

THE DEPARTMENT OF MATHEMATICAL SCIENCES PROUDLY PRESENTS

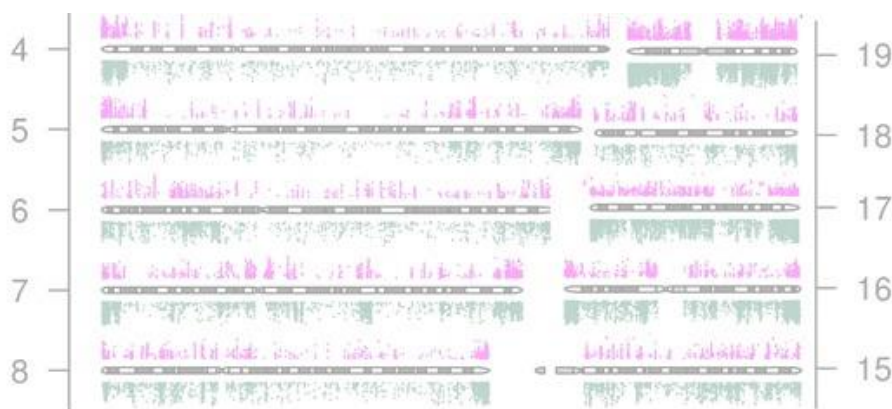
COLLOQUIUM

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Algebraic Methods for Biological Data Science

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Biological data science is an important field for making decisions based on data collected from both laboratory and clinical settings. Carefully planned experiments are key as they have a direct impact on the efficacy of modeling, and likewise the choice of model directly influences the direction of future research. In this talk we describe an algebraic framework to unify these two processes for discrete data and polynomials over a finite field. Input data, viewed as an affine variety, are paired with standard monomial sets, representing bases of polynomial models. This pairing enables the simultaneous execution of experimental design and model selection, and an equivalence relation on data sets provides a comprehensive view of all possible model bases associated to a data set. We highlight recent work on determining tighter upper bounds for the number of polynomial models for biological data.

Enlace: meet.google.com/urm-rhmx-dhw

Hora: 10:30 am

