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

2011 – 2015 **B.S. Operations Research: Engineering Management Systems**, *cum laude*
COLUMBIA UNIVERSITY

Grants, honors & awards

2021 – 2023 Chan Zuckerberg Initiative Essential Open Source Software for Science grant in support of scvi-tools (Key personnel; PI: Nir Yosef, [Link])
2019 – 2020 NHGRI Genomics and Computational Biology T32 trainee
2012 – 2015 Ralph W. Haines Scholarship, Columbia Engineering
2014 Tau Beta Pi induction, Columbia Engineering (top 1/8 of class)

Publications

MANUSCRIPTS IN SUBMISSION

1. Tal Ashuach, Daniel A. Reidenbach, **Adam Gayoso**, and Nir Yosef. "PeakVI: A Deep Generative Model for Single Cell Chromatin Accessibility Analysis". In: *bioRxiv* (2021). [PDF].

2. **Adam Gayoso***, Romain Lopez*, Galen Xing*, Pierre Boyeau, Katherine Wu, Michael Jayasuriya, Edouard Mehlman, Maxime Langevin, Yining Liu, Jules Samaran, Gabriel Misrachi, Achille Nazaret, Oscar Clivio, Chenling Xu, Tal Ashuach, Mohammad Lotfollahi, Valentine Svensson, Eduardo da Veiga Beltrame, Carlos Talavera-Lopez, Lior Pachter, Fabian J Theis, Aaron Streets, Michael I Jordan, Jeffrey Regier, and Nir Yosef. "scvi-tools: a library for deep probabilistic analysis of single-cell omics data". In: *bioRxiv* (2021). [PDF].

JOURNAL ARTICLES

1. Mohammad Lotfollahi, Mohsen Naghipourfar, Malte D. Luecken, Matin Khajavi, Maren Büttner, Marco Wagenstetter, Ziga Avsec, **Adam Gayoso**, Nir Yosef, Marta Interlandi, Sergei Rybakov, Alexander V. Misharin, and Fabian J. Theis. "Mapping single-cell data to reference atlases by transfer learning". In: *Nature Biotechnology* (2021). [PDF].

2. **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].

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

4. 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].

5. 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].

Review Articles

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

Refereed Workshop Papers

1. 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].

2. 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].

3. **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].

Presentations

Invited talks

Oct 2021	Research in progress seminar, Division of Pulmonary and Critical Care Medicine, Northwestern University
May 2021	Seminar, Celsius Therapeutics
May 2021	Single cell user group, NIH
Apr 2021	Kundaje Lab Journal Club, Stanford University
Feb 2021	Microsoft Research Health Futures Biomedical Computing team
Oct 2020	Single cell workshop, Pfizer
Feb 2020	Journal club, 10x Genomics

Contributed talks

Oct 2021	CZI Single Cell Biology Annual Meeting
Apr 2021	CZI Seed Networks Computational Biology Meeting
Mar 2021	UC Berkeley Center for Computational Biology Retreat
Nov 2020	CZI Seed Networks Annual Meeting

Posters

Oct 2021	UC Berkeley Center for Computational Biology Retreat
Apr 2021	Cold Spring Harbor conference on Probabilistic Modeling in Genomics
Oct 2019	UC Berkeley Center for Computational Biology Retreat **(Best poster award)**

Other meetings and events

Apr 2021	SingleCellOpenProblems: jamboree for expanding OpenProblems framework
Nov 2020	AstraZeneca single-cell genomics group tutorial
Nov 2020	UC Berkeley Computational Biology skills seminar
Nov 2019	Normjam: normalization workshop for scRNA-seq data, CZI/NY Genome Center

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.

Software

2019 – scvi-tools – A library for deep probabilistic analysis of single-cell omics data.
2017 – DoubletDetection – A package for detecting doublets in scRNA-seq data.

Teaching and mentorship experience

2020 – scvi-tools team. University of California, Berkeley
Recruited and mentored three research engineers, one master's student, and one undergraduate student. Designed screening exams, conducted interviews, and managed project.

Fall 2021 — Introduction to Computational Molecular and Cell Biology (BIO ENG C131)
Graduate Student Instructor, University of California, Berkeley

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

PLOS Computational Biology, 2021
Machine Learning in Computational Biology Workshop (MLCB), 2020

Press

"TotalVI: A transformative algorithm". Berkeley Engineering News. Mar 2021.