

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 training grant
- 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 Nazon, 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. [\[PDF\]](#).

Employment

- | | |
|----------------|---|
| Jan – Jun 2018 | <p>Junior Computational Biologist. SLOAN KETTERING INSTITUTE
 <i>Advisor:</i> Dana Pe’er</p> <p>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.</p> |
| Summer 2017 | <p>Research Assistant. SLOAN KETTERING INSTITUTE
 <i>Advisor:</i> Dana Pe’er</p> <p>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.</p> |
| Spring 2016 | <p>Research Assistant. UC BERKELEY SCHOOL OF PUBLIC HEALTH
 <i>Advisor:</i> Lee W. Riley</p> <p>Developed pipeline to process and analyze RNA-seq data with application to carbapenem-resistant bacteria.</p> |

Presentations

INVITED TALKS

- | | |
|----------|---|
| Apr 2021 | <p>Kundaje Lab Journal Club, Stanford University
 <i>“scvi-tools: a library for deep probabilistic analysis of single-cell omics data”.</i></p> |
| Feb 2021 | <p>Microsoft Research Health Futures Biomedical Computing team,
 <i>“Deep generative modeling for single-cell multimodal omics”.</i></p> |
| Nov 2020 | <p>Berkeley Computational Biology skills seminar,
 <i>“Single-cell data analysis with Scanpy and scvi-tools”.</i></p> |
| Oct 2020 | <p>Single cell workshop at Pfizer,
 <i>“Deep generative modeling for single-cell transcriptomics and proteomics”.</i></p> |
| Feb 2020 | <p>Journal club at 10x Genomics,
 <i>“Bayesian modeling and automatic interpretation of scRNA-seq data”.</i></p> |

CONTRIBUTED TALKS

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

OTHER MEETINGS AND EVENTS

- Apr 2021 [SingleCellOpenProblems](#): jamboree for expanding OpenProblems framework
- Nov 2019 [Normjam](#): normalization workshop for scRNA-seq data, CZI/NY Genome Center

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.