NCBS ANNUAL TALKS 2018

Celebrating Diversity in Biology

3rd – 5th January

Modern Biology presents tremendous opportunities to address questions at all spatiotemporal scales using a range of tools, techniques, and model organisms. This meeting celebrates this diversity.

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Poster design: Deepti Trivedi

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NCBS ANNUAL TALKS 2018: **CELEBRATING DIVERSITY IN BIOLOGY** **3RD-5TH JANUARY 2018** Dasheri Auditorium, live streaming to Haapus		
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ABSTRACTS FOR THE ANNUAL TALKS 2018 CELEBRATING DIVERSITY IN BIOLOGY

Wednesday, January 3, 2018

Session 1: Love on the Fly

Chair: Girish Ratnaparikh
IISER Pune

09:00 – 09:45

Fly Genetics to study Growth Control in Development and its aberration in cancer

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Elaborate network of signalling pathways ensure growth control during animal development such that various organs and tissues attain specific size and shape. This network also allows certain degree of plasticity to respond to environmental cues such as availability of nutrition adjusting size of organs and tissues, at the same time restricting their development appropriate to the overall body size. Disturbance in any component of this intricate growth control mechanism in human would result in cancer and many ageing-related disorders.
I discuss our efforts in identifying key regulators of growth during epithelial tissue morphogenesis using *Drosophila* genetics. Human orthologues of many of those players are implicated in aggressive tumors and metastasis.

09:45 – 10:15

Tuning of lipid transfer reactions at membrane contact sites in Drosophila photoreceptors

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During phospholipase C (PLC) signalling, the hydrolysis of phosphatidylinositol 4,5 bisphosphate (PIP2) generates signalling intermediates that mediate information transfer and key cellular functions. However, given the low abundance of PIP2, the consumption of this lipid by PLC signalling needs to be matched by its resynthesis from phosphatidylinositol (PI). In eukaryotic cells a sequence of metabolic reactions couples PIP2 hydrolysis to its resynthesis. The lipid intermediates of these reactions cannot diffuse across aqueous cytosol; yet the enzymes that mediate these reactions are distributed between two membrane compartments, the plasma membrane (PM) and the endoplasmic reticulum (ER). To sustain the PIP2 cycle, lipid intermediates need to be transported between the endoplasmic reticulum (ER) and the plasma membrane (PM); this is thought to be mediated by lipid transport proteins located at membrane contact sites. However, the mechanism by which such lipid transport is regulated remains unclear. We address this question in the context of the Drosophila RDGB protein that is located at the ER-PM contact site in photoreceptors, contains a PI transfer domain and is required to sustain PIP2 signalling in photoreceptors. We find that multiple non-PITP domains of RDGB regulate the function of its PI transfer domain. Further, using a genome wide in vivo genetic screen, we define novel regulators of RDGB function during PIP2 signalling. Thus, our work defines novel molecular

mechanisms by which lipid transfer is regulated at contact sites during PLC signalling in Drosophila photoreceptors.

10:15 – 10:30

Neuropeptide driven store-operated Ca2+ entry regulates central dopaminergic neuron activity and flight

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Calcium ions (Ca2+) function at the critical interface of membrane excitability and cellular signaling in neurons. In non-excitable cells a significant fraction of Ca2+ entry is via the STIM/Orai pathway of store-operated calcium entry (SOCE). The physiological significance of STIM/Orai mediated SOCE in mature neurons however, needs better understanding. Work from our lab has previously demonstrated that maturation of the central nervous system of Drosophila melanogaster during pupal development, specifically dopamine synthesizing neurons, require GPCR signaling as well as SOCE. In this talk, I will discuss about a specific neuropeptide receptor driven SOCE pathway that is required in central dopaminergic neurons for maintenance of acute flight. Furthermore, I will provide genetic and cellular evidence to demonstrate that this neuropeptide signaling pathway and downstream SOCE are both required to maintain neural activity in mature dopaminergic neurons for proper functioning of the flight circuit.

Session 2: Ta(l)king Shape

Chair: Sreelaja Nair
TIFR Mumbai

11:00 – 11:15

Role of super enhancer in regulating INK4a/ARF locus

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Distal DNA regulatory elements known as enhancers regulate gene expression by looping with the promoter of the target gene. It has been estimated that human genome contains around 1 million enhancers. Enhancers are cell type specific, hence at a given time only a few thousand enhancers are active which may drive the gene expression. Interestingly, it has been seen that highly expressed critical genes are often associated with cluster of enhancers which have been termed as super enhancers where they show higher enrichment of various transcription factors and drive gene expression exponentially. It is assumed that constituent enhancers of a super enhancer act in synergy, such that cumulative sum of these individual enhancers is the final output delivered to the target gene for its expression rate. However, this model does not account for enhancer mediated enhancer regulation within a specific super enhancer where, enhancer hierarchy may be playing a lead role in cell/tissue-type specific manner. In order to study the mechanism of action of individual enhancers within a super enhancer, we chose GWAS and senescence hot spot, INK4a/ARF locus. We show a super

enhancer network in adjacent gene desert region controls this locus positively.
We also report the importance of non-coding RNAs (eRNAs) transcribed from these enhancers in gene regulation. Further we show a probable mechanism of action by individual enhancers via recruitment of histone modifiers on their target genes. Our findings suggest a network of enhancers, which regulates INK4/ARF locus in a combinatorial and hierarchical manner.

11:15 – 11:30

Atypical activities of Rice RNA dependent RNA polymerase 3 and its role in plant growth and development

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RNA silencing is an evolutionarily conserved mechanism to regulate gene expression as well as a defense mechanism against viruses in plants. Production of dsRNA is the trigger for this pathway. Plant specific RNA-dependent RNA polymerases (RDR) catalyze the synthesis of dsRNA from ssRNAs, so that requisite substrates for Dicer-mediated cleavage are generated. There are at least 6 members in plant RDR family. Among these members, functions of RDR1, RDR2, and RDR6 are well known among different plants. However, RDR3 that belong to a unique clade (gamma), has not been characterized, mainly because it is a pseudo-gene in the model plant Arabidopsis. However, extensive expression data indicates that, in higher plants with bigger genomes such as rice, RDR3 is highly expressed tissue specifically. Sequence and phylogenetic analysis revealed that OsRDR3 has unusual conserved motifs when compared to other RDRs. In order to study functional and biochemical properties of OsRDR3, it was expressed in E. coli cells and recombinant protein was purified. We found that OsRDR3 can synthesize complementary strands not only from ssRNA substrates, but also from ssDNA.
Surprisingly, OsRDR3 can recognize circular viral ssDNA substrates to generate complementary RNA. OsRDR3 activity is inhibited at pH below 7.0, it requires a divalent cation, and active in a wide range of temperature. O. sativa and Nicotiana tabacum

plants over-expressing OsRDR3 exhibit vigorous growth of plants, while its silencing in rice impairs development and growth. These data suggests that OsRDR3 acts as an unusual template-independent polymerase with important roles in growth and development.

11:30 – 12:00

The assembly, maintenance and repair of muscle.

Dhananjay Chaturvedi, Rajesh Gunage, Nagaraju Dhanyasi, M. Umashankar and **K. VijayRaghavan**
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The laboratory studies how the nervous system and muscles develop and, with Mani Ramaswami's group, how neural circuits function. Early in development sets of muscle progenitors cells are set aside, in each segment of the fruitfly. In the second thoracic segment these cells proliferate during larval life in a regulated manner to create a large pool of myoblasts that will fuse to form the giant multinucleate muscle fibres that power flight. The formation of muscle sarcomeres upon myoblast fusion is a carefully choreographed process, involving the dynamic partnership of microtubules and actin. The nervous system also plays role in selecting the right combination of muscle structural proteins that are needed. We had previously deciphered the molecular mechanism of how muscle stem cells are central to the formation of the large myoblast pool need for flight muscle formation. We now show that these stem cells persist in the adult and, upon muscle damage, proliferate fuse and participate in repair of muscle. Important molecular players have been identified. Taken together we have shown for the first time in any organism that muscles progenitor use symmetric and asymmetric proliferation of stem cells to grown in number. We have discovered that muscles in insects can be repaired by satellite cells, much the same way as in mammals, making Drosophila flight muscle a very tractable preparation to study muscle maintenance, damage and repair.

