

## Ritambhara Singh

---

Center of Computational Molecular Biology, Brown University, 164 Angell St., Providence, RI-02912  
*e-mail:* ritambhara@brown.edu, *Phone:* +1 (401) 863-9925

### Education

Institute	Major	Degree, Year
University of Pune, Pune, India	Computer Engineering	Bachelors, 2012
University of Virginia, Charlottesville, United States	Computer Science	Masters, 2014
University of Virginia, Charlottesville, United States	Computer Science	Doctoral, 2018
University of Washington, Seattle, United States	Genome Sciences	Post-Doctoral, 2018-2019

### Appointments

2019-present	Assistant Professor, Computer Science, Brown University
2018-2019	Senior Research Fellow, Genome Sciences, University of Washington
Summer 2017	Research Intern, Microsoft Research New England
2013-2018	Research Assistant, Computer Science, University of Virginia
2012-2013	Teaching Assistant, Computer Science, University of Virginia

### Awards

NHGRI Genomic Innovator Award (2021)  
OVPR Salomon Faculty Research Award (2021)  
COBRE CBHD Pilot Award at Brown University (2020)  
Algorithms and Models for Single Cell Genomics Workshop Travel Award (2019)  
Conference on Neural Information Processing Systems Travel Award (2017)  
Grace Hopper Celebration of Women in Computing Student Scholarship (2017)  
Graduate Student Award for Outstanding Research (2016-2017)  
First Prize in Podium Presentation at 13th Annual UVA Engineering Research Symposium (2017)  
European Conference on Computational Biology Travel Fellowship (2016)  
L. William Ballard Fellowship (2015)  
Chief of Army Staff Best Outgoing Student Award (2012)  
TATA Merit Scholarship Award (2010)

### Publications

- [1] Pinar Demetci, Rebecca Santorella, Bjorn Sandstede, William Stafford Noble, and **R. Singh**. Gromov-wasserstein optimal transport to align single-cell multi-omics data. *International Conference on Research in Computational Molecular Biology (RECOMB)*, 2021.
- [2] Giancarlo Bonora, Vijay Ramani, **R. Singh**, He Fang, Dana L Jackson, Sanjay Srivatsan, Ruolan Qiu, Choli Lee, Cole Trapnell, Jay Shendure, et al. Single-cell landscape of nuclear configuration and gene expression during stem cell differentiation and x inactivation. *Genome Biology*, 22(1):1–36, 2021.
- [3] Jacob Schreiber and **R. Singh**. Machine learning for profile prediction in genomics. (*Invited Review*) *Current Opinion in Chemical Biology*, 65:35–41, 2021.

