

Travis S. Johnson

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Education

The Ohio State University, Columbus, OH – *College of Medicine*

- **PhD Biomedical Sciences:** *May 2020*
 - Specialization in bioinformatics
 - Multi-Modeling and Integrative Data Analytics Departmental Fellowship (T15)
 - National Research Service Award Individual Fellowship (F31)

The Ohio State University, Columbus, OH - *College of Public Health*

- **MS Public Health:** *May 2016*
 - Specialization in biomedical informatics
 - Bioinformatics lab assistant

Ohio University, Athens, OH - *College of Arts and Sciences*

- **BS Plant Biology:** *May 2014*
 - Bioinformatics certificate
 - Plant cell biology lab assistant

United States Air Force, Maxwell Air Force Base, AL - *Community College of the Air Force*

- **AS Scientific Analysis Technology:** *Feb 2015*
 - Basic military training honor graduate
 - Student leader during technical training

Professional Experience

Indiana Biosciences Research Institute, Indianapolis, IN – *Applied Data Sciences Center*

- **Visiting Assistant Research Professor:** *July 2021 – Present*
 - Applied bioinformatics analysis
 - Bioinformatics pipeline development

Indiana University School of Medicine, Indianapolis, IN - *Department of Biostatistics and Health Data Science*

- **Assistant Research Professor:** *July 2020 – Present*
 - Single cell and spatial transcriptomic method development
 - Machine learning and deep learning
 - Transfer learning and domain adaptation
 - Integrative methods
 - Disease focus: Alzheimer's disease, myeloma, diabetes
 - Grant writing

Vascugen, Madison, WI

- **Consultant:** *Oct 2020 – June 2021*
 - Implementation of single cell workflows
 - Generating reports on product quality control
 - Advising on single cell analysis and interpretation

Medasource, Indianapolis, IN – *IU Health*

- **Contractor:** *May 2019 – May 2020*
 - SQL queries of EMR records
 - Statistical modeling on EMR data
 - Predictive machine learning on EMR data

- Advising students on their capstone projects
- Generation of reports based on data mining

The Ohio State University College of Medicine, Columbus, OH - *Department of Biomedical Informatics*

Indiana University School of Medicine, Indianapolis, IN - *Department of Medicine*

- **Graduate Fellow:** *February 2019 – May 2020*
- **Graduate Research Associate:** *May 2018 – February 2019*
- **Affiliate Indiana University School of Medicine:** *August 2017 – May 2020*
- **Graduate Fellow:** *May 2016 – May 2018*
- **Lab Assistant:** *September 2014 – May 2016*
 - Grant writing
 - HPC computing
 - Feature selection and feature reduction
 - Machine learning method development in biomedical data
 - Data analysis pipeline implementation for high performance computing
 - Interface development for online tools
 - RNA sequence alignment and quantification
 - Analysis of sequencing data

Ohio University, Athens, OH - *Department of Environmental and Plant Biology*

- **Lab Assistant:** *September 2011-2014*
 - Completed bio-hazard and radiation safety training
 - Basic wet-lab protocols
 - Basic statistical analyses

Ohio Air National Guard, Dayton, OH – *125th IS*

- **Scientific Applications Specialist:** *March 2009 – March 2015*
 - Staff sergeant (honorably discharged)
 - Production analyst on remote sensing data
 - Student leader during technical training
 - Honor Graduate from basic military training

Additional Skills

- Single cell analysis (clustering, trajectory, integration)
- Python, TensorFlow, NumPy, Pandas, Scikit-Learn
- HPC computing
- UNIX/LINUX
- R, MATLAB, RShiny
- SQL
- Statistical methods
- Bioinformatics tools
- Machine learning architectures
- Basic wet-lab protocols

Awards, Honors, and Memberships

- IU Melvin and Bren Simon Comprehensive Cancer Center *full member 2022 – present*
- American Society of Hematology (ASH) *member 2022 – present*
- Frontiers in Genetics, Cancer Genetics and Oncogenomics *review editor 2021 – present*
- Institute of Electrical and Electronics Engineers (IEEE) *member 2021 – present*
- American Society of Human Genetics (ASHG) *member 2017 – present*

