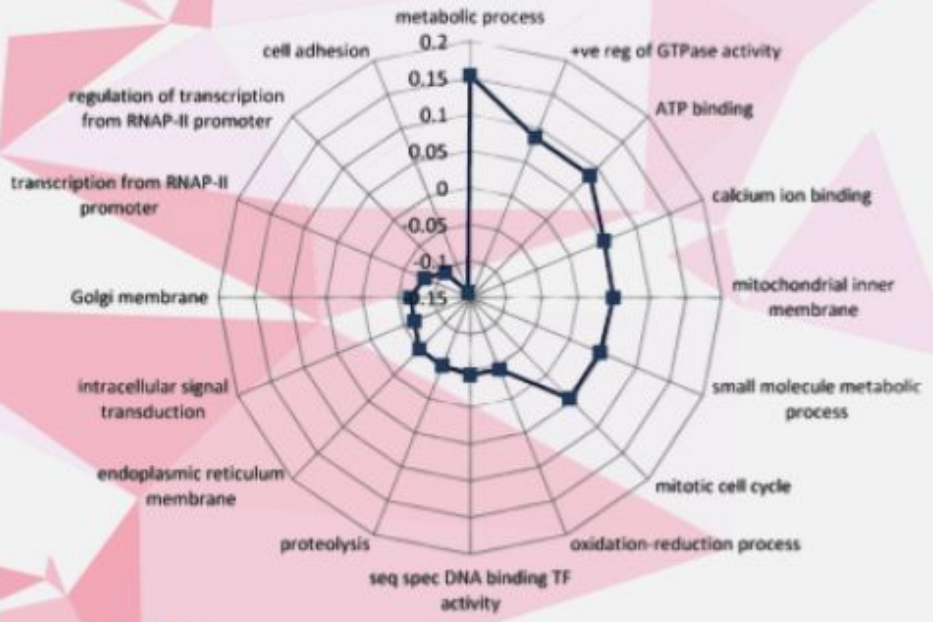
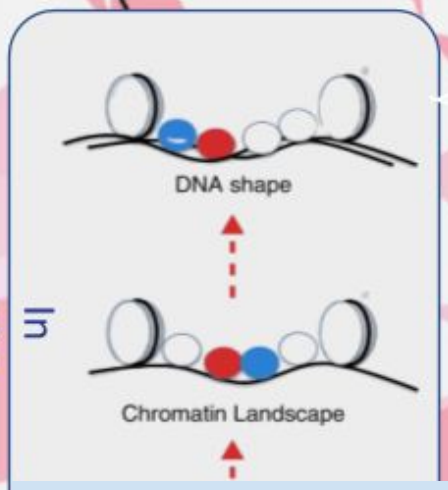
1ST ONLINE INDIA-UK BILATERAL SPARC SYMPOSIUM ON

TRANSCRIPTIONAL DYNAMICS IN DEVELOPMENTAL BIOLOGY

August 10-11,2020, 1:00 PM to 6:30PM IST





FOR DETAILS, SCAN QR CODE BELOW OR VISIT:

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Inaugural Session Schedule

Day 1: Monday, August 10, 2020			
IST	**GMT+1**	**Title**	**Speaker**
13:00-13:30	8:30-9:00	Registration of Participants	
13:30-14:30	9:00-10:00	Inaugural program	
13.30-13.40	9.00-9.10	Introduction to the SPARC program	Sharad K Soni
13.40-13.50	9.10-9.20	Welcome to participants and Introduction to Partcipating Labs-I:	Shandar Ahmad
13,50-14.00	9.20-9.30	Introduction to Partcipating Labs-II: Nicoletta Lab	Nicoletta Bobola
14.00-14.10	9.30-9.40	Introduction to Partcipating Labs-III: Rakesh Bhatnagar's lab	Rakesh Bhatnagar
14.10-14.20	9.40-9.50	Introduction to Partcipating Labs-IV: Rupesh Chaturvedi's lab	Rupesh Chaturvedi
14.20-14.30	9.50-10.00	Inaugual address by the Chief Guest	M Jagdesh Kumar

