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Websites:

- [Personal Github](#), [Organizational Github](#)
- [Web-based Tools](#)
- [NCBI Bibliography](#)

Professional Summary

Bioinformatics scientist and computational biology lead with a Ph.D. in Genomics and 8+ years of experience providing end-to-end computational support for large-scale, high-throughput genomic research. **Leads the Computational Biology Unit within the Biostatistics and Computational Biology Shared Resource at the University of Florida Health Cancer Institute**, partnering with investigators to define experimental design and analytical strategy across a broad range of NGS platforms, including spatial transcriptomics, single-cell multimodal omics, bulk and single-cell RNA-seq, ChIP-seq/CUT&RUN, and whole exome/genome sequencing. Builds and maintains automated, reproducible analysis pipelines (Snakemake, Nextflow) in HPC environments, develops documentation and SOPs to standardize workflows across a shared-resource core, and trains and mentors staff and trainees in reproducible analysis practices. Regularly contributes computational expertise to manuscripts and grant proposals, and communicates complex analyses clearly to investigators and collaborators across a range of technical backgrounds.

Current position

University of Florida Health Cancer Institute
Biostatistics and Computational Biology Shared Resource
Computational Biology Unit Lead

Gainesville, FL

Feb 2026-present

Skills

Pipeline Development: Workflow orchestration (Snakemake, Nextflow), containerization (Docker, Singularity, Podman), version control (Git), HPC environments (10+ years), cloud computing familiarity

Web Development & Infrastructure: Web application development and deployment using Podman, interactive visualization tools, knowledge management systems, collaborative research infrastructure

NGS & Multi-Omics: RNA-seq (bulk and single-cell), spatial transcriptomics/proteomics, single-cell multimodal omics, ChIP-seq/CUT&RUN, epigenomics assays, whole exome/genome sequencing, variant calling/annotation, untargeted metabolomics

Programming & Analysis: Python, R (10+ years each), bash/Linux, statistical modeling, machine learning (scikit-learn, regression/classification methods), database design (SQLite)

Domain Expertise: Computational genomics, cancer biology, biomarker discovery, clinical data integration, cross-functional collaboration with scientific and clinical teams

Core & Collaborative Research Support: Experimental design consultation with PIs and study teams, SOP development and documentation, cross-project workflow standardization, staff and trainee training/mentorship, grant and manuscript support

Education

University of Florida, College of Medicine

Gainesville, FL

Ph.D., Genetics & Genomics

December 2017

Oberlin College

Oberlin, OH

Bachelor of Arts, Biology

June 2011

Work Experience

Computational Biology Lead | UF Health Cancer Institute, Gainesville, FL | Feb 2026–Present

- Drive research initiatives in spatial transcriptomics and multi-omics, taking end-to-end ownership from analysis design through publication
- Hands-on development and maintenance of web-deployed research tools, analytical pipelines and infrastructure
- Consult with PIs and study teams to guide experimental design and analytical strategy, provide exploratory analyses, present data clearly in sharable notebooks, and communicate insights relevant to next steps
- Bridge spatial transcriptomics and imaging/ML domains by collaborating with image analysis scientists to integrate modalities and advance mechanistic disease research
- Lead trainings in reproducible analysis practices
- Contribute computational expertise to grant proposals and manuscript preparation across multi-omics cancer research

Bioinformatics Analyst III | UF Health Cancer Institute, Gainesville, FL | Feb 2025–Feb 2026

- Design and deploy scalable, containerized analysis pipelines for diverse NGS platforms (scRNA-seq, spatial proteomics, ATAC-seq, CUT&RUN) using Snakemake/Nextflow
- Established organizational GitHub, documentation hub, SOPs, and web-deployed research applications, transforming siloed workflows into collaborative, reproducible infrastructure
- Develop automated reporting systems and interactive visualization tools that streamline data delivery and improve researcher accessibility
- Lead computational strategy for multi-omics cancer research projects, integrating datasets to identify molecular signatures of disease progression and treatment response
- Provide bioinformatics training and mentorship to graduate students in reproducible analysis practices
- Contribute computational expertise to grant proposals and manuscript preparation

Bioinformatics Analyst III | UF Health Dept. of Pathology & Immunology, Gainesville, FL | Oct 2023–Feb 2025

