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**Assistant Professor, Department of Computer Science and Engineering**  
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## Education and Training

### Education

08/2007-06/2012 BM, Piano Performance, Ohio University, Athens, OH  
08/2007-06/2012 BS, Computer Science, Ohio University, Athens, OH  
08/2012-05/2016 MS, Computer Science, The University of North Carolina at Chapel Hill, Chapel Hill, NC  
08/2012-08/2017 PhD, Computer Science, The University of North Carolina at Chapel Hill, Chapel Hill, NC

### Postdoctoral Training

08/2017-08/2018 Postdoctoral Research Fellow, Computational Biology and Neuroscience, Broad Institute of Harvard and MIT, Cambridge, MA  
08/2018 Visiting Scholar, Broad Institute of Harvard and MIT, Cambridge, MI

## Academic, Administrative, Clinical, Research and Military Appointments

### Academic Appointments

08/2018-present Assistant Professor of Computational Medicine and Bioinformatics, University of Michigan, Ann Arbor, MI  
08/2018-present Assistant Professor of Computer Science and Engineering, University of Michigan, Ann Arbor, Michigan

## Grants

### Current Grants

*5 R01 HG010883-05: Quantitative Definition of Cell Identity by Integrating Transcriptomic, Epigenomic, and Spatial Features of Individual Cells* NIH-DHHS-US- 19-PAF04686

Joshua Welch, PI  
09/2019-06/2024. \$1,508,385 (\$341,121)

*5 RF1 MH123199-03: Linking molecular and anatomical features of brain cell identity through computational data integration* NIH-DHHS-US- 20-PAF01160

Joshua Welch, PI  
09/2020-08/2023. \$1,121,254 (\$373,752)

*5 R01 AI149669-05: Integrative Single-Cell Analysis of Transcriptome, Epigenome, and Lineage in HIV Latency and Activation; co-PI Welch supervises single-cell integration and lineage analyses* NIH-DHHS-US- 19-PAF05566

Kathleen L Collins co-PI; Joshua D. Welch co-PI, Co-PI  
12/2019-11/2024. \$3,360,219 (\$673,441)

*1R01DE03063001: Craniofacial skeletal cell lineage plasticity for reconstituting stem cells and their niches; co-PI Welch supervises single-cell analyses* NIH-DHHS-US- 20-PAF07172

Noriaki Ono co-PI; Wanida Ono co-PI; Joshua Welch co-PI, Co-PI  
04/2021-02/2026. \$2,332,515

*1UC2AR081033: Immunogenomics and Systems Biology Core-UC2-SBC; co-PI Welch supervises single-cell multi-omic integration analyses* NIH

Tsoi, Lam Alex co-PI; Gudjonsson, Johann co-PI; Zhou, Xiang co-PI; Welch, Joshua co-PI, Co-PI  
03/2022-12/2026. \$11,901,944

*Adipose tissue diversity in infants, children, and adolescents; co-PI Welch supervises single-cell multi-omic integration and velocity analyses* Chan Zuckerberg Initiative, LL- 21-PAF06428  
Lumeng, Carey Nien-Kai;Gadepalli, Samir Kumar;Ohye, Richard G;Singer, Kanakadurga VNL;Welch, Joshua; Woolford, Susan Jennifer, Co-PI  
10/2021-09/2024. \$1,962,705

*LAMA21AB0: Divergence of RAS and BOS Phenotypes of CLAD; co-PI Welch supervises single-cell data analyses* Cystic Fibrosis Foundation  
Lama, Vibha co-PI; Welch, Joshua co-PI, Co-PI  
02/2022-01/2024. \$336,000 (\$168,000)

*Predicting the Impact of Genomic Variation on Cellular States* NIH-DHHS-US- 21-PAF02189  
Co-I with Effort (Principal Investigator: Boyle, Alan P)  
07/2021-06/2026. \$3,829,187

*Uncover the role of H3.3-G343R mutation in shaping the DNA damage response, anti-tumor immunity and mechanisms of resistance in glioma.* NIH-DHHS-US- 21-PAF05156  
Co-I with Effort (Principal Investigator: Castro, Maria)  
01/2022-08/2026. \$3,228,160

