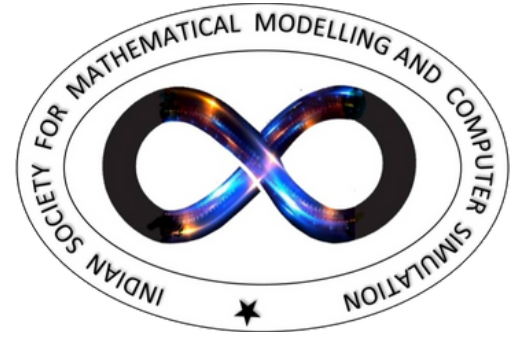




Faculty Development Program (FDP) on Advances in Mathematical Modeling Techniques, AI/ML and Bioinformatics



As part of the **Centenary Celebrations of our Founder Chancellor Bhagawan Sri Sathya Sai Baba**, The Centre for Excellence in Mathematical Biology (CEMB) of Sri Sathya Sai Institute of Higher Learning (SSSIHL), in collaboration with Indian Society for Mathematical Modelling and Computer Simulation (ISMMACS), along with the Departments of Mathematics and Computer Science (DMACS), Biosciences (DBIO), and Food and Nutritional Sciences (DFNS) of SSSIHL, organized an online Faculty Development Program (FDP) on Advances in Mathematical Modeling Techniques, AI/ML and Bioinformatics from April 12th - 19th, 2025.

This online FDP focused on advanced mathematical methods, and covered key topics such as Machine Learning, Optimal Control Theory, Parameter Estimation, Network Modeling, Stochastic Modeling, Bifurcation Theory, Bioinformatics and Nutritional Science. Combining theoretical insights with hands-on training, the program was open to faculty members, post-doctoral researchers, PhD students, and industry professionals working in allied areas, and aimed to enhance research and practical applications.

Day 1 : April 12, 2025 (Morning Session)

Speaker: Dr. Krishna Kiran Vamsi, SSSIHL

Dr. Krishna Kiran Vamsi's session in the Faculty Development Program provided a foundational overview of essential mathematical concepts needed for modeling and bioinformatics. He began with the basics of set theory, relations, and functions, gradually building up to derivatives and differential equations, which are vital for understanding dynamic changes in biological systems. He explained how these mathematical tools help model real-life scenarios like population growth and disease spread. The session aimed to prepare participants—especially those from non-mathematics backgrounds—for advanced topics in mathematical modeling, emphasizing the practical use of these concepts in biology, simulations, and applied machine learning (AI/ML).

Speaker : Dr. Anuj Kumar, TIET

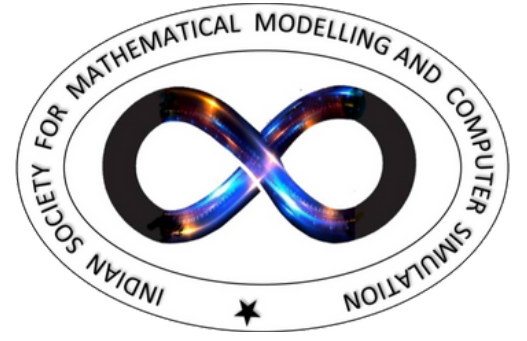
The lecture by Dr. Anuj Kumar focused on the application of optimal control theory to mathematical modeling, particularly in the context of infectious disease dynamics. He explained how optimal control helps in designing efficient intervention strategies—like vaccination or treatment—by balancing health outcomes with economic costs. The talk covered fundamental mathematical concepts, including the use of differential equations, Hamiltonian formulation, and Pontryagin's Maximum Principle to find optimal solutions. Dr. Kumar demonstrated how control variables influence system dynamics and discussed numerical methods, such as the forward-backward sweep, for solving complex, real-world problems where analytical solutions are not feasible. The session emphasized the importance of tailoring cost functions (linear, quadratic, or more complex forms) to reflect real-world constraints and concluded with a dynamic Q&A exploring practical modeling challenges and theoretical limitations.

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Faculty Development Program (FDP) on Advances in Mathematical Modeling Techniques, AI/ML and Bioinformatics



Day 1 : April 12, 2025 (Evening session)

Speaker : Dr. Surabhi Pandey, Founder, BL Foundation for Social Initiatives, Delhi NCR

Dr. Surabhi Pandey's lecture focused on the importance of parameter estimation in mathematical models for policy-focused research, especially in public health. She explained how accurate, data-driven parameter values are crucial for creating reliable simulations that inform decisions like vaccine rollout or disease control strategies. Using examples from her work on tuberculosis and malaria, she demonstrated methods like data synthesis from systematic reviews, Monte Carlo simulations, and ensemble modeling to estimate key parameters and address uncertainty. She emphasized the need to use real-world, up-to-date data from trusted sources such as WHO, NFHS, and government reports, rather than relying solely on existing literature. The session highlighted how precise parameter estimation helps bridge the gap between research and practical implementation, ensuring better-informed public health policies.

Speaker : Mr. D. Bhanu Prakash, SSSIHL

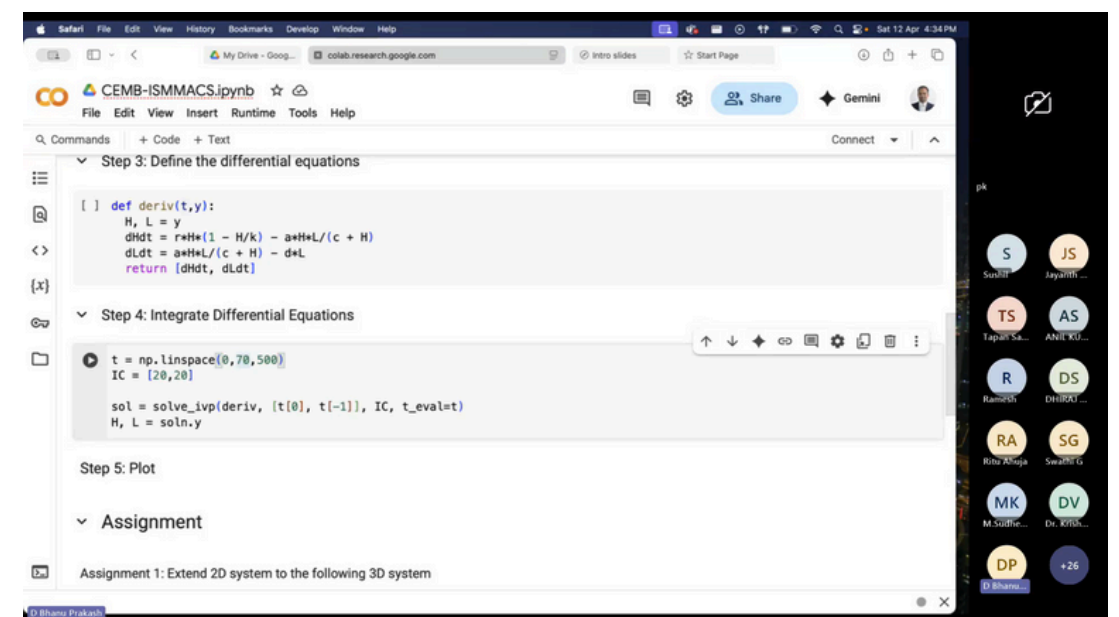
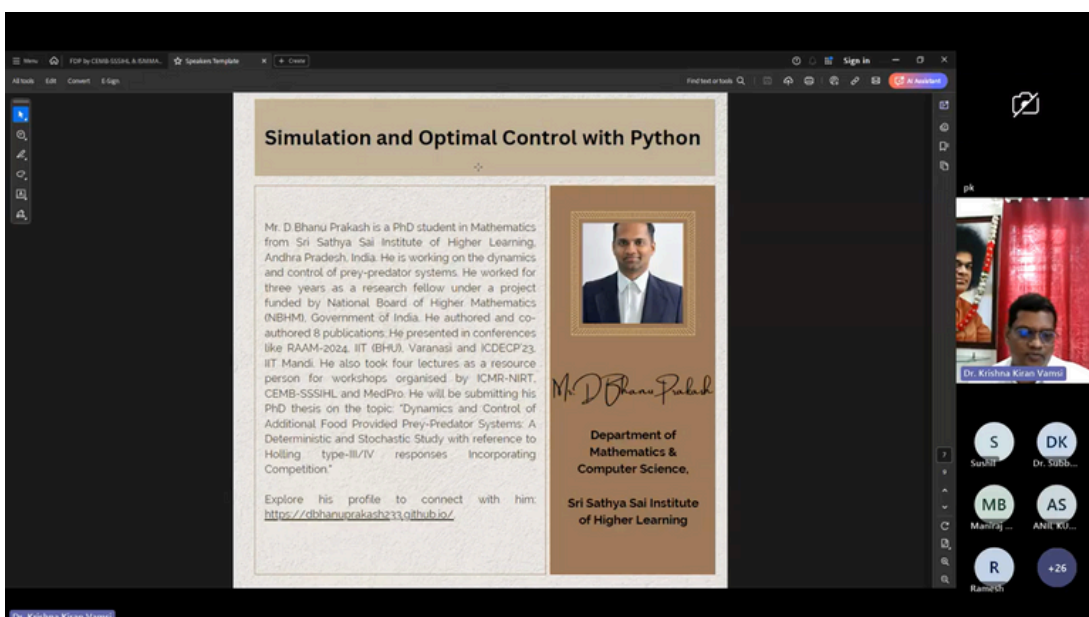
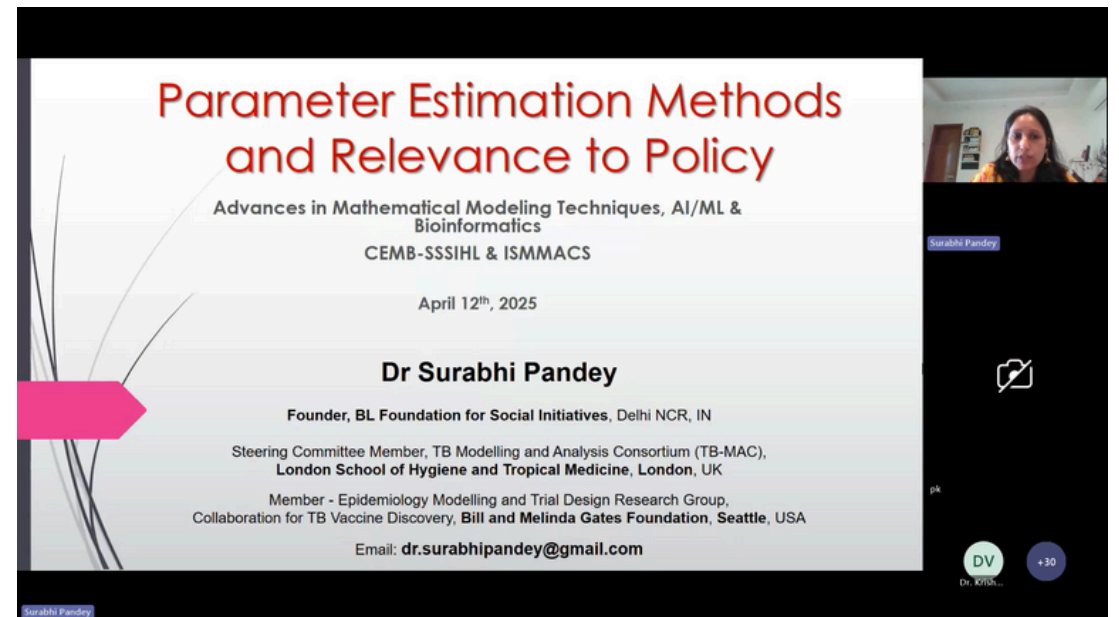
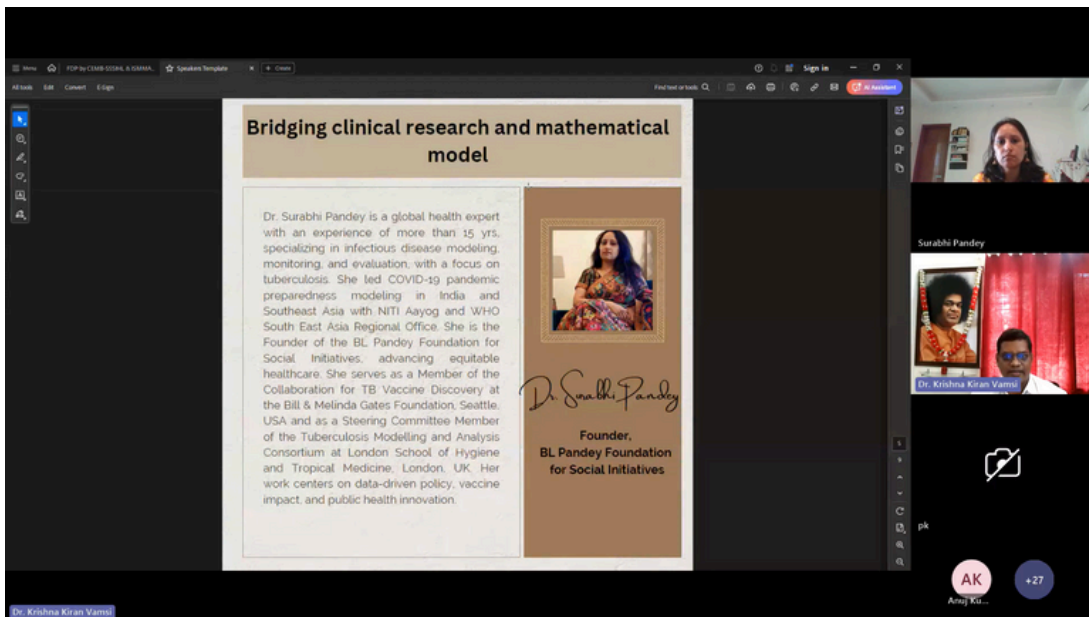
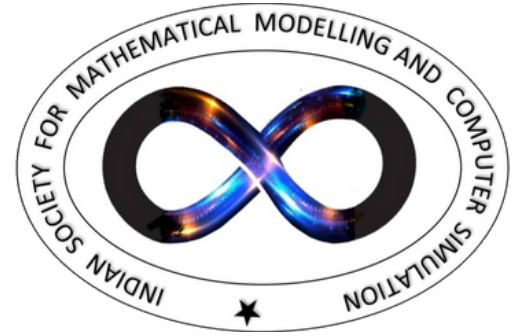
Mr. D. Bhanu Prakash conducted a hands-on session on solving optimal control problems using Python, with a focus on differential equation modeling. He began with a real-world example—the soft landing problem from the Apollo 11 moon mission—to explain the relevance of optimal control in space missions. The session gradually moved into practical implementation, introducing participants to Google Colab, a free online platform for coding in Python. He guided attendees through the step-by-step process of solving a system of ordinary differential equations (ODEs) using Python libraries like NumPy, SciPy, and Matplotlib. The core example used was the Rosenzweig-MacArthur predator-prey model, and the process involved defining parameters, setting initial conditions, solving using `solve_ivp()`, and plotting time-series and phase diagrams. Mr. Prakash also encouraged participants to explore forward-backward sweep methods, compare different numerical solvers like `solve_ivp` vs `odeint`, and test model behavior under various parameter changes. The session was highly interactive, with coding exercises, error debugging, and insights into extending models for advanced control analysis.

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Faculty Development Program (FDP) on Advances in Mathematical Modeling Techniques, AI/ML and Bioinformatics



Day 2 : April 13, 2025 (Morning session)

Speaker : Dr. Tanuja Das, University of Montreal, Canada

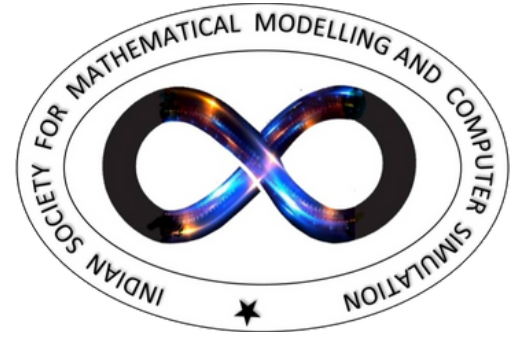
The session focused on the importance of parameter estimation in mathematical modeling, particularly within epidemiology and medical research. Dr. Tanuja Das explained how parameters like transmission rate and recovery rate influence disease dynamics in models such as the SIR model. She demonstrated how different parameter values affect infection peaks and emphasized that estimating these parameters using real-world data can inform better decision-making in healthcare, such as determining required treatment capacities. She also presented an example from cancer research, highlighting how patient-specific parameters (like immune status and tumor growth) influence drug efficacy, and how parameter estimation helps in designing personalized treatment plans. The talk covered challenges in data availability—such as missing or noisy data—and discussed strategies to overcome them using surrogate datasets, statistical methods, and open-access platforms. The session concluded with a brief introduction to using MATLAB for solving ODEs and fitting models to data, including practical steps for participants to access MATLAB either through institutional licenses or limited-time trials.

