

JOSHUA D. WELCH, PH.D.

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PROFESSIONAL EXPERIENCE

Assistant Professor (2018-present)
Department of Computational Medicine and Bioinformatics
Department of Computer Science and Engineering
University of Michigan, Ann Arbor, MI

Visiting Scholar (2018-present)
Stanley Center for Psychiatric Research
Broad Institute of MIT and Harvard, Cambridge, MA

Postdoctoral Associate (2017-2018)
Stanley Center for Psychiatric Research
Broad Institute of MIT and Harvard, Cambridge, MA
Advisor: Evan Z. Macosko

EDUCATION

Ph.D. in Computer Science (2012-2017)
The University of North Carolina at Chapel Hill
Advisor: Jan F. Prins

M.S. in Computer Science (2012-2016)
The University of North Carolina at Chapel Hill
Advisor: Jan F. Prins

B.S. in Computer Science (2007-2012)
Specialization in Bioinformatics
Ohio University
Overall GPA: 3.99

B.Mus. in Piano Performance (2007-2012)
Ohio University
Overall GPA: 3.99

PUBLICATIONS

1. Liu J*, Gao C*, Sodicoff J, Kozareva V, Macosko EZ, **Welch JD**. Jointly Defining Cell Types from Multiple Single-Cell Datasets Using LIGER. Nature Protocols 2020 (in press). *Equal contribution
2. Matsushita Y, Nagata M, Kozloff K, **Welch J**, Mizuhashi K, Tokavanich N, Hallett S, Link D, Nagasawa T, Ono W, and Ono N. A Wnt-mediated transformation of the bone marrow stromal cell identity orchestrates skeletal regeneration. Nature Communications. 11, 332 (2020).
3. Zhou Y, Liu Z, **Welch JD**, Gao X, Wang L, Garbutt T, Keepers B, Ma H, Prins JF, Shen W, Liu J, Qian L. Single-Cell Transcriptomic Analyses of Cell Fate Transitions during Human Cardiac Reprogramming. Cell Stem Cell. 2019 Jun 12. pii: S1934-5909(19)30224-3. doi: 10.1016/j.stem.2019.05.020.

4. **Welch JD***, Kozareva V, Ferreira A, Vanderburg C, Martin C, Macosko EZ*. Single-cell multi-omic integration compares and contrasts features of brain cell identity. *Cell* 2019. <https://doi.org/10.1016/j.cell.2019.05.006>.
*Co-corresponding
5. Rodriques SG*, Stickels RR*, Goeva A, Martin CA, Murray E, Vanderburg CR, **Welch JD**, Chen LM, Chen F+, Macosko EZ+. Slide-seq: A Scalable Technology for Measuring Genome-Wide Expression at High Spatial Resolution. *Science* 29 Mar 2019: Vol. 363, Issue 6434, pp. 1463-1467 DOI: 10.1126/science.aaw1219
6. Liu Z*, Wang L*, **Welch JD***, Ma H, Zhou Y, Vaseghi HR, Yu S, Wall JB, Alimohamadi S, Zheng M, Yin C, Shen W, Prins JF, Liu J, Qian L. Single-cell transcriptomics reconstructs fate conversion from fibroblast to cardiomyocyte. *Nature* (02 November 2017). 551, 100104 doi:10.1038/nature24454
*Equal contribution
7. **Welch JD**, Hartemink AJ, Prins JF. MATCHER: Manifold alignment reveals correspondence between single cell transcriptome and epigenome dynamics. *Genome Biology* 2017, 18:138. doi:10.1186/s13059-017-1269-0
8. Lackey P, **Welch JD**, Marzluff WM. TUT7 Catalyzes the Uridylation of the 3' End of Histone mRNA for Rapid Degradation. *RNA* 2016. doi:10.1261/rna.058107.116
9. **Welch JD***, Williams LA*, DiSalvo M*, Brandt AT, Marayati R, Sims CE, Allbritton NL, Prins JF, Yeh JJ, Jones CD. Selective Single Cell Isolation for Genomics Using Microarray Arrays. *Nucleic Acids Research* 2016. doi: 10.1093/nar/gkw700
*Equal contribution
10. Lyons SM, Cunningham CH, **Welch JD**, Groh B, Guo AY, Wei B, Whitfield ML, Xiong Y, Marzluff WF. A subset of replication-dependent histone mRNAs are expressed as polyadenylated RNAs in terminally differentiated tissues. *Nucleic Acids Research* 2016. doi: 10.1093/nar/gkw620
11. **Welch JD**, Hartemink AJ, Prins JF. SLICER: Inferring branched, nonlinear cellular trajectories from single cell RNA-seq data. *Genome Biology* 2016, 17:106 doi:10.1186/s13059-016-0975-3
12. **Welch JD**, Hu Y, Prins JF. Robust Detection of Alternative Splicing in a Population of Single Cells. *Nucleic Acids Research* 2016. doi: 10.1093/nar/gkv1525
*Also accepted as a highlight at ISMB 2016
13. Brooks L, Lyons SM, Mahoney JM, **Welch JD**, Liu Z, Marzluff WM, Whitfield ML. A multi-protein occupancy map of the mRNP on the 3' end of histone mRNAs. *RNA* 2015.
14. **Welch JD***, Slevin MK*, Tatomer D, Duronio RJ, Prins JF, Marzluff WF. EnD-Seq and AppEnD: Sequencing 3' ends to identify nontemplated tails and degradation intermediates. *RNA* 2015.
*Equal contribution
15. **Welch JD**, Baran-Gale J, Perou C, Sethupathy P, Prins JF. Pseudogenes Transcribed in Breast Invasive Carcinoma Show Subtype-Specific Expression and ceRNA Potential. *BMC Genomics* 2015.
16. Slevin MK, Meaux S, **Welch JD**, Bigler R, Miliani de Marval PL, Su W, Rhoads RE, Prins JF, Marzluff WF. Deep Sequencing Shows Multiple Oligouridylation Are Required for 3' to 5' Degradation of Histone mRNAs on Polyribosomes. *Molecular cell* 53 (6), 1020-1030. March 2014.
17. Lichtenberg J, Kurz K, Liang X, Al-ouran R, Neiman L, Nau LJ, **Welch JD**, Jacox E, Bitterman T, Ecker K, Elnitski L, Drews F, Lee SS, Welch LR. WordSeeker: concurrent bioinformatics software for discovering genome-wide patterns and word-based genomic signatures. *BMC Bioinformatics*. 2010 Dec 21;11 Suppl 12:S6.

