CENTRE FOR INTEGRATIVE BIOLOGY AND SYSTEMS MEDICINE

IBSE NEWSLETTER

YEAR 2021–2022

https://ibse.iitm.ac.in

OBJECTIVES

The Centre for Integrative Biology and Systems mEdicine (IBSE) will establish state-of-the-art research cores and will continue to work to maintain, improve, and promote the interactions, collaborations, and Internationalisation by expanding current partnerships through increased faculty mobility into and out of IBSE. As an interdisciplinary group dedicated to pioneering innovative approaches and algorithms that integrate multi-dimensional data across scales to understand, predict and manipulate complex biological system, IBSE will conduct data-driven disease and clinical research

RESEARCH IMPACT

IBSE conducted some cutting-edge research work which was published in reputed international journals. The research can be broadly classified into the development of a computational tool for bio-production, computational tools for cancer research, computational tools for basic research, anti-cancer treatment studies and design principles for adaptation. Here is a summary of the research work.

KEY RESEARCH AREAS

- Development of algorithms using machine learning, data and graph mining to study clinical data to understand and predict clinical outcomes and generate disease risk models
- Biological network analysis, which includes the prediction of molecular function in cells and populations, and environmental and evolution-dependent modulation of networks

IBSE FACULTY

HIMANSHU SINHA, Biotechnology

KARTHIK RAMAN, Biotechnology

NIRAV BHATT, Biotechnology

RAVINDRAN BALARAMAN, Computer Science

MANIKANDAN NARAYANAN, Computer Science

RAGHUNATHAN RENGASWAMY, Chemical Engineering

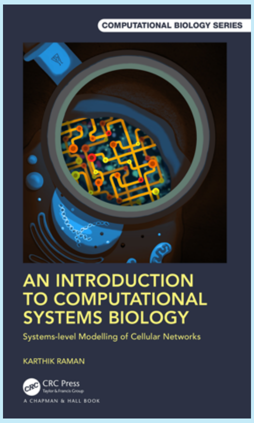
RESEARCH HIGHLIGHTS

COMPUTATIONAL TOOLS TO OPTIMIZE BIO-PRODUCTION

Manufacturing of chemicals and products via microbial means is considered a more sustainable and eco-friendly way of production than chemical means. With a vision to make bio-production more economical and feasible, IBSE researchers worked to develop computational tools that can help increase the efficiency of bio-production.

co-FSEOF (co-production using Flux Scanning based on Enforced Objective Flux)
Manufacturing of chemicals and products via microbial means is considered a more sustainable and eco-friendly way of production than chemical means. With a vision to make bio-production more economical and feasible, IBSE researchers worked to develop computational tools that can help increase the efficiency of bio-production (https://doi.org/10.3389/fbioe.2021.779405)

CAMP (Co-culture/Community Analyses for Metabolite Production)
CAMP is a bacterial matchmaking tool that suggests how to bundle two or more bacteria together such that the community produces the desired products in the maximum quantity. The tool works by using the information of various protein interaction taking place in bacteria that leads to the production of various metabolites. The tool was tested by identifying the best species pair for the production of commercially important metabolite – lactate.
Apart from publishing their research work, IBSE researchers also published a comprehensive review entitled “*Modelling microbial communities: Harnessing consortia for biotechnological applications*”. The review talks about the use of microbial communities for biotechnological applications and the major challenges in the way. It discusses the latest approaches, models and tools which are being employed to understand the interactions between the microbes and how it governs bio-production. (https://doi.org/10.1101/2020.10.24.353805)



BOOK OF THE MONTH

How can we model complex biological systems at various levels

How can we understand, model and simulate massive biological networks

A comprehensive and insightful account of applying mathematical modelling approaches to very large biological systems and networks

COMPUTATIONAL TOOLS FOR CANCER RESEARCH

Understanding the factors and mechanisms responsible for cancer progression remains an important area of research. Towards this, IBSE has developed model/tools/methods to predict driver genes (genes in which the mutations have been linked to the progression of cancer) and driver mutations.

cTaG model
cTAG model uses a ratio-metric approach for identifying driver genes where both the repeated occurrence of mutations and the functional impact of the mutations are taken into consideration to categorize a gene as a driver gene. The USP of the model is that it overcomes two major challenges of low recall and bias toward genes with high mutation rate while predicting new driver genes. (https://doi.org/10.1038/s41598-021-04015-y)

