

Combi Seminar

Wednesday, 5.15.24 | Foege Auditorium | 1:30

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



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“Causal Discovery in Biological Systems”

Estimation of high-dimensional directed graphs arises naturally in many biological applications, including the study of biomolecular systems using various -omics measurements. While several existing algorithms can be used for this task, these general-purpose algorithms do not account for features of biological networks and do not take advantage of the properties of biological networks and data. In this talk we discuss alternative algorithms that are specifically designed to take properties of biological networks and data into account and can offer reliable estimates under potentially less stringent assumptions.

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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