MICHAEL I. LOVE
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University of North Carolina-Chapel Hill
Department of Biostatistics
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EDUCATION

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 POSITIONS

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 and Computational Biology, Dana-Farber Cancer Institute
Department of Biostatistics, Harvard TH Chan School of Public Health

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HONORS, AWARDS, SCHOLARSHIPS

- Junior Faculty Development Award 2017, University of North Carolina at Chapel Hill.
- National Institutes of Health Cancer Training Grant Postdoctoral Fellowship (5T32CA009337-33), 2013 - present.
- International Max Planck Research School Scholarship, 2010 - 2013.

- Robert Byrd Honors Scholarship, 2001-2005.
- National Merit Scholarship, 2001-2005.

PROFESSIONAL SERVICE

- **Develop and maintain** open-source biostatistical software.
- **Referee** for the following journals and conferences:

  2017: Nature Methods, BMC Bioinformatics
  2016: Biostatistics, Briefings in Bioinformatics, Bioinformatics
  2015: Journal of Computational and Graphical Statistics, Bioinformatics, PLOS ONE
  2014: Bioinformatics, Nucleic Acids Research, PLOS Computational Biology, Genomics, BMC Genomics
  2013: RECOMB Conference, German Conference on Bioinformatics (GCB)
  2012: PLOS ONE
  2011: Bioinformatics, ISMB/ECCB Conference

PROFESSIONAL MEMBERSHIPS

- American Statistical Association (ASA), 2015 - present.
- Eastern North American Region (ENAR), 2016 - present.

PEER-REVIEWED PUBLICATIONS

1. **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.
   Nucleic Acids Research, AA, (2016). doi:10.1093/nar/gkw1163

2. **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

3. Leonardo Collado Torres, Abhinav Nellore, Alyssa C Frazee, Christopher Wilks, **Michael I Love**, Ben Langmead, Rafael A Irizarry, Jeffrey Leek, Andrew E Jaffe, Flexible expressed region analysis for RNA-seq with derfinder.
   Nucleic Acids Research, AA, (2016). doi:10.1093/nar/gkw852

4. 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.
   Genome Biology, 17(74), (2016). doi:10.1186/s13059-016-0940-1

5. 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

6. **Michael I Love**, Simon Anders, Vladislav Kim, Wolfgang Huber, RNA-seq workflow: gene-level exploratory analysis and differential expression.
   F1000Research, 4(1070), (2015). doi:10.12688/f1000research.7035.1

7. 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.
Human Molecular Genetics, Epub ahead of print, (2015). doi:10.1093/hmg/ddv414

8. 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.
Genome Research, 25(6):825–835, (2015). doi:10.1101/gr.185157.114

9. Wolfgang Huber, Vincent J Carey, Robert Gentleman, Simon Anders, Marc Carlson, Benilton S Carvalho, Hector Corrada Bravo, Sean Davis, Laurent Gatto, Thomas Girke, Raphael Gottardo, Florian Hahne, Kasper D Hansen, Rafael A Irizarry, Michael Lawrence, **Michael I Love**, James MacDonald, Valerie Obenchain, Andrzej K Oleś, Hervé Pagès, Alejandro Reyes, Paul Shannon, Gordon K Smyth, Dan Tenenbaum, Levi Waldron, Martin Morgan, Orchestrating high-throughput genomic analysis with Bioconductor.
Nature Methods, 12(2):115–121, (2015). doi:10.1038/nmeth.3252

