

## **Data Science Seminar Series**

Monday, September 18, 9:30-10:30 am, virtual/Teams

### **TITLE**

Decoding the human genome through interpretable, robust and integrative machine learning

### **SPEAKER**

Dr. Maxwell Libbrecht, the School of Computing Science at Simon Fraser University, BC Canada.

### **ABSTRACT**

Two decades ago, the human genome was sequenced. That is, we learned the string of three billion letters A/C/T/G that make up our genetic code. Since then, we have collected thousands of genome-wide measurements about the activity of the genome. These measurements span hundreds of biochemical properties of the genome, such as the measurement of which base pairs a given protein binds to, and span hundreds of human tissues. In total, we have on the order of  $10^{13}$  genomic measurements. Yet despite these massive data sets, much of how the genome functions remains unknown. My group's research focuses on developing machine learning methods that yield insight into genome biology. I will present our work addressing problems in genomics by developing methods for learning neural networks, building probabilistic graphical models, and interpreting machine learning models.

[https://www.tru.ca/science/masters-degrees/mscnds/Data\\_Science\\_Seminar\\_Series.html](https://www.tru.ca/science/masters-degrees/mscnds/Data_Science_Seminar_Series.html)