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Faculty Development Program (FDP) on Advances in Mathematical Modeling Techniques, AI/ML and Bioinformatics



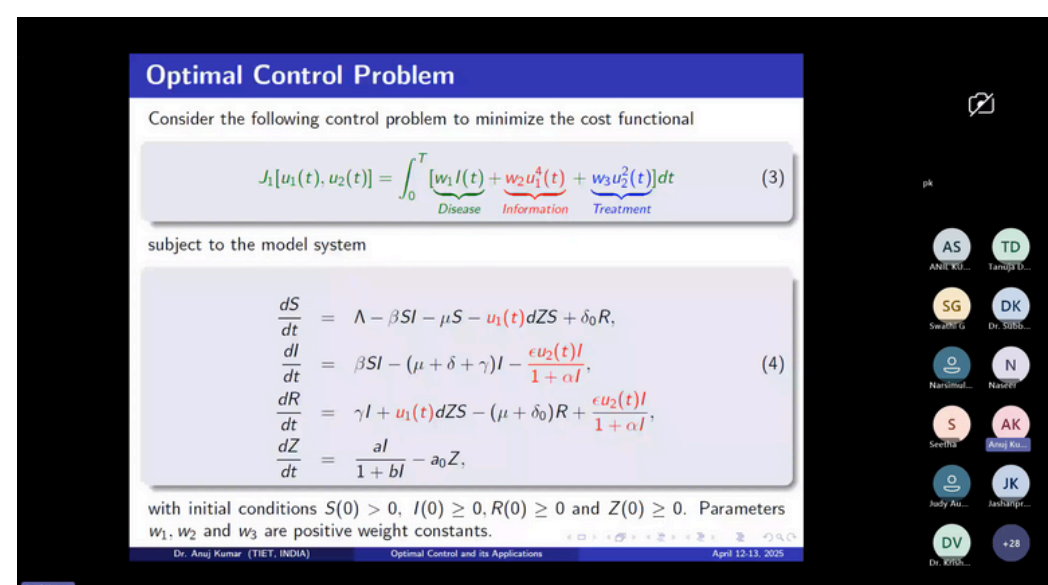
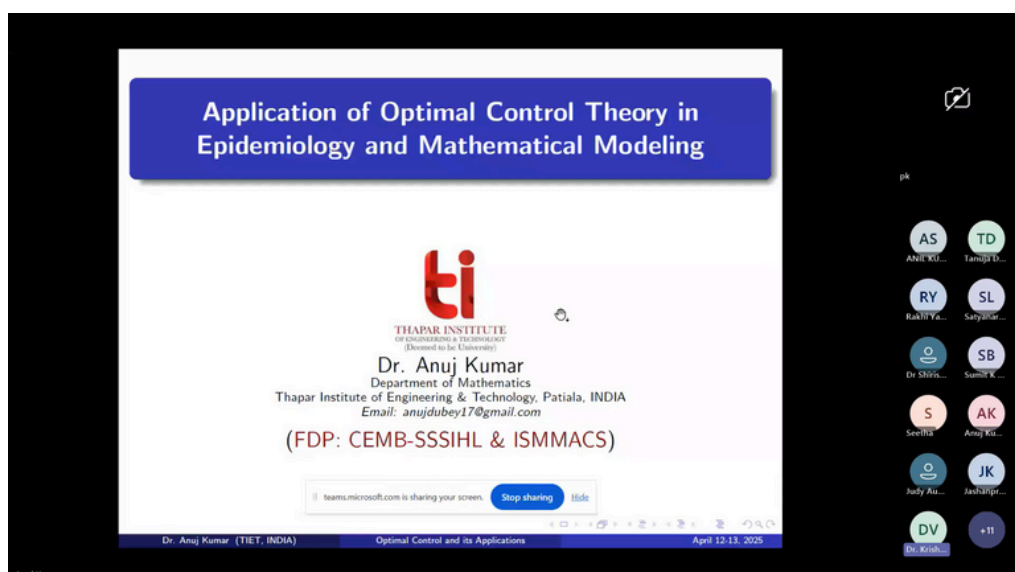
Speaker : Dr. Anuj Kumar , TIET

The session focused on the application of mathematical modeling and optimal control strategies in the context of infectious disease spread. Various compartmental models such as SIR, SEIR, and vector-borne frameworks were discussed, incorporating realistic features like demographic effects, behavioral responses, vaccination strategies, and information dynamics. Emphasis was placed on the importance of the basic reproduction number (R_0) in determining disease persistence, and the use of Pontryagin's Maximum Principle to derive optimal control policies. Control strategies included behavioral interventions and treatment, with numerical simulations showing that combined interventions are most effective in reducing infection peaks and total cost. Advanced concepts like backward and Hopf bifurcations, treatment saturation, and cost-effectiveness analysis were also explored, highlighting how model parameters influence epidemic outcomes and control efficiency.

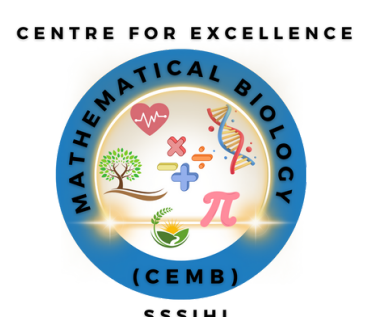
Day 2 : April 13, 2025 (Evening session)

Speaker : Dr. Tanuja Das, University of Montreal, Canada

The session led by Dr. Tanuja Das focused on the fundamental principles of epidemiology and mathematical modeling of infectious diseases. She began with an overview of infectious disease transmission and its public health implications, emphasizing how mathematical models help in understanding, predicting, and controlling disease spread. Dr. Das explained the structure and significance of compartmental models (like SIR models), including how differential equations describe transitions between susceptible, infected, and recovered populations. She elaborated on parameter definitions, model assumptions, and the process of deriving equations based on biological insights. The lecture covered stability and bifurcation analysis, showing how equilibrium points help understand long-term disease outcomes, and how the stability of these points changes with system parameters. She also introduced basic reproduction number (R_0) and its biological meaning, especially in determining whether a disease will die out or persist. The session concluded with discussions on the importance of initial conditions, parameter sensitivity, and biological interpretations of mathematical results, while setting the stage for the next session focused on hands-on MATLAB implementation.

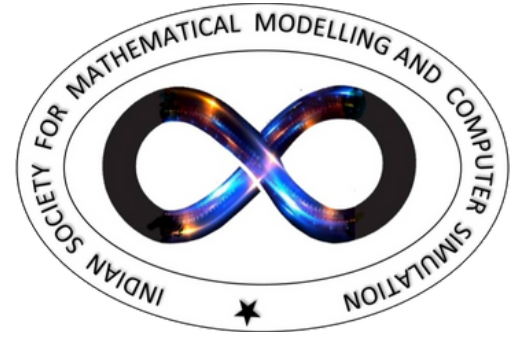


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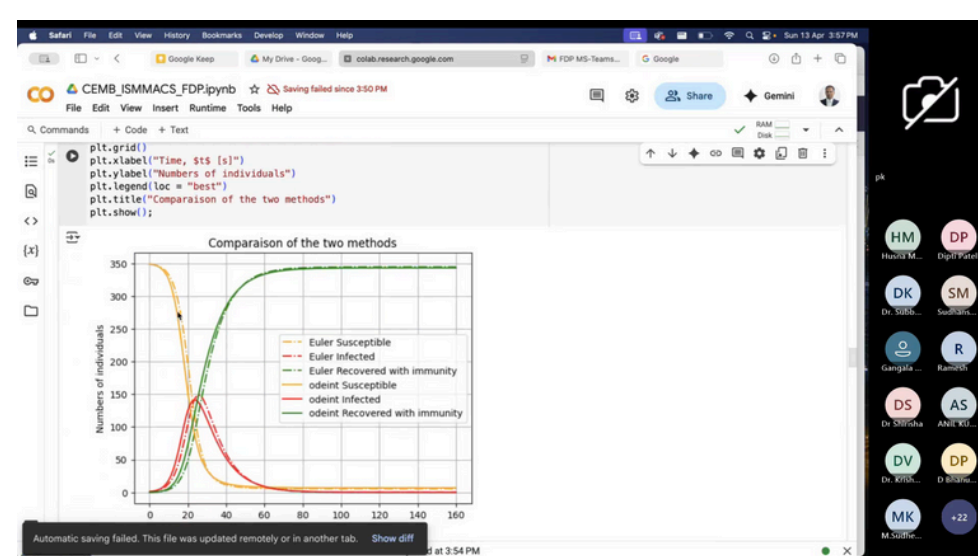
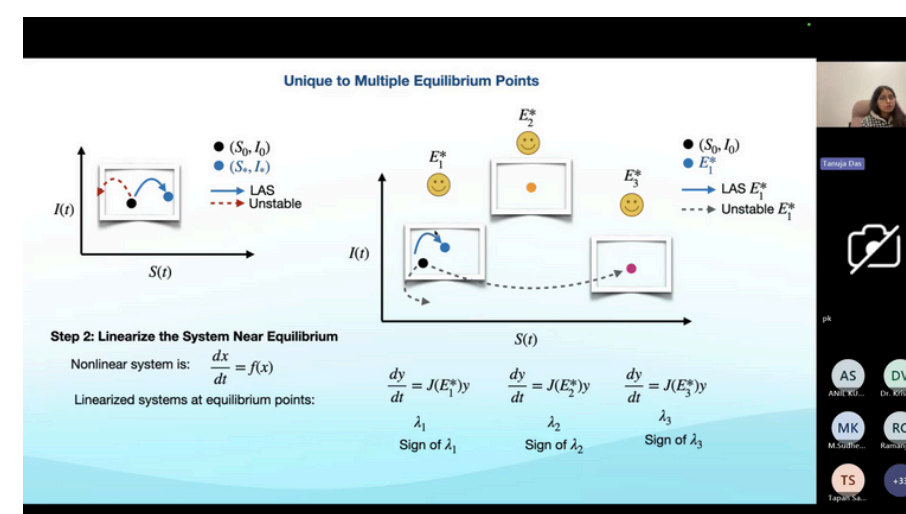
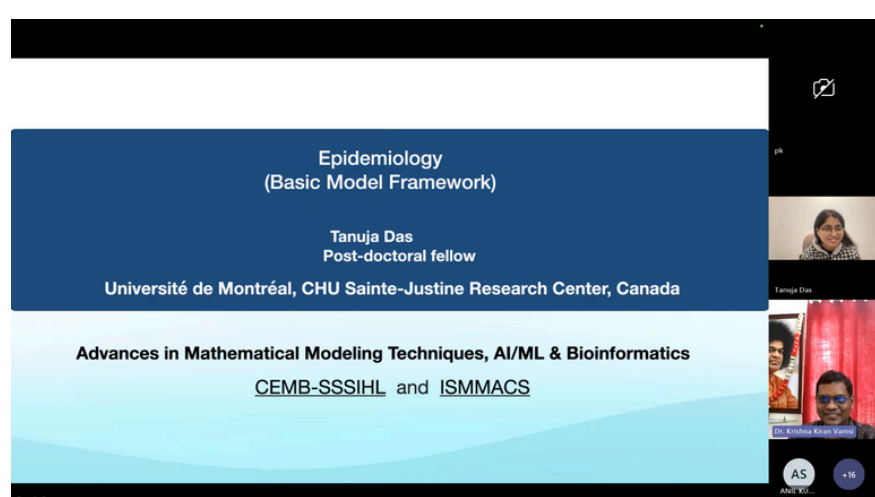
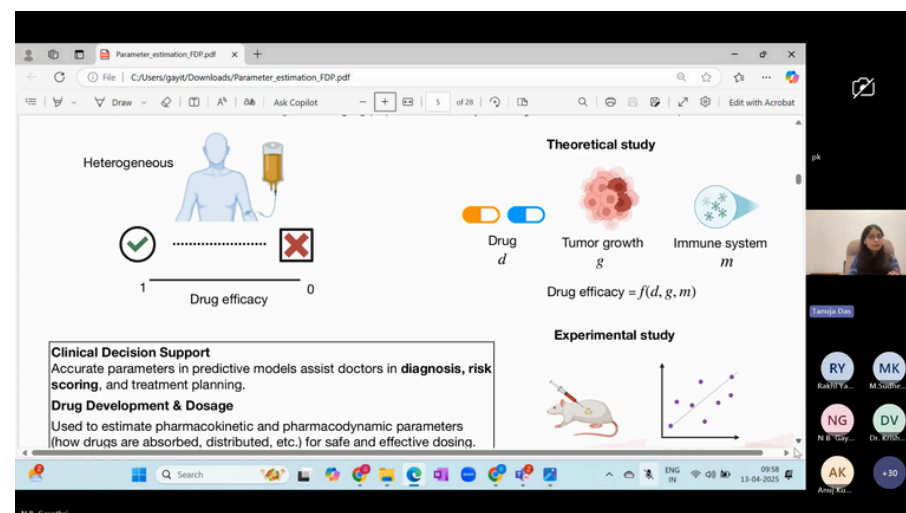
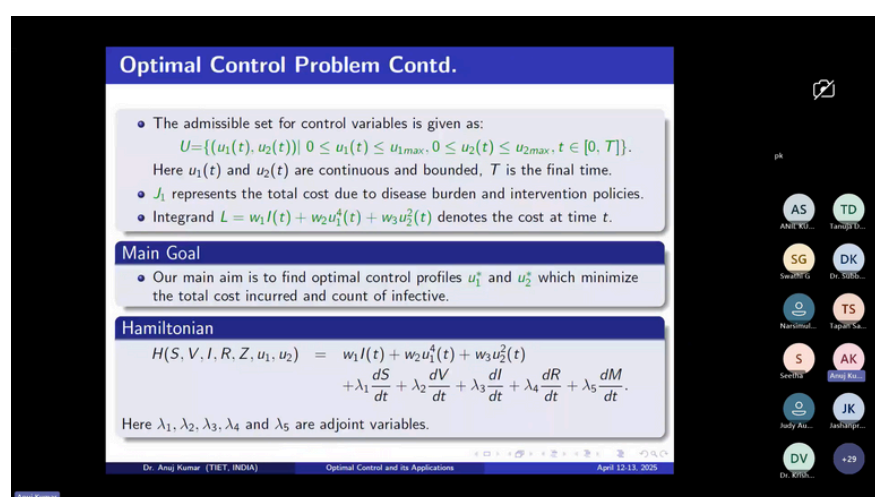


Faculty Development Program (FDP) on Advances in Mathematical Modeling Techniques, AI/ML and Bioinformatics



Speaker : Mr. D Bhanu Prakash, SSSIHL

The final session of the Faculty Development Program (FDP) held on April 13, 2025, focused on solving optimal control problems using Python. Led by Mr. D. Bhanu Prakash, the session began with a review of solving differential equations, particularly using a five-step solution approach and extending models from 2D to 3D. Participants explored multiple numerical methods—solve_ivp, odeint, Euler, and Runge-Kutta 4 (RK4)—and their applicability to simple and complex systems like the SAR model. A hands-on demonstration included plotting population dynamics and implementing forward-backward sweep methods to solve Hamiltonian-based optimal control problems, using a lunar landing scenario modeled after Apollo 11 data. Key concepts such as adjoint equations, switching functions, Bang-Bang control, and numerical approximation errors were discussed. The session concluded with a critical reflection on modeling assumptions, boundary conditions, and advanced solution methods (e.g., direct transcription, multiple shooting, and libraries like CasADi and GEKKO), offering insights into numerical stability and global optimality for real-world applications.

