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🌐 minhtran1309.github.io

# Minh Tran

in minh-ngoc-1309

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## EDUCATION

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- **The University of Queensland (UQ)** QLD, Australia  
*Ph.D. Candidate in Computational Biology* Oct. 2019 - Mar. 2023
- **Myongji University** Yongin, S. Korea  
*M.Sc. in Electronics and Electrical Engineering* Feb. 2016 - Mar. 2018
- **National Economics University** Hanoi, Vietnam  
*B.Sc. in Computer Science* Sep. 2011 - July. 2015

## WORK EXPERIENCE

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- **PhD Candidate** *University of Queensland, Australia, Oct 2019 - Present*
  - Conduct research and analysis for cellular communication within spatial context in cancer using imaging and sequencing data
  - Propose a novel computation package called STRISH to identify cells colocalisation with ligand-receptor throughout the tissue using spatially resolved multi-omics data (spatial transcriptomic and proteomic data)
  - Adapt the spatial analyses (i.e. Delaunay triangulation, K nearest neighbors, Ripley's K function) and heterogeneity scoring measurements (i.e. Shannon entropy, Rao's quadratic entropy, graph modularity) to identify the spatial differences across cancer subtype
  - Collaborate with other research groups to develop and conduct the analysis for scRNA-seq, ATAC-seq and spatial omic data
  - Present results to a wide variety of audience including both scientific/technical and clinical colleagues
- **Bioinformatic Scientist** *Vingroup Big Data Institute, Vietnam, Mar. 2019 - Oct. 2019*
  - Design the workflow to analyse DNA sequencing data to build the largest population-scale biomedical database for Vietnamese genome
  - Develop API to automate data QC process and upload meta data to the genomic variant database for Vietnamese population
  - Benchmark for accuracy and speed of the performance of variant calling platforms including Dragen (Illumina), DeepVariant (Google), and GATK. Regarding accuracy, DeepVariant outperformed GATK and Dragen with higher F1 score 0.2 and 0.1 respectively. Meanwhile, Dragen reduced the computational time significantly by 75% comparing to DeepVariant
- **AI Engineer** *Cinnamon AI Startup, Vietnam, Oct. 2018 - Mar. 2019*
  - Develop backbone of document analysis solution using machine learning (ML) and deep learning (DL) to extract information from contracts
  - Leverage state-of-the-art NLP transformers BERT as the alternative solution for information extraction models to deliver higher accuracy 90%+ overall and F1 score at 0.86 with limited training data (approx. 100 samples)
- **Visiting Scholar** *Genome Center, Uni of California Davis, USA, Mar. 2018 - Sep. 2018*
  - Chromosome conformation capture techniques (Hi-C) provide a wealth of data on the three-dimensional architecture of genomes
  - Introduce dimensional reduction including Autoencoder, PCA and SVG and robust differential analysis for noisy and high dimensional Chromosome 3D maps
  - Autoencoder achieved higher true positive value compared to PCA by 15%-30% proportion to the size of consideration block

## SKILLS AND TECHNOLOGIES

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**Programming Languages:** Python, R, Bash Shell, JavaScript, Java, C/C++, SQL,  $\LaTeX$ ,

**Developer Tools:** Git, Docker, Anaconda, Slurm, PBS

**Framework and Tools:** sklearn, pandas, skimage, scipy, SimpleITK, tensorflow, Keras, QuPath, CellProfiler, napari, Seurat, scanpy

## PUBLICATIONS

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### First(co-first) author

1. *Tran, M.* and Yoon, S. and Teoh, M. and Andersen, S. and Lam, PY. and Purdue, B. W. and Raghubar, A. and Hanson, SJ. and Devitt, K. and Jones, K. and Walters, S. and Monkman, J. and Kulasinghe, A. and Tuong, ZK. and Soyer, HP. and Frazer, I. H. and Nguyen, Q. “A robust experimental and computational analysis framework at multiple resolutions, modalities and coverages”. *Frontiers in Immunology* vol 13. 1664-3224 (2022).
2. *Tran, M.*, Su, A. Lee, HJ. Cruz, R. Pflieger, L. Dean, A. Nguyen, Q. Ji, H.P. Rhodes, T. “Understanding the tumour immune microenvironment of stage III colorectal cancer using multiplexed imaging mass cytometry”. *Royal College of Pathologists of Australasia-Pathology update* vol 53. S36-S37 (2021)
3. *Ngoc, M.T.*, Park, DC. “Centroid Neural Network with Pairwise Constraints for Semi-supervised Learning”. *Neural Processing Letters* vol 48. 1721–1747 (2018).
4. Carlos Rojas, *Minh N. Tran*, Linh Huynh, Fereydoun Hormozdiari “Machine learning approaches for comparative genome structure analysis”, *American Society of Human Genetics Annual Meeting (ASHG)* (2018).

### Co-author

1. Naval-Sanchez, M. Deshpande, N. *Tran, M.* Zhang, J. Alhomrani, M., Alsanie, W. Nguyen, Q. and Nefzger, C.M.. “Benchmarking of ATAC Sequencing Data From BGI’s Low-Cost DNBSEQ-G400 Instrument for Identification of Open and Occupied Chromatin Regions”. *Frontiers in Molecular Biosciences* vol 9. (2022).
2. Tan, X., Su, A.T., Hajiabadi, H., *Tran, M.*, Nguyen, Q.. “Applying Machine Learning for Integration of Multi-Modal Genomics Data and Imaging Data to Quantify Heterogeneity in Tumour Tissues”. *Artificial Neural Networks. Methods in Molecular Biology*, vol 2190 (2021).
3. Tan, X. Su, A.T. *Minh, T.*, Nguyen, Q.. “SpaCell: integrating tissue morphology and spatial gene expression to predict disease cells”. *Bioinformatics*, vol 36. 2293–2294 (2020).

## REFERENCES

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References Available Upon Request