Ritambhara Singh

POSITION	Assistant Professor
DEPARTMENT	Computer Science

CONTACT INFORMATION

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Computer Science Department
Brown University
Providence, RI 02906 USA

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Website: www.ritambharasingh.com
Lab Website: www.rsinghlab.org

RESEARCH INTERESTS

Machine Learning, Data Mining, Computational Biology, Health Sciences

EDUCATION

University of Virginia, Charlottesville, Virginia USA

Ph.D., Computer Science, May 2018

- Dissertation Topic: Fast and Interpretable Classification of Sequential Data in Biology
- Advisor: Dr. Yanjun Qi

M.S., Computer Science, December 2014

Savitribai Phule Pune University, Pune, Maharashtra INDIA

B.E., Computer Engineering, May 2012

PROFESSIONAL APPOINTMENTS

Brown University, Providence, Rhode Island USA
Assistant Professor, Computer Science   **September, 2019 - present**

University of Washington, Seattle, Washington USA
Senior Research Fellow, Genomic Sciences   **August, 2018 - July, 2019**

Microsoft Research New England, Cambridge, Massachusetts USA
Research Intern   **May, 2017 - August, 2017**

University of Virginia, Charlottesville, Virginia USA
Research Assistant, Computer Science   **September, 2013 - May, 2018**
Teaching Assistant, Computer Science   **September, 2012 - May, 2013**

PEER REVIEWED PUBLICATIONS

(Underlined authors are trainees in the lab, # indicates undergraduate students, ∗ indicates joint first or last authors)

CONFERENCE PROCEEDINGS

<u>Zheng S</u>∗, <u>Thakkar N</u>∗#, Harris HL, Zhang M, Liu S, Gerstein M, Aiden EL, Rowley MJ, Noble WS, Gürsoy G∗, **Singh R**∗. Predicting A/B compartments from histone modifications using deep learning. *International Conference on Bioinformatics, Computational Biology and Health Informatics (ACM BCB) 2023.*

Tran QH, Janati H, Courty N, Flamary R, Redko I, <u>Demetci P</u>, **Singh R.** (author order based on contribution) Unbalanced co-optimal transport. *AAAI Conference on Artificial Intelligence 2023.*

<u>Demetci P</u>, Santorella R, Sandstede B, **Singh R**. Unsupervised integration of single-cell multi-omics datasets with disproportionate cell-type representation. *International Conference on Research in Computational Molecular Biology (RECOMB) 2022.*

Demetci P∗, Santorella R∗, Sandstede B, Noble WS, **Singh R**. Gromov-Wasserstein optimal transport to align single-cell multi-omics data. *International Conference on Research in Computational Molecular Biology (RECOMB) 2021.*

Saueressig C, Berkley A, Kang E#, Munbodh R∗, **Singh R**∗. Exploring graph-based neural networks for automatic brain tumor segmentation. *From Data to Models and Back: 9th International Symposium, DataMod 2020.*

Singh R, Demetci P, Bonora G, Ramani V, Lee C, Fang H, Duan Z, Deng X, Shendure J, Disteche C, Noble WS. Unsupervised manifold alignment for single-cell multi-omics data. *ACM International Conference on Bioinformatics, Computational Biology and Health Informatics (ACM BCB) 2020.*

Singh R, Lanchantin J, Sekhon A, Qi Y. Attend and predict: Understanding gene regulation by selective attention on chromatin. *Advances in neural information processing systems (NeurIPS) 2017.*

Singh R, Sekhon A, Kowsari K, Lanchantin J, Wang B, Qi Y. GaKCo: A Fast Ga pped k-mer String K ernel Using Co unting. *Joint European Conference on Machine Learning and Knowledge Discovery in Databases (ECML-PKDD) 2017.*

Lanchantin J, **Singh R**, Wang B, Qi Y. Deep motif dashboard: visualizing and understanding genomic sequences using deep neural networks. *Pacific Symposium on Biocomputing (PSB) 2017.*

