

Statistical Mechanics in Chemistry and Biology (SMCB)

An online conference, 23-26 January 2021



Board Room, Temporary Campus, IIT Tirupati

The “*Statistical Mechanics in Chemistry and Biology (SMCB-2021)*” conference is jointly organised by IIT Tirupati, IISER Tirupati and IIT Goa over an online platform. The idea of this conference is conceived and nurtured by the country’s legendary researcher in this domain **Prof. Biman Bagchi**, who is a National Science Chair Professor at IISc Bangalore. The coordinators for the pioneer event are **Dr. Rajib Biswas** (Asst. Prof. of Chemistry, IIT Tirupati), **Dr. Rakesh S. Singh** (Asst. Prof. of Chemistry, IISER Tirupati) and **Dr. Mantu Santra** (Asst. Prof. of Chemistry, IIT Goa). This was created to provide the young researchers a platform to discuss their research works.



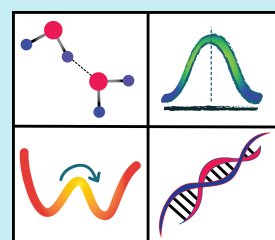
DR. RAJIB BISWAS
IIT Tirupati



DR. RAKESH S SINGH
IISER Tirupati



DR. MANTU SANTRA
IIT Goa



SMCB - 2021



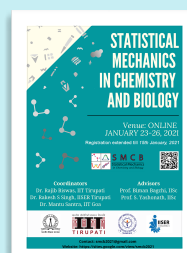
Prof. Biman Bagchi
National Science Chair
Professor, IISc
Bangalore

Coordinators

Dr. Rajib Biswas
Dr. Rakesh S. Singh
Dr. Mantu Santra

Advisors

Prof. Biman Bagchi
Prof. S. Yashonath



Inauguration of SMCB-2021



Board Room, Temporary Campus, IIT Tirupati

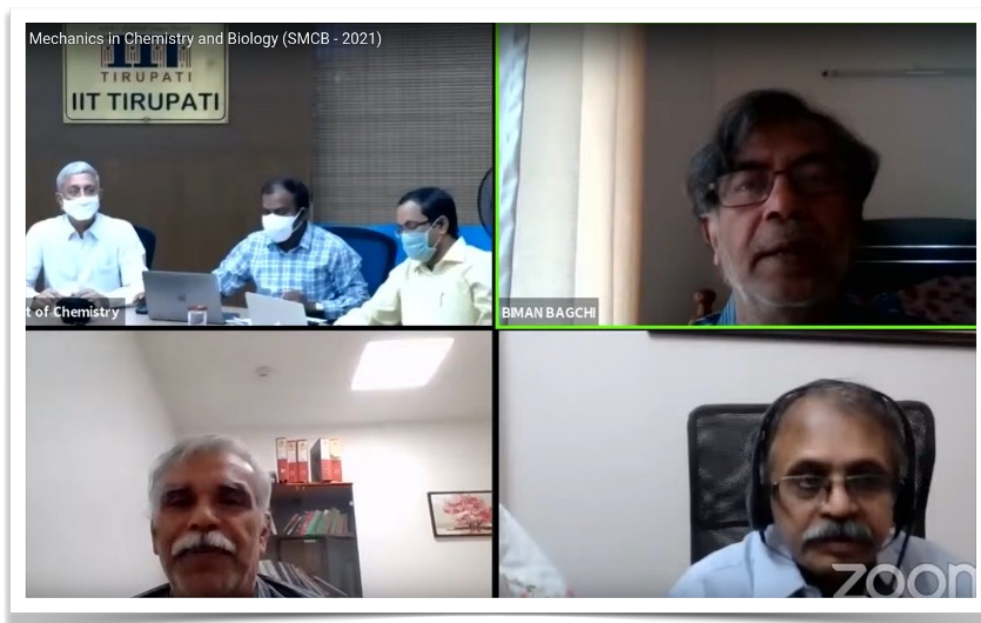
The 4 days long online conference SMCB-2021 is formally inaugurated by Prof. K. N. Satyanarayana, Director, IIT Tirupati; Prof. K. N. Ganesh, Director, IISER Tirupati; Prof. C. P. Rao, HoD, Chemistry, IIT Tirupati, and Prof. K. Vijayamohanan Pillai, Chair, Chemistry, IISER Tirupati. The inaugural session was attended by near about 200 participants over ZOOM video conferencing platform.