NBDriver for predicting Driver mutations
Distinguishing a driver mutation responsible for cancer progression from a neutral passenger mutation remains a challenge. IBSE has developed a cancer mutation effect prediction tool named NBDriver. The tool is based on neighbourhoods features of driver and passenger genes extracted from the experimentally validated cancer mutation data. Using this tool, the researchers have identified 138 known driver genes. (https://doi.org/10.3390/cancers13102366)

COMPUTATIONAL TOOLS FOR BASIC RESEARCH

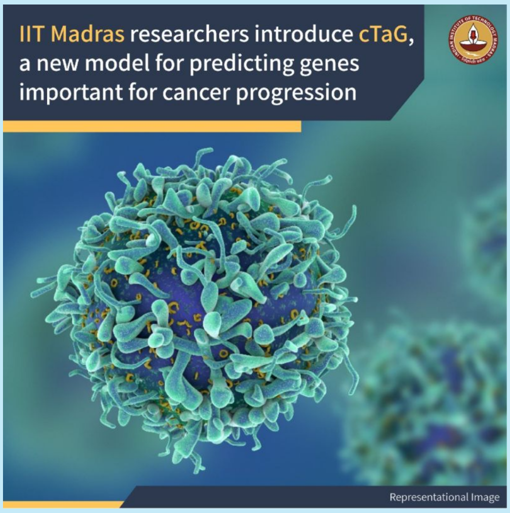
BioEmbedS and BioEmbedS-TS Model
Knowledge about inter-tissue communication taking place in the body is central to understanding the human body completely. One of the most important interactions that govern inter-tissue communication is gene-hormone interaction but our knowledge in this area is sparse. IBSE researchers have developed two models to fill this gap: BioEmbedS and BioEmbedS-TS. BioEmbedS model predicts whether a gene and a hormone pair are associated or not whereas BioEmbedS-TS, whether a gene is involved in the production of the hormone or, is responding to the presence of a hormone. (https://doi.org/10.1101/2021.01.28.428707)

NetGenes database
Essential genes are the ones which are indispensable for the growth and reproduction of an organism. Netgenes is a database collection of around 2.1 million essential genes predicted from 2700+ bacteria. The essential genes present in this database were predicted using features derived from STRING protein-protein functional association networks. (https://doi.org/10.3389/fgene.2021.722198)

Gut microbes and anti-cancer treatment
Certain gut microbes such as Enterococcus spp. are known to have anticancer potential and therefore it is essential to study the effect of anti-cancer treatments on such microbes. IBSE studied the effect of silver nanoparticles that are promising candidates for cancer treatment on the Enterococcus spp and found that the silver nanoparticles treated Enterococcus cells were successful in decreasing the viability of colorectal cancer cells. The study also observed the production of folate in Enterococcus cells treated with silver nanoparticles. While the previous studies show that folate helps in the progression of colorectal cancer cells, this new study by IBSE researchers signals that folate may instead help in killing colorectal cancer cells. (https://doi.org/10.1038/s41540-021-00210-9)

Synthetic biology
All living systems work via a large network of biological entities. Although there is a seamless integration of these biological entities, a biological system is not entirely perturbed due to a change in the behaviour of a single entity. This study sought to determine the principles underlying how biological systems

adapt to fluctuations and come back to their original state. The study used a systems-theoretic approach to deduce mathematical principles obeyed by the system for adaptation. This work was published in PLoS Computational Biology, one of the top journals in systems/synthetic biology. A review was also published in another leading journal, ACS Synthetic Biology, on Designing Biological Circuits: From Principles to Applications. (https://doi.org/10.1371/journal.pcbi.1009769)



RBC DSAI

3RD IBSE INTERNATIONAL SYMPOSIUM

CLINICAL GENOMICS TO SYSTEMS MEDICINE: Computational Approaches for Transforming Healthcare (VIRTUAL)

1 - 4 February 2022

We bring biomedical scientists, computational biologists, and data scientists to present and discuss the latest developments in various omics technologies transforming clinical and translational research. A key focus will be novel techniques, methods and algorithms to dissect omics data at multiple levels, enabling a deeper understanding of complex human diseases.