JOURNAL ARTICLES Jain A, Laidlaw DH, Bajcsy P∗, **Singh R**∗. Memory-efficient semantic segmentation of large microscopy images using graph-based neural networks. *Microscopy. 2023.*

Zhang J, **Singh R**. Investigating the Complexity of Gene Co-expression Estimation for Single-cell Data. *Journal of Machine Learning for Modeling and Computing. 2023.*

Guetta-Terrier C, Karambizi D, Akosman B, Zepecki JP, Chen JS, Kamle S, Fajardo JE, Fiser A, **Singh R**, Toms SA, Lee CG. Chi3l1 is a modulator of glioma stem cell states and a therapeutic target in glioblastoma. *Cancer Research. 2023.*

Berkley A, Saueressig C, Shukla U, Chowdhury I, Munoz-Gauna A#, Shehu O, **Singh R**∗, Munbodh R∗. Clinical capability of modern brain tumor segmentation models. *Medical Physics. 2023.*

Golovanevsky M, Eickhoff C∗, **Singh R**∗. Multimodal attention-based deep learning for Alzheimer's disease diagnosis. *Journal of the American Medical Informatics Association. 2022.*

Demetci P, Santorella R, Chakravarthy M#, Sandstede B, **Singh R**. Scotv2: Single-cell multiomic alignment with disproportionate cell-type representation. *Journal of Computational Biology (Special RECOMB Edition). 2022.*

de Lima Camillo LP#, Lapierre LR, **Singh R**∗. A pan-tissue DNA-methylation epigenetic clock based on deep learning. *npj Aging. 2022.*

Bigness J, Loinaz X#, Patel S#, Larschan E, **Singh R**. Integrating long-range regulatory interactions to predict gene expression using graph convolutional networks. *Journal of Computational Biology. 2022.*

Demetci P∗, Santorella R∗, Sandstede B, Noble WS, **Singh R**. SCOT: single-cell multi-omics alignment with optimal transport. *Journal of Computational Biology (Special RECOMB Edition). 2022.*

Bonora G, Ramani V, **Singh R**, Fang H, Jackson DL, Srivatsan S, Qiu R, Lee C, Trapnell C,

Shendure J, Duan Z. Single-cell landscape of nuclear configuration and gene expression during stem cell differentiation and X inactivation. *Genome Biology. 2021.*

Conard AM, Goodman N, Hu Y, Perrimon N, **Singh R**, Lawrence C, Larschan E. TIMEOR: a web-based tool to uncover temporal regulatory mechanisms from multi-omics data. *Nucleic Acids Research. 2021.*

Schreiber J, **Singh R**, Bilmes J, Noble WS. A pitfall for machine learning methods aiming to predict across cell types. *Genome biology. 2020*

Blakely D, Collins E, **Singh R**, Norton A, Lanchantin J, Qi Y. FastSK: fast sequence analysis with gapped string kernels. *Bioinformatics. 2020*

Sekhon A, **Singh R**, Qi Y. DeepDiff: DEEP-learning for predicting DIFFerential gene expression from histone modifications. *Bioinformatics. 2018*

Wang B, **Singh R**, Qi Y. A constrained $l-1$ minimization approach for estimating multiple sparse Gaussian or nonparanormal graphical models. *Machine Learning. 2017*

Qin P, Parlak M, Kuscu C, Bandaria J, Mir M, Szlachta K, **Singh R**, Darzacq X, Yildiz A, Adli M. Live cell imaging of low-and non-repetitive chromosome loci using CRISPR-Cas9. *Nature communications. 2017*

Singh R, Lanchantin J, Robins G, Qi Y. DeepChrome: deep-learning for predicting gene expression from histone modifications. *Bioinformatics. 2016*

Singh R, Lanchantin J, Robins G, Qi Y. Transfer string kernel for cross-context DNA-protein binding prediction. *IEEE/ACM Transactions on Computational Biology and Bioinformatics. 2016*

Singh R, Kuscu C, Quinlan A, Qi Y, Adli M. Cas9-chromatin binding information enables more accurate CRISPR off-target prediction. *Nucleic acids research. 2015*