- International Society for Computational Biology (ISCB) *member 2012 – present*
- Organization of Computational Neuroscience (OCNS) *member 2017 – 2018*
- ISCB travel fellowship *recipient 2017*
- ISCB travel fellowship *recipient 2016*
- Ohio Air National Guard *non-commissioned officer 2013-2015*
- Choose Ohio First Bioinformatics scholarship *recipient 2011-2014*
- Phi Kappa Theta, *president 2012-2014*
- Mortar Board National Honors Society *member 2013*
- 2nd place Ohio University Research Expo *recipient 2012*

Funding

Awarded

- American Cancer Society Institutional Research Grant, **role: PI (19-144-34)**
- Multiple Myeloma Research Foundation, 2021 Research Fellow Award, **role: PI**
- National Institutes of Health, National Library of Medicine, Ruth L. Kirschstein Predoctoral Individual National Research Service Award, **role: PI (1F31LM013056)**
- National Institutes of Health, National Library of Medicine, Multi-Modeling and Integrative Data Analytics Fellowship, **role: trainee (4T15LM011270)**

Pending

- National Institutes of Health, National Cancer Institute, Development of Innovative Informatics Methods and Algorithms for Cancer Research and Management, **impact score: 27, role: MPI (1R21CA264339)**
- National Science Foundation, Division of Mathematical Sciences and National Institute of General Medical Sciences, Initiative to Support Research at the Interface of the Biological and Mathematical Sciences, **role: Co-PI**
- National Institutes of Health, Research Project Grant, **role: Co-I**
- Chan Zuckerberg Initiative, Single-Cell Biology Data Insights, **role: Co-PI**

Publications

1. **Johnson, T.**, Abrams, Z., Zhang, Y., & Huang, K. (2017). Mapping neuronal cell types using integrative multi-species modeling of human and mouse single cell RNA sequencing. In *PACIFIC SYMPOSIUM ON BIOCOMPUTING 2017* (pp. 599-610).
2. **Johnson, T.**, Liebner, D., & Chen, J. L. (2017). Opportunities for patient matching algorithms to improve patient care in oncology. *JCO Clinical Cancer Informatics*, 1.
3. **Johnson, T. S.**, Abrams, Z. B., Mo, X., Zhang, Y., & Huang, K. (2017). Lack of human cytomegalovirus expression in single cells from glioblastoma tumors and cell lines. *Journal of neurovirology*, 23(5), 671-678.
4. Han, Z., **Johnson, T.**, Zhang, J., Zhang, X., & Huang, K. (2017). Functional virtual flow cytometry: a visual analytic approach for characterizing single-cell gene expression patterns. *BioMed research international*, 2017.
5. **Johnson, T. S.**, Li, S., Kho, J. R., Huang, K., & Zhang, Y. (2018). Network analysis of pseudogene-gene relationships: from pseudogene evolution to their functional potentials. In *PACIFIC SYMPOSIUM ON BIOCOMPUTING 2018: Proceedings of the Pacific Symposium* (pp. 536-547).
6. Wang, T., **Johnson, T.**, Zhang, J., & Huang, K. (2018). Topological methods for visualization and analysis of high dimensional single-cell RNA sequencing data. In *BIOCOMPUTING 2019: Proceedings of the Pacific Symposium* (pp. 350-361).
7. Huang, Z., Zhan, X., Xiang, S., **Johnson, T.S.**, Helm, B., Yu, C.Y., Zhang, J., Salama, P., Rizkalla, M., Han, Z. and Huang, K. (2019). SALMON: Survival Analysis Learning With Multi-Omics Neural Networks on Breast Cancer. *Frontiers in genetics*, 10, 16.

