Travis S. Johnson, PhD, MSPH
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Education

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

- **PhD Biomedical Sciences:** *May 2020*
  - Specialization in bioinformatics
  - National Research Service Award Individual Fellowship (F31)
  - Clinical and Translational Research Informatics Training Program (T15)

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

- **Agnes Beaudry Investigator in Myeloma Research:** *May 2023 – Present*
- **Assistant Professor:** *August 2022 – Present*
- **Assistant Research Professor:** *July 2020 – August 2022*
  - Single cell and spatial transcriptomic method development
  - Machine learning and deep learning
  - Transfer learning and domain adaptation
  - Integrative methods and multiomics
  - Disease focus: Myeloma, Alzheimer's disease, breast cancer, and diabetes
  - Grant writing

Indiana Biosciences Research Institute, Indianapolis, IN – *Integrated Data Sciences*

- **Director of Bioinformatics:** *July 2022 – Present*
  - Grant development
  - Recruitment and supervision of bioinformatics staff
  - Development and implementation of bioinformatics pipelines
  - Bioinformatics support and guidance
- **Visiting Assistant Research Professor:** *July 2021 – July 2022*
  - Applied bioinformatics analysis
  - Bioinformatics pipeline development

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

- BMC Bioinformatics *Associate Editor 2024 - present*
- Agnes Beaudry Endowment *Recipient 2023 – present*
- International Biometric Society *Member 2023 – present*
- International Myeloma Society *Member 2022 – present*
- BioCrossroads 23 PAIR Award: Promising Achievers in Innovation and Research *Recipient 2022*
- International Myeloma Society Young Investigator Award *Recipient 2022*
- IU Melvin and Bren Simon Comprehensive Cancer Center *Full Member Experimental and Developmental Therapeutics 2022 – present*
- American Society of Hematology (ASH) *Member 2022 – present*
- Center for Computational Biology and Bioinformatics *Member 2021 – present*
- Frontiers in Genetics, Cancer Genetics and Oncogenomics *Associate Editor 2024 – 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*

Professional Service

Reviewer

- Nucleic Acids Research
- Nature Computational Science
- Genome Biology
- Genome Medicine
- Briefings in Bioinformatics
- Bioinformatics
- Genomics Proteomics and Bioinformatics
- Communications Biology
- Inflammation
- Frontiers in Genetics (review editor)
- Computational and Structural Biotechnology
- BMC Supplements
- Transaction on Computational Biology and Bioinformatics

Conferences

- ITCR Annual Meeting *Organizing committee 2024*
- DahShu Data Science Symposium *Organizing committee and Session chair 2024*
- IEEE International Conference on Bioinformatics and Biomedicine (BIBM) *Program committee 2021,2023, 2024*
- Regenstrief Institute Artificial Intelligence in Healthcare Innovation: Moving from Reactive to Proactive *Session Moderator: Harnessing the Real-World Clinicaogenomics Data for AI 2023*
- International Conference on Intelligent Biology and Medicine (ICIBM) *Session chair 2022, 2024*

Teaching

- B302 Biostatistics for Informatics, Instructor (Fall 2022, Fall 2023, Fall 2024, Spring 2025)

Mentorship

High school

- Isabella Wu (research mentor)
- Fatima Gbenro (SEED-STEM internship supervisor)
- Sahanna Nishkaran (SEED-STEM internship supervisor)

Undergraduate

- Carter Parrish (internship supervisor)
- Emmanual Gichaba (summer internship advisor)
- Andree Kortokolliegbo (summer internship advisor)
- Allison Luo (summer internship advisor)
- Rameesha Syed (IBRI bioinformatics internship supervisor and IUSM internship supervisor)
- Olivia Lazaro (IBRI bioinformatics internship supervisor)
- Chitra Sunil (DataWiz internship supervisor)
- Sahiti Somalraju (IBRI bioinformatics internship supervisor)
- Nicholas Dibley (IBRI bioinformatics internship supervisor)
- Alexander Pitchford (IBRI bioinformatics internship supervisor)
- Kristina Cazares (summer internship supervisor)
- Priyanka Paradkar (summer internship advisor)

