Sciences, University of Washington.

Mitchell Volger. Department of Genome Sciences, University of Washington.

Jared Mohr. Department of Genome Sciences, University of Washington.

Anthony Valente. Department of Genome Sciences, University of Washington.

Deanna Plubell. Department of Genome Sciences, University of Washington.

Natalie Sauerwald. CMU-Pitt Computational Biology Program, Carnegie Mellon University.

Michael Goldberg. Department of Genome Sciences, University of Washington.

Daniel Jones. Paul G. Allen School of Computer Science and Engineering, University of Washington.

Kathleen Abadie. Department of Bioengineering, University of Washington.

Hyeon-Jin Kim. Department of Genome Sciences, University of Washington.

Chengxiang Qiu. Department of Genome Sciences, University of Washington.

Sean Windle. Department of Pathology, University of Washington.

## Teaching

“GENOME 373: Genomic Informatics.” This course provides a survey of bioinformatics methodologies. The course is taught in an alternating format, with one week focusing on the application of bioinformatics programs, followed by a week in which I describe the inner workings of those same programs. First offered spring quarter 2004, I taught the course jointly with Jim Thomas for four years, then we did not teach the course in 2008, and I taught it myself in 2009.

“GENOME 475: Debates in Genetics.” This course is organized into three-class units, where each unit addresses a current topic on genetics. The introductory class involves a lecture and discussion of the topic background, with readings from the popular press and the scientific literature. The second class is a formal debate, with student teams debating and students evaluating the debate. The third class is a discussion of the debate. I co-taught the course for five years (2012–2016).

“GENOME 541: Introduction to Computational Molecular Biology: Genome and Protein Sequence Analysis.” This is the second half of a two-quarter graduate course in the core methods of computational biology. The course, which I organize, covers a variety of topics, with each of five faculty members teaching a two-week block. My portion of the course focuses on machine learning methods for computational biology. I have taught this course every year since 2003, except during my sabbaticals in 2010 and 2017.

“GENOME 559: Introduction to Statistical and Computational Genomics.” This was originally a 5-week course that introduced graduate students to the basics of statistical analysis and programming in Perl. I taught the course for seven years from autumn 2002 through spring 2009. In 2007, we switched from Perl to Python, and in 2008, we switched from a 5-week to a 10-week format and a co-teaching format. I started teaching the course again in winter 2018.

“CSE590C: Reading and Research in Computational Biology.” This ongoing seminar is offered through the UW Department of Computer Science and serves as the journal club for the Computational Molecular Biology program. The course is organized jointly by Martin Tompa, Larry Ruzzo, Joe Felsenstein and myself. I have taught this course every year since 2002–2003, except during my sabbaticals spring 2010 and 2017.

“Introduction to Bioinformatics.” Three-week course taught at the African Institute for Mathematical Sciences, Muizenberg, South Africa, in February, 2013. AIMS draws post-baccalaureate students from across Africa and provides them with a one-year masters degree to prepare them for entry to graduate school. My course taught basic bioinformatics using Python.

Ad hoc teaching at the University of Washington:

- “MEDCHEM 541: Mass Spectrometry Based Proteomics.” 2008, 2009.
- “MEBI/BIME 590: Biomedical and Health Informatics Lecture Series.” 2008, 2009, 2011, 2017.
- Data science masters program, 2016, 2017.

“Computational Genomics.” I designed this course to be offered to undergraduate and graduate students at Columbia. It was cross-listed in computer science, biomedical engineering and medical informatics and was offered as an elective in all three departments. The course focused on microarray expression analysis, protein sequence analysis, and gene finding. Students worked in interdisciplinary teams on two projects per semester. I taught the course in spring 2000 (35 students) and 2001 (65 students). After I left Columbia, the course was taught by Prof. Christina Leslie.



