

Ritambhara Singh

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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

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) (in press)*, 2021.
- [2] Camillo Saueressig, Adam Berkley, Elliot Kang, Reshma Munbodh, and **R. Singh**. Exploring graph-based neural networks for automatic brain tumor segmentation. *Lecture Notes in Computer Science (LNCS, Springer) (in press)*, 2021.
- [3] 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.
- [4] **R. Singh**, Pinar Demetci, Giancarlo Bonora, Vijay Ramani, Choli Lee, He Fang, Zhijun Duan, Xinxian Deng, Jay Shendure, Christine Disteche, 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.
- [5] 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.
- [6] 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.
- [7] Arshdeep Sekhon, **R. Singh**, and Yanjun Qi. Deepdiff: Deep-learning for predicting differential gene expression from histone modifications. *Bioinformatics*, 34(17):i891–i900, 2018.

- [8] **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.
- [9] **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.
- [10] 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.
- [11] 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.
- [12] **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.
- [13] **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.
- [14] **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.
- [15] 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.
- [16] **R. Singh**, Cem Kuscu, 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.
- [17] 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 dot11 to mll-af9 defines level of h3k79 di-and tri-methylation on target genes and transformation potential. *Cell reports*, 11(5):808–820, 2015.
- [18] 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.
- [19] Cem Kuscu, 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. (*Selected Paper*) “Unsupervised manifold alignment for single-cell multi-omics data”
ACM Conference on Bioinformatics, Computational Biology, and Health Informatics 2020 (Virtual)

2. (*Selected Paper*) “Jointly embedding multiple single-cell omics measurement”
Workshop on Algorithms in Bioinformatics 2019 (Niagara Falls, NY)
3. (*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)
4. (*Invited*) “Attend and Predict: Understanding Gene Regulation by Selective Attention on Chromatin”
Banff International Research Stations (BIRS) Workshop (Oaxaca, Mexico)
5. (*Selected Abstract*) “DeepChrome+”
Thirteenth University of Virginia Engineering Research Symposium
(*Winner of first prize award*)
6. (*Selected Paper*) “DeepChrome: Deep-learning for predicting gene expression from histone modifications”
European Conference on Computational Biology 2016 (The Hague, Netherlands)
7. (*Invited*) “Transfer String Kernel for Cross-Context Sequence Specific DNA-Protein Binding Prediction”
Indraprastha Institute of Information Technology, Delhi (India)

Poster Presentations

1. (*Selected Paper*) “Jointly embedding multiple single-cell omics measurement”
Workshop on Algorithms in Bioinformatics 2019 (Niagara Falls, NY)
2. (*Selected Paper*) “Attend and Predict: Understanding Gene Regulation by Selective Attention on Chromatin”
Conference on Neural Information Processing Systems 2017 (Long Beach, CA)
3. (*Selected Abstract*) “Transfer String Kernel for Cross-Context Sequence Specific DNA-Protein Binding Prediction”
European Conference on Computational Biology 2016 (The Hague, Netherlands)

Teaching Service

Instructor

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

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

- **Reviewer:**

National Science Foundation (NSF)

Nature Communications

PLOS Computational Biology

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

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

Awards and Honors

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)