Kuntimaddi A, Achille NJ, Thorpe J, Lokken AA, **Singh R**, Hemenway CS, Adli M, Zeleznik-Le NJ, Bushweller JH. Degree of recruitment of DOT1L to MLL-AF9 defines level of H3K79 Di-and tri-methylation on target genes and transformation potential. *Cell reports. 2015*

Qin F, Song Z, Babiceanu M, Song Y, Facemire L, **Singh R**, Adli M, Li H. Discovery of CTCF-sensitive Cis-spliced fusion RNAs between adjacent genes in human prostate cells. PLoS genetics. 2015

Kuscu C, Arslan S, **Singh R**, Thorpe J, Adli M. Genome-wide analysis reveals characteristics of off-target sites bound by the Cas9 endonuclease. *Nature biotechnology. 2014*

INVITED REVIEW | Schreiber J, **Singh R.** Machine learning for profile prediction in genomics. *Current Opinion in Chemical Biology. 2021.*

WORKSHOP PROCEEDINGS | <u>Murtaza G</u>, Wagner J, Zook JM, **Singh R**. GraPhiC: An integrative graph based approach for imputing missing Hi-C reads. *BIOKDD 2023.*

<u>Demetci P</u>, Tran QH, Redko I∗, **Singh R**∗. Jointly aligning cells and genomic features of single-cell multi-omics data with co-optimal transport. *Learning Meaningful Representations of Life (LMRL) Workshop at NeurIPS 2022.*

Saueressig C, Berkley A, Munbodh R∗, **Singh R**∗. A joint graph and image convolution network for automatic brain Tumor segmentation. *International MICCAI Brainlesion Workshop 2021.*

Liu J, Huang Y, **Singh R**, Vert JP, Noble WS. Jointly embedding multiple single-cell omics measurements. *Workshop on Algorithms and Bioinformatics (WABI) 2019.*

Singh R, Qi Y. Character based string kernels for bio-entity relation detection. *Workshop on Biomedical Natural Language Processing (BioNLP) 2016*

PRE-PRINTS
(UNDER REVIEW)

Demetci P, Tran QH, Redko I∗, **Singh R**∗. Revisiting invariances and introducing priors in Gromov-Wasserstein distances. *arXiv preprint. 2023.*

Golovanevsky M, Schiller E#, Nair A#, **Singh R**∗, Eickhoff C∗. One-Versus-Others Attention: Scalable Multimodal Integration. *arXiv preprint. 2023.*

Abdullahi TA, Mercurio L, **Singh R**∗, Eickhoff C∗. Retrieval-Based Diagnostic Decision Support. *JMIR Preprints. 2023.*

Murtaza G, Jain A, Hughes M#, Wagner J, **Singh R**. Investigating the performance of deep learning methods for Hi-C resolution improvement. *bioRxiv preprint. 2022.*

INVITED LECTURES

2023
Workshop on Computational Tools for Single-Cell Omics (ICERM) *(scheduled)*
Mini-symposium on Optimal transport and mean field games with applications in data science and biology (ICIAM)
Computational Genomics Summer Institute program (UCLA)
Integration Initiative: Sex, Aging, Genomics, & Evolution (IISAGE) Research Talk Series

2022
Department of Biomedical Informatics Seminar (Columbia University)
Department of Computational Medicine Bioinformatics Seminar (University of Michigan)
Biomedical Informatics Lecture Series (University of Pittsburgh)
Banff International Research Stations (BIRS) Workshop (UBC, Kelwona)
Workshop on Optimal Transport: Theory, Computation, and Biology (UC Irvine)
3rd International IBSE Symposium (IIT, Madras)

2021
National Institute of Standards and Technology (NIST)
Virtual North East Regional IDeA Conference
Math and Computer Science Zoom Colloquium (Providence College)