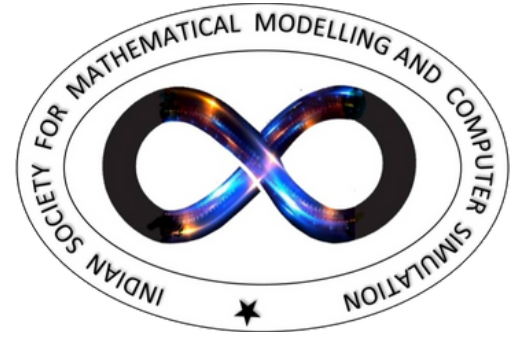


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Faculty Development Program (FDP) on Advances in Mathematical Modeling Techniques, AI/ML and Bioinformatics



Day 3 : April 14, 2025 (Morning session)

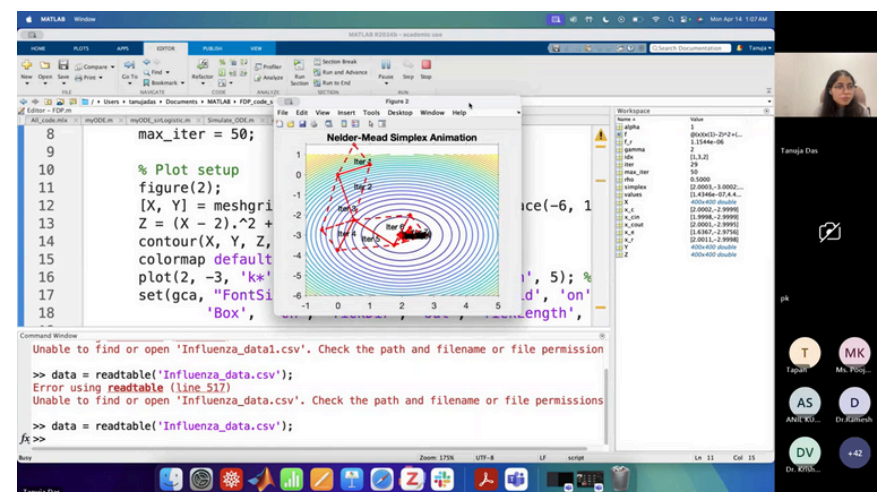
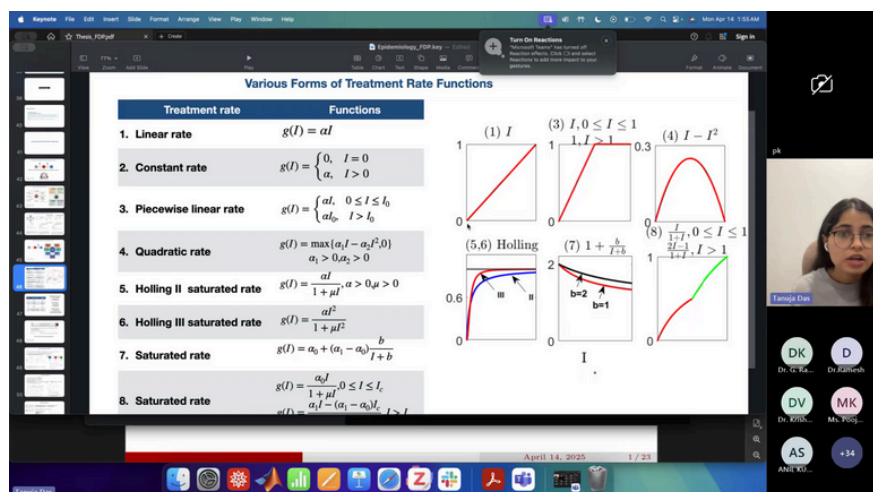
Speaker : Dr. Tanuja Das, University of Montreal, Canada

Dr. Tanuja Das delivered an insightful session during the Faculty Development Program (FDP), focusing on the role of complex epidemiological models in capturing real-world disease dynamics. The session highlighted how incorporating factors like awareness, treatment limitations, and behavioral responses can significantly influence model outcomes. Using compartmental models such as SEIR and SIR, Dr. Das discussed nonlinear incidence and treatment rate functions, emphasizing parameters like awareness sensitivity (m), treatment saturation, and self-protection rate (θ). She introduced functional responses like Holling Type II and III, adapted from ecological models, to simulate realistic treatment scenarios. The analysis involved bifurcation theory, identifying phenomena such as backward bifurcation, transcritical bifurcation, and Hopf bifurcation, all of which can lead to multistability and disease outbreaks, even when the basic reproduction number $R_0 < 1$. The session concluded by underscoring the role of cooperative effects, non-monotonic interactions, and parameter sensitivity in understanding long-term epidemic behavior and planning effective control strategies.

Day 3 : April 14, 2025 (Evening session)

Speaker : Prof. Deepa Sinha, South Asian University

Prof. Deepa Sinha from South Asian University delivered a session on encryption and decryption using signed Cayley graphs, coinciding with the International Day of Quantum Computing. After a foundational introduction to graph theory and signed graphs, she explained unitary Cayley graphs and their signed extensions, setting the stage for their application in cryptography. Prof. Sinha proposed an innovative encryption-decryption scheme where messages are encoded as signed graphs, superimposed with unitary signed Cayley graphs, and encrypted using a trapdoor function (symmetric key). The scheme transforms plain text into graph-based ciphertext, offering enhanced security. She elaborated on both encryption and decryption processes using real examples, matrix representations, and edge-weight transformations. The session concluded with a discussion on computational complexity, showing how graph structure and traversal can be leveraged for secure communication, especially in sensitive areas like military or government networks. Participants appreciated the novel approach and its relevance in modern cryptographic applications.

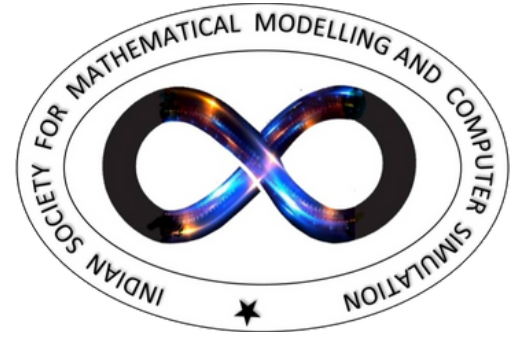


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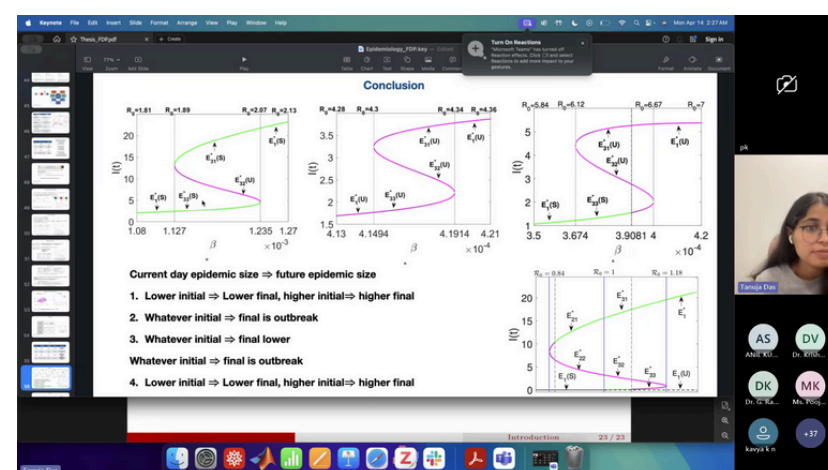
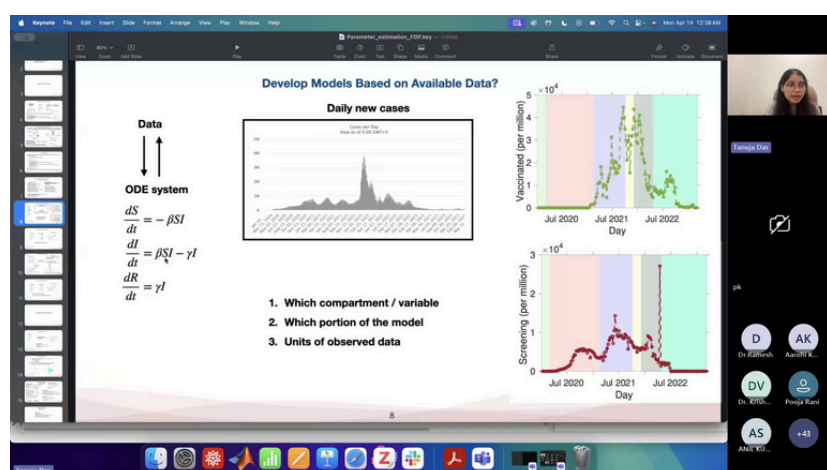


Speaker : Prof. Ritesh Dubey, SRM IST

Prof. Ritesh Dubey delivered an FDP session on integrating deep learning with the numerical solution of hyperbolic conservation laws, particularly focusing on ENO (Essentially Non-Oscillatory) and WENO (Weighted ENO) reconstruction techniques. He began by discussing the challenges of solving hyperbolic PDEs numerically due to discontinuities and shock formations, which standard interpolation methods struggle to handle. Prof. Dubey introduced the idea of posing interpolation as a learning problem, using shallow neural networks to classify and reconstruct smooth polynomials for accurate flux approximation. He explained how synthetic data was generated from smooth and discontinuous functions, the importance of grid spacing (Δx) in model training, and how imbalanced datasets affect classification performance. Models were trained using supervised learning, leveraging classification techniques to select appropriate stencils for reconstruction. A hybrid multimodal approach combining models trained on both smooth and discontinuous data was proposed, yielding better accuracy and non-oscillatory behavior. The session concluded by highlighting open research questions in scientific machine learning and encouraging future exploration of model generalizability and regression corrections for more reliable PDE solvers.

Speaker : Dr. Abhishek Pandey, Yale School of public health, USA

The Faculty Development Program (FDP) session, featured Dr. Abhishek Pandey, a research scientist at Yale University, who conducted a comprehensive, hands-on lecture on parameter estimation in infectious disease modeling. He discussed the construction and application of compartmental models (e.g., SIR models) to simulate disease spread and estimate critical parameters like transmission and recovery rates. The session covered both deterministic and probabilistic approaches, including least squares and likelihood-based methods, emphasizing the significance of model validation, data quality, and incorporating uncertainty. Dr. Pandey also shared real-world applications, such as modeling the Ebola outbreak, and compared mechanistic models with machine learning techniques, highlighting their roles in public health decision-making. The interactive discussion set the foundation for an advanced follow-up on Bayesian MCMC methods in the next session.

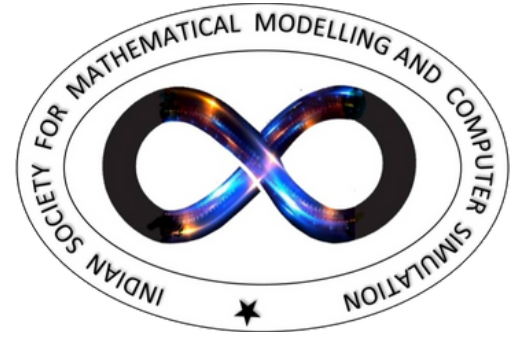


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Faculty Development Program (FDP) on Advances in Mathematical Modeling Techniques, AI/ML and Bioinformatics



Day 4 : April 15, 2025 (Morning Session)

Speaker : Prof. Shruti Dubey, IIT Madras

Professor Shruti Dubey from the Department of Mathematics, IIT Madras, delivered a comprehensive lecture during a Faculty Development Program (FDP) session on the topic of Extreme Learning Machine (ELM). The session, hosted by Dr. Krishna Kiran Vamsi, began with an introduction to Dr. Dubey's academic background and contributions in the field of differential equations and mathematical modeling. Dr. Dubey explained the mathematical foundations of ELM, including concepts like Singular Value Decomposition (SVD), pseudo-inverse, and least squares solution of systems. She then transitioned into an overview of classical feed-forward neural networks, highlighting their structure, function, and limitations related to learning rate, iteration dependency, and overfitting. The focus then shifted to the ELM approach, where Dr. Dubey emphasized its speed and simplicity in training single-layer feed-forward networks by randomly assigning input weights and biases, and solving a linear system analytically without iterations. The session included live demonstrations of Python code implementing ELM for function approximation tasks. Dr. Dubey concluded by highlighting ELM's advantages in speed and generalization performance, and offered to share supplementary material and references for further exploration. The session was interactive and appreciated for its depth, clarity, and practical relevance.

Day 4 : April 15, 2025 (Evening Session)

Speaker : Dr. Prashant Kumar Srivastava, ISMMACS and Dr. Krishna Kiran Vamsi, CEMB-SSSIHL

This session featured Dr. Prashant Kumar Srivastava and Dr. Krishna Kiran Vamsi, who shared insights on academic societies and interdisciplinary research. Dr. Srivastava introduced the Indian Society for Mathematical Modelling and Computer Simulation (ISMMCS), highlighting its contributions to research through international collaborations, annual events, and member benefits, encouraging young researchers to join for enhanced networking and academic growth. Dr. Vamsi then presented the activities of the Center for Excellence in Mathematical Biology (CEMB) at Sri Sathya Sai Institute of Higher Learning (SSSIHL), emphasizing its focus on applied mathematical biology in areas such as cancer metastasis prediction, leprosy and tuberculosis modeling, cardiovascular and ecological systems, diabetes reversal, and the role of diet and music in health. The center collaborates with national institutes and hospitals, develops tools like a TB patient retention predictor (with a patent filed), and promotes outreach through specialized courses, research internships, and national FDPs. With multiple publications and new programs underway, including a planned Executive Master's in Computational Biology, the center remains open to multidisciplinary collaboration and aims to bridge research with real-world healthcare impact.

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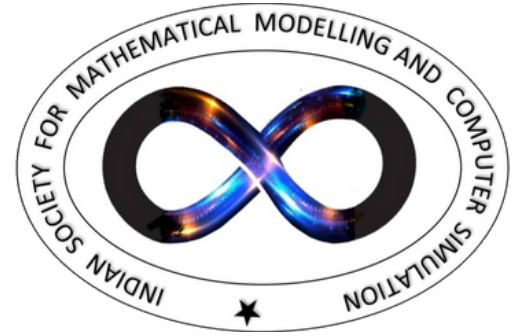




Faculty Development Program (FDP)

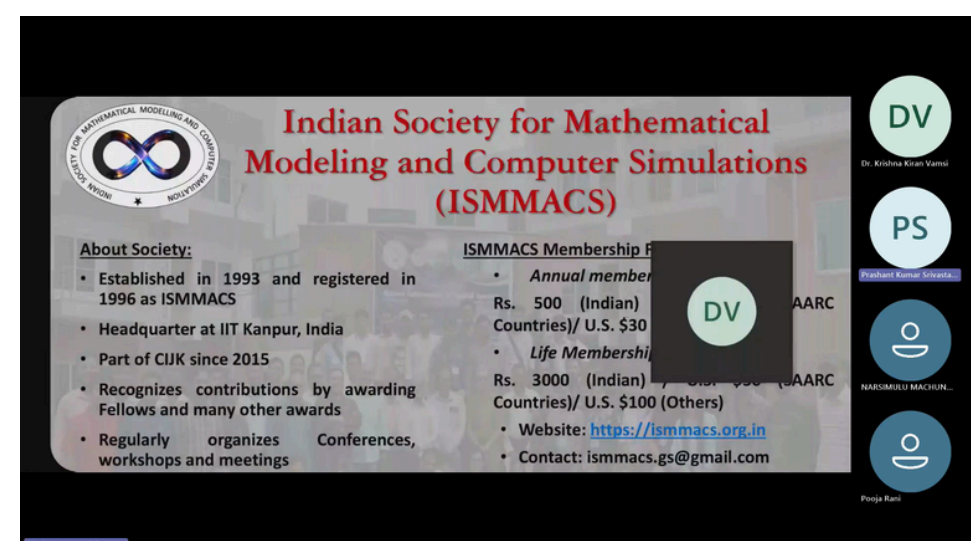
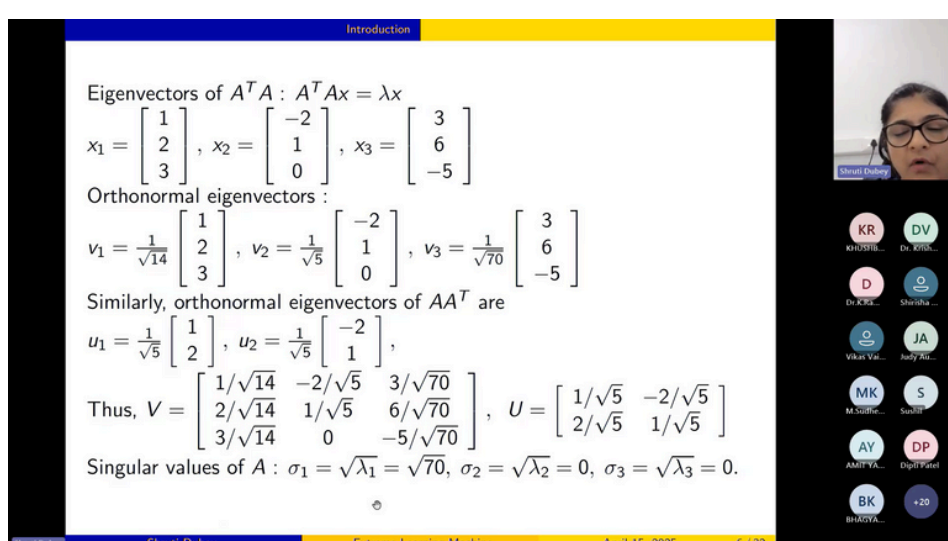
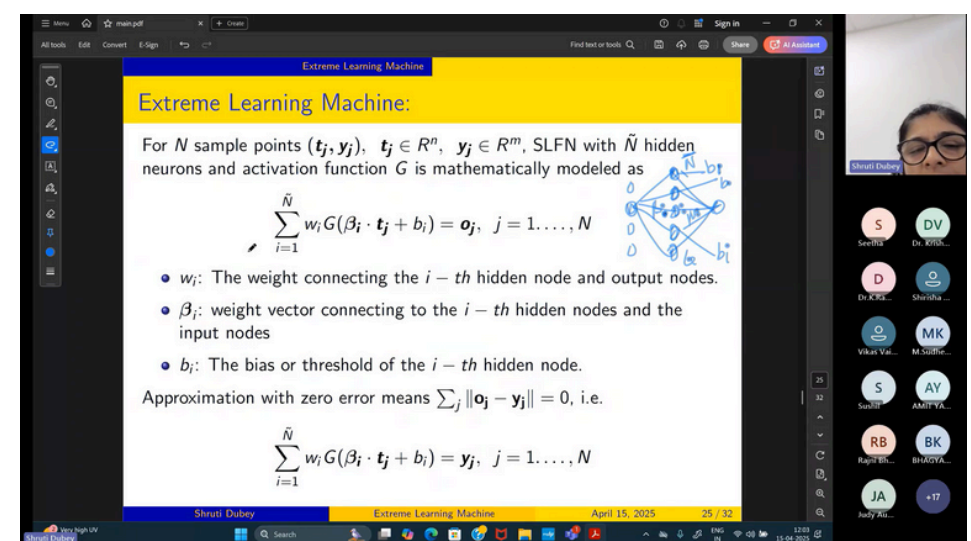
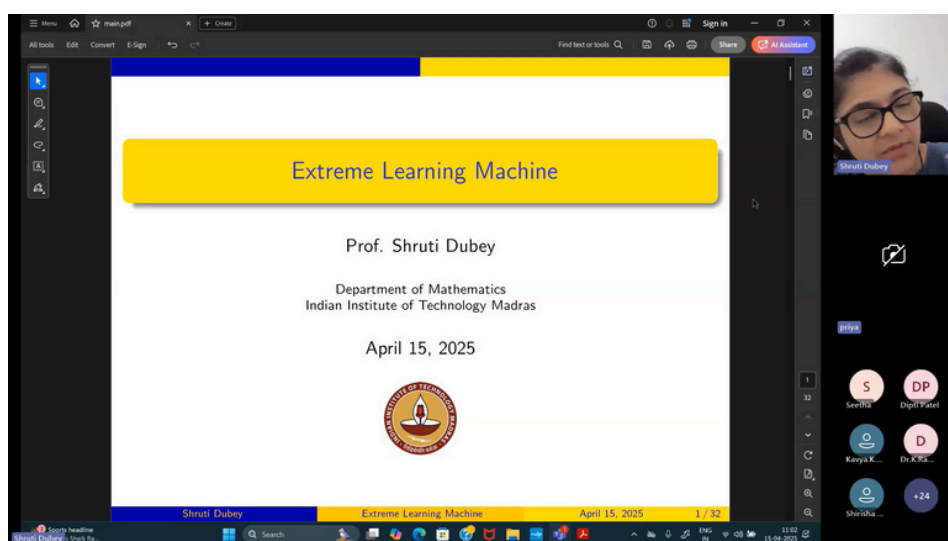
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Advances in Mathematical Modeling Techniques, AI/ML and Bioinformatics