12:00 – 12:30

Coordinating Cell Shape changes during Early Inner Ear Morphogenesis

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The inner ear arises from non-neural ectoderm as a result of instructions sent by surrounding tissues. These interactions progressively restrict the potential of the ectoderm and result in the formation of the otic placode, a disk of thickened ectoderm that will exclusively give rise to all of the inner ear as well as its neurons. While otic placode is a surface structure, the inner ear is internalized, embedded within the cranial mesenchyme. In this talk I want to discuss our progress in understanding the mechanisms that result in these morphological changes. How does the ectoderm become thick when it is induced? How does it invaginate? How does the invaginated ectoderm close? How are these cell-level events coordinated across the tissue?

12:30 – 13:00

The mammalian adult brain: inside the health and wellbeing of the new and the old neurons

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Neurons are one of the most complex and elaborate cell types in any organism. While they need to function through the entire lifespan of an organism, once formed during development, these cells are largely incapable of repair or regeneration. What underlies the heathy maintenance of such a long-living, complex and indispensable cell type? While long-living neurons represent the majority of the neuronal population, a couple of very specific neurogenic locations in the adult brain continuously produce new neurons by the process of adult neurogenesis. The molecular regulation that governs various aspects of adult neurogenesis, such as optimal production and fate decisions, remain poorly understood. My talk will focus on two specific aspects of neuronal cell biology in the adult brain — maintenance of mature neurons and genesis of new neurons.

Session 3: Form and Function

Chair: N Srinivasan

IISc Banglore

16:30 – 17:00

Exploring domain diversity in the protein sequence space using computational approaches

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Domains are the basic building blocks of proteins which can combine to give rise to different combinations of domain architectures. Ascribing a biological context to domains in a protein is the first step towards understanding its biological function. I will present some of the attempts in our lab to bridge the gap between protein sequence and structural space. A computational approach of multi-pronged sequence searches were carried out to recognise remote homologues within genomes of around ~160000 different organisms, starting from nearly 11000 domains of known structure. Co-existing domains of such remote homologues are also recognized using Hidden Markov Models. The distribution of remote homologues across different protein structural classes, folds and superfamilies will be discussed. Finally, illustrative collaborative projects will be described that exemplifies direct applications of such a repository in classical biology.

17:00 – 17:30

Matters of the Heart: Fluid Flows Talk to the Electrical System

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An elaborate and well-tuned electrical system generates the cardiac Action Potential (cardiac AP), which underlies the beating of the heart. The shape and duration of the cardiac AP is held within close tolerances as small variations can lead to cardiac arrhythmias and even catastrophic heart failure. The firing of the Action Potential, in turn, results in contractions of the musculature of the heart and hence blood flow through the body. The effect of mechanical forces at work during the heart beat on the electrical system of the heart have not, surprisingly, been investigated in detail so far. The ventricles lack specialist mechanosensitive channels i.e. channels that are relatively insensitive to other stimuli but mediate ionic currents in response to membrane deformation. Here we investigate the influence of mechanical shear on a critical component of the electrical system – a voltage-gated ion channel that plays a major role in the repolarization of the cardiac Action Potential. The product of the human ether-a-go-go related gene (hERG) is the channel underlying the fast component of the delayed rectifier potassium currents, Ikr. When HEK293T cells expressing hERG1a channels were exposed to laminar shear stress, there was a 30% to 40% increase in whole cell current. Modulation of the whole cell current upon application of shear stress was reversible and found to be dependent on the integrin pathway. Our data indicates that mechanoelectric feedback modulates hERG channel activity through the integrin pathway, demonstrating for the first time that mechanical forces in the heart influence its electrical activity.

17:30 – 18:00

Computational protein folding and function.

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I will talk about folding simulations of ubiquitin and what one might infer about ubiquitin function from these simulations.

18:00 – 18:45

Deconstruction of the Ras switching cycle through saturation mutagenesis

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Ras proteins are highly conserved signaling molecules that exhibit regulated, nucleotide-dependent switching between active and inactive states. The high sequence conservation of Ras requires mechanistic explanation, especially given the general mutational tolerance of proteins. In collaboration with Rama Ranganathan (UTSW), we have used deep mutational scanning, biochemical analysis and molecular simulations to understand constraints on Ras sequence. Ras exhibits global sensitivity to mutation when regulated by a GTPase activating protein and a nucleotide exchange factor. Removing the regulators shifts the distribution of mutational effects to be largely neutral, and reveals hotspots of activating mutations in residues that restrain Ras dynamics and promote the inactive state. Evolutionary analysis, combined with structural and mutational data, argue that Ras has coevolved with its regulators in the vertebrate lineage. Overall, our results show that sequence conservation in Ras depends strongly on the biochemical network in which it operates, providing a framework for understanding the origin of global selection pressures on proteins.

Thursday, January 4, 2018

Session 4: A 'Health'y Session

Chair: Suresh Subramani
UCSD

09:00 – 09:45

Interface between cytoskeletal dynamics and tumor biology

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Abstract awaited.

09:45 – 10:15

Update on "DNA tumour virus cancers" and off campus health sciences research

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Studies of DNA tumour viruses have been a major driving force in understanding mechanisms of carcinogenesis. The major focus of our group has been in delineating the signals that complement the function of human papillomaviruses and analyzing key sub-sets that drive progression in human cervical cancers. In particular, we have focused on ligand dependent Notch signaling and the CD66+ subset. In this talk, I will discuss recent data by Calvin Rodrigues and Leanna Rose Joy, which examines the role of Suv39H1, a chromatin regulator, and TGF-B signaling, respectively, in driving migratory phenotypes in such subpopulations. These results expand our understanding of chromatin driven switches during early phases of cancer metastasis, and begin an exploration of the functional role of CD66.

Beyond these directions, Reety Arora has an independent program supported by the Wellcome Trust/ DBT India Alliance, investigating mechanisms of tumor progression by Merkel cell polyomavirus, focusing on the cell of origin in these cancers. I will also briefly allude to our off-campus activities that we began in 2008 as a teaching effort, and then expanded to build laboratories at St. John's medical college campus with the support of a DBT glue grant. The grant was centred around hematological malignancies and genomics, and there has been a transition with younger colleagues from the NCBS campus moving there to drive the program further. One of the unanticipated but potentially far reaching programs that emerged from this interaction was a viral

discovery metagenomics effort initiated and sustained by Chitra Pattabiraman and her team. With the support of a philanthropic grant, we are creating a “Dengue consortium” in both India and Africa extending the metagenomics effort.

10:15 – 10:30

Autophagy-Endocytosis nexus in the control of intracellular mycobacterial infection

Harmanjit SIngh[1], **Manisha Goel[1]**, Shanthanu Singh[2], Varadha Sundaramurthy[1]
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Intracellular pathogens alter multiple pathways in the host cell for their survival, with manipulations of trafficking pathways being the most common. We are dissecting the pathways of autophagy and endocytosis to study their influence on intracellular mycobacterial survival. Endocytosis and autophagy interact with each other at multiple levels, they share common molecular mediators and have a similar fate i.e. they fuse with lysosomes and degrade their contents. While both the pathways are individually well studied in the context of bacterial infections, their inter-relationship and possible cross-regulation via the shared lysosome is not clear. We are developing high content analysis tools to understand this nexus. Using chemical perturbations and multiplexed high content assays, we have uncovered compounds that alter the two trafficking pathways in distinct ways and have differential bacterial survival rates and vice versa. Our results validate known control mechanisms in intracellular mycobacterial survival, reveal potentially new ones and offer interesting insights into the broader connections between endocytosis and autophagy.

