

## 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
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## PROFESSIONAL EXPERIENCE

- Assistant Professor** 2016 - present  
Department of Biostatistics, Department of Genetics  
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

- **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](https://doi.org/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/>
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## SELECTION OF PEER-REVIEWED PUBLICATIONS

For complete list of publications and preprints, refer to [mikelove.github.io](http://mikelove.github.io) or [Google Scholar](#).

1. 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](https://doi.org/10.1016/j.ajhg.2021.07.011)
2. 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](https://doi.org/10.1093/biostatistics/kxab013)
3. Anqi Zhu\* <sup>1</sup>, Nana Matoba<sup>1</sup>, 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](https://doi.org/10.1371/journal.pgen.1009455)

4. 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](https://doi.org/10.1371/journal.pgen.1009398)
5. 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](https://doi.org/10.1093/nar/gkab031)
6. 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](https://doi.org/10.1186/s13059-020-1942-6)
7. 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](https://doi.org/10.1002/gepi.22324)
8. 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](https://doi.org/10.1371/journal.pcbi.1007664)
9. 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](https://doi.org/10.1093/nar/gkz622)
10. 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](https://doi.org/10.1093/bioinformatics/bty895)
11. 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](https://doi.org/10.1038/nmeth.4197)
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](https://doi.org/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](https://doi.org/10.1186/s13059-014-0550-8)

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## 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)