

Department of Biotechnology, IIT Madras

MS (by Research) admissions July 2022

List of Stream-wise Project titles, Faculty names and vacancies

1) CB- Computational Biology Stream

Si. No.	Faculty Name	Project title(s), Number of vacancies
1	Karthik Raman	<p>1. Machine learning approaches to design biological circuits (1 student) With the advent of synthetic biology, which involves the de novo design of biological networks, a common question that arises is as to how one designs a biological network that performs a specific function. For example, how does one design a circadian oscillator? Or, how does one design a (tuneable) switch? Also, are there any clear design principles underlying the construction of these systems? Current approaches to designing such systems are based on trial and error, or brute force explorations of the design space. We have also developed systems-theoretic approaches to design such networks. In this project, the idea is to use machine learning, alongside ODE modelling, to identify circuits capable of performing specific biological functionalities. Candidates wishing to work on this project are expected to have either a strong background in ML, or in computational methods and programming.</p> <p>2. Identifying correlated mutations from cancer genomic data (1 student) Cancer is essentially a disease of the genome. While many studies have identified single mutations (driver mutations) that 'cause' cancer, there are only a few approaches that can identify correlated mutations, which have a similar role in cancer progression. Through this project, we will use a combination of machine learning and statistical approaches to identify combinations of mutations. Candidates wishing to work on this project are expected to have a strong background in ML/statistics.</p>
2	V S Chakravarthy	Modeling the basal ganglia to understand Parkinson's disease (1 student)
3	Madhulika Dixit	Computational integration and analysis of multi-omics data for better understanding of vascular diseases (1 student)
4	Sanjib senapati	Structure-based designing of a novel class of HIV Protease drugs effective against both apo and mutant variants: A comprehensive study using Molecular Dynamics (MD) Simulations and In-vitro studies (1 student)
5	M. Hamsa Priya	Machine Learning aided modelling of viral capsids (1 student)
6	Michael Gromiha	Sequence and structural studies on protein aggregation (1 student)
7	Nirav Bhatt	Integrated Modeling and Control of Biological Disease Networks using Omics, Literature Data, and clinical Data: The objective of this project is to develop integrated (regulator-signalling-metabolic) biological networks using omics and literature data. The integrated models will be used for developing optimal therapeutic strategies using networked control approaches (Theory/Computational) (1 student)
8	N Manoj	Molecular evolution of G-protein coupled receptors (1 student)
9	Vani	Understanding molecular mechanisms of bacterial interactions (1 student)
11	Himanshu Sinha	Modelling GARBH-Ini cohort data for preterm risk prediction: (1 student) Predicting preterm birth risk has been a tough challenge due to the ambiguity and heterogeneity of the disease and the complexity of the relationship between the predictors. Using data from the GARBH-Ini cohort, consisting of more than 10 million data points collected from 8000+ pregnant women participants, we want to develop a dynamic preterm birth risk prediction model that helps stratify women early enough for clinical interventions to delay preterm birth to as close to normal term.

		<p>Application of multivariate and machine learning approaches for biomarker discovery from Influenza vaccine trial (INCENTIVE) cohort data: The INCENTIVE consortium is a partnership between Indian and European/US groups to address the global health and the economic challenge posed by influenza. INCENTIVE's strategic goals are to provide seminal knowledge on the underlying mechanisms of poor responsiveness to influenza vaccines in vulnerable individuals and advance the development of next-generation universal influenza vaccines. We plan to develop computational methods to perform integrated analysis of immune response, conventional and systems serology, T, and B and immune cell analyses, and metadata generated including transcriptome, proteome, and metabolome generated from influenza vaccine candidates trials in different populations in India.</p>
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2) **BS- Biological Sciences Stream**

Si.No	Faculty Name	Project title(s), Number of vacancies
1	Madhulika Dixit	CRISPR-Cas9 based engineering of vascular cells (1 student)
2	Sanjib senapati	Stabilizing DNA and RNA at Room Temperature using a new class of green solvents (1 student)
3	S. Mahalingam	RAS effector RASS7 mediated inflammasome on autophagy regulation in cancer (1 student)
4	Nitish Mahapatra	Molecular genetics of chronic kidney disease in Indian population (1 student)
5	Himanshu Sinha	<p>Role of yeast ribosomal protein variants in phenotypic adaptation and evolution (1 student)</p> <p>Ribosomal proteins are among the most conserved proteins across eukaryotes, and ribosomes are considered invariant in structure and function. However, recent evidence shows that ribosomal proteins are structurally variable and have a phenotypic function beyond translation. We have identified several yeast ribosomal protein-coding variants, which we are testing for their novel role in adaptation to diverse environments. The outcome of this project will be to uncover the role of universal and essential cell machinery, ribosome, in regulating phenotypic variation in genetically variable populations in response to changing environments – providing evidence for the concept of “specialized ribosome”, which proposes that across organisms, variable ribosome exist to differentially regulate translation, modifying phenotypic outcomes.</p>

3) **BE- Biological Engineering Stream**

Si.No	Faculty Name	Project title(s), Number of vacancies
1	Guhan Jayaraman	Bioprocess Monitoring and Control using in-situ NIR Spectroscopy. (1 student)
2	Karthik Raman	Machine learning approaches to design biological circuits (1 student) With the advent of synthetic biology, which involves the de novo design of biological networks, a common question that arises is as to how one designs a biological network that performs a specific function. For example, how does one design a circadian oscillator? Or, how does one design a (tunable) switch? Also, are there any clear design principles underlying the construction of these systems? Current approaches to designing such systems are based on trial and error, or brute force explorations of the design space. We have also developed systems-theoretic approaches to design such networks. In this project, the idea is to use machine learning, alongside ODE modelling, to identify circuits capable of performing specific biological functionalities. Candidates wishing to work on this project are expected to have either a strong background in ML, or in computational methods and programming.
3	Madhulika Dixit	CRISPR-Cas9 based engineering of vascular cells. (1 student)
4	Smita Srivastava	To study the effect of fungal endophytes on growth and secondary metabolism of the host plant <i>Nothapodytes nimmoniana</i> . (1 student)
5	M. Hamsa Priya	Analyzing protein-solvent network and its implication on protein structure (1 student)
6	Nirav Bhatt	1: On-site Food Authentication using Handheld NIR spectroscopy and Design of Experiments (1 student) 2: Model Predictive Control of Bioprocesses using Low-cost and UV-Vis Spectroscopy (1 student)