8. Yu, C.Y., Xiang, S., Huang, Z., **Johnson, T.S.**, Zhan, X., Han, Z., Huang, K. (2019). Gene Co-expression Network and Copy Number Variation Analyses Identify Transcription Factors Associated with Multiple Myeloma Progression. *Frontiers in genetics*, *10*, 468.
9. **Johnson, T.S.**, Li, S., Franz, E., Huang, Z., Li, S.D., Campbell, M.J., Huang, K., Zhang, Y. (2019). PseudoFuN: Deriving functional potentials of pseudogenes from integrative relationships with genes and microRNAs across 32 cancers. *Gigascience*, *8*(5), giz046.
10. **Johnson, T.S.**, Wang, T., Huang, Z., Yu, C.Y., Wu, Y., Han, Y., Zhang, Y., Huang, K., Zhang, J. (2019). LAmbDA: Label Ambiguous Domain Adaptation Dataset Integration Reduces Batch Effects and Improves Subtype Detection. *Bioinformatics*, *35*(22), 4696-4706.
11. Wang, T., **Johnson, T. S.**, Shao, W., Lu, Z., Helm, B. R., Zhang, J., & Huang, K. (2019). BERMUDA: a novel deep transfer learning method for single-cell RNA sequencing batch correction reveals hidden high-resolution cellular subtypes. *Genome biology*, *20*(1), 1-15.
12. Abrams, Z. B., **Johnson, T. S.**, Huang, K., Payne, P. R., & Coombes, K. (2019). A protocol to evaluate RNA sequencing normalization methods. *BMC bioinformatics*, *20*(24), 1-7.
13. Mason, M. J., Schinke, C., Eng, C. L., Towfic, F., Gruber, F., Dervan, A., **Multiple Myeloma DREAM Consortium**, ... & Cui, Y. (2020). Multiple Myeloma DREAM Challenge reveals epigenetic regulator PHF19 as marker of aggressive disease. *Leukemia*, *34*(7), 1866-1874.
14. Smerekanych, S.* , **Johnson, T. S.***, Huang, K., Zhang, Y. (2020). Pseudogene-gene functional networks are prognostic of patient survival in breast cancer. *BMC Medical Genomics*. *13*(5), 1-13.
15. Huang, Z., **Johnson, T.**, Han, Z., Helm, B., Cao, S., Zhang, C., ... Huang, K. (2020) Deep Learning-based Cancer Survival Prognosis from RNA-seq Data: Approaches and Evaluations. *BMC Medical Genomics*, *13*(5), 1-12.
16. Sharpnack, M. F., Cho, J. H., **Johnson, T. S.**, Otterson, G. A., Shields, P. G., Huang, K., ... & He, K. (2020). Clinical and Molecular Correlates of Tumor Mutation Burden in Non-Small Cell Lung Cancer. *Lung Cancer*. *146*, 36-41.
17. **Johnson, T. S.**, Xiang, S., Helm, B. R., Abrams, Z. B., Neidecker, P., Machiraju, R., Zhang, Y., ... & Zhang, J. (2020). Spatial Cell Type Composition in Normal and Alzheimers Human Brains is Revealed Using Integrated Mouse and Human Single Cell RNA Sequencing. *Scientific Reports*. *10*(1), 1-14.
18. **Johnson, T.***, Xiang, S.* , Dong, T., Huang, Z., Cheng, M., Wang, T., ... & Zhang, J. (2020). Combinatorial analyses reveal that cellular composition changes have different impact on transcriptomic changes of cell type specific genes in Alzheimer's Disease brains. *Scientific Reports*.
19. Awasthi, A., Tan, S., **Johnson, T. S.**, Mo, X. M., Fan, K., & Zhang, Y. (2021). PgenePapers: a novel database and search tools of reported regulatory pseudogenes. *International Journal of Computational Biology and Drug Design*, *13*(5-6), 504-519.
20. Xu, C., Sun, S., **Johnson, T.**, Qi, R., Zhang, S., Zhang, J., & Yang, K. (2021). The glutathione peroxidase Gpx4 prevents lipid peroxidation and ferroptosis to sustain Treg cell activation and suppression of antitumor immunity. *Cell Reports*, *35*(11), 109235.
21. Huang, X., Huang, K., **Johnson, T.**, Radovich, M., Zhang, J., Ma, J., & Wang, Y. (2021). ParsVNN: parsimony visible neural networks for uncovering cancer-specific and drug-sensitive genes and pathways. *NAR Genomics and Bioinformatics*, *3*(4), lqab097.
22. Lu, Z., **Johnson, T.S.**, Shao, W., Zhang, M., Zhang, J., Huang, K. (2021). Optimal transport- and kernel-based early detection of mild cognitive impairment patients based on magnetic resonance and positron emission tomography images. *Alzheimer's Research & Therapy*, *14*(1), 1-12.
23. **Johnson, T. S.**, Christina, Y. Y., Huang, Z., Xu, S., Wang, T., Dong, C., ... & Zhang, Y. (2022). Diagnostic Evidence GAuge of Single cells (DEGAS): A flexible deep-transfer learning framework for prioritizing cells in relation to disease. *Genome Medicine*, *14*(1), 1-23.
24. Sharpnack, M. F.* , **Johnson, T. S.***, Chalkley, R., Han, Z., Carbone, D., Huang, K., He, K. (2022). TSAFinder: Exhaustive Tumor Specific Antigen Detection with RNAseq. *Bioinformatics*.