INAUGURATED BY



From Left: Prof. K. N. Satyanarayana (Director, IIT Tirupati); Prof. C. P. Rao (HoD Chemistry, IIT Tirupati); Prof. K. N. Ganesh (Director, IISER Tirupati); Prof. K. Vijayamohanan Pillai (Chair, Chemistry, IISER Tirupati)

Glimpses of Inaugural Session



Chairpersons of the Technical Sessions

The conference has six technical sessions, comprise of 24 presentations by faculty members and 31 presentations by young research scholars.



Dr. Sangeeta Saini
Kurukshetra University



Dr. Sayan Bagchi
CSIR-NCL Pune



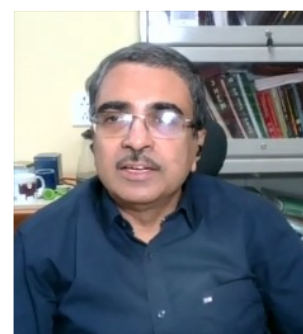
Dr. Hemant Kashyap
IIT Delhi



Dr. Manju Sharma
University of Hyderabad



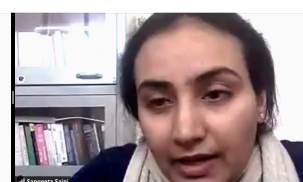
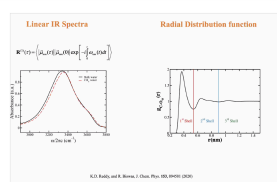
Dr. Sandip Paul
IIT Guwahati



Prof. Anindya Datta
IIT Bombay

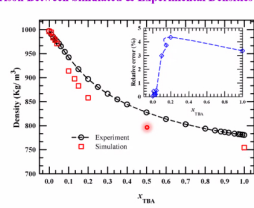
Aggregation of lysozyme in presence and absence of mixed bilayer

Shahee Islam, Chaitali Mukhopadhyay*
Department of Chemistry, University of
Calcutta, West Bengal
e-mail: cmchem@caluniv.ac.in



Simulations of Water + TBA: Fidelity Check via Comparison Between Simulated & Experimental Densities

x_{TBA}	Present simulations	Experiments	Relative Error (%)
0.01	996.56	990.41	0.649
0.02	994.30	984.98	0.394
0.03	983.48	980.15	0.152
0.04	978.44	975.61	0.174
0.06	971.20	965.05	0.45
0.10	913.86	942.10	2.99
0.13	897.70	-----	-----
0.15	883.00	917.47	3.75
0.17	883.07	-----	-----
0.20	858.08	896.99	4.33
1.00	754.40	780.43	3.34



- All Atom Potential by Kossick et al.; IPC B 2000
- TIP4P/2005 Model for Water
- NVT ensemble, 2 ns production run
- Average over 10 blocks
- GROMACS4.5.6; TRAVIS, VMD



Glimpses of the Technical Sessions

Statistical Mechanics in Chemistry and Biology (SMCB-2021)

Allostery and Hydrogen Bond Network: A Tale of Two Proteins

Suman Chakrabarty

Department of Chemical, Biological & Macromolecular Sciences
S.N. Bose National Centre for Basic Sciences, Kolkata

ClyA – paradigms of membrane oligomerization

- Nature of intermediates, pre-pores/arcs ?
- Distinguish between oligomerization pathways ?

will ganapathy ayappa

Statistical Mechanics in Chemistry and Biology (SMCB-2021)

Each Protomer:

1. Generate unique contact information; 2. Feed Hamiltonian the contact information

Roy et al., JPCL 2020

Method Pipeline of Building Super-Symmetric Contact Map

Trimeric SARS-CoV2 spike protein template (pdb:6vsh)
(ChainA:up; ChainB:down; ChainC:down)

Homology modelling and missing loop building using SWISS-MODEL

Intra-chain contact map generation

Using Shadow contact map generation tool

Isolate unique contacts for RBD-up from ChainA (C_{up})

Isolate unique contacts for RBD-down from ChainB (C_{down})

Isolate shared contacts for RBD-up & down comparing ChainA and B contact-pairs (C_{shared})

