

# 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 and Computational Biology T32 trainee
- 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].

## Presentations

### INVITED TALKS

- Apr 2021 Kundaje Lab Journal Club, Stanford University  
“*scvi-tools: a library for deep probabilistic analysis of single-cell omics data*”.
- Feb 2021 Microsoft Research Health Futures Biomedical Computing team,  
“*Deep generative modeling for single-cell multimodal omics*”.
- Oct 2020 Single cell workshop at Pfizer,  
“*Deep generative modeling for single-cell multimodal omics*”.
- Feb 2020 Journal club at 10x Genomics,  
“*Bayesian modeling and automatic interpretation of scRNA-seq data*”.

### CONTRIBUTED TALKS

- Apr 2021 CZI Seed Networks Computational Biology Meeting,  
“*scvi-tools: a library for deep probabilistic analysis of single-cell omics data*”.
- Mar 2021 UC Berkeley Center for Computational Biology Retreat,  
“*scvi-tools: a library for deep probabilistic analysis of single-cell omics data*”.
- Nov 2020 CZI Seed Networks Annual Meeting,  
scvi-tools software demonstration

### POSTERS

- Apr 2021 Cold Spring Harbor conference on Probabilistic Modeling in Genomics,  
“*scvi-tools: a library for deep probabilistic analysis of single-cell omics data*”.
- Oct 2019 UC Berkeley Center for Computational Biology Retreat  
“*A joint model of RNA expression and surface protein abundance in single cells*”.

### OTHER MEETINGS AND EVENTS

- Apr 2021 [SingleCellOpenProblems](#): jamboree for expanding OpenProblems framework
- Nov 2020 UC Berkeley Computational Biology skills seminar,  
“*Single-cell data analysis with Scanpy and scvi-tools*”.
- 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 single-cell RNA-sequencing data.

## 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

- 2021 – PLOS Computational Biology  
 2020 – Machine Learning in Computational Biology (MLCB)

## Press

- Mar 2021 ["TotalVI: A transformative algorithm"](#). Berkeley Engineering News.