

## TIMOTHY D. MAJARIAN

### WORK HISTORY

#### **Computational Associate, The Broad Institute of MIT and Harvard, Cambridge MA**

Joint appointment, Clinical and Translational Epidemiology Unit,  
Massachusetts General Hospital, Boston MA  
August 2017 – Present  
PI: Dr. Alisa K. Manning

#### **Research Assistant, Carnegie Mellon University, Pittsburgh PA**

January – September 2017  
PI: Dr. Robert F. Murphy

#### **Teaching Assistant, Carnegie Mellon University, Pittsburgh PA**

August – December 2016  
Professor: Dr. Phillip Compeau

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### EDUCATION

#### **Master of Science, Carnegie Mellon University, Pittsburgh PA, 2017**

Computational Biology Department - Distinguished Research Award  
Selected Coursework – Computational genomics, Machine learning, Biological modeling and  
Simulation, Automation in biological research, Bioimage informatics

#### **Bachelor of Arts, The University of Vermont, Burlington VT, 2013**

Dual major – Biology and Applied Mathematics  
Selected Coursework – Cell biology, Microbiology, General Chemistry, Organic  
Chemistry, Differential Equations, Abstract analysis, Numerical methods,  
Statistics and probability

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### PUBLICATIONS

Laville, V., **Majarian, T. D.**, Sung, Y. J., *et al.* (2019) Genome-wide Interaction Studies by the  
CHARGE Gene-Lifestyle Interactions Working Group: what we have learned and what is  
coming next. *bioRxiv*. doi.org/10.1101/562157

**Majarian, T. D.**, Murphy, R.F. and Lakdawala, S. (2019) Learning the sequence of influenza A  
genome assembly during viral replication using point process models and fluorescence in  
situ hybridization. *PLoS Comp Bio*. doi.org/10.1371/journal.pcbi.1006199

**Majarian T. D.**, Cao-Berg I., Ruan X. and Murphy R. F. (2019) CellOrganizer: Learning and Using  
Cell Geometries for Spatial Cell Simulations. In: Hlavacek W. (eds) *Modeling Biomolecular  
Site Dynamics*. *Methods in Molecular Biology*, vol 1945. Humana Press, New York, NY.  
doi.org/10.1007/978-1-4939-9102-0\_11

Johnson, G. R., Kangas, J. D., Dovzhenko, A., Trojok, R., Voigt, K., **Majarian, T. D.**, Palme, K. and  
Murphy, R. F. (2017), A method for characterizing phenotypic changes in highly variable cell

populations and its application to high content screening of Arabidopsis thaliana protoplasts. Cytometry, 91: 326–335. doi.org/10.1002/cyto.a.23067

Li, Y., **Majarian, T. D.**, Naik, A. W., Johnson, G. R. and Murphy, R. F. (2016), Point process models for localization and interdependence of punctate cellular structures. Cytometry, 89: 633–643. doi.org/10.1002/cyto.a.22873

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PROJECTS,  
PRESENTATIONS,  
ABSTRACTS,  
CONFERENCES

**The American Society for Human Genetics meeting, Houston TX, 2019**

Poster presentation: *Colocalizing gene-lifestyle interaction associations with molecular signatures of smoking and alcohol consumption.*

Poster presentation: *Understanding the genetic basis of type 2 diabetes risk: Whole genome sequence analysis of glycemic traits from the NHLBI's TOPMed Program.*

Poster presentation: *Large-scale multi-ancestry gene-environment interaction screenings point towards different genetic mechanisms by population and exposure.*

Interactive Workshop: *Reproducible Analysis on the Cloud: Creating and Sharing Methods and Analyses with Terra.*

**The Cohorts for Heart and Aging Research in Genomic Epidemiology Consortium meeting, St. Louis MI, 2019**

Oral presentation: *Colocalizing gene-lifestyle interaction associations with molecular signatures of smoking and alcohol consumption*

**World Preclinical Congress, Boston MA, 2018**

Invited oral presentation: *Machine Learning of the Assembly Instructions of a Cell*

**All of Us Data Sciences Team, Cambridge MA, 2017-2018**

Member, contributed to interactive computing platform for the NIH sponsored, All of Us Research Program.

**American Society of Human Genetics, San Diego CA, 2018**

Poster presentation: *Leveraging T2D specific omics data in rare variant association analysis in TOPMed*

**Towards a Functional Understanding of the Diabetic Genome meeting, NIH, Bethesda MD, 2018**

Attendee

**The Cohorts for Heart and Aging Research in Genomic Epidemiology Consortium meeting, Boston MA, 2017**

Attendee

**National Center for Multiscale Modeling of Biological Systems Cell Modeling workshop, Pittsburgh PA, 2016**

Oral presentation: *Approaches to modeling protein distributions: vesicle modeling in CellOrganizer through Gaussian mixture and point process models*

**CellOrganizer Galaxy distribution, Carnegie Mellon University, Pittsburgh PA, 2016**

Deployment of CellOrganizer program on the Galaxy server

**CellOrganizer, Carnegie Mellon University, Pittsburgh PA, 2015-2017**

Researcher and software developer; software for generative modeling of cellular organization and protein distribution derived from microscopy images

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**REFERENCES**

**Dr. Alisa K. Manning, PHD**

Instructor of Medicine, Harvard Medical School  
Assistant Investigator, Massachusetts General Hospital  
Associated Scientist, The Broad Institute of MIT and Harvard  
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**Dr. James B. Meigs, MD, MPH**

Professor of Medicine, Harvard Medical School  
Associate Member, The Broad Institute of MIT and Harvard  
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**Dr. Robert F. Murphy, PHD**

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