

Brief Project Summaries

• RNA localization

Formulate and analyze a mathematical model (with differential equations) of RNA localization. This will involve doing background reading on the topic and then working with Prof. Urbinati (from Biology) to formulate a model and better understand RNA localization. He will clarify this biological process but you will formulate the model. In the process of formulating the model Prof. Urbinati will tell you if your assumptions and hypothesis sound reasonable. Once a model is formulated, mathematical analysis will be done and the results analyzed. If necessary, the model will then be re-adjusted and the process repeated.

References:

“RNA localization in yeast: moving towards a mechanism” by G.Gonsalvez et al.

Also see http://mpf.biol.vt.edu/research/budding-yeast_model/pp/index.php

• Spread of ideologies

This project will involve a differential equation model of groups of people with varying degrees of fanaticism toward an idea/ideology. Previous work on this has looked at this in hopes of gaining insight into fanatic behavior of terrorists. Many other possibilities also exist for fanaticism and the spread of ideologies. Some preliminary results show that recruitment and retentions are key in such systems. For example, political ideologies or social ideologies could be examined. A specific example will be chosen and you will come up with a model and estimates on the parameters. A mathematical analysis will be done and the results analyzed. If necessary, the model will then be re-adjusted and the process repeated.

References:

“The Mathematics of Infectious Diseases” by H.Hethcote

“Models for Transmission Dynamics of Fanatic Behaviors” by C.Castillo-Chavez and B.Song

• SIR network model

The SIR model is a basic mathematical model used to study the spread of an epidemic through a population with people that are susceptible to a disease, infected with a disease, and recovered from the disease. The differential equation model and results are well-known; however, this DE model assumes that the population is homogeneous and that everyone interacts with each other with equal probability and this is not realistic in our current society. E.g., if we consider the population of students at LMU, everyone does not interact with everyone else. This project will examine how the interactions and structure of a given population will affect the outcome of the disease under the SIR framework. The initial stages of this work will involve developing a computer code that describes how individuals in a population interact with each and this code will be used to answer various questions. Computation will be an integral part of this project.

References:

“The Structure and Function of Complex Networks” by M.Newman

“The Mathematics of Infectious Diseases” by H.Hethcote

I will serve as an advisor in all of these projects, helping you formulate a model, clarifying things, and giving you suggestions and direction but you will do all the work.