- [4] Ashley Mae Conard, Nathaniel Goodman, Yanhui Hu, Norbert Perrimon, **R. Singh**, Charles Lawrence, and Erica Larschan. Timeor: a web-based tool to uncover temporal regulatory mechanisms from multi-omics data. *Nucleic Acids Research*, 49(W1):W641–W653, 2021.
- [5] Camillo Saueressig, Adam Berkley, Elliot Kang, Reshma Munbodh, and **R. Singh**. Exploring graph-based neural networks for automatic brain tumor segmentation. In *From Data to Models and Back: 9th International Symposium, DataMod 2020, Virtual Event, October 20, 2020, Revised Selected Papers 9*, pages 18–37. Springer International Publishing, 2021.
- [6] Jacob Schreiber, **R. Singh**, Jeffrey Bilmes, and William Stafford Noble. A pitfall for machine learning methods aiming to predict across cell types. *Genome biology*, 21(1):1–6, 2020.
- [7] **R. Singh**, Demetci, Pinar, Giancarlo Bonora, Vijay Ramani, Choli Lee, He Fang, Zhijun Duan, Xinxian Deng, Jay Shendure, Christine Disteché, and William Stafford Noble. Unsupervised manifold alignment for single-cell multi-omics data. *ACM Conference on Bioinformatics, Computational Biology, and Health Informatics (ACM-BCB)*, 2020.
- [8] Derrick Blakely, Eamon Collins, **R. Singh**, Andrew Norton, Jack Lanchantin, and Yanjun Qi. Fastsk: fast sequence analysis with gapped string kernels. *Bioinformatics*, 36(Supplement\_2):i857–i865, 2020.
- [9] Jie Liu, Yuanhao Huang, **R. Singh**, Jean-Philippe Vert, and William Stafford Noble. Jointly embedding multiple single-cell omics measurements. In *Workshop on Algorithms and Bioinformatics (WABI)*, 2019.
- [10] Arshdeep Sekhon, **R. Singh**, and Yanjun Qi. Deepdiff: Deep-learning for predicting differential gene expression from histone modifications. *Bioinformatics*, 34(17):i891–i900, 2018.
- [11] **R. Singh**, Jack Lanchantin, Arshdeep Sekhon, and Yanjun Qi. Attend and predict: Understanding gene regulation by selective attention on chromatin. In *Advances in neural information processing systems (NeurIPS)*, pages 6785–6795, 2017.
- [12] **R. Singh**, Arshdeep Sekhon, Kamran Kowsari, Jack Lanchantin, Beilun Wang, and Yanjun Qi. Gakco: a fast gapped k-mer string kernel using counting. In *Joint European Conference on Machine Learning and Knowledge Discovery in Databases (ECML-PKDD)*, pages 356–373. Springer, 2017.
- [13] Jack Lanchantin, **R. Singh**, Beilun Wang, and Yanjun Qi. Deep motif dashboard: Visualizing and understanding genomic sequences using deep neural networks. In *Pacific Symposium on Biocomputing (PSB)*, pages 254–265. World Scientific, 2017.
- [14] Beilun Wang, **R. Singh**, and Yanjun Qi. A constrained  $l - 1$  minimization approach for estimating multiple sparse gaussian or nonparanormal graphical models. *Machine Learning*, 106(9-10):1381–1417, 2017.
- [15] Peiwu Qin, Mahmut Parlak, Cem Kuscu, Jigar Bandaria, Mustafa Mir, Karol Szlachta, **R. Singh**, Xavier Darzacq, Ahmet Yildiz, and Mazhar Adli. Live cell imaging of low-and non-repetitive chromosome loci using crispr-cas9. *Nature communications*, 8:14725, 2017.
- [16] **R. Singh**, Jack Lanchantin, Gabriel Robins, and Yanjun Qi. Deepchrome: deep-learning for predicting gene expression from histone modifications. *Bioinformatics*, 32(17):i639–i648, 2016.
- [17] **R. Singh** and Yanjun Qi. Character based string kernels for bio-entity relation detection. In *Proceedings of the 15th Workshop on Biomedical Natural Language Processing*, pages 66–71, 2016.

- [18] **R. Singh**, Jack Lanchantin, Gabriel Robins, and Yanjun Qi. Transfer string kernel for cross-context dna-protein binding prediction. *IEEE/ACM transactions on computational biology and bioinformatics*, 2016.
- [19] **R. Singh**, Cem Kucsu, Aaron Quinlan, Yanjun Qi, and Mazhar Adli. Cas9-chromatin binding information enables more accurate crispr off-target prediction. *Nucleic acids research*, 43(18):e118–e118, 2015.
- [20] Aravinda Kuntimaddi, Nicholas J Achille, Jeremy Thorpe, Alyson A Lokken, **R. Singh**, Charles S Hemenway, Mazhar Adli, Nancy J Zeleznik-Le, and John H Bushweller. Degree of recruitment of dot1l to mll-af9 defines level of h3k79 di- and tri-methylation on target genes and transformation potential. *Cell reports*, 11(5):808–820, 2015.
- [21] Fujun Qin, Zhenguang Song, Mihaela Babiceanu, Yansu Song, Loryn Facemire, **R. Singh**, Mazhar Adli, and Hui Li. Discovery of ctf- sensitive cis-spliced fusion rnas between adjacent genes in human prostate cells. *PLoS genetics*, 11(2):e1005001, 2015.
- [22] Cem Kucsu, Sevki Arslan, **R. Singh**, Jeremy Thorpe, and Mazhar Adli. Genome-wide analysis reveals characteristics of off-target sites bound by the cas9 endonuclease. *Nature biotechnology*, 32(7):677, 2014.