Inaugural Speakers

M Jagadesh Kumar
Vice-Chancellor, JNU,
(Chief Guest)

Rakesh Bhatnagar
(Vice-Chancellor, BHU)
SBT, JNU (SPARC Co-PI)

Shandar Ahmad
SCIS, JNU
(SPARC PI & Host)

Nicoletta Bobola
The Univ. of Manchester
(Principal collaborator)

Sharad Soni
(International
Collaboration Unit, JNU)

Rupesh Chaturvedi
SBT, JNU
(SPARC Co-PI)

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13:30-14:30	**9:00-10:00**	**Inaugral program**	
Session-I (Chair: Shandar Ahmad)			
14:30-15:15	**10:00-10:45**	Human embryonic development/organogenesis	Nicoletta Bobola
15:15-16:00	**10:45-11:30**	Rewiring of Transcriptional Regulators in the Human Fungal Pathogen *Candida albicans*	Krishnamurthy Natarajan
16:00-16:15	**11.30-11:45**	**BREAK**	
Session-II (Chair: K. Natarajan)			
16:15-17:00	**11:45-12:30**	Retinoic acid signaling regulates morphogenesis of the developing forebrain roof plate	Jonaki Sen
17:00-17:45	**12:30-13:15**	Transcriptional control and effects of mutations in regulatory elements during development	Araceli Garcia Mora
17:45-18:30	**13:15-14:00**	Sequence, structure and conformational dynamics signatures in genome wide regulatory programs of transcription factors	Shandar Ahmad
18:15-18:30	**13:45-14:00**	**Valedictory Program**	

Session Chairs

Shandar Ahmad

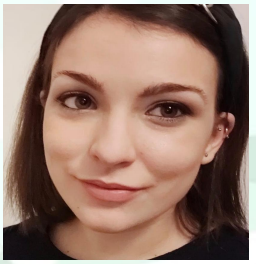
Krishnamurthy Natarajan

Speakers

Nicoletta Bobola

Krishnamurthy Natarajan

Jonaki Sen



Araceli Garcia Mora

Shandar Ahmad

Day 2 Schedule

Day 2: Tuesday, August 11, 2020			
Session-III (Chair: Mukesh Jain)			
13:30-14:15	**9:00-9:45**	Patterning and morphogenesis/ molecular control	Nicoletta Bobola
14:15-15:00	**9:45-10:30**	Sequence and structural variations in slow and fast transcription factor binding sites	Manisha Kalsan
15:00-15:45	**10:30-11:15**	Transcriptional signature modulating plant architectural traits enhances chickpea yield	Swarup K Parida
15:45-16:00	**11:15-11:30**	**BREAK**	
Session-IV (Chair: Brojen Singh)			
16:00-16:45	**11:30-12:15**	Unified representation of single cells states with pathways and its utility for developmental biology and stem cell studies	Vibhor Kumar
16:45-17:30	**12:15-13:00**	Identifying diversity in transcriptional regulation from high-throughput experiments	Leelavati Narlikar
17:30-18:15	**13:00-13:45**	Genomics and Molecular genetics approaches to study Transcription Factor function.	Arnab Mukhopadhyay
18:15-18:30	**13:45-14:00**	**Valedictory Program**	

Session Chairs

Mukesh Jain
SCIS, JNU

R.K.Brojen Singh
SCIS, JNU

Speakers

Nicoletta Bobola

Manisha Kalsan

Swarup K Parida

Vibhor Kumar

Leelavati Narlikar

Arnab Mukhopadhyay

Inaugural Program Speakers

M Jagadesh Kumar
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SCIS, JNU (SPARC PI & Host)

Nicoletta Bobola
The Univ. of Manchester, UK (Principal collaborator)

