MICHAEL I. LOVE

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EDUCATION

Dr. rer. nat., Computational Biology *Magna cum laude*   **2013**
Freie Universität, Berlin, Germany
Max Planck Institute for Molecular Genetics, Berlin, Germany
Advisors: Prof. Dr. Martin Vingron, Prof. Dr. Knut Reinert, Dr. Stefan Haas
Dissertation title: *Statistical Analysis of High-Throughput Sequence Count Data*

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

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

PROFESSIONAL EXPERIENCE

Associate Professor   **2022 - present**
Department of Biostatistics, Department of Genetics
University of North Carolina-Chapel Hill

Assistant Professor   **2016 - 2022**
University of North Carolina-Chapel Hill

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

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BOOKS AND CHAPTERS

- <u>**Michael I Love**</u>, "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 mikelove.github.io or Google Scholar.

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

2. 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, <u>**Michael I. Love**</u>, 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

3. 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

4. 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

5. 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

6. 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

7. 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

8. Sarah A. Reifeis*, Michael G. Hudgens, Mete Civelek, Karen L. Mohlke, **Michael I. Love**. Assessing exposure effects on gene expression.
Genetic Epidemiology, 44(6):601–610, (2020). doi: 10.1002/gepi.22324

9. **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

10. 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

11. 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

12. **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

13. **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

1. **DESeq2**: Differential expression analysis for RNA-seq. (Bioc)

2. **apeglm**: Approximate posterior estimation for GLM coefficients. (Bioc)

3. **tximport** / **tximeta**: Import transcript quantification with automatic metadata detection. (Bioc)

4. **fishpond**: Nonparametric differential transcript expression with inferential replicates. (Bioc)