10. Hao Hu, Stefan A Haas, Jamel Chelly, Hilde Van Esch, Martine Raynaud, Arjan PM de Brouwer, Stefanie Weinert, Guy Froyen, Suzanna GM Frints, Frédéric Laumonnier, Tomasz Zemojtel, **Michael I Love**, Hughes Richard, Anne-Katrin Emde, Melanie Bienek, Corinna Jensen, Melanie Hambrock, Ute Fischer, Claudia Langnick, Mirjam Feldkamp, Willemijn Wissink-Lindhout, Nicolas Lebrun, Laetitia Castelnau, Julien Rucci, Rodrick Montjean, Olivier Dorseuil, Pierre Billuart, Till Stuhlmann, Marie Shaw, Mark A Corbett, Alison Gardner, Saffron Willis-Owen, Chuan Tan, Kathryn L Friend, Stefanie Belet, Kees EP van Roozendaal, Mélanie Jimenez-Pocquet, Marie-Pierre Moizard, Nathalie Ronce, Ruping Sun, Sean O'Keeffe, Ramu Chenna, Alena van Bömmel, Jonathan Göke, Anna Hackett, Michael Field, Louise Christie, Jackie Boyle, Eric Haan, John Nelson, Gillian Turner, Gareth Baynam, Gabriele Gillessen-Kaesbach, Ulrich Müller, Daniela Steinberger, Bartlomiej Budny, Magdalena Badura-Stronka, Anna Latos-Bieleńska, Lilian B Ousager, Peter Wieacker, Germán Rodríguez Criado, Marie-Louise Bondeson, Göran Annerén, Andreas Dufke, Monika Cohen, Lionel Van Maldergem, Catherine Vincent-Delorme, Bernard Echenne, Brigitte Simon-Bouy, Tjitske Kleefstra, Michèl Willemsen, Jean-Pierre Fryns, Koenraad Devriendt, Reinhard Ullmann, Martin Vingron, Klaus Wrogemann, Thomas F Wienker, Andreas Tzschach, Hans van Bokhoven, Jozef Gécz, Thomas J Jentsch, Wei Chen, Hans-Hilger Ropers, Vera M Kalscheuer, X-exome sequencing of 405 unresolved families identifies seven novel intellectual disability genes.
Molecular Psychology, Epub ahead of print, (2015). doi:10.1038/mp.2014.193

11. **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

12. 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.
Genome Biology, 15(12):554+, (2014). doi:10.1186/s13059-014-0554-4

13. Jonas Ibn-Salem*, Sebastian Köhler*, **Michael I Love**, Ho-Ryun Chung, Ni Huang, Matthew E Hurles, Melissa Haendel, Nicole L Washington, Damian Smedley, Christopher J Mungall, Suzanna E Lewis, Claus-Eric Ott, Sebastian Bauer, Paul N Schofield, Stefan Mundlos, Malte Spielmann, Peter N Robinson, Deletions of chromosomal regulatory boundaries are associated with congenital disease. *Genome Biology*, 15(9):423+, (2014). doi:10.1186/s13059-014-0423-1

14. Owen D Solberg*, Edwin J Ostrin*, **Michael I Love**, Jeffrey C Peng, Nirav R Bhakta, Lydia Hou, Christine Nguyen, Margaret Solon, Cindy Nguyen, Andrea J Barczak, Lorna T Zlock, Denitza P Blagev, Walter E Finkbeiner, K Mark Ansel, Joseph R Arron, David J Erle, Prescott G Woodruff, Airway epithelial miRNA expression is altered in asthma.
American Journal of Respiratory and Critical Care Medicine, 186(10):965–974, (2012).
doi:10.1164/rccm.201201-0027oc

15. 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

16. **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), (2011).
doi:10.2202/1544-6115.1732

SUBMITTED MANUSCRIPTS

1. Rob Patro, Geet Duggal, **Michael I Love**, Rafael A Irizarry, Carl Kingsford, Salmon provides accurate, fast, and bias-aware transcript expression estimates using dual-phase inference.
`http://biorxiv.org/content/early/2016/08/30/021592`
submitted, under review

BOOKS

- 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/`

PUBLICLY AVAILABLE SOFTWARE

1. **DESeq2**: Differential expression analysis for RNA-seq.(Bioc)
2. **exomeCopy**: Detection of copy number variants for Exome-seq. (Bioc)
3. **alpine**: Correction of fragment sequence bias for RNA-seq transcript abundance estimation. (Bioc)
4. **tximport**: Import and summarize transcript-level estimates for gene-level analysis. (Bioc)
5. **SparseData**: Efficient calculation of basic statistics for large sparse genomic datasets.
6. **GenomicFiles** *(contributor)*: Infrastructure for parallel queries of large genomic files. (Bioc)

