

Combi Seminar

Wednesday, 2.15.23 | Foege Auditorium | 1:30

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



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<http://saramostafavi.github.io/>

“Using sequence-to-activity neural network models to understand gene regulation”

We develop and apply machine learning and statistical methods to study biology, including mechanisms of human health and disease. Most recently, we have been applying our methods to understand immune response(s) across different contexts, mechanisms of psychiatric disorders, and causes of rare genetic diseases in children. We are especially interested in developing models for combining association evidence across multiple types of molecular/genomics data, such as gene expression and genotype data, and modeling prior biological pathways and networks for disentangling spurious from meaningful correlations.

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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