18. Lichtenberg J, Yilmaz A, **Welch JD**, Kurz K, Liang X, Drews F, Ecker K, Lee SS, Geisler M, Grotewold E, Welch LR. The word landscape of the non-coding segments of the Arabidopsis thaliana genome. BMC Genomics. 2009 Oct 8;10:463.
19. Lichtenberg J, Jacox E, **Welch JD**, Kurz K, Liang X, Yang MQ, Drews F, Ecker K, Lee SS, Elnitski L, Welch LR. Word-based characterization of promoters involved in human DNA repair pathways. BMC Genomics. 2009 Jul 7;10 Suppl 1:S18.

PREPRINTS

Alghamri MS, Avvari RP, Thalla R, Kamran N, Zhang L, Ventosa M, Taher A, Faisal SM, Nez FJ, Fabiani MBG, Haase S, Carney S, Orringer D, Hervey-Jumper S, Heth J, Patil PG, Al-Holou WN, Eddy K, Merajver S, Ulintz PJ, **Welch JD**, Gao C, Liu J, Nez G, Hambardzumyan D, Lowenstein PR, Castro M. G-CSF Secreted by Epigenetically Reprogrammed Mutant IDH1 Glioma Stem Cells Reverses the Meloid Cells-Mediated Immunosuppressive Tumor Microenvironment. bioRxiv. <https://doi.org/10.1101/2020.07.22.215954>. Submitted to Cancer Discovery.

Liu J*, Gao C*, Sodicoff J, Kozareva V, Macosko EZ, **Welch JD**. Jointly Defining Cell Types from Multiple Single-Cell Datasets Using LIGER. bioRxiv. <https://doi.org/10.1101/2020.04.07.029546> *Equal contribution. In press at Nature Protocols.