- Designed end-to-end analysis pipelines for NGS platforms (snRNA-seq, ChIP-seq, spatial proteomics) serving pathology and immunology researchers
- Applied machine learning to high-dimensional metabolomics data for clinical trial analysis, identifying molecular signatures predictive of glioblastoma treatment response (published *Int. J. Mol. Sci.*, 2024)
- Improved turnaround time for pay-for-service molecular pathology core by implementing reproducible R-based pipelines
- Led bioinformatics aspects of cancer biomarker projects investigating immune modulation in breast cancer and HuBMAP consortium spatial profiling research

Data Management Analyst III | UF Health Dept. of Pathology & Immunology, Gainesville, FL | Jan 2022–Oct 2023

- Implemented production pipelines for bulk RNA-seq, spatial transcriptomics, and untargeted metabolomics serving clinical researchers
- Applied advanced statistical methods and ML approaches to complex biological datasets
- Designed and coordinated data management systems for multi-investigator research projects

Postdoctoral Researcher | University of Florida, Gainesville, FL | Jan 2018–Dec 2021

- Developed computational workflows for analyzing 20 TB of NGS data across phylogenomic projects
- Published methods for extracting biological signals from complex genetic datasets spanning 1,000+ species (*Nature Communications*, 2024)
- Designed database systems (SQLite) for efficient querying of large-scale genomic data

Graduate Research Fellow | University of Florida, Gainesville, FL | Aug 2011–Dec 2017

- Designed computational workflows for analysis of NGS data.
- Published and presented research results in academic and public outlets.

Honors & Awards

- Basic Science Staff Researcher of the Year, UF Health Cancer Institute (2026)
 - Berns' Award for Excellence in Genetics, University of Florida Genetics Institute (2016)
 - University of Florida Alumni Fellowship, University of Florida Genetics Institute (2011–2015)
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Invited Talks & Workshops

Invited Workshop Leader, “Integrative Navigation and Analysis of Spatial Omics and Histology.” 2026 PCEN Virtual Scientific Symposium, Pediatric Centers of Excellence in Nephrology. March 23, 2026 (virtual).

Invited Speaker, “FUSION: Extracting Value from Images.” Scientific Highlights: Datasets and Tools, HuBMAP Last Hurrah, Rockville, MD. June 15, 2026 (in person).

Invited Workshop Leader, “Bioinformatics Workshop - Basics of Bulk RNA-Seq Analysis” UF Health Cancer Institute, Gainesville, FL. March 9, 2026 (in person). <https://ufhcc-bcbsr.github.io/res-bioinfo-rnaseq-workshop/>

Publications

Lightsey S, **Kates HR**, Shirlekar K, Brant JO, Sharma B. A Defined 3D Hydrogel Model Recapitulates Key Transcriptomic Features of Lung Adenocarcinoma. *Tissue Eng Part C Methods*. 2026 May;32(5):195-207. PubMed PMID: 42175837.

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Anvar S, Maharjan C, Chen Z, Somers JD, Jin Z, **Kates HR**, Ramirez SH, Andrews AM, Runyon BM, Carelock ME, Zhang Y, Liu J, Zhang W, Cui L. Senescent cancer cells facilitate metastasis by adhesion-mediated clustering and immune modulation. *Cancer Research. AACR*; 2026 April 17; San Diego, CA, United States

Tithi, T. I., Mo, J., Borcharding, N., Jo, S., **Kates, H. R.**, Cho, E., Cash, K. E., Honda, M., Wang, L., & Ahmed, K. K. (2025). The distinct roles of MSH2 and MLH1 in basal-like breast cancer and immune modulation. *bioRxiv*, 2023.07.20.549745.

Cuaycal, A. E., Fu, D. A., **Kates, H.**, Ewing, S., Chen, J., Brusko, M., Campbell-Thompson, M., & Mathews, C. E. (2025). GeoMx Digital Spatial Profiler Immuno-oncology (IO) Proteome Atlas (IPA) Assay for Human Pancreas.

Tasci E., Popa M., Zhuge Y., Chappidi S., Zhang L., Zgela T. C., Sproull M., Mackey M., **Kates H. R.**, ... & Krauze A. V. (2024). MetaWise: Combined Feature Selection and Weighting Method to Link the Serum Metabolome to Treatment Response and Survival in Glioblastoma. *Int. J. Mol. Sci.* 2024, 25, 10965. <https://doi.org/10.3390/ijms252010965>

Gibbons JA, Worthington LM, Chiu EG, **Kates HR**, Carter RR, Nelson R, Zhang M, Garrett TJ, Ho TTB. Severe anemia in preterm infants associated with increased bacterial virulence potential and metabolic disequilibrium. *Pediatr Res.* 2024 Oct 22. doi: 10.1038/s41390-024-03669-4. Epub ahead of print. PMID: 39438713.