2017
Banff International Research Stations (BIRS) Workshop (Oaxaca, Mexico)

2016
Indraprastha Institute of Information Technology, Delhi (India)

ACTIVE GRANTS

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

NSF Biology Integration Institutes (BII) Award (Riddle)   09/01/22 – 08/30/27
NSF $2,533,059
IISAGE - Discovering the mechanisms and evolution of aging differences between females and males
The proposed research program will focus on studying the differences in aging between females and males using data from multiple species. Through experimentation, data integration, and data modeling we will understand the genomic and evolutionary mechanisms underlying these differences.
Role: Co-PI

NIDCD R01 (Fleischmann)   03/01/23 – 02/28/28
NIH $499,714
Gene regulatory network control of olfactory cortex cell type specification
The goal is to understand the underlying gene regulation for olfactory cortex cell type specification. This goal will be achieved by mapping single-cell gene expression to open chromatin regions to extract regulatory elements involved in expressing genes and by performing network modeling of the regulatory genes.
Role: Co-PI

COMPLETED GRANTS	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

SERVICE TO THE DEPARTMENT AND UNIVERSITY	Computer Science Diversity Committee Chair - 2023 - present

Computer Science Diversity Committee Member - 2022-2023
Center for Computational Molecular Biology Faculty Search - 2022-2023
Computer Science Ph.D. Admissions Committee - 2019-2023
Computational Biology Ph.D. Admissions Committee - 2019-2023
Computer Science Concentration Advisor - 2020-2023
Computational Biology Concentration Advisor - 2021-2023

Program Chair for Brown Unconference 2020 (organized at the start of COVID lockdown to engage research community)
Reviewer for Office of the Vice President for Research (OVPR) - 2022, 2023

SERVICE TO THE PROFESSION	**Program Chair**

RECOMB Seq 2024

Program Committee
RECOMB - 2021 - 2023
RECOMB Highlights - 2023
ISMB/ECCB Machine Learning in Computational and Systems Biology (MLCSB) COSI - 2023
Machine Learning in Computational Biology (MLCB) - 2021
ACM BCB - 2019-2021
ACM-BCB Workshop on Machine-learning methods for single-cell analysis - 2021

Conference Area Chair
Machine Learning in Computational Biology (MLCB) - 2023

Editorial Board
Journal of Computational Biology - 2023-present

Guest Editor
Journal of Machine Learning for Modeling and Computing (Special Issue)- 2022-2023

Scientific Panels
National Science Foundation (NSF)
National Institute of Health (NIH)
Department of Energy (DoE)
Fonds de recherche du Québec (FRQNT)
UK Research and Innovation Medical Research Council (UKRI MRC) *(Ad-hoc reviewer)*

Invited Participant
NSF-NIH Joint Workshop on Emerging AI in Biology (CMU, 2023)
NSF MODULUS Conference (GMU, 2022)

Conference Reviewer
ICML, ICLR, NeurIPS, ISMB/ECCB, BIOKDD

Journal Reviewer
Nature Methods, Nature Protocols, Nature Communications, Communications Biology (Nature), PLOS Computational Biology, PLOS One, Cell Systems, Bioinformatics, Journal of Computational Biology, IEEE/ACM Transactions on Computational Biology and Bioinformatics

Invited Opinion
Voices (Cell Systems 13, October 19, 2022): What are the keys to succeeding as a computational biologist in today's research climate? Contributors: Bonnie Berger, Dechao Tian, Wei Vivian Li, Mohammed El-Kebir, Alexandru I Tomescu, Ritambhara Singh, Niko Beerenwinkel, Yu Li, Christina Boucher, Ziv Bar-Joseph.