*Transcriptional Control of HIV Latency in Hematopoietic Stem and Progenitor Cells* NIH-DHHS-US- 20-PAF09036  
Co-I without Effort (Principal Investigator: Virgilio, Maria)  
07/2021-06/2024. \$128,282

*5 R35 NS122302-08: Mechanisms of neurodegenerative diseases: intersections with ubiquitin pathways* NIH-DHHS-US- 20-PAF08998  
Co-I without Effort (Principal Investigator: Henry L Paulson)  
05/2021-04/2029. \$8,306,640 (\$1,038,330)

*1R01DE0291810101: Dental Follicle: A Central Regulator of Tooth Root Formation and Regeneration* NIH-DHHS-US- 20-PAF04857  
Co-I with Effort (Principal Investigator: Wanida Ono)  
02/2021-01/2026. \$1,852,500

*5R01DE02666604: Dynamics and Regulation of Bone Stem Cells in vivo - Supplement Proposal* NIH-DHHS-US- 17-PAF03798; 19-PAF05903  
Co-I with Effort (Principal Investigator: Noriaki Ono)  
01/2018-12/2022. \$2,080,003

*5R01DE02666604: Dynamics and Regulations of Bone Stem Cells in Vivo* NIH-DHHS-US- 19-PAF05903; 17-PAF03798  
Co-I with Effort (Principal Investigator: Noriaki Ono)  
01/2018-12/2022. \$2,080,003

*F31HG012715: Leveraging Spatial Location for Single-Cell Molecular and Morphological Characterization* NIH/NHGRI  
Co-I without Effort (Principal Investigator: April Kriebel)  
12/2022-11/2024

*An Atlas of Human Brain Cell Variation* NIH  
Co-I with Effort (Principal Investigator: Macosko, Evan; McCarroll, Steven)  
07/2022-06/2027. \$1,416,517

*The role of circulating meta-inflammatory monocytes in adolescent insulin resistance* NIH-DHHS-US- 21-PAF04066  
Co-I with Effort (Principal Investigator: Singer, Kanakadurga VNL)  
09/2021-08/2026. \$3,181,634

*Linking single-neuron morphology and gene expression using deep learning.* Lee F31/Welch NIH-DHHS-US- 21-PAF06378  
Co-I without Effort (Principal Investigator: Lee, Hojae)  
09/2021-08/2023. \$90,013

## **Submitted Grants**

*Exploiting the T-cell lymphoma ecosystem to improve disease classification and treatment* NIH

Co-I with Effort (Principal Investigator: Wilcox, Ryan)

10/2022-09/2027. \$5,000,000

*Building Mechanistic Models of Cell Fate Transition from Single-Cell Multi-Omic Data* NOT FUNDED Pew Charitable Trust

Welch, Joshua, PI

08/2022-08/2025. \$300,000

*Dual Gene Therapy with Nivolumab for GBM* NOT FUNDED NIH

Co-I with Effort (Principal Investigator: Lowenstein, Pedro)

07/2022-06/2027

*Characterization and Applications of Mathematical Invariance in Deep Learning* NOT FUNDED NSF-US- 21-PAF07531

Co-I with Effort (Principal Investigator: Bieri, Lydia;Dinov, Ivo;Fessler, Jeffrey A;Garikipati, Krishna;Veerapaneni, Shravan)

01/2022-12/2024. \$1,143,707

*University of Michigan Senescence Tissue Mapping Center* NOT FUNDED NIH-DHHS-US- 21-PAF06320

Co-I with Effort (Principal Investigator: Gudjonsson, Johann E;Bitzer, Markus;Hodgin, Jeffrey B)

12/2021-11/2026. \$16,819,018

*Interrogating tissues from ancestrally diverse Hispanic/Latino populations; co-PI Welch supervises single-cell analyses* NOT FUNDED Chan Zuckerberg Initiative, LL- 21-PAF07335