Postgraduate (BS)

- Oluwamayowa (Mayowa) Awosika (IBRI bioinformatics internship supervisor)
- Daivic Akala (IBRI bioinformatics internship supervisor)

Masters

- Xiuxiu Yang (research mentor)
- Lujain Alsaleh (thesis committee chair)
- Amwaj Almalki (thesis committee member)
- Madeline Peyton (thesis committee chair)
- Manasi Somasundaram (internship supervisor)
- Anusha Bellapu (IBRI bioinformatics internship supervisor)
- Soumya Yennapureddy (IBRI bioinformatics internship supervisor)
- Adrian Gomez (rotation advisor)

Doctoral

- Valerie Dorsant Ardon (rotation advisor)
- Sihong Li (dissertation committee chair)
- Justin Couetil (research mentor)
- Debolina Chatterjee (GRA supervisor)
- Ben Duggan (rotation advisor)
- Ziyu Liu (research mentor)
- Tianhan Dong (research mentor)
- Madeline Peyton (dissertation committee chair)
- Jiahui Liu (research mentor)
- Caleb Beimfohr (rotation advisor)

Post-doctoral

- Debolina Chatterjee (postdoctoral supervisor)

Research staff

- Li Lin (research mentor)
- Sylvia Robertson (bioinformatician supervisor)
- Olivia Lazaro (bioinformatician supervisor)

Funding

Awarded

- Indiana University Melvin and Bren Simon Comprehensive Cancer Center Experimental and Developmental Therapeutics Pilot Award, **role: MPI**
- National Institutes of Health, National Institute of General Medical Sciences, Initiative to Support Research at the Interface of the Biological and Mathematical Sciences, **role: Co-PI (1R01GM148970)**
- National Institutes of Health, National Cancer Institute, Development of Innovative Informatics Methods and Algorithms for Cancer Research and Management, **role: MPI (1R21CA264339)**
- 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, Clinical and Translational Research Informatics Training Program, **role: trainee** (**4T15LM011270**)

Pending

- National Institutes of Health, National Institute of Diabetes and Digestive and Kidney Diseases, Research Project Grant, **role: MPI (1R01DK139384)**
- National Institutes of Health, National Cancer Institute, Secondary Analysis and Integration of Existing Data to Elucidate Cancer Risk and Related Outcomes, **role: MPI (1R01CA300423)**
- National Institutes of Health, National Institute on Aging, Multi-Scale Models Bridging Levels of Analysis in Aging and Alzheimer's Disease (AD) and AD-Related Dementias (ADRD), **role: MPI (1R01AG092654)**

Media Coverage

1. Drury, C. IU School of Medicine researchers draw analogies between art and science in new study. (2022). *Indiana CTSI Newsroom*
2. Russell, J. AI tools are helping researchers discover new drugs more quickly. (2023). *Indianapolis Business Journal*
3. Harton T. Pervasive AI: Artificial Intelligence and Machine Learning are transforming the life sciences in Indiana and beyond. (2024). *BioFutures by Indianapolis Business Journal*
4. Harris, M. Finding a signal in the noise. (2025). *IU Medicine Magazine*

