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Minh Tran

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WORK EXPERIENCE

- **PhD Candidate** *University of Queensland, Australia, Oct 2019 - Present*
 - Research about cellular communication within spatial context in cancer using imaging and sequencing data
 - Collaborate with other research groups to develop preprocessing pipeline for RNA sequencing and spatial omic data
- **Bioinformatic Scientist** *Vingroup Big Data Institute, Vietnam, Mar. 2019 - Oct. 2019*
 - Design workflows to analyse next-generation sequencing data from 1000 Vietnamese individuals
- **AI Engineer** *Cinnamon AI Startup, Vietnam, Oct. 2018 - Mar. 2019*
 - Develop software using machine learning (ML) and deep learning (DL) to extract information from contracts
- **Visiting Scholar** *Genome Center, Uni of California Davis, USA, Mar. 2018 - Sep. 2018*
 - Conduct a research project about ML-based comparison of 3D genome architectures

EDUCATION

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

PROJECT EXPERIENCE

- **Develop methods to analyse cellular communication using spatial multi-omics data** *UQ, Present*
 - Propose a novel cells colocalization detection throughout the tissue using spatially resolved multi-omics data and demonstrate the significant of the results through statistical tests
 - Adapt the spatial analyses and heterogeneity scoring metric to identify cell crosstalk within the tissue microenvironment
- **Automated information retrieval of legal contracts** *Cinnamon AI, Dec 2018*
 - ML-based approaches for information retrieval from legal contracts
 - Adapt pre-trained BERT as an alternative approach achieve 90%+ overall accuracy and F1 score at 0.86
- **Comparison of genome 3D structural with machine learning approaches** *UC Davis, May 2018*
 - Dimensional reduction and robust differential analysis for noisy and high dimensional Chromosome 3D maps
 - Apply preprocessing methods including Autoencoder, PCA and SVG, capturing the interaction between inactive and active genes via 3D space proximity
- **Centroid neural network with pairwise constraints for semi-supervised clustering** *Myongji, Feb 2017*
 - A new algorithm, combining hierarchical clustering method Cent.NN with a new cost function for pairwise constraints.
 - The proposed method shows substantial advantages over existing algorithms including better stability (20% lower std) and more optimal running time.

SKILLS AND TECHNOLOGIES

Programming Languages Python, R, Bash Shell, JavaScript, Java, C/C++ , SQL, ~~LaTeX~~, \LaTeX ,

Framework and Tools GitHub, scikit-learn, pandas, skimage, scipy, SimpleITK, Keras, QuPath

SELECTED PUBLICATIONS

1. [Minh Tran](#), SoHye Yoon, Quan Nguyen “A robust experimental and computational analysis framework at multiple resolutions, modalities and coverages”, *Frontiers in Immunology* (2022)
2. [Minh N. Tran](#), Park Dong Chul “Centroid Neural Network with Pairwise Constraints for Semi-supervised Learning”, *Neural Processing Letters* (2018)
3. 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)