Spence, Jason co-PI; Sexton, Jonathan Zachary co-PI;Welch, Joshua co-PI, Co-PI

12/2021-11/2024. \$3,452,370

*Unraveling the Cellular Dynamics of the Cranial Base Synchondroses Throughout Postnatal Craniofacial Development* NOT FUNDED NIH-DHHS-US- 21-PAF06196

Co-I without Effort (Principal Investigator: Hallett, Shawn)

09/2021-08/2025. \$390,788

*Characterization and Applications of Mathematical Invariance in Deep Learning* NOT FUNDED National Science Foundation

Co-I with Effort (Principal Investigator: Lydia Bieri)

09/2021-08/2024. \$1,143,707 (\$372,777)

*Joshua Welch Sloan Research Fellowship* NOT FUNDED Sloan, Alfred P., Foundation- 21-PAF01054

Welch, Joshua, PI

09/2021-09/2023. \$75,000

*In vivo spatial profiling of mosaic stem cell interactions in chondrosarcoma initiation; co-PI Welch supervises single-cell computational analyses* NOT FUNDED NIH-DHHS-US- 20-PAF05027

Ono, Noriaki co-PI; Welch, Joshua co-PI, Co-PI

04/2021-03/2023. \$424,295

*Mapping and modeling the human gut across the developmental continuum; co-PI Welch supervises single-cell computational analyses* NOT FUNDED Helmsley Charitable Trust

Rao, Arvind; Higgins, Peter; Camp, Gray; Colacino, Justin; Spence, Jason; Welch, Joshua; Zhou, Xiang, Co-PI

07/2019-07/2022. \$2,991,042

## **Past Grants**

*Integrative single cell genomic analysis of mesenchymal stem cells* MCubed

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

01/2019-04/2020. \$20,000 (\$20,000)

Grant Number: 2018-183155: *Integrating Single Cell Profiles across Modalities Using Manifold Alignment* Chan  
Zuckerberg Initiative (CZ- 18-PAF04549  
Welch, Joshua, PI  
04/2018-08/2019. \$171,000 (\$171,000)

COMPUTATIONAL MODELING OF HETEROGENEOUS GENE EXPRESSION IN SINGLE CELLS NIH  
Welch, Joshua, PI  
06/2016-05/2017. \$45,016 (\$33,259)

## Honors and Awards

### International

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

### National

2012-2014 National Science Foundation Graduate Research Fellowship

2016-2017 Ruth L. Kirschstein National Research Service Award

### Institutional

2013 Graduate Student Mentoring Award, UNC Office of Undergraduate Research

2015 Big Data to Knowledge Fellowship (BD2K T32 at University of North Carolina)

2017 University of North Carolina Horizon Award

2021 Institutional Nominee for Pew Biomedical Scholars

## Memberships in Professional Societies

2015-present Member, International Society for Computational Biology (ISCB)

2022-present Member, American Association for the Advancement of Science

2022-present Member, Association for Computing Machinery

2022-present Member, Society for Neuroscience

## Editorial Positions, Boards, and Peer-Review Service

### Study Sections

#### National

2020 GNOM-G Study Section, National Human Genome Research Institute, NIH (Ad Hoc)

2021 ETTN-B(55), National Institute of Mental Health (Ad Hoc)

2021 GCAT Study Section, National Human Genome Research Institute (Ad Hoc)

2021 INCLUDE Down Syndrome Study Section, NIH Common Fund (Ad Hoc)

2021 ZDE1 JK(07) Study Section, National Institute of Dental and Craniofacial Research (Ad Hoc)

2022 RFA-AI-22-025 Study Section, National Institute of Allergy and Infectious Disease (Ad Hoc)

2022 ZDE1 JFR (03) Study Section, National Institute of Dental and Craniofacial Research (Ad Hoc)

#### Editorial Boards

2019-2021 Program Committee Member, ACM Conference on Bioinformatics, Computational Biology, and Health Informatics (ACM BCB) Program Committee