Speaker : Dr. Abhishek Pandey ,Yale School of public health, USA

Dr. Abhishek Pandey delivered an insightful session as part of the Faculty Development Program, focusing on parameter estimation techniques in infectious disease modeling. Building on previous sessions, he introduced maximum likelihood estimation (MLE) as a probabilistic approach to parameter estimation, emphasizing its ability to incorporate uncertainty by assessing how likely observed data is under a given model. He demonstrated the application of likelihood functions, assumptions around normal, Poisson, and negative binomial distributions, and contrasted MLE with traditional least squares fitting. Dr. Pandey then introduced the Bayesian approach, particularly the Metropolis-Hastings MCMC algorithm, explaining how it provides a full posterior distribution of parameters rather than single-point estimates—enabling better uncertainty quantification. The session included detailed demonstrations using Jupyter notebooks, exploring convergence, proposal distributions, and model fitting. He concluded with a comparative analysis of mechanistic models vs. AI/ML-based models, highlighting the strengths of hybrid approaches and the emerging potential in integrating neural networks with epidemiological modeling for real-time decision-making. The session was well-received for its practical depth, clarity, and relevance to modern mathematical biology.



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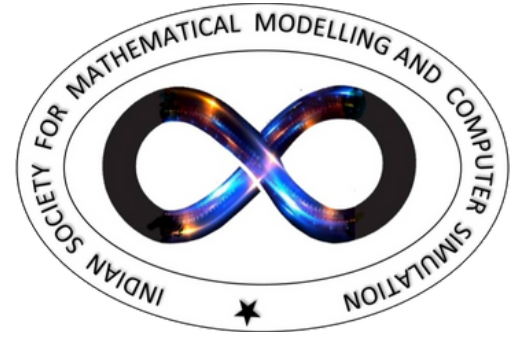




Faculty Development Program (FDP)

on

Advances in Mathematical Modeling Techniques, AI/ML and Bioinformatics



Day 5 : April 16, 2025 (Morning Session)

Speaker : Dr. Bapan Ghosh, IIT Indore

First Session

In this session, Dr. Bapan Ghosh delivered an in-depth lecture on Delay Differential Equations (DDEs) with a focus on stability analysis and population models. The talk was structured in two parts: the first explored the classification, solution techniques, and existence and uniqueness theorems for DDEs, including types like constant, state-dependent, and distributed delays. It highlighted the distinction between retarded and neutral DDEs, emphasizing the infinite-dimensional nature of these systems due to their dependence on history functions. The second part centered on the qualitative behavior of solutions, including positivity, oscillations, and continuity of derivatives, using both analytical examples and visual illustrations. Dr. Ghosh emphasized how delay can significantly alter system dynamics compared to standard ODEs and concluded with theoretical insights that lay the groundwork for applications in mathematical biology and ecological modeling.

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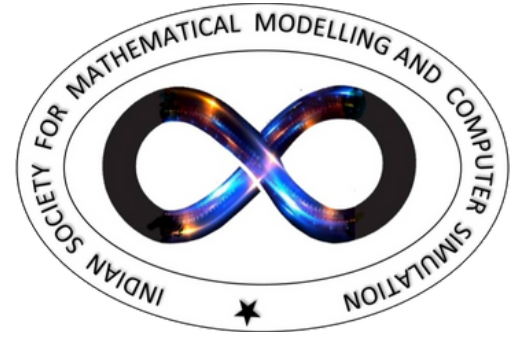




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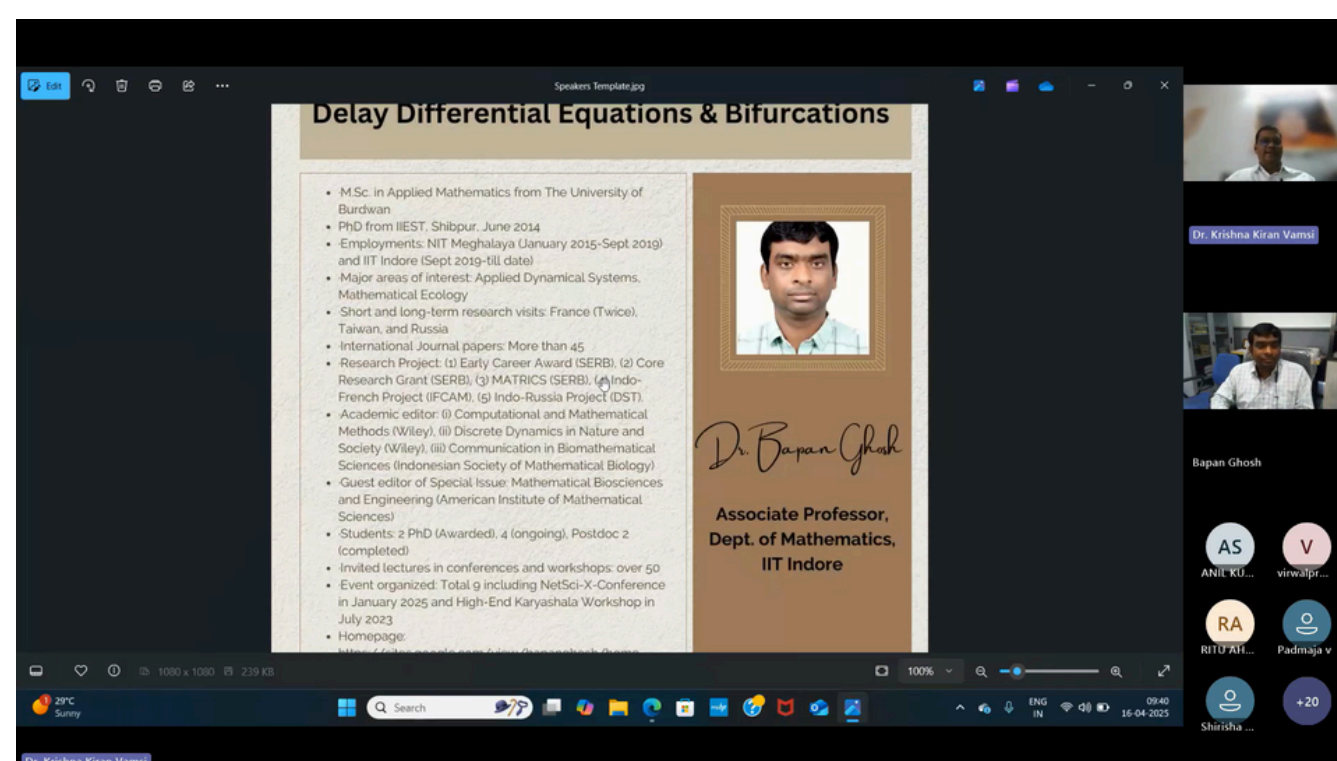
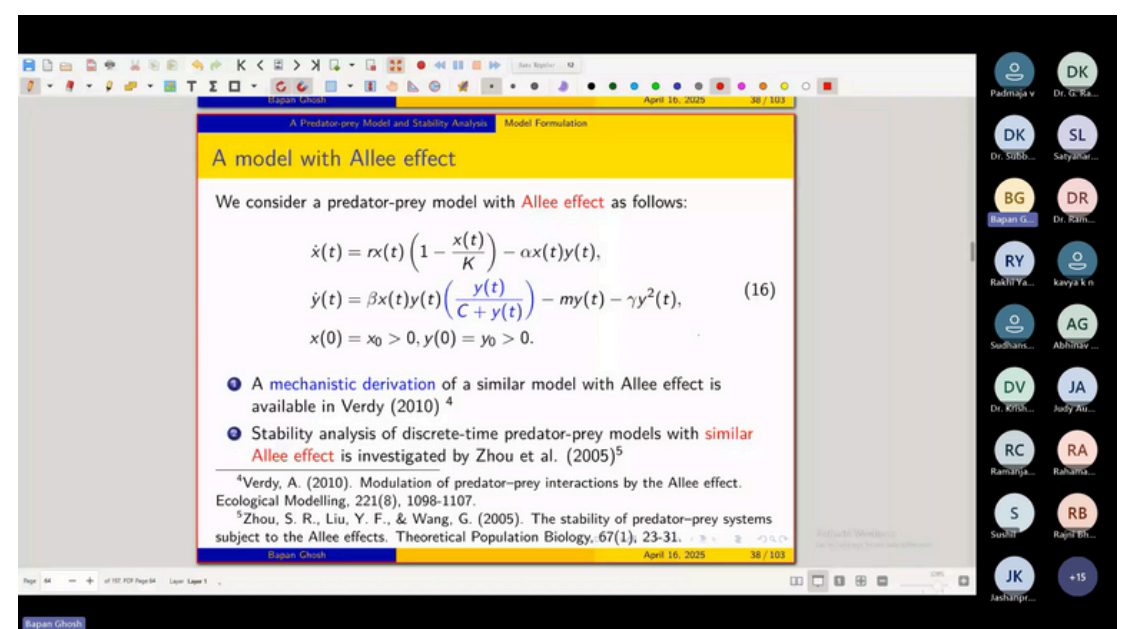
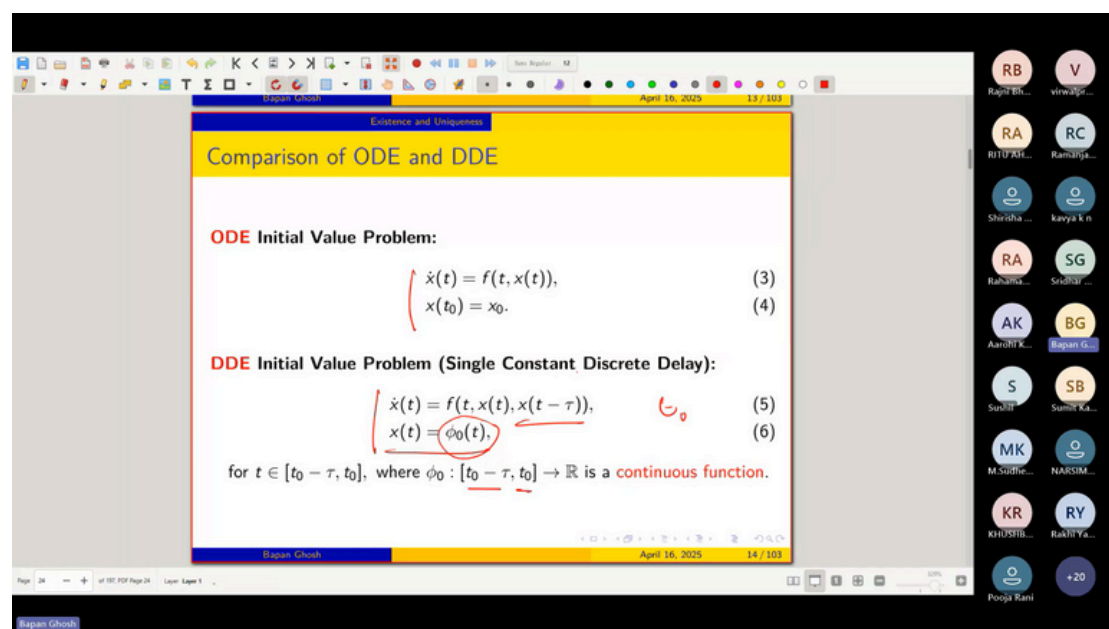
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Advances in Mathematical Modeling Techniques, AI/ML and Bioinformatics



Second session

In this session, Dr. Bapan Ghosh elaborated on the applications and stability analysis of Delay Differential Equations (DDEs), focusing on real-world models in ecology, epidemiology, and mathematical biology. He presented models involving dispersal delays, epidemic recovery cycles, bacterial growth, and distributed delays, demonstrating how delays significantly influence system dynamics. A major highlight was the detailed discussion on stability switching, invariance, and Hopf bifurcations, grounded in his research. Dr. Ghosh introduced a unique model exhibiting multiple dynamic behaviors (e.g., stability change, instability switching) and shared the geometric approach to analyze eigenvalue transitions. The session concluded with insights into open problems, recent research, and the importance of DDEs in understanding complex biological interactions.

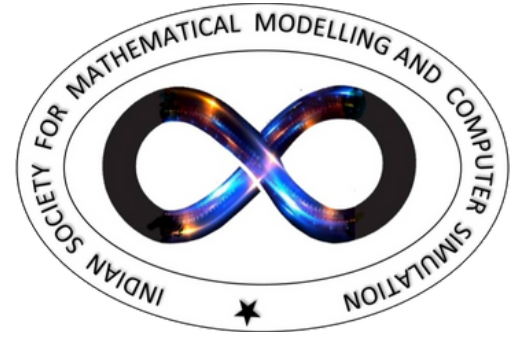


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Faculty Development Program (FDP) on Advances in Mathematical Modeling Techniques, AI/ML and Bioinformatics



Day 6 : April 17, 2025 (Morning Session)

Speaker : Dr. Partha Sarathi Mandal , NIT Patna

First Session

In this session, Dr. Partha Sarathi Mandal presented an insightful talk on stochastic modeling and its applications to population growth and epidemic models. Unlike deterministic models, which produce fixed outcomes from initial conditions, stochastic models incorporate randomness and probabilistic elements, making them more realistic for systems with inherent uncertainty, especially in small populations. He developed a stochastic population model using Continuous-Time Markov Chains (CTMCs), based on a birth-death process, and extended it to an SIS epidemic model, incorporating infection and recovery rates. Using transition probabilities, he derived Kolmogorov forward equations and demonstrated through numerical simulations that finite-time extinction—not possible in deterministic models—can be effectively captured. The session highlighted how stochastic frameworks offer a more accurate and flexible approach to modeling real-world dynamics influenced by demographic and environmental variability.

