NEVA CHERNIAVSKY DURAND

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RESEARCH INTERESTS

Computational genomics: developing robust analysis and visualization tools that employ cutting-edge technologies, such as deep learning, to enable fundamental discovery in biology and improve human health.

EDUCATION

2004-2009 Ph.D. in Computer Science
University of Washington, Seattle, WA
Thesis: Activity Analysis of Sign Language Video
Advisors: Richard Ladner and Eve Riskin

2002-2004 M.S. in Computer Science
University of Washington, Seattle, WA
Thesis: Grammar-based Compression of DNA Sequences
Advisor: Richard Ladner

1997-2001 B.S. in Computer Science and Mathematics (summa cum laude)
Tufts University, Medford, MA

EXPERIENCE

2021-present **Senior Scientist** **Broad Institute of MIT and Harvard**

Senior scientist working at the intersection of computational biology, deep learning, and genome regulation.

* Developed novel deep learning models for interpreting DNA methylation and chromatin accessibility from Nanopore sequencing, advancing understanding of cell state and epigenetic memory.
* Led analysis for the dGTEx consortium, integrating hundreds of single-cell and spatial multi-omic datasets from dozens of tissues to build a comprehensive regulatory atlas across developmental time.
* Designed and maintained scalable pipelines for single-cell multiomic assays (scRNA + scATAC), supporting experiments with over 1 million cells.
* Created visual analytics tools for interpreting deep learning predictions, multiomic patterns, and regulatory element function.
* Drove scientific vision for large collaborative projects, contributed to multiple publications, and supervised junior team members.

2023-2024 **Technology Transfer Engineer** **INRIA Startup Studio (France)**

Principal software engineer in incubator, hardening existing research technology and inventing new methods for CellEMax, a cancer therapy startup. Created new deep learning algorithm for early detection of cell death from microscopy images; built single cell gene analysis pipeline; fortified and expanded microscopy image analysis pipeline; developed support software to automate experimental results and increase the speed at which biologists can evaluate their methods.

2019-2021 **Assistant Professor, non-tenure track** **Aiden Lab at Baylor College of Medicine**
2014-2019 **Staff Scientist** **Aiden Lab at Baylor College of Medicine**
2012-2014 **Computational Biologist** **Aiden Lab at the Broad Institute**

Chief computationalist in biological lab focused on 3D reconstruction of the genome. Devised analyses and software for novel assay combining whole genome bisulfite sequencing and proximity ligation; supervised project employing deep learning for feature annotation; created one-click data pipeline for analysis of whole genome sequencing Hi-C experiments; invented algorithms for diploid analysis and feature detection; built Java software for visualization of massive data sets; and helped author scientific papers describing our work. Oversaw widespread adoption of the software by the larger research community via publication and forum creation, including as the standard for NHGRI consortia. Managed lab's data production for the ENCODE consortium. Other projects include ancestral genome reconstruction and reconciling the results of diverse proximity ligation experiments via linear algebraic techniques. Code at https://github.com/aidenlab/juicer and https://github.com/aidenlab/juicebox

2010-2011 **Postdoctoral Researcher in Computer Vision, Massachusetts Institute of Technology, Center for Biological and Computational Learning:** Built an object recognition system for aerial video that includes refinement of neuromorphic features, dictionary learning and feature selection, classification, and tracking. Other projects include action recognition in real-world video data, semi-supervised learning on large image datasets, and experiments on crowd-sourcing for vision tasks.

2009-2010 **Postdoctoral Researcher in Computer Vision, INRIA (France), Willow project**: Classification of person attributes from video data to aid sociologists in describing and analyzing change over time. We extract facial descriptors and train a classifier via semi-supervised learning on image and video data to predict attributes on movies.

2006-2009 **MobileASL**: Compressing sign language video to enable deaf users to communicate via mobile phone. We automatically recognize activity specific to sign language video, such as turn-taking and finger spelling, and adjust parameters in real-time to save power and bits while preserving intelligibility.

