
Biological Networks
(Org: **Elena Dimitrova** (Clemson))

LEONID CHINDELEVITCH, Simon Fraser University
Metabolic networks: geometry, optimization, and complexity

Metabolic network models are simple to describe, yet complicated to analyze at the genome-scale. They pose a number of interesting questions that can be tackled with tools from discrete geometry, linear and convex optimization, as well as complexity theory. This talk will give an overview of the key issues underlying the analysis of metabolic network models, highlight the connections to a variety of mathematical and algorithmic areas, and present some results exploiting those connections in order to elucidate the structure of metabolism.

LUAY NAKHLEH, Rice University
Phylogenetic Networks

Phylogenetic trees are central to evolutionary biology and have been the focus of much research in mathematics, statistics, and computer science for several decades. Though appropriate for several groups of taxa, a phylogenetic tree may be inadequate for other groups. In particular, horizontal gene transfer is ubiquitous in bacteria, hybridization is very common in many groups of eukaryotes, and recombination is a hallmark of sexual species. All these processes result in reticulate evolutionary histories best modeled with phylogenetic network. I will describe phylogenetic networks, approaches to their inference, and mathematical and computational challenges that arise in their inference and analysis.

SVETLANA POZNANOVIK, Clemson University
The Structure of the Branching Polytopes for RNA Structures

Finding a method that can quickly and reliably identify the structure of a given RNA has been an important problem in computational biology. However, the methods developed still vary widely in the prediction accuracy. An important component of this problem is predicting the secondary structure, which identifies both the canonically base-paired regions (helices) and non-paired regions (loops). In this work we focus on understanding the effects of the parameters used for scoring the multibranch loops in the nearest-neighbor thermodynamic model. For this purpose, for each RNA we built and analyzed a branching polytope. Here I will present our findings.

KRIS VASUDEVAN, University of Calgary
Brain network structure and dynamics: Mathematical modelling of epileptic seizures

Spectral graph theory of graphs containing only attractive (or positive) interactions has been the subject of detailed studies. However, in brain networks, these graphs can carry interactions which are repulsive (or negative) to a degree. We have investigated how properties of signed graph adjacency matrices change for differing ratios of negative interactions to positive interactions by considering graph structures of the correlational matrices from intracranial electroencephalogram (iEEG) data during an episode of epileptic seizure. Furthermore, we have also examined how non-linear dynamics on such graphs describes the seizure behaviour. Joint work with M. Cavers and P. Federico (University of Calgary).

NORA YOUNGS, Colby College
Neural ideals and stimulus space visualization

A neural code C is a collection of binary vectors that record the co-firing patterns of a set of neurons. We look at codes arising from place cells, neurons that respond to geographic stimulus. The stimulus space is visualized as a subset of \mathbb{R}^2 covered by

convex sets \mathcal{U} which form an Euler diagram for C . There are some methods to determine if a realization \mathcal{U} exists; however, these do not construct a realization. We consider the problem of algorithmically drawing diagrams using two polynomial ideals: the neural ideal, a pseudo-monomial ideal; and the neural toric ideal, a binomial ideal.