MICHAEL I. LOVE
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PERSONAL

University of North Carolina at Chapel Hill

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EDUCATION

Postdoctoral Research Fellow **2013 - 2016**
Supervisor: Rafael Irizarry
Department of Biostatistics and Computational Biology, Dana-Farber Cancer Institute
Department of Biostatistics, Harvard TH Chan School of Public Health

Dr. rer. nat., Computational Biology **2013**
Magna cum laude
Freie Universität, Berlin, Germany
Max Planck Institute for Molecular Genetics, Berlin, Germany
International Max Planck Research School for Computational Biology and Scientific Computing
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 **2005**
With distinction
Stanford University, Stanford, CA

PROFESSIONAL EXPERIENCE

Associate Professor **2022 - present**
Assistant Professor **2016 - 2022**
Department of Genetics,
Department of Biostatistics,
Member of Lineberger Comprehensive Cancer Center
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HONORS

- MAQC 2021 Scientist Research Award (3rd place)
- UNC Gillings Departmental Teaching Excellence and Innovation Award for 2020-21.
- UNC Center for Environmental Health and Susceptibility (CEHS) Recruitment Award for 2019.
- UNC Junior Faculty Development Award for 2017.

BIBLIOGRAPHY

Books and chapters:

1. **Michael I. Love**, "Statistical modeling of high dimensional counts." *RNA Bioinformatics*, 2nd ed., edited by Ernesto Picardi, Springer US, 2021, pp. 97–134. doi: 10.1007/978-1-0716-1307-8
2. Rafael A. Irizarry and **Michael I. Love**, *Data Analysis for the Life Sciences with R*, Chapman and Hall/CRC, 2016, 376 pages. doi: 10.1201/9781315367002

Refereed papers/articles:

Key: " * " for work first authored by an advisee.

1. Andrea Walens, Sarah C Van Alsten, Linnea T Olsson, Markia A Smith, Alex Lockhart, Xiaohua Gao, Alina M Hamilton, Erin L Kirk, **Michael I Love**, Gaorav P Gupta, Charles M Perou, Cyrus Vaziri, Katherine A Hoadley, Melissa A Troester. RNA-based classification of homologous recombination deficiency in racially-diverse patients with breast cancer.
Cancer Epidemiology, Biomarkers and Prevention, OAP, (2022). doi: 10.1158/1055-9965.EPI-22-0590

2. Markia A Smith, Sarah C Van Alsten, Andrea Walens, Jeffrey S Damrauer, Ugwuji N Maduekwe, Russell R Broaddus, **Michael I Love**, Melissa A Troester, Katherine A Hoadley. DNA Damage Repair Classifier Defines Distinct Groups in Hepatocellular Carcinoma.
Cancers, 14(17):4282, (2022). doi: 10.3390/cancers14174282

3. Dan Liang, Nil Aygün, Nana Matoba, Folami Y. Ideraabdullah, **Michael I. Love**, Jason L. Stein. Inference of putative cell-type specific imprinted regulatory elements and genes during human neuronal differentiation.
Human Molecular Genetics, ddac207, (2022). doi: 10.1093/hmg/ddac207

4. Amber N Hurson, Mustapha Abubakar, Alina M Hamilton, Kathleen Conway, Katherine A Hoadley, **Michael I Love**, Andrew F Olshan, Charles M Perou, Montserrat Garcia-Closas, Melissa A Troester. Prognostic significance of RNA-based TP53 pathway function among estrogen receptor positive and negative breast cancer cases.
NPJ Breast Cancer 8(1):1–10, (2022). doi: 10.1038/s41523-022-00437-7

5. 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

6. Nicole E. Kramer, Eric S. Davis, Craig D. Wenger, Erika M. Deoudes, Sarah M. Parker, **Michael I. Love**, Douglas H. Phanstiel. Plotgardener: cultivating precise multi-panel figures in R.
Bioinformatics, 38(7):2042–2045, (2022). doi: 10.1093/bioinformatics/btac057