$\{C_{up}, C_{down}, C_{shared}\}$

Inter-chain contact map generation

Shadow contact map generation of dimeric interface

Asymmetric inter-chain contact-map from AB dimer (up-down)

Symmetric inter-chain contact from BC dimer (down-down)

Isolate unique inter-chain up-down interfacial contacts

Isolate unique inter-chain down promoting contacts

$\{C_{asym}, C_{sym}\}$

"The shadow criterion"

In contact

Not in contact

Roll-off

Hoel JK, Whitford PC, Onuchic JN. (2012) : A general contact definition for capturing the dynamics of biomolecular (solid) and

Statistical Mechanics in Chemistry and Biology

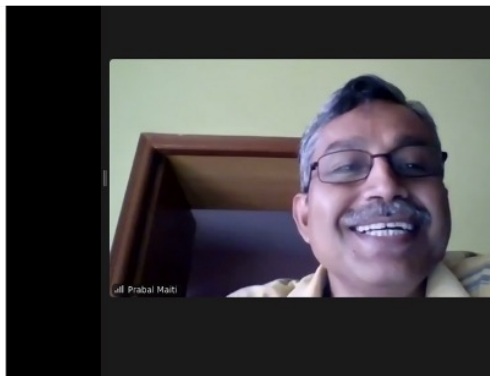
MEASURING THE AGGREGATION PROPENSITY OF AMYLOID- β AND ITS FAD MUTANTS

Parbati Biswas,
Dept. of Chemistry,
University of Delhi

23rd Jan. 2021

Understanding HIV invasion mechanism and designing efficient inhibitor through computational techniques

Prabal K. Maiti
Centre for Condensed Matter Theory
Dept. of Physics, Indian Institute of Science (IISc)
Bangalore, India.



Motor proteins walking on the cellular track



<http://www.statidaily.com/2020/10/10/motor-proteins-walking-on-the-cellular-track/>



<https://www.youtube.com/watch?v=7v3hug8P8k>

Perhaps the most important entity in living cells. Walks on microtubule or actin filament while carrying important cellular cargo. Converts chemical energy of ATP/GTP hydrolysis to produce mechanical energy.

Features:

- What are the different states in the mechanochemical cycle?
- How two heads coordinate between them to produce a long distance walk?
- How multiple motors work as a team?

Questions:

- Molecular mechanism of ATP/GTP hydrolysis in motor proteins?
- How specific mutations of motor proteins lead to disease or small molecule binding lead to anesthesia?



A statistical Approach to Understand Bacterial Cytoplasm

Jagannath Mondal
TIFR Hyderabad

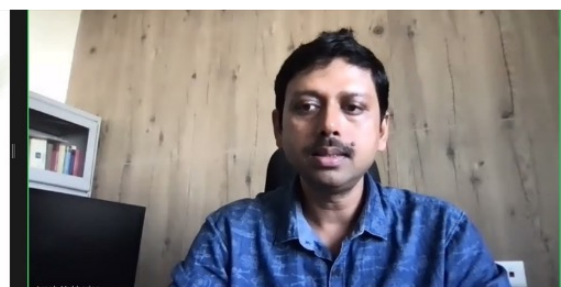


Surface Complementarity in Proteins using Unsupervised Learning and robust Curvature Measure



SMCB-Jan 2021

Arnab Mukherjee
Chemistry Department



Noise-induced symmetry breaking of self-regulators: Nonequilibrium transition towards homochirality

Debasish Mondal

Department of Chemistry
Indian Institute of Technology Tirupati



SMCB2021, 24th January, 2021



Activity and crowding, two major players in single probe dynamics



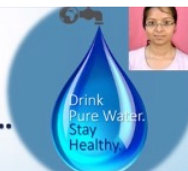
Rajarshi Chakrabarti
Department of Chemistry
Indian Institute of Technology Bombay

Statistical Mechanics in Chemistry and Biology (SMCB), 23-26 January 2021



Thank You

Save water ...



