

## **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

**United States Air Force**, MAFB - *Community College of the Air Force*

**AS Scientific Analysis Technology** *Feb 2015*

- Graduated from AF technical training with positive reviews from instructors

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

**BS Plant Biology** *May 2014*

- Bioinformatics certificate
- Plant cell biology lab assistant

### **Professional Experience**

**Vascugen**, Madison, WI

- **Consultant:** *Oct 2020 – Present*
  - Implementation of single cell workflows
  - Generating reports on product QC
  - Advising on single cell analysis and interpretation

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

- **Assistant Research Professor:** *July 2020 – Present*
  - Single cell method development
  - Machine learning and deep learning
  - Transfer learning and domain adaptation
  - Integrative methods
  - Grant writing

**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 – March 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 – *125<sup>th</sup> IS***

- **Scientific Applications Specialist:** *March 2009 – March 2015*
  - Staff sergeant rank (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**

- 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*
- 2<sup>nd</sup> place Ohio University Research Expo *recipient 2012*

## **Funding**

- 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**)
- The Ohio State University Comprehensive Cancer Center, Translational Therapeutics Seed Award, role: project member

## **Publications**

1. **Johnson, T.S.**, Abrams, Z., Zhang, Y., Huang, K. (2016). Mapping neuronal cell types using integrative multi-species modeling of human and mouse single cell RNA sequencing *Pacific Symposium on Biocomputing*, Vol. 22, 599-610.
2. **Johnson, T.S.**, Liebner, D., Chen, J. (2017). Opportunities for Patient Matching Algorithms to Improve Patient Care in Oncology *JCO Clinical Cancer Informatics*, Vol. 1, 1-8.
3. **Johnson, T.S.**, Abrams, Z., Mo, X., Zhang, Y., Huang, K. (2017). Lack of human cytomegalovirus expression in single cells from glioblastoma tumors and cell lines *Journal of Neurovirology*, 23:271-278.
4. Han, Z., **Johnson, T.S.**, 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*, Article ID 3035481.
5. **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*, Vol. 23, 536-547.
6. Wang, T., **Johnson, T.S.**, Zhang, J., Huang, K. (2019). Topological Methods for Visualization and Analysis of High Dimensional Single-Cell RNA Sequencing Data. *Pacific Symposium on Biocomputing*, Vol. 24, 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*, 1-9.
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*.
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*.
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*.
17. **Johnson, T. S.**, Xiang, S., Helm, B. R., Abrams, Z. B., Neidecker, P., Machiraju, R., Zhang, Y., ... & Zhang, J. (2019). Spatial Cell Type Composition in Normal and Alzheimers Human Brains is Revealed Using Integrated Mouse and Human Single Cell RNA Sequencing. *Scientific Reports*.
18. Xiang, S.\*, **Johnson, T.\***, 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. **Johnson, T. S.**, Christina, Y. Y., Huang, Z., Xu, S., Wang, T., Dong, C., ... & Zhang, Y. (2020). Diagnostic Evidence GAuge of Single cells (DEGAS): A flexible deep-transfer learning framework for prioritizing cells in relation to disease. **Under Review**
20. Xu, X., Sun, S., **Johnson, T.S.**, Qi, R., Zhang, S., Zhang, J., Yang, K. (2020). The glutathione peroxidase Gpx4 prevents lipid peroxidation and ferroptosis to sustain Treg cell activation and suppression of antitumor immunity. *Cell Reports*. **In Press**

### **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.**