Adam Joseph Gayoso

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Education

2018 – **Ph.D. Computational Biology**
University of California, Berkeley
Advisors: Nir Yosef, Aaron Streets

2016 – 2017 **M.S. Computer Science**
Columbia University
Track: Machine Learning

2011 – 2015 **B.S. Operations Research: Engineering Management Systems**
Columbia University
Honors: Cum Laude

Grants, honors & awards

2019 – 2020 NHGRI Genomics training grant
2019 Best poster award, UC Berkeley Center for Computational Biology retreat
2012 – 2015 Ralph W. Haines Scholarship, Columbia Engineering
2014 Tau Beta Pi induction, Columbia Engineering

Publications

Journal Articles

Adam Gayoso*, Zoë Steier*, Romain Lopez, Jeffrey Regier, Kristopher L Nazor, Aaron Streets, and Nir Yosef. "Joint probabilistic modeling of single-cell multi-omic data with totalVI". In: *Nature Methods* (2021). [PDF].

Romain Lopez, **Adam Gayoso**, and Nir Yosef. "Enhancing scientific discoveries in molecular biology with deep generative models". In: *Molecular Systems Biology* (2020). [PDF].

Valentine Svensson, **Adam Gayoso**, Nir Yosef, and Lior Pachter. "Interpretable factor models of single-cell RNA-seq via variational autoencoders". In: *Bioinformatics* (2020). [PDF].

Manu Setty, Vaidotas Kiseliovas, Jacob Levine, **Adam Gayoso**, Linas Mazutis, and Dana Pe'er. "Characterization of cell fate probabilities in single-cell data with Palantir". In: *Nature Biotechnology* (2019). [PDF].

Sheila Adams-Sapper, **Adam Gayoso**, and Lee. W. Riley. "Stress-adaptive responses associated with high-level carbapenem resistance in KPC-Producing Klebsiella pneumoniae". In: *Journal of Pathogens* (2018). [PDF].

Refereed Workshop Papers

Pierre Boyeau, Romain Lopez, Jeffrey Regier, **Adam Gayoso**, Michael I. Jordan, and Nir Yosef. "Deep Generative Models for Detecting Differential Expression in Single Cells". In: *Machine Learning in Computational Biology*. 2019. [PDF].

Oscar Clivio, Romain Lopez, Jeffrey Regier, **Adam Gayoso**, Michael I. Jordan, and Nir Yosef. "Detecting Zero-Inflated Genes in Single-Cell Transcriptomics Data". In: *Machine Learning in Computational Biology*. 2019. [PDF].

Adam Gayoso, Romain Lopez, Zoë Steier, Jeffrey Regier, Aaron Streets, and Nir Yosef. "A Joint Model of RNA Expression and Surface Protein Abundance in Single Cells". In: *Machine Learning in Computational Biology*. 2019. [PDF].

Employment

Jan – Jun 2018 — Junior Computational Biologist. Sloan Kettering Institute
Advisor: Dana Pe'er

Developed an unsupervised classifier to detect doublets, technical artifacts in single-cell RNA-seq data, and built infrastructure to process and distribute single-cell datasets to collaborators.

Summer 2017 — Research Assistant. Sloan Kettering Institute
Advisor: Dana Pe'er

Designed methods to identify genes predictive of cell fate decisions in single-cell trajectory pseudotime data, as well as clustering of genes based on pseudotemporal patterns.

Spring 2016 — Research Assistant. UC Berkeley School of Public Health
Advisor: Lee W. Riley

Developed pipeline to process and analyze RNA-seq data with application to carbapenem-resistant bacteria.

Presentations

Invited talks

Feb 2021 — Microsoft Research Health Futures Biomedical Computing team
Nov 2020 — Berkeley Computational Biology skills seminar
Oct 2020 — Single cell workshop at Pfizer
Feb 2020 — Journal club at 10x Genomics

Contributed talks

Nov 2020 — CZI Seed Networks Annual Meeting, `scvi-tools` software demonstration

Other meetings and events

Nov 2019 — Normjam: normalization workshop for scRNA-seq data, CZI/NY Genome Center

Teaching experience

Spring 2021 — Doctoral Seminar in Computational Biology (COMPBIO 293)
Graduate Student Instructor, University of California, Berkeley

University service

2020 – 2021 — Admissions committee for UC Berkeley Computational Biology Graduate Group
2020 – 2021 — UC Berkeley Computational Biology Skills Seminar Coordinator

Journal and conference reviewing

2020 – — Machine Learning in Computational Biology (MLCB)