Second session

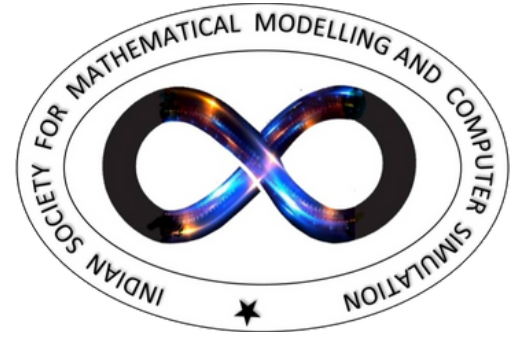
In this advanced session, Dr. Partha Sarathi Mandal explored the application of stochastic modeling, specifically using Continuous-Time Markov Chains (CTMC) and Stochastic Differential Equations (SDEs), to analyze the dynamics of zoonotic diseases, with a focus on bubonic plague transmission from rats to humans via fleas. He detailed a compartmental model involving eight populations (rat, flea, human compartments) and discussed the limitations of deterministic models, especially their inability to capture finite-time extinction or account for random outbreaks in small populations. Using a stochastic framework, he analyzed the probability of disease extinction, first passage time to spillover, and the effects of noise-induced extinction. Numerical simulations demonstrated how increased noise intensity can drive systems to extinction even when deterministic models predict persistence. He concluded by showing how environmental randomness can be incorporated via white noise perturbations, offering a more realistic perspective on disease dynamics and ecosystem interactions.

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Faculty Development Program (FDP) on Advances in Mathematical Modeling Techniques, AI/ML and Bioinformatics



Day 6 : April 17, 2025 (Evening Session)

Speaker : Dr. Akhil Kumar Srivastava, Barcelona Institute for Global Health

First Session

In this session, Dr. Akhil Kumar Srivastava delivered a comprehensive session on stochastic modeling in epidemiology, focusing on how to transition from traditional deterministic models to stochastic differential equations (SDEs). Emphasizing the role of randomness in real-world disease dynamics—especially in early outbreak stages or small populations—he explained the SIR model as a base and showed how to incorporate random perturbations through probability-driven transitions using tools like Continuous-Time Markov Chains (CTMCs) and Ito calculus. He detailed how to construct expectation and covariance matrices, develop the M-matrix, and ultimately derive a complete stochastic model, using an advanced COVID-19 model with multiple compartments (e.g., exposed, symptomatic, asymptomatic, hospitalized, quarantined). Dr. Srivastava also highlighted practical aspects such as simulating these models using MATLAB, and emphasized that stochastic models better capture variability and uncertainties in epidemiological data compared to deterministic models.

Second session

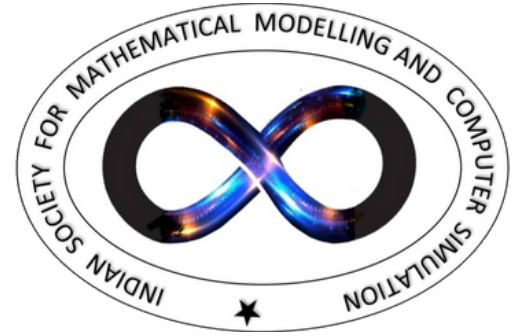
In this hands-on session, Dr. Akhil Kumar Srivastava guided participants through implementing stochastic epidemiological models in MATLAB, using the SIRS model as an example. He explained how to define biologically meaningful parameters, initial conditions, and time steps, emphasizing the importance of maintaining positive values in epidemiological simulations. The session covered how to code the stochastic differential equations (SDEs), construct the M matrix representing noise terms, and simulate multiple runs to observe variability. He also demonstrated how to compare stochastic simulations to deterministic solutions within the same code framework, highlighting the differences in behavior due to random fluctuations. Participants were shown how to generate plots of multiple simulation paths, as well as the mean trajectory, illustrating how stochastic models provide richer insights into uncertainty and variability in disease dynamics. Dr. Srivastava concluded by offering to share his MATLAB codes and relevant references, encouraging further exploration and collaboration.

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Faculty Development Program (FDP) on Advances in Mathematical Modeling Techniques, AI/ML and Bioinformatics



Stochastic Models in Epidemiology

Arsh Kumar Sinhasaria is a postdoctoral researcher at Barcelona Institute of Global Health (BIGH). His work focuses on the study and management of disease transmission and the implementation of strategies control policies for various diseases, in particular infectious vector borne diseases, COVID-19, tuberculosis. His research interests include: infectious disease dynamics, data analysis, mathematical modeling of social problems, nonlinear dynamics, optimal control and complex networks.

He was awarded with prestigious postdoctoral fellowship from Spanish Government in 2022 and worked in Barcelona Centre for Applied Mathematics (BICAM).

During his research career, he conducted his research in different countries such as China, Italy, Portugal as a visiting researcher.

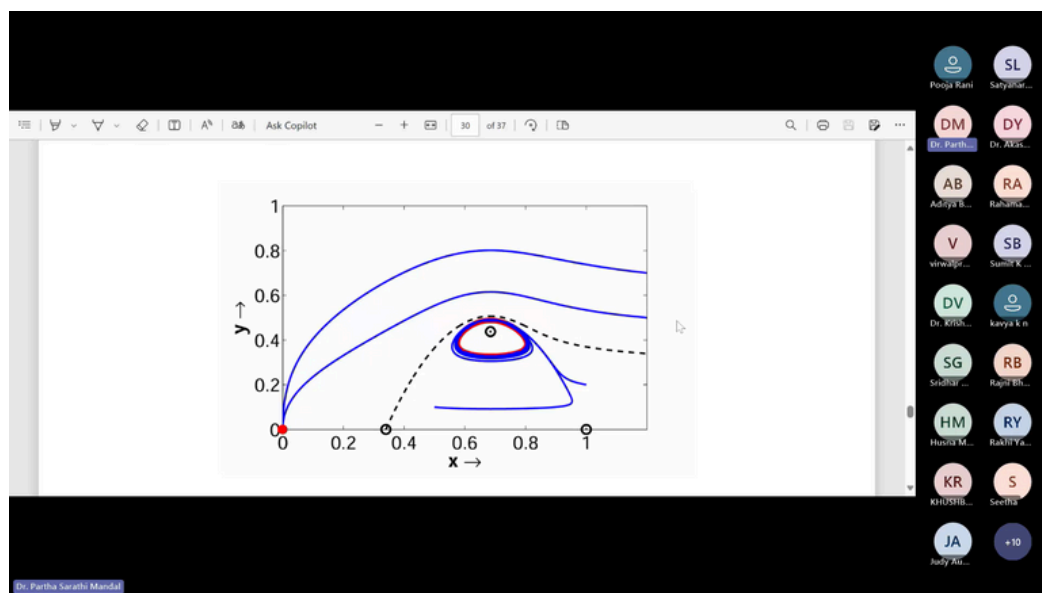
He is a trained mathematical epidemiologist who obtained his MPhil and PhD degrees in Mathematical Epidemiology from the School of Advanced Sciences, Vellore Institute of Technology with under supervision of Prof. Arsh Choudh. During his MPhil and PhD, he worked on modeling infectious diseases, such as vector borne diseases and influenza. His focus is on COVID-19 modelling and dengue disease, as well as developing a good model, analyzing data with the model, and discussing control interventions optimal control.

Throughout his career, he has published 20 scientific papers in 15 peer-reviewed high-impact mathematical journals, spoken at 10 Symposia, and given 10 talks.

Google Scholar Link: <https://scholar.google.com/citations?user=Qp8J5JAMAAJ&hl=en>

Dr. Arsh Kumar Sinhasaria
Barcelona Institute of Global Health, Barcelona, Spain.

Mathematical model

$$\begin{aligned}\frac{dS}{dt} &= \Lambda - \beta_1(1 - \epsilon_m c_m) S I_s - \beta_2(1 - \epsilon_m c_m) S I_a - \mu S, \\ \frac{dE}{dt} &= \beta_1(1 - \epsilon_m c_m) S I_s + \beta_2(1 - \epsilon_m c_m) S I_a - \sigma E - \mu E, \\ \frac{dI_s}{dt} &= (1 - a) \sigma E + \alpha_a I_a - (\mu_s + \mu) I_s - \phi_s I_s, \\ \frac{dI_a}{dt} &= a \sigma E - \gamma_a I_a - \alpha_a I_a - \mu I_a, \\ \frac{dH}{dt} &= \phi_s I_s - (\gamma_h + \mu_h + \mu) H, \\ \frac{dQ_h}{dt} &= \gamma_a I_a - \alpha_h Q_h - \mu Q_h, \\ \frac{dR}{dt} &= \alpha_h Q_h + \gamma_h H - \mu R.\end{aligned}\quad (1)$$


CTMC model for population growth

Birth births in $(t, t + \Delta t | N(t) = n) = \left(\prod_{i=1}^n b_i \Delta t \right) (1 - b_n \Delta t)^{n-1}, n = 0, \dots, \infty$.

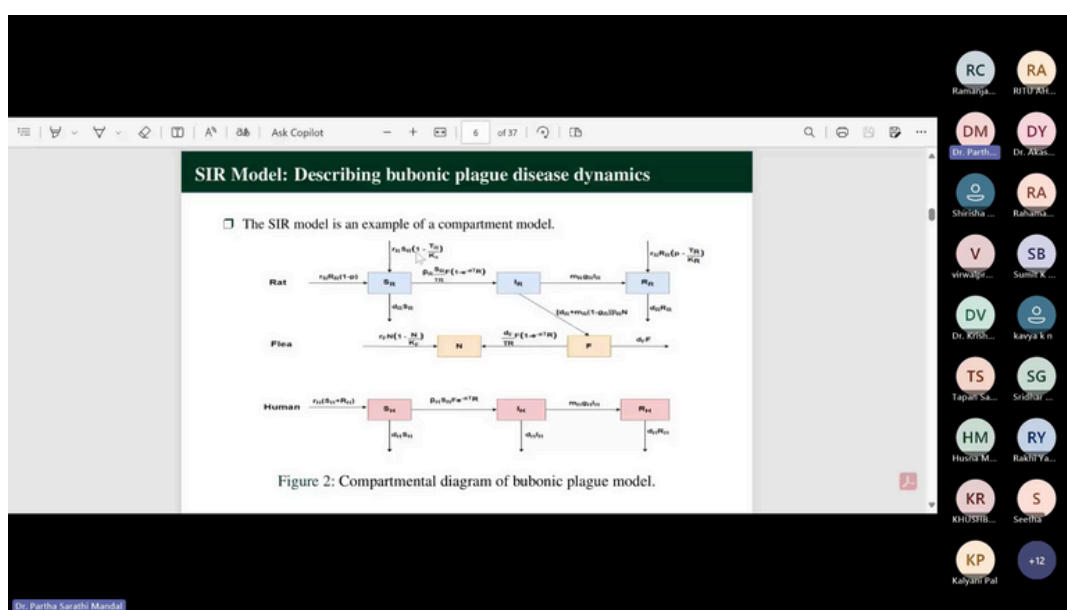
If $t = 0$, we have

Birth births in $(0, t + \Delta t | N(t) = n) = (1 - b_n \Delta t)^n (1 - b_n \Delta t) + o(\Delta t)$,

whereas for $t = 1$,

Birth births in $(1, t + \Delta t | N(t) = n) = b_n \Delta t (1 - b_n \Delta t)^{n-1} + o(\Delta t)$.

Birth deaths in $(t, t + \Delta t | N(t) = n) = \left(\prod_{i=1}^n d_i \Delta t \right) (1 - d_n \Delta t)^{n-1}, n = 0, \dots, \infty$.



Stochastic epidemic model

CTMC model formulation

The infinitesimal transition probabilities are defined as follows:

$$p_j(\Delta t) = \begin{cases} \frac{b(i) \Delta t}{b(i) \Delta t + d(i) \Delta t + o(\Delta t)}, & j = i + 1 \\ \frac{d(i) \Delta t}{b(i) \Delta t + d(i) \Delta t + o(\Delta t)}, & j = i - 1 \\ 1 - \frac{b(i) \Delta t + d(i) \Delta t}{b(i) \Delta t + d(i) \Delta t + o(\Delta t)}, & j = i \\ o(\Delta t), & \text{otherwise.} \end{cases}$$

Because Δt is sufficiently small, there are only three possible changes in states:

$$i \rightarrow i + 1, \quad i \rightarrow i - 1, \quad i \rightarrow i.$$

Let $b(i)$ denote a birth (new infection) and $d(i)$ denote a death or recovery. Then

$$p_j(\Delta t) = \begin{cases} \frac{b(i) \Delta t}{b(i) \Delta t + d(i) \Delta t + o(\Delta t)}, & j = i + 1 \\ \frac{d(i) \Delta t}{b(i) \Delta t + d(i) \Delta t + o(\Delta t)}, & j = i - 1 \\ 1 - \frac{b(i) \Delta t + d(i) \Delta t}{b(i) \Delta t + d(i) \Delta t + o(\Delta t)}, & j = i \\ o(\Delta t), & \text{otherwise.} \end{cases}$$

One Slide Summary

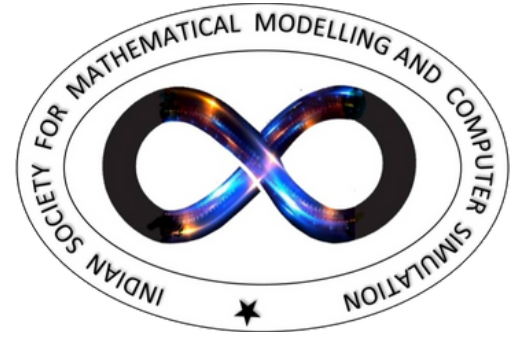
- Zoomosis
- Spillover
- A continuous-time stochastic zoonotic disease model describing Bubonic-plague disease dynamics and focuses on:
 - Disease Extinction Probability
 - First Passage Time to Spillover event
- Our results include
 - Analytical and Numerical estimates of approximate extinction probability of disease
 - Analytical expression of First passage time distribution and validate it by numerical example
 - Mean of the first passage time of the distribution.

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Faculty Development Program (FDP) on Advances in Mathematical Modeling Techniques, AI/ML and Bioinformatics



Day 7 : April 18, 2025 (Morning Session)

Speaker : Dr. Naresh K.N. , SSSIHL

First Session

Dr. Naresh K. N. delivered a comprehensive introduction to bioinformatics, emphasizing its interdisciplinary nature at the intersection of biology, mathematics, computer science, and statistics. He began with the fundamentals of genetics—explaining the structure and function of DNA, genes, chromosomes, and the genome—and illustrated how biological instructions within a single cell give rise to the complexity and diversity of human life. Highlighting the sheer volume of genomic data, Dr. Naresh emphasized the need for computational tools to store, organize, and analyze this data, giving rise to the field of bioinformatics. He defined bioinformatics as the application of computational techniques for the management, analysis, and interpretation of biological and biomedical data, with applications ranging from disease diagnostics to personalized medicine. The session also touched upon central dogma (DNA → RNA → Protein), molecular networks, genotype-phenotype relationships, and the use of databases and algorithms for genomic research. Dr. Naresh introduced key concepts like genomics, proteomics, and metabolomics, and underscored how bioinformatics is revolutionizing healthcare through AI and ML-based predictive tools for disease detection and drug development.

Second session

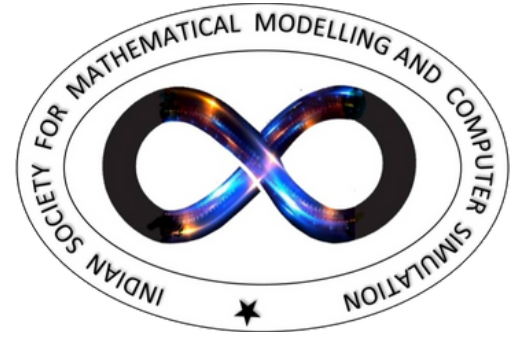
Dr. Naresh K. N. delivered an in-depth session on bioinformatics, emphasizing its significance as an interdisciplinary field that combines biology, mathematics, computer science, and statistics to process and interpret massive biological data. He walked participants through the journey from DNA to RNA to proteins, illustrating how information is stored in the genome and expressed differently across cell types, depending on the need. The session highlighted major databases (like NCBI, PDB, ATCC) and discussed how genomic data is organized, analyzed, and used for purposes ranging from disease diagnosis to drug discovery. Dr. Naresh showcased applications like HIV drug design, biomarker discovery, and personalized medicine, including examples such as early cancer detection through gene sequencing. He introduced the concept of model organisms, discussed the Human Genome Project, and explained how bioinformatics tools are used for pattern recognition, disease prediction, and comparative genomics. The lecture concluded by underlining the importance of algorithms, machine learning, and high-performance computing in transforming raw genomic data into actionable medical and biological insights.