2005-2006 **Multimedia**: Broadcasting compressed variable bit rate movies to satisfy video-on-demand. Casting this problem as a version of generalized windows scheduling, we achieve low delay with a practical and efficient algorithm.

2005 **MultiStage**: Compressing video to obtain constant quality at a target average bit rate. We mapped the problem of bit allocation to the multiple choice knapsack problem and implemented our solution inside H.264, the newest standard for video compression.

2004-2005 **Auction Theory**: Selling items to impatient bidders. We prove bounds on the competitiveness of deterministic and randomized algorithms compared with the optimal offline solution.

2002-2004 **DNASequitur**: Compressing DNA sequences. We apply a linear time grammar compression algorithm that creates a unique grammar for DNA.

1998-2002 **Software developer in image processing, National Institutes of Health, Bethesda, MD:** Important member of a programming team that is developing a general-purpose image-processing product to support research in the NIH intramural program. The MIPAV (Medical Image Processing, Analysis, and Visualization) application enables quantitative analysis and visualization of medical images to support NIH scientists and physicians. Java software modules implemented include automated image registration technique used in a variety of physician research; surface visualization tool for modeling structures found in medical images; interactive "intelligent scissors" tool for delineating tumors; and reusable graph component used in analysis of image data

PUBLICATIONS

Y. Hu, M. Horlbeck, R. Zhang, S. Ma, R. Shrestha, V. K. Kartha, F. M. Duarte, C. Hock, R. E. Savage, A. Labade, H. Kletzien, A. Meliki, A. Castillo, **N. C. Durand**, E. Mattei, L. J. Anderson, T. Tay, A. S. Earl, N. Shoresh, C. B. Epstein, A. Wagers, J. D. Buenrostro. "Multiscale footprints reveal the organization of cis-regulatory elements," *Nature*, January 2025.

M. Sandoval-Velasco, O. Dudchenko, J. A. Rodríguez, C. P. Estrada, M. Dehasque, C. Fontsere, S. ST Mak, R. Khan, V. G. Contessoto, A. B. Oliveira Jr, A. Kalluchi, B. J. Zubillaga Herrera, J. Jeong, R. P. Roy, I. Christopher, D. Weisz, A. D. Omer, S. S. Batra, M. S. Shamim, **N. C. Durand**, B. O'Connell, A L Roca, MV Plikus, MA Kusliy, SA Romanenko, NA Lemskaya, NA Serdyukova, SA Modina, PL Perelman, EA Kizilova, SI Baiborodin, NB Rubtsov, G Machol, K Rath, Ri Mahajan, P Kaur, A Gnirke, I Garcia-Treviño, R Coke, JP Flanagan, K Pletch, A Ruiz-Herrera, V Plotnikov, IS Pavlov, NI Pavlova, AV Protopopov. M Di Pierro, AS Graphodatsky, ES Lander, MJ Rowley, PG Wolynes, JN Onuchic, L Dalén, MA Marti-Renom, MTP Gilbert, EL Aiden. "Three-dimensional genome architecture persists in a 52,000-year-old woolly mammoth skin sample," *Cell*, July 2024.

P. A. Adastra,, **N. C. Durand**, N. Mitra, S. G. Pulido, R. Mahajan, A. Blackburn, Z. L. Colaric, J. W. M. Theisen, D. Weisz, O. Dudchenko, A. Gnirke, S. S. P. Rao, P. Kaur, E. L. Aiden, A. P. Aiden. "A rapid, low cost, and highly sensitive SARS-CoV-2 diagnostic based on whole genome sequencing," *PLoS ONE 18(11),* November 2023.