SPEAKERS

Anshul Kundaje
Stanford University, US

Giriraj Chandak
CCMB Hyderabad, IN

Irene Papatheodorou
EMBL-EBI Cambridge, UK

Irit Gat-Viks
Tel Aviv University, IL

Jason Pitt
CSI Singapore, SG

Joshua Millstein
University of
Southern California, US

Julien Gagneur
TUM Munich, DE

Manikandan Narayanan
IITM Chennai, IN

Maria Secrier,
University College London, UK

Nikolai Slavov
Northeastern University, USA

Oliver Stegle
DKFZ Heidelberg, DE

Rithambhara Singh
Brown University, US

Samsiddhi Bhattacharjee
NIBMG Kolkata, IN

Shweta Ramdas,
Azim Premji University,
Bengaluru, IN

Sridhar Sivasubbu
IGIB New Delhi, IN

Thangaraj K
CCMB Hyderabad, IN

Vijay Tiwari
Queens University Belfast, UK

Xia Yang
University of California
Los Angeles, US

REGISTRATION FEE :
Student/Postdoc : ₹3,000 ($40) • Faculty : ₹6,000 ($80) • Industry : ₹12,000 ($160)

SCAN TO REGISTER

Register at : https://bit.ly/3rd-IBSE-Symp-Register

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ibse.iitm.ac.in ibse.symposium@gmail.com

FLAGSHIP PROJECTS

GARBH-Ini - modelling of preterm birth risk

In collaboration with our clinical partners, the Translational Health Science and Technology Institute (THSTI), we are analysing the GARBH-Ini cohort, a hospital-based observational pregnancy cohort to study multidimensional correlates of preterm birth in India. GARBH-Ini is one of the five “Atal Jai Anusandhan Biotech Missions – UNaTI” launched by the Government of India. We are building regression and machine learning models using anthropometric, clinical and obstetric characteristics of the mothers to estimate gestational age and predict preterm birth. These models, when validated and deployed will be instrumental reducing maternal and child mortality in India. We have developed gestational age dating model for first trimester and showed that it was as accurate as previous formula but had better accuracy and sensitivity in determining preterm birth rate. We then developed machine learning random forest based late trimester gestational age dating model for second and third trimesters. This model was based on foetal ultrasound characteristics. This model was significantly more accurate in determining gestational age and improved preterm birth estimation by almost 50% compared the established formula.

GenomeIndia: Cataloguing the genetic variations in Indians

Human genome mapping studies have shown that there are substantial differences in genomes of the populations across the world. The most commonly represented Caucasian genome diverged from the Indian population over 30-50 thousand years ago. Furthermore, unlike homogeneous Caucasian populations, the Indian population is very heterogeneous with over 4,500 genetically distinct subpopulations. The aim of the ‘GenomeIndia: Cataloguing the Genetic Variation in Indians’ project is to do whole genome sequencing (WGS) for 10,000 healthy individuals of the country’s diverse populace. This project will generate a unique dataset which will catalogue the unique variations of representative population groups across the country to create a catalogue of genomic variants for Indians.

The project will help in cataloguing the common as well as low-frequency genetic variations in the Indian population, along with a comprehensive understanding of the copy number variations specific to our population and thus facilitate future large-scale genome-wide association studies for researchers across India. This project is jointly run with Initiative for Biological Systems Engineering (IBSE) and Robert Bosch Center for Data Science and AI (RBCDSAI).

INCENTIVE – Indo-European Consortium for Next Generation Influenza Vaccine

The INCENTIVE consortium represents a true partnership between Indian and European/US groups to address the global health and the economic challenge posed by influenza infections. 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 two next-generation universal influenza vaccines. As a data science partner in INCENTIVE, we strengthen the partnership between India and European partners through exchanges of the state-of-the-art technology and methodology for vaccine research. INCENTIVE’s goal of better preparing the international community for future pandemics becomes highly relevant in the current COVID19 pandemic.

RECENT EVENTS

3rd IBSE International Symposium

1–4 February 2022

The theme of the virtual symposium was “Clinical Genomics to Systems Medicine: Computational Approaches for Transforming Healthcare”. This symposium brought biomedical scientists, computational biologists, and data scientists to present and discuss the latest developments in various omics technologies transforming clinical and translational research. A key focus was on novel techniques, methods and algorithms to dissect omics data at multiple levels, enabling a deeper understanding of complex human diseases. Spread over four days, the symposium had 17 seminars on various topics, ranging from the application of machine learning for multi-omics and data integration; personalised medicine for rare genetic diseases and cancer therapy; precision definition of diseases states; single-cell proteomics; deep learning algorithms for genome-wide pattern discovery; application of AI for voice-enabled cancer discovery; and genome-wide association studies. Over 150 enthusiastic students and researchers attended the symposium. A large proportion of these attendees were students of IITM Online BSc in Data Science and AI. The videos of the workshop lectures can be found here.