Session 5: Cellular Struggles

Chair: Amit Singh

IISc Banglore

11:00 – 11:30

Diversity in bacteria-virus ecosystems may be facilitated by restriction-modification systems

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Virulent bacteriophage and their bacterial hosts represent an unusual sort of predator-prey system where hundreds of new predators are born each time a single prey is eaten. It is puzzling how, despite the apparent effectiveness of the phage predators, they manage to avoid driving their bacterial prey to extinction. Bacteria, of course, have developed multiple mechanisms to defend against phage. I'll talk about some mathematical models, which suggest that restriction-modification systems, which are at best a weak and temporary defence against bacteriophage, may enhance long-term coexistence of multiple bacterial strains. The models suggest that this diversity can be as large as the burst size of the phage but no larger - a curious correspondence between a number at the level of species and a biophysical parameter that characterises individual phage.

11:30 – 11:45

The evolutionary impact of tRNA modifications on bacterial tRNA gene content

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Bacteria exhibit large diversity in key aspects of translation, including tRNA genes and codon use. However, the evolutionary processes that generated this diversity remain unclear. We analyzed the evolution of a major component of translation: tRNA modifications that allow specific ("target") tRNAs to recognize multiple codons. Phylogenetic ancestral reconstruction shows that most modifications are ancestral to the eubacterial clade, but were lost multiple times subsequently. Interestingly, most modification losses (or gains) are associated with increased (or reduced) tRNA diversity. Specifically, modification gain (or loss) events were co-incidental with the evolutionary loss (or gain/retention) of "non-target" tRNAs that are necessary to decode all sense codons in the absence of modifications. Additionally, such shifts in tRNA diversity were also correlated with increased bias in genomic GC content and associated codon use. Thus, our analysis provides the first clear evidence for the hypothesis that modifications played a key role during the early evolution of key aspects of translation, by shaping the tRNA gene content of bacteria. We hypothesize that major shifts in genome GC and codon use selected for an altered tRNA pool, weakening selection on modifications and allowing their repeated loss through drift.

11:45 – 12:00

Survival in low-nutrition: study on a small colony size variant of *Escherichia coli* isolated in prolonged stationary phase

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Bacteria passes through four distinct phases of growth in rich media: lag, log, stationary and death. Upon further incubation without addition of nutrients, the remnant population can sustain itself for long periods of time with no change in the total population size; a phase known as the prolonged stationary phase. In this phase, younger subpopulation tends to take over pre-existing, older subpopulation, a phenomenon known as Growth Advantage in Stationary Phase (GASP) [1]. We evolved a GASP strain (*E.coli* K12 ZK819) in prolonged stationary phase for a month. We describe a Small Colony size Variant (SCV), which repeatedly came up in a specific time window of 19th to 23rd day in prolonged stationary phase. This strain is characterized by slower growth compared to parent and is able to outcompete parent strain as well as co-existing large colony variant in spent media. SCV also has higher tolerance to specific antibiotics. Whole Genome sequencing led us to a putative mutation responsible for the small colony phenotype, which we verified by transferring the mutation to different genetic backgrounds, and looking at the colony-size phenotype. We found that a single point mutation in the *rpoC* gene (coding for beta-clamp of RNA polymerase machinery) is responsible for the small colony size phenotype. This mutation also confers competitive advantage to SCV over its ancestors.

Reference :
1. Microbial competition: Escherichia coli mutants that take over stationary phase
cultures. Kolter et al. Science(1993)

12:00 – 12:30

Cells under extreme perturbations

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Not all cells (organisms) can survive extreme perturbations such as complete freezing or desiccation of their bodies. While short enough durations of these perturbations invoke stress response in the cells, prolonged periods result in a transition to dormancy (eg. sporulation). Often, survival goes together with the ability of the cell to make a perturbation-triggered material phase transition, such as the solidification of the cytoplasm. However the nature of these transitions and their underlying mechanisms are unclear. Further, these extreme states of living matter and the accompanying biochemical processes, if any, could have implications in understanding not only cellular organization and function but also the ecoevolutionary traces of cells. Using physicists' yeast as a model system, we combine approaches from experimental evolution, molecular biology and materials science to study their behaviour under freezing and thawing.

12:30 – 13:00

Possible and impossible cells

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In my research I use the eukaryotic membrane traffic system as a window to study the emergence of cellular complexity. Homeostasis is a central issue in cell biology: how are the compositions of distinct membrane-bound organelles maintained in the face of constant exchange of material via vesicles? Applying methods from graph theory, I will show how homeostasis renders many vesicle traffic topologies impossible and places strict constraints on the dynamics of the SNARE proteins that mediate vesicle fusion. Conversely, among possible or probable homeostatic vesicle traffic topologies unexpected levels of organisation emerge spontaneously, including collections of compartments that resemble the Golgi apparatus. These models suggest pathways by which new organelles might be added to the eukaryotic cellular plan over evolutionary timescales.

Session 6: Actin' Up

Chair: Roop Mallik

TIFR Mumbai

16:30 – 17:00

TBA

Madan Rao
National Centre for Biological Sciences
NCBS-TIFR
Bangalore

Abstract awaited.

17:00 – 17:30

Endocytic regulation of cell membrane tension

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Cells regulate their membrane area and tension by finely tuned mechanisms. However, the cellular processes and molecular mechanisms behind this regulation are poorly understood. Exo-endocytic processes undoubtedly play a major role in controlling these physical properties of the membrane. We find that a specific mode of endocytosis, the clathrin and dynamin-independent endocytic pathway is a key component of the cellular machinery that sets the resting membrane tension and may be responsible for maintaining area homeostasis. In my talk I will discuss our efforts in understanding the molecular machinery that regulates this pathway and how this may tie in with regulating membrane tension.

17:30 – 18:15

Recent progress on the kinesin mechanism

Daniel R. Peet, Algirdas Toleikis, Nicholas J. Carter, Nigel J. Burroughs,
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Kinesin-1 is a walking machine that steps processively towards the fast growing (plus) ends of microtubules, hauling molecular cargo to specific reaction sites in cells. At low loads kinesin typically takes about 100 x 8 nm steps per diffusional encounter with the microtubule, with a very strong directional bias towards the microtubule plus end. Under hindering loads, kinesin starts to take backsteps, and at stall force, it takes an equal number of backsteps and forward steps. Neither the mechanism of choosing the stepping direction nor the mechanism of backstepping is fully understood. We have been using single molecule optical trapping to apply loads to kinesins *in vitro* in order to study the forestep-backstep decision process and especially their backstepping mechanism. We are counting forward steps, backward steps and detachments at particular forces, and investigating how different factors influence the forestep-backstep decision process. So far, we found that Drosophila kinesin-1 walking on unstabilised pig brain GDP-microtubules has a reduced stall force compared to the same motor walking on taxol-microtubules. Furthermore, when walking on *S. pombe* microtubules, kinesin-1 dwells for longer at any particular load, stall force is reduced to ~6pN and detachments are less likely at any particular force, indicating an increase in processivity. These findings show that kinesin's forestep-backstep decision is taken not by the motor domain alone, but by the motor-microtubule complex.

In related work, we have recently found that kinesin-1 can modulate microtubule dynamics. By capping dynamic microtubules with GMPCPP tubulin, tethering them in a microfluidic flow and introducing kinesin, we have found that strong-state (ATPand apo-) kinesin-1 motor domains inhibit the shrinkage of GDP-MTs by up to 2 orders of magnitude and expand their lattice spacing by 1.6%. Overall, our work is revealing unexpected new ways in which the mechanochemical cycles of kinesin and tubulin interlock, allowing kinesins to influence the structure, stability and mechanics of microtubules, and microtubules to influence the stepping action of kinesin.

Friday, January 5, 2018

Session 7: What's the Buzz?

