

Combi Seminar

Wednesday, 1.16.19 | 1:30 | Foege Auditorium



Dr. Erick Matsen

Associate Member

Fred Hutchinson Cancer Research Center

“Classical and “deep” probabilistic models for adaptive immune receptor sequences”

The Matsen Lab: We develop and apply evolutionary methods for molecular sequence data (i.e. DNA and RNA). We enjoy all facets of computational biology research, from diving deeply into biological questions, to mathematical and statistical analysis, algorithm development, and efficient algorithm implementation. Our recent work has developed new methods to analyze metagenomic, viral, and immune cell sequence data, as well as pursued more abstract methodological questions in evolutionary tree reconstruction. We also work to improve the software environment for computational biologists, both by developing our own open-source tools and contributing to work on larger projects.

<https://matsen.fhrc.org/research.html>

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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