

Combi Seminar

Wednesday, 10.27.21 | 1:30 | Foege Auditorium

remote viewing option: <https://depts.washington.edu/gsrestrc/remote.htm>



Dr. William Noble

University of Washington

“Deep learning analysis of tandem mass spectrometry data”

Our research group develops and applies computational techniques for modeling and understanding biological processes at the molecular level. Our research emphasizes the application of statistical and machine learning techniques, such as hidden Markov models and support vector machines. We apply these techniques to various types of biological data, including protein and DNA sequences, data from high-throughput genomic assays such as ChIP-seq and Hi-C, and tandem mass spectrometry. We are currently developing methods for analyzing shotgun proteomics data, for characterizing protein function, structure and interactions, and for understanding the structure and regulatory influence of chromatin.

<https://noble.gs.washington.edu/>

Questions? Contact Brian Giebel at bgiebel@uw.edu or visit the Combi website at <http://www.gs.washington.edu/news/combi.htm>

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