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 *PACIFIC SYMPOSIUM ON 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*.
26. Alsaleh, L., Li, C., Couetil, J., Ye, Z., Huang, K., Zhang, J., Chen, C., **Johnson, T.S.** (2022). Spatial Transcriptomic Analysis Reveals Transcriptomic and Cellular Topology Associations in Breast and Prostate Cancers. *Cancers. 14*(19), 4856.
27. Jafari, E., **Johnson, T.**, Wang, Y., Liu, Y., Huang, K. and Wang, Y. (2022). AIscEA: Unsupervised Integration of Single-cell Gene Expression and Chromatin Accessibility via Their Biological Consistency. *Bioinformatics*. *38*(23), 5236-5244.
28. **Johnson, T.,** Steere, B., Zhang, P., Zang, Y., Higgs, R., Milch, C., Reinisch, W., Panés, J., Huang, K., D'Haens, G., Krishnan, V. (2023). Mirikizumab-induced transcriptome changes in ulcerative colitis patient biopsies at week 12 are maintained through week 52. *Clinical and Translational Gastroenterology (CTG)*.
29. Lin, L., Basu, R., Chatterjee, D., Templin, A.T., Flak, J., **Johnson, T.S.** (2023). Disease Associated Astrocyte and Microglia Markers are Dysregulated in Mice Fed High Fat Diet. *Scientific Reports*. 13, 12919
30. Obarorakpor, N., Patel, D., Boyarov, R., Amarsaikhan, N., Cepeda, J.R., Eastes, D., Robertson, S., **Johnson, T.,** Yang, K., Tang, Q. and Zhang, L. (2023). Regulatory T cells targeting a pathogenic MHC class II: Insulin peptide epitope postpone spontaneous autoimmune diabetes. *Frontiers in Immunology*, *14*, p.1207108.
31. Basu, R., Elmendorf, A. J., Lorentz, B., Mahler, C. A., Lazzaro, O., App, B., Zhou, S., Yamamoto, Y., Suber, M., Wann, J.C., Cheol Roh, H., Sheets, P.L., **Johnson, T.S.,** Flak, J. N. (2024). Ventromedial hypothalamic nucleus subset stimulates tissue thermogenesis via preoptic area outputs. *Molecular Metabolism*, *84*, 101951.
32. **Johnson, T.S.,** Sudha, P., Liu, E., Becker, N., Robertson, S., Blaney, P., Morgan, G., Chopra, V., Dos Santos, C., Nixon, M., Huang, K., Suvannasankha, A., Abu Zaid, M., Abonour, R., Walker, B. (2024). 1q amplification and PHF19 expressing high-risk cells are associated with relapsed/refractory multiple myeloma. *Nature Communications*, *15*(1), 4144.
33. Jury-Garfe, N., Redding-Ochoa, J., You, Y., Martínez, P., Karahan, H., Chimal-Juárez, E., **Johnson, T.S.**, Zhang, J., Resnick, S., Kim, J., Troncoso, J., Lasagna-Reeves, C. A. (2024). Enhanced microglial dynamics and a paucity of tau seeding in the amyloid plaque microenvironment contribute to cognitive resilience in Alzheimer's disease. *Acta Neuropathologica*, *148*(1), 15.
34. Yang, X.*, Chatterjee, D.*, Couetil, J., Ardon, V., Zhang, J., Huang, K., **Johnson, T.** (2024). Gradient boosting reveals spatially diverse cholesterol gene signatures in colon cancer. *Frontiers in Genetics.*
35. Roy, G., Syed, R., Lazaro, O., Robertson, S., McCabe, S.D., Rodriguez, D., Mawla, A.M., **Johnson, T.S.***, Kalwat, M.A.* (2024) Identification of type 2 diabetes- and obesity-associated human β-cells using deep transfer learning. *eLife*. **Reviewed Preprint**
36. Huang, X., Jannu, A.J., Song, Z., Jury-Garfe, N., Lasagna-Reeves, C.A., Alzheimer's Disease Neuroimaging Initiative, **Johnson, T.S.**, Huang, K., Zhang, J. (2025). Predicting Alzheimer's disease subtypes and understanding their molecular characteristics in living patients with transcriptomic trajectory profiling. *Alzheimer's and Dementia*. 2024;e14241
37. Li, S., Liu, J., Peyton, M., Lazaro, O., Huang, X., Shi, Z., Zhang, Z., Walker, B.A., **Johnson, T.S.** (2025) Multiple Myeloma Insights from Single-Cell Analysis: Clonal Evolution, the Microenvironment, Therapy Evasion, and Clinical Implications. *Cancers*.