UM1 HG011531 (Noble, Disteche, Shendure) NIH	9/18/20–6/31/25 \$1,316,000	2.4 cal. mo.
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**UW 4-Dimensional Genomic Organization of Mammalian Embryogenesis Center**  
The UW 4D Genome Organization of Mammalian Embryogenesis Center (UW 4D GENOME) will carry out systematic generation of sequencing and imaging data during mouse embryogenesis, summarizing and visualizing the resulting data using machine learning models.  
Role: Multi-PI

U54 DK107979 (Noble, Shendure) NIH	9/30/15–7/31/21 \$278,542	1.8 cal. mo.
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**University of Washington Center for Nuclear Organization and Function**  
This project develops novel experimental and computational methods to characterize genome 3D architecture, validate the methods using mouse and human cells, and demonstrate the utility of the resulting data for improving our understanding of fundamental biology and human disease.  
Role: Multi-PI

R01 GM121818 (Noble) NIH/NIGMS	2/01/17–1/31/21 \$111,873	1.44 cal. mo.
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**Optimization and joint modeling for peptide detection by tandem mass spectrometry**  
This project develops and applies statistical and machine learning methods for interpreting mass spectra.  
Role: PI

R35 GM131745 (Disteche) NIH/NIGMS	5/1/19–4/30/24 \$374,589	1.2 cal. mo.
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**X chromosome regulation and role in aneuploidy**  
The main goal of this project is to understand the role of the sex chromosomes in sex differences and sex chromosome disorders in vivo. The Noble lab is developing statistical and machine learning methods to interpret the resulting data sets.  
Role: Co-investigator

P41 GM103533 (MacCoss) NIH/NIGMS	7/1/17–3/31/21 \$137,667 (subaward)	1.08 cal. mo.
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**Comprehensive biology: Exploiting the yeast genome**  
The mission of the YRC is to facilitate the identification and characterization of protein complexes in the yeast *Saccharomyces cerevisiae*.  
Role: Co-investigator

1633939 (Nunn) NSF	10/1/16–9/30/20 \$7,241 (subaward)	0.36 cal. mo.
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**Collaborative research: Proteins as functional biomarkers: integrating organic characterization with proteomics to track routes for carbon and nitrogen recycling and preservation**  
This project aims to produce a metaproteomic pipeline to provide insights into the distribution of taxonomy-specific biological functions to unravel ecosystem processes.  
Role: co-PI

Grant (Villen) Keck Foundation	1/1/17–6/30/21 \$40,000	0.36 cal. mo.
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**Limited mistranslation mutagenesis: A proteome-wide technology to assess the effects of amino acid substitutions on protein function**  
This project will develop a novel, non-genetic mutagenesis technology to assess the effects of amino acid substitutions on protein function on a proteome-wide scale  
Role: Co-Investigator

U01 HG009395 (Leslie) 12/1/16–11/30/21 0.54 cal. mo.  
NIH/NHGRI \$65,533 (subcontract)

**Encoding genomic architecture in the encyclopedia: linking DNA elements, chromatin state, and gene expression in 3D**

This project will develop methods to integrate gene expression, DNA sequence, chromatin accessibility, and chromatin 3D architecture data to gain insights into gene regulation.

Role: Co-investigator

U24 HG009446 (Weng) 2/1/17–1/31/22 0.96 cal. mo.  
NIH/NHGRI \$71,419 (subcontract)

**EDAC: ENCODE Data Analysis Center**

The EDAC is a multi-disciplinary group of scientists who integrate data from all groups in the ENCODE Consortium.

Role: Co-investigator

R01 AI136511 (Le Roch) 7/01/18–6/30/23 1.02 cal. mo.  
NIH/NIGMS \$99,665

**Chromatin structure and control of gene expression in the human malaria parasite**

This project will characterize the molecular drivers of chromatin organization and gene regulation in *Plasmodium falciparum*, elucidating their importance in parasite development, virulence, and sexual differentiation.

Role: Co-investigator

R61 DA047010 (Mullins, Duan) 8/15/18–5/31/20 0.6 cal. mo.  
NIH/NIGMS \$56,218

**Impact of methamphetamine use on the HIV nucleome in individuals on antiretroviral therapy**

This project aims to understand the mechanisms of HIV latency using state-of-the-art genomic tools as well as complementary cellular and molecular methods.