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Faculty Development Program (FDP) on Advances in Mathematical Modeling Techniques, AI/ML and Bioinformatics



Day 7 : April 18, 2025 (Evening Session)

Speaker : Dr. Naresh K. N. , SSSIHL

Dr. Naresh K. N. conducted an advanced hands-on session exploring bioinformatics techniques through a case study on colon cancer. The session began with a family-based scenario involving pedigree analysis, introducing the genetic condition FAP (Familial Adenomatous Polyposis)—a hereditary disorder caused by mutations in the APC gene, a tumor suppressor gene that controls cell division. Using a simulated case involving two siblings, the session demonstrated how a defective APC gene leads to uncontrolled cell proliferation and potential cancer. Dr. Naresh guided participants through practical steps: retrieving Sam's APC gene sequence, comparing it with the normal APC sequence from the NCBI nucleotide database, and performing pairwise sequence alignment using BLAST to detect mutations. A key finding was a single nucleotide mutation (T to A at position 1748), which introduced a premature stop codon, truncating the APC protein and leading to loss of function. The session also introduced tools like the ORF Finder to identify the start and stop points of protein synthesis and discussed the implications of truncated proteins, loss of beta-catenin regulation, and how this leads to malignancy. Dr. Naresh concluded with the importance of genetic testing, early diagnosis, and preventive care, such as regular colonoscopies, in managing hereditary cancers.

Speaker : Dr. Anuj Kumar Umrao, Hebrew University of Jerusalem

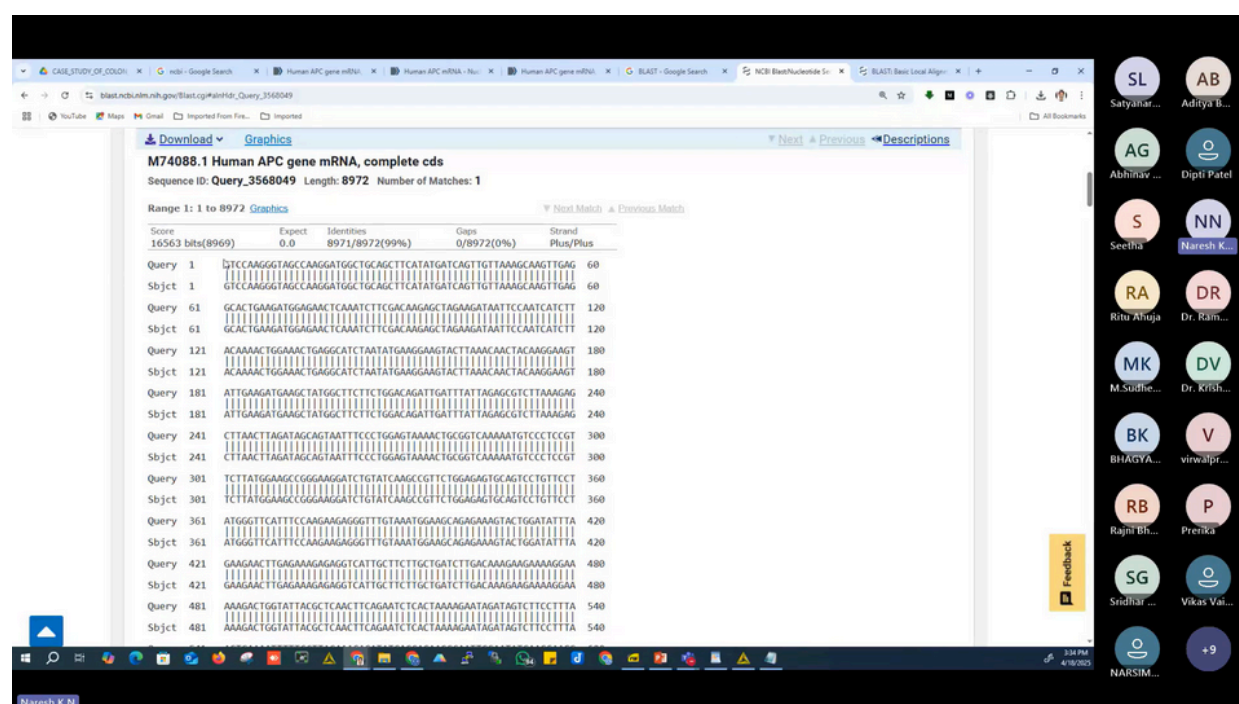
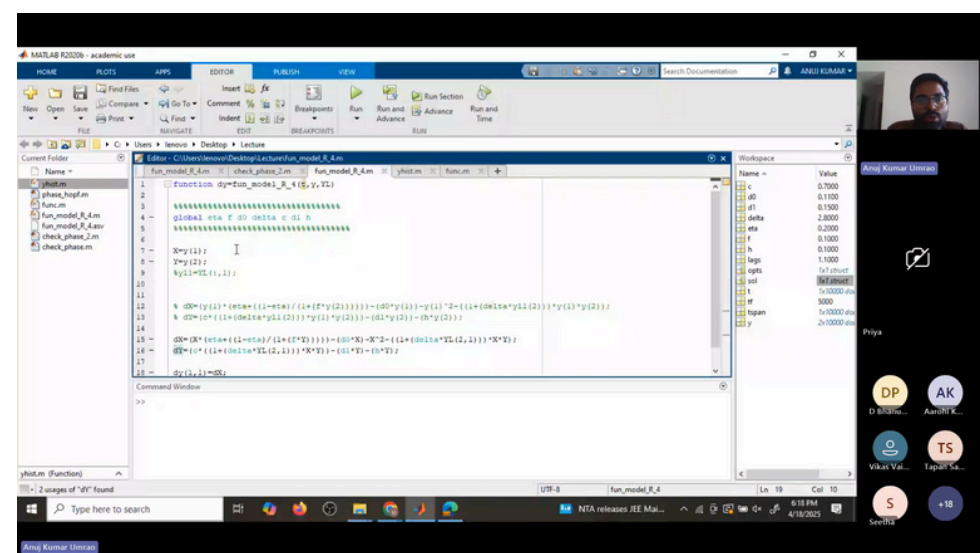
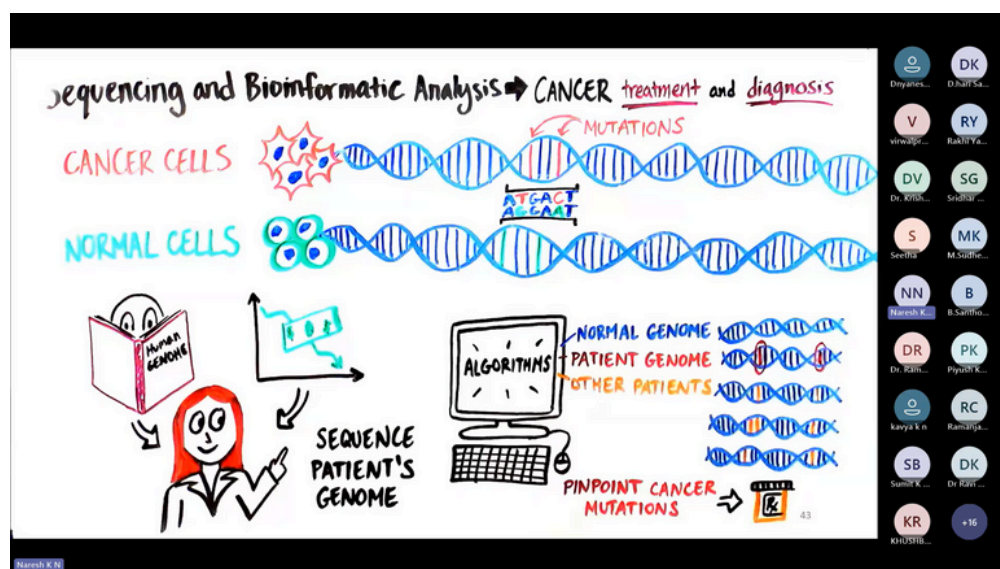
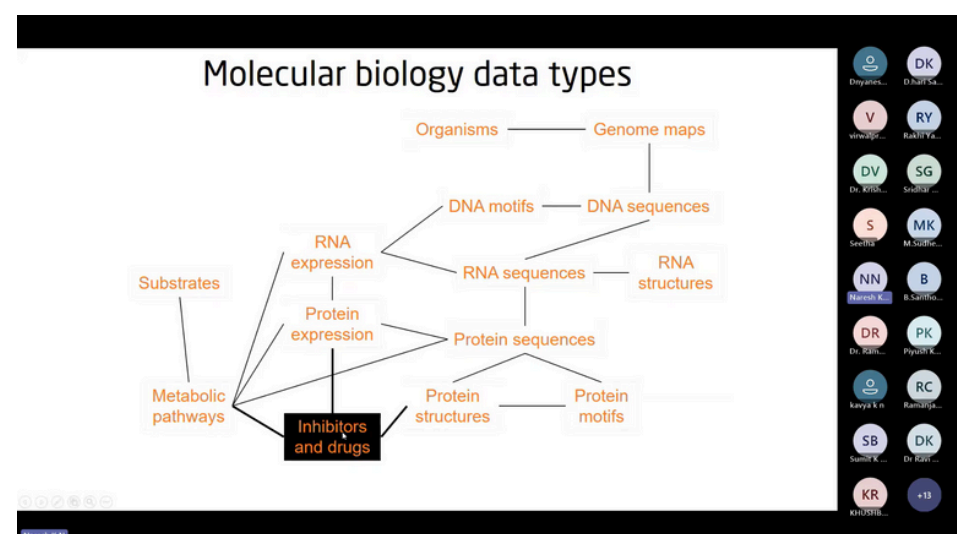
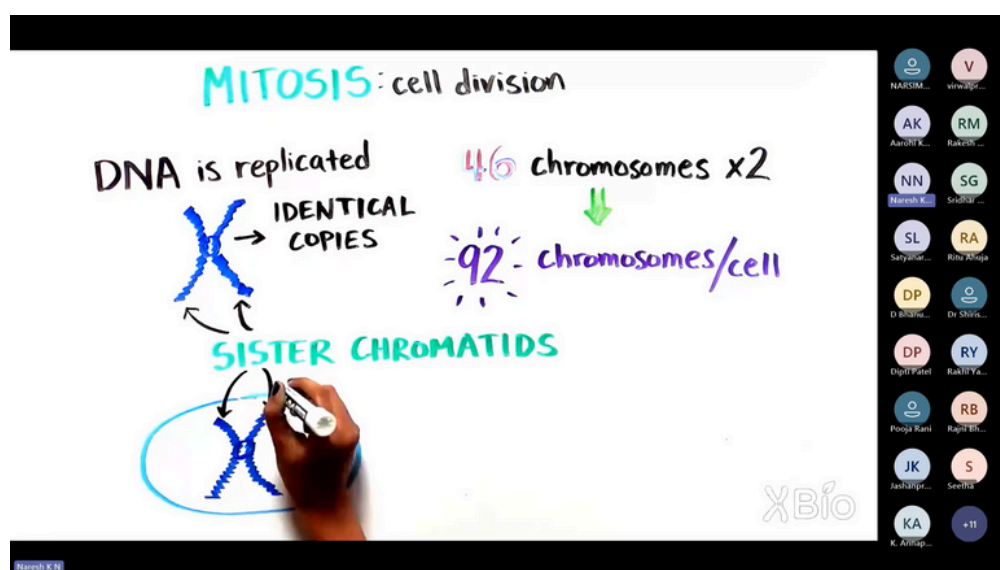
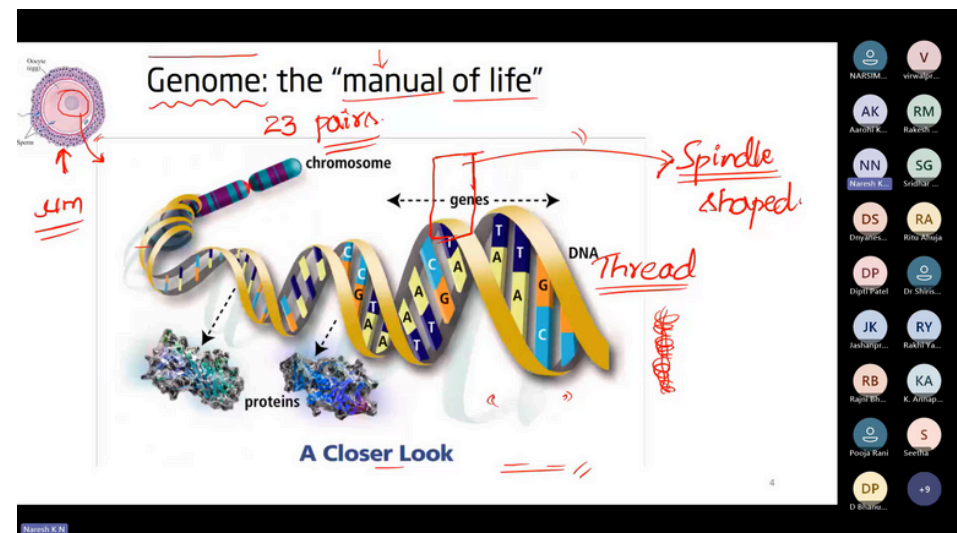
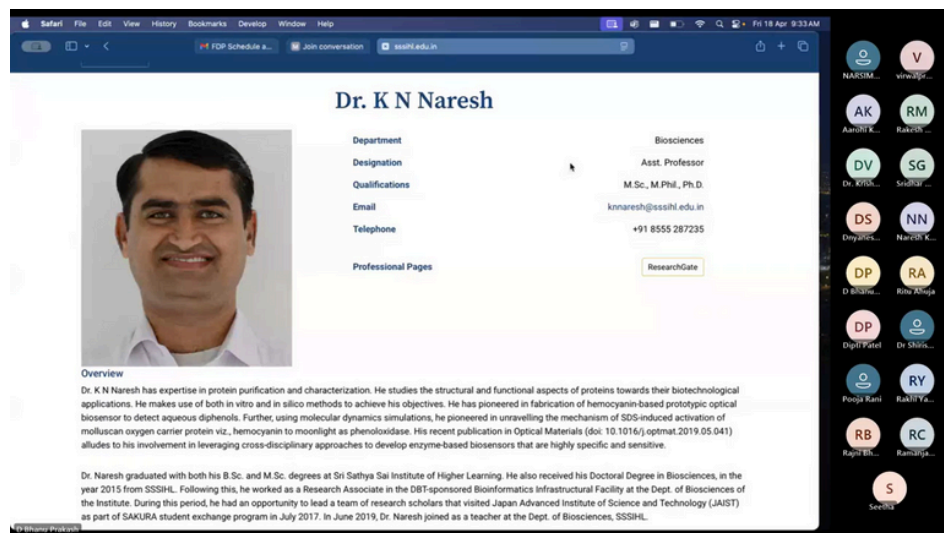
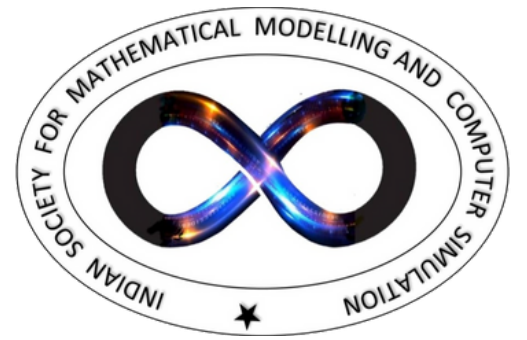
In this hands-on session, Dr. Anuj Kumar Umrao guided participants through the numerical solution and simulation of delay differential equations (DDEs), particularly within ecological models such as predator-prey systems. Using MATLAB, he demonstrated how to define DDEs involving time delays, implement global variables, and use MATLAB's built-in dde23 solver for solving systems with constant delays. The tutorial walked through plotting time series, phase portraits, and performing one-parameter bifurcation analysis by varying delay values. The core example discussed involved a two-species predator-prey model with cooperation and harvesting, where delays influenced both prey and predator populations. Dr. Umrao showed how small changes in delay parameters could shift the system from stable equilibria to oscillatory behaviors, thus emphasizing the impact of delays on system stability. He detailed the process of defining the function file, using delay variables, setting up simulations with linspace, and extracting solution values using deval for visualization. The session concluded with coding strategies for plotting bifurcation diagrams, showing how long-term dynamics (e.g., maxima and minima) evolve with increasing delay. Dr. Umrao also addressed participant questions on code structure, optimization, and suggested key textbooks for further study on DDEs.

