Department of Mathematics and Statistics Colloquium

Student Research Presentations

KMC Dynamics: The Evolution of Crystal Structures

Michael Boyle

Channing Parker

Molly Rowland

Abstract: We consider a solid-on-solid atomistic model for homo-epitaxial growth. Atoms evaporate from, condensate on, and diffuse (hop) across the crystal surface. Facets reflect a long-range order of the atoms on the crystal surface. To explore the mathematics of facet formation, we numerically simulate a one-dimensional discrete silicon on silicon model. We then generalize this to a two-dimensional silicon on silicon model. We want to analyze the geometry of the emerging structure, and whether a facet evolves as a consequence of this atomistic model.

Modeling Crystalline Structures with Monte Carlo

Ben Delaney

Abstract: Due to the widespread use of crystalline materials in manufacturing and technology, we find it beneficial to study how certain parameters influence the mobility of a crystal's surface atoms and the resulting structure generated. The cross-section of a silicon film deposited on a silicon substrate is considered. We employ a solid-on-solid bond counting model in which a surface atom can undergo one of three events: hopping, evaporation, or condensation. Experimentally verified rates, obtained by ab-initio calculations, are utilized to predict the outcome of an event occurring at a given site along the film. A kinetic Monte Carlo algorithm then can be used to simulate the evolution of the crystal over time, allowing us to analyze the effect that varying our parameters has on crystalline growth. We also consider how our rates must be altered in order to model a silicon-germanium film deposited on a silicon substrate.

An Exact Product Formula for Abelian Varieties of Odd Prime Dimension

Jonathan Gerhard

Abstract: An abelian variety is a higher dimensional analogue of an elliptic curve and, like elliptic curves, is of great interest to both number theorists and algebraic geometers. One major interest is counting the number of abelian varieties in a fixed isogeny class. Progress towards this goal is made through a beautiful intertwining of the theory of class groups of certain number fields and the study of conjugacy classes of a certain matrix group.

Meta-Analysis of Parkinsons Disease Genomic Data

Justin Taylor

Abstract: Gene expression studies allow for the relative quantification of tens of thousands of messenger RNA transcripts. In this work, we attempt to elucidate the mechanisms of Parkinsons disease (PD) development in the human brain using six genomic studies. Meta-analysis is a statistical technique for combining results from different independent studies, useful for increasing the power of a test. We used meta-analysis based on logit method to detect differentially expressed set of genes. These genes are then used to identify Parkinsons disease related pathways and their statistical significance.

Monday, April 24 at 3:45 in Roop 103

Refreshments at 3:30