

# Vipul Singhal

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CONTACT INFORMATION	60 Biopolis Street, Singapore, 138672 Genome Institute of Singapore <i>website</i> : <a href="https://vipulsinghal02.github.io/">https://vipulsinghal02.github.io/</a>	<i>Phone</i> : (+65) 97726038 <i>E-mail</i> : <a href="mailto:vipuls@gis.a-star.edu.sg">vipuls@gis.a-star.edu.sg</a>
OBJECTIVE	Develop new algorithms for spatial and multi omics, with a particular interest in optimization, Bayesian inference and deep learning. These methods should be developed in close collaboration with clinicians and biologists, and leverage the multi omic nature of the data.	
EXPERIENCE	<b>Genome Institute of Singapore</b> : helped organize the efforts of a team of 12 people, comprising biologists, engineers, bioinformaticians and physicists to develop the BANKSY spatial clustering algorithm: <ul style="list-style-type: none"><li>• 2-60 times more scalable and 10-1000 times faster than existing algorithms</li><li>• presented our work at various meetings (HCA Asia, AGBT, SSCN and internal seminars)</li><li>• published in Nature Genetics and Bioconductor</li><li>• independently benchmarked and recommended as a best practice, for instance for Xenium data (DOI: 10.1101/2023.02.13.528102), in the identification of domains in diffuse midline glioma (DMG) (DOI: 10.1038/s41467-023-36707-6) or even for analyzing MRI imaging (non-genomics) datasets (DOI: 10.1007/s00429-023-02748-2)</li></ul> <b>California Insitute of Technology</b> : worked in the Murray lab on bringing tools from control theory into synthetic biology <ul style="list-style-type: none"><li>• singular perturbation theory for timescale separation in dynamical models of transcription</li><li>• built an experimentally validated framework using Bayesian inference for batch effect removal</li><li>• a MATLAB toolbox for modeling and consensus Bayesian parameter inference involving genetic circuits</li><li>• additionally: mentored various undergraduate and masters students over the years</li></ul>	
EDUCATION	Ph.D., 2019, <b>California Institute of Technology</b> , Pasadena, California, USA B. Eng., <i>First Class Hons.</i> , Electrical Eng., 2010 <b>Imperial College London</b> , London, UK	
SKILLS	<b>Software/computational</b> : deep/machine learning (pytorch, tensorflow, scikit-learn), Python, Linux, AWS, Git R, genomics packages (Seurat, SingleCellExperiment, Scanpy, etc), MATLAB, LaTeX, Illustrator. <b>Mathemetical</b> : convex optimization, linear operator theory, differential geometry, probability theory	
HONORS AND AWARDS	Niche Skills Award (2022) National Science Scholarship, PhD (2011) National Science Scholarship, BS (2007)	
ACADEMIC EXPERIENCE	<b>Genome Institute of Singapore</b> , Singapore <i>Senior Postdoctoral Fellow</i> <span style="float: right;"><b>2022–2023</b></span> <i>Postdoctoral Fellow</i> <span style="float: right;"><b>2018–present</b></span> <b>California Institute of Technology</b> , Pasadena, California, USA <i>Graduate Student</i> <span style="float: right;"><b>2011–2018</b></span>	
PUBLICATIONS	<u>Vipul Singhal</u> , Nigel Chou, Joseph Lee, Yifei Yue, Jinyue Liu, Wan Kee Chock, Li Lin, Yun-Ching Chang, Erica Teo, Hwee Kuan Lee, Kok Hao Chen, Shyam Prabhakar, “BANKSY unifies cell typing and tissue domain segmentation for scalable spatial omics data analysis”, <b>Nature Genetics</b> , <a href="https://www.nature.com/articles/s41588-024-01664-3">https://www.nature.com/articles/s41588-024-01664-3</a> .	

Li Lin\*, Tzuen Yih Saw, Nigel Chou\*, Jolene Goh Jie Lin, Eugene Kwa Jing, Wan Kee Chock, Vipul Singhal, Zheng Li, Mike J. Huang, Huck Hui Ng, Chiea Chuen Khor, Hwee Kuan Lee, Kok Hao Chen, Shyam Prabhakar, Jinyue Liu, Mosaic neuronal disarray and developmental asynchrony converge on dysregulated progenitor adhesion in autism, (**Submitted, Nature Neuroscience**).

