

NEVA CHERNIAVSKY DURAND, Ph.D.

Senior Scientist | Computational Biology, Machine Learning & Scientific Software

Broad Institute of MIT and Harvard, Cambridge, MA | neva@broadinstitute.org | personal.broadinstitute.org/neva/

RESEARCH PROFILE

I'm a computational biologist and machine learning researcher focused on developing technologies that drive biological discovery, particularly in gene regulation. I build tools - ranging from deep learning models and scalable analysis pipelines to interactive visualizations - that help researchers extract meaning from complex biological data. My work spans single-cell multiomics, long read methylation, regulatory and 3D genomics, biomedical image analysis, and computer vision.

EXPERIENCE

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

- Work at the intersection of computational biology, machine learning, and genome regulation, developing analysis and visualization methods for complex genomic and multiomic data.
- Lead analysis for the dGTEX consortium, integrating single-cell, spatial, and multiomic datasets across dozens of tissues and developmental stages to build a resource for understanding gene regulation in pediatric donors and non-human primates.
- Design and maintain scalable pipelines for single-cell multiomic assays, including scRNA-seq and scATAC-seq, supporting experiments with more than one million cells.
- Apply and fine-tune deep learning models to DNA methylation, chromatin accessibility, regulatory activity, and sequence-to-function problems; develop visual analytics for interpreting model predictions.
- Contribute to studies of enhancer-gene regulation, 3D genome organization, cellular senescence, and cancer biology, working closely with experimental scientists across large collaborative projects.
- Drive scientific direction, troubleshoot analysis and data-quality problems, develop reproducible workflows, contribute to publications, and supervise junior scientists.

Technology Transfer Engineer / Principal Software Engineer | Inria Startup Studio / CellEmax, France | 2023-2024

- Contributed to an AI-powered live-cell imaging platform for identifying next-generation immunotherapy targets in oncology.
- Developed a deep learning algorithm for early detection of cell death from microscopy images and expanded the live-cell image-analysis pipeline.
- Developed analysis software linking imaging-defined single-cell phenotypes with transcriptomic measurements, with standardized data management and graphical interfaces for experimental biologists.
- Contributed computational methods underlying FateSeqNN/fate-seq 2.0, including image analysis, signal processing, fate forecasting, and a unified database of more than 20,000 time-resolved single-cell trajectories with same-cell transcriptomes.

Assistant Professor / Staff Scientist / Computational Biologist | Aiden Lab, Baylor College of Medicine & Broad Institute | 2012-2021

- Chief computationalist in a biological laboratory focused on 3D genome organization. Devised analyses and software for new genomic assays and helped drive experimental and computational projects.
- Created Juicer, a one-click analysis pipeline for Hi-C experiments, and Juicebox, an interactive visualization system for massive genomic contact maps; both became widely used community tools.
- Invented algorithms for diploid genome analysis and genomic feature detection; supervised work using deep learning for feature annotation; managed ENCODE consortium data production.
- Worked across algorithm development, production scientific software, visualization, biological interpretation, consortium coordination, and collaborative publication.

Postdoctoral Researcher, Computer Vision | MIT, Center for Biological and Computational Learning | 2010-2011

- Built an object-recognition system for aerial video combining feature refinement, dictionary learning, feature selection, classification, and tracking; also worked on action recognition, semi-supervised learning, and large image datasets.

Postdoctoral Researcher, Computer Vision | Inria WILLOW, France | 2009-2010

- Developed methods for classification of human attributes from image and video data, using facial descriptors and semi-supervised learning to improve generalization from unlabeled video.

Software Developer, Image Processing | National Institutes of Health | 1998-2002

- Developed components of MIPAV, a general-purpose medical image processing, analysis, and visualization platform used by NIH scientists and physicians, including image registration, surface visualization, tumor delineation, and reusable visualization components.

EDUCATION

Ph.D., Computer Science | University of Washington | 2009

- Thesis: Activity Analysis of Sign Language Video. Advisors: Richard Ladner and Eve Riskin.

M.S., Computer Science | University of Washington | 2004

- Thesis: Grammar-based Compression of DNA Sequences. Advisor: Richard Ladner.

B.S., Computer Science and Mathematics, summa cum laude | Tufts University | 2001

SELECTED PUBLICATIONS

Gschwind AR, Mualim KS, Karbalayghareh A, et al., including **Durand NC**. "An encyclopedia of human enhancer-gene regulatory interactions." *Nature* (2026). doi:10.1038/s41586-026-10781-4.

Torlai Triglia E*, Miller TE*, **Durand NC**, et al. "Chromatin topology and distal elements underlie divergent cell-type-specific regulation of 9p21 locus cell cycle genes." *Cell Genomics* (2026):101304. doi:10.1016/j.xgen.2026.101304.

Guckelberger P, et al., including **Durand NC**. "Quantitative changes in 3D contact predict changes in enhancer-promoter regulation upon cohesin depletion." *Nature Communications*, accepted in principle.

Hu Y, Horlbeck M, Zhang R, et al., including **Durand NC**. "Multiscale footprints reveal the organization of cis-regulatory elements." *Nature* (2025).