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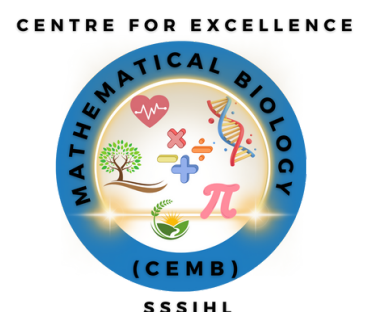




Faculty Development Program (FDP) on Advances in Mathematical Modeling Techniques, AI/ML and Bioinformatics

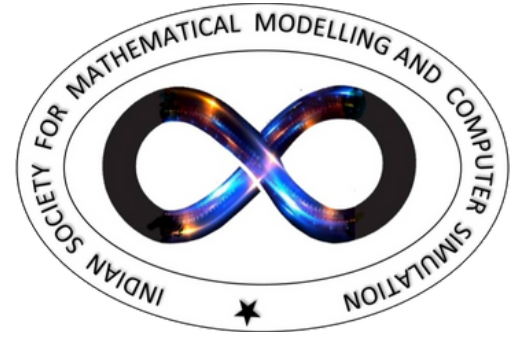


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Faculty Development Program (FDP) on Advances in Mathematical Modeling Techniques, AI/ML and Bioinformatics



Day 8: April 19, 2025 (Morning Session)

Speaker : Dr. Satyanarayana Labani, Vice President for Biostatistics Consortium of India

First Session

Dr. Satyanarayana Labani's session focused on the epidemiology of cervical cancer, the role of screening programs, and the application of biostatistics in public health research. He began by emphasizing the global burden of cervical cancer, particularly in low- and middle-income countries, and stressed that early detection and prevention through screening can drastically reduce mortality. Dr. Labani explained key epidemiological terms like incidence, prevalence, sensitivity, specificity, and predictive values used to evaluate the effectiveness of screening methods. The session delved into HPV infection as the primary cause of cervical cancer and described tools such as the Pap smear test, HPV DNA testing, and colposcopy for early detection. He highlighted the natural history of disease progression, underlining the importance of identifying pre-cancerous lesions before they develop into malignancy. Dr. Labani also discussed biostatistical methods for analyzing screening data, including the use of Kaplan-Meier survival analysis and Cox proportional hazards models. Throughout, he emphasized the importance of study design, sample size estimation, error types, and P-values, encouraging health researchers to apply robust statistical tools in cancer control programs. The session concluded with insights on integrating epidemiology, screening, and biostatistics for effective cancer prevention strategies.

Second session

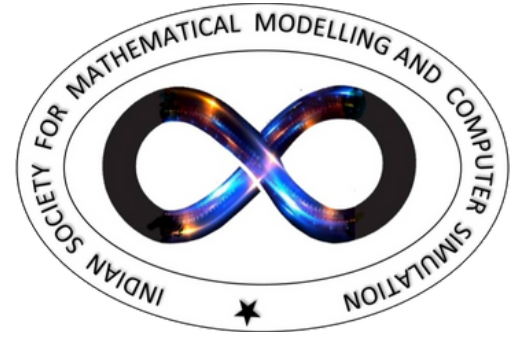
The session, led by Dr. Satyanarayana Labani, provided an in-depth exploration of screening and diagnostic tests for cervical cancer, focusing on evaluating test accuracy through metrics like sensitivity, specificity, positive predictive value, and negative predictive value. He emphasized the importance of using a gold standard (e.g., biopsy) for validation and discussed the interpretation of errors such as false positives and false negatives in medical testing. The session also covered ROC curves for selecting optimal cutoff points and comparing multiple tests, supported by real-world community studies involving HPV, Pap, and VIA tests. Dr. Labani additionally touched on the application of various statistical and mathematical models—including deterministic, stochastic, agent-based, survival analysis, and spatial models—to improve understanding and cost-effectiveness of screening strategies. He shared insights from his collaborative Indo-US projects and advocated for the integration of advanced modeling in public health research.

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Faculty Development Program (FDP) on Advances in Mathematical Modeling Techniques, AI/ML and Bioinformatics



Day 8 : April 19, 2025 (Evening Session)

Speaker : Dr. Satyanarayana Labani, Vice President for Biostatistics Consortium of India
First Session

In this hands-on FDP session, Dr. Satyanarayana Labani guided participants through practical data analysis using the JAMOV statistical software. The session focused on how to import data from Excel, code and label variables, and perform basic descriptive statistics, such as computing means, standard deviations, and generating frequency tables for categorical data. Participants learned to create and interpret scatter plots, understand and calculate correlation coefficients, and conduct regression analysis to examine relationships between variables like BMI and birth weight. The session also covered group comparisons using t-tests and ANOVA, and the structuring of data for such analyses (e.g., combining measurements and identifiers in a single column format). Dr. Labani demonstrated how to copy results to Word documents, customize outputs, and emphasized the ease and flexibility of using JAMOV, especially as a free alternative to SPSS for quantitative research.

Second Session

In this FDP session, Dr. Satyanarayana Labani delivered a practical demonstration on using JAMOV for statistical analysis. He began by revisiting independent sample t-tests, emphasizing the importance of checking normality and homogeneity of variances before choosing between parametric (t-test) or non-parametric (Mann-Whitney U) tests. He then demonstrated ANOVA for comparing three groups, showing how to interpret post-hoc tests like Tukey's to identify specific group differences. The session also covered reliability analysis using Cronbach's alpha to assess internal consistency of survey instruments, followed by factor analysis—both confirmatory and exploratory—to evaluate data constructs and validity. Dr. Labani explained the use of QQ plots, factor loadings, and percentage variance explained, and concluded by guiding participants to JAMOV's manual, book, and YouTube resources for further learning. The session reinforced JAMOV as a free, effective alternative to proprietary software for epidemiological and social science research.

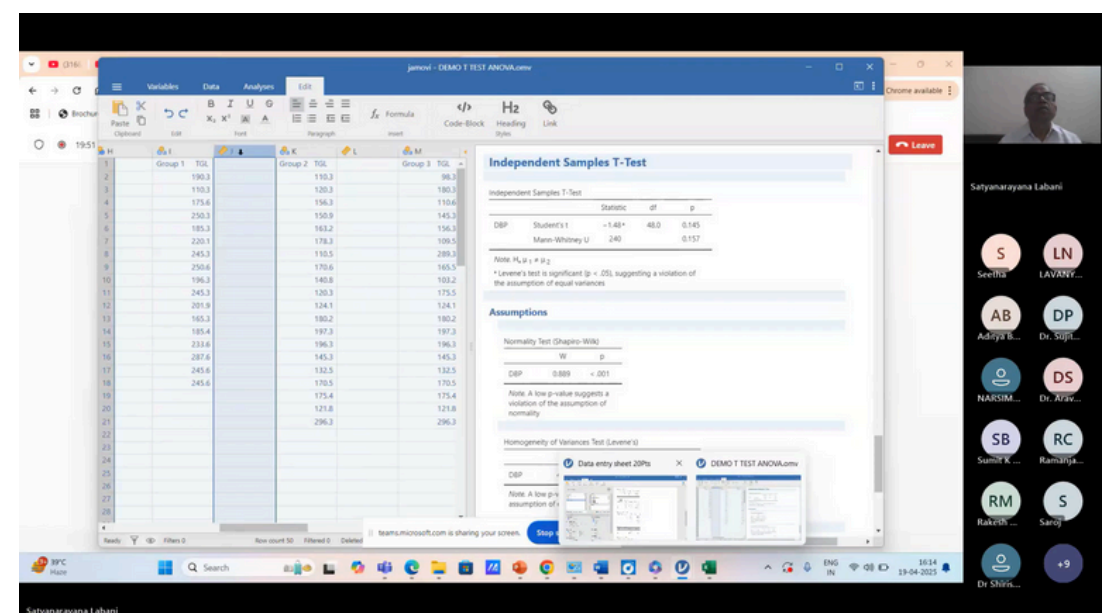
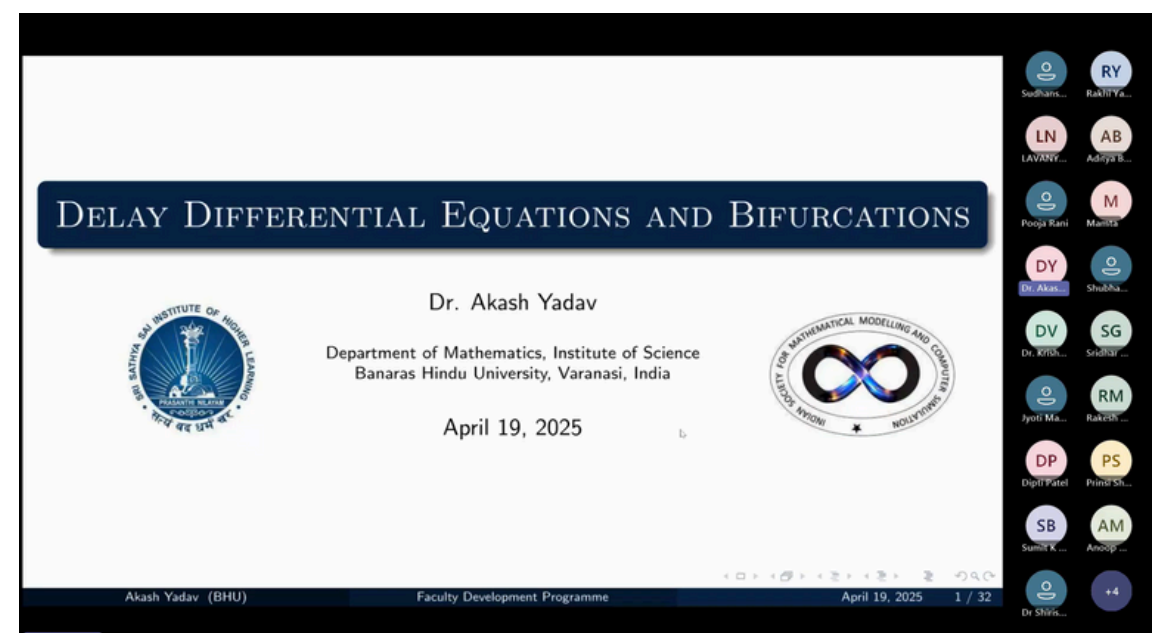
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In the final FDP session, Dr. Akash Yadav, Senior Research Fellow at BHU, delivered a technical lecture on delay differential equations (DDEs) and their application in modeling insecticide effects on crop production. He introduced a mathematical model involving immature and mature insect populations, a vegetable crop, and external efforts like irrigation. Using MATLAB, he demonstrated how to implement DDEs to simulate population dynamics, emphasizing the role of maturation delay (τ) and one-time insecticide application. The session covered key modeling concepts like equilibrium analysis, time series plots, phase portraits, and bifurcation diagrams to study system behavior under varying parameters. Dr. Yadav showcased modular MATLAB coding practices, including splitting the function and run files, and explained how to extract maximum and minimum values from simulations to generate equilibrium curves. The interactive session concluded with clarification on code structure, plotting syntax, and best practices for analyzing nonlinear biological systems using delay-based models.

S_No	Women_name	Age	Women_ID	Education	Marital_Sta	Religion	Menstr_His	Clinical_Sig	VA_Result	VLU_Result	Cyto_result
1	Savitri	35	13-001	1	2	1	1	1	2	1	2
2	Ramkati	35	13-002	1	2	1	3	2	2	2	2
3	Shanti	35	13-003	2	2	1	2	3	2	2	2
4	Nirmala	35	13-004	1	2	1	1	4	2	2	2
5	Bedwati	35	13-005	2	2	1	3	2	1	1	2
6	Rakha	35	13-006	1	2	1	1	1	2	2	1
7	Sudesh	42	13-007	1	2	1	2	3	2	2	2
8	Rajesh	40	13-008	1	2	1	2	2	2	2	2
9	Shashi	50	13-009	1	2	1	3	2	1	1	1
10	Roshni	30	13-010	1	2	1	2	1	2	2	2
11	Jaibun Nisha	40	13-011	3	3	2	2	1	2	2	2
12	Nimlesh	30	13-012	1	2	1	1	1	2	2	2
13	Bali	45	13-013	1	2	1	2	2	2	2	2
14	Poojpa	50	13-014	3	2	1	3	3	2	2	1
15	Rambati	50	13-015	1	3	1	3	2	2	2	2
16	Vidya	55	13-016	2	2	1	3	2	2	2	2
17	Santa	30	13-017	4	2	1	1	1	2	2	2
18	Kamlesh	49	13-018	4	2	1	2	1	1	1	1
19	Perveen	40	13-019	1	2	2	1	2	2	2	2
20	Saroj	45	13-020	1	2	1	2	3	2	2	2

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Faculty Development Program (FDP) on Advances in Mathematical Modeling Techniques, AI/ML and Bioinformatics

