

# 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

### MANUSCRIPTS IN SUBMISSION

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

**Adam Gayoso**<sup>\*</sup>, Romain Lopez<sup>\*</sup>, Galen Xing<sup>\*</sup>, Pierre Boyeau, Katherine Wu, Michael Jayasuriya, Edouard Mehlman, Maxime Langevin, Yining Liu, Jules Samaran, Gabriel Mirrachi, 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

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. “Query to reference single-cell integration with transfer learning”. In: *Nature Biotechnology* (*In press*) (2021). [\[PDF\]](#).

**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). [\[PDF\]](#).

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). [\[PDF\]](#).

#### REVIEW ARTICLES

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

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

|          |   |
|----------|---|
| 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 at Pfizer                              |
| Feb 2020 | Journal club at 10x Genomics                                |

#### CONTRIBUTED TALKS

|          |  |
|----------|--|
| 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

|          |   |
|----------|---|
| Apr 2021 | Cold Spring Harbor conference on Probabilistic Modeling in Genomics |
| Oct 2019 | UC Berkeley Center for Computational Biology Retreat                |

## 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 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 Workshop (MLCB)

**Press**

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