*Type of event/activity	R&D
Name/Title of the Activity/Event	Ph. D viva voce
Date of Organization	21-12-2021
Venue	Virtual Platform
Objectives of the event/activity	Objective of R&D is to encourage and sustain excellence in Research and Innovation by cultivating and promoting a research culture among its teachers, staff and students. This would be leveraged for inspiring and enhancing the professional competence of the faculty members; for developing and promoting scientific temperament and research aptitudes among the students.
Participants	15 participants
Mention organized	PROF. Divyamani M K & PROF. Supriya H S

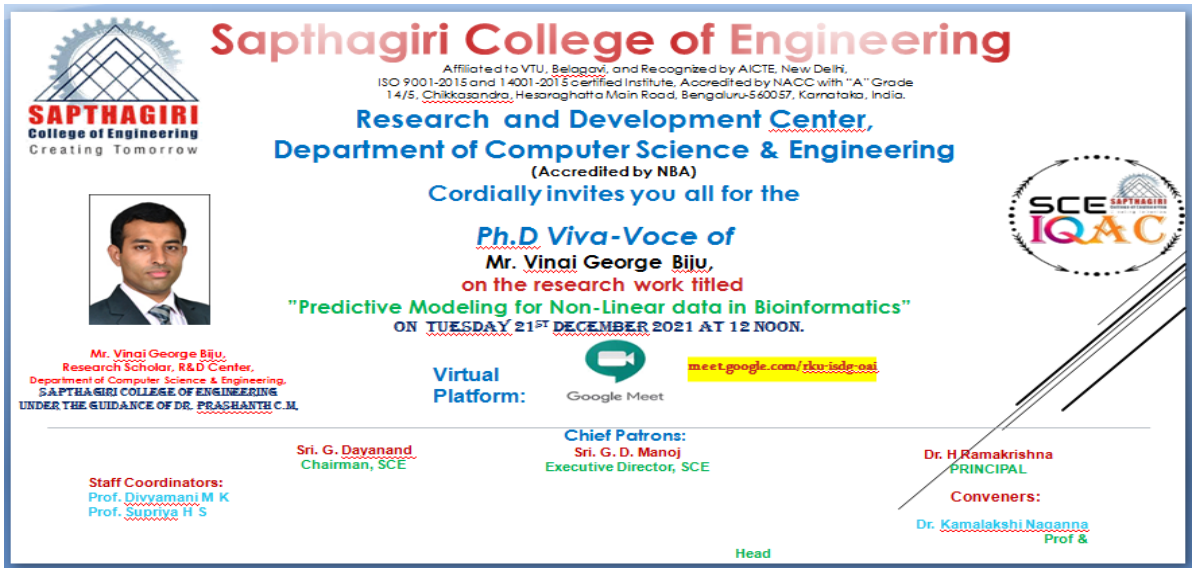
Event Description:

Research and Development Center, Department of Computer Science & Engineering conducted Ph. D viva voce of Mr.Vinai George Biju, on the research work titled **"Predictive Modeling for Non-Linear data in Bioinformatics"**. The research work is about Identifying molecular signatures of disease phenotypes is studied using two mainstream approaches: (i) Predictive modeling methods such as linear classification and regression algorithms are used to find signatures predictive of phenotypes from genomic data, which may not be robust due to limited sample size or highly correlated nature of genomic data. (ii) Gene set analysis methods are used to find gene sets on which phenotypes are linearly dependent by bringing prior biological knowledge into the analysis, which may not capture more complex nonlinear dependencies. Thus, formulating an integrated model of gene set analysis and nonlinear predictive modeling is of great practical importance.