Sandoval-Velasco M, Dudchenko O, et al., including **Durand NC**. "Three-dimensional genome architecture persists in a 52,000-year-old woolly mammoth skin sample." *Cell* (2024).

Fulco CP*, Nasser J*, et al., including **Durand NC**. "Activity-by-contact model of enhancer-promoter regulation from thousands of CRISPR perturbations." *Nature Genetics* 51 (2019):1664-1669.

Durand NC*, Robinson JT*, et al. "Juicebox Provides a Visualization System for Hi-C Contact Maps with Unlimited Zoom." *Cell Systems* 3(1) (2016). *Co-first author.

Durand NC*, Shamim MS*, et al. "Juicer Provides a One-Click System for Analyzing Loop-Resolution Hi-C Experiments." *Cell Systems* 3(1) (2016). *Co-first author.

Sanborn AL*, Rao SSP*, et al., including **Durand NC**. "Chromatin extrusion explains key features of loop and domain formation in wild-type and engineered genomes." *PNAS* 112(47) (2015).

Rao SSP*, Huntley MH*, **Durand NC**, et al. "A 3D Map of the Human Genome at Kilobase Resolution Reveals Principles of Chromatin Looping." *Cell* 159(7) (2014).

Dudchenko O, Batra SS*, Omer AD*, et al., including **Durand NC**. "De Novo Assembly of the *Aedes aegypti* Genome Using Hi-C Yields Chromosome-Length Scaffolds." *Science* 356(6333) (2017).

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

Vian L*, Pękowska A*, Rao SSP*, et al., including **Durand NC**. "The Energetics and Physiological Impact of Cohesin Extrusion." *Cell* 173(4) (2018).

Gate RE, Cheng CS, Aiden AP, et al., including **Durand NC**. "Genetic Determinants of Co-Accessible Chromatin Regions in Activated T Cells Across Humans." *Nature Genetics* 50(8) (2018).

Nakamura R, Motai Y, Kumagai M, et al., including **Durand NC**. "CTCF looping is established during gastrulation in medaka embryos." *Genome Research* (2021).

Wike CL, Guo Y, Tan M, et al., including **Durand NC**. "Chromatin architecture transitions from zebrafish sperm through early embryogenesis." *Genome Research* (2021).

Complete publication list: Google Scholar (linked from personal.broadinstitute.org/neva/)

SELECTED RESEARCH SOFTWARE & METHODS

- Juicer - one-click system for analyzing loop-resolution Hi-C experiments; designed for reproducible analysis of large sequencing datasets.
- Juicebox / Juicebox.js - interactive desktop and web visualization systems for exploring very large Hi-C contact maps.
- Single-cell multiomic workflows - scalable processing, QC, integration, visualization, and annotation for scRNA-seq/scATAC-seq and related assays.
- Cell-events pipeline / FateSeqNN contributions - live-cell microscopy segmentation, tracking, event detection, quantitative trajectory analysis, and integration with same-cell transcriptomic data.

INVITED TALKS & WORKSHOPS

2026 Invited workshop, "Beginning with Multi-Omics Data Integration," Festival of Genomics, Biodata & AI, Boston. Workshop faculty/presenter.

2019 "Visualizing the 3D Genome with Juicebox and Spacewalk." Broad Institute Nuclear Architecture Symposium.
2019 "Learning How the Genome Folds in 3D." Re*Work Deep Learning Summit.
2016 "NGS and 3D Genomes: Exploring Genome Architecture with Juicebox." Visualizing Biological Data (VizBi).
2010 "Semi-supervised learning of facial attributes in video." MIT Vision Group.
2009 "Activity Analysis of Sign Language Video." Inria WILLOW.

TEACHING

Instructor, Data Structures, University of Washington (2006). Sole instructor for 28 computer science majors; supervised a teaching assistant, developed course materials and a programming project, lectured, and wrote and graded exams.
Teaching Assistant, University of Washington: Data Compression; Discrete Structures; Introduction to Computer Science; Graduate Algorithms; Professional Master's Program Algorithms.

HONORS & SERVICE

BCM Woman of Excellence Award (2018); UW SWE Outstanding Female Graduate Award in CSE (2007); NSF Graduate Research Fellowship (2002-2005); Phi Beta Kappa (2002); Benjamin Brown Scholarship, Tufts University (2001).
Reviewer / program committee: Nature Computational Science, Genome Biology, PLOS Computational Biology, Nature Protocols, Bioinformatics, IEEE Transactions on Image Processing, IEEE Transactions on Multimedia, IEEE Transactions on Circuits and Systems for Video Technology, Journal of Discrete Algorithms, ACM CHI, and the International Conference on Intelligent User Interfaces.
Earlier service: graduate admissions committee; graduate student senator and liaison; seminar coordinator; undergraduate tutor; mentor for Making Connections, a program matching disadvantaged high school women with mentors.

TECHNICAL SKILLS

Programming: Python, R, Java, C, C++, Matlab, OpenCV, awk, Perl, shell, HTML/JavaScript. Machine learning: Keras/TensorFlow, deep learning, computer vision, segmentation, classification, model interpretation. Computing/workflows: Google Cloud, AWS, Terra/WDL, Unix. Fluent in French.