7. Xiaoliang Wang, Hongjie Chen, Pooja Middha Kapoor, Yu-Ru Su, Manjeet K. Bolla, Joe Dennis, Alison M. Dunning, Michael Lush, Qin Wang, Kyriaki Michailidou, Paul D.P. Pharoah, John L. Hopper, Melissa C. Southey, Stella Koutros, Laura E. Beane Freeman, Jennifer Stone, Gad Rennert, Rana Shibli, Rachel A. Murphy, Kristan Aronson, Pascal Guénel, Thérèse Truong, Lauren R. Teras, James M. Hodge, Federico Canzian, Rudolf Kaaks, Hermann Brenner, Volker Arndt, Reiner Hoppe, Wing-Yee Lo, Sabine Behrens, Arto Mannermaa, Veli-Matti Kosma, Audrey Jung, Heiko Becher, Graham G. Giles, Christopher A. Haiman, Gertraud Maskarinec, Christopher Scott, Stacey Winham, Jacques Simard, Mark S. Goldberg, Wei Zheng, Jirong Long, Melissa A. Troester, **Michael I. Love**, Cheng Peng, Rulla Tamimi, Heather Eliassen, Montserrat García-Closas, Jonine Figueroa, Thomas Ahearn, Rose Yang, D. Gareth Evans, Anthony Howell, Per Hall, Kamila Czene, Alicja Wolk, Dale P. Sandler, Jack A. Taylor, Anthony J. Swerdlow, Nick Orr, James V. Lacey, Sophia Wang, Håkan Olsson, Douglas F. Easton, Roger L. Milne, Li Hsu, Peter Kraft, Jenny Chang-Claude, Sara Lindström. A Genome-Wide Gene-Based Gene–Environment Interaction Study of Breast Cancer in More than 90,000 Women.
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8. Gieira S Jones, Katherine A Hoadley, Halei Benefield, Linnea T Olsson, Alina M Hamilton, Arjun Bhattacharya, Erin L Kirk, Heather J Tipaldos, Jodie M Fleming, Kevin P Williams, **Michael I Love**, Hazel B Nichols, Andrew F Olshan, Melissa A Troester. Racial differences in breast cancer outcomes by hepatocyte growth factor pathway expression.
Breast Cancer Research and Treatment 192(2):447–455, (2022). doi: 10.1007/s10549-021-06497-w

9. Sanah N. Vohra, Katherine E. Reeder-Hayes, Hazel B. Nichols, Marc A. Emerson, **Michael I. Love**, Andrew F. Olshan, Melissa A. Troester. Breast cancer treatment patterns by age and time since last pregnancy in the Carolina Breast Cancer Study Phase III.
Breast Cancer Research and Treatment, 192:435–445, (2022). doi: 10.1007/s10549-022-06511-9

10. Amber N. Hurson, Mustapha Abubakar, Alina M. Hamilton, Kathleen Conway, Katherine A. Hoadley, **Michael I. Love**, Andrew F. Olshan, Charles M. Perou, Montserrat Garcia-Closas and Melissa A. Troester. TP53 pathway function, estrogen receptor status, and breast cancer risk factors in the Carolina Breast Cancer Study.
Cancer Epidemiology, Biomarkers, and Prevention, 31(1):124–131, (2022). doi: 10.1158/1055-9965.EPI-21-0661

11. Achal Patel, Montserrat Garcia-Closas, Andrew F. Olshan, Charles M. Perou, Melissa A. Troester, **Michael I. Love**, Arjun Bhattacharya. Gene-level germline contributions to clinical risk of recurrence scores in Black and White breast cancer patients.

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12. Nana Matoba, **Michael I. Love**, Jason L. Stein. Evaluating brain structure traits as endophenotypes using polygenicity and discoverability.
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13. Gieira S. Jones, Katherine A. Hoadley, Linnea T. Olsson, Alina M. Hamilton, Arjun Bhattacharya, Erin L. Kirk, Heather J. Tipaldos, Jodie M. Fleming, **Michael I. Love**, Hazel B. Nichols, Andrew F. Olshan, Melissa A. Troester Hepatocyte growth factor pathway expression in breast cancer by race and subtype.
Breast Cancer Research, 23(1):1–10, (2022). doi: 10.1186/s13058-021-01460-5

14. Hannah J. Perrin, Kevin W. Currin, Swarooparani Vadlamudi, Gautam K. Pandey, Kenneth K. Ng, Martin Wabitsch, Markku Laakso, **Michael I. Love**, Karen L. Mohlke. Chromatin accessibility and gene expression during adipocyte differentiation identify context-dependent effects at cardiometabolic GWAS loci.
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15. 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.
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16. Dan Liang, Angela L. Elwell, Nil Aygün, Michael J. Lafferty, Oleh Krupa, Kerry E. Cheek, Kenan P. Courtney, Marianna Yusupova, Melanie E. Garrett, Allison Ashley-Koch, Gregory E. Crawford, **Michael I. Love**, Luis de la Torre-Ubieta, Daniel H. Geschwind, Jason L. Stein. Cell-type specific effects of genetic variation on chromatin accessibility during human neuronal differentiation.
Nature Neuroscience, 24:941–953 (2021). doi: 10.1038/s41593-021-00858-w

17. Scott Van Buren*, Hirak Sarkar, Avi Srivastava, Naim U. Rashid, Rob Patro, **Michael I. Love**. Compression of quantification uncertainty for scRNA-seq counts.
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18. Arjun Bhattacharya*, Alina M. Hamilton, Melissa A. Troester, **Michael I. Love**. DeCompress: tissue compartment deconvolution of targeted mRNA expression panels using compressed sensing.
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19. Arjun Bhattacharya* [1], Alina M. Hamilton[1], Helena Furberg, Eugene Pietzak, Mark P. Purdue, Melissa A. Troester, Katherine A. Hoadley†, **Michael I. Love**†. An approach for normalization and quality control for NanoString RNA expression data.
Briefings in Bioinformatics, 22(3):bbaa163, (2021). doi: 10.1093/bib/bbaa163

