



Initiative for **Biological Systems Engineering (IBSE)**

**Robert Bosch Center for Data Science
and Artificial Intelligence (RBCDSAI)**
Indian Institute of Technology Madras,
Chennai





Mission

IBSE is an interdisciplinary group dedicated to pioneering innovative approaches and algorithms that integrate multi-dimensional data across scales to understand, predict and manipulate complex biological systems.

In so doing, we aim not only to advance fundamental understanding of cells and their interactions as populations forming complex organs, but also to empower personalised medicine.

IBSE closely works with the **Robert Bosch Centre for Data Science and Artificial Intelligence (RBCDSAI), IITM**



Reference: EMBL-EBI Data servers

Key Research Themes

Biological network analysis

- Molecular function prediction in cells and populations
- Environmental and evolution dependent modulation of biological networks

Algorithms: machine learning, graph mining, linear programming...

- Studying protein folding pathways, protein function prediction, predicting novel metabolic pathways
- Understanding disease-causing mutations

Flagship projects – GARBH-Ini

Preterm birth – 3.6M births annually; India average rate 13%

High mortality (~50%) with long term health consequences

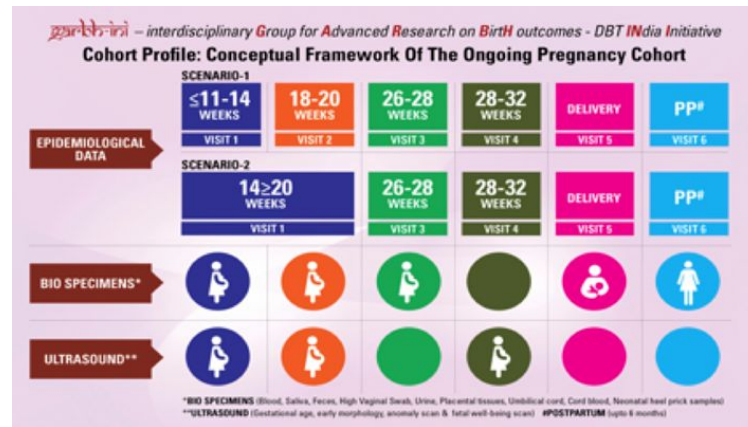
GARBH-Ini – a longitudinal study of birth outcomes

Population : Urban & semi-urban population covering 750 sq. km around Gurugram, India

Cohort size : 8,000 women

Total no. of variables : 1,900

Ultrasound images in the repository : 330,000



OBJECTIVE

To apply data-driven machine learning approaches to develop an accurate and clinically useful model to predict risk of preterm birth

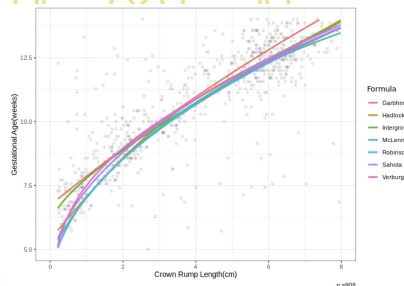
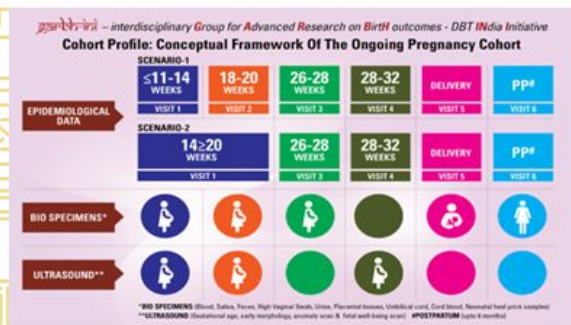
END GOAL

Dynamic prediction models that can predict, at different periods of gestation, the preterm birth risk using the clinical, epidemiological and imaging data

GARBH-Ini Preterm Birth Cohort

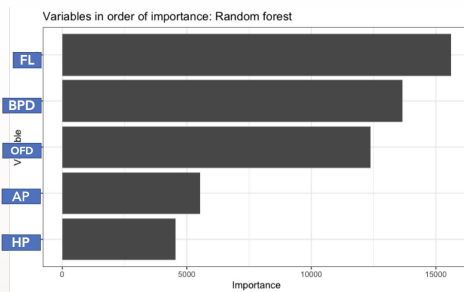
THSTI-IITM collaboration for data analyses to predict preterm birth in Indian population