Service to the community
Invited speaker for Brown University's WiSE Speaker Series (2022)
Invited faculty for Brown University's WiCS Fireside Chat/Q&A (2021)
Featured in Brown University's Graduate Women/Womxn in STEM's campaign #thisiswhatascientistslookslike (2020)

HONORS AND AWARDS	NHGRI Genomic Innovator Award, 2021
	OVPR Salomon Faculty Research Award, 2021
	COBRE Center for Computational Biology of Human Disease (CBHD) Pilot Award, 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, 2017
	First Prize 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

TEACHING

Deep Learning: CSCI1470/2470 (Spring 2022, 2023), Brown University. (Enrollment: 250 students)
Deep Learning in Genomics: CSCI2952G (Fall 2019, 2020, 2021), Brown University. (Enrollment: 20 students)
Deep Learning in Genomics: CSCI1850 (Spring 2020, 2021), Brown University. (Enrollment: 30 students)

GRADUATE STUDENT ADVISING

Current Graduate Students
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 microscopy image 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
Award/Honor: T32 Predoctoral Training Program in Biological Data Science Fellowship

Tassallah (Amina) Abdullahi, Ph.D, Computer Science
Dates: 2021-present
Project: Data-driven Decision Support System (DDS) for rare diagnoses
Award/Honor: 2022 ACM SIGHPC Computational and Data Science Fellowship

Hyeyeon Hwang, Ph.D, Computational Biology
Dates: 2021-present
Project: Modeling Glioblastoma datasets using machine learning

Whitney Sloneker, Ph.D, Computational Biology
Dates: 2022-present
Project: Interpretable graph-based neural networks for applications to biology

Former Graduate Students
Pinar Demetci, Ph.D, Computational Biology
Dates: 2020-2023
Thesis: Probabilistic Algorithms for Integrative Analysis of Single-cell Multi-omics data
Award/Honor: Rising Stars in EECS program
Current Position: Schmidt Fellow at Broad Institute

Jeremy Bigness, Ph.D, Computational Biology
Dates: 2019-2022
Thesis: Using Deep Learning to Understand Spatiotemporal Gene Regulation
Current Position: Research Scientist at Agilent Technologies

Hardy Bright, M.S, Data Science
Dates: Summer 2022
Practicuum: Predicting gene expression from epigenetic data in Glioblastoma patients
Current Position: Research assistant in the lab

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
Current Position: Graduate student at Yale University

DISSERTATION COMMITTEES

Ashley Conrad. "It's About Time: Interpretable Methods and Associated Interactive Platforms to Uncover Regulatory Mechanisms from Temporal and Multi-Omics Data". Center for Computational Molecular Biology, Brown University, 2022.

Wei Cheng. "Interpretable Multi-Scale Statistical Methods for Genetic Association Studies". Center for Computational Molecular Biology, Brown University, 2022.

Rebecca Santorella. "Data-Driven Mathematical Analysis with Applications in Dynamical Systems, Biology, and Social Justice". Division of Applied Mathematics, Brown University, 2022.

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

UNDERGRADUATE STUDENT ADVISING

Honors Thesis Advised
Lucas Paulo de Lima ('21, UTRA awardee, Leallyn B. Clapp Prize for Outstanding Senior Honors Thesis in Biochemistry), Xavier Loinaz ('21), Ishaani Kahtri ('21, UTRA awardee), Muhammad Haider Asif ('22), Justin Sanders ('22, Outstanding graduating senior award), Hossam Zaki ('22, UTRA awardee), Madeline Hughes ('22), Jordan Idehen ('22), Sally Zhi ('22, UTRA awardee), David (Inho) Lee ('23), Momoka Kobayashi ('23), Alexander Le ('23, UTRA Awardee), Yuan Pu ('23), Nitya Thakkar ('23, CS Senior Prize), Shalin Patel ('23)

Independent Study
Elliot Kang ('20), Giselle Garcia ('21), Shreya D'Souza ('21), Akira Nair ('24), Wangdrak Dorji ('24), Manav Chakravarthy ('24), Jay Gopal ('25), Eva Schiller ('25), Bumjin Joo ('25),

Summer Research
Colin Baker (Summer 2023, UTRA awardee), Peter Zhu (Summer 2023, IISAGE REU 2023), Mikayla Walsh (Summer 2023, IISAGE REU 2023), Thulasi Varatharajan (Summer 2021, University of Pittsburgh, Leadership Alliance Summer Research Program).

High-school Students Advised
Carmen Boyan (Summer 2022, Classical High School, Providence RI), Sara Nath (Summer 2023, The Gatton Academy, KY)