Anyone who can solve the problems of water will be worthy of two Nobel prizes - one for peace and one for science



John F. Kennedy

So why waiting , start now to design a nanomembrane , give it to the experimentalist and solve the water problem



Homeoviscous Adaptation of Cell Membrane: Defying Cold Stress



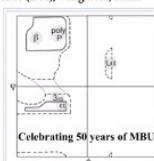
Snehasis Daschakraborty
Department of Chemistry
IIT Patna
India



Conformational sampling of proteins with funnelled, multi-funnelled and weakly multi-funnelled free-energy landscapes

Anand Srivastava
anand@iisc.ac.in

Molecular Biophysics Unit, Indian Institute of Science (IISc), Bangalore, India



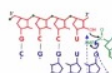
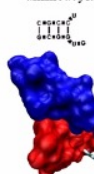
Celebrating 50 years of MBU

Acknowledgement: Dr. Rajeswari Appadurai, DST-ECR, DBT-IISc partnership, Wellcome Trust (ECR to Rajeswari), HPC resources through Compute Canada (Dr. Jayashree Nagesh)

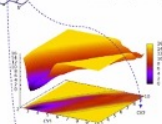


Results

□ An active site in a 5 nucleotide unit performing aminoacylation



Substrates (RNA and PheAMP)
Enzyme (ribo-)



Example of classical metadynamics calculation of approach of L-PheAMP towards the 5' active site. No convergence for D- is achieved unless the base pairing of 5ut is perturbed. (S. Chowdhury, A. Saha, N. Nandi, Unpublished)



Polymorphism

❖ Phenomenon of existing in multiple crystal structures

Ice has 18 known crystalline structures

Thermodynamic Anomalies and Ice Nucleation in Deeply Stretched Water

Rakesh S. Singh
Indian Institute of Science Education and Research
Trirupati

SMCB-2021

Finding the correspondence between real time and mc step

Eq. MD Simulations

- A system of equimolar mixture of neopentane and *n*-hexane in zeolite NaY at a loading of 1mpc is simulated with equilibrium molecular dynamics at 300K temperature.
- The timestep is 1fs.
- The system is equilibrated for 1ns, and then production ran for 5ns.
- The system dimension is 2x2x2.

$D_{neopentane}^{MD} = 5.07 \times 10^{-9} \text{ m}^2/\text{sec}$
 $D_{n-hexane}^{MD} = 4.06 \times 10^{-9} \text{ m}^2/\text{sec}$

yashonath

Examining the origin of two-step crystal nucleation from vapor phases using molecular theory for non-classical nucleation

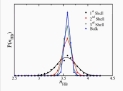
Sudheep N. Punathanam
Department of Chemical Engineering,
Indian Institute of Science, Bengaluru

Structural Polymorphism Driven Thermodynamic Variability Effectively Predicts Disease Phenotype

Statistical Mechanics in Chemistry and Biology 23rd - 26th Jan, 2021

Hydrogen bond analysis

1. The inter-oxygen distance is less than 3.5 Å
2. The hydrogen acceptor distance is less than 2.6 Å
3. $H-O\cdots O$ angle is less than 30°

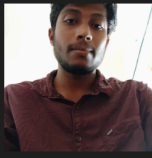


A. Lohar and D. Chakraborty, J. Chem. Phys. 148, 084701 (2018)

Conclusions

1. We observe a blue-shifted narrow inewidth linear IR response in the case of the methanol-water system.
2. OH stretching frequency of water towards blue shift those are facing towards methanol.
3. Water molecules facing towards methanol behave like high temperature water.
4. Some of the first shell water molecules behave like low temperature water.

References
1. K.D. Raddly and R. Biswas, J. Chem. Phys. 153, 094501 (2020)



KAMBHAM DEVENDRA

Reparameterization Strategy: Our aim is to reproduce experimental dielectric coefficient

Experimental fact: Higher dielectric constant + higher conductance present

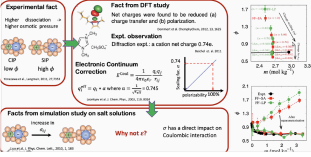
Fact from GFT study: Net charges were found to be reduced (a) charge transfer and (b) polarization.

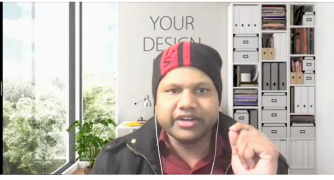
Expt. observation: Diffraction exp. a carbon net charge 0.74e

Electronic Continuum Correction: $\epsilon_{\text{net}} = 1.00$ (Bjork, 1974)

Fact from simulation study on salt solutions: $\epsilon_{\text{net}} = 0.74$ (a) has a direct impact on Coulombic interaction

Why not 0.7?