Role: Co-investigator

R01 GM127327 (Deng) 9/01/18–8/31/20 0.6 cal. mo.  
NIH \$40,443

**Gene-by-gene studies of dosage regulation pathways of the mammalian X chromosome.**

The goal of this study is to identify mechanisms of adaptation in response to gene dosage changes such as copy number variants, using the X chromosome as a model.

Role: Co-investigator

Grant (Noble) 6/01/20–5/31/21 0.6 cal. mo.  
Chan-Zuckberg \$200,000

**The Percolator analysis engine for tandem mass spectrometry data**

We propose to improve Percolator, which is the dominant software for analyzing spectrum identifications produced by protein tandem mass spectrometry, by making the software faster, more robust, and applicable to more types of mass spectrometry data.

Role: PI

**Pending support**

Dollar amounts indicate the first year direct cost.

R01 HG11466 (Noble) 9/01/20–8/31/25 1.2 cal. mo.  
NIH \$250,000

**Deep tensor genomic imputation**

This project will develop a machine learning approach to predicting various types genomic experiments before they are performed by leveraging big, heterogeneous compendia of existing data.

Role: PI



## Previous support

Dollar amounts indicate the total direct cost for the full award period.

U01 CA200147 (Henikoff, Shendure, Noble) 9/1/17–8/31/19 0.6 cal. mo.  
NIH \$38,745 (subaward)

### **Tethered nuclease strategies for *in situ* mapping of 3D nuclear organization**

This proposal refines and extends a modern genomic profiling method, called CUT&RUN, that enables accurate mapping with relatively low-coverage deep sequencing.

Role: co-I

R01 RR021692, R01 GM103544 (Noble, Bailey) 8/01/05–8/31/18 0.12 cal. mo.  
NIH/NIGMS \$174,460

### **The MEME suite of motif-based sequence analysis tools**

This project supports, maintains and develops the MEME software suite of motif analysis software.

Role: Multi-PI

R01 AI106775 (Noble, Le Roch) 6/7/13–5/31/18 0.78 cal. mo.  
NIH/NHGRI \$79,265

### **The spatial organization of the *Plasmodium* genome throughout its infectious cycle**

This project, a collaboration with Karine Le Roch's lab at UC Riverside, will use a recently developed technique to discover the three-dimensional structure of the *P. falciparum* genome at three time points during the parasite's life cycle, assay the chromatin modification landscape of the genome over the same time points, and then build an integrated model of gene expression.

Role: Multi-PI

R01 GM106056 (Rohs) 2/1/14–1/31/18 0.66 cal. mo.  
NIH \$157,590 (subcontract)

### **Genome analysis based on the integration of DNA sequence and shape**

This project integrated analysis of 1D sequence at genome-wide scale with 3D structure at atomic resolution, developing novel genome analysis tools and furthering our understanding of genome function.

Role: Co-Investigator

U41 HG007000 (Weng) 9/12/12–7/31/17 0.96 cal. mo.  
NIH/NHGRI \$89,482 (no new funds)

### **EDAC: ENCODE Data Analysis Center**

This proposal aims to create the ENCODE Data Analysis Center consisting of a multi-disciplinary group of leading scientists who will respond to directions from the ENCODE Analysis Working Group and thus integrate data from all groups in the ENCODE Consortium in an unbiased manner. The Noble lab developed unsupervised and semi-supervised learning methods for interpreting the data tracks.

Role: Co-investigator

1549932 (Noble, Bilmes, MacCoss) 9/1/15–8/31/17 0.3 cal. mo.  
NSF \$61,534

### **EAGER: Cloud-based analysis of mass spectrometry proteomics data**

This project will develop novel machine learning algorithms to enable proteomics researchers to make sense of one experiment within the context of all the previous experiments stored in the cloud.

Role: Multi-PI

R01 ES024917 (Noble) 9/10/14–8/31/17 0.12 cal. mo.  
NIH/NIEHS \$94,139

**Machine learning methods to impute and annotate epigenomic maps**

This project develops and applies novel unsupervised machine learning methods to make sense of epigenomic data sets. The project will produce novel computational methods as well as two primary analysis products: virtual experiments for combinations of assays and cell types that have not yet been carried out and annotations that identify various types of biochemical and functional activity along the human genome.