IITM-EBI Winter School

6–9 December 2021

The IITM-EMBL-EBI Winter School virtual 4-day course was jointly organised by the BioModelsTeam from EMBL-EBI, Hinxton, UK, along with the Centre for Integrative Biology and Systems Medicine (IBSE) and the Robert Bosch Centre for Data Sciences and Artificial Intelligence (RBCDSAI) from IITM. This course was aimed at experimental biologists, bioinformaticians and mathematicians who just started in systems biology, are familiar with the basic terminology in this field and are now keen on gaining a better knowledge of systems. Thirty-seven participants had interactive workshop lectures, research talks, break-out rooms, group projects, flash talks, poster presentations and hands-on sessions during

IBSE-RBCDSAI HPC Symposium: 4–7 January 2022

This online symposium aimed to bring scientists working in high-performance computing (HPC) and those from disciplines that apply HPC, particularly to AI & biology, to present and discuss the latest HPC developments that transform research across disciplines. A key focus was a pedagogical touch to cater to participating students and early career researchers to pique their interest. More than 15 speakers from all over the world shared their work with 48 students and young researchers. The following sessions in different domains of HPC were covered:

- HPC Fundamentals for Data Scientists/ Engineers
- HPC Advances in Numerical Computing
- HPC Powering Data Science & ML
- HPC Applications in Computational Biology

The videos of the workshop can be found here.

this course. Various modelling approaches and tools were introduced to the participants. The BioModels Team trained participants on kinetic modelling of signalling pathways, curation and annotation of mathematical models, and standards in modelling (SBML, SED-ML, etc.). It introduced other paradigms such as constraint-based modelling, e.g., Flux Balance Analysis (FBA), to analyse metabolic pathways. Videos of the workshop can be found here.

COLLOQUIA

8th IBSE Colloquium

The 8th IBSE Colloquium was conducted on 15 September 2021. A talk was delivered by Dr. Yana Bromberg, Professor, Dept. of Biochemistry and Microbiology, Rutgers University, USA, titled “Are DNA variants bugs or features?”. The online event Dr. Yana Bromberg is a fellow of the Institute for Advanced Study at the Technical University of Munich, Germany. She is also the vice-president of the Board of Directors of the International Society for Computational Biology and actively participates in the organization of the ISMB/ECCB conferences. She is known for her seminal work on a machine learning-based method for screening for effects of genetic variation (SNAP). The talk elaborated on the machine learning-based tools developed by her lab for the analysis of synonymous and non-synonymous variants, and its use as a means for interpretation of the whole exome collection of variant effects in light of disease to reveal disease-associated pathways.

9th IBSE Colloquium

The 9th IBSE Colloquium took place online in Zoom on 9 December 2021. Dr. James A. Glazier, Professor of Physics, Adjunct Professor of Informatics and Biology and Director of the Biocomplexity Institute at Indiana University, USA delivered his talk on “From Network Models to Multiscale Virtual-Tissue Computer Simulations of Development, Homeostasis and Disease”. His research focusses on applying physics-based computer simulation to understand various aspects of development of infectious diseases. He held faculty positions in reputed universities in the USA, France, Australia, and Japan. He is an active member of several interesting consortia and particularly he leads the CompuCell3D multi-scale modelling environment. In this talk, Dr. James discussed the need for novel approaches in medicine and listed various challenges associated with the traditional approach. Dr. James discussed the virtual tissues approach to constructing quantitative, predictive mechanistic models starting from cell behaviours and combining sub-cellular network kinetics models, the physical and mechanical behaviours of cells and the longer-range effects of the extracellular environment. The colloquium ended with an interactive Q&A session. There were around 100 participants, including students, researchers, faculty, and industrialists.

9th IBSE Internal Workshop

This was an internal event aimed at IITM faculty and students to know more about the research, connect and work with IBSE. It was conducted in hybrid mode on 27 October 2021. Five research students from IBSE presented their work in different areas, ranging from latent variable modelling to microbial community interactions to genome graphs.

IN THE NEWS

1. IIT Madras develops AI-based Algorithm to identify Cancer-causing Alterations | Education News
2. IITs make giant strides in precision oncology research
3. How computational biology is helping industrial manufacture of metabolites - The Hindu Business Line
4. IIT Madras researchers develop model to detect cancerous mutations - Hindustan Times
5. Why is Big data on Biology so big - Times of India
6. Biotechnology 2.0: IIT Madras Prof on the era of biology, math and programming combined

NEXT FOCUS AREAS

- As COVID pandemic has subsided, we plan to send a few senior PhD students for a short 3-month research internships along with attending conferences/workshops in foreign laboratories to gain research experience.
- We are going to co-organize international workshop "The role of AI in transforming healthcare" in collaboration with THSTI and University of Oxford from 11-12 June 2022, in Goa. We also plan to organize workshops for INCENTIVE project later this year.
- IBSE plans to host a foreign research faculty later this year as part of their CoE activities.
- IBSE faculty will develop courses in domain of AI in healthcare for IITM Online BSc in Data Science and AI degree program.

