DIMACS REU Projects

K. Mischaikow

Project 1. Led by Ewerton Viera

Title: Identifying bifurcation for combinatorial dynamical systems

Methodically and reliably understanding robust dynamics of ordinary differential equation (ODE) models of multi scale system (think biology) is extremely challenging as variables and parameters are typically numerous and poorly measured. This challenge motivates our development of coarser modeling tools based on combinatorics and algebraic topology.

These combinatorial and algebraic topological tools lend themselves to efficient and scalable computations. For gene regulatory networks we have developed a software tool Dynamic Signatures Generated by Regulatory Networks (DSGRN) that can take as input a regulatory network and output a database that describes the global dynamics over a large high dimensional parameter space. This output takes the form of partially ordered sets and associated chain complexes. In other words, DSGRN can be thought of as a function that maps a parameter to an homological representation of dynamics.

This leads to the following questions: How in this approach should one characterize (in combinatorial/algebraic topological terms) the changes in dynamics as one varies parameters? How can one find the parameter values where changes occur? What is the biological significance of these changes?

To address these questions we propose to begin our investigations by studying 2 and 3 dimensional systems since we can visualize the results and have user friendly software in this setting. With success we can move on to more general systems.

Project 2. Led by William Cuello

Title: Taking a Step Away from Traditional Analyses for Ecological Models

Mathematical ecologists have traditionally explored species dynamics using ordinary differential equations (ODEs). These ODEs describe the instantaneous growth rates of species within the system via non-linear functions and are typically parameterized with unknown constants. For lower dimensional systems, e.g., a 2-dimensional competitive system, one can linearize the system around its equilibria (or steady states) to determine global dynamics of species under different parameter choices. One choice of parameters could lead to coexistence amongst the species, while another choice could lead to competitive exclusion. However, such an analysis becomes more and more challenging (or even impossible) as more species are added to the system. In particular, more species means more parameterized equations (i.e., more parameter space to explore). Without taking advantage of specific symmetries or functional forms, one can at most do parameter sweeps to determine differing qualitative dynamics.

To address this problem, we propose that we study an approximate system. Here, we replace the non-linear, functional components with simple step functions. We can then use recently developed tools from combinatorics, algebraic topology, and dynamical systems theory to solve for long-term solutions of the system in different parameter regimes. We are then confronted with some natural questions: under this framework, is it possible to find parameter regions in which species coexist (or are excluded)? Are the regions for coexistence and exclusion preserved when modelled with traditional ODEs that correspond to our approximate system? Can this framework help us understand larger trophic networks that are traditionally challenging to analyze using ODEs?

Project 3. Led by Marcio Gameiro

Title: Data driven dynamics

Computing dynamics from data is a very important and challenging problem, specially when the data is high dimensional. Our approach to extract dynamics from data is to discretize the system by constructing a grid decomposition of the space where the data lives and then use the data to determine a mapping between grid elements. This discretization is represented by a directed graph and graph algorithms are used to efficiently extract region with recurrent dynamics (called Morse sets). We can then validate and further characterize the dynamics using Algebraic topology (Conley index). Examples and software to perform these computations on rectangular grids are available at `https://github.com/marciogameiro/CMGDB`.

These methods are very effective for low dimensional data using a structured grid (such as a rectangular grid) to decompose the space. In this project we propose to explore alternative methods to decompose the space to discretize the dynamics and investigate how efficient these methods are for high dimensional data.

One alternative decomposition we propose in this project is to use a Voronoi decomposition. Give a collection of points $P = \{x_1, \ldots, x_n\} \subset \mathbb{R}^N$ a Voronoi decomposition of $\mathbb{R}^N$ is a decomposition of $\mathbb{R}^N$ into Voronoi cells $V_1, \ldots, V_n$ where V_i is the set of points in $\mathbb{R}^N$ closer to x_i than to any other points x_j for $j \neq i$. More formally $V_i = \{x \in \mathbb{R}^N \mid d(x, x_i) \leq d(x, x_j) \text{ for } j \neq i\}$. The point x_i is the center of the Voronoi cell V_i. Notice that we can determine in which Voronoi cell a given point is just by computing its distances to all points in P. Hence we can use a Voronoi decomposition to discretize the space without actually constructing the Voronoi cells, rather we just compute the distances of the mapped point to the centers of the Voronoi cells to determine to which cell the point is mapped. Hence this method should be effective for high dimensional data.

Project 4. Led by Shane Kepley

Title: Studying gene regulatory dynamics via sloppy models

Reliably modeling the dynamics of regulatory networks is one of the most important challenges in modern systems biology. Numerous advances in molecular and systems biology has led to the identification of complex networks involving dozens of genes interacting with one another. On the mathematical side these networks are often modeled as systems of nonlinear differential equations. To analyze these networks requires a choice of nonlinearities and one popular choice involves Hill functions. A serious challenge is that the use of Hill functions for complex networks results in systems with tens to hundreds of state variables and parameters making it difficult or impossible to study the global dynamics.

This has led to the development of coarser modeling tools which incorporate combinatorial methods and algebraic topology into classical dynamical systems theory to study complex networks over large regions of parameter space. These coarse models are much more amenable to efficient, large scale computation, but at the same time, they can be systematically identified with the Hill function models.

In this project, we aim to explore computational methods for mapping between system parameters of the Hill function systems and coarse systems based on "sloppy models". Sloppy modeling is a framework for studying hierarchies of models using tools from differential geometry. The models themselves are identified with manifolds in a Euclidean space and simplifications of these models arise naturally as boundaries of this manifold or lower dimensional submanifolds.

Our goal would be to design and implement a computational method based on sloppy modeling which provides a means for mapping parameters in coarse systems to manifolds of parameters in Hill systems which produce similar dynamics.