Role: PI

R01 CA180777 (Noble) 4/1/13–3/31/17 0.12 cal. mo.  
NIH/NCI \$76,247 (no new funds)

**BIGDATA: Small: DA: Interpreting massive genomic data sets via summarization**

This proposal develops submodular summarization methods for drawing inferences from massive genomic data sets. We will apply these methods to five big data problems in genomics: 1) identifying functional elements characteristic of a given human cell type; 2) identifying genomic features associated with particular subclasses of cancer; 3-4) identifying genomic variants representative of ancestrally or phenotypically defined human populations; and 5) finding a set of microbial genes that characterize a given site on the human body.

Role: PI

R01 GM096306 (Noble) 3/01/07–5/31/16 0.3 cal. mo.  
NIH/NIGMS \$3,400,159

**Machine learning analysis of tandem mass spectra**

This project applies techniques and tools from the field of machine learning to the analysis of mass spectrometry data. The aims include developing better methods for identifying and quantifying proteins in complex mixtures, including proteins with post-translational modifications.

Role: PI

R01 GM098039 (Blau) 7/01/11–4/30/14 \$1,801,829  
NIH/NIGMS

**Modeling mammalian genomes**

In this project we used our previously described genome architecture assay to understand the relationship between genome architecture and allele specific expression in mammalian development.

Role: Co-investigator

R01 DC03829 (Rubel) 12/1/09–10/31/13 \$9520 (salary only)  
NIH/NIDCD

**Afferent influences on auditory system ontogeny**

The overall goals of this program are to understand the cellular basis of experience-dependent maturation and maintenance of neurons in the brainstem auditory pathways of birds and mammals.

Role: Co-investigator

DBI 085008 (Weng) 5/15/09–4/31/13 \$292,803  
NSF

**Computational analysis of nucleosome positioning signals in eukaryotic genomes**

This project aims to develop machine learning methods that model the relationship between DNA sequence and local chromatin structure.

Role: Co-investigator

U54 HG004695 (Birney) 4/1/08–12/31/12 \$630,978  
NIH/NHGRI

**EDAC: ENCODE Data Analysis Center**

This project established a multi-disciplinary group of scientists to provide integrative analysis of functional information from the NIH ENCODE consortium.

Role: Co-investigator

U65 HG004592 (J Stamatoyannopoulos) NIH/NHGRI	9/29/07–6/30/12	\$13,971,444
<b>A comprehensive catalog of human DNaseI hypersensitive sites</b>		
The overall aim of this proposal is to establish a comprehensive, high quality catalog of human DNaseI hypersensitive sites spanning all major tissue lineages.		
Role: Co-investigator		
P41 RR0011823 (Davis) NIH/NCRR	9/1/06–8/31/11	\$2,427,687
<b>Comprehensive biology: Exploiting the yeast genome</b>		
The mission of the YRC is to facilitate the identification and characterization of protein complexes in the yeast <i>Saccharomyces cerevisiae</i> .		
Role: Co-investigator		
R01 GM074257 (Leslie) NIH/NCRR	5/1/05–6/30/11	\$211,974 (subcontract)
<b>Recognizing protein folds with discriminative learning</b>		
This project develops discriminative methods for classifying proteins into structural families based upon their amino acid sequences.		
Role: Co-investigator		
R01 EB007057 (Noble) NIH/NIBIB	3/1/07–2/28/11	\$2,427,687
<b>Machine learning analysis of tandem mass spectra</b>		
This project applies techniques and tools from the field of machine learning to the analysis of mass spectrometry data. The primary aim is to produce software that increases the sensitivity and specificity of protein identifications from complex mixtures.		
Role: PI		
Grant (Noble) NIH	4/1/09–3/31/10	\$24,816
<b>Facilitating and improving mass spectrometry analyses in the Center for Ecogenetics and Environmental Health</b>		
This project improved the documentation and user interface for the Crux mass spectrometry analysis toolkit and applied Crux to several data sets being produced under the auspices of the CEEH.		
Role: PI		
R33 HG003070 (Noble) NIH/NHGRI	9/1/04–8/31/08	\$1,226,036
<b>Detecting relations among heterogeneous genomic datasets</b>		
This project developed a computational framework for integrating and drawing inferences from a collection of genome-wide measurements. The project included subcontracts at three other institutions.		
Role: PI		
R01 GM071923 (J Stamatoyannopoulos) NIH/NIGMS	9/1/04–8/31/08	\$1,746,932
<b>Computational discovery of <i>cis</i>-regulatory sequences</b>		
This project used quantitative chromatin profiling to identify <i>cis</i> -regulatory elements in a high-throughput fashion. This proposal received a percentile ranking of 2.2%.		
Role: Co-investigator		

