Vipul Singhal

CONTACT INFORMATION

60 Biopolis Street, Singapore, 138672
Genome Institute of Singapore
LinkedIn: linkedin.com/in/vipul-singhal-a0012436

Phone: (+65) 97726038
E-mail: vipuls@gis.a-star.edu.sg
GitHub: github.com/vipulsinghal02

OBJECTIVE

Develop new algorithms for spatial omics, with a particular interest in optimization, Bayesian inference and deep learning methods. Ultimately, these methods should be developed in close collaboration with clinicians and biologists, and leverage the spatial and/or multi omic nature of the data.

EXPERIENCE

Genome Institute of Singapore: helped organize the efforts of a team of 12, comprising biologists, engineers, bioinformaticians and physicists to develop the BANKSY spatial clustering algorithm:
- 2-60 times more scalable and 10-1000 times faster than existing algorithms
- presented our work at various meetings (HCA Asia, AGBT, SSCN and internal seminars)
- paper accepted at Nature Genetics and Bioconductor
- 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)

California Insitute of Technology: worked in the Murray lab on bringing tools from control theory into synthetic biology
- singular perturbation theory for timescale separation in models of transcription
- system identification and Bayesian inference for batch effect removal
- a MATLAB toolbox for modeling and consensus Bayesian parameter inference involving genetic circuits
- additionally: mentored various undergraduate and masters students over the years

EDUCATION

California Institute of Technology, Pasadena, California, USA

Ph.D., Computation and Neural Systems, 2019

Imperial College London, London, UK

B. Eng., *First Class Hons.*, Electrical and Electronic Engineering, 2010

SKILLS

Software/computational: deep/machine learning (pytorch, tensorflow, scikit-learn), Python, Linux, AWS, Git R, genomics packages (Seurat, SingleCellExperiment, Scanpy, etc), MATLAB, LaTeX, Illustrator.

Mathemetical: 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

Genome Institute of Singapore, Singapore

Senior Scientist I	**2023–present**
Senior Postdoctoral Fellow	**2022–2023**
Postdoctoral Fellow	**2018–2022**

California Institute of Technology, Pasadena, California, USA

Graduate Student	**2011–2018**

PUBLICATIONS

Vipul Singhal*, 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: A Spatial Omics Algorithm that Unifies Cell Type Clustering and Tissue Domain Segmentation", bioRxiv, (*accepted, Nature Genetics*).

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*).

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." Nat Commun 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 prototyping 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/WO201613 (Patent)