Chair: Renee Borges
IISc Banglore

09:00 – 09:30

Molecular evolution and functional diversity of doublesex, a master regulator of polymorphisms in insects

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Doublesex is a well-known transcription factor that controls early sexual differentiation in insects. Increasingly, a wide array of secondary sexual traits and adult polymorphisms are shown to be governed by developmental regulation of doublesex, ever expanding our understanding of the developmental genetic power of this key gene. In this talk I will show how accelerated molecular evolution, some of it under positive selection, in parts of this gene has modulated a differential pace of evolution in critical sex-specific exons. This molecular evolution has influenced the structural and functional diversity of doublesex. This work highlights the role of doublesex as a magical gene that has potentially facilitated a singular diversification of sex-limited traits in the incredibly diverse set of insects.

09:30 – 10:00

Tritrophic interactions mediated by infochemicals

Radhika Venkatesan
National Centre for Biological Sciences
NCBS-TIFR
Bangalore.
radhika@ncbs.res.in

Plants-insect interactions are complex, dynamic and subject to variation with time and space. Upon insect attack, plants release specific bouquet of volatile organic compounds as signals to attract parasitic wasps. These wasps utilize herbivore induced plant volatiles (HIPVs) to locate suitable oviposition site. We study such tritrophic interactions in our lab asking how HIPV production is regulated and whether herbivorous insects can use HIPVs to upregulate their own defence mechanisms as a counter-adaptation to parasitization. We use Gossypium hirsutum, Spodoptera litura and Bracon brevicornis as study systems to understand these interactions. In this talk, results on HIPV emission from various plant systems would be discussed. The role of HIPVs in parasitoid attraction and defence priming in herbivores would be shown. Our data suggest that upon exposure, S. litura can escape parasitization by priming immune response. Further, elevated immune defense confers additional advantage of anti-microbial activity. Priming of S. litura was found to be associated with trade-offs like developmental alterations. Our results demonstrate for the first time that HIPVs can mediate adaptation mechanisms in insect herbivores. These findings are crucial to understand tri-trophic interactions.

10:00 – 10:15

A universal insecticide from an Indian medicinal plant activates broad spectrum olfactory receptor neurons.

Srishti Batra and Shannon Olsson
National Centre for Biological Sciences
NCBS-TIFR
Bangalore.
srishtib@ncbs.res.in

We have recently identified a plant-derived compound from an Indian medicinal plant, *Artemisia pallens* that serves as a broad spectrum fumigant insecticide across several insect orders. Electroanntenogram recordings revealed that the chemosensory systems of diverse insect species, ranging from Archaeogantha to Dipterans can detect this volatile. With the aim of understanding conserved chemosensory detection of this compound across all insect orders, we used various approaches- toxicology, behavioural bio-assays; neurogenetics, and electrophysiological recordings from insect olfactory sensory neurons (OSNs). To confirm how this compound interacts with insect chemoreceptors, we examined the response of various chemosensory mutants and heterologously-expressed insect ORs in HEK293 cell lines using calcium imaging. This compound is able to activate all OSNs expressing the ORx/ Orco complex in Drosophila melanogaster except for highly specialised olfactory receptors such as pheromone OSNs. IR and Grexpressing cells do not respond, nor do Orco-null mutants, heterologouslyexpressed specialized ORs/Orco, or receptor-specific knockouts, suggesting that the ORx/Orco complex, rather than Orco itself, is activated. Behavioural assays also indicate that several species are repelled by compound. The mode of toxicity, however, is different from olfactory detection, correlating to activation of Na+/K+ - ATPase via fumigation. We are now using this information to better

understand the functioning of insect olfactory receptors with the help of bioinformatics approaches. The unique multiple activities of this compound provide new opportunities for both insect control and understanding the molecular mechanisms of olfaction and ion exchange in insects.

10:15 – 10:30

Time memory and Egr-1 expression in honey bee foragers

Aridni Shah, and Axel Brockmann
National Centre for Biological Sciences
NCBS-TIFR
Bangalore.
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Training honey bees to an artificial feeder has been one of the most successful behavioral paradigms to identify insect sensory and cognitive capabilities. Studies on molecular changes occurring during foraging provide the possibility to identify brain regions and molecular processes involved in insect cognition. For example, we recently demonstrated that continuous foraging in honey bees is accompanied by a sustained upregulation of the transcription factor Egr-1 (early growth response protein-1) and candidate downstream genes involved in learning and memory. Since Egr-1 expression changes were strongly associated with onset of foraging, we asked if the time of foraging affects Egr-1 expression. We found that Egr-1 expression was upregulated at the time of training in morning (8-10 am) and evening (4-6 pm) feeder trained foragers. At all the other tested time points, expression levels were low. More importantly, when we prevented time trained foragers from flying using artificial rain, these foragers showed slight but significant increases in Egr-1 expression around the time of feeder training. Interestingly, the increase in Egr1 expression appeared shortly before the time of training. Additionally, in situ hybridization studies demonstrated that foraging- and feeder time-training lead to an up regulation of Egr- 1 in the small-type Kenyon cells of the mushroom bodies. Our finding nicely corresponds with earlier studies indicating that the Kenyon cells are involved in information processing during foraging and orientation flights. Based on our results, we propose that Egr-1 is a potential molecular link between the output of the

circadian clock and the learning and memory systems involved in foraging.

Session 8: It's Electric!

Chair: Upi Bhalla

NCBS Banglore

11:00 – 11:45

TBA

Michael Hausser
Wolfson Institute for Biomedical Research
University College London
London

Abstract awaited.

11:45 – 12:00

Precise excitation-inhibition balance controls gain and timing in the hippocampus

Aanchal Bhatia, and Upinder S. Bhalla
National Centre for Biological Sciences
NCBS-TIFR
Bangalore.
aanchalb@ncbs.res.in

Excitation and inhibition (EI) are normally closely balanced throughout the brain. EI balance has been seen in response to stimuli in vitro and in vivo, but it is unknown if balance emerges out of complex network dynamics or if it exists at the level of presynaptic connections. We used patterned optical stimulation to activate hundreds of distinct CA3 neuron groups. We found that even arbitrarily chosen CA3 subsets elicited very tightly coupled excitation and inhibition at the postsynaptic CA1 neurons (precise balance). This revelaed an exceptional degree of structure at the level of connectivity of the network. Integration of these tightly balanced inputs lead to divisive normalization at the subthreshold level. Divisive normalization of firing rates is a canonical neural computation, observed in several cortices. On the other hand, Subthreshold Divisive Normalization (SDN) is a novel form of gain control, which normalizes and gates inputs in the subthreshold domain, before the neuron spikes. Mechanistically, SDN emerges from balance due to decrease in EI onset latency with increase in input. This also results in input information being shared between amplitude and timing of the response. In summary, precise balance in feedforward networks could be a general mechanism of independent gain and timing control in individual neurons of sparsely coding balanced networks.

12:00 – 12:15

Fighting fire with fire: rolling back the effects of stress after it has happened.

Prabahan Chakrabarty, and Sumantra Chattarji
National Centre for Biological Sciences
NCBS-TIFR
Bangalore.
prabahanc@ncbs.res.in

A single, traumatic exposure to stress can often lead to delayed emergence of symptoms, as in Post-Traumatic Stress Disorder (PTSD). Although a hallmark of PTSD is the elevation in circulating levels of glucocorticoids, a number of counterintuitive clinical observations also suggest a protective role of the stress hormone in this context. For example, patients in intensive care units (ICU) who received stresslevels of glucocorticoid as a part of their treatment were less likely to develop ICUrelated PTSD symptoms in the future (*Schelling et al, 2006*). We examined this paradoxical relationship between PTSD and glucocorticoid by using an animal model of the disorder, with the broader aim of understanding intervention strategies once the stress has already happened.

12:15 – 13:00

Serotonin and mitochondrial biogenesis

Vidita Vaidya
Department of Biological Sciences
Tata Institute of Fundamental Research
Mumbai

Abstract awaited.

