

## PERSONAL DATA

Birthplace: Atlanta, Georgia

## EDUCATION

2014-2022 MD/PhD in Genomic Medicine, Augusta University, Augusta, GA

2011-2014 Bachelor of Biology and Chemistry, University of North Georgia, Dahlonega, GA

## HONORS

NIH Ruth L. Kirschstein National Research Service Award (NRSA) Individual Fellowship (F30DK121461)

Annual Faculty Club Award for Outstanding Graduate Student  
Genomic Medicine Best Poster Award

## PUBLICATIONS

John J. Wallbillich, **Paul M.H. Tran**, Shan Bai, Lynn K.H. Tran, Ashok K. Sharma, Sharad A. Ghamande and Jin-Xiong She. Identification of a transcriptomic signature with excellent survival prediction for squamous cell carcinoma of the cervix. *AJCR*, 2020

Tran LKH, **Tran PMH**, Mysona DP, Purohit SB, Myers E, Lee WS, Dun B, Xu D, Liu H, Hopkins D, Nechtman J, Scelsi CL, Mittal PK, Kleven D, Wallbillich JJ, Rungruang B, Ghamande S, She JX. A 73-gene proliferative transcriptomic signature predicts uterine serous carcinoma patient survival and response to primary therapy. *Gynecol Oncol*. 2020 Feb 14;. doi: 10.1016/j.ygyno.2020.02.015. [Epub ahead of print] PubMed PMID: 32067813.

Purohit S, Ferris DG, Alvarez M, **Tran PMH**, Tran LKH, Mysona DP, Hopkins D, Zhi W, Dun B, Wallbillich JJ, Cummings RD, Wang PG, She JX. Better

survival is observed in cervical cancer patients positive for specific anti-glycan antibodies and receiving brachytherapy. *Gynecol Oncol*. 2020 Jan 16;. doi: 10.1016/j.ygyno.2020.01.014. [Epub ahead of print] PubMed PMID: 31955861.

Mysona DP, Tran LKH, **Tran PMH**, Gehrig PA, Van Le L, Ghamande S, Rungruang BJ, Java J, Mann AK, Liao J, Kapp DS, Santos BD, She JX, Chan JK. Clinical calculator predictive of chemotherapy benefit in stage 1A uterine papillary serous cancers. *Gynecol Oncol*. 2020 Jan;156(1):77-84. doi: 10.1016/j.ygyno.2019.10.017. Epub 2019 Nov 30. PubMed PMID: 31796203.

Mysona D, Pyrzak A, Purohit S, Zhi W, Sharma A, Tran L, **Tran P**, Bai S, Rungruang B, Ghamande S, She JX. A combined score of clinical factors and serum proteins can predict time to recurrence in high grade serous ovarian cancer. *Gynecol Oncol*. 2019 Mar;152(3):574-580. doi: 10.1016/j.ygyno.2018.12.015. Epub 2018 Dec 18. PubMed PMID: 30578005.

## SELECT ABSTRACTS

**Paul M. H. Tran**, Ashok Sharma, Ph.D., Shan Bai, M.S., Jin-Xiong She, Ph.D. “Discovery of a Proliferative Gene Signature Predictive of Patient Survival in Renal Cancer.” 32nd MD/PhD National Student Conference. June 14-16, 2017, Keystone, Co. (poster)

**Paul M. H. Tran**, Hai-Tao Liu, Shuchun Li, Lynn Tran, Boying Dun, and Jin-Xiong She. “Discovery of a Proliferative Gene Signature Predictive of Cancer Patient Survival.” American Physician Scientist Association 14th Joint Annual Meeting with Association of American Physicians and American Society for Clinical Investigation. April 20-22, 2018, Chicago, IL. (poster)

**Paul M. H. Tran**, Hai-Tao Liu, Shuchun Li, Lynn Tran, Boying Dun, and Jin-Xiong She. “Applications of a Cellular Proliferation Gene Signature in Precision Oncology.” 33<sup>rd</sup> MD/PhD National Student Conference. June 13-15, 2018, Keystone, Co. (poster)

**Paul Tran**, Bruno dos Santos, Dakota Booth, Khaled bin Sattar, Lynn Tran, Sharad Purohit, Jin-Xiong She. “Machine Learning Based Classification of Brain Cancers using Transcriptome Profiling.” Presented at the *AACR Annual Meeting*, Georgia World Congress Center, Atlanta, GA. April 1, 2019.

APPLICATIONS OF MACHINE LEARNING TO GENOMICS: STUDIES IN  
TYPE 1 DIABETES AND CANCER

ABSTRACT:

**Introduction:** A major aim of modern medicine is to translate basic genomics findings using machine learning and other data analysis methods into clinical tests for improving patient care. Herein, I applied machine learning methods to publicly available genetic and genomic data to address three clinical problems in cancer and type 1 diabetes (T1D) research.

**Project 1:** Cancer classification mostly depends on the anatomic pathology workforce; hence, diagnosis is slow, stepwise, and prone to errors and systemic bias. Using a transcriptome-based cancer classification method, I reconciled the 18% disagreement rate between histology and mutation-based classifier for brain cancer.

**Project 2:** I applied the same transcriptome-based classification method to lung adenocarcinoma and identified 3 novel subgroups comprising ~30% of lung adenocarcinoma.

**Project 3:** The estimated genetic heritability of T1D is up to 80%. Identifying those most genetically susceptible to T1D can lead to reduction of the number of islet autoimmunity cases and the number diabetic ketoacidosis episodes. I developed a genetic risk prediction model using neural networks which performs better than currently published methods. I applied model interpretation methods to the neural network and identified important genetic drivers for characterizing T1D molecular subgroups.

**Conclusion:** These projects are small steps in translating genomic medicine projects to clinical applications but represent a future with more objective and automated tools to aid in clinical decision making.

The Graduate School  
Augusta University

Final Oral Examination  
For

PAUL TRAN

For the Degree of  
DOCTOR OF PHILOSOPHY

Friday, April 3, 2020

Department of Genomic Medicine  
Virtual

COMMITTEE

Advisor: Dr. Jin-Xiong She

Dr. Daniel Albo                      Dr. Richard McIndoe  
Dr. Sharad Purohit                 Dr. Ashok Sharma

Reader: Dr. Nagla Karim