## Selected Talks

1. *(Invited)* “Towards data modeling in genomics and medicine using graph-based neural networks”  
National Institute of Standards and Technology (NIST)
2. *(Invited)* “Integrating long-range regulatory interactions to predict gene expression using graph convolutional networks”  
Virtual North East Regional IDeA Conference 2021
3. *(Invited)* “Towards data integration in genomics using machine learning”  
Math and Computer Science Zoom Colloquium (Providence College)
4. *(Selected Paper)* “Unsupervised manifold alignment for single-cell multi-omics data”  
ACM Conference on Bioinformatics, Computational Biology, and Health Informatics 2020 (Virtual)
5. *(Selected Paper)* “Jointly embedding multiple single-cell omics measurements”  
Workshop on Algorithms in Bioinformatics 2019 (Niagara Falls, NY)
6. *(Selected Abstract)* “Unsupervised manifold alignment for single-cell genomics”  
Algorithms and Models for Single Cell Genomics Workshop (UC Irvine)  
and BBI Single Cell Symposium (Fred Hutch Cancer Research Center)
7. *(Invited)* “Attend and Predict: Understanding Gene Regulation by Selective Attention on Chromatin”  
Banff International Research Stations (BIRS) Workshop (Oaxaca, Mexico)
8. *(Selected Abstract)* “DeepChrome+”  
Thirteenth University of Virginia Engineering Research Symposium  
*(Winner of first prize award)*
9. *(Selected Paper)* “DeepChrome: Deep-learning for predicting gene expression from histone modifications”  
European Conference on Computational Biology 2016 (The Hague, Netherlands)

10. (*Invited*) “Transfer String Kernel for Cross-Context Sequence Specific DNA-Protein Binding Prediction”  
 Indraprastha Institute of Information Technology, Delhi (India)

## Teaching

### Instructor

Fall 2021	Deep Learning in Genomics (Graduate Level)	Brown University
Spring 2021	Deep Learning in Genomics (Undergraduate Level)	Brown University
Fall 2020	Deep Learning in Genomics (Graduate Level)	Brown University
Spring 2020	Deep Learning in Genomics (Undergraduate Level)	Brown University
Fall 2019	Deep Learning in Genomics (Graduate Level)	Brown University

### Teaching Assistant

Fall 2015	Machine Learning (Graduate Level)	University of Virginia
Spring 2013	Theory of Computation (Undergraduate Level)	University of Virginia
Fall 2012	Algorithms (Undergraduate Level)	University of Virginia

## Advising

### Current Graduate Students

**Jeremy Bigness**, Ph.D, Computational Biology

Dates: 2019-present

Project: Using Deep Learning to Understand Spatiotemporal Gene Regulation

**Pinar Demetci**, Ph.D, Computational Biology

Dates: 2020-present

Project: Probabilistic Algorithms to Enable Integrated Analysis of Single-cell Multi-omics Data

**Ghulam Murtaza**, Ph.D, Computer Science

Dates: 2021-present

Project: Improving HiC data quality using Graph Neural Networks

**Atishay Jain**, Ph.D, Computer Science

Dates: 2021-present

Project: Efficient Neutron Tomography segmentation using Graph Neural Networks

**Jiaqi Zhang**, Ph.D, Computer Science

Dates: 2021-present

Project: Modeling gene regulation in single-cells using Gaussian graphical model

**Michal Golovanevsky**, Ph.D, Computer Science

Dates: 2021-present

Project: Cross-modality integration of genomics and clinical data

**Tassallah (Amina) Abdullahi**, Ph.D, Computer Science

Dates: 2021-present

Project: Data-driven Decision Support System (DDS) for rare diagnoses

### **Former Graduate Students**

**Adam Berkley**, M.S, Computer Science

Dates: 2019-2021

Thesis: Clinical Capability of Modern Brain Tumor Segmentation Models

Current Position: Associate Professional Staff at John Hopkins University

**Camillo Saueressig**, M.S, Computer Science

Dates: 2020-2021

Thesis: Exploring graph-based neural networks for automatic brain tumor segmentation