Poster Session

Day 1 - January 3, 2018

1. Analysis of a metazoan specific phosphoinositide kinase

Harini K, Ramya Viswanathan, Sanjeev Sharma and Padinjat Raghu
National Centre for Biological Sciences, Bengaluru, India

4. The Mouse Genome Engineering Facility - Services and Technologies to enhance laboratory mouse quality

Jaya Purushotham, ShilpaKumari B A, Reena Vemula, Kamlesh KV, Latha Chukki, **Aurelie Jory**
National Centre for Biological Sciences, Bengaluru, India

7. Next Generation Genomics and Sanger Sequencing Facility

Tejali Naik, Greeshma Venugopal, Riaz Basha Shaik, Awadhesh Pandit
National Centre for Biological Sciences, Bengaluru, India
Center for Cellular and Molecular Platforms, Bengaluru, India

10. Precise excitation-inhibition balance controls gain and timing in the hippocampus

Aanchal Bhatia, Sahil Moza, Upinder S. Bhalla
National Centre for Biological Sciences, Bengaluru, India

13. NCBS Museum and Field Stations Facility - Infrastructure and facilities for biodiversity studies in India

Varad B. Giri, Tarun Karmakar and Krushnamegh Kunte
National Centre for Biological Sciences, Bengaluru, India

16. Warming & N-deposition: Boon or Bane for the heavily invaded Nilgiri grasslands?

Manaswi Raghurama, Mahesh Sankaran
National Centre for Biological Sciences, Bengaluru, India

19. Understanding the role of insulin-like peptide producing neurons in regulation of Drosophila flight

Anamika Sharma, Gaiti Hasan
National Centre for Biological Sciences, Bengaluru, India

22. Community assembly and diversity of ants in the Andaman Islands

Gaurav Agavekar[1,2,3], Francisco Hita Garcia[3], Deepa Agashe[2], Evan Economo[3]
1. Master's Program in Wildlife Biology and Conservation, Wildlife Conservation Society - India Program & National Centre for Biological Sciences, Bengaluru, India
2. Adaptation Lab, National Centre for Biological Sciences, Bengaluru, India
3. Biodiversity and Biocomplexity Unit, Okinawa Institute of Science and Technology Graduate University, Okinawa, Japan.

25. Organization of double-strand break ends during homology search in vivo

Afroze Chimthanawala, Julia Hitschfel, Anjana Badrinarayanan
National Centre for Biological Sciences, Bengaluru, India

28. Evidence of sinks and sources in the PLC activated PIP2 cycle

Rohit Suratekar, Padinjat Raghu, Sandeep Krishna
National Centre for Biological Sciences, Bengaluru, India

31. How does the dimensions of unfolded state change during folding?

Sandhya Bhatia, G. Krishnamoorthy and Jayant B. Udgaonkar
NCBS, Anna University and IISER, Pune

34. An autism-susceptibility candidate gene controls variability of escape responses in larval zebrafish

Urvashi Jha, Igor Kondrychyn, Vladimir Korzh and Vatsala Thirumalai
National Centre for Biological Sciences, Bengaluru, India

37. Airflow mediated flight initiation in cephalic mechanosensors of Oleander hawkmoths

Maitri M, **Chinmayee LM**, Sanjay P Sane
National Centre for Biological Sciences, Bengaluru, India

40. Fly facility: A resource for your fly genetics needs

Anitha VA, Basavaraj V, Gajendra SG, Hemavathy C, Janani SV, Kishore V,
Manna Ghalia, Nataraj N, Shwetha H, Srividhya A, Vinitha CM, Yashvantha
and **Deepti Trivedi**
National Centre for Biological Sciences, Bengaluru, India
Center for Cellular and Molecular Platforms, Bengaluru, India

43. Investigating the role of Arabidopsis RAB proteins during salt stress

Divya Rajagopal, M.K. Mathew
National Centre for Biological Sciences, Bengaluru, India

46. Re-visiting the classification of myosins in the entire sequence database

Naseer Pasha, **Meenakshi Iyer** and R. Sowdhamini
National Centre for Biological Sciences, Bengaluru, India

49. Why are the same bird species not found throughout the Himalayas? Understanding the bird diversity gradient in the Himalayas using macroecological and phylogeographic approaches

Bela Arora, Vivek Ramachandran and Uma Ramakrishnan
National Centre for Biological Sciences, Bengaluru, India

52. Investigating the cause of domain swapping in Protein G mutant

Vishram Terse, and Shachi Gosavi
National Centre for Biological Sciences, Bengaluru, India

55. Microfluidics and Microfabrication facility

Feroz Musthafa
National Centre for Biological Sciences, Bengaluru, India
Center for Cellular and Molecular Platforms, Bengaluru, India

58. The interplay between actin cortex and different non-muscle myosins template a dynamic plasma membrane heterogeneity

Thomas S. van Zanten, **Parijat Sil** and Satyajit Mayor
National Centre for Biological Sciences, Bengaluru, India

61. Bush encroachment influences nocturnal rodent community and behaviour in a semi-arid grassland in Gujarat, India

Anisha Jayadevan[1,2], Shomen Mukherjee[3,4], Abi Tamim Vanak[4,5]
[1] Postgraduate Program in Wildlife Biology and Conservation, National Centre for Biological Sciences
[2] Wildlife Conservation Society – India Program, Centre for Wildlife Studies
[3] Azim Premji University
[4] Ashoka Trust for Research in Ecology, and the Environment
[5] Fellow, Wellcome Trust/DBT India Alliance Program
School of Life Sciences, University of KwaZulu-Natal, Durban

64. Central Imaging and Flow Cytometry Facility

Divya A, Ranjana Neelagar, **H. Krishnamurthy**, Manoj K. Mathew, Anil Kumar HV., Badrinarayan N
National Centre for Biological Sciences, Bengaluru, India
Center for Cellular and Molecular Platforms, Bengaluru, India

67. Autophagy-Endocytosis nexus in the control of intracellular bacterial infections

Manisha Goel, Harmanjit Singh, Shantanu SIngh, Varadha Sundaramurthy
National Centre for Biological Sciences, Bengaluru, India

70. An insight into the dynamics of Atx2 granules and regulation of its cellular RNA targets.

Amanjot Singh, Devasena Thiagarajan, Devam Purohit, Joern Huelsmeier, Jens Hillebrand, VijayRaghavan, Baskar Bakthavachalu and Mani Ramaswami.
National Centre for Biological Sciences, Bengaluru, India

73. Nest structure and social behaviour in Asian dwarf honey bee, Apis florea

Hemalatha Bhagavan and Axel Brockmann
National Centre for Biological Sciences, Bengaluru, India

76. Atypical endonuclease activity of viral silencing suppressor protein Beta C1

Ashwin Nair, P.V. Shivaprasad
National Centre for Biological Sciences, Bengaluru, India

79. Adaptations of S. cerevisiae to freezing and thawing

Charuhansini Kulkarni, Shashi Thutupalli
National Centre for Biological Sciences, Bengaluru, India

82. Biodiversity in a changing world: small mammal communities and pathogens in a mixed-use landscape

Ansil BR, Vivek Ramachandran and Uma Ramakrishnan
National Centre for Biological Sciences, Bengaluru, India

85. Developing an Air Quality Index for Pollinators

Geetha GT, Abhinav Raina, Susan Mullen, Shannon Olsson
National Centre for Biological Sciences, Bengaluru, India

88. Preventing the effects of stress with environmental enrichment

Giselle M Fernandes, Sumantra Chattarji
National Centre for Biological Sciences, Bengaluru, India

91. Direct iron sensing by riboswitches regulates iron homeostasis in bacteria

Susmitnarayan Chowdhury, Dolly Mehta and Arati Ramesh
National Centre for Biological Sciences, Bengaluru, India

94. DNA damage recovery in bacteria results in asymmetric cell division

Suchitha Raghunathan, Varshit Dusad, Anjana Badrinarayanan
National Centre for Biological Sciences, Bengaluru, India

97. How do individual honey bees communicate new food source information?

Arumoy Chatterjee, Prabhudev M.V., Ebi A. George, Pallab Basu, Axel Brockmann
National Centre for Biological Sciences, Bengaluru, India

100. Insights into the lone transmembrane helix of STIM1

Sahil Lall and MK Mathew
National Centre for Biological Sciences, Bengaluru, India