Sharad Soni
Int. Collab Unit (ICU), JNU

Rupesh Chaturvedi
SBT, JNU (SPARC Co-PI)

Technical Session Speakers

Nicoletta Bobola
The University of Manchester, United Kingdom

Jonaki Sen
Indian Institute of Technology, Kanpur

Krishnamurthy Natarajan
School of Life Sciences, JNU

Arnab Mukhopadhyay
National Institute of Immunology, New Delhi

Swarup K Parida
National Institute of Plant and Genomics Research, New Delhi

Vibhor Kumar
Indraprastha Institute of Information Technology, New Delhi

Leelavati Narlikar
CSIR- National Chemical Laboratory, Pune

Shandar Ahmad
School of Computational & Integrative Sciences, JNU

Araceli Garcia Mora
The University of Manchester, United Kingdom

Manisha Kalsan
School of Computational & Integrative Sciences, JNU

Introduction to Technical Session Speakers

SHANDAR AHMAD

Shandar Ahmad is a Computational Biologist interested in the role of genomic DNA shape in transcription factor/ target interactions and he investigates this using machine learning and deep learning techniques. Currently, the Dean of School of Computational & Integrative Sciences, Jawaharlal Nehru University, he heads SciWhyLab, which is involved in an integrated approach to study life science and health related problems. Relevant to this workshop, his works on predicting DNA-binding proteins, genomic DNA conformational ensemble dictionaries, integrative functional annotations employing transcriptomic, sequence and structure based signatures and clustering patterns of conserved residues in transcription factors are some of the techniques he has developed.

NICOLETTA BOBOLA

Nicoletta Bobola is Professor of Developmental Biology and Genomics at the University of Manchester, UK. She obtained her PhD at the University of Genoa, Italy; as part of her training and during her postdocs, she worked in Austria, Germany and the USA. She first established her independent group at the Max-Plack Institute of Immunobiology in Freiburg (Germany) and later moved to the University of Manchester as Lecturer in 2006. She has a career-long expertise in the field of transcriptional regulation. Her research aims at understanding how transcription factors instruct gene expression programs to generate specific cell fates in vertebrate embryonic development, using mouse and zebrafish model systems (Development 2003, 2005 and 2008; Dev Biol 2009; MCB 2011, Nucleic Acids Research 2012; Development 2013; Dev Cell 2015; Elife 2017; Elife 2018). A complementary area of research investigates the role of the non-coding genome in instructing human development, and how changes in non-coding regulatory information lead to disease (Elife 2016; Nat Comm 2020).

JONAKI SEN

Jonaki Sen completed her graduate studies from Albert Einstein College of Medicine, New York, where she studied the development of dorsal-ventral polarity in the Drosophila embryo. This was followed by postdoctoral studies on vertebrate retinal development in the laboratory of Prof. Constance Cepko in the Genetics Dept. at Harvard Medical School, Boston. At present, she is a Professor in the Department of Biological Sciences and Bioengineering at IIT Kanpur. The research interest of her laboratory lies in understanding various aspects of neuronal development. Her group studies the molecular mechanisms that regulate morphogenesis, differentiation and neuronal migration, using the chick and mouse embryo as models.

KRISHNAMURTHY NATARAJAN

Krishnamurthy Natarajan is currently a Professor at the Laboratory of Eukaryotic Gene Regulation in School of Life Sciences, JNU, Delhi. His broad area of research is Cell and Molecular biology/Molecular genetics: Transcription, chromatin and gene regulation with specialized work in TAF complexes and Mechanism of Transcription in *Saccharomyces cerevisiae, Candida albicans*; Gene regulation during Iron Homeostasis in *Candida albicans* and Transcriptional Regulatory Network controlling Melanogenesis and pigment disorders using Mouse Melanoma cell lines. He is also a Co-founder of Ahammune Biosciences which focuses on translating scientific research to provide a treatment to immunity based dermatological disorders such as vitiligo.