B. Hitz, J-W. Lee, O. Jolanki, M. S. Kagda, K. Graham, P. Sud, I. Gabdank, J. S. Strattan, C. A. Sloan, T. Dreszer, L. D. Rowe, N. R. Podduturi, V. S. Malladi, E. T. Chan, J. M. Davidson, M. Ho, S. Miyasato, M. Simison, F. Tanaka, Y. Luo, I. Whaling, E. L. Hong, B. T. Lee, R. Sandstrom, E. Rynes, J. Nelson, A. Nishida, A. Ingersoll, M. Buckley, M. Frerker, D. S Kim, N. Boley, D. Trout, A. Dobin, S. Rahmanian, D. Wyman, G. Balderrama-Gutierrez, F. Reese, **N. C. Durand**, O. Dudchenko, D. Weisz, S. S. P. Rao, A. Blackburn, D. Gkountaroulis, M. Sadr, M. Olshansky, Y. Eliaz, D. Nguyen, I. Bochkov, M. S. Shamim, R. Mahajan, E. Aiden, T. Gingeras, S. Heath, M. Hirst, W. J. Kent, A. Kundaje, A. Mortazavi, B. Wold, J. M. Cherry. "The ENCODE Uniform Analysis Pipelines," *bioRxiv*, April 2023.

V. Garg*, O. Dudchenko*, J. Wang, A. W. Khan, S. Gupta, P. Kaur, K. Han, R. K. Saxena, S. M. Kale, M. Pham, J. Yu, A. Chitikineni, Z. Zhang, G. Fan, C. Lui, V. Valluri, F. Meng, A. Bhandari, X. Liu, T. Yang, H. Chen, B. Valliyodan, M. Roorkiwal, C. Shi, H. B. Yang, **N. C. Durand**, M. K. Pandey, G. Li, R. Barmukh, X. Wang, X. Chen, H-M. Lam, H. Jiang, X. Zong, X. Liang, X. Liu, B. Liao, B. Guo, S. Jackson, H. T. Nguyen, W. Zhuang, W. Shubo, X. Wang, E. L. Aiden, J. L. Bennetzen, R. K. Varshney. "Chromosome-length genome assemblies of six legume species provide insights into genome organization, evolution, and agronomic traits for crop improvement," *Journal of Advanced Research* 42, December 2022

R. Nakamura, Y. Motai, M. Kumagai, C. L. Wike, H. Nishiyama, Y. Nakatani, **N. C. Durand**, K. Kondo, T. Kondo, T. Tsukahara, A. Shimada, B. R. Cairns, E. L. Aiden, S. Morishita, H. Takeda. "CTCF looping is established during gastrulation in medaka embryos," *Genome Research*, May 2021.

C. L. Wike, Y. Guo, M. Tan, R. Nakamura, D. K. Shaw, N. Díaz, A. F. Whittaker-Tademy, **N. C. Durand**, E. L. Aiden, J. M. Vaquerizas, D. Grunwald, H. Takeda, B. R. Cairns. "Chromatin architecture transitions from zebrafish sperm through early embryogenesis," *Genome Research*, May 2021.

C. P. Fulco*, J. Nasser*, T. R. Jones, G. Munson, D. T. Bergman, V. Subramanian, S. R. Grossman, R. Anyoha, B. Doughty, T. A. Patwardhan, T. H. Nguyen, M. Kane, E. M. Perez, **N. C. Durand**, C. A. Lareau, E. K. Stamenova, E. L. Aiden, E. S. Lander, J. M. Engreitz. "Activity-by-contact model of enhancer–promoter regulation from thousands of CRISPR perturbations," *Nature Genetics* 51, November 2019.

G. Nir*, I. Farabella*, C. P. Estrada*, C. G. Ebeling*, B. J. Beliveau, H. M. Sasaki, S. D. Lee, S. C. Nguyen, R. B. McCole, S. Chattoraj, J. Erceg, J. A. Abed, N. M. C. Martins, H. Q. Nguyen, M. A. Hannan, S. Russell, **N. C. Durand**, S. S. P. Rao, J. Y. Kishi, P. Soler-Vila, M. Di Pierro, J. N. Onuchic, S. P. Callahan, J. M. Schreiner, J. A. Stuckey, P. Yin, E. L. Aiden, M. A. Marti-Renom, C. Wu. "Walking Along Chromosomes with Super-Resolution Imaging, Contact Maps, and Integrative Modeling," *PLOS Genetics* 14(12), December 2018.