20. 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.
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21. Arjun Bhattacharya*, Yun Li, **Michael I. Love**. MOSTWAS: multi-omic strategies for transcriptome-wide prediction and association studies.
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22. Halei C. Benefield, Katherine E. Reeder-Hayes, Hazel B. Nichols, Benjamin C. Calhoun, **Michael I. Love**, Erin L. Kirk, Joseph Geradts, Katherine A. Hoadley, Stephen R. Cole, H. Shelton Earp, Andrew F. Olshan, Lisa A. Carey, Charles M. Perou, Melissa A. Troester. Outcomes of Hormone-Receptor Positive, HER2-Negative Breast Cancers by Race and Tumor Biological Features.
JNCI Cancer Spectrum, 5(1):pkaa072, (2020). doi: 10.1093/jncics/pkaa072

23. Hyo Young Choi, Heejoon Jo, Xiaobei Zhao, Katherine A. Hoadley, Scott Newman, Jeremiah Holt, Michele C. Hayward, **Michael I. Love**, J. S. Marron, D. Neil Hayes. SCISSOR: a framework for identifying structural changes in RNA transcripts.
Nature Communications, 12(286), (2021). doi: 10.1038/s41467-020-20593-3

24. Sanah N. Vohra, Andrea Walens, Alina M. Hamilton, Mark E. Sherman, Pepper Schedin, Hazel B. Nichols, Katherine E. Reeder-Hayes, Andrew F. Olshan, **Michael I. Love** and Melissa A. Troester. Molecular and clinical characterization of postpartum-associated breast cancer in the Carolina Breast Cancer Study Phase I-III, 1993-2013.
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25. 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

26. Joshua P. Zitovsky, **Michael I. Love**. Fast effect size shrinkage software for beta-binomial models of allelic imbalance.
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Genome Biology, 21(1):42, (2020). doi: 10.1186/s13059-020-1942-6

28. Avi Srivastava, Laraib Malik, Hirak Sarkar, Mohsen Zakeri, Fatemeh Almodaresi, Charlotte Soneson, **Michael I. Love**, Carl Kingsford, Rob Patro. Alignment and mapping methodology influence transcript abundance estimation.
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30. Sarah A. Reifeis*, Michael G. Hudgens, Mete Civelek, Karen L. Mohlke, **Michael I. Love**. Assessing exposure effects on gene expression.
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32. Charlotte Soneson, Federico Marini, Florian Geier, **Michael I. Love**, Michael B. Stadler. ExploreModelMatrix: Interactive exploration for improved understanding of design matrices and linear models in R.
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Americal Journal of Human Genetics, 105(4):773–787, (2019). doi: 10.1016/j.ajhg.2019.09.001

37. 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

38. Charlotte Soneson, **Michael I. Love**, Rob Patro, Shobbir Hussain, Dheeraj Malhotra, Mark D. Robinson. A junction coverage compatibility score to quantify the reliability of transcript abundance

estimates and annotation catalogs.
Life Science Alliance, 2(1):e201800175, (2019). doi: 10.26508/lsa.201800175

39. Lindsay A. Williams, Katherine A. Hoadley, Hazel B. Nichols, Joseph Geradts, Charles M. Perou, **Michael I. Love**, Andrew F. Olshan, Melissa A. Troester. Differences in race, molecular and tumor characteristics among women diagnosed with invasive ductal and lobular breast carcinomas.
Cancer Causes & Control, 30(1):31–39, (2019). doi: 10.1007/s10552-018-1121-1

40. Yoh Isogai, Zheng Wu, **Michael I.Love**, Michael Ho-Young Ahn, Dhananjay Bambah-Mukku, Vivian Hua, Karolina Farrell, Catherine Dulac. Multisensory Logic of Infant-Directed Aggression by Males.
Cell, 175(7):1827–1841, (2018). doi: 10.1016/j.cell.2018.11.032

41. 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

42. **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

43. Yuchen Yang, Ruth Huh, Houston W. Culpepper, Yuan Lin, **Michael I. Love**, Yun Li. SAFE-clustering: Single-cell Aggregated (From Ensemble) Clustering for Single-cell RNA-seq Data.
Bioinformatics, 35(8):1269–1277, (2018). doi: 10.1093/bioinformatics/bty793

44. Alena van Bömmel, **Michael I. Love**, Ho-Ryun Chung, Martin Vingron. coTRaCTE predicts co-occurring transcription factors within cell-type specific enhancers.
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45. Edward W. Pietryk, Kiristin Clement, Marwa Elnagheeb, Ryan Kuster, Kayla Kilpatrick, **Michael I. Love**, Folami Y. Ideraabdullah. Intergenerational response to the endocrine disruptor vinclozolin is influenced by maternal genotype and crossing scheme.
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46. Koen Van den Berge[1], Fanny Perraudeau[1], Charlotte Soneson, **Michael I. Love**, Davide Risso, Jean-Philippe Vert, Mark D. Robinson, Sandrine Dudoit[†], Lieven Clement[†]. Observation weights unlock bulk RNA-seq tools for zero inflation and single-cell applications.
Genome Biology, 19(1):24, (2018). doi: 10.1186/s13059-018-1406-4

47. Lindsay A. Williams, Hazel B. Nichols, Katherine A. Hoadley, Chiu Kit Tse, Joseph Geradts, Mary Elizabeth Bell, Charles M. Perou, **Michael I. Love**, Andrew F. Olshan, Melissa A. Troester. Reproductive risk factor associations with lobular and ductal carcinoma in the Carolina Breast Cancer Study.