Preterm births: need for early predictions



GARBHINI-GA1

$$GA = -0.02294(CRL)^2 + 1.15018(CRL) + 6.73526$$

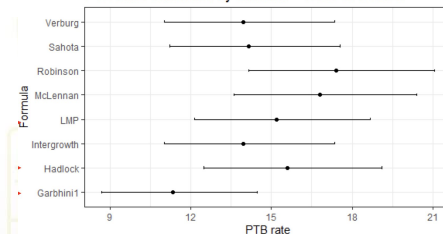


GARBHINI RANDOM FOREST

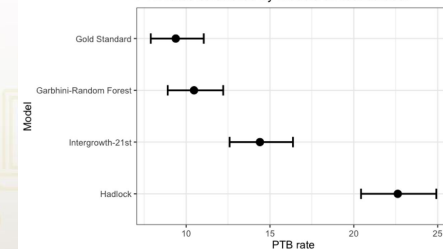
Preterm birth prediction

Garbhini-GA1 and Garbhini Random Forest classifies preterm birth more accurately than Hadlock's formula, currently used in India

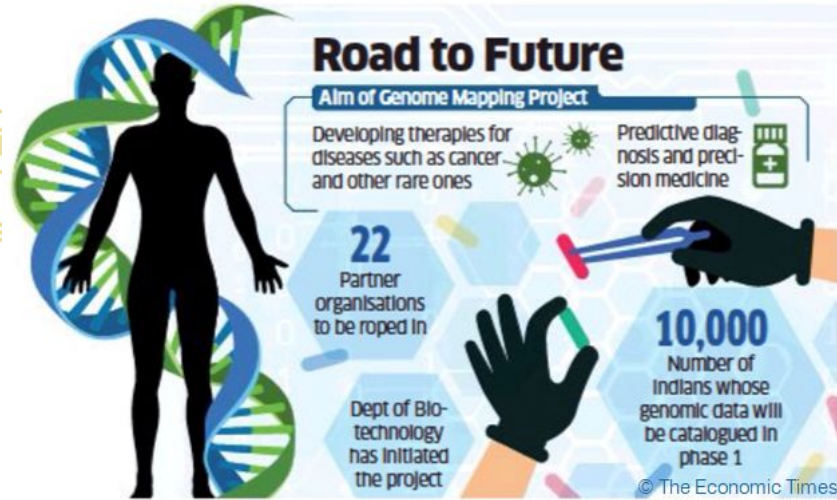
PTB rates calculated by formulae - TEST DATASET



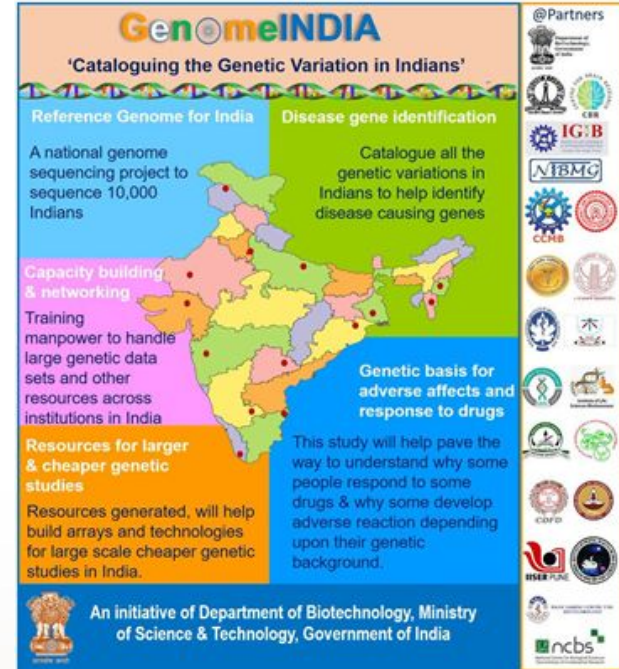
PTB rates calculated by models on test dataset



Flagship projects: GenomeIndia



DEPARTMENT OF BIOTECHNOLOGY
Ministry of Science & Technology



GenomeIndia - Cataloguing the genetic variations in Indians

A ₹2.5 billion multi-institutional project to sequence whole genomes of 10K Indians to map the genetic diversity of Indian population

Flagship projects – INCENTIVE



European Union and India flagship call

#H2020
#OpenToTheWorld
#DBTIndia

Fighting flu together

Apply for funding now
new research and innovation opportunities

€30 million
to develop
a next generation
influenza vaccine



The illustration shows a white pot with the Indian national flag (saffron, white, and green horizontal stripes) on its side. A blue thermometer is stuck in the pot, which contains yellow liquid. A lemon is next to the pot. The background is dark purple with faint virus-like icons.