(Bioc): R package within the Bioconductor Project

PRESENTATIONS

Invited talks

- *Modeling of RNA-seq sequence biases*, Triangle Statistical Genetics Meeting, SAS Campus, Cary, NC., October, 2016.
- *Technical bias in sequencing data and solutions*, Quantitative Issues in Cancer Research Working Seminar, Harvard TH Chan School of Public Health, October, 2014.
- *Shrinkage estimators for differential analysis of RNA-seq*, Immunology Division Bioinformatics Seminar, Harvard Medical School, May, 2014.
- *Analysis of RNA-seq at the gene level*, Quantitative Issues in Cancer Research Working Seminar, Harvard TH Chan School of Public Health, November, 2013.

Contributed talks

- *Simplified processing of large genomic datasets with GenomicFiles*, Bioconductor Conference, August, 2014.
- *Multiple group comparisons for RNA-seq and stable effect size estimates*, HiTSeq, Intelligent Systems for Molecular Biology (ISMB), July, 2014.
- *RNA-seq workflows in Bioconductor*, Trends in genomic data analysis in R/Bioconductor workshop, Intelligent Systems for Molecular Biology (ISMB), July, 2014.
- *Normalization of DNase-seq data for classification of cell types*, 22nd Annual Workshop on Mathematical and Statistical Aspects of Molecular Biology (MASAMB), April, 2012.

TEACHING

Courses

- PH525x: *Biomedical Data Science*, online HarvardX eight course series.
  Teaching Fellow, February - June, 2015.
  Instructor for PH525.2x: Linear Models and PH525.5x: RNA-seq Case Study.
  `http://genomicsclass.github.io/book/`
  7,000+ active students (watching lectures and completing assignments)
- PH525x: *Data Analysis for Genomics*, HarvardX online course.
  Teaching Fellow, February - June, 2014.
  `https://www.edx.org/course/harvardx/harvardx-ph525x-data-analysis-genomics-1401`
  4,000+ active students (watching lectures and completing assignments)

Short courses, workshops

- *RNA-seq data analysis and differential expression*, Harvard Medical School Immunology Division RNA-seq Summer Course, July, 2015.
- *Differential expression, manipulation, and visualization of RNA-seq reads*, workshop, Bioconductor Conference, Seattle, July, 2015.
- *RNA-Seq data analysis and differential expression I-III* and *Statistical aspects of gene set enrichment analysis*, Statistics and Computing in Genome Data Science, one week course, Bressanone-Brixen, June, 2015.
- *Statistical aspects of differential gene expression*, Next Generation Sequencing Data Analysis Course taught by the Bioinformatics Core, Harvard TH Chan School of Public Health, May, 2015.
- *Analysis of RNA-seq using the DESeq2 package*, workshop, Bioconductor Conference, August, 2014.

- *RNA-seq: differential expression at the gene level*, Otto Warburg International Summer School and Research Symposium in Berlin on Next Generation Sequencing and its Impact on Genetics, August, 2013.
- *RNA-seq analysis*, four session introductory course, European Molecular Biology Laboratory, Heidelberg, November, 2012.
- *Statistical Inference and Linear Modeling*, four session introductory course, Max Planck Institute for Molecular Genetics, Berlin, March, 2012.

Advising

- Co-advisor of Anqi Zhu, PhD student in Biostatistics, UNC-Chapel Hill (2016-)
- Co-advisor of Sean McCabe, PhD student in Biostatistics, UNC-Chapel Hill (2016-)
- Advisor of Bachelor's Thesis of Stefan Budach, *Technical artifacts and batch effects in RNA-seq data*, Freie Universität, Berlin, Department of Mathematics and Informatics, Bioinformatics Program, July, 2013.