Cancer Causes & Control, 29(1):25–32, (2017). doi: 10.1007/s10552-017-0977-9

48. Doug H. Phanstiel, Kevin Van Bortle, Damek Spacek, Gaelen T. Hess, Muhammad S. Shamim, Ido Machol, **Michael I. Love**, Erez L. Aiden, Michael C. Bassik, Michael P. Snyder. Static and Dynamic DNA Loops form AP-1-Bound Activation Hubs during Macrophage Development.
Molecular Cell, 67(6):1037–1048, (2017). doi: 10.1016/j.molcel.2017.08.006

49. Rob Patro, Geet Duggal, **Michael I. Love**, Rafael A. Irizarry, Carl Kingsford, Salmon provides fast and bias-aware quantification of transcript expression.
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50. **Michael I. Love**, Matthew Huska, Marcel Jurk, Robert Schopflin, Stephan Starick, Kevin Schwahn, Samantha Cooper, Keith Yamamoto, Morgane Thomas-Chollier, Martin Vingron, Sebastiaan Meijsing. Role of the chromatin landscape and sequence in determining cell type-specific genomic glucocorticoid receptor binding and gene regulation.
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Nucleic Acids Research, 45(2):e9, (2016). doi: 10.1093/nar/gkw852

53. Mingxiang Teng, **Michael I. Love**, Carrie A. Davis, Sarah Djebali, Alexander Dobin, Brenton R. Graveley, Sheng Li, Christopher E. Mason, Sara Olson, Dmitri Pervouchine, Cricket A. Sloan, Xintao Wei, Lijun Zhan, Rafael A. Irizarry, A benchmark for RNA-seq quantification pipelines.
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54. Charlotte Soneson, **Michael I. Love**, Mark D. Robinson, Differential analyses for RNA-seq: transcript-level estimates improve gene-level inferences.
F1000Research, 4:1521, (2015). doi: 10.12688/f1000research.7563.1

55. **Michael I. Love**, Simon Anders, Vladislav Kim, Wolfgang Huber, RNA-seq workflow: gene-level exploratory analysis and differential expression.
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56. Raman Kumar, Mark A. Corbett, Bregje WM van Bon, Alison Gardner, Joshua A. Woenig, Lachlan A. Jolly, Evelyn Douglas, Kathryn Friend, Chuan Tan, Hilde Van Esch, Maureen Holvoet, Martine Raynaud, Michael Field, Melanie Leffler, Bartłomiej Budny, Marzena Wisniewska, Magdalena Badura-Stronka, Anna Latos-Bieleńska, Jacqueline Batanian, Jill A. Rosenfeld, Lina Basel-Vanagaite,

Corinna Jensen, Melanie Bienek, Guy Froyen, Reinhard Ullmann, Hao Hu, **Michael I. Love**, Stefan A. Haas, Pawel Stankiewicz, Sau Wai Cheung, Anne Baxendale, Jillian Nicholl, Elizabeth M Thompson, Eric Haan, Vera M Kalscheuer, Jozef Gecz, Increased STAG2 dosage defines a novel cohesinopathy with intellectual disability and behavioural problems.
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57. Stephan R. Starick, Jonas Ibn-Salem, Marcel Jurk, Céline Hernandez, **Michael I. Love**, Ho-Ryun Chung, Martin Vingron, Morgane Thomas-Chollier, Sebastiaan H. Meijsing, ChIP-exo signal associated with DNA-binding motifs provide insights into the genomic binding of the glucocorticoid receptor and cooperating transcription factors.
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61. Wei Li, Han Xu, Tengfei Xiao, Le Cong, **Michael I. Love**, Feng Zhang, Rafael A. Irizarry, Jun S. Liu, Myles Brown, Xiaole X. Liu, MAGeCK enables robust identification of essential genes from genome-scale CRISPR/Cas9 knockout screens.