103. Sustained release of insulin for glycemic control in Type I Diabetes using biocompatible hydrogels

Ashish D, Kiran Kumar MN, Ashok Kumar HG, Preethem Srinath, Sujoy Bej, Saheli Chakraborty, S. Ramakrishnan, Praveen Kumar Vemula
National Centre for Biological Sciences, Bengaluru, India

106. CTCF and RNA dependent clustering of enhancers

Deepanshu Soota and Dimple Notani
National Centre for Biological Sciences, Bengaluru, India

109. Active Trafficking Dynamics on Closed Membranes

Stefan Alexandru Rautu, Kripa Gowrishankar, Richard G. Morris, Madan Rao
National Centre for Biological Sciences, Bengaluru, India

112. Cx35 encoded gap junctions guide Purkinje neuron dendritic arborization

Sahana Sitaraman, Shaista Jabeen, Gnaneshwar Yadav, Vandana Agarwal and Vatsala Thirumalai
National Centre for Biological Sciences, Bengaluru, India

115. Fluid shear stress in a healthy and diseased heart - from an Ion channel perspective

Samrat Roy and MK Mathew
National Centre for Biological Sciences, Bengaluru, India

118.'Growth stunting' and Severe Mental illness & Of Birds, Brains and Voices

121. Extinction recall of fear memories formed before stress is not affected despite amygdalar hyperactivity

Mohammed Mostafizur Rahman, Sumantra Chattarji
National Centre for Biological Sciences, Bengaluru, India

124. The SUMO ligase activity of human cytomegalovirus transactivator IE2 is regulated by the kinase CK2

Vasvi Tripathi, Kiran S Chatterjee and Ranabir Das
National Centre for Biological Sciences, Bengaluru, India

127. Membrane receptor signaling generates functional nanodomains at the plasma membrane of living cells.

Joseph Mathew Kalappurakkal[1], Anupama Ambika Anilkumar[1,2],Chandrima Patra[1], Thomas vanZanten[1], Michael P. Sheetz[3] and Satyajit Mayor [1,4].
[1]National Centre for Biological Sciences, Bengaluru, India
[2]St Johns Research Institute, Bangalore, India
[3]Mechanobiology Institute, National University of Singapore, Singapore
[4]Institute for Stem Cell Biology and Regenerative Medicine, Bengaluru, India

Day 2 - January 4, 2018

2. Mechanics of Dipteran wing hinge

Abin Ghosh, Tanvi Deora, Akash Vardhan, Namrata Gundiah, and Sanjay.P.Sane
National Centre for Biological Sciences, Bengaluru, India

5. An Algorithmic Barrier to Neural Circuit Understanding

Venkat Ramaswamy
National Centre for Biological Sciences, Bengaluru, India

8. Transcriptional regulation of Cyclin D2 by Hes1: Therapeutic implications in a subset of plasma cell neoplasms

Sasikala P.S, Deepak Arya, Shuling Zhang, Vairavan L, Rakesh Sharma, Akhilesh Pandey, Dasaradhi
Palakodeti, Beverly A. Mock, Sudhir Krishna
National Centre for Biological Sciences, Bengaluru, India
Institute for Stem Cell Biology and Regenerative Medicine, Bengaluru, India
Institute of Bioinformatics, Bengaluru
NCI-NIH,USA

11. Stochastic Dynamics of Cell Nucleus

Amit Kumar Singh, JF Rupprecht, Jacques Prost, Madan Rao
National Centre for Biological Sciences, Bengaluru, India
MBI Singapore

14. Towards a Push-Pull Strategy for the Coffee White Stem Borer

Santosh Rajus, Sriraksha Bhagavan, Shannon Olsson
National Centre for Biological Sciences, Bengaluru, India

17. Regulation of error-prone polymerase activity during trans-lesional synthesis repair

Asha Joseph, Ismath Sadhir, Prachi Shinde
National Centre for Biological Sciences, Bengaluru, India

20. The IP3 receptor and SOCE in human neural precursor cells

Pragnya Chakraborty, Bipan Kumar Deb, Renjitha Gopurappilly, Gaiti Hasan
National Centre for Biological Sciences, Bengaluru, India

23. A cluster of miRNAs regulate anthocyanin biosynthesis in Vitis vinifera

Varsha Tirumalai, Swetha Chenna, Ashwin Nair, P.V. Shivaprasad
National Centre for Biological Sciences, Bengaluru, India

26. Genomics approach helps in understanding complex neuropsychiatric disorders

Soujanya M S, Husayn Ahmed P, Odity Mukherjee,
ADBS Consortium
National Centre for Biological Sciences, Bengaluru, India
Institute for Stem Cell Biology and Regenerative Medicine, Bengaluru, India
National Institute for Mental Health and Neuroscience
Institute for Bioinformatics and Biotechnology

29. Mass spectrometric quantification of amine titers in single honey bee brains and brain parts

Divya Ramesh and Axel Brockmann
National Centre for Biological Sciences, Bengaluru, India

32. Decoding the paradoxical effects of an adenylate cyclase mutant in E.coli

Shweta Chakraborty, Aalap Mogre, Aswin Sai Narain Seshasayee
National Centre for Biological Sciences, Bengaluru, India

35. Translation regulation of actin modulators fine tune dendrite growth in developing neurons

Sreenath R, Ravi Muddashetty
Institute for Stem Cell Biology and Regenerative Medicine, Bengaluru, India

38. Information Processing and Discrimination at Receptor Clusters

Kabir Husain, Marcus J. Taylor, Satyajit Mayor, Madan Rao
National Centre for Biological Sciences, Bengaluru, India

41. Evolution of Ontogenic colour change in Swallowtail butterflies

Nikhil Gaitonde, Jahnavi Joshi and Krushnamegh Kunte
National Centre for Biological Sciences, Bengaluru, India

44. Demonstration of animating your favourite biological process

Ipsa Jain, Renaud Chabrier, Minhaj Sirajuddin
Institute for Stem Cell Biology and Regenerative Medicine, Bengaluru, India

47. Systems biology approach to study cardiomyopathy genes

Pankaj Chauhan, Farah Haque, Dhandapani Perundurai and R. Sowdhamini
National Centre for Biological Sciences, Bengaluru, India

50. Tbx6 is a mesoderm switch in bipotent neuromesoderm progenitors

Aritra Misra, Alok Javali, Karolis Leonavicius, Debalina Acharya, Bhakti Vyas and Ramkumar Sambasivan
Institute for Stem Cell Biology and Regenerative Medicine, Bengaluru, India
National Centre for Biological Sciences, Bengaluru, India
Oxford University

53. Neural Substrates of Speciation

Hinal Kharva, Cheyenne Tait, Marco Schubert, Jeffrey Feder, Shannon Olsson
National Centre for Biological Sciences, Bengaluru, India
Transdisciplinary University

56. Effect of climate warming on plant–pollinator interactions in the alpine meadow ecosystems of the Eastern Himalayas

Joyshree Chanam, Dharmendra Lamsal, Yuvaraj Ranganathan, Shannon Olsson, Mahesh Sankaran
National Centre for Biological Sciences, Bengaluru, India

59. Second order neuron for bitter taste processing in Drosophila

Ali Asgar Bohra, Heinrich Reichert and K VijayRaghavan
National Centre for Biological Sciences, Bengaluru, India

62. Phosphorylation of Pcdh15 by FgfR1 in inner ear stereocilia

Akira Honda, **Shri Vidhya Seshadri, Debadutta Deb**, Raj Ladher
National Centre for Biological Sciences, Bengaluru, India

65. Ligand-induced segregation of chromatin domains

Bharath Sarvanan and Dimple Notani
National Centre for Biological Sciences, Bengaluru, India

68. Assessing the energy landscapes of designed proteins

Sridhar Neelamraju, David Wales, Shachi Gosavi
National Centre for Biological Sciences, Bengaluru, India
University of Cambridge

