Adam Gayoso

Research Scientist
Google DeepMind
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Education

Ph.D. Computational Biology   2018 - 2023
University of California, Berkeley
Advisors: Aaron Streets, Nir Yosef

M.S. Computer Science   2016 - 2017
Columbia University

B.S. (cum laude) Operations Research: Engineering Management Systems   2011 - 2015
Columbia University

Employment

Research Scientist   2023 -
Google DeepMind, *London, UK*

Research Scientist Intern   May 2022 - Sep 2022
DeepMind, *London, UK*

Junior Computational Biologist, Pe'er Lab   Jan 2018 - Jun 2018
Sloan Kettering Institute, *New York, NY*

Research Assistant, Pe'er Lab   Summer 2017
Sloan Kettering Institute, *New York, NY*

Research Assistant, Riley Lab   Spring 2016
UC Berkeley School of Public Health, *Berkeley, CA*

Publications

(* denotes equal contribution)

Journal Articles

1. **Adam Gayoso***, Philipp Weiler*, Mohammad Lotfollahi, Dominik Klein, Justin Hong, Aaron Streets, Fabian J. Theis, Nir Yosef. "Deep generative modeling of transcriptional dynamics for RNA velocity analysis in single cells". In: *Nature Methods* (2023) [link]

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, Scverse Community. "The scverse project provides a computational ecosystem for single-cell omics data analysis". In: *Nature Biotechnology* (2023) [link]

3. Pierre Boyeau, Jeffrey Regier, **Adam Gayoso**, Michael I. Jordan, Romain Lopez, 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* (2023) [link]

4. The Tabula Sapiens Consortium. "The tabula sapiens: A multiple-organ, single-cell transcriptomic atlas of humans". In: *Science* (2022) [link]

5. Tal Ashuach, Daniel A. Reidenbach, **Adam Gayoso**, Nir Yosef. "PeakVI: A deep generative model for single-cell chromatin accessibility analysis". In: *Cell Reports Methods* (2022) [link]

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 Veiga Beltrame da, Vitalii Kleshchevnikov, Carlos Talavera-Lopez, Lior Pachter, Fabian J Theis, Aaron Streets, Michael I Jordan, Jeffrey Regier, Nir Yosef. "A Python library for probabilistic analysis of single-cell omics data". In: *Nature Biotechnology* (2022) [link]

7. 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, Omer Ali Bayraktar. "Cell2location maps fine-grained cell types in spatial transcriptomics". In: *Nature Biotechnology* (2022) [link]

8. 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, Fabian J. Theis. "Mapping single-cell data to reference atlases by transfer learning". In: *Nature Biotechnology* (2022) [link]

9. **Adam Gayoso***, Zoë Steier*, Romain Lopez, Jeffrey Regier, Kristopher L Nazor, Aaron Streets, Nir Yosef. "Joint probabilistic modeling of single-cell multi-omic data with totalVI". In: *Nature Methods* (2021) [link]

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

11. Manu Setty, Vaidotas Kiseliovas, Jacob Levine, **Adam Gayoso**, Linas Mazutis, Dana Pe'er. "Characterization of cell fate probabilities in single-cell data with Palantir". In: *Nature Biotechnology* (2019) [link]

12. Sheila Adams-Sapper, **Adam Gayoso**, Lee. W. Riley. "Stress-adaptive responses associated with high-level carbapenem resistance in KPC-Producing Klebsiella pneumoniae". In: *Journal of Pathogens* (2018) [link]

Review Articles

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

Refereed Workshop Papers

1. Pierre Boyeau, Justin Hong, **Adam Gayoso**, Michael I. Jordan, Elham Azizi, Nir Yosef. "Deep generative modeling for quantifying sample-level heterogeneity in single-cell omics". In: *Machine learning in computational biology (oral presentation)* (2022) [link]

2. Pierre Boyeau, Romain Lopez, Jeffrey Regier, **Adam Gayoso**, Michael I. Jordan, Nir Yosef. "Deep generative models for detecting differential expression in single cells". In: *Machine learning in computational biology* (2019) [link]

3. **Adam Gayoso**, Romain Lopez, Zoë Steier, Jeffrey Regier, Aaron Streets, Nir Yosef. "A joint model of RNA expression and surface protein abundance in single cells". In: *Machine learning in computational biology* (2019) [link]

4. Oscar Clivio, Romain Lopez, Jeffrey Regier, **Adam Gayoso**, Michael I. Jordan, Nir Yosef. "Detecting zero-inflated genes in single-cell transcriptomics data". In: *Machine learning in computational biology (oral presentation)* (2019) [link]

Grants, honors & awards

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

Software

scverse - Core developer for consortium organized around Scanpy ecosystem and maintenance of core single-cell omics software.	2022 - 2023
scvi-tools - A library for deep probabilistic analysis of single-cell omics data.	2021
DoubletDetection - A package for detecting doublets in scRNA-seq data.	2017

Presentations

Invited talks

Wellcome Sanger Institute, Bayraktar Group	May 2022
Indiana University CNS Showcase	Apr 2022
CZI Essential Open Source Software for Science Annual Meeting	Nov 2021
Research in progress seminar, Division of Pulmonary and Critical Care Medicine, Northwestern University	Oct 2021
Seminar, Celsius Therapeutics	May 2021
Single cell user group, NIH	May 2021
Kundaje Lab Journal Club, Stanford University	Apr 2021
Microsoft Research Health Futures Biomedical Computing team	Feb 2021

Single cell workshop, Pfizer	Oct 2020
Journal club, 10x Genomics	Feb 2020

Contributed talks

CSHL Single Cell Analyses (Lightning talk)	Nov 2021
CZI Single Cell Biology Annual Meeting	Oct 2021
CZI Seed Networks Computational Biology Meeting	Apr 2021
UC Berkeley Center for Computational Biology Retreat	Mar 2021
CZI Seed Networks Annual Meeting	Nov 2020

Posters

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

Other meetings and events

CZI Single-Cell Biology Annual Meeting Pre-Meeting	Nov 2022
Assembling tissue references meeting, CZI Science	May 2022
SingleCellOpenProblems: jamboree for expanding OpenProblems framework	Apr 2021
AstraZeneca single-cell genomics group tutorial	Nov 2020
UC Berkeley Computational Biology skills seminar	Nov 2020
Normjam: normalization workshop for scRNA-seq data, CZI/NY Genome Center	Nov 2019

Teaching and mentorship experience

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)	2020 - 2023
Introduction to Computational Molecular and Cell Biology (BIO ENG C131) Graduate Student Instructor, University of California, Berkeley	Fall 2021
Doctoral Seminar in Computational Biology (COMPBIO 293) Graduate Student Instructor, University of California, Berkeley	Spring 2021

University service

UC Berkeley Computational Biology Skills Seminar Co-coordinator	2020 - 2023
Admissions committee for UC Berkeley Computational Biology Graduate Group	2020 - 2022

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   Dec 2022
Zuckerberg Initiative Science Blog.

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