2019 Program Committee Member, High Performance Computational Biology (HICOMB) 2019 Program Committee

2021 Guest Editor, PLoS Computational Biology

2022 program committee member, ISMB/ECCB Program Committee

2022 program committee member, RegGen SIG Program Committee

## **Journal Reviewer**

2017-2021	Bioinformatics (Ad Hoc)
2017-2021	Genome Biology (Ad Hoc)
2017-2021	Nature Communications (Ad Hoc)
2018	Nature Reviews Genetics (Ad Hoc)
2019-2020	Genome Research (Ad Hoc)
2019-2020	Nature Methods (Ad Hoc)
2019	IEEE/ACM Transactions on Computational Biology (Ad Hoc)
2020-2021	Nature (Ad Hoc)
2020-2021	Nature Protocols (Ad Hoc)
2021	Nature Biotechnology (Ad Hoc)
2022	PLoS Computational Biology (Ad Hoc)

## **Teaching**

### **Advanced Post Graduate Fellow**

04/2021-03/2022	Shreepriya Das, PhD, University of Michigan
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### **Graduate Student**

08/2018-08/2020	Yuwei Bao, MS, University of Michigan
08/2018-06/2022	Hengshi Yu, PhD, University of Michigan
10/2018-present	Hojae Lee, PhD, University of Michigan
01/2019-present	Jialin Liu, MS/PhD, University of Michigan
04/2019-05/2021	Ruohan Liao, MS, University of Michigan
06/2019-present	Chao Gao, PhD, University of Michigan
03/2020-present	Angel Ka Yan Chu, MS, University of Michigan
04/2020-present	Lu Lu, MS, University of Michigan
05/2020-present	April Kriebel, PhD, University of Michigan
06/2020-present	Yichen Gu, PhD, University of Michigan
07/2020-present	Chen Li, PhD, University of Michigan
11/2021-present	Yuxuan Song, MS, University of Michigan

### **Postdoctoral Fellow**

02/2021-present	Maryam Bagherian, PhD, University of Michigan
08/2022-present	Justin Lee, PhD, University of Michigan

### **Undergraduate Student**

04/2019-present	Joshua Sodicoff, BS, University of Michigan
01/2022-present	Zaid Siddiqui, B.S., University of Michigan

## **Teaching Activity**

### **Institutional**

01/2016-05/2016	Co-Instructor of Record COMP 790-201: Predictive Models for High-Dimensional Data Analysis The University of North Carolina at Chapel Hill
03/2018	Co-Instructor Single-Cell Sequencing Nanocourse Harvard Medical School
09/2019-12/2020	Co-Instructor, Bioinformatics Journal Club (BIOINF 602/603)
10/2019-10/2021	Guest lecturer, BIOINF 500
01/2020-04/2020	Co-Instructor, Computational Genomics (BIOINF 525)
04/2020	Guest Lecturer, Single-Cell Genomics (BME)

11/2020 Guest Lecturer, Cancer Genomics (BIOINF 590)  
09/2021-12/2021 Co-Instructor of BIOINF 593/CSE 598