E. Stamenova*, **N. C. Durand***, O. Dudchenko, M. S. Shamim, S-C. Huang, Y. Jiang, I. D. Bochkov, S. S. P. Rao, E. S. Lander, A. Gnirke, E. L. Aiden. "The Hi-Culfite Assay Reveals Relationships Between Chromatin Contacts and DNA Methylation State," *bioRxiv,* November 2018.

R. E. Gate, C. S. Cheng, A. P. Aiden, A. Siba, M. Tabaka, D. Lituiev, I. Machol, M. G. Gordon, M. Subramaniam, M. Shamim, K. L. Hougen, I. Wortman, S-C. Huang, **N. C. Durand**, T. Feng, P. L. De Jager, H. Y. Chang, E. L. Aiden, C. Benoist, M. A. Beer, C. J. Ye, A. Regev. "Genetic Determinants of Co-Accessible Chromatin Regions in Activated T Cells Across Humans," *Nature Genetics* 50(8), July 2018.

L. Vian*, A. Pękowska*, S. S. P. Rao*, K-R. Kieffer-Kwon*, S. Jung*, L. Baranello, S-C. Huang, L. El Khattabi, M. Dose, N. Pruett, A. L. Sanborn, A. Canela, Y. Maman, A. Oksanen, W. Resch, X. Li, B. Lee, A. L. Kovalchuk, Z. Tang, S. Nelson, M. Di Pierro, R. R. Cheng, I. Machol, B. G. St Hilaire, **N. C. Durand**, M. S. Shamim, E. K. Stamenova, J. N. Onuchic, Y. Ruan, A. Nussenzweig, D. Levens, E. Lieberman Aiden, R. Casellas. "The Energetics and Physiological Impact of Cohesin Extrusion," *Cell* 173(4), May 2018.

J. T. Robinson, D. Turner, **N. C. Durand**, H. Thorvaldsdóttir, J. P. Mesirov, E. Lieberman Aiden. "Juicebox.js Provides a Cloud-Based Visualization System for Hi-C Data," *Cell Systems* 6(2), January 2018.

O. Dudchenko, M. S. Shamim, S. S. Batra, **N. C. Durand**, N. T. Musial, R. Mostofa, M. Pham, B. G. St Hilaire, W. Yao, E. Stamenova, M. Hoeger, S. K. Nyquist, V. Korchina, K. Pletch, J. P. Flanagan, A. Tomaszewicz, D. McAloose, C. P. Estrada, B. J. Novak, A. D. Omer, E. L. Aiden. "The Juicebox Assembly Tools module facilitates de novo assembly of mammalian genomes with chromosome-length scaffolds for under $1000," *bioRxiv*, January 2018.

P. A. Larsen, R. A. Harris, Y. Liu, S. C. Murali, C. R. Campbell, A. D. Brown, B. A. Sullivan, J. Shelton, S. J. Brown, M. Raveendran, O. Dudchenko, I. Machol, **N. C. Durand**, M. S. Shamim, E. Lieberman Aiden, D. M. Muzny, R. A. Gibbs, A. D. Yoder, J. Rogers, K. C. Worley. "Hybrid De Novo Genome Assembly and Centromere Characterization of the Gray Mouse Lemur (Microcebus Murinus)," *BMC Biology* 15(110), November 2017.

O. Dudchenko, S. S. Batra*, A. D. Omer*, S. K. Nyquist, M. Hoeger, **N. C. Durand**, M. S. Shamim, I. Machol, E. S. Lander, A. P. Aiden, E. Lieberman Aiden. "De Novo Assembly of the Aedes Aegypti Genome Using Hi-C Yields Chromosome-Length Scaffolds," *Science* 356(6333), April 2017.

N. C. Durand*, J. T. Robinson*, M. S. Shamim, I. Machol, J. P. Mesirov, E. S. Lander, E. Lieberman Aiden. "Juicebox Provides a Visualization System for Hi-C Contact Maps with Unlimited Zoom," *Cell Systems* 3(1), July 2016.

