

# John D. Blischak

Website: [jdblischak.com](http://jdblischak.com)  
Email: [jdblischak@gmail.com](mailto:jdblischak@gmail.com)  
LinkedIn: [linkedin.com/in/jdblischak](https://www.linkedin.com/in/jdblischak)  
GitHub: [github.com/jdblischak](https://github.com/jdblischak)

## EXPERIENCE

---

- JDB Software Consulting, LLC** Copley, OH, USA  
Freelance Scientific Software Developer 2019–Present
- **Genentech Inc** - Built bioinformatics pipelines to support scientists in Human Genetics
  - **AbbVie Inc** - Built a backend data management system in R to interface with an interactive dashboard to explore differential expression results
  - **University of Chicago** - Continued developing workflow software for organized + reproducible + shareable data science in R
  - **Penn State University** - Taught a 3-day virtual workshop on bioinformatics and reproducibility for incoming PhD students
- University of Chicago** Chicago, IL, USA  
Postdoctoral Scholar 2016–2019
- Created workflow software for organized + reproducible + shareable data science in R
  - Built bioinformatics pipelines with Python and R to process single-cell RNA-seq data

## EDUCATION

---

- University of Chicago** Chicago, IL, USA  
PhD Genetics, Advisor: Yoav Gilad 2010–2016
- Thesis: Transcriptomic approaches to investigate tuberculosis susceptibility
- Ohio University** Athens, OH, USA  
BS Biological Sciences 2006–2010

## PUBLICATIONS

---

\* denotes equal authorship

1. Hsiao CJ, Tung P, **Blischak JD**, Burnett JE, Barr KA, Dey KK, Stephens M, Gilad Y. Characterizing and inferring quantitative cell cycle phase in single-cell RNA-seq data analysis. *Genome Research*, 2020, doi: 10.1101/gr.247759.118
2. **Blischak JD**, Carbonetto P, Stephens M. Creating and sharing reproducible research code the workflow way. *F1000Research*, 2019, doi: 10.12688/f1000research.20843.1
3. Sarkar AK\*, Tung PY\*, **Blischak JD**, Burnett JE, Li YI, Stephens M, and Gilad Y. Discovery and characterization of variance QTLs in human induced pluripotent stem cells. *PLOS Genetics*, 2019, doi: 10.1371/journal.pgen.1008045
4. Blake LE\*, Thomas SM\*, **Blischak JD**, Hsiao CJ, Chavarria C, Myrthil M, Gilad Y, and Pavlovic BJ. A comparative study of endoderm differentiation in humans and chimpanzees. *Genome Biology*, 2018, doi: 10.1186/s13059-018-1490-5
5. Engelmann BW\*, Hsiao CJ\*, **Blischak JD**, Fourne Y, Khan Z, Ford M, and Gilad Y. A Methodological Assessment and Characterization of Genetically-Driven Variation in Three Human Phosphoproteomes. *Scientific Reports*, 2018, doi: 10.1038/s41598-018-30587-3