V. Singhal, Z. A. Tuza, Z. Z. Sun, R. M. Murray, “A MATLAB Toolbox for Modeling Genetic Circuits in Cell-Free Systems”, **OUP Synthetic Biology**, 2021; doi: 10.1101/2020.08.05.237990

B. Ranjan, W. Sun, J. Park, K. Mishra, F. Schmidt, R. Xie, F. Alipour, V. Singhal, I. Joanito, M. A. Honardoost, N. A. Rayan, J. M. Y. Yong, E. T. Koh, K. P. Leong, N. A. Rayan, M. G. Liang Lim, “DUBStepR is a scalable correlation-based feature selection method for accurately clustering single-cell data.” **Nature Communications** 12, 5849 (2021). <https://doi.org/10.1038/s41467-021-26085-2>

X. F. Meng, A.-A. Baetica\*, V. Singhal\*, R. M. Murray. “Recursively computing analytic forms for equilibrium distributions of stochastic biochemical reaction networks.” **J. R. Soc. Interface**, (2017), 14 20170157. DOI: 10.1098/rsif.2017.0157.

M. K. Takahashi, J. Chappell, C. A. Hayes, Z. Z. Sun, J. Kim, V. Singhal, K. J. Spring, S. Al-Khabouri, C. P. Fall, V. Noireaux, R. M. Murray, and J. B. Lucks. “Rapidly Characterizing the Fast Dynamics of RNA Genetic Circuitry with Cell-Free Transcription–Translation (TX-TL) Systems.” **ACS Synth. Biol.**, (2015), 4:503-515. DOI: 10.1021/sb400206c.

Z. Z. Sun, J. Kim, V. Singhal, R. M. Murray. “Protein degradation in a TX-TL cell-free expression system using ClpXP protease.” **bioRxiv**, (2015), 019695; doi: DOI: 10.1101/019695.

CONFERENCES AND MEETINGS Vipul Singhal, “BANKSY: Scalable and Accurate Clustering of Spatial Omics Data”, **Singapore Single Cell Network** (2023).

Vipul Singhal, Nigel Chou, Joseph Lee, Jinyue Liu, Wan Kee Chock, Li Lin, Yun-Ching Chang, Erica Teo, Hwee Kuan Lee, Kok Hao Chen, Shyam Prabhakar, “BANKSY: A Spatial Omics Algorithm that Unifies Cell Type Clustering and Tissue Domain Segmentation”, *Advances in Genome Biology and Technology*, (2022), and **Human Cell Atlas, Asia**, (2021).

V. Singhal and R. M. Murray, “Transforming Data Across Environments Despite Structural Non-Identifiability.” Conference Paper, **American Control Conference**, (2019), Philadelphia, PA, USA, pp. 5639-5646. doi: 10.23919/ACC.2019.8814953.

V. Singhal, R. M. Murray. “Data Driven Reduction of Extract to Extract Variability in Cell Free Systems.” Poster Presentation, **1st European Congress on Cell-Free Synthetic Biology**, (2017), Ascona, Switzerland.

V. Singhal, R. M. Murray. “Quantification of Variability in Cell-Free Biomolecular Breadboards.” Oral Presentation, **Molecular Programming Project Meeting**, (2016), Boston, USA.

V. Singhal, R. M. Murray. “Model-Based Calibrations for Extract Variability Reduction in Cell Free Systems.” Poster Presentation, **Engineering Biology Research Consortium Meeting**, (2016), Pasadena, USA.

V. Singhal, J. Kim and R. M. Murray. “Model Reduction of Transcription Mass Action Models in the Presence of Resource Consumption.” Poster Presentation, **Winter qBio**, (2016), Oahu, Hawaii, USA.

Z. A. Tuza, V. Singhal, J. Kim and R. M. Murray, “An in silico modeling toolbox for rapid prototyp-

ing of circuits in a biomolecular “breadboard” system,” Conference Paper, **52nd IEEE Conference on Decision and Control**, (2013), Florence, Italy, pp. 1404-1410. doi: 10.1109/CDC.2013.6760079.

PATENTS AND  
TECHNOLOGY  
DISCLOSURES

Li Lin, Vipul Singhal, Liu Jinyue, “Methodology for accurate assignment of discrete RNA molecules to single cells in tissue images” GIS/Z/13390 A\*STAR reference (Technology Disclosure)

V. Singhal, S. Prabhakar, H. K. Lee, K. H. Chen, (Singapore, A\*STAR 2020) “Building Aggregates with a Neighbourhood Kernel and a Spatial Yardstick (BANKSY)” GIS/Z/12142 A\*STAR reference (Technology Disclosure)

Z. Z. Sun (Pittsburgh, PA, USA), R. M. Murray (Pasadena, CA, USA), V. Singhal (Pasadena, CA, USA) 2017 Cell-Free Biomolecular Breadboards and Related Methods and Arrangements, United States, California Institute of Technology, (Pasadena, CA, USA) WO2016134069A1 url: <https://patents.google.com/patent/WO2016134069A1/en>. (Patent)