

# PIMS - LUNCHBOX LECTURE

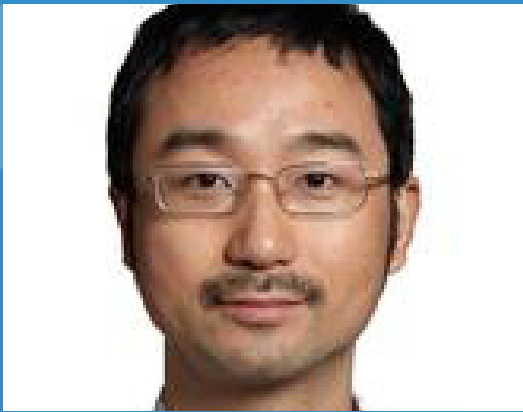
# DR. QUAN LONG



Thursday, October 20, 2022  
12pm - 1pm MDT

Room 416, 906-8 Ave SW  
University of Calgary,  
Downtown

## TRANSFER LEARNING FOR MACHINE LEARNING WITH APPLICATIONS



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Quan Long is an Associate Professor at University of Calgary, hosted by the Dept. of Biochemistry and Molecular Biology. Additionally, with a joint appointment in the Dept. of Medical Genetics and an adjunct appointment in the Dept. of Math and Stat. Currently he is leading a research group to develop computational and statistical tools, focusing on genomic problems with high-dimensional features and low sample sizes. He is also interested in theoretical problems in machine learning. Quan Long's works have been published in leading journals, attracting 30,000+ citations. His group is funded by federal agencies including NSERC, CIHR, and NFRF.

### Abstract

Machine Learning including deep learning techniques have been successfully used in many big-data fields. However, a limitation of many machine learning tools is that one needs to have a very large sample size to train a model with many parameters. This may prevent the broader use of machine learning in sample-sparse domains. For instance, in medical genetics, the number of patients of a particular disease available for a research project may be at the level of hundreds or even dozens, which is way lower than the requirement of many machine learning techniques that are sample-hungry. Towards this line, researchers have developed a technique called "transfer-learning", which can re-task an established general model (that are usually trained by very large sample) to a specific target using tailored samples of limited size. Such transfer-learning models open the door of developing many tools tailored to specific tasks using small samples with nimble training procedure. In this talk, I will first explain the basic theory of transfer-learning, followed by an introduction of its use in computer science including natural language process. I will also present a project using transfer-learning to characterize genetic basis of complex diseases by retasking a large general model.

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