### **Dissertation Committees**

Present	April Kriebel, Computational methods for Single-cell and spatial data integration, University of Michigan, DCMB, Chair
Present	Brad Crone, Computational methods for GWAS with LD, University of Michigan, DCMB, Committee Member
Present	Chao Gao, Single-cell multi-omic integration, University of Michigan, DCMB, Chair
Present	Charlie Childs, Human gut development, University of Michigan, Cell and Developmental Biology, Committee Member
Present	Chen Li, Learning computational models of gene regulation from single-cell multi-omic data, University of Michigan, DCMB, Chair
Present	Chen Sun, Algorithms for structural variant detection, University of Michigan, DCMB, Committee Member
Present	D. Ford Hannum, Single-cell analysis of female reproductive tract, University of Michigan, DCMB, Committee Member
Present	Hanbyul Cho, Single-cell analysis of cancer, University of Michigan, DCMB, Committee Member
Present	Hanrui Zhang, Predicting combination treatment response by machine learning, University of Michigan, DCMB, Committee Member
Present	Hengshi Yu, Deep generative models for single-cell perturbation data, University of Michigan, Biostatistics, Co-Chair
Present	Hojae Lee, Deep generative models for linking gene expression and morphology, University of Michigan, ECE, Chair
Present	Hsiangyu Hu, Molecular and Cellular Pathology, University of Michigan, Molecular and Cellular Pathology, Committee Member
Present	Jacqueline Larouche, Single-cell analysis of aging muscle, University of Michigan, Biomedical Engineering, Committee Member
Present	Jialin Liu, Computational methods for inferring cell-cell communication, University of Michigan, DCMB, Chair
Present	Jiaqiang Zhu, Statistical models for spatial transcriptomics, University of Michigan, Biostatistics, Committee Member
Present	Marcus Sherman, Open-source Python library for processing SAM files, University of Michigan, DCMB, Committee Member
Present	Maria Virgilio, Determinants of HIV latency, University of Michigan, Immunology, Committee Member
Present	Nanxiang Zhao, Genome-wide Interrogation of Human Positive Regulatory Elements, Michigan, DCMB, Committee Member
Present	Renee Conway, Organoid models and development of human lung mesenchymal stem cells, University of Michigan, Cell and Developmental Biology, Committee Member
Present	Shuze Wang, Single-cell analysis of the ear, University of Michigan, DCMB, Committee Member
Present	Yichen Gu, Computational methods for RNA velocity inference, University of Michigan, ECE, Co-Chair
Present	Ying Ma, Statistical methods for spatial transcriptomics, University of Michigan, Biostatistics, Committee Member
Present	Yuanhao Huang, Machine learning methods for predicting epigenome data, University of Michigan, DCMB, Committee Member

### **Committee and Administrative Services**

## Committee Services

### International

2018-present	Association for Computing Machinery conference on Bioinformatics and Computational Biology, Program Committee
2021	Machine-learning methods for single-cell analysis, Workshop at ACM-BCB 2021, Co-Chair
2022-present	Intelligent Systems for Molecular Biology, Program Committee
2022-present	Intelligent Systems for Molecular Biology, Regulatory and Systems Genomics Special Interest Group, Program Committee Member
2022	Research in Computational Molecular Biology (RECOMB) 2022, Session Chair

### Institutional

2020-present	Department of Computational Medicine and Bioinformatics Seminar Committee, Co-Chair
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## Visiting Professorships and Extramural Invited Presentations

### Extramural Invited Presentations

1. Quantitative definition of cell identity by integrating transcriptomic, epigenomic, and spatial features., Broad Institute of MIT and Harvard, March 2019, Cambridge, MA
2. Quantitative definition of cell identity through single-cell data integration. Hosted by David Arnosti, Michigan State University, September 2019, Lansing, MI
3. Quantitative Definition of Cellular Identity by Single-Cell Multi-Omic Integration (MIT Bioinformatics Seminar). Hosted by Bonnie Berger, Massachusetts Institute of Technology, February 2020, Cambridge, MA
4. Quantitative Definition of Cellular Identity by Single-Cell Multi-Omic Integration, Biogen, February 2020, Cambridge, MA
5. Learning Representations of Cell Identity by Single-Cell Multi-Omic Integration. MIT 6.874,6.802,20.390,20.490: Deep Learning in the Life Sciences (via zoom). Hosted by Manolis Kellis., Massachusetts Institute of Technology, March 2021, Cambridge, MA (via Zoom)
6. Jointly Defining Cell States from Single-Cell Multi-Omic and Spatial Transcriptomic Datasets. Hosted by Yun Li, International Chinese Statistical Association annual meeting, September 2021, Virtual
7. Modeling neuronal identity changes with single-cell multimodal integration. Stanley Center Symposium. Hosted by Steve Hyman, Broad Institute of Harvard and MIT, September 2021, Cambridge, MA
8. Quantitative Definition of Cellular Identity from Single-Cell Multi-Omic Data. Hosted by Bernie Daigle., University of Memphis, November 2021, Memphis, TN (by zoom)
9. Jointly defining cell states from Single-Cell Multiomic and Spatial Transcriptomic datasets. Hosted by Steven Hoffman., Illumina/10X Genomics, November 2021, Virtual
10. Single-cell multi-omic velocity infers dynamic and decoupled gene regulation. Hosted by Mingyao Li., University of Pennsylvania, November 2021, Philadelphia, PA (by zoom)
11. Iterative Single-Cell Multi-Omic Integration Using Online Learning. Hosted by Jonah Cool., Chan Zuckerberg Biohub, December 2021, Palo Alto, CA (by zoom)
12. Single-cell multi-omic velocity infers dynamic and decoupled gene regulation. Hosted by Youping Deng, University of Hawaii - Manoa, February 2022, Honolulu, Hawaii, USA (by zoom)
13. Sampling from disentangled representations of single-cell data using generative adversarial networks. Hosted by Martin Treppner., Institute of Medical Biometry and Statistics, University of Freiburg, March 2022, Freiburg, Germany (by zoom)
14. Iterative single-cell multi-omic integration using online learning, Allen Institute for Brain Science, May 2022, Zoom (Virtual Event)
15. UINMF performs mosaic integration of single-cell multi-omic datasets using nonnegative matrix factorization. Hosted by Liang Sun., Boston Children's Hospital, October 2022, Boston, MA (by zoom)
16. Single-cell multi-omic integration using LIGER. Hosted by Giuseppe Testa., Human TechnoPole, November 2022, Milan, Italy

