Lambda Moses (aka Dongyi/Lambda Lu)
Postdoctoral Scholar

Curriculum Vitae
February 2025

Department of Statistics,
Columbia University
she/her
+1 424 666 5899
dl3764@columbia.edu
lambdamoses

Research experiences

2024-present — **Postdoctoral scholar** — Columbia University
New York, NY
- ➤ Implementing on-disk functionalities of SpatialFeatureExperiment for interoperable analyses of large spatial -omics data
- ➤ Finding effects of technology and spatial aggregation scale on common downstream spatial -omics analyses
- ➤ Using Moran eigenvector spatial filtering to identify global and local negative spatial autocorrelation in spatial -omics data
- ➤ PI: Bianca Dumitrascu

2023-2024 — **Postdoctoral scholar** — California Institute of Technology
Pasadena, CA
- ➤ Implemented functionalities to work with large images and transcript spot geometries in SpatialFeatureExperiment
- ➤ 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
- ➤ Integrated geospatial data structure into SingleCellExperiment as a new data structure SpatialFeatureExperiment
- ➤ 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. (2025). *Alabaster.sfe: Language agnostic on disk serialization of SpatialFeatureExperiment*. https://pachterlab.github.io/alabaster.sfe/
2. Moses, L., Huseynov, A., Jackson, K., Luebbert, L., & Pachter, L. (2024). *Voyager: From geospatial to spatial omics*. https://doi.org/10.18129/B9.bioc.Voyager
3. Moses, L., Huseynov, A., & Pachter, L. (2024). *Integrating SingleCellExperiment with simple features in sf*. https://doi.org/10.18129/B9.bioc.SpatialFeatureExperiment

4. Moses, L., Jackson, K., & Pachter, L. (2024). *SFEData: Example SpatialFeatureExperiment datasets*. https: //doi.org/10.18129/B9.bioc.SFEData
5. Jackson, K., Booeshaghi, A. S., Galvez-Merchan, A., Moses, L., & Pachter, L. (2024). *concordexR: Calculate the concordex coefficient*. https://doi.org/10.18129/B9.bioc.concordexR
6. Corso, D., Malfait, M., & Moses, L. (2021). *spatialDE: R wrapper for SpatialDE*. https://doi.org/10.18129/B9.bioc. spatialDE
7. Moses, L., & Pachter, L. (2019). *BUSpaRse: Kallisto | bustools r utilities*. https://doi.org/10.18129/B9.bioc.BUSpaRse
8. Moses, L. (2019). *TENxBUSData: Single cell dataset from 10x in BUS format*. https://doi.org/10.18129/B9.bioc. TENxBUSData

Presentations

2024 **Exploratory spatial data analysis from single molecules to multiple samples**
Workshop, Bioconductor Conference, Van Andel Institute, Grand Rapids, MI
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*, 2023–2007.
2. Moses, L., & Pachter, L. (2022). Museum of spatial transcriptomics. *Nature Methods*, *19*(5), 534–546.
3. Rich, J. M., Moses, L., Einarsson, P. H., Jackson, K., Luebbert, L., Booeshaghi, A. S., Antonsson, S., Sullivan, D. K., Bray, N., Melsted, P., et al. (2024). The impact of package selection and versioning on single-cell RNA-seq analysis. *bioRxiv*.
4. Hutchison, W. J., Keyes, T. J., Consortium, T., Crowell, H. L., Serizay, J., Soneson, C., Davis, E. S., Sato, N., Moses, L., Tarlinton, B., et al. (2024). The tidyomics ecosystem: Enhancing omic data analyses. *Nature Methods*, 1–5.
5. Jackson, K. C., Booeshaghi, A. S., Gálvez-Merchán, Á., Moses, L., Chari, T., Kim, A., & Pachter, L. (2024). Identification of spatial homogeneous regions in tissues with concordex. *bioRxiv*.
6. 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*, 2023–2006.
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.
9. 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*, 2023–2011.
10. Moses, L. (2024). From geospatial to spatial-omics. *XRDS: Crossroads, The ACM Magazine for Students*, *30*(2), 16–19.