25. Liu, Y., Wang, T., Duggan, B., Huang, K., Zhang, J., Ye, X., **Johnson, T.S.** (2022). SPCS: A Spatial and Pattern Combined Smoothing Method for Spatial Transcriptomics Expression. *Briefings in Bioinformatics*.

Abstracts and presentations

1. Abrams, Z., Armbruster, M., Burns, E., Clay, S., Cottrill, E., Fenstemaker, S., Garcia, K., Hayden, M., **Johnson, T.**, Lyall, K., Parisi, D., Presley, W., Thompson, O., Williams, D., Williams, T., Wyatt, S. (2012). Mining and Annotation of Gene Lists: A Comparative Study *Great Lakes Bioinformatics Conference (GLBC)*, Ann Arbor, MI. May 2012. Poster presented by Abrams, Z.
2. Abrams, Z., Armbruster, M., Burns, E., Clay, S., Cottrill, E., Fenstemaker, S., Garcia, K., Hayden, M., **Johnson, T.**, Lyall, K., Parisi, D., Presley, W., Thompson, O., Williams, D., Williams, T., Wyatt, S. (2013). Mining and Annotation of Gene Lists: A Comparative Study *Ohio Plant Biology Conference (OPBC)*, Columbus, OH. October 2013. **Poster presented by Johnson, T.**
3. **Johnson, T.**, Kho, J., Çatalyürek, Ü.V., Huang, K., Zhang, Y. (2016). Identification of Key Mutation Signatures from Conservation Analysis of Gene-pseudogene Families in Human. *Intelligent Systems in Molecular Biology (ISMB)*, Orlando, FL. July 2016. Poster presented by Zhang, Y.
4. Zhang, Y., **Johnson, T.**, Aldana, R., Feng, G., Huang, K. (2016). Comparing Variant Concordance in DNA-seq and RNA-seq from Matched Samples *Intelligent Systems in Molecular Biology (ISMB)*, Orlando, FL. July 2016. Poster presented by Zhang, Y.
5. **Johnson, T.**, Kho, J., Çatalyürek, Ü.V., Huang, K., Zhang, Y. (2016). Identification of Key Mutation Signatures from Conservation Analysis of Gene-pseudogene Families in Human *Intelligent Systems for Molecular Biology (ISMB)*, Orlando, FL. July 2016. Poster presented by Zhang, Y.
6. **Johnson, T.S.**, Abrams, Z., Zhang, Y., Huang, K. (2017). Mapping neuronal cell types using integrative multi-species modeling of human and mouse single cell RNA sequencing *Pacific Symposium on Biocomputing (PSB)*, Waimea, HI. January 2017. **Poster presentation by Johnson, T.S.**
7. Zhang, Y., **Johnson, T.**, Yu, S., Huang, K. (2017). Evaluating Relationships between Pseudogenes and Genes: From Pseudogene Evolution to Their Functional Potentials 67th *Annual Meeting of The American Society of Human Genetics (ASHG)*, Orlando, FL. October 2017. **Poster presented by Johnson, T.**
8. **Johnson, T.S.**, Li, S., Kho, J., Huang, K., Zhang, Y. (2018). Network analysis of pseudogene-gene relationships: from pseudogene evolution to their functional potentials *Pacific Symposium on Biocomputing (PSB)*, Waimea, HI. January 2018. **Oral presentation by Johnson, T.S.**
9. Sharpnack, M. F., **Johnson, T.**, Otterson, G. A., Carbone, D. P., Huang, K., & He, K. (2018). A cell cycle-related RNA expression signature of neoantigen burden in lung adenocarcinoma. *American Society of Clinical Oncology (ASCO)*, Chicago, IL. June 2018. Poster presented by Sharpnack, M.F.
10. **Johnson, T.S.**, Abrams, Z.B., Helm, B.R., Neidecker, P., Machiraju, R., Zhang, Y., Huang, K., Zhang, J. (2019). Integration of Mouse and Human Single-cell RNA Sequencing Infers Spatial Cell-type Composition in Human Brains *Research in Computational Molecular Biology (RECOMB)*, Washington, DC. May 2019. **Poster presentation by Johnson, T.S.**
11. Smerekanych, S. *, **Johnson, T. S. ***, Huang, K., Zhang, Y. (2019). Pseudogene-gene functional networks are prognostic of patient survival in breast cancer. *International Conference on Intelligent Biology and Medicine (ICIBM)*, Columbus, OH. June 2019. **Oral presentation by Johnson, T.S.**