Indo-EU Consortium INCENTIVE

A €20 million project to develop of next generation influenza vaccines for European and Indian populations

Funding



Alumni Endowment of
US\$1 million in stocks
(over four years) from IIT
alumnus,
Dr Prakash Arunachalam

The interest from this
endowment aims to fund
~₹40 lakhs p.a. for
various
IBSE activities



International symposium



An international Symposium
on synthetic biology from 30
Jan – 1 Feb 2020
funded by **European Molecular
Biology Organising (EMBO)**
and **India Alliance
(Wellcome-DBT)**



IndiaAlliance
DBT wellcome

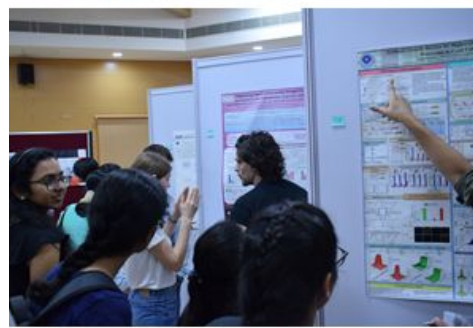
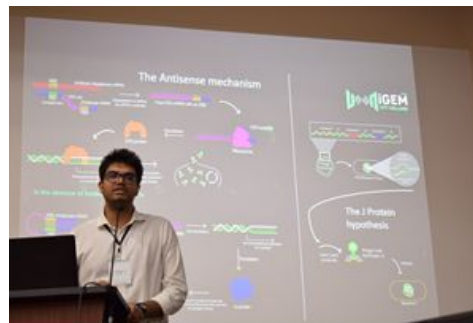


EMBO
Molecular
Medicine





From the Symposium



International workshop



An international workshop on BioModels jointly organised by IBSE and European Bioinformatics Institute (EBI), Cambridge UK and funded by IBSE **to train 46 participants from India to learn to build and analyse bio-mathematical models**



IBSE in the news



IIT-M team develops fresh algorithm to study genes, diseases

TIMES NEWS NETWORK

Chennai: Faculty of Indian Institute of Technology, Madras, working with researchers across the world, have developed computational algorithms to link diseases to underlying genes. Their algorithms not only detects gene groups that cause diseases but also the links between various related diseases and these gene groups, an official release said.

The IIT-M team analysed existing module identification algorithms and developed an improved system that achieved 50% better performance. The team hopes to develop detailed maps of tissue and disease-specific networks to understand links between genes, proteins and diseases better.

hind it. Now, researchers have improvised these algorithms to perform a task that could save lives.

Researchers at IIT-Madras have developed algorithms that could detect proteins and genes that cause cancer, hypertension or diabetes. The algorithms could also help find link between various related diseases and their gene groups. When many such underlying genes and proteins associated with diseases are identified, the algorithm could eventually help in identifying an individual or a community that

disease modules in related diseases

helps look at a person's friends and breaks it down into clusters, for example people who studied in the same college. The algorithm that finds tightly connected groups of people is applied to proteins to find connected groups of proteins or genes associated with a disease," he said. "The algorithm that is used in social networks can be used in case of coronavirus," he added.

The research was led by professor B Ravindran, head

CHENNAI IIT-M researchers have developed algorithms to detect disease causing dysfunctional proteins and genes in biological networks.



Through their initiative, they hope to develop detailed maps of tissue and disease specific net-

nature|methods

ANALYSIS

<https://doi.org/10.1038/s41592-019-0509-5>

OPEN

Assessment of network module identification across complex diseases

Sarvenaz Choobdar^{1,2,20}, Mehmet E. Ahsen^{3,117}, Jake Crawford^{4,117}, Mattia Tomasoni^{1,2}, Tao Fang⁵, David Lamparter^{1,2,6}, Junyuan Lin⁷, Benjamin Hescott⁸, Xiaozhe Hu⁷, Johnathan Mercer^{9,10}, Ted Natoli¹¹, Rajiv Narayan¹¹, The DREAM Module Identification Challenge Consortium¹², Aravind Subramanian¹¹, Jitao D. Zhang¹³, Gustavo Stolovitzky^{3,13}, Zoltán Kutalik^{2,14}, Kasper Lage^{9,10,15}, Donna K. Slonim^{4,16}, Julio Saez-Rodriguez^{17,18}, Lenore J. Cowen^{4,7}, Sven Bergmann^{1,2,19,21*} and Daniel Marbach^{1,2,5,21*}
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<https://doi.org/10.1038/s41592-019-0509-5>

- Lockdown compliance decreased with every subsequent stage of lockdown.
- High correlation between busy areas and COVID-19 infection rates.
- Movement patterns are different in weekdays compared to weekends.