Zizhen Yao, Hanqing Liu, Fangming Xie, Stephan Fischer, A. Sina Boeshaghi, Ricky S Adkins, Andrew I. Aldridge, Seth A. Ament, Antonio Pinto-Duarte, Anna Bartlett, M. Margarita Behrens, Koen Van den Berge, Darren Bertagnolli, Tommaso Biancalani, Hector Corrada Bravo, Tamara Casper, Carlo Colantuoni, Heather Creasy, Kirsten Crichton, Megan Crow, Nick Dee, Elizabeth L Dougherty, Wayne I. Doyle, Sandrine Dudoit, Rongxin Fang, Victor Felix, Olivia Fong, Michelle Giglio, Jesse Gillis, Jeff Goldy, Mike Hawrylycz, Hector Roux de Bzieux, Brian R. Herb, Ronna Hertzano, Xiaomeng Hou, Qiwen Hu, Jonathan Crabtree, Jayaram Kancherla, Matthew Kroll, Kanan Lathia, Yang Eric Li, Jacinta D. Lucero, Chongyuan Luo, Anup Mahurkar, Delissa McMillen, Naeem Nadaf, Joseph R. Nery, Sheng-Yong Niu, Joshua Orvis, Julia K. Osteen, Thanh Pham, Olivier Poirion, Sebastian Preissl, Elizabeth Purdom, Christine Rimorin, Davide Risso, Angeline C. Rivkin, Kimberly Smith, Kelly Street, Josef Sulc, Thuc Nghi Nguyen, Michael Tieu, Amy Torkelson, Herman Tung, Eeshit Dhaval Vaishnav, Valentine Svensson, Charles R. Vanderburg, Vasilis Ntranos, Cindy van Velthoven, Xinxin Wang, Owen R. White, Z. Josh Huang, Peter V. Kharchenko, Lior Pachter, John Ngai, Aviv Regev, Bosiljka Tasic, **Joshua D. Welch**, Joseph R. Ecker, Evan Z Macosko, Bing Ren, BRAIN Initiative Cell census Network (BICCN), Hongkui Zeng, Eran A. Mukamel. An integrated transcriptomic and epigenomic atlas of mouse primary motor cortex cell types. bioRxiv. <https://doi.org/10.1101/2020.02.29.970558>. In revision at Nature.

Gao C, Preissl S, Luo C, Castanon R, Sandoval J, Rivkin A, Nery JR, Behrens MM, Ecker JR, Ren B, **Welch JD**. Iterative Refinement of Cellular Identity from Single-Cell Data Using Online Learning. bioRxiv. <https://doi.org/10.1101/2020.01.16.909861>. Accepted for presentation at RECOMB 2020. In revision at Nature Biotechnology.

HONORS AND AWARDS

Horizon Award, The UNC Graduate School (2017)

NIH Predoctoral Fellowship (F31) (2016).

Proposal title: “Computational Modeling of Heterogeneous Gene Expression in Single Cells”

Big Data to Knowledge Fellowship (BD2K T32) (2015)

Elected President of the Computer Science Student Association (2014)

Selected to attend Heidelberg Laureate Forum (200 students selected) (2014)

Graduate Student Mentoring Award, UNC Office of Undergraduate Research (2013)

NSF Graduate Research Fellowship (2012)

Outstanding Senior in Computer Science, Ohio University Russ College of Engineering (2011)

Ohio University Concerto Competition Winner (2011)

Outstanding Junior in Computer Science, Ohio University Russ College of Engineering (2009)

GRANTS

Linking Molecular and Anatomical Features of Brain Cell Identity through Computational Data Integration

NIH/NIMH (1R01MH123199-01)

Joshua D. Welch (PI)

09/01/2020-08/31/2023.

Total: \$1,275,913

Integrative Single-Cell Analysis of Transcriptome, Epigenome, and Lineage in HIV Latency and Activation

NIH/NIAID (1R01AI149669-01)

Kathleen Collins (PI), Joshua D. Welch (PI)

12/19/2019-12/31/2024.

Total: \$3,360,219

Quantitative Definition of Cell Identity by Integrating Transcriptomic, Epigenomic, and Spatial Features of Individual Cells

NIH/NHGRI (1R01HG010883-01)

Joshua D. Welch (PI), Noriaki Ono (co-I)

09/03/2019-06/30/2024.

Total: \$1,508,385

Dynamics and Regulations of Bone Stem Cells In Vivo (Supplement)

NIH/NIDCR (3R01DE026666-02S1)

Noriaki Ono (PI), Joshua D. Welch (Co-I)

06/2019-05/2020.

Total: \$228,690

Integrative Single Cell Genomic Analysis of Mesenchymal Stem Cells

MCubed, University of Michigan

Noriaki Ono, Wanida Ono, Joshua D. Welch (Co-PI)

01/2019-04/2020.

Total: \$20,000

Integrating Single Cell Profiles across Modalities Using Manifold Alignment

Chan Zuckerberg Initiative (2018-183155)

Joshua Welch (PI)

04/2018-08/2019.

Total: \$171,000

ABSTRACTS

Chao Gao, **Joshua D. Welch**: Iterative Refinement of Cell Identity from Single-Cell Data Using Online Learning, Research in Computational Molecular Biology, 2020.

Joshua D. Welch: Validating Joint Analysis of Single-Cell Transcriptome and Epigenome Data Using scNMT-seq and SNARE-seq, BIRSBioIntegration, 2020.