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64. Ruping Sun, **Michael I. Love**, Tomasz Zemojtel, Anne-Katrin Emde, Ho-Ryun Chung, Martin Vingron, Stefan A. Haas, Breakpointer: Using local mapping artifacts to support sequence breakpoint discovery from single-end reads.
Bioinformatics, 28(7):1024–1025, (2012). doi: 10.1093/bioinformatics/bts064

65. **Michael I. Love**, Alena Mysickova, Ruping Sun, Vera Kalscheuer, Martin Vingron, Stefan A. Haas, Modeling read counts for cnv detection in exome sequencing data.
Statistical Applications in Genetics and Molecular Biology, 10(1):52, (2011). doi: 10.2202/1544-6115.1732

Digital and other novel forms of scholarship:

Open source software

The following list comprises open source software packages maintained by the Love Lab. The number of monthly unique IP downloads are listed for software packages maintained by the Love Lab that are widely used in genomics research pipelines in academia and industry.

Key:
(Bioc) - R package within the Bioconductor Project;
(GitHub) - software hosted as a GitHub repository.

1. **DESeq2**: Differential expression analysis for RNA-seq. (Bioc)
    - **Greater than 19,000 monthly unique IP downloads**
    - 5th most accessed article published by *Genome Biology*
    - Awarded and funded as a CZI *Essential Open Source Software* (EOSS) project, out of 72 projects
    - Press: "Love wins CZI funding for open source software to analyze genomics data"
      UNC Gillings School of Public Health News

2. **apeglm**: Approximate posterior estimation for GLM coefficients. (Bioc)
    - **Greater than 3,000 monthly unique IP downloads**
3. **tximport**: Import and summarization of transcript-level estimates for gene-level analysis. (Bioc)
    - **Greater than 3,000 monthly unique IP downloads**
4. **tximeta**: Transcript data import with automatic metadata for computational reproducibility. (Bioc)
    - **Greater than 1,200 monthly unique IP downloads**
5. **fishpond**: Nonparametric differential transcript expression with inferential replicates. (Bioc)
6. **airpart**: Differential cell-type-specific allelic imbalance using single-cell allelic count data. (Bioc)
7. **nullranges**: Generation of sets of genomic features representing the null hypothesis. (Bioc)
8. **MRLocus**: Mendelian Randomization analysis at the genomic locus, or *cis*-MR. (GitHub)
9. **MOSTWAS**: Multi-Omic Strategies for TWAS. (GitHub)
10. **DeCompress**: Tissue compartment deconvolution for targeted RNA panels. (GitHub)
11. **ACTOR**: LDA model to compare isoform expression to a reference panel. (GitHub)
12. **alpine**: Correction of fragment sequence bias for RNA-seq transcript abundance estimation. (Bioc)
13. **exomeCopy**: Detection of copy number variants for Exome-seq. (Bioc)

Data science workflows

Reproducible genomic data science workflows maintained or co-authored by the Love Lab. The workflows are "literate programming" documents, which weave prose, figures, and code together to demonstrate completion of a data science task. These are submitted and hosted both on Bioconductor servers, where they are tested against current R and package ecosystem, and on *F1000Research* where they are subjected to peer-review.

1. **RNA-seq workflow: gene-level exploratory analysis and differential expression**
    - Bioconductor hosted workflow (the top downloaded Bioconductor workflow, out of 29)
    - F1000Research peer-reviewed publication (more than 75,000 views)
    - Press: Gibbs, W. Wayt, "A test drive of a DNA-analysis toolkit in the cloud". *Nature*, 552:137–138, (2017). doi: 10.1038/d41586-017-07833-1
      "*...Also available are peer-reviewed tutorials, known as workflows, which are updated as the platform evolves. One, co-authored by Love, walks readers through a differential-expression analysis of RNA-sequencing data. I used his workflow to guide my exploration.*"
2. **RNA-seq workflow for differential transcript usage following Salmon quantification**
    - Bioconductor hosted workflow
    - F1000Research peer-reviewed publication (more than 20,000 views)
3. **Fluent genomics with plyranges and tximeta**
   (first author: Stuart Lee, of Monash University)
    - Bioconductor hosted workflow
    - F1000Research peer-reviewed publication (more than 1400 views)

Invited presentations

1. November 2022 - Texas A&M University, Statistics Department
2. October 2022 - University of Washington, Biostatistics Department
3. April 2022 - ENAR, "Statistical Methods for Single-Cell Sequencing Data"
4. March 2022 - MRC Integrative Epidemiology Unit, University of Bristol
5. December 2021 - Institute for Genome Sciences, School of Medicine, University of Maryland, Baltimore
6. September 2021 - Dept. of Biostatistics, Virginia Commonwealth University
7. September 2021 - ICSA Applied Statistics Symposium - Organized Invited Sesssion "Integrative multi-omics inference"
8. August 2021 - JSM, "Genomics in Neuroscience"
9. June 2021 - Genetics, Genomics and Informatics Virtual Seminar, The University of Tennessee Health Science Center
10. December 2020 - Dept. of Statistics, Penn State University
11. December 2020 - Institute for Personalized Medicine Seminar Series, Icahn School of Medicine, Mount Sinai Hospital
12. June 2020, Banff International Research Station (BIRS), "Mathematical Frameworks for Integrative Analysis of Emerging Biological Data Types"
13. March 2020 - ENAR, "Recent advanced and opportunities in large scale and multi-omic single cell data analysis"
14. March 2020 - Human Genetics Seminar Series, Dept. of Genetics, University of Utah
15. December 2019 - Statistical Genetics Seminar, Dept. of Biostatistics, Johns Hopkins University
16. November 2019 - APHA, Spiegelman Awardee Invited Session
17. July 2019 - JSM, "Making an Impact in Statistics Education through Innovation and Outreach"
18. May 2019 - ASA Symposium on Data Science & Statistics, "Democratizing Data Science through Workflows"
19. March 2019 - ENAR, "Teaching Data Science through Case Studies"
20. March 2019 - Dept. of Biostatistics and Bioinformatics, Emory University
21. February 2019 - Epigenetics and Stem Cell Biology, NIEHS
22. November 2018 - Epigenetics and Epigenomics Program, Duke University
23. October 2018 - Computational Biology & Bioinformatics, Duke University
24. September 2018 - School of Public Health Statistics Seminar, Brown University