12. Sharpnack, M., Cho, J. H., **Johnson, T.**, Otterson, G., Shields, P., Huang, K., ... & He, K. (2019). P1. 04-15 Smoking Status Is Not a Replacement Biomarker for Tumor Mutation Burden in Non-Small Lung Cancer. *World Conference on Lung Cancer (WCLC)*, September 2019, Poster presentation by Sharpnack, M.
13. Dong, C., Yu, C.Y., **Johnson, T.S.**, Reiter, J.L., Abu Zaid, M.I., Abonour, R., ... & Liu, Y. (2019). A Highly Robust Model for Predicting Outcome of Multiple Myeloma Patients By Inferring Patient-Specific Transcription Factor Activity. *American Society of Hematology (ASH)*, December 2019, Poster presented by Dong, D.
14. **Johnson, T.S.**, Yu, C.Y., Dong, C., Wang, T., Abu Zaid, M.I., Abonour, R., ... & Huang, K. (2019). Development of a Novel Deep Transfer Learning Framework to Characterize Inter-and Intra-Tumor Heterogeneity in Myeloma Patients. *American Society of Hematology (ASH)*, December 2019, **Poster presented by Johnson, T.S.**
15. Sharpnack, M., **Johnson, T.**, Chalkley, R., Han, Z., Carbone, D., Huang, K., & He, K. (2021). Exhaustive tumor specific antigen detection with RNAseq. *Cancer Res July 1 2021 (81) (13 Supplement)*, **Poster presentation at AACR by Sharpnack, M.**
16. **Johnson, T.**, Steere, B., Zhang, P., Zang, Y., Higgs, R., Gottlieb, K., ... & Krishnan, G. (2021). DOP09 Mirikizumab-induced transcriptome changes in patient biopsies at Week 12 are maintained through Week 52 in patients with Ulcerative Colitis. *Journal of Crohn's and Colitis, 15(Supplement_1)*. **Oral presentation at ECCO 2021 by Krishnan, G.**
17. **Johnson, T.**, Steere, B., Zhang, P., Zang, Y., Higgs, R., Gottlieb, K., ... & Krishnan, V. (2021). S806 Mirikizumab-Induced Transcriptome Changes in Patient Biopsies at Week 12 Are Maintained Through Week 52 in Patients With Ulcerative Colitis, *The American Journal of Gastroenterology: October 2021 - Volume 116 - Issue - p S374-S375*. **Presented at the ACG 2021**
18. Couetil, J., Zhang, J., Huang, K., **Johnson, T.S.** (2021). DEGAS: Mapping clinical metrics to spatial transcriptomics with deep learning. Rocky Mountain Bioinformatics Conference 2021. **Oral presentation by Couetil, J.**
19. **Johnson, T.S.** (2022). Identifying high risk components of disease from single cell, spatial, and imaging data. University of Louisville Department of Bioinformatics and Biostatistics Seminar. **Oral presentation by Johnson, T.S.**