38. Couetil, J.L., Liu, Z., Alomari, A.K., Zhang, J., Huang, K., **Johnson, T.S.** (2025). Diagnostic Evidence Gauge of Spatial Transcriptomics (DEGAS): Using transfer learning to map clinical data to spatial transcriptomics in prostate cancer. *Genomics Proteomics and Bioinformatics*. **In Revision (R1)**
39. Lazaro, O.*, Li, S.*, Carter, W., Robertson, S., Hickey, B.E., Angus, S.P., House, A., Clapp, W., Qadir, A.S.#, **Johnson, T.S.#**, Rhodes, S.D.# (2025). A novel induced pluripotent stem cell model of schwann cell differentiation reveals NF2-related gene regulatory networks of the extracellular matrix. *Frontiers in Cellular Neuroscience*. **Under Review**
40. Liu, Z., Couetil, J., Sudha, P., Becker, N., Walker, B.A., Huang, K., Zhang, J., **Johnson, T.S.** (2025). Optimal transport enabled deep transfer learning reveals subtypes of myeloma cells that are associated with short term sham treatment response and high-risk of progression. **In preparation**

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.S.**
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. *Indiana University Purdue University Indianapolis Department of Mathematics Statistis Seminar.* **Oral presentation (invited) by Johnson, T.S.**
20. **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 (invited) by Johnson, T.S.**
21. Yang, X., Flak, J., **Johnson, T.S.** (2022) Single cell deconvolution analysis identified an inhibitory neuron subtype associated with high fat diet in the bed nucleus of the stria terminalis. *American Diabetes Association (ADA) 2022*. Poster presentation by Yang, X.
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36. Couetil J.L. Liu Z. Zhang J. Huang K. **Johnson TS.** (2023). DEGAS: Identifying markers of the epithelial to mesenchyme transition in morphologically normal prostate cancer using deep transfer learning. *International Biometrics Society Eastern North American Region (ENAR) Spring Meeting.* Oral presentation by Couetil J.L.
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prognostic cell types. *International Biometrics Society Eastern North American Region (ENAR) Spring Meeting.* Oral presentation by Liu, Z.