6. Knowles DA\*, Burrows CK\*, **Blischak JD**, Patterson KM, Serie DJ, Norton N, Ober C, Pritchard JK, and Gilad Y. Determining the genetic basis of anthracycline-cardiotoxicity by molecular response QTL mapping in induced cardiomyocytes. *eLife*, 2018, doi: 10.7554/eLife.33480
7. **Blischak JD\***, Tailleux L\*, Myrthil M, Charlois C, Bergot E, Dinh A, Morizot G, Chény O, Platen CV, Herrmann JL, Brosch R, Barreiro LB, and Gilad Y. Predicting susceptibility to tuberculosis based on gene expression profiling in dendritic cells. *Scientific Reports*, 2017, doi: 10.1038/s41598-017-05878-w
8. Tung PY\*, **Blischak JD\***, Hsiao CJ\*, Knowles DA, Burnett JE, Pritchard JK, and Gilad Y. Batch effects and the effective design of single-cell gene expression studies. *Scientific Reports*, 2017, doi: 10.1038/srep39921
9. Kariuki SN, **Blischak JD**, Nakagome S, Witonsky DB, and Di Rienzo A. Patterns of transcriptional response to 1,25-Dihydroxyvitamin D3 and bacterial lipopolysaccharide in primary human monocytes. *G3*, 2016, doi: 10.1534/g3.116.028712
10. **Blischak JD**, Davenport ER, and Wilson G. A quick introduction to version control with Git and GitHub. *PLOS Computational Biology*, 2016, doi: 10.1371/journal.pcbi.1004668
11. **Blischak JD**, Tailleux L, Mitrano A, Barreiro LB, and Gilad Y. Mycobacterial infection induces a specific human innate immune response. *Scientific Reports*, 2015, doi: 10.1038/srep16882
12. Banovich NE, Lan X, McVicker G, van de Geijn B, Degner JF, **Blischak JD**, Roux J, Pritchard JK, and Gilad Y. Methylation QTLs are associated with coordinated changes in transcription factor binding, histone modifications, and gene expression levels. *PLOS Genetics*, 2014, doi: 10.1371/journal.pgen.1004663

## SELECTED PRESENTATIONS

---

- Why R? Webinar Series 2020  
*Reproducible research with workflow*
- The Quantitative & Applied Ecology Group, University of Melbourne 2018  
*Introduction to reproducible research with R Markdown, Git, and workflow*
- useR! 2018  
*The workflow R package: a framework for reproducible and collaborative data science*
- Workshop in Biostatistics, Stanford University 2018  
*The workflow R package: a framework for reproducible and collaborative data science*

## TEACHING

---

- Teaching Assistant, Quantitative Analysis Bootcamp, UChicago 2020
- Instructor, Bioinformatics Data Reproducibility Bootcamp, Penn State 2020
- Co-Instructor, Create and share reproducible code with R Markdown and workflowr, useR!2020 2020
- Guest Lecturer, Reproducible Research with workflowr, UChicago 2019
- Instructor, DataCamp Course (online), Differential Expression Analysis in R with limma 2018
- Guest Lecturer, Effective Strategies for Computational Reproducibility, UChicago 2018
- Guest Lecturer, Differential Expression Analysis of RNA-seq data with R/Bioconductor, UChicago 2017
- Guest Lecturer, Differential Expression Analysis of RNA-seq data with R/Bioconductor, UChicago 2016
- Instructor and Organizer, Software Carpentry Workshop, UChicago 2016
- Guest Lecturer, Differential Expression Analysis of RNA-seq data with R/Bioconductor, UChicago 2015
- Instructor and Organizer, Software Carpentry Workshop, UChicago 2015
- Guest Lecturer, Differential Expression Analysis of RNA-seq data with R/Bioconductor, UChicago 2014
- Instructor and Organizer, Software Carpentry Workshop, UChicago 2014

- Instructor and Organizer, Software Carpentry Workshop, UChicago 2013
- Teaching Assistant, Genomics and Systems Biology, UChicago 2012
- Teaching Assistant, Introduction to Probability and Statistics for Geneticists, UChicago 2012

## COMMUNITY

---

- Journal Reviewer  
*Journal of Statistical Software, NAR Genomics and Bioinformatics, Nature Genetics, PLOS Computational Biology, PLOS Genetics, PLOS One, The R Journal*
- SatRday Columbus 2020  
*Co-Organizer of 1-day virtual conference on R and data science*
- Greater Cleveland R Group 2020–Present  
*Co-Organizer*
- Reproducible Research CRAN Task View 2019–Present  
*Co-Maintainer*
- conda-forge | community driven packing for conda 2017–2018  
*Co-Maintainer of conda binaries for R packages*
- Software Carpentry 2014–2016  
*Co-Maintainer of R lessons*

## RECENT AWARDS

---

- Nan Xiao Prize for Computational Reproducibility, University of Chicago 2018