

Lambda Moses (aka Dongyi/Lambda Lu)

Postdoctoral Fellow

Curriculum Vitae

August 2023

📍 Division of Biology and Biological Engineering,
California Institute of Technology
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Education

- 2017-2023 **PhD in biology** California Institute of Technology
Pasadena, CA
- Built Voyager geospatial exploratory spatial data analysis (ESDA) framework for spatial -omics
 - Analyses of history and sociology of the field of spatial transcriptomics in Museum of Spatial Transcriptomics book and review paper
 - Contributed to the kallisto bustools single cell RNA-seq pseudoalignment framework
 - PI: Lior Pachter
- 2013-2017 **Bachelor of Science** University of California, Los Angeles
Los Angeles, CA
- Molecular, cell, and developmental biology (highest departmental honors)
 - Computational and systems biology (valedictorian)
 - Summa cum laude, Phi Beta Kappa
 - Genome wide association study of liver lipid and iron phenotypes in hybrid mouse diversity panel
 - PI: Aldons J. Lysis

Research experiences

- 2023-present **Postdoctoral Fellow** California Institute of Technology
Pasadena, CA
- Comprehensive analyses of mouse adipose control and Itih5 knockout spatial transcriptomics data
 - Extension of Voyager to case control, multiple biological replica, and 3D data
 - PI: Lior Pachter

Software

1. Moses, L., Jackson, K., Luebbert, L., & Pachter, L. (2023). *Voyager: From geospatial to spatial omics*. <https://doi.org/10.18129/B9.bioc.Voyager>
2. Moses, L., & Pachter, L. (2023). *Integrating SingleCellExperiment with simple features in sf*. <https://doi.org/10.18129/B9.bioc.Voyager>
3. Moses, L., Jackson, K., & Pachter, L. (2023). *SFEData: Example SpatialFeatureExperiment datasets*. <https://doi.org/10.18129/B9.bioc.SFEData>
4. Jackson, K., Boeshaghi, A. S., Galvez-Merchan, A., Moses, L., & Pachter, L. (2023). *concordexR: Calculate the concordex coefficient*. <https://doi.org/10.18129/B9.bioc.concordexR>
5. Corso, D., Malfait, M., & Moses, L. (2021). *spatialDE: R wrapper for SpatialDE*. <https://doi.org/10.18129/B9.bioc.spatialDE>
6. Moses, L., & Pachter, L. (2019). *BUSpaRse: Kallisto | bustools r utilities*. <https://doi.org/10.18129/B9.bioc.BUSpaRse>
7. Moses, L. (2019). *TENxBUSData: Single cell dataset from 10x in BUS format*. <https://doi.org/10.18129/B9.bioc.TENxBUSData>

Presentations

- 2023 **Voyager: Exploratory spatial data analysis from geospatial to spatial -omics**
Workshop, Bioconductor Conference, Dana-Farber Cancer Institute, Harvard Medical School
- 2023 **Voyager: Exploratory spatial data analysis from geospatial to spatial -omics**
Invited talk, Cedars-Sinai Medical Center, Los Angeles

- 2023 **From geospatial to spatial -omics with SpatialFeatureExperiment and Voyager**
Invited talk, Advanced Biomedical Computation series, Brigham & Women's Hospital, Harvard Medical School
- 2022 **SpatialFeatureExperiment: An S4 Class Bringing Geospatial Tools To Spatial Omics**
Package demo, Bioconductor Conference, Seattle Children's Research Institute
- 2020 **Museum of Spatial Transcriptomics**
Short talk, Bioconductor Conference, virtual

Publications

1. Moses, L., Einarsson, P. H., Jackson, K., Luebbert, L., Booeshaghi, A. S., Antonsson, S., Melsted, P., & Pachter, L. (2023). *Voyager: Exploratory single-cell genomics data analysis with geospatial statistics*. <https://doi.org/10.1101/2023.07.20.549945>
2. Jackson, K., Booeshaghi, A. S., Gálvez-Merchán, Ángel, Moses, L., Chari, T., & Pachter, L. (2023). *Quantitative assessment of single-cell RNA-seq clustering with CONCORDEX*. <https://doi.org/10.1101/2023.06.28.546949>
3. Fuqua, B. K., Moses, L., McLachlan, S., Pan, C., Davis, R. C., Hui, S. T., Che, N., Zhou, Z., Ng, C., Charugundla, S., Blencowe, M., Saleem, Z., Miikeda, A., Ozdemir, B., Hui, C., Li, T., Stolin, C. L., Kozuch, M., Zhou, J., ... Lusk, A. J. (2023). *The genetic architecture of dietary iron overload and associated pathology in mice*. <https://doi.org/10.1101/2023.06.05.543764>
4. Moses, L., & Pachter, L. (2022). Museum of spatial transcriptomics. *Nature Methods*. <https://doi.org/10.1038/s41592-022-01409-2>
5. Melsted, P., Booeshaghi, A. S., Liu, L., Gao, F., Lu, L., Min, K. H., Veiga Beltrame, E. da, Hjörleifsson, K. E., Gehring, J., & Pachter, L. (2021). Modular, efficient and constant-memory single-cell RNA-seq preprocessing. *Nature Biotechnology*, 39(7), 813–818. <https://doi.org/10.1038/s41587-021-00870-2>