Sahithya S Iyer

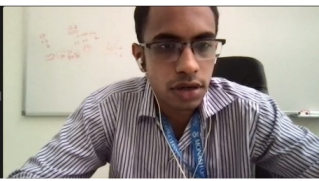
Rouse model with fluctuating internal friction

R. Kallasham, Rajarshi Chakrabarti, and J. Ravi Prakash

Email address for correspondence: rkallasham@itb.ac.in, rajarshi@chems.itb.ac.in, ravi.jagadeesham@monash.edu

ITB-Monash Research Academy
An Indian Australian research partnership

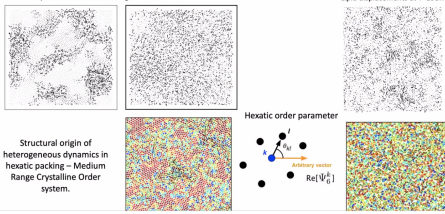




Heterogeneous Dynamics in single L_o phase in lipid membranes

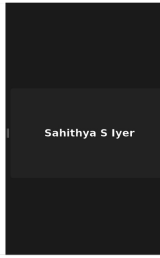
Particle displacements in 2D Model glass formers: $T = 1.0$ and $T = 2.0$

Lipid displacements at $T = 298K$



Hexatic order parameter

Structural origin of heterogeneous dynamics in hexatic packing – Medium Range Crystalline Order system.



Sahithya S Iyer

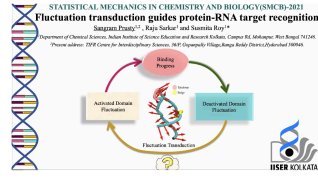
STATISTICAL MECHANICS IN CHEMISTRY AND BIOLOGY (SMCB)-2021

Fluctuation transduction guides protein-RNA target recognition

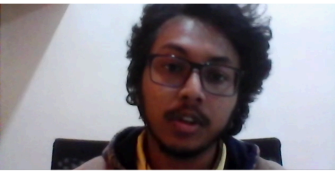
Satish Kumar, Rajarshi Chakrabarti, and Ravi Prakash

Department of Chemical Science, Indian Institute of Science Education and Research Kolkata, Campus K1, Mohanpur, West Bengal 741245

Present address: IISER Kolkata for Interdisciplinary Science, IISER Hyderabad (Hyderabad Science Centre, Hyderabad)

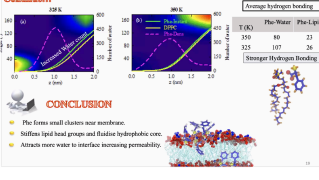


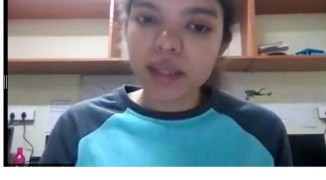
IISER KOLKATA



CONCLUSION

- The forms small clusters near membrane.
- Stiffens lipid head groups and fluidize hydrophobic core.
- Attracts more water to increase membrane permeability.





Recent experimental study

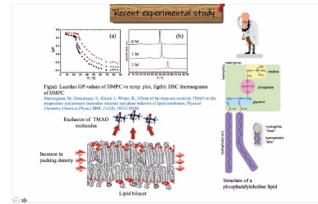
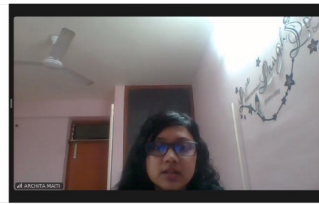


Figure 1: Lipid order parameter (OP) values of DOPC in water plus lipid. DSC thermograms of DOPC. DSC thermograms of DOPC in water plus lipid. DSC thermograms of DOPC in water plus lipid.