N. C. Durand*, M. S. Shamim*, I. Machol, S. S. P. Rao, M. H. Huntley, E. S. Lander, E. Lieberman Aiden. "Juicer Provides a One-Click System for Analyzing Loop-Resolution Hi-C Experiments," *Cell Systems* 3(1), July 2016.

E. M. Darrow*, M. H. Huntley*, O. Dudchenko, E. K. Stamenova, **N. C. Durand**, Z. Sun, S. Huang, A. L. Sanborn, I. Machol, M. S. Shamim, A. P. Seberg, E. S. Lander, B. P. Chadwick, E. Lieberman Aiden. "Deletion of DXZ4 on the human inactive X chromosome alters higher-order genome architecture," *PNAS* 113(31), July 2016.

A. L. Sanborn*, S. S. P. Rao*, S. Huang, **N. C. Durand**, M. H. Huntley, A. I. Jewett, I. D. Bochkov, D. Chinnappan, A. Cutkosky, J. Li, K. P. Geeting, A. Gnirke, A. Melnikov, D. McKenna, E. K. Stamenova, E. S. Lander, E. Lieberman Aiden. "Chromatin extrusion explains key features of loop and domain formation in wild-type and engineered genomes," *PNAS* 112(47), September 2015.

S. S. P. Rao*, M. H. Huntley*, **N. C. Durand**, E. K. Stamenova, I. D. Bochkov, J. T. Robinson, A. L. Sanborn, I. Machol, A. D. Omer, E. S. Lander, E. Lieberman Aiden. "A 3D Map of the Human Genome at Kilobase Resolution Reveals Principles of Chromatin Looping," *Cell* 159(7), December 2014.

N. Cherniavsky, I. Laptev, J. Sivic, and A. Zisserman, "Semi-supervised Learning of Facial Attributes in Video," in *First International Workshop on Parts and Attributes*, in conjunction with ECCV 2010, September 2010.

N. Bansal, N. Chen, **N. Cherniavsky**, A. Rudra, B. Scheiber, and M. Sviridenko, "Dynamic Pricing for Impatient Bidders," *ACM Transactions on Algorithms*, 6(2), March 2010.

N. Cherniavsky, J. Chon, J. O. Wobbrock, R. E. Ladner, and E. A. Riskin, "Activity Analysis Enabling Real-time Video Communication on Mobile Phones for Deaf Users," in *UIST '09: Proceedings of the ACM Symposium on User Interface Software and Technology*, pages 79-88, October 2009.

N. Cherniavsky, "Activity Analysis of Sign Language Video," PhD thesis, University of Washington, March 2009.

J. Chon, **N. Cherniavsky**, E. A. Riskin, and R. E. Ladner, "Enabling Access through Real-time Sign Language Communication over Cell Phones," in *Asilomar Conference on Signals, Systems, and Computers*, November 2009.

N. Cherniavsky, R. E. Ladner, and E. A. Riskin, "Activity Detection in Conversational Sign Language Video for Mobile Telecommunication," in *IEEE Int'l Conference on Automatic Face and Gesture Recognition*, September 2008.

N. Cherniavsky, A. C. Cavender, R. E. Ladner, and E. A. Riskin, "Variable Frame Rate for Low Power Mobile Sign Language Communication", in *ASSETS '07: Proceedings of the Ninth International ACM SIGACCESS Conference on Computers and Accessibility*, pages 163-170, October 2007.

N. Cherniavsky, G. Shavit, M. F. Ringenburg, R. E. Ladner, and E. A. Riskin, "MultiStage: A MINMAX Bit Allocation Algorithm for Video Coders," *IEEE Transactions on Circuits and Systems for Video Technology* volume 17, number 1, pages 59-67, January 2007.

N. Bansal, **N. Cherniavsky**, N. Chen, A. Rudra, B. Scheiber and M. Sviridenko, "Dynamic Pricing for Impatient Bidders," in *Symposium on Discrete Algorithms (SODA),* pages 726-735, January 2007.