Ravi, S., Barroso, D., Acosta, G., Kamat, M., **Kates, H.R.**, Garrett, T.J., & Abisambra, J.F. (2024). Repetitive Mild Traumatic Brain Injury Alters Microgliosis in the Thalamic Region and Disrupts Lipid Profile in Distinct Brain Regions. *Abstracts, Neurotrauma 2024*, San Francisco, California, June 9-12, 2024.

Finegan, C., Kates, H. R., Guralnick, R. P., Soltis, P. S., Resende Jr, M. F. R., Ané, J. M., Kirst, M., Folk, R. A., & Soltis, D. E. (2025). Convergent evolution of NFP-facilitated root nodule symbiosis. *Proceedings of the National Academy of Sciences*, 122(37), e2424902122.

Liu, S. Y., Yang, Y. Y., Tian, Q., Yang, Z. Y., Li, S. F., Valdes, P. J., Farnsworth, A., Kates, H. R., Siniscalchi, C. M., & Guralnick, R. P. (2025). An integrative framework reveals widespread gene flow during the early radiation of oaks and relatives in Quercoideae (Fagaceae). *Journal of Integrative Plant Biology*, 67(4), 1119-1141.

Folk, R. A., Maassoumi, A. A., Siniscalchi, C. M., **Kates, H. R.**, Soltis, D. E., Soltis, P. S., Belitz, M. B., & Guralnick, R. P. (2024). Phylogenetic diversity and regionalization in the temperate arid zone. *Journal of Systematics and Evolution*, 62(6), 1201-1217.

Gu, W., Zhang, T., Liu, S. Y., Tian, Q., Yang, C. X., Lu, Q., Fu, X. G., **Kates, H. R.**, Stull, G. W., & Soltis, P. S. (2024). Phylogenomics, reticulation, and biogeographical history of Elaeagnaceae. *Plant Diversity*, 46(6), 683-697.

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Gobin, C., Inkabi, S., Lattimore, C.C., Gu, T., Menefee, J.N., Rodriguez, M., **Kates, H.**, ... & Fredenburg, K.M. (2023). Investigating miR-9 as a mediator in laryngeal cancer health disparities. *Frontiers in Oncology*, 13, 1096882. doi: 10.3389/fonc.2023.1096882.

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Siniscalchi, C.M., **Kates, H.R.**, Soltis, P.S., Soltis, D.E., Guralnick, R.P., & Folk, R.A. (2022). Testing the evolutionary drivers of nitrogen-fixing symbioses in challenging soil environments. *bioRxiv*.

Fu, X.G., Liu, S.Y., Velzen, R., Stull, G.W., Tian, Q., Li, Y.X., ... **Kates, H.R.**, & Jin, J.J. (2022). Phylogenomic analysis of the hemp family (Cannabaceae) reveals deep cyto-nuclear discordance and provides new insights into generic relationships. *Journal of Systematics and Evolution*.

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Kates, H.R., Soltis D.E., and Soltis, P.S. 2016. Evolutionary and domestication history of *Cucurbita* (pumpkin and squash) species inferred from 44 nuclear loci. (Botany 2016 Abstracts, Botanical Society of America, ©2016, Savannah)

Garcia, N., Tharp E., **Kates, H.R.** et al. Preliminary analyses of genome size and secondary metabolite evolution in Lamiaceae. (Botany 2016 Abstracts, Botanical Society of America, ©2016, Savannah)

Kates, H.R., Soltis D.E., and Soltis, P.S. 2015. Species tree estimation in *Cucurbita* provides new insight into the genetic origins of crop species. (Florida Genetics Symposium 2015 Abstracts, University of Florida, ©2015, Gainesville)

Barrera, D., **Kates, H.R.,** Soltis, P.S., Soltis, D.E. 2016. Preparing nonviable *Cucurbita* seeds for next generation DNA sequencing to enable diverse collaborations in studies of crop wild relatives. (Botany 2016 Abstracts, Botanical Society of America, ©2016, Savannah)

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