Evolution of DSC thermograms

Decrease in packing density

Membrane is a phospholipid bilayer



Arginine

Insulin Monomer

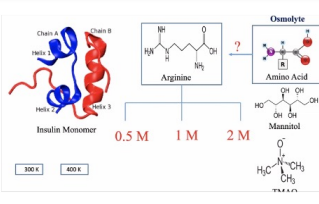
0.5 M 1 M 2 M

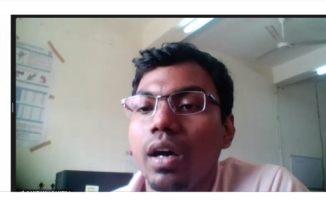
Osmolyte

Amino Acid

Mannitol

CH₃ (CH₂)₁₀CH₃






Dynamical Anomaly of Aqueous Amphiphilic Solutions: Connection to Solution H-bond Fluctuation Dynamics?

Ranjit Biswas

S. N. Bose National Centre for Basic Sciences, Salt Lake, Kolkata 700 106, India




Acknowledgement: Atanu Baks (Simulations)

Thankful to: Dr. Rajib Biswas, Dr. Rakesh S. Singh, Dr. Mantu Santra


Focus: Anomaly in Solute-Centered Relaxation Dynamics in Aqueous Solutions

Method: Molecular Dynamics Simulations



A FEW PROPOSALS TO THINK ABOUT ..

- Frequency of SMCB Conference
- Seminar Series Call it SMCB Seminar Series – Frequency?



