



# Genome Sciences Seminar

Wednesday, 12.6.17 | 3:30 | Foege Auditorium

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## Dr. Bin Ma

Professor, Cheriton School of Computer Science  
University of Waterloo

## “De novo peptide and protein sequencing with mass spectrometry”

### Research Interests:

Professor Bin Ma's research interests are in bioinformatics algorithms and software. He studies the mathematical problems that are abstracted from molecular biology, and develops algorithms and computer software for biologists to use. In particular, his work in recent years is focused on two areas: homology search and mass spectrometry data analysis. Homology search finds similarities in DNA and protein sequence database. This is a basic task that modern biologists need to perform regularly. The large size of the database raised the requirement for extremely efficient searching algorithm. Together with Professor Ming Li and other coworkers, he has developed the PatternHunter program for homology search.

Mass spectrometry is a wet-lab experimental method to identify and quantify proteins in given biological samples. However, the data obtained from the experiments are complicated and contain errors and noises. The analysis of the data requires the right mathematical model, efficient algorithm, and user friendly software. Together with his coworkers, he developed the PEAKS software package, which is now one of the industrial standard packages for such analysis.

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Refreshments served outside the Auditorium at 3:20pm

Questions? Contact Brian Giebel at [bgiebel@uw.edu](mailto:bgiebel@uw.edu) or visit the Seminar website at <http://www.gs.washington.edu/news/seminars.htm>

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