## Patents

### Application in Process

U.S. Patent Application NO.: 17/876,493 Title: Designing Chemical or Genetic Perturbations using Artificial Intelligence Inventors: Joshua D. Welch and Hengshi Yu UM Reference: 2022-338-01, Co-inventor, Submitted on 07/2022

## Bibliography

### Peer-Reviewed Journals and Publications

1. 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* 10 Suppl 1: S18, 2009. PM19594877/PMC2709261
2. 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* 10: 463, 2009. PM19814816/PMC2770528
3. 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* 11 Suppl 12: S6, 2010. PM21210985/PMC3040532
4. 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. *Mol Cell* 53(6): 1020-30, 2014. PM24656133/PMC4403670
5. Brooks L 3rd, Lyons SM, Mahoney JM, **Welch JD**, Liu Z, Marzluff WF, Whitfield ML: A multiprotein occupancy map of the mRNP on the 3' end of histone mRNAs. *RNA* 21(11): 1943-65, 2015. PM26377992/PMC4604434
6. **Welch JD**, Slevin MK, Tatomer DC, Duronio RJ, Prins JF, Marzluff WF: EnD-Seq and AppEnD: sequencing 3' ends to identify nontemplated tails and degradation intermediates. *RNA* 21(7): 1375-89, 2015. PM26015596/PMC4478355
7. **Welch JD**, Baran-Gale J, Perou CM, Sethupathy P, Prins JF: Pseudogenes transcribed in breast invasive carcinoma show subtype-specific expression and ceRNA potential. *BMC Genomics* 16: 113, 2015. PM25765044/PMC4344757
8. Lackey PE, **Welch JD**, Marzluff WF: TUT7 catalyzes the uridylation of the 3' end for rapid degradation of histone mRNA. *RNA* 22(11): 1673-1688, 2016. PM27609902/PMC5066620
9. 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 Res* 44(19): 9190-9205, 2016. PM27402160/PMC5100578
10. **Welch JD**, Hu Y, Prins JF: Robust detection of alternative splicing in a population of single cells. *Nucleic Acids Res* 44(8): e73, 2016. PM26740580/PMC4856971
11. **Welch JD**, Hartemink AJ, Prins JF: SLICER: inferring branched, nonlinear cellular trajectories from single cell RNA-seq data. *Genome Biol* 17(1): 106, 2016. PM27215581/PMC4877799
12. **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 microwell arrays. *Nucleic Acids Res* 44(17): 8292-301, 2016. PM27530426/PMC5041489
13. 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* 551(7678): 100-104, 2017. PM29072293/PMC5954984
14. **Welch JD**, Hartemink AJ, Prins JF: MATCHER: manifold alignment reveals correspondence between single cell transcriptome and epigenome dynamics. *Genome Biol* 18(1): 138, 2017. PM28738873/PMC5525279
15. **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* 177(7): 1873-1887, 2019. PM31178122



