Lambda Moses (aka Dongyi/Lambda Lu)
Postdoctoral Scholar

Curriculum Vitae
March 2024

📍 Division of Biology and Biological Engineering, California Institute of Technology
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Research experiences

2023-present   **Postdoctoral scholar**   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

2017-2023   **Graduate researcher**   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

2015-2017   **Undergraduate researcher**   University of California, Los Angeles
Los Angeles, CA
➤ Genome wide association study of liver lipid phenotypes in iron overload in hybrid mouse diversity panel
➤ PI: Aldons J. Lusis

Education

2017-2023   **PhD in biology**   California Institute of Technology
Pasadena, CA

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

Software

Bioconductor R packages:

1. Moses, L., Huseynov, A., Jackson, K., Luebbert, L., & Pachter, L. (2023). *Voyager: From geospatial to spatial omics*. https://doi.org/10.18129/B9.bioc.Voyager
2. Moses, L., Huseynov, A., & Pachter, L. (2023). *Integrating SingleCellExperiment with simple features in sf*. https://doi.org/10.18129/B9.bioc.SpatialFeatureExperiment
3. Moses, L., Jackson, K., & Pachter, L. (2023). *SFEData: Example SpatialFeatureExperiment datasets*. https://doi.org/10.18129/B9.bioc.SFEData
4. Jackson, K., Booeshaghi, 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., Bray, N., Melsted, P., & Pachter, L. (2023). Voyager: Exploratory single-cell genomics data analysis with geospatial statistics. *bioRxiv*.

2. Moses, L., & Pachter, L. (2022). Museum of spatial transcriptomics. *Nature Methods*, *19*(5), 534–546.

3. Fuqua, B. K., Moses, L., McLachlan, S., Pan, C., Davis, R. C., Hui, S. T., Che, N., Zhou, Z., Ng, C., Charugundla, S., et al. (2023). The genetic architecture of dietary iron overload and associated pathology in mice. *bioRxiv*.

4. Moses, L. (2024). From geospatial to spatial -omics. *XRDS*, *30*(2), 16–19. https://doi.org/10.1145/3637459

5. Jackson, K. C., Booeshaghi, A. S., Gálvez-Merchán, Á., Moses, L., Chari, T., & Pachter, L. (2023). Quantitative assessment of single-cell RNA-seq clustering with CONCORDEX. *bioRxiv*.

6. Sullivan, D. K., Min, K. H., Hjörleifsson, K. E., Luebbert, L., Holley, G., Moses, L., Gustafsson, J., Bray, N. L., Pimentel, H., Booeshaghi, A. S., et al. (2023). Kallisto, bustools, and kb-python for quantifying bulk, single-cell, and single-nucleus RNA-seq. *bioRxiv*.

7. 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.

8. Gao, F., Veiga Beltrame, E. da, Gehring, J. A., Hjoerleifsson, K. E. E., Lu, L., Melsted, P., Ntranos, V., Pachter, L., & Svensson, V. (2019). The BUS format for single-cell RNA-seq processing and analysis. *Journal of Biomolecular Techniques: JBT*, *30*(Suppl), S62.