

Schedule

Online Workshop on Fundamentals of Mathematical Biology

Day 1 (May 11, 2023)

Time	Speaker	Topics
9:45-10:00 AM		Inauguration
10:00-11:30 AM	Prof. Malay Banerjee	Analytical detection of stationary patterns Turing instability is a well-known mechanism behind the formation of stationary spatial patterns by reaction-diffusion systems in population biology. However, the existence of such heterogeneous solutions depends on the stability of non-constant steady-states associated with the corresponding boundary value problem. The main objective of this talk is to discuss the existence of various stationary Turing patterns within a bounded domain and detection of relevant bifurcations through numerical continuation. The talk is aimed to discuss the detection of multiple stationary patterns within and outside of Turing instability domain.

11:30AM-1:00 PM	Dr. Prashant Kumar Srivastava	<p>Modeling and analysis of infectious diseases</p> <p>In this talk, I shall briefly discuss various infectious disease models and their properties. Analytical results such as stability of equilibrium, basic reproduction number, local and global stability etc. will be explored. These models will be then simulated on Matlab numerically for certain parameters and effect of parameters will be explored on the model properties.</p>
<i>01:00 PM – 03:00 PM</i>		<i>Lunch Break</i>
3:00-4:30 PM	Prof. Amit Chakraborty	<p>Design-based dynamic approaches in mathematical biology</p> <p>Bio-complexity is a thriving research area in the 21st century, focusing mainly on organisms-environment interactions across the levels of biological organizations. However, biological levels of organizations have classically divided into two mainstream science disciplines. The first one is molecular and cell biology, at which the evolutionary mechanism of natural selection plays a key role in shaping the organization and has remained to be a primary force interlinking the molecule/cell structures with the biological functions. The other one is ecological and environmental sciences that neglect the evolutionary effects with the reasonable assumption that ecological changes are taking place at a much faster time scale than the evolutionary changes. The recognizable gap between these two has remained open until recently, mainly due to technological barriers of generating and processing a large volume of molecular data. Rapid development of genomic science methods and high-throughput molecular data-generating techniques are stimulating the bio-complexity research with great opportunities of addressing ambitious questions of determining a general underlying principle of biological regulations observed and measured across the levels. Along this line of research, in this presentation, I will introduce a design-based dynamic approach combining graph and dynamical systems tools to deal with emerging problems in biology with high-throughput information.</p>

4:30-6:00 PM	Dr. Sanjay Lamba	<p><i>SARS-CoV-2 infection dynamics and genomic surveillance reveals early variant transmission in urban wastewater</i></p> <p>Wastewater-based epidemiology (WBE) offers a powerful tool for tracking the spread of SARS-CoV-2. Using wastewater testing as an environmental surveillance tool can provide an unbiased snapshot of community health. We describe an early warning system and how wastewater monitoring can be used for community-level detection and tracking of the SARS-CoV-2 virus. In conclusion, monitoring temporal variation in viral loads in wastewater combined with other analyses can detect a virus outbreak at least 7–14 days in advance. The findings from this study have been discussed regularly with local authorities to inform policy-making decisions.</p>
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Day 2 (May 12, 2023)

Time	Speaker	Topics
10:00-11:30AM	Prof. Sandip Banerjee	Estimation of System Parameters using MATHEMATICA
11:30 AM – 01:00	Prof. Kamalraj Pardasani	Modeling Calcium Dynamics in Neuron Cells
<i>01:00 PM – 03:00 PM</i>		<i>Lunch Break</i>

3:00-4:30 PM	Dr. Amiya Ranjan Bhowmick	<p>Statistical Inference on Biological Growth Curve Models</p> <p>Growth curve models serve as a theoretical framework for the quantitative studies of growth in many areas of applied sciences. When fitting growth equations to real data sets, the model parameters are assumed to be fixed which are estimated by using non-linear least-squares or maximum likelihood estimation method. In this workshop, we shall discuss about various growth curve models which are commonly used in the mathematical biology literature. We shall explicitly consider the statistical issues related to the fitting of these growth equations to the real data sets. We will also discuss statistical inference related to derived quantities, like point of inflection, nonlinear functions of growth parameters. All the computations will be done using R. This workshop will contain practical hands on experience in solving differential equations (which are growth curve models) and their fitting to real data sets using software R. Some recent advancement will also be discussed at the end.</p>
4:30-5:30 PM	Dr. B.S. Sanjeev	
5:30-5:45PM		Valedictory Note