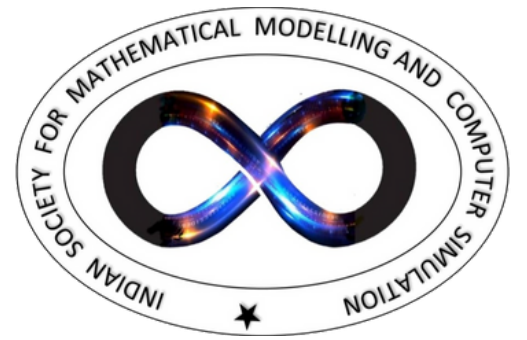
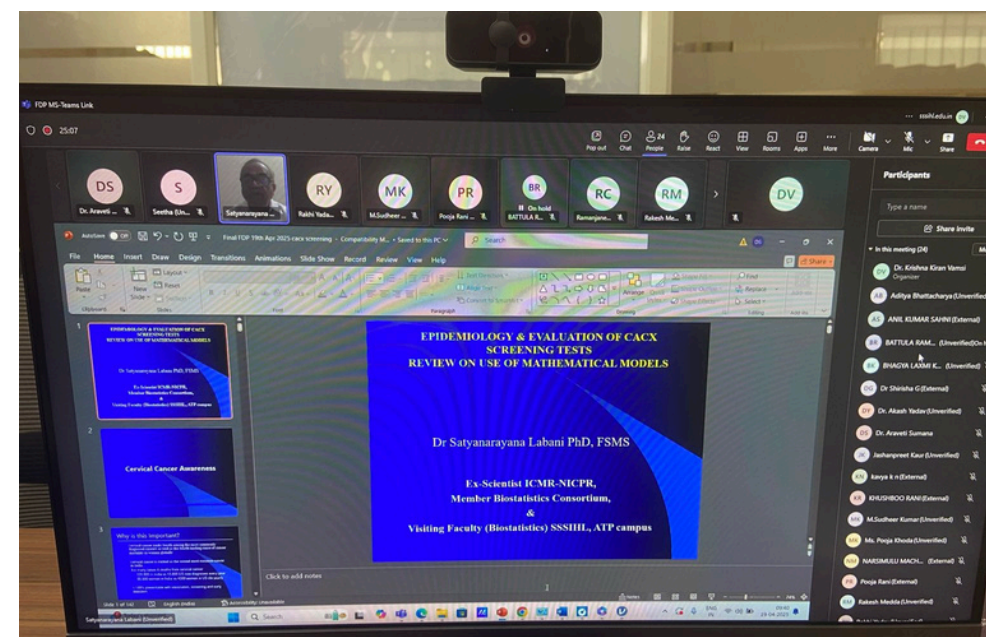
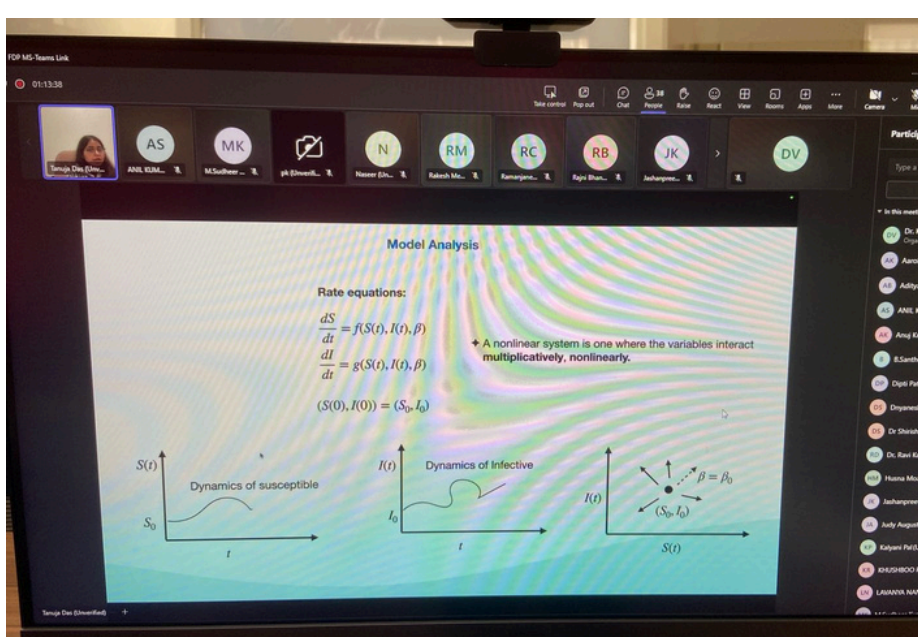
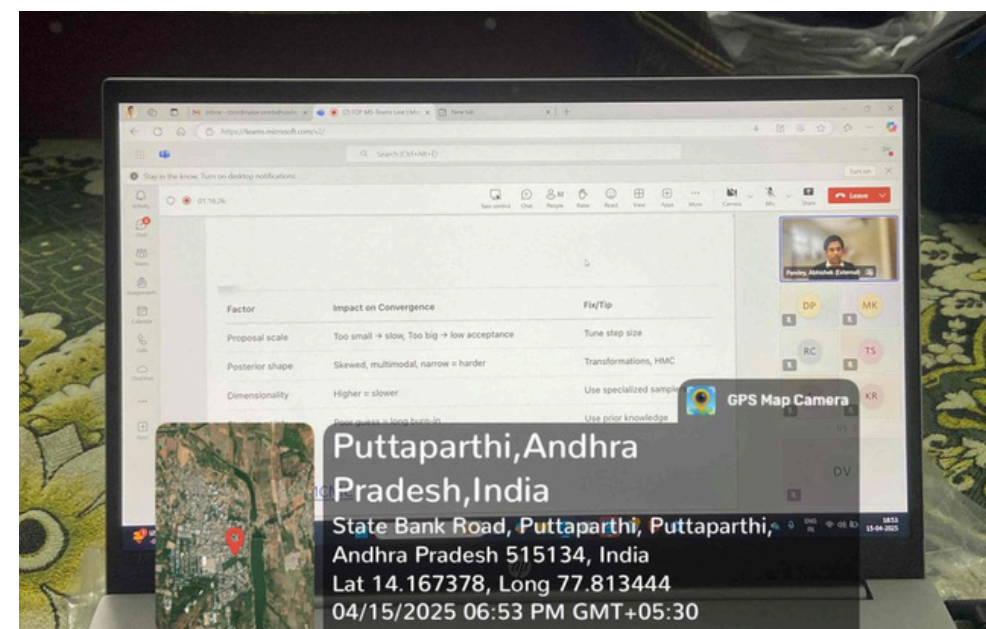
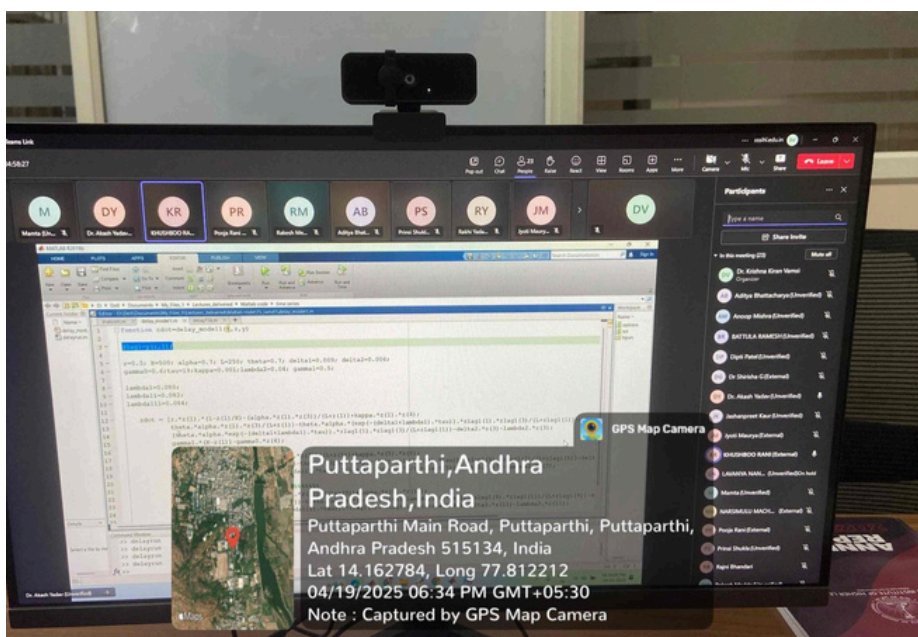
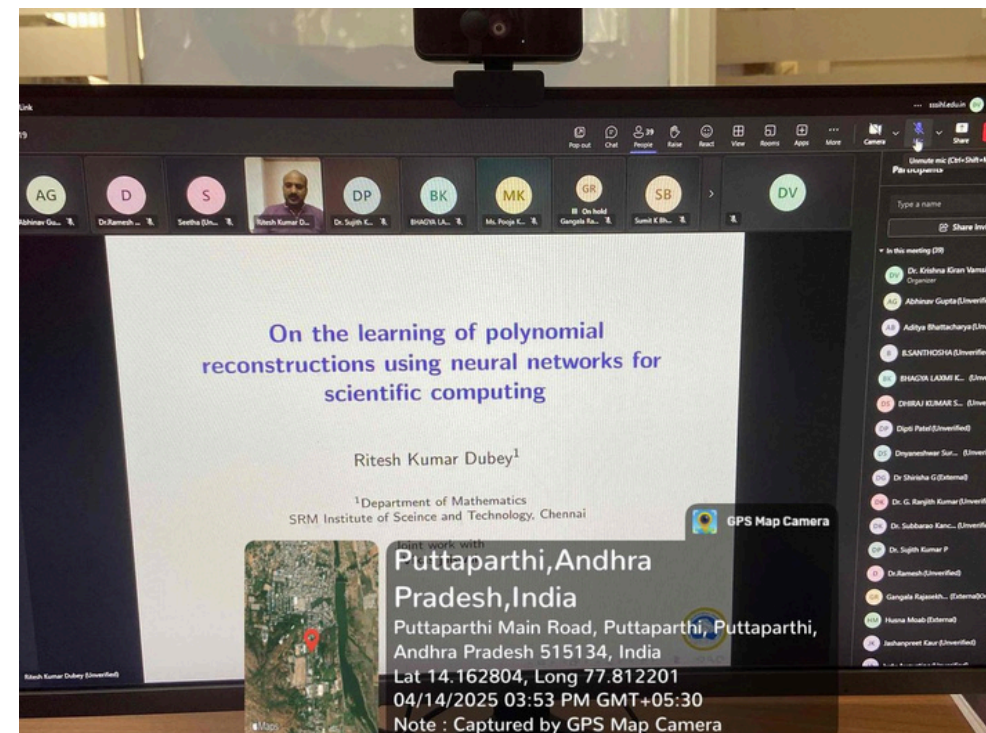


PHOTO GALLERY

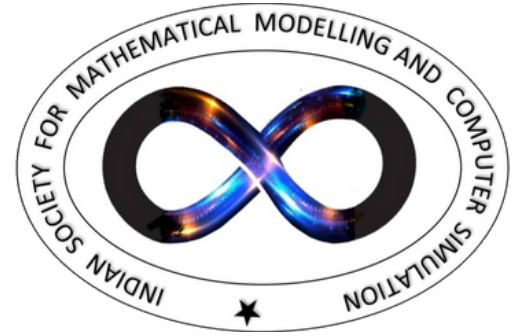


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Faculty Development Program (FDP) on Advances in Mathematical Modeling Techniques, AI/ML and Bioinformatics



FDP DETAILS

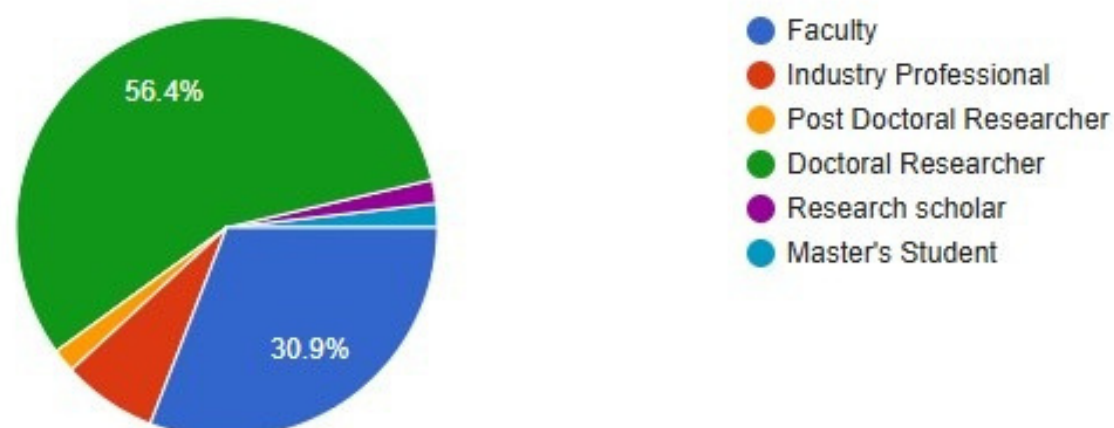
Participants Profiles for the FDP

Number of Participants - 72 (17 from SSSIHL and 55 from other Institutions spread across India)

The participants for the FDP included faculty, industry professionals, post-doctoral & doctoral research scholars, post graduate and graduate students who were spread across different parts of India.

Applicants Occupation

55 responses



Applicants Occupation

17 responses



[Click here for
the Flyer of FDP](#)

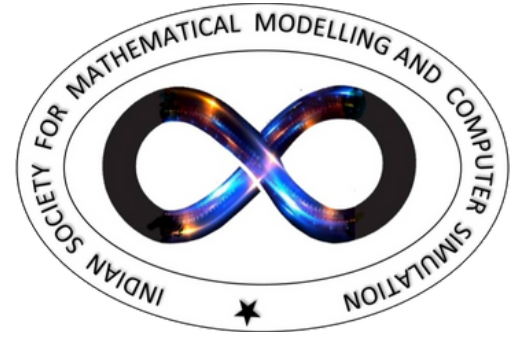
[Click here for the
Detailed Schedule of FDP](#)

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Faculty Development Program (FDP) on Advances in Mathematical Modeling Techniques, AI/ML and Bioinformatics



Feedback from Participants on FDP

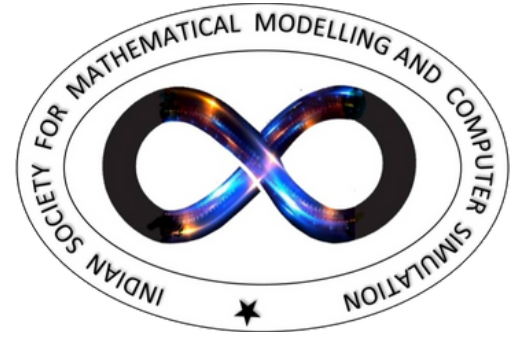
- Firstly, I would like to thank the coordinators for organizing such a insightful FDP. The information and knowledge shared by distinguished resource persons during the FDP and the hands on sessions provides valuable in sights to research direction and helps to enhance the basic knowledge of the delay differential equations, optimal control, parameter estimation, stochastic and many more. Looking forward for more such kinds of workshops.
- The FDP was extremely well-organized, intellectually stimulating, and highly relevant to current research trends in mathematical biology and control theory. The invited speakers were clearly experts in their domains, and they presented complex topics in a comprehensible manner, making it accessible for participants from diverse backgrounds. The sessions ran smoothly without technical glitches. Communication regarding schedule and materials was clear and timely. Thank you to the organizing teams at CEMB-SSSIHL and ISMMACS for putting together such a valuable program.
- The Faculty Development Program was highly informative and well-organized. The sessions were engaging, and the professors provided practical insights that were easy to understand. The interactive discussions were particularly helpful in applying the concepts to real-life scenarios. Such programs are valuable for professional growth, and I look forward to attending future sessions.
- The FDP is conducted smoothly and punctually. The theme chosen for FDP was excellent. The presentations by all the speakers were excellent and really helped to improve our knowledge. Thanks to the organising committee for giving such platform and all the best.
- The sessions delivered by subject experts were insightful and offered a fine balance between theoretical concepts and practical applications. The inclusion of interdisciplinary topics helped broaden our perspectives, particularly in understanding how AI/ML tools can be integrated with mathematical modeling and biological data analysis.
- Very thankful to the team for organising this FDP. The content, the speakers and the overall management of the FDP was complementing and refined my knowledge further. Particularly, I really liked that video recordings of the session were available so if somehow I could not attend the live session, I could see the video and learn. Thanks again to the team.
- First of all, I want to give heartfelt thanks to the organizer for conducting such a nice, smooth program. Here, I have learned a lot about modeling, programming for their simulation, and some bioinformatics ideas. I believe this insightful knowledge shared by the honoured speakers would be of great benefit to my future research growth and career advancement. Hopefully, we will meet again at some other FDP where I get a chance to learn from such speakers.
- I attended the Online Faculty Development Program (FDP) held from April 12th to 19th, 2025, by CEMB-SSSIHL & ISMMACS on 'Advances in Mathematical Modeling Techniques, AI/ML & Bioinformatics.' The program was highly interactive and enriching, particularly in the context of epidemiology. I gained valuable insights into optimal control, simulation techniques, and the application of AI/ML in this field. Overall, the conference was extremely beneficial, and I would like to extend my gratitude for such an informative and well-organized event.
- It was excellent to learn all the concepts from basics which was very helpful for someone like me who is just getting started with mathematical modeling and control studies. Thank you for all the excellent sessions.

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Faculty Development Program (FDP) on Advances in Mathematical Modeling Techniques, AI/ML and Bioinformatics



Feedback from Participants on FDP

- The Faculty Development Programme on mathematical modeling and use of AI was a resounding success, thanks to the organizers efforts in bringing together experts in the field. It was a privilege to learn from them and gain valuable insights. We're truly grateful for the opportunity.
- I would like to express my sincere gratitude for organizing this Faculty Development Program. It was a truly enriching and insightful experience. The sessions were well-structured, informative, and highly relevant to current academic and professional practices. I gained valuable knowledge and practical strategies that I can apply in my teaching and research.
- The FDP sessions were extremely informative and engaging, offering valuable insights into the latest advancements in mathematical modeling, AI/ML, and bioinformatics. The content was well-structured and the sessions were highly beneficial, providing practical knowledge that will help in both academic and professional growth.
- This FDP that was part of the Sri Sathya Sai Centenary Celebrations provided a great opportunity to examine interdisciplinary overlaps across mathematics, artificial intelligence, epidemiology, and bioinformatics. The combination of both theory, applications, and practical work provided a holistic overview. The sessions were carefully programmed, and the speakers offered both conceptual clarity and a reality perspective. Not only has it broadened our technical repertoire, but we have also gained a fresh research perspective.
- I am in my first year of Ph.D., and I literally prayed to Swami for guidance in carrying out my research work. This FDP feels like a great gift from Swami. While I understood some of the theory, I was eager to learn more about programming, particularly in real data fitting, parameter estimation, Delay Differential Equations (DDE), and bifurcation analysis. As a beginner, the hands-on sessions on parameter estimation and statistical analysis were highly insightful. The availability of materials and recordings is extremely helpful for a deeper understanding. My heartfelt gratitude goes to Swami, all the respected professors, and the coordinator for organizing this FDP and enlightening us. I am eagerly awaiting the live sessions in the future. Thank you. Jai Sairam!
- Although I missed a few sessions due to my non-mathematical background, the sessions I did attend were excellent. The resource person often made a commendable effort to help those without a mathematics background understand the content. Overall, a great experience. Thanks a lot. Sairam
- This FDP has been extremely helpful in expanding my knowledge in mathematical biology, ML, AI and other aspects of mathematical modelling. This FDP offered incredible sessions and hands on session from experts of all over the world. It was a wonderful experience of learning. Thank you for giving me the opportunity to attend this FDP.
- The Online Faculty Development Program (FDP) titled "Advances in Mathematical Modeling Techniques, AI/ML & Bioinformatics" offered a unique and interdisciplinary blend of mathematics, disease biology, and artificial intelligence. With expert insights from diverse domains, the program proved to be both enriching and rewarding for all participants. I extend my sincere thanks to the organizers for their commendable efforts in making the event a success.
- First, I would like to extend my sincere appreciation to the organizing committee for conducting such an engaging and insightful sessions. The sessions were well-structured and balanced theoretical concepts with hands-on activities. I would highly recommend similar type of FDPs to anyone interested in Mathematical Modeling.
- FDP program was very insightful for me. Program coordination is commendable. There is a vast variety of speakers from different fields in mathematical biology. Highlight of the FDP program is the hands-on session, which is extremely useful for everyone. Thanks to SSIHL and ISMMACS for providing us such a academic treat to us.

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