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

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.

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

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

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

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

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

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 Microraft Arrays. Nucleic Acids Research 2016. doi: 10.1093/nar/gkw700
*Equal contribution

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

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

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

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.

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

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.

Slevin MK, Meaux S, **Welch JD**, Bigler R, Miliani de Marval PL, Su W, Rhoads RE, Prins JF, Marzluff WF Deep Sequencing Shows Multiple Oligouridylations Are Required for 3' to 5' Degradation of Histone mRNAs on Polyribosomes. Molecular cell 53 (6), 1020-1030. March 2014.

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.

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.

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.

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

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.

Dynamics and regulations of bone stem cells in vivo
NIH/NIDCR (3R01DE026666-02S1)
Noriaki Ono (PI), Joshua D. Welch (Co-I)
06/2019-05/2020.

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.

Integrating Single Cell Profiles across Modalities Using Manifold Alignment
Chan Zuckerberg Initiative (2018-183155)
Joshua Welch, PI
04/2018-08/2019.

ABSTRACTS

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 Microrafts, 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.

PEER-REVIEW SERVICE

Program Committee Member
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

GRADUATE STUDENT ADVISING

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

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

Hojae Lee, PhD, ECE, University of Michigan (10/2018-present)

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

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

TEACHING

BIOINF 500, Fall 2019 (Co-Instructor)
BIOINF 602/603, Fall 2019 (Co-Instructor)
BIOINF 590, Fall 2019 (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, Michigan, DCMB

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

Maria Virgilio, Molecular and Cellular Biology

Jacqueline Larouche, Biomedical Engineering

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