MICHAEL I. LOVE
http://mikelove.github.io
February 27, 2026

EDUCATION

Dr. rer. nat., Computational Biology *Magna cum laude* **2013**
Freie Universität, Berlin, Germany & Max Planck Institute for Molecular Genetics

M.S., Statistics **2010**
Stanford University, Stanford, CA

B.S., Mathematics *With distinction* **2005**
Stanford University, Stanford, CA

PROFESSIONAL EXPERIENCE

Associate Professor **2022 - present**
Associate Director of Bioinformatics & Computational Biology (BCB) **2023 - present**
Assistant Professor **2016 - 2022**
Department of Genetics, Department of Biostatistics
University of North Carolina-Chapel Hill

Postdoctoral Research Fellow **2013 - 2016**
Supervisor: Rafael Irizarry
Department of Biostatistics, Harvard TH Chan School of Public Health

BOOKS AND CHAPTERS

- **Michael I Love**, "Statistical modeling of high dimensional counts." Ernesto Picardi (Ed.), *RNA Bioinformatics*, 2nd ed., (2021). Springer US. doi: 10.1007/978-1-0716-1307-8
- Rafael A Irizarry and **Michael I Love**, *Data Analysis for the Life Sciences with R*. (2016). Chapman and Hall/CRC. Available as PDF: https://leanpub.com/dataanalysisforthelifesciences/

SELECTION OF PEER-REVIEWED PUBLICATIONS

For complete list of publications and preprints, refer to my Google Scholar page.

1. Euphy Wu*, Noor P. Singh, Kwangbom Choi, Mohsen Zakeri, Matthew Vincent, Gary A. Churchill, Cheryl L. Ackert-Bicknell, Rob Patro, **Michael I. Love**. SEESAW: detecting isoform-level allelic imbalance accounting for inferential uncertainty.
Genome Biology, (2023). doi: 10.1186/s13059-023-03003-x

2. Wancen Mu*, Eric Davis, Stuart Lee, Mikhail Dozmorov, Douglas H. Phanstiel, **Michael I. Love**. bootRanges: Flexible generation of null sets of genomic ranges for hypothesis testing.
Bioinformatics, (2023). doi: 10.1093/bioinformatics/btad190

3. Eric S. Davis, Wancen Mu*, Stuart Lee, Mikhail G. Dozmorov, **Michael I. Love**, Douglas H. Phanstiel. matchRanges: Generating null hypothesis genomic ranges via covariate-matched sampling.
Bioinformatics, (2023). doi: 10.1093/bioinformatics/btad197

4. Wancen Mu*, Hirak Sarkar, Avi Srivastava, Kwangbom Choi, Rob Patro, **Michael I. Love**. Airpart: Interpretable statistical models for analyzing allelic imbalance in single-cell datasets.
Bioinformatics, btac212, (2022). doi: 10.1093/bioinformatics/btac212

5. Nil Aygün, Angela L. Elwell, Dan Liang, Michael J. Lafferty, Kerry E. Cheek, Kenan P. Courtney, Jessica Mory, Ellie Hadden-Ford, Oleh Krupa, Luis de la Torre-Ubieta, Daniel H. Geschwind, **Michael I. Love**, Jason L. Stein. Brain-trait-associated variants impact cell-type-specific gene regulation during neurogenesis.
American Journal of Human Genetics, (2021). doi: 10.1016/j.ajhg.2021.07.011

6. Sean D. McCabe*, Andrew B. Nobel, **Michael I. Love**. ACTOR: a latent Dirichlet model to compare expressed isoform proportions to a reference panel.
Biostatistics, kxab013, (2021). doi: 10.1093/biostatistics/kxab013

7. Anqi Zhu* [1], Nana Matoba[1], Emmaleigh Wilson, Amanda L. Tapia, Yun Li, Joseph G. Ibrahim, Jason L. Stein, **Michael I. Love**. MRLocus: identifying causal genes mediating a trait through Bayesian estimation of allelic heterogeneity.
PLOS Genetics, 17(4):e1009455, (2021). doi: 10.1371/journal.pgen.1009455

8. Arjun Bhattacharya*, Yun Li, **Michael I. Love**. Multi-omic strategies for transcriptome-wide prediction and association studies.
PLOS Genetics, 17(3):e1009398, (2021). doi: 10.1371/journal.pgen.1009398

9. Arjun Bhattacharya*, Alina M. Hamilton, Melissa A. Troester, **Michael I. Love**. DeCompress: tissue compartment deconvolution of targeted mRNA expression panels using compressed sensing.
Nucleic Acids Research, 49(8):e48, (2021). doi: 10.1093/nar/gkab031

10. Arjun Bhattacharya*, Montserrat Garcia-Closas, Andrew F. Olshan, Charles M. Perou, Melissa A. Troester, **Michael I. Love**. A framework for transcriptome-wide association studies in breast cancer in diverse study populations.
Genome Biology, 21(42) (2020). doi: 10.1186/s13059-020-1942-6

11. **Michael I. Love**, Charlotte Soneson, Peter F. Hickey, Lisa K. Johnson, N. Tessa Pierce, Lori Shepherd, Martin Morgan, Rob Patro. Tximeta: Reference sequence checksums for provenance identification in RNA-seq.
PLOS Computational Biology, (2020). doi: 10.1371/journal.pcbi.1007664

12. Anqi Zhu*, Avi Srivastava, Joseph G. Ibrahim, Rob Patro, **Michael I. Love**. Nonparametric expression analysis using inferential replicate counts.
Nucleic Acids Research, 47(18):e105, (2019). doi: 10.1093/nar/gkz622

13. Anqi Zhu*, Joseph G. Ibrahim, **Michael I. Love**. Heavy-tailed prior distributions for sequence count data: removing the noise and preserving large differences.
Bioinformatics, 35(12):2084-2092, (2018). doi: 10.1093/bioinformatics/bty895

14. **Michael I. Love**, Charlotte Soneson, and Rob Patro. Swimming downstream: statistical analysis of differential transcript usage following Salmon quantification.
F1000Research, 7:952, (2018). doi: 10.12688/f1000research.15398.3

15. Rob Patro, Geet Duggal, **Michael I Love**, Rafael A Irizarry, Carl Kingsford, Salmon provides fast and bias-aware quantification of transcript expression.
Nature Methods, 14(4):417, (2017). doi: 10.1038/nmeth.4197

16. **Michael I Love**, John B Hogenesch, Rafael A Irizarry, Modeling of RNA-seq fragment sequence bias reduces systematic errors in transcript abundance estimation.
Nature Biotechnology, 32(12):1287-1291, (2016). doi: 10.1038/nbt.3682

17. **Michael I Love**, Wolfgang Huber, Simon Anders, Moderated estimation of fold change and dispersion for RNA-seq data with DESeq2.
Genome Biology, 15(12):550+, (2014). doi: 10.1186/s13059-014-0550-8

DIGITAL SCHOLARSHIP

- **Tidyomics Project**: Open source software for tidy analysis of omics data. (GitHub)
- **DESeq2**: Differential expression analysis for RNA-seq. (Bioc)
- **apeglm**: Approximate posterior estimation for GLM coefficients. (Bioc)
- **tximport** / **tximeta**: Import transcript quantification with automatic metadata detection. (Bioc)
- **fishpond**: Nonparametric differential transcript expression with inferential replicates. (Bioc)
- **MRLocus**: Identifying causal genes affecting traits through summary QTL and GWAS data.
- **nullranges**: Modular tool to generate genomic ranges representing the null hypothesis. (Bioc)