U01 HG003161 (G Stamatoyannopoulos) 9/30/03-7/31/07  
NIH/NHGRI  
**Identification of Functional DNA Elements by HSqPCR**  
This was an ENCODE project, aimed at detecting DNaseI hypersensitive sites *in vivo* using a high-throughput screen.  
Role: Co-investigator

IIS-0093302 / IIS-0431725 (Noble) 3/1/01-2/28/07 \$445,074 (direct)  
NSF  
**CAREER: Support vector methods for functional genomics**  
This project develops gene functional classification techniques based upon the support vector machine algorithm.  
Role: PI

P41 RR0011823 (Davis) 9/1/01-8/31/06  
NIH/NCRR  
**Comprehensive biology: Exploiting the yeast genome**  
The mission of the YRC is to facilitate the identification and characterization of protein complexes in the yeast *Saccharomyces cerevisiae*.  
Role: Co-investigator

EIA-0312706 (Leslie) 9/15/03-8/31/06 \$200,000 (direct)  
NSF  
**ITR: Machine learning approaches to protein sequence comparison: discriminative, semi-supervised, scalable algorithms**  
This project developed, implemented and disseminated machine learning algorithms for pairwise biological sequence comparison.  
Role: Co-investigator

BR-4031T (Noble) 9/16/01-9/15/05 \$40,000  
Sloan  
**Alfred P. Sloan Foundation Research Fellow**  
The Sloan Research Fellowships were established in 1955 to provide support and recognition to young scientists. Currently, 100 grants are awarded annually in six fields: chemistry, computer science, economics, mathematics, neuroscience, and physics. In 2001, 14 grants were awarded in computer science.  
Role: PI

BDI-0078523 / BDI-0243257 (Noble) 8/1/00-7/31/05 \$412,195 (direct)  
NSF  
**Generative and discriminative methods for gene finding and functional annotation**  
This project developed an integrated gene finding and protein homology detection system based upon a generalized expectation-maximization learning algorithm.  
Role: PI

Grant (Grundy) 6/1/00-5/31/02 \$60,000  
Pharmaceutical Research and Manufacturers of America Foundation  
**Data-driven computational gene finding and functional annotation**  
This award provided salary support for the development of gene finding and functional annotation techniques.  
Role: PI

Grant (Grundy) 3/01/01-2/28/02 \$91,580  
Rigel, Inc.

**Inferring gene function from yeast two-hybrid data**

This project used yeast two-hybrid data, in conjunction with sequence and expression data, to functionally characterize yeast genes.

Role: PI

Grant (Honig) 6/1/01-5/31/04 \$2,319,096  
NIH

**Center for Computational Biology and Bioinformatics**

The Center for Computational Biology and Bioinformatics serves as a focal point for research and education at Columbia. The center provides core resources, sponsors retreats, workshops and a seminar series, and assists in the development of a coherent curriculum throughout the university.

Role: Co-investigator

BES-0088001 (Leonard) 1/1/01-12/31/03 \$500,000 (direct)  
NSF

**Curriculum in Genomic Engineering**

This project developed and operated a course track in Genomic Engineering that is related to research activities undertaken by the proposers and their colleagues at Columbia University. Prof. Noble taught "Computational Genomics," one of the five courses in this track, until leaving Columbia.

Role: Co-investigator

RO1 HD41689 (Hirsch) 12/1/02-7/31/04 \$80,734 (subcontract)  
NIH/NICHHD

**The molecular pathogenesis of health disparities in infection-induced preterm birth**

This project used microarrays to identify genes involved in infection-induced preterm labor.

Role: Co-investigator