25. May 2018 - Bioinformatics Research Center, NCSU
26. March 2018 - ENAR, "Teaching Data Science at all Levels"
27. February 2018 - Center for Public Health Genomics, UVA
28. December 2016 - Computational Biology, Bioinformatics & Genomics, UMD
29. October 2016 - Triangle Statistical Genetics Meeting, Cary, NC

Non-refereed papers/articles:

The following are non-refereed papers/articles and all titles are indicated with an asterisk. † indicates first-author work from an advisee.

1. Euphy Wu†, Noor P. Singh, Kwangbom Choi, Mohsen Zakeri, Matthew Vincent, Gary A. Churchill, Cheryl L. Ackert-Bicknell, Rob Patro, **Michael I. Love** Detecting isoform-level allelic imbalance accounting for inferential uncertainty*.
bioRxiv, (2022). doi: 10.1101/2022.08.12.503785
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*.
bioRxiv, (2022). doi: 10.1101/2022.09.02.506382
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*.
bioRxiv, (2022). doi: 10.1101/2022.08.05.502985
4. Kathleen S. M. Reed, Eric S. Davis, Marielle L. Bond, Alan Cabrera, Eliza Thulson, I. Yoseli Quiroga, Shannon Cassel, Kamisha T. Woolery, Isaac Hilton, Hyejung Won, **Michael I. Love**, Douglas H. Phanstiel Temporal analysis suggests a reciprocal relationship between 3D chromatin structure and transcription*.
bioRxiv, (2022). doi: 10.1101/2022.05.05.490836
5. Sarah A. Reifeis†, Michael G. Hudgens, Melissa A. Troester, **Michael I. Love**, Assessing Etiologic Heterogeneity for Multinomial Outcome with Two-Phase Outcome-Dependent Sampling Design*.
medRxiv, (2022). doi: 10.1101/2022.07.20.22277805
6. Nil Aygün, Dan Liang, Wesley L. Crouse, Gregory R. Keele, **Michael I. Love**, Jason L. Stein. Inferring cell-type-specific causal gene regulatory networks during human neurogenesis*.
bioRxiv, (2022). doi: 10.1101/2022.04.25.488920
7. Jessica C. McAfee, Sool Lee, Jiseok Lee, Jessica L. Bell, Oleh Krupa, Jessica Davis, Kimberly Insigne, Marielle L. Bond, Douglas H. Phanstiel, **Michael I. Love**, Jason L. Stein, Sriram Kosuri, Hyejung Won. Systematic investigation of allelic regulatory activity of schizophrenia-associated common variants*.
medRxiv, (2022). doi: 10.1101/2022.09.15.22279954
8. Hunyong Cho, Chuwen Liu, Boyang Tang, Bridget M. Lin, Jeffrey Roach, Apoena de Aguiar Ribeiro, **Michael I. Love**, Kimon Divaris, Di Wu. Distribution-based comprehensive evaluation of methods for differential expression analysis in metatranscriptomics*.
bioRxiv, (2021). doi: 10.1101/2021.07.14.452374

9. Kim-Anh Lê Cao, Al J. Abadi, Emily F. Davis-Marcisak, Lauren Hsu, Arshi Arora, Alexis Coullomb, Atul Deshpande, Yuzhou Feng, Pratheepa Jeganathan, Melanie Loth, Chen Meng, Wancen Mu, Vera Pancaldi, Kris Sankaran, Amrit Singh, Joshua S. Sodicoff, Genevieve L. Stein-O'Brien, Ayshwarya Subramanian, Joshua D. Welch, Yue You, Ricard Argelaguet, Vincent J. Carey, Ruben Dries, Casey S. Greene, Susan Holmes, **Michael I. Love**, Matthew E. Ritchie, Guo-Cheng Yuan, Aedin C. Culhane, Elana Fertig. Community-wide hackathons to identify central themes in single-cell multi-omics*.
Genome Biology, (2021). doi: 10.1186/s13059-021-02433-9