71. Mistranslation influences the bacterial stress response

Laasya Samhita, Parth Raval and Deepa Agashe
National Centre for Biological Sciences, Bengaluru, India

74. Responses of interspecific associations in mixed-species bird flocks to selective logging

Binod Borah 1, Suhel Quader 2, Umesh Srinivasan 3
1.Master's Program in Wildlife Biology and Conservation, Wildlife Conservation Society - India Program & National Centre for Biological Sciences, Bangalore, India
2. Nature Conservation Foundation, Bangalore, India
3. Princeton University, Princeton, USA

77. Regulation of mature neuronal maintenance in the adult brain

Md. Shariq, Dipannita Sarkar, Deepanjali Dwivedi, Upi Bhalla and Hiyaa Ghosh
National Centre for Biological Sciences, Bengaluru, India

80. Functional diversity and structural complexity of doublesex gene

Saurav Baral, Gandhimathi Arumugam, Riddhi Deshmukh, Krushnamegh Kunte
National Centre for Biological Sciences, Bengaluru, India

83. Effects of origin of replication on chromosomal architecture and gene expression in E. coli.

Terence Christie, Akshara Dubey and Aswin Sai Narain Seshasayee
National Centre for Biological Sciences, Bengaluru, India

86. Chromosomal inversion as a strategy to compensate for the loss of origin of replication in E.coli

Reshma T V, Soumya Nayak, Aswin Sai Narain Seshasayee
National Centre for Biological Sciences, Bengaluru, India

89. Context dependent regulation of gene expression in neurons by SOCE

Rishav Mitra, Shlesha Richhariya and Gaiti Hasan
National Centre for Biological Sciences, Bengaluru, India

92. Investigating the role of store operated calcium entry in mouse purkinje neurons

Sreeja Kumari Dhanya, Gaiti Hasan
National Centre for Biological Sciences, Bengaluru, India

95. Gut microbes reveal dietary specialization in dragonfly populations

Rittik Deb and Deepa Agashe
National Centre for Biological Sciences, Bengaluru, India

98. Visually guided landing behaviour in houseflies

Sujay B, Satish Raja K, Sanjay.P.Sane
National Centre for Biological Sciences, Bengaluru, India

101. 2-photon imaging of mouse hippocampal activity during trace conditioning

Kambadur Ananthamurthy, Soumya Bhattacharjee, Upinder S. Bhalla
National Centre for Biological Sciences, Bengaluru, India

104. Diversity, stability, and reproducibility in stochastically assembled microbial ecosystems

Akshit Goyal, Sergei Maslov, Sandeep Krishna
National Centre for Biological Sciences, Bengaluru, India
UIUC

107. Wing shape and flight morphology analysis in butterfly mimicry rings of the Western Ghats

Dipendra Nath Basu, Vaishali Bhaumik, Krushnamegh Kunte
National Centre for Biological Sciences, Bengaluru, India

110. Electron Microscopy: Eye to ultrastructure analysis in molecular and cellular world

Deepti Negi, Saloni Sharma and Nagendra Pratap Singh
National Centre for Biological Sciences, Bengaluru, India

113. Confocal Imaging and Analysis@Screening Facility

Chandan Mithra and Shahab Uddin
National Centre for Biological Sciences, Bengaluru, India

116. Regulation of lipid transfer in Phospholipase C mediated signalling at membrane contact sites [MCS]

Bishal Basak, Shirish Mishra, Rajan Thakur, Harini K, Padinjat Raghu
National Centre for Biological Sciences, Bengaluru, India

119. Phospholipase D regulates synaptic vesicle cycle

Rajan Thakur and Padinjat Raghu
National Centre for Biological Sciences, Bengaluru, India

122. Towards Understanding the Dynamics of Development and Differentiation of the Inner Ear Hair Cells

Nishant Singh, Sharada and Raj Ladher
National Centre for Biological Sciences, Bengaluru, India

125.The Hamming Model to Study the Steady States of Biological Systems

Rahul Kumar and Mukund Thattai
National Centre for Biological Sciences, Bengaluru, India

Day 3 - January 5, 2018

3. The NCBS Animal Care and Resource Center

Sangeetha Raajkamal, Sreenivasulu T, Kamlesh KV, Vinod Kumar D, Manjunatha AM, Rupa Kumari, Shrruthi M, Akshay Bhatt, Latha Chukki, **Mohan GH**, **Aurelie Jory**
National Centre for Biological Sciences, Bengaluru, India

6. Activation of lncRNA hub by cancer-associated enhancer

Kaivalya Walavalkar, Dimple Notani
National Centre for Biological Sciences, Bengaluru, India

9. Pleiotropy and trade-offs among new mutations in bacteria

Mrudula Sane, Deepa Agashe
National Centre for Biological Sciences, Bengaluru, India

12. Multi-species connectivity in a fragmented landscape-theoretical predictions, empirical investigation and future simulations

Prachi Thatte, Uma Ramakrishnan
National Centre for Biological Sciences, Bengaluru, India

15. Mass Spectrometry Applications in Life Sciences

Raviswamy, Kamala Lakshmi, Padma R, **Dhananjay Shinde**
National Centre for Biological Sciences, Bengaluru, India

18. Negative regulation of G2-M in the presence of Cdc25/String facilitates tracheoblast growth and tracheal hypertrophy in Drosophila

Amrutha K, Archit Bagul, Arjun Guha
Institute for Stem Cell Biology and Regenerative Medicine, Bengaluru, India

21. Models of synaptic CaMKII activation time course with and without subunit exchange

Dilawar Singh, Upinder S. Bhalla
National Centre for Biological Sciences, Bengaluru, India

24. Investigating the alterations in liver tissue during Plasmodium liver-stage development using 3D quantitative image analysis

Lakshmi B, Vanessa Zuzarte Luis, Maria Mota, Varadha Sundaramurthy
National Centre for Biological Sciences, Bengaluru, India

27. A five-residue motif for the design of domain swapping in proteins

Neha Nandwani, Parag Surana, Nahren M. Mascarenhas, Jayant B. Udgaonkar, Ranabir Das and Shachi Gosavi
National Centre for Biological Sciences, Bengaluru, India
IISER, Pune
Sacred Heart college Tirupattur Tamil Nadu

30. Effect of Actomyosin activity on the spatiotemporal organization and kinetics of membrane proteins: An in-vitro reconstitution based approach

Abrar A Bhatt, Sankarshan Talluri, Darius V Koster, Kabir Hussain, Amit Das, Madan Rao, Satyajit Mayor
National Centre for Biological Sciences, Bengaluru, India

33. Small RNAs regulate lipid metabolism in mycobacteria

Anjali K, Dolly Mehta and Arati Ramesh
National Centre for Biological Sciences, Bengaluru, India

36. BAR domain of IRSp53 and Membrane Tension regulates CLIC/GEEC Endocytosis

Rashmi Godbole, Mugdha Sathe, Joseph Thottacherry, Satyajit Mayor
National Centre for Biological Sciences, Bengaluru, India

39. Myrmecochory: The elaiosome and its significance

Rohit Sasidharan, Radhika Venkatesan
National Centre for Biological Sciences, Bengaluru, India

42. Regulation of tumour progression and the migratory states in cervical carcinomas

Leanna Rose Joy, Calvin Rodrigues, Sanjukta Mukherjee, Sudhir Krishna
National Centre for Biological Sciences, Bengaluru, India

45. Computational analysis of cold stress responsive genes in Rosaceae family

Mohamed Shafi, Mahantesha Naika, Varalakshmi, Lavanya, R. Sowdhamini
National Centre for Biological Sciences, Bengaluru, India

48. Designed for degradation: FAT10 and Ubiquitin

Hitendra Negi, Ranabir Das
National Centre for Biological Sciences, Bengaluru, India

51. Activation profiles of Purkinje neurons during optomotor adaptation in larval zebrafish

Sriram Narayanan, Vatsala Thirumalai
National Centre for Biological Sciences, Bengaluru, India