16. 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* 25(1): 149-164.e9, 2019. PM31230860/PMC6684137
17. Rodrigues SG, Stickels RR, Goeva A, Martin CA, Murray E, Vanderburg CR, **Welch J**, Chen LM, Chen F, Macosko EZ: Slide-seq: A scalable technology for measuring genome-wide expression at high spatial resolution. *Science* 363(6434): 1463-1467, 2019. PM30923225
18. Liu J, Gao C, Sodicoff J, Kozareva V, Macosko EZ, **Welch JD**: Jointly defining cell types from multiple single-cell datasets using LIGER. *Nat Protoc* 15(11): 3632-3662, 2020. PM33046898
19. Matsushita Y, Nagata M, Kozloff KM, **Welch JD**, Mizuhashi K, Tokavanich N, Hallett SA, Link DC, Nagasawa T, Ono W, Ono N: A Wnt-mediated transformation of the bone marrow stromal cell identity orchestrates skeletal regeneration. *Nat Commun* 11(1): 332, 2020. PM31949165/PMC6965122
20. BRAIN Initiative Cell Census Network (BICCN): A multimodal cell census and atlas of the mammalian primary motor cortex. *Nature* 598(7879): 86-102, 2021. PM34616075/PMC8494634
21. Yao Z, Liu H, Xie F, Fischer S, Adkins RS, Aldridge AI, Ament SA, Bartlett A, Behrens MM, Van den Berge K, Bertagnolli D, de Bézieux HR, Biancalani T, Boeshaghi AS, Bravo HC, Casper T, Colantuoni C, Crabtree J, Creasy H, Crichton K, Crow M, Dee N, Dougherty EL, Doyle WI, Dudoit S, Fang R, Felix V, Fong O, Giglio M, Goldy J, Hawrylycz M, Herb BR, Hertzano R, Hou X, Hu Q, Kancherla J, Kroll M, Lathia K, Li YE, Lucero JD, Luo C, Mahurkar A, McMillen D, Nadaf NM, Nery JR, Nguyen TN, Niu SY, Ntranos V, Orvis J, Osteen JK, Pham T, Pinto-Duarte A, Poirion O, Preissl S, Purdom E, Rimorin C, Risso D, Rivkin AC, Smith K, Street K, Sulc J, Svensson V, Tieu M, Torkelson A, Tung H, Vaishnav ED, Vanderburg CR, van Velthoven C, Wang X, White OR, Huang ZJ, Kharchenko PV, Pachter L, Ngai J, Regev A, Tasic B, **Welch JD**, Gillis J, Macosko EZ, Ren B, Ecker JR, Zeng H, Mukamel EA: A transcriptomic and epigenomic cell atlas of the mouse primary motor cortex. *Nature* 598(7879): 103-110, 2021. PM34616066/PMC8494649
22. Alghamri MS, McClellan BL, Avvari RP, Thalla R, Carney S, Hartlage MS, Haase S, Ventosa M, Taher A, Kamran N, Zhang L, Faisal SM, Núñez FJ, Garcia-Fabiani MB, Al-Holou WN, Orringer D, Hervey-Jumper S, Heth J, Patil PG, Eddy K, Merajver SD, Ulintz PJ, **Welch J**, Gao C, Liu J, Núñez G, Hambardzumyan D, Lowenstein PR, Castro MG: G-CSF secreted by mutant IDH1 glioma stem cells abolishes myeloid cell immunosuppression and enhances the efficacy of immunotherapy. *Sci Adv* 7(40): eabh3243, 2021. PM34586841/PMC8480930
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24. Matsushita Y, Chu AKY, Ono W, **Welch JD**, Ono N: Intercellular Interactions of an Adipogenic CXCL12-Expressing Stromal Cell Subset in Murine Bone Marrow. *J Bone Miner Res* 36(6): 1145-1158, 2021. PM33651379
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