10. Anushka Rajesh, Yutong Chang, Malak S. Abedalthagafi, Annie Wong-Beringer, **Michael I. Love**, Serghei Mangul. Improving the completeness of public metadata accompanying omics studies*.
Genome Biology, 22(1):106, (2021). doi: 10.1186/s13059-021-02332-z

11. Miheer Dewaskar, John Palowitch, Mark He, **Michael I. Love**, Andrew Nobel. Finding stable groups of cross-correlated features in multi-view data*.
arXiv, September 2020. arXiv: 2009.05079

12. Koen Van Den Berge, Katharina M. Hembach, Charlotte Soneson, Simone Tiberi, Lieven Clement, **Michael I. Love**, Rob Patro, and Mark D. Robinson. RNA sequencing data: hitchhiker's guide to expression analysis*.
Annual Review of Biomedical Data Science, October 2018. doi: 10.1146/annurev-biodatasci-072018-021255

TEACHING RECORD

Classroom teaching:

- BIOS 784 / BCB 784: *Computational Biology*, elective, 3 credits.
Instructor, Fall 2022, Spring 2021, Fall 2017.
$\sim$ 25 students enrolled.
Notes and syllabus: https://biodatascience.github.io/compbio

- BIOS 663: *Intermediate Linear Models*, required for Masters, 4 credits.
Instructor, Spring 2022, Spring 2020. $\sim$ 45 students enrolled.

- BIOS 735: *Statistical Computing*, required for PhD, 4 credits.
Co-Instructor with Dr. Naim Rashid, Spring 2019.
23 students enrolled.
Notes and syllabus: https://biodatascience.github.io/statcomp

- *Biomedical Data Science*, HarvardX online series.
Teaching Fellow, 2014-2016.
Instructor for "Linear Models" and "RNA-seq Case Study".
http://genomicsclass.github.io/book/

Graduate students supervised:

- Yuriko Harigaya, PhD in Bioinformatics & Computational Biology. (Co-supervized with Dr. Valdar)

- Rachel Sharp, PhD in Bioinformatics & Computational Biology. (Co-supervized with Dr. Won)

- Euphy Wu, PhD in Biostatistics. (Co-supervized with Dr. Rashid)
- Wancen Mu, PhD in Biostatistics.
- Ji-Eun Park, PhD in Biostatistics. (Co-supervised with Dr. Wu)
- Achal Patel, PhD in Epidemiology. Graduated Summer 2022. (Co-supervised with Dr. Troester)
- Alex Lockhart, M.S. in Biostatistics, Graduated Fall 2020.
- Sarah Reifeis, PhD in Biostatistics, Graduated Fall 2020. (Co-supervised with Dr. Hudgens)
- Arjun Bhattacharya, PhD in Biostatistics, Graduated Summer 2020.
- Scott Van Buren, PhD in Biostatistics, Graduated Summer 2020. (Co-supervised with Dr. Rashid)
- Sean McCabe, PhD in Biostatistics, Graduated Spring 2020. (Co-supervised with Dr. Lin)
- Anqi Zhu, PhD in Biostatistics, Graduated Fall 2019. (Co-supervised with Dr. Ibrahim)

GRANTS

All award amounts are direct costs for the current project year.

Ongoing:

Sorted by project start date.

- **Principal Investigator** UM1-HG012003 (Won) 09/01/2021 - 05/31/2026
  NIH (NHGRI) $1,196,078
  Systematic in vivo characterization of disease-associated regulatory variants
  10% effort
- **Co-Investigator** R01-MH125236 (Crawford) 04/01/2021 - 01/31/2026
  NIH (NIMH) $1,225,816
  Beyond GWAS: High Throughput Functional Genomics and Epigenome Editing to Elucidate the Effects of Genetic Associations for Schizophrenia
  8% effort
- **Co-Investigator** R01-CA253450 (Troester) 04/01/2021 - 03/31/2026
  NIH (NCI) $391,413
  P53, DNA Repair, and Immune Response in Breast Cancer Mortality Disparities
  10% effort
- **Principal Investigator** Essential Open Source Software (Love) 01/01/2021 - 12/31/2022
  Chan Zuckerberg Initiative $74,000
  5% effort
- **Principal Investigator** R01-MH118349 (Stein) 12/10/2018 - 11/30/2023
  NIH (NIMH) $303,438
  pathQTL: Integrative Multi-Omics Causal Inference of Molecular Mechanisms Leading to Neuropsychiatric Illness
  25% effort

- **Principal Investigator** R01-HG009937 (Patro) 09/18/2018 - 06/30/2023
  NIH (NHGRI) $256,486
  A Modular Framework for Accurate, Efficient, and Reproducible Analysis of RNA-Seq Data
  27% effort

- **Co-Investigator** P50-CA058223 (Perou) 09/01/2018 - 08/31/2023
  NIH (NCI) $1,531,225
  SPORE in Breast Cancer - Project 1: The Carolina Breast Cancer Study (CBCS)
  5% effort

