

Adam Gayoso

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Professional experience

2023 – Research Scientist
Google DeepMind, London, UK

Education

2018 – 2023 **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

Publications

MANUSCRIPTS IN SUBMISSION

1. **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* (2023). [PDF].

JOURNAL ARTICLES

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: *Proceedings of the National Academy of Sciences (in press)* (2023). [PDF].

2. Isaac Virshup*, Danila Bredikhin*, Lukas Heumos*, Giovanni Palla*, Gregor Sturm*, **Adam Gayoso***, Ilia Kats, Mikaela Koutrouli, Philipp Angerer, Volker Bergen, Pierre Boyeau, Maren Büttner, Gokcen Eraslan, David Fischer, Max Frank, Justin Hong, Michal Klein, Marius Lange, Romain Lopez, Mohammad Lotfollahi, Malte D. Luecken, Fidel Ramirez, Jeffrey Regier, Sergei Rybakov, Anna C. Schaar, Valeh Valiollah Pour Amiri, Philipp Weiler, Galen Xing, Bonnie Berger, Dana Pe’er, Aviv Regev, Sarah A. Teichmann, Francesca Finotello, F. Alexander Wolf, Nir Yosef, Oliver Stegle, Fabian J. Theis, and Scverse Community. “The scverse project provides a computational ecosystem for single-cell omics data analysis”. In: *Nature Biotechnology* (2023). [PDF].

3. 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].

4. 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). [\[PDF\]](#).
5. 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). [\[PDF\]](#).
6. **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). [\[PDF\]](#).
7. **The Tabula Sapiens Consortium**. “The Tabula Sapiens: A multiple-organ, single-cell transcriptomic atlas of humans”. In: *Science* (2022). [\[PDF\]](#).
8. **Adam Gayoso***, Zoë Steier*, Romain Lopez, Jeffrey Regier, Kristopher L Nazon, Aaron Streets, and Nir Yosef. “Joint probabilistic modeling of single-cell multi-omic data with totalVI”. In: *Nature Methods* (2021). [\[PDF\]](#).
9. Valentine Svensson, **Adam Gayoso**, Nir Yosef, and Lior Pachter. “Interpretable factor models of single-cell RNA-seq via variational autoencoders”. In: *Bioinformatics* (2020). [\[PDF\]](#).
10. Manu Setty, Vaidotas Kisieliovas, 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). [\[PDF\]](#).
11. 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)

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)

Prior employment

May – Sep 2022	Research Scientist Intern, DeepMind, <i>London, UK</i>
Jan – Jun 2018	Junior Computational Biologist, Pe’er Lab, Sloan Kettering Institute, <i>New York, NY</i>
Summer 2017	Research Assistant, Pe’er Lab, Sloan Kettering Institute, <i>New York, NY</i>
Spring 2016	Research Assistant, Riley Lab, UC Berkeley School of Public Health, <i>Berkeley, CA</i>

Software

2022 – 2023	scverse – Core developer for consortium organized around Scanpy ecosystem and maintenance of core single-cell omics software.
2019 – 2023	scvi-tools – A library for deep probabilistic analysis of single-cell omics data.
2017 – 2023	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

Nov 2022 CZI Single-Cell Biology Annual Meeting Pre-Meeting
 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 – 2023 scvi-tools team. UNIVERSITY OF CALIFORNIA, BERKELEY
 Recruited and mentored four research engineers, one master's student, and one undergraduate student. Designed screening exams, conducted interviews, and managed project. Team members advanced to top PhD programs (UC Berkeley, Stanford, Columbia).
 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 – 2023 UC Berkeley Computational Biology [Skills Seminar](#) Co-coordinator
 2020 – 2022 Admissions committee for UC Berkeley Computational Biology Graduate Group

Journal and conference reviewing

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

Press

["Meet the Single-Cell Scientists Mapping Cells in the Human Body"](#). Chan Zuckerberg Initiative Science Blog. Dec 2022.

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