ACKNOWLEDGMENTS

- IBSE appreciates generous support from the Prakash Arunachalam endowment that has helps run several student initiatives, conferences and meetings.
- IBSE also appreciates support from Ashok Venkitaraman, Director CSI-NUS Singapore and Mehta Chair Professor, Dept of Biotechnology, Bhupat and Jyoti Mehta School of Biosciences, IIT Madras for his advise and support.
- IBSE acknowledges advise and support of IBSE Technical Advisory Board members – Ashok Venkitaraman, Krishnan Ramanathan, Partha Majumder, Seshadri Srinivasan, Srinivasan Parthasarathy and Yana Bromberg.

EMBL-EBI

RBC DSAI

2021 IITM-EMBL-EBI Winter School

Reproducible Modelling in Systems Biology

6-9 December, 2021
VIRTUAL

COURSE CONTENT

During this course you will learn :
- Introduction to kinetic modelling
- Model curation and annotation with COPASI
- Data resources for modelling
- Constraint-based modelling
- Reproducibility in systems biology modelling

LEARNING OUTCOMES

After the course, participants should be able to:
- Identify strength and weakness of systems biology modelling approaches
- Access, query and retrieve data or models from public repositories for systems biology modelling
- Use modelling software to develop reproducible systems biology models
- Discuss real-life application of models in fundamental and industrial research

Course Fees Student/Postdoc : ₹**2,500** • Faculty : ₹**5,000** • Industry : ₹**10,000**

Last date to apply : **25th October**
(only 40 participants will be selected)

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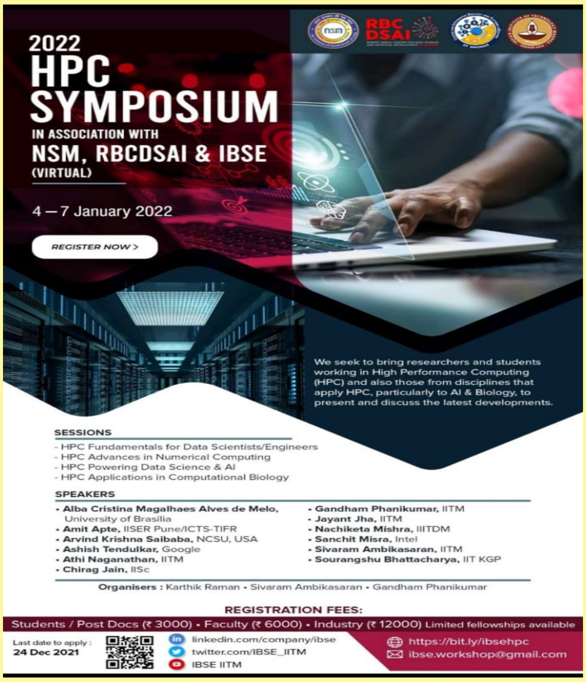
IBSE IITM @ YouTube

https://linktr.ee/IBSE_IITM
ibse.workshop@gmail.com



2022
HPC SYMPOSIUM
IN ASSOCIATION WITH
NSM, RBCDSAI & IBSE
(VIRTUAL)

4 — 7 January 2022

REGISTER NOW >

We seek to bring researchers and students working in High Performance Computing (HPC) and also those from disciplines that apply HPC, particularly to AI & Biology, to present and discuss the latest developments.

SESSIONS

- HPC Fundamentals for Data Scientists/Engineers
- HPC Advances in Numerical Computing
- HPC Powering Data Science & AI
- HPC Applications in Computational Biology

SPEAKERS

- **Alba Cristina Magalhaes Alves de Melo,** University of Brasilia
- **Amit Apte,** IISER Pune/ICTS-TIFR
- **Arvind Krishna Saibaba,** NCSU, USA
- **Ashish Tendulkar,** Google
- **Athi Naganathan,** IITM
- **Chirag Jain,** IISc
- **Gandham Phanikumar,** IITM
- **Jayant Jha,** IITM
- **Nachiketa Mishra,** IIITDM
- **Sanchit Misra,** Intel
- **Sivaram Ambikasaran,** IITM
- **Sourangshu Bhattacharya,** IIT KGP

Organisers : Karthik Raman • Sivaram Ambikasaran • Gandham Phanikumar

REGISTRATION FEES:

Students / Post Docs (₹ 3000) • Faculty (₹ 6000) • Industry (₹ 12000) Limited fellowships available

Last date to apply :
24 Dec 2021

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