In the news

THE HINDU

SCIENCE

IIT Madras study reveals metabolism of key gut microbiota



Little is known about differences between different strains of Bifidobacterium genus and their individual commercial uses

A study by IIT Madras researchers of 36 strains of gut bacteria commonly found in the gut reveals their metabolism and could bring added rigour into the development of probiotics. Probiotics are cocktails of helpful bacteria which, among other uses, are prescribed to alleviate digestive imbalances.

scientific reports

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Journal information ▾

nature > scientific reports > articles > article

Article | [Open Access](#) | Published: 03 December 2019

Deciphering the metabolic capabilities of Bifidobacteria using genome-scale metabolic models

N. T. Devika & Karthik Raman 

Scientific Reports **9**, Article number: 18222 (2019) | [Cite this article](#)

1654 Accesses | **2** Citations | **29** Altmetric | [Metrics](#)

In the news

THE HINDU BusinessLine

Scientists identify 21 microbes that help build a healthy gut

TV Jayan : | New Delhi | Updated on July 07, 2020 | Published on July 07, 2020



Representational image only

‘By highlighting these 21 species, we will spur research into exploring their use as probiotics, independently and in combination with other existing probiotics’

nature ecology & evolution

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Journal information ▾

[nature](#) > [nature ecology & evolution](#) > [articles](#) > [article](#)

Article | Published: 06 July 2020

Metagenome-wide association analysis identifies microbial determinants of post-antibiotic ecological recovery in the gut

Kern Rei Chng, Tarini Shankar Ghosh, Yi Han Tan, Tannistha Nandi, Ivor Russel Lee, Amanda Hui Qi Ng, Chenhao Li, Aarthi Ravikrishnan, Kar Mun Lim, David Lye, Timothy Barkham, Karthik Raman, Swaine L. Chen, Louis Chai, Barnaby Young , Yunn-Hwen Gan  & Niranjan Nagarajan 

Nature Ecology & Evolution **4**, 1256–1267(2020) | [Cite this article](#)

2653 Accesses | **1** Citations | **115** Altmetric | [Metrics](#)

In the news



Home > Category > Indian Science News

A novel algorithm for enhanced crop productivity



India Science Wire

New Delhi, Thursday, August 06, 2020

Microbes always exist in communities. They are also used in commercial applications. In industries like probiotics and biofuels, co-cultivations of these microbes are performed under controlled conditions for improved yield and productivity of the given product. These co-cultures are designed randomly based on hit and trial methods.

To quickly ascertain the right combination and to understand how these microbes interact with in a co-culture, researchers from Indian Institute of Technology (IIT) Madras have developed and demonstrated an effective method. The study applies computer-based modelling to develop novel algorithms to identify metabolic interactions between bacteria. This understanding may help in identify the perfect combination for a co-culture.



Computational and Structural
Biotechnology Journal

Volume 18, 2020, Pages 1249-1258



Investigating metabolic interactions in a microbial co-culture through integrated modelling and experiments

Aarthi Ravikrishnan ^{a, b, c, d, 1}, Lars M. Blank ^d, Smita Srivastava ^a, Karthik Raman ^{a, b, c}

Interactions



IBSE Colloquia

- Prof. Radhakrishnan Mahadevan, University of Toronto
- Prof. Partha Majumder, National Institute of Biomedical Genomics (NIBMG)

IBSE Seminars

- Dr. Ranjeeta Menon, Univ. of Sydney
- Dr. Nathan Bachmann, Univ. of Sydney
- Dr. Anshu Bhardwaj, IMTECH

IBSE Workshops: showcase research activities through talks by IBSE students and faculty

- IITM-NUS Workshop
- IBSE-inSTEM MiniSymposium



Fellowships



IBSE Post Baccalaureate Fellowship (12 months)
Rachita K. Kumar, Tamizhini L, Shreyansh Umale

IBSE Junior Research Fellow (2 years) – Sai Sruthi A

Student Achievement



Gayathri Sambamoorthy

Institute Blues Award 2020 @ IITM



Other Publications



Thank you