ARNAB MUKHOPADHYAY

Arnab Mukhopadhyay is currently Staff Scientist VI at the National Institute of Immunology (NII), New Delhi. He completed his MSc (1997) and PhD (2003) in Plant Molecular Biology from Delhi University South Campus followed by a postdoctoral stint (2003-2008) at UMASS medical school, Worcester, Massachusetts, USA. Since 2009, his lab at NII has been studying various molecular mechanisms of aging and longevity assurance using *Caenorhabditis elegans* as the model system. He is an elected fellow of The National Academy of Science, India (NASI) and Guha Research Conference (GRC) Society. He is a recipient of the Ramalingaswami Re-entry Fellowship (2009-2014), National Bioscience Award for Career Development (2016) and SERB-Science Technology Award for Research (STAR) award (2019).

SWARUP K PARIDA

Swarup Parida is currently a Staff Scientist IV at National Institute of Plant Genome Research (NIPGR), New Delhi, India. He completed his Ph.D. in Biotechnology from Jamia Hamdard University and National Research Centre on Plant Biotechnology (NRCPB), New Delhi. He specializes in Agricultural Biotechnology, Plant Genomics, Genetics and Molecular Breeding. He is a recipient of several prestigious Young Scientist Awards, including Indian National Science Academy (INSA), National Academy of Sciences India (NASI) and National Academy of Agricultural Sciences (NAAS), ELSEVIER-NASI-SCOPUS, NAAS-Associateship, to name a few. He is also currently a member of Crop Science Society of America and Editor of multiple international journals.

VIBHOR KUMAR

Vibhor Kumar received his PhD in Computational systems biology from Helsinki University of Technology (now Aalto), Finland. During his PhD, he solved the first and highest resolution (so far) structure of LDL (bad cholesterol) in native state at human body temperature. After completing PhD, he started applying computational approach to genomic data. He has worked at Genome Institute of Singapore (GIS) for more than 8 years and published some fundamental research findings. At GIS, he was primarily working on epigenome and gene regulation and applied his findings to other branches such as cancer and stem cell study. Currently, he is working on deriving functional genomic insights from single cell transcriptome and epigenome

LEELAVATI NARLIKAR

Leelavati Narlikar received her Bachelor's degree in Computer Engineering from University of Pune and a PhD in Computer Science from Duke University. She now works at the National Chemical Laboratory, Pune and is a part of a group of scientists there who use mathematics and computation to understand diverse aspects of biology. She is generally interested in designing new probabilistic models as well as algorithms to learn them, all with the hope of solving fundamental problems in biology and healthcare.

ARACELI GARCIA MORA

Araceli Garcia Mora is originally from Valencia, Spain and studied her Bachelors degree in biological sciences at the “Universidad Autónoma de Madrid”. Already at an undergraduate level she focused on bioinformatics and carried out her final year research project at the Centre for Molecular Biology Severo Ochoa (CBMSO), investigating the mitochondrial genome of *Leishmania*. She continued her studies at The University of Manchester, where she completed an MSc in Bioinformatics and Systems Biology. During her masters she joined the Bobola Lab group and decided to continue her research career in this group after graduating in 2018. Currently she is halfway through her PhD in Genomics, funded by the Medical Research Council UK. Her research interests focus on understanding combinatorial binding of Transcription Factors and investigating how disruptions in Transcription Factor binding to enhancers can cause developmental disorders and misregulation of transcription.

MANISHA KALSAN

Manisha Kalsan received her Master’s in Bioinformatics from Delhi Technological University and, is currently a PhD student at School of Computational & Integrative Sciences, Jawaharlal Nehru University. Her research interest lies in the applications of computational techniques to study the sequential and structural features of different transcription factors and their target sites, and to predict the different states of a genome on the basis of the conformational parameters of the DNA to annotate the genome for novel insights. She is also interested in developing predictors based on shape profiles for different types of target sites for a transcription factor, showing different temporal patterns.