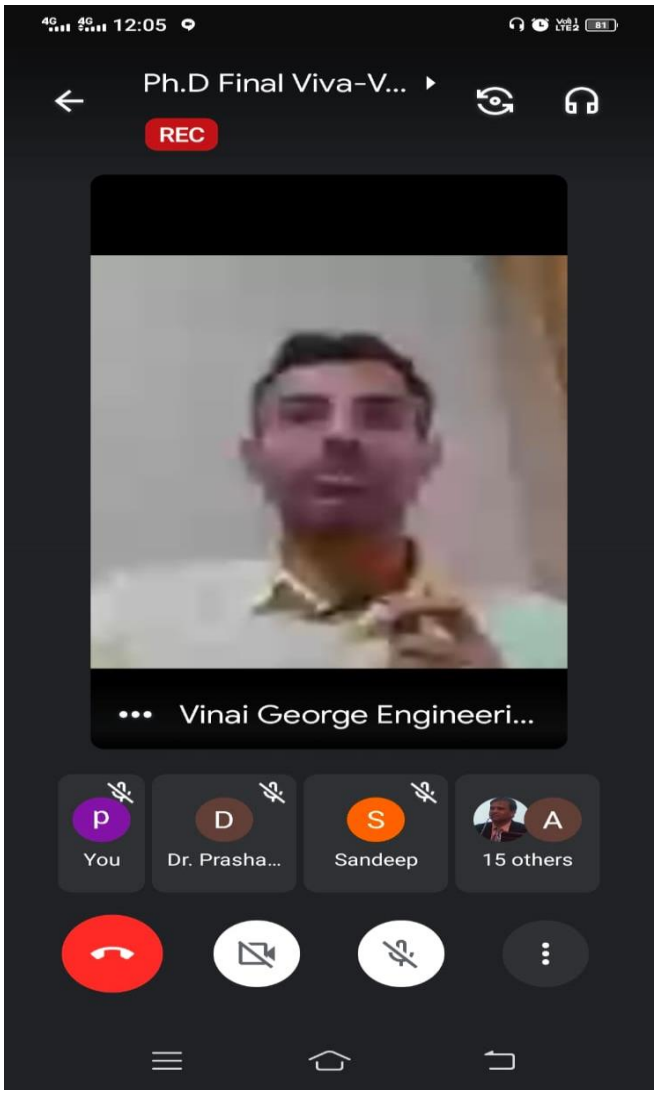
In the study, a Bayesian binary classification framework is proposed to integrate gene set analysis and nonlinear predictive modeling. It is then generalized and formulated to multitask learning setting to model multiple related datasets conjointly. The main novelty is the probabilistic nonlinear formulation that enables ti robustly capture nonlinear dependencies between genomic data and phenotype even with small sample sizes. It is demonstrated the performance of algorithms using repeated random subsampling validation experiments.

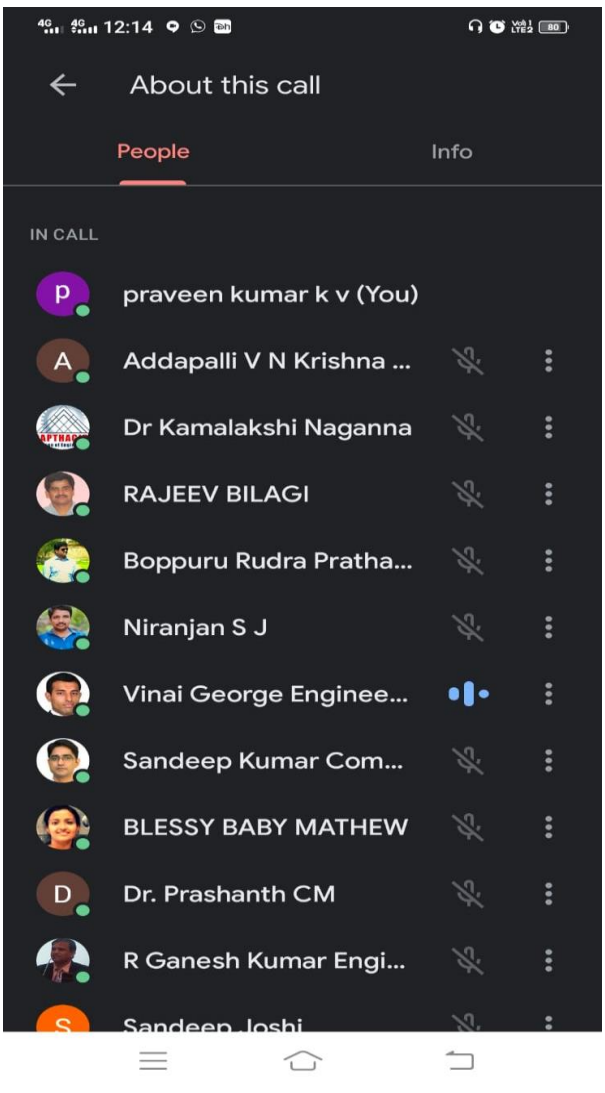
Images:

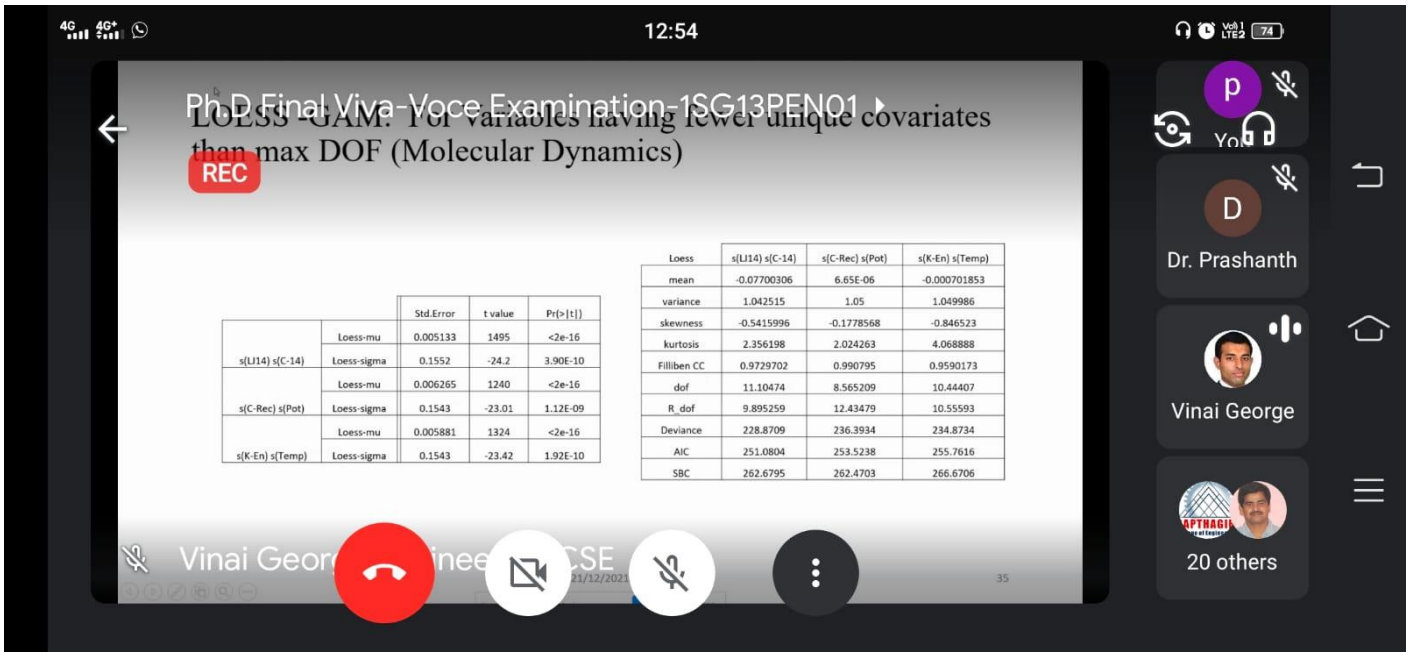
BROCHURE



SOME CLICKS OF EVENT

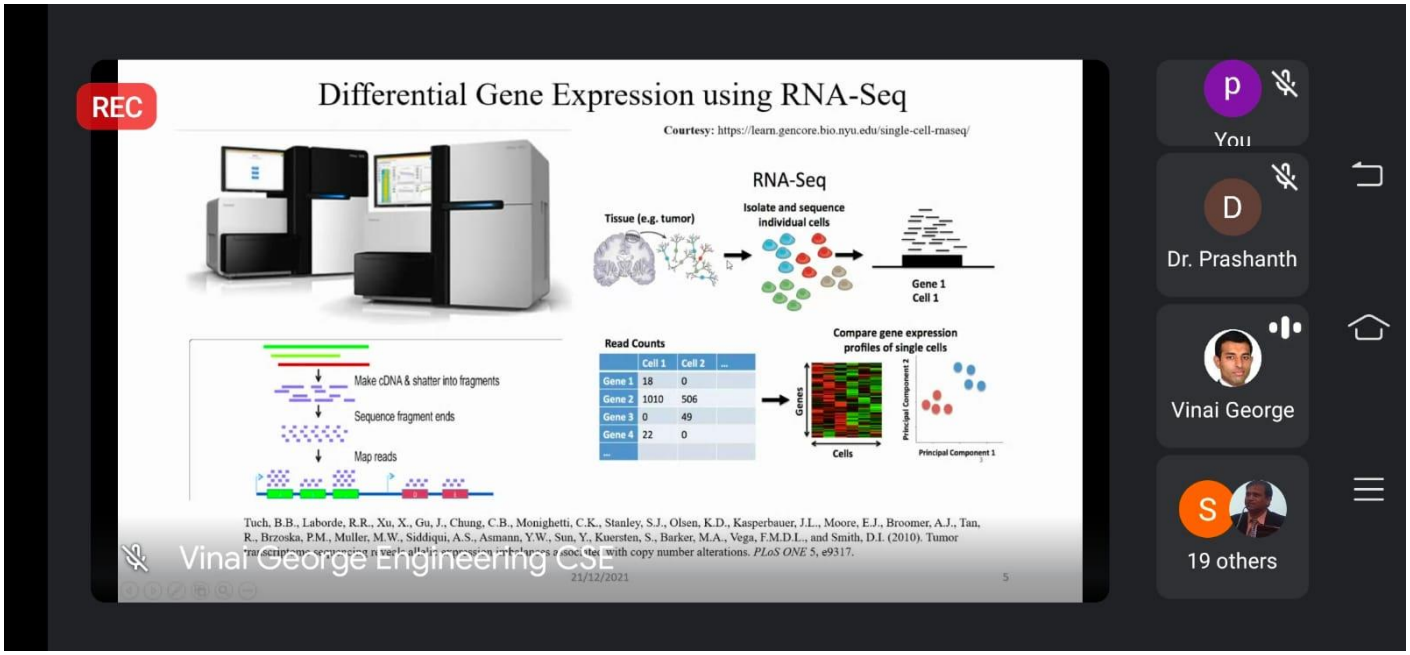






		Std.Error	t value	Pr(>|t|)
s(LI14) s(C-14)	Loess-mu	0.005133	1495	<2e-16
	Loess-sigma	0.1552	-24.2	3.90E-10
s(C-Rec) s(Pot)	Loess-mu	0.006265	1240	<2e-16
	Loess-sigma	0.1543	-23.01	1.12E-09
s(K-En) s(Temp)	Loess-mu	0.005881	1324	<2e-16
	Loess-sigma	0.1543	-23.42	1.92E-10

Loess	s(LI14) s(C-14)	s(C-Rec) s(Pot)	s(K-En) s(Temp)
mean	-0.07700306	6.65E-06	-0.000701853
variance	1.042515	1.05	1.049986
skewness	-0.5415996	-0.1778568	-0.846523
kurtosis	2.356198	2.024263	4.068888
Filliben CC	0.9729702	0.990795	0.9590173
dof	11.10474	8.565209	10.44407
R_dof	9.895259	12.43479	10.55593
Deviance	228.8709	236.3934	234.8734
AIC	251.0804	253.5238	255.7616
SBC	262.6795	262.4703	266.6706



Gene	Cell 1	Cell 2	...
Gene 1	18	0	
Gene 2	1010	506	
Gene 3	0	49	
Gene 4	22	0	
...			

PO1	PO2	PO3	PO4	PO5	PO6	PO7	PO8	PO9	PO10	PO11	PO12
3	2					3	2		2		3

Type of activity:
Ph. D viva voce

Coordinators:
Prof. Divyamani M k
Prof. Supriya H S

Signature of the HOD
[Dr. KamalakshiNaganna]

Date of Submission: 29-12-2021