Joshua Sodicoff, **Joshua D. Welch**: Application of LIGER to integration of seqFISH and scRNA-seq, BIRSBioIntegration, 2020.

Maria C. Virgilio, Jay Lubow, **Joshua D Welch**, Kathleen L Collins: The impact of HIV-1 Vpr on host transcription in macrophages, Cold Spring Harbor Laboratory meeting: Retroviruses, 2020.

Yutong Wang, Clay Scott, Laura Balzano, **Joshua D. Welch**: Domain adaptation for spatial and dissociated gene expression data integration, Learning Meaningful Representations of Life, Workshop at NeurIPS, Vancouver, Canada, 2019.

Maria C. Virgilio, Mark M. Painter, Valeri H. Terry, Francisco Gomez-Rivera, **Joshua D. Welch**, Kathleen L. Collins: Single-cell RNA sequencing analysis of HSPCs harboring latent and active HIV infections, Midwest Virology Symposium, 2019.

Joshua D. Welch, Evan Z. Macosko: Single-Cell Multi-omic Integration Compares and Contrasts Features of Brain Cell Identity, Intelligent Systems for Molecular Biology, Basel, Switzerland, 2019.

Joshua D. Welch, Evan Z. Macosko: Single-Cell Multi-omic Integration Compares and Contrasts Features of Brain Cell Identity, Algorithms and Models for Single-Cell Genomics, Irvine, CA, USA, 2019.

Joshua D. Welch, Velina Kozareva, Ashley Ferreira, Carly Martin, Evan Macosko: Comparing and contrasting heterogeneous single-cell datasets, Single Cell Genomics, Cambridge, MA, 2018.

Joshua D. Welch, Alexander J. Hartemink, Jan F. Prins: MATCHER: Manifold Alignment Reveals Correspondence between Single Cell Transcriptome and Epigenome Dynamics, Intelligent Systems for Molecular Biology (ISMB), Chicago, IL, 2018.

Joshua D. Welch, Alexander J. Hartemink, Jan F. Prins: E Pluribus Unum: United States of Single Cells, Research in Computational Molecular Biology, Hong Kong, 2017.

Joshua D. Welch, Yin Hu, Jan F. Prins: Robust Detection of Alternative Splicing in a Population of Single Cells, Intelligent Systems for Molecular Biology, Orlando, FL, 2016.

Joshua D. Welch, Alexander J. Hartemink, Jan F. Prins. SLICER: Inferring Branched, Nonlinear Cellular Trajectories from Single Cell RNA-seq Data, Research in Computational Molecular Biology (RECOMB), Santa Monica, CA, 2016.

Joshua D. Welch, Jan F. Prins: Finding Life in High-Dimensional Space: Identifying Cell Types from Single Cell Gene Expression Data, NSF Data Science Workshop, Seattle, WA, 2015.

Joshua D. Welch, Lindsay Williams, Matthew DiSalvo, Jan F. Prins, Nancy Allbritton, Christopher Sims, Jen Jen Yeh, Corbin D. Jones: Selective Single Cell Isolation and RNA Sequencing Using Magnetic Micrafts, RNA Conference, Madison, WI, 2015.

Joshua D. Welch. Decoding the Symbols of Life: Learning Cell Types and Properties from RNA Sequencing Data, Dagstuhl Seminar 14381, "Neural-Symbolic Learning and Reasoning", 2014.

Joshua D. Welch, Michael K. Slevin, Jan F. Prins, William Marzluff: EnD-seq: A method for finding the 3 ends of RNA molecules using next-generation sequencing with application to mRNA exonuclease degradation, Symposium on RNA Biology X, North Carolina RNA Society Meeting, Chapel Hill, NC, 2013.

Joshua D. Welch, Charles Perou, Praveen Sethupathy, Jan F. Prins: Investigating the Role of Transcribed Pseudogenes in Breast Cancer, Intelligent Systems for Molecular Biology (ISMB), Berlin, Germany, 2013.

INVITED TALKS

Quantitative Definition of Cellular Identity by Single-Cell Multi-Omic Integration, George O'Brien
Kidney Center Research Seminar, University of Michigan, March 2020, Ann Arbor, MI

United States of Single Cells (Taubman Tech Talk), University of Michigan, February 2020, Ann Arbor,
MI

Quantitative Definition of Cellular Identity by Single-Cell Multi-Omic Integration, Biogen, February
2020, Cambridge, MA

Quantitative Definition of Cellular Identity by Single-Cell Multi-Omic Integration (MIT Bioinformatics
Seminar), Massachusetts Institute of Technology, February 2020, Cambridge, MA

Quantitative definition of cell identity by integrating transcriptomic, epigenomic, and spatial features,
Broad Institute of MIT and Harvard, March 2019, Cambridge, MA

Quantitative definition of cell identity through single-cell data integration (Science at the Edge Seminar
Series), Michigan State University, September 2019, Lansing, MI

Life in High-Dimensional Space: Modeling Sequential Changes in Gene Expression, Penn State Uni-
versity, March 2017, State College, PA.

