

STATISTICS COLLOQUIUM

TUESDAY, FEBRUARY 19, 2013

TALK: 4:15 PM — SCIENCE CENTER RM. 705

RECEPTION: 3:50 PM — SCIENCE CENTER, 7TH FLOOR

“Geometric Constraints in Causal Inference and Chromosome Packing”

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ABSTRACT

Taking a geometric approach we analyze the constraints involved in two very different problems: first, causal inference using the prominent PC-algorithm and second, chromosome organization in the human cell nucleus.

We first analyze the so-called "strong-faithfulness assumption", one of the main constraints of the PC-algorithm. We show that this assumption is in fact extremely restrictive, implying fundamental limitations for the PC-algorithm and other structure-learning algorithms based on partial correlations. We then discuss a more applied problem, namely the spatial organization of chromosomes. A chromosome arrangement can be viewed as a minimal overlap configuration of ellipsoids of various sizes and shapes inside an ellipsoidal container, the cell nucleus. We describe a bilevel optimization formulation to find such minimal overlap configurations of ellipsoids and analyze the geometric constraints involved in chromosome packing.