

# Combi Seminar

Wednesday, 7.17.19 | 1:30 | Foege Auditorium

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## Dr. William Noble

University of Washington

## “Traveling across spaces: the power of embedding genomic and proteomic data into a latent space”

Many machine learning methods work by translating data points from the space in which they reside to a new, latent space of either higher or lower dimension. In this talk, I will describe three settings in which a latent representation can help us make sense of complex genomic or proteomic data. In one case, we train a deep tensor factorization model to learn latent representations of genomics assay types, cell types and genomic positions. These learned embeddings then turn out to be useful not only for imputing new genomics experiments, but also for a variety of other downstream machine learning tasks. In a second setting, we train a siamese deep neural network to embed tandem mass spectra into a latent space, such that spectra generated by the same peptide are close together. This learned embedding then provides a flexible framework for jointly analyzing hundreds of mass spectrometry experiments. Finally, I will describe how an unsupervised embedding approach can map diverse types of single-cell measurements into a latent space, effectively providing an in silico co-assay for experiments performed on similar sets of cells but using different experimental techniques.

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

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