Life in High-Dimensional Space: Modeling Sequential Changes in Gene Expression, University of Michi-
gan, February 2017, Ann Arbor, MI.

Life in High-Dimensional Space: Modeling Sequential Changes in Gene Expression, Virginia Tech,
February 2017, Blacksburg, VA.

Life in High-Dimensional Space: Modeling Sequential Changes in Gene Expression, University of Ken-
tucky, February 2017, Lexington, KY.

PEER-REVIEW SERVICE

Program Committee Member

11th ACM Conference on Bioinformatics, Computational Biology, and Health Informatics (ACM-BCB)
Program Committee (2020)

10th ACM Conference on Bioinformatics, Computational Biology, and Health Informatics (ACM-BCB)
Program Committee (2019)

High Performance Computational Biology (HICOMB) 2019

Ad Hoc Reviewer

Bioinformatics

Genome Biology

Nature Communications

Nature Methods

Nature Reviews Genetics

Genome Research

IEEE/ACM Transactions on Computational Biology

PLoS Computational Biology

Temporary Member

GNOM-G Study Section, National Human Genome Research Institute

GRADUATE STUDENT ADVISING

Yuwei Bao, MS, DCMB/CSE, University of Michigan (08/2018-08/2019)

Hengshi Yu, PhD, Biostatistics, University of Michigan (08/2018-present)

Hojae Lee, PhD, Electrical and Computer Engineering, University of Michigan (10/2018-present) - **NSF Graduate Research Fellowship**

Jialin Liu, MS, DCMB, University of Michigan (01/2019-present)

Chao Gao, PhD, DCMB, University of Michigan (06/2019-present)

Yuwei Bao, PhD (joint with Satish Narayanasamy), Computer Science and Engineering, University of Michigan (08/2019-present)

April Kriebel, PhD, DCMB, University of Michigan (06/2020-present) - **University of Michigan Genomics Training Grant**

Chen Li, PhD, DCMB, University of Michigan (06/2020-present) - **University of Michigan Bioinformatics Training Grant**

Yichen Gu, PhD (joint with David Blaauw), Computer Science and Engineering, University of Michigan (07/2020-present)

TEACHING

BIOINF 500, Fall 2019 (Co-Instructor)

BIOINF 602/603, Fall 2019 (Co-Instructor)

BIOINF 590, Fall 2019 (Co-Instructor)

BIOINF 602/603, Winter 2020 (Co-Instructor)

BIOINF 602/603, Fall 2020 (Co-Instructor)

The University of Michigan, Ann Arbor, MI

COMP 790-201: Predictive Models for High-Dimensional Data Analysis (Co-Instructor)

The University of North Carolina at Chapel Hill (01/2016-05/2016)

Single-Cell Sequencing Nanocourse (Co-Instructor)

Harvard Medical School (03/2018)

DISSERTATION COMMITTEES

Marcus Sherman, Open-source Python library for processing SAM files, University of Michigan, Computational Medicine and Bioinformatics

Nanxiang Zhao, Genome-wide Interrogation of Human Positive Regulatory Elements, University of Michigan, Computational Medicine and Bioinformatics

Renee Conway, Organoid models and development of human lung mesenchymal stem cells, University of Michigan, Cell and Developmental Biology

Maria Virgilio, Single-cell analysis of HIV latency, University of Michigan, Molecular and Cellular Biology

Jacqueline Larouche, Single-cell analysis of volumetric muscle loss, University of Michigan, Biomedical Engineering

Jiaqiang Zhu, Statistical methods for spatial transcriptomics, University of Michigan, Biostatistics

Chen Sun, Algorithms for somatic variant detection in single neurons, University of Michigan, Computational Medicine and Bioinformatics

OPEN-SOURCE SOFTWARE PACKAGES

AppEnD: Mapping 3' additions from RNA-seq data

<https://github.com/jw156605/append>

SingleSplice: Detection of alternative splicing in single cells

<https://github.com/jw156605/SingleSplice>

SLICER: Single cell trajectory inference

<https://github.com/jw156605/SLICER>

MATCHER: Single cell multi-modal integration

<https://github.com/jw156605/MATCHER>

LIGER: Linked inference of genomic experimental relationships

<https://github.com/MacoskoLab/LIGER>