54. Inactivation of the Ubiquitin pathway by glutamine deamidation

Rashmi, Priyesh Mohanty, Ranabir Das
National Centre for Biological Sciences, Bengaluru, India

57. Chemical Ecology program enables researchers to deconstruct chemical interactions in biodiversity rich northeast region of India

Dhruba Sharma, Sushma Krishnan, Lucy Nongbri, Uma Ramakrishnan, Shannon Olsson
National Centre for Biological Sciences, Bengaluru, India

60. Understanding the mechanism of prion-like propagation of tau fibrils

Harish Kumar, Jayant B. Udgaonkar
National Centre for Biological Sciences, Bengaluru, India,
IISER Pune

63. Code decoded: Priming of insect herbivore defence

Enakshi Ghosh, Radhika Venkatesan
National Centre for Biological Sciences, Bengaluru, India

66. Structural insights into signal-responsive control of transcription in bacteria

Anirudh KN, Harish Prasad, Dolly Mehta, Arati Ramesh
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69. NMR facility@NCBS-TIFR

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72. Ligand induced cooperativity in a non-cooperative mutant of PI3K SH3

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75. Role of soil moisture in mound building by termites

Sree Subha Ramaswamy, Amritansh Vats, Sanjay.P.Sane
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78. Regulation of chromatin domain organization by Euchromatic Histone Methyltransferases during aging

Alhad Ketkar, Radhika Rao,Neelam Kedia, Febina Ravindran, Vairavan Lakshman, Akash Guliyani, Dasaradhi Palakodeti, Shravanti Rampalli
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81. Arabidopsis PARK7 homolog protein AtDJ-1D is a DNA deglycase

Melvin Prasad, Kondalarao B, Patrick D'Silva, P.V. Shivaprasad
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84. Reaction kinetics in crowded environments

Anupam Singh, Manoj Kumar, Madan Rao, Shashi Thutupalli
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87. Endo-Lysosomal containment of intracellular mycobacteria in macrophages

Kuldeep Sachdeva, Manisha Goel, Prerna Tripathi, Varadha Sundaramurthy
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90. Climate warming amplifies soil respiration in a tropical montane grassland ecosystem

Yadugiri V Tiruvaimozhi, Mahesh Sankaran
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93. Control of passive particles in an active bath

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96. Fight like sea sponges: origin of immune system in animals

Anshika Singh, Sudhir Krishna
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99. The NCBS/InStem X-ray Facility

Vinod Nayak
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102. Role of Vinculin in regulating bulge stem cell quiescence

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105. Urea-TMAO Paradigm and Protein Folding Cooperativity

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108. Muscle repair in Drosophila Flight Muscles

Dhananjay Chaturvedi, K VijayRaghavan
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111. Partners in stress: Plant – Bacterial interaction against Heavy metal.

Shiksha Ajmera, Radhika Venkatesan
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114. Strategies for post-stress intervention against the delayed effects of stress on the amygdala

Prabahan Chakraborty, Sumantra Chattarji
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117. Understanding the early morphogenetic events leading to otic vesicle formation

M Arockia Catherin, Varsha NT, Raj K Ladher
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120. Methionine drives an anabolic transformation through Gcn4

Adhish Walvekar, Rajalakshmi Srinivasan, Ritu Gupta, Sunil Laxman
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123. Sphingolipid Signaling Regulates Muscle Development in Drosophila

Krishan Badrinath, Julie Saba, K. VijayRaghavan
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126. Engaging children and adults in documenting a changing world

Swati Sidhu1, Ramit Singal2, Muhammed Nizar1, Geetha Ramaswami2, Suhel Quader1
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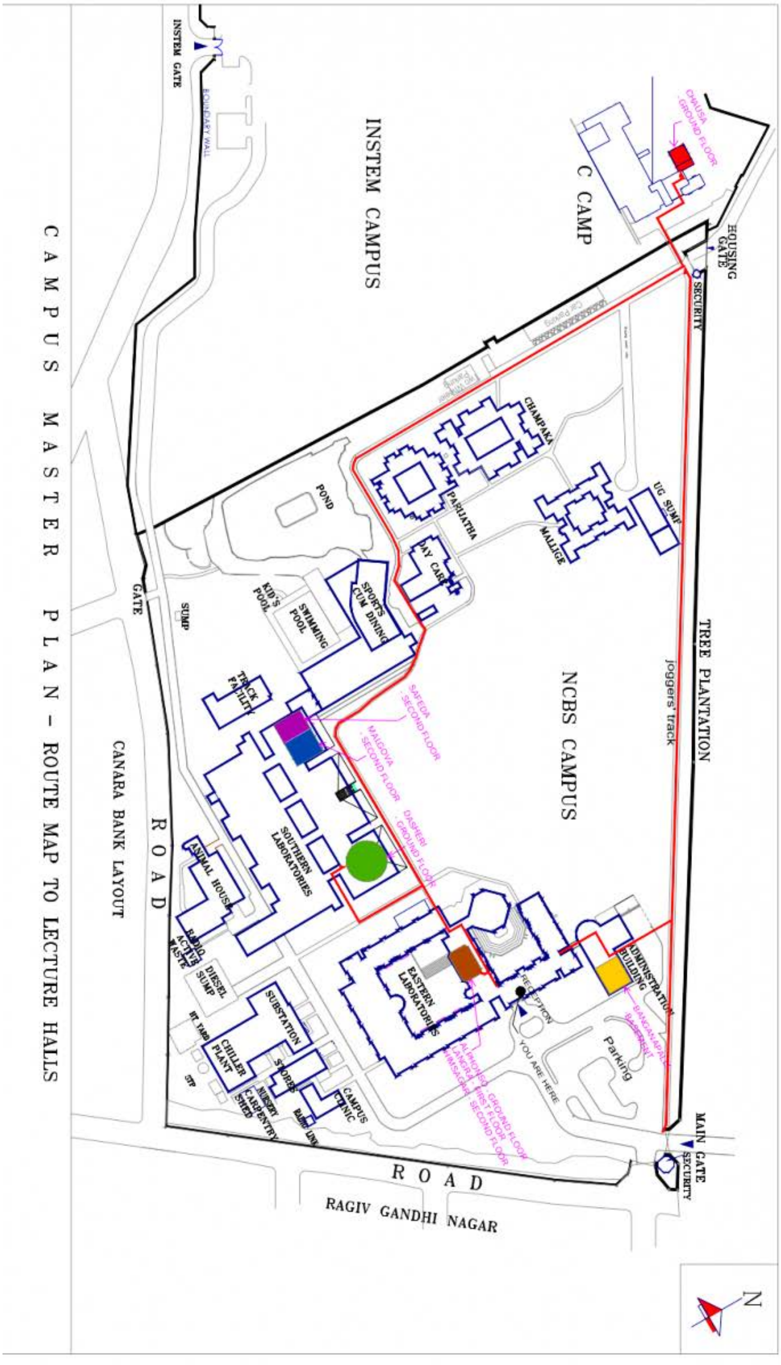
2.Nature Conservation Foundation


CAMPUS MASTER PLAN – ROUTE MAP TO LECTURE HALLS
INSTEM GATE
INSTEM CAMPUS
C CAMP
CHALISA - GROUND FLOOR
HOUSING GATE
SECURITY
TREE PLANTATION
joggers' track
NCBS CAMPUS
CHAMPAKA
PARIJATHA
MALLIGE
UG SUMP
POND
DAY CARE
SPORTS CUM DINING
SWIMMING POOL
KID'S POOL
SUMP
GATE
TRACK FACILITY
SAFEDA - SECOND FLOOR
MALGOVA - SECOND FLOOR
DASHERI - GROUND FLOOR
SOUTHERN LABORATORIES
ANIMAL HOUSE
RADIO ACTIVE WASTE
DIESEL SUMP
SUBSTATION
CHILLER PLANT
STORES
CAMPUS CLINIC
EASTERN LABORATORIES
ADMINISTRATION BUILDING
RECEPTION
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Parking
MAIN GATE
SECURITY
CANARA BANK LAYOUT
ROAD
ROAD
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