- **Co-Investigator** R01-DK093757 (Mohlke) 08/01/2017 - 05/31/2023
  NIH (NIDDK) $477,414
  Genetic Epidemiology of Rare and Regulatory Variants for Metabolic Traits
  5% effort

Completed:

- **Co-Investigator** P30-ES010126 (Troester) 04/01/2021 - 02/28/2026
  NIH (NIEHS) $302,838
  UNC-CH Center for Environmental Health and Susceptibility - Biostatistics and Bioinformatics Facility Core
  15% effort

- **Co-Investigator** P01-CA142538 (Lin) 04/01/2019 - 03/31/2020
  NIH (NCI) $416,534
  Statistical Methods for Cancer Clinical Trials - Project 3: Statistical/Computational Methods for Pharmacogenomics and Individualized Therapy
  10% effort

- **Co-Investigator** UL1-TR002489 (Buse) 03/01/2019 - 02/29/2020
  NIH (NCATS) $6,281,669
  NC TraCS Institute
  10% effort

- **Co-Investigator** R01-HG009125 (Nobel) 09/07/2016 - 06/30/2020
  NIH (NHGRI) $299,936
  Multi-Tissue and Network Models for Next-Generation EQTL Studies
  10% effort

SERVICE

Professional service:

- **Member** of Technical Advisory Board for Bioconductor Project (2020 - present)

- **Member** of Code of Conduct Committee for Bioconductor Project (2021 - present)

- **Member** of organizing committee for BioC conference 2021, 2022.

- **Reviewer** for R01 Leveraging Existing ADRD Data Resources, NIH NINDS Review Panel, February 25, 2022.

- **Reviewer** for BRAIN Initiative, NIH NIMH Review Panel, June 11, 2021.
- **Temporary Member** of Biodata Management and Analysis (BDMA) NIH Study Section, October 22-23, 2020.
- **Developer and maintainer** for widely-used open-source software packages. Maintenance of software packages entails addressing feature requests as well as software support requests. DESeq2 typically receives more than 10 support requests per week on https://support.bioconductor.org.
- **Referee** for the following journals:

  Bioinformatics, Nucleic Acids Research, Genome Biology, Genome Research, Journal of the American Statistical Association, Biometrics, American Journal for Human Genetics, PLOS Computational Biology, PLOS Genetics, Statistical Applications in Genetics and Molecular Biology, Nature Biotechnology, Nature Methods, Nature Communications, Nature Reviews Molecular Cell Biology, Cell Reports, BMC Bioinformatics, Briefings in Bioinformatics, F1000Research, R Journal.

Departmental service:

- **Member** - Biological & Biomedical Sciences Program Admissions Committee (August 2022 - present)
- **Member** - Biostatistics Communications Committee (August 2021 - present)
- **Member** - Genetics Advisory Committee (August 2021 - present)
- **Chair** - Biostatistics Communications Committee (August 2021 - August 2022)
- **Member** - Biostatistics Masters Exam Committee (January 2020 - August 2022)
- **Member** - Biostatistics Computing Committee (August 2016 - July 2021)
- **Co-Chair** - Biostatistics Seminar Committee (August 2016 - July 2020)

Community engagement:

- **UNC PREP Mentor** to Kwame Forbes (PREP year 2020-2021).
- **Instructor/organizer** of "Statistical Methods for Functional Genomics" (two weeks NIH-sponsored course, 24 international students), Cold Spring Harbor Laboratories, Cold Spring Harbor, NY, for the years 2017, 2018, 2019, 2022.
- **Instructor/organizer** of "Statistics and Computing in Genome Data Science" (5 day course, Bioconductor-sponsored event), Bressanone-Brixen, Italy, for the years: 2015, 2016, 2018.
- **Workshop lead** for RNA-seq and genomic data science topic at numerous events including: BioC conference 2014, 2015, 2016, 2018, 2019, 2020, 2022, R-Ladies Tunis 2020 (Tunisian local chapter of R-Ladies Global), ENAR 2018, UC Davis ANGUS 2017, Harvard Medical School 2015, Harvard School of Public Health 2015. I have also given 1 hour lectures in genomic data science to the UNC PREP cohort (2020) and the UNC Educational Pathways to Diversity in Genomics (EDGE) cohort (2021).

  Examples of publicly available workshop material:

- BioC2022 - Statistical Estimation Of Allelic Expression Using Salmon And Swish
- BioC2020 - Importing alevin scRNA-seq counts into R/Bioconductor
- BioC2019 - Overlapping differential expression and differential chromatin accessibility
- BioC2018 - RNA-seq data analysis with DESeq2, MultiQC, Glimma, and ZINB-WaVE
- BioC2016 - Low-level exploratory data analysis and methods development for RNA-seq
- BioC2015 - Differential expression, manipulation, and visualization of RNA-seq reads

PROFESSIONAL SOCIETY MEMBERSHIPS

- Eastern North American Region (ENAR), 2016 - present.
- American Statistical Association (ASA), 2015 - present.
- American Society of Human Genetics (ASHG), 2021 - present.