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41. **Johnson, T.S.** (2023). Multiomic data integration. *Regenstrief Institute Artificial Intelligence in Healthcare Innovation: Moving from Reactive to Proactive*. **Oral presentation (invited) by Johnson T.S.**
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44. **Johnson, T.S.** (2023). Diagnostic evidence gauge of single cells and spatial transcriptomics. *National Cancer Institute (NCI) Informatics Technology for Cancer Research (ITCR) Annual Meeting*. **Oral presentation by Johnson, T.S.**
45. **Johnson, T.S.,** Sudha, P., Liu, E., Chopra, V.S., Dos Santos, C., Nixon, M., Huang, K., Abonour, R., Abu Zaid, M., Walker, B.A. (2023). Connecting 1q amplification and PHF19 expression in high-risk myeloma clones. *International Myeloma Society (IMS) Annual Meeting.* **Poster presentation by Johnson, T.S.**
46. **Johnson, T.S.** (2023). Data science solutions for large scale clinical and genomic data integration. *Health Services Research (HSR) Work In Progress (WIP)*. **Oral presentation (invited) by Johnson, T.S.**
47. **Johnson, T.S.** (2023). Integrative omics and risk inference. *Eli Lilly*. **Oral presentation (invited) by Johnson, T.S.**
48. Chatterjee, D., Couetil, J., Zhang, J., Huang, K., **Johnson, T.S.** (2024). Exploring spatially resolved transcriptomics: Disease risk prediction and insights into Alzheimer’s disease-associated gene expression. *International Biometrics Society Eastern North American Region (ENAR) Spring Meeting.* Oral presentation by Chatterjee, D.
49. **Johnson, T.S.** (2024). Research Panel. *Tech: Don’t Be Afraid of Health Care Indiana Life Sciences Collaboration Conference Series.* **Oral presentation and panel discussion (invited) by Johnson, T.S.**
50. Couetil, J.L., Liu, Z., Alomari, A.K., Zhang, J., Huang, K., **Johnson, T.S.** (2024). Diagnostic Evidence Gauge of Spatial Transcriptomics (DEGAS-ST): Using transfer learning to map clinical data to spatial transcriptomics in prostate cancer. *Association for Clinical and Translational Science Annual Meeting.* Oral presentation by Couetil, J.L.
51. Lazaro, O.*, Li, S.*, Carter, W., Awosika, O., Robertson, S., Hickey, B.E., Angus, S.P., House, A., Clapp, D.W., Qadir, A.S.$^{\#}$, **Johnson, T.S.$^{\#}$**, Rhodes, S.D.$^{\#}$ (2024). A novel induced pluripotent stem cell model of Schwann cell differentiation reveals NF2-related gene regulatory networks of the extracellular matrix. *DahShu Data Science Symposium*. Poster presentation by Li S.
52. Peyton, M., Sunil, C., Zhang, P., McCabe, S.D., Zhang J., Huang, K., **Johnson, T.S.** (2024). Single-cell Approach to Repurposing of Drugs for Alzheimer’s Disease. *DahShu Data Science Symposium*. Poster presentation by Peyton, M.
53. Peyton, M., Sunil, C., Zhang, P., McCabe, S.D., Zhang, J., Huang, K., **Johnson, T.S.** (2024). Spatio-topological characterization of repurposed drugs for Alzheimer’s disease via single-cell and spatial transcriptomics. *STATGEN Conference on Statistics in Genomics and Genetics*. Oral presentation by Petyton, M.

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55. Liu, J., Zhang, J., Huang, K., Johnson, T.S. (2024). Plasticity of Human Microglia and Brain Perivascular Macrophages in Aging and Alzheimer's Disease. *TREAT-AD*. Oral presentation by Liu, J.
56. **Johnson, T.S.** (2024). CRA-I – GenAI for Research and Science Roundtable. *Computing Research Association Industry*. **Oral presentation and panel discussion (invited) by Johnson, T.S.**
57. Chatterjee, D., Couetil, J.L., Dong, T., Zhang, J., Huang, K., Chen, C., **Johnson, T.S.** (2024). Identification of high-risk cells in spatially resolved transcriptomics of cancer biopsies using deep transfer learning. *NCI Informatics Technology for Cancer Research (ITCR) Trainee Symposium*. Oral presentation by Chatterjee, D.
58. Liu, J., Zhang, J., Huang, K., **Johnson, T.S.** (2024). Identifying High Risk Cellular interactions in Alzheimer's Disease. *TREAT-AD*. Oral presentation by Liu, J.
59. **Johnson, T.S.,** (2024). AI Applications in Pharmaceuticals. *The Alliance: A Forum of Indiana Business Leaders*. **Oral presentation (invited) by Johnson, T.S.**
60. Chatterjee, D., Couetil, J.L., Dong, T., Zhang, J., Huang, K., Chen, C., **Johnson, T.S.** (2024). Identification of High-Risk Cells in Spatially Resolved Transcriptomics of Cancer Biopsies Using Deep Transfer Learning. *National Cancer Institute (NCI) Informatics Technology for Cancer Research (ITCR) Annual Meeting*. Oral presentation by Chatterjee, D.
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64. Liu, J., Zhang, J., Huang, K., **Johnson, T.S.** (2024). Exploring Disease-Associated Microglia in Alzheimer's Disease. *TREAT-AD*. Oral presentation by Liu, J.
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References

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