N. Cherniavsky and R. E. Ladner, "Practical Low Delay Broadcast of Compressed Variable Bit Rate Movies," in *Data Compression Conference (DCC)*, pages 362-371, March 2006.

N. Cherniavsky and R. E. Ladner, "Grammar-based compression of DNA Sequences", UW CSE Technical Report (TR2007-05-02), presented at the *DIMACS Working Group on the Burrows-Wheeler Transform*, August 2004.

M.J. McAuliffe, D.P. McGarry, W. Gandler, **N. Cherniavsky**, D.A. Parsons, H.J. Singh, and B.L. Trus, "Medical Image Processing, Analysis, and Visualization", presented at the National Institutes of Health Research Festival, Oct 2000.

*****These authors contributed equally to the work

INVITED TALKS

Nov 21, 2019	**Visualizing the 3D Genome with Juicebox and Spacewalk.** Broad Institute Nuclear Architecture Symposium.
May 23, 2019	**Learning How the Genome Folds in 3D.** Re*Work Deep Learning Summit.
Oct 5, 2016	**Reading and Writing Genomes in 3D.** INRIA Algorithms Biology Structure seminar.
Mar 25, 2015	**NGS and 3D Genomes: Exploring Genome Architecture with Juicebox.** Visualizing Biological Data (VizBi) 2015.
Oct 21, 2010	**MobileASL: Overcoming the technical challenges of mobile video conversation in sign language.** Tufts University Computer Science Colloquium.
Oct 13, 2010	**Semi-supervised learning of facial attributes in video.** MIT Vision group meeting.
Mar 13, 2009	**Activity Analysis of Sign Language Video**. INRIA WILLOW group meeting.

TEACHING EXPERIENCE

Summer 2006	**Instructor, *Data Structures***: I served as the sole instructor for a 28 student class consisting of computer science majors, supervising one teaching assistant. I taught three weekly lectures, combining previous material with original work; held office hours; prepared a new project, including a new code base with visualization; wrote and graded exams; answered student questions via a newsgroup and private email; and maintained the course website with up-to-date lecture materials and assignments.
Winter 2004-Spring 2005	**Teaching Assistant, *Data Compression; Discrete Structures; Introduction to Computer Science; Graduate Algorithms; Professional Masters Program Algorithms*:** Depending on the course, duties included teaching hour-long weekly sessions; holding office hours for individual help; website maintenance;

grading assignments and exams; writing solutions to assignments; and setting up and maintaining project code.

HONORS

2018	BCM Woman of Excellence Award
2007	UW SWE Outstanding Female Graduate Award in CSE
2002-2005	NSF Graduate Research Fellowship
2002	Phi Beta Kappa, Tufts University
2001	Benjamin Brown Scholarship, Tufts University
1998	Dean's Prize for Academic Excellence, Tufts University

SERVICE

Program committee	International Conference on Intelligent User Interfaces
Reviewer	Nature Computational Science Genome Biology PLOS Computational Biology Nature Protocols Bioinformatics IEEE Transactions on Multimedia IEEE Transactions on Circuits and Systems for Video Technology Journal of Discrete Algorithms ACM SIGCHI conference on Human Factors in Computing Systems IEEE Transactions on Image Processing EURASIP Journal on Bioinformatics and Systems Biology IEEE Transactions on Broadcasting
2005-2009	Tutor, CSE undergraduates
2006-2007	Graduate student seminar coordinator
2006	Editor for disabilities office: translated mathematics portions of textbooks into Latex to make them accessible to blind students
2005-2006	CSE graduate student coordinator: served as the liaison between the faculty and the graduate students
2005-2006	Graduate admissions committee
2004-2005	Graduate and Professional Student senator
2004-2006	Mentor for Making Connections, a program that matches disadvantaged high school women with successful mentors

SKILLS

Extensive programming experience in Java, C, C++, Python, R, Matlab, OpenCV, awk, Perl, shell scripts, and HTML/Javascript. Comfortable using Google Cloud, Amazon AWS, Terra/WDL, Keras/Tensor Flow, Unix, IntelliJ, and ChatGPT. Fluent in French.