Current Position: Attending Medical School at Technical University of Munich (TUM) and Ludwig Maximilian University of Munich (LMU) (joint program)

**Suchen Zheng**, M.S, Computer Science

Dates: 2020-2021

Project: Predicting the three-dimensional organization of the genome one organizational unit at a time

Current Position: Research Assistant (Gerstein Lab, Yale University)

### **Thesis committee membership**

Rebecca Elyanow. “Analyzing RNA-seq data using prior knowledge of gene and cell relationships”. Department of Computer Science, Brown University, 2020

### **Academic Service**

- **Program Committee Member:**

International Conference on Research in Computational Molecular Biology (RECOMB) - 2021

ACM Conference on Bioinformatics, Computational Biology, and Health Informatics (ACM-BCB) - 2019, 2020, 2021

ACM-BCB Workshop on Machine-learning methods for single-cell analysis - 2021

- **Scientific Panels:**

National Science Foundation (NSF)

- **Reviewer:**

Nature Communications

Communications Biology (Nature)

PLOS Computational Biology

Bioinformatics

IEEE/ACM Transactions on Computational Biology and Bioinformatics

International Conference on Learning Representations (ICLR) - 2021

International Conference on Research in Computational Molecular Biology (RECOMB) - 2019, 2020

International Conference on Machine Learning (ICML) - 2020, 2021

Conference on Neural Information Processing Systems (NeurIPS) - 2019, 2020, 2021

Conference on Intelligent Systems for Molecular Biology (ISMB/ECCB) - 2019

International Workshop on Biological Knowledge Discovery from Big Data (BIOKDD)- 2019

Women in Machine Learning (WIML) at NeurIPS - 2017

- **Program Chair and Organizer:**

Brown Unconference - 2020

## Department Service

- **Computer Science**  
Ph.D. Admissions Committee - 2019, 2020  
Concentration Advisor - 2020
- **Center for Computational Molecular Biology**  
Ph.D. Admissions Committee - 2019, 2020  
Concentration Advisor - 2021

## Training

- “Anchor Course Design Institute to Prepare for Online Courses”, *Brown University*, 1 week
- “2019-2020 Launch Course Design Institute”, *Brown University*, 1 week.
- “New Computer Science Faculty Teaching Workshop 2018”, *NSF*, 3 days

## Current Support

NHGRI Genomic Innovator Award (Singh)                      09/01/21 – 08/30/26  
NIH                      \$1,883,807

### **Deep learning for understanding gene regulation in diseases via ‘omics’ integration**

The proposed research program will focus on data integration and interpretation efforts across a variety of genomics and genetics datasets to understand gene regulation in diseases.

**Role:** PI

COBRE Phase 2 Renewal Grant (Rand)                      09/01/21 – 06/30/26  
NIH                      \$226,216

### **Renewal of Centers of Biomedical Research Excellence (COBRE) (Phase 2)**

The goal of the research project on this grant will be to develop machine learning methods to model gene regulation in bulk and single-cell datasets.

**Role:** Co-PI

NIST PREP Program (Larson)                      09/01/21 – 08/31/22  
NIST                      \$122,004

### **3D-Based Measurements from Neutron Tomography**

The goal of the project is to segment 4D datasets (3D location plus phase) and quantify the confidence of the 3D measurements derived from segmenting 3D tomographic reconstructions. The impact of this research includes computational overhead reduction using graph-based models and their explainability.

**Role:** Other Significant Person