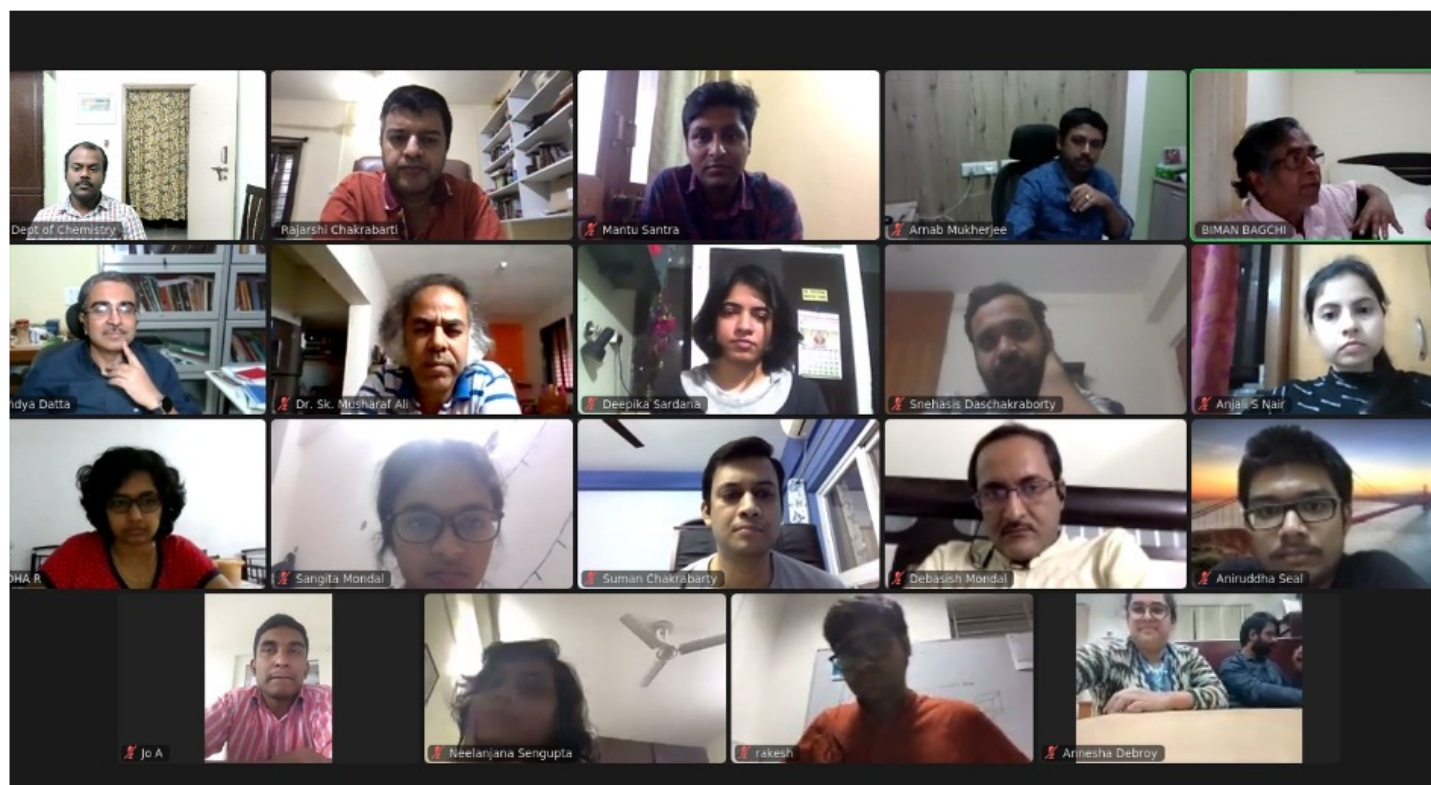
BIMAN BAGCHI

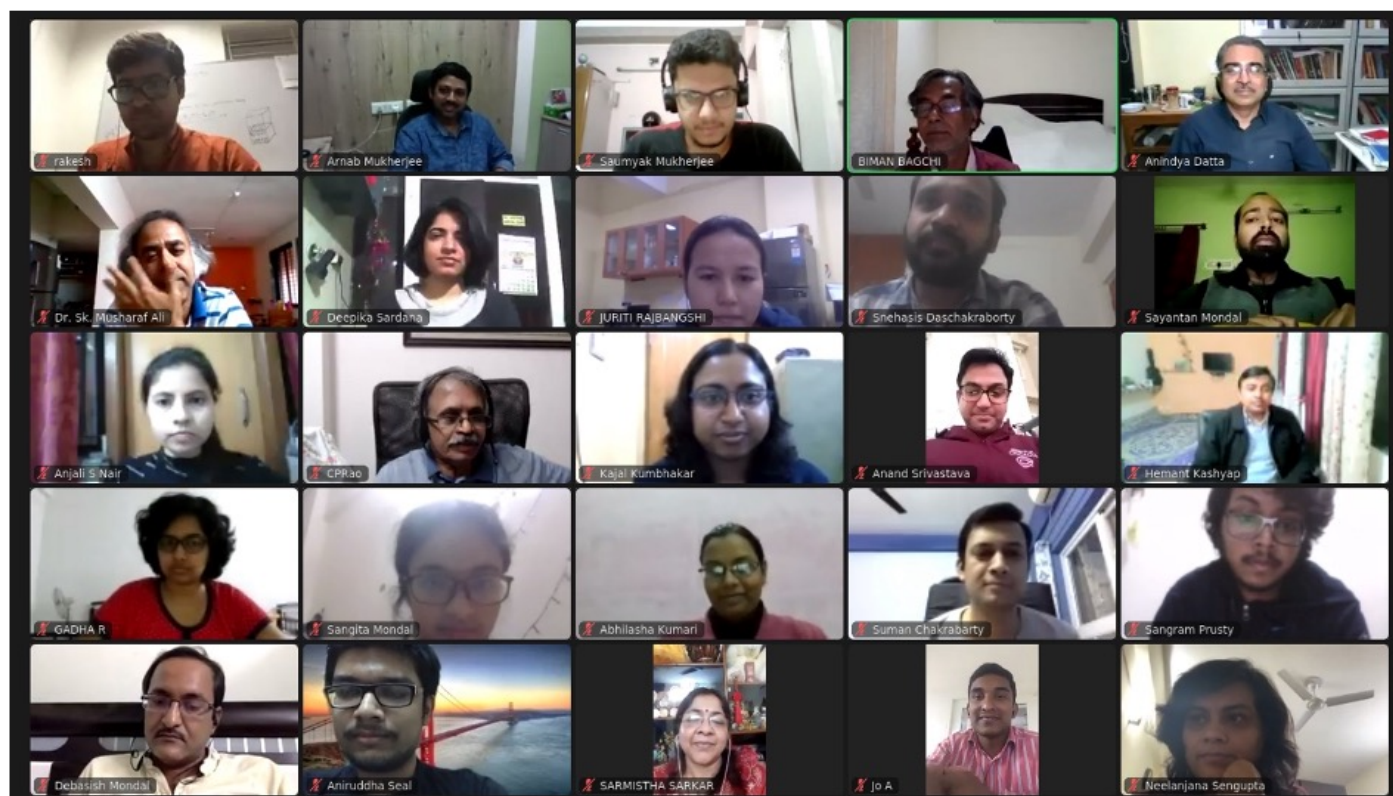
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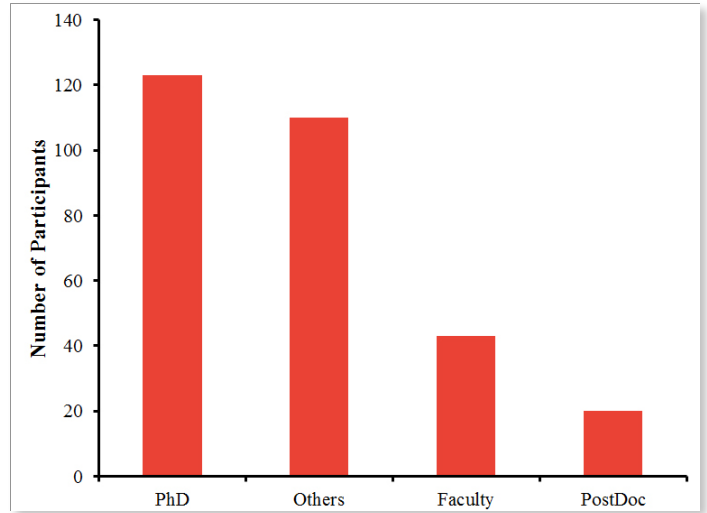
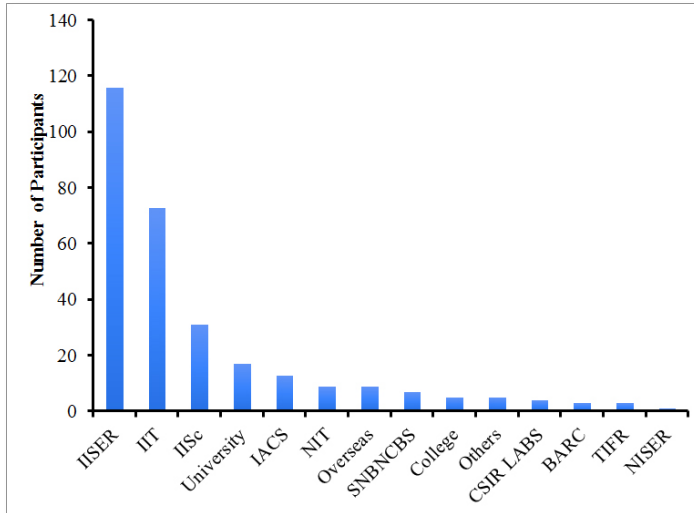




