

Adam Gayoso

adamgayoso@berkeley.edu | adamgayoso.com | github.com/adamgayoso

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

Employment

- May – Sep 2022 Research Scientist Intern, Science team
DEEPMIND
Advisor: Sara-Jane Dunn
- Jan – Jun 2018 Junior Computational Biologist
SLOAN KETTERING INSTITUTE
Advisor: Dana Pe'er
- Summer 2017 Research Assistant
SLOAN KETTERING INSTITUTE
Advisor: Dana Pe'er
- Spring 2016 Research Assistant
UC BERKELEY SCHOOL OF PUBLIC HEALTH
Advisor: Lee W. Riley

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. Pierre Boyeau, Jeffrey Regier, **Adam Gayoso**, Michael I. Jordan, Romain Lopez, and Nir Yosef. “An Empirical Bayes Method for Differential Expression Analysis of Single Cells with Deep Generative Models”. In: *bioRxiv* (2022). [\[PDF\]](#).

2. **Adam Gayoso***, Philipp Weiler*, Mohammad Lotfollahi, Dominik Klein, Justin Hong, Aaron Streets, Fabian J. Theis, and Nir Yosef. “Deep generative modeling of transcriptional dynamics for RNA velocity analysis in single cells”. In: *bioRxiv* (2022). [\[PDF\]](#).

JOURNAL ARTICLES

1. Tal Ashuach, Daniel A. Reidenbach, **Adam Gayoso**, and Nir Yosef. “PeakVI: A deep generative model for single-cell chromatin accessibility analysis”. In: *Cell Reports Methods* (2022). [\[PDF\]](#).
2. Vitalii Kleshchevnikov, Artem Shmatko, Emma Dann, Alexander Aivazidis, Hamish W. King, Tong Li, Rasa Elmentaite, Artem Lomakin, Veronika Kedlian, **Adam Gayoso**, Mika Sarkin Jain, Jun Sung Park, Lauma Ramona, Elizabeth Tuck, Anna Arutyunyan, Roser Vento-Tormo, Moritz Gerstung, Louisa James, Oliver Stegle, and Omer Ali Bayraktar. “Cell2location maps fine-grained cell types in spatial transcriptomics”. In: *Nature Biotechnology* (2022). [\[PDF\]](#).
3. 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* (2022). [\[PDF\]](#).
4. **Adam Gayoso***, Romain Lopez*, Galen Xing*, Pierre Boyeau, Valeh Valiollah Pour Amiri, Justin Hong, 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, Vitalii Kleshchevnikov, Carlos Talavera-Lopez, Lior Pachter, Fabian J Theis, Aaron Streets, Michael I Jordan, Jeffrey Regier, and Nir Yosef. “A Python library for probabilistic analysis of single-cell omics data”. In: *Nature Biotechnology* (2022). [\[PDF\]](#).
5. **The Tabula Sapiens Consortium**. “The Tabula Sapiens: A multiple-organ, single-cell transcriptomic atlas of humans”. In: *Science* (2022). [\[PDF\]](#).
6. **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). [\[PDF\]](#).
7. Valentine Svensson, **Adam Gayoso**, Nir Yosef, and Lior Pachter. “Interpretable factor models of single-cell RNA-seq via variational autoencoders”. In: *Bioinformatics* (2020). [\[PDF\]](#).
8. 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). [\[PDF\]](#).
9. 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, Justin Hong, **Adam Gayoso**, Michael I. Jordan, Elham Azizi, and Nir Yosef. “Deep generative modeling for quantifying sample-level heterogeneity in single-cell omics”. In: *Machine Learning in Computational Biology (Oral presentation)*. 2022. [\[PDF\]](#).
2. 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. [\[PDF\]](#).
3. 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 (Oral presentation)*. 2019. [\[PDF\]](#).
4. **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. [\[PDF\]](#).

(* denotes equal contribution)

Software

- 2022 – [scverse](#) – Core developer for consortium organized around Scanpy ecosystem and maintenance of core single-cell omics 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.

Presentations

INVITED TALKS

- | | |
|----------|---|
| May 2022 | Wellcome Sanger Institute, Bayraktar Group |
| Apr 2022 | Indiana University CNS Showcase |
| Nov 2021 | CZI Essential Open Source Software for Science Annual Meeting |
| 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

Nov 2021	CSHL Single Cell Analyses (Lightning talk)
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

Nov 2021	CSHL Single Cell Analyses
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

May 2022	Assembling tissue references meeting, CZI Science
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

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 – 2022	Admissions committee for UC Berkeley Computational Biology Graduate Group
2020 – 2022	UC Berkeley Computational Biology Skills Seminar Co-coordinator

Journal and conference reviewing

ICML Workshop on Computational Biology, Program Committee, 2022
PLOS Computational Biology, 2021
Machine Learning in Computational Biology Workshop (MLCB), 2020 – 2021

Press

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