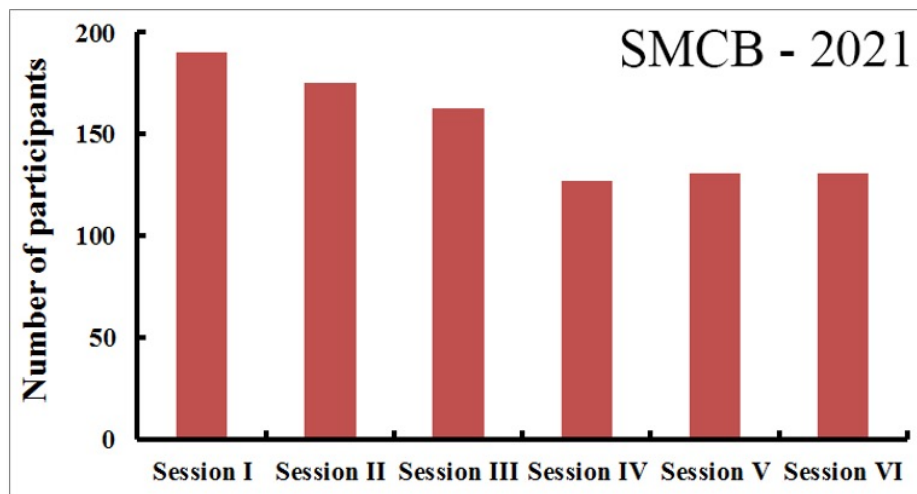


Statistics

The conference has received overwhelming responses from the community. More than 300 participants registered for the conference across the country and a few from overseas as well.



Details of registered participants.



Total number of participants attended at least one full talk in each session.

Thank You!