MORNING I 9.15AM–12.20PM

9.15AM — Opening Remarks

9:30AM–10.00AM — Kavita Isvaran (Let's Talk Science!)
Animal Personality in the Wild

10.00AM–10.10AM — Nitin Saxena (Behind the Scenes)
An epically failed attempt of Runaway

10.10AM–10.25AM — Pragyadeep Roy (Let's Talk Science!)
Diversity within lookalikes:Exploring the Indian Indotyphlops

10.25AM–10.40AM — Sarath P K (Let's Talk Science!)
Late Quaternary Paleoecological Reconstruction of Sandynallah
Based on Multiproxy Analysis of Peat Deposits.

10.40AM–11.00AM — Break

11.00AM–11.30AM — Priti Bangal (Let's Talk Science!)
Patterns of flock assembly and species interactions in mixed-species bird flocks

11.30AM–11.35AM — Manasa Kulkarni, Tanveen Kaur Randhawa(Lights Out!)
Born Assassin: Life of a Ninja bug

11.35AM–12.05PM — Ankur Shringi (Let's Talk Science!)
A comparison of forest biomass estimation using vegetation indices (such as NVDI/EVI) and textural indices

12.05PM–12.20PM — Dilip Naidu (Let's Talk Science!)
Synchrony in community dynamics

12.20PM–2.00PM — Lunch

Day 1

2.00PM-2.15PM   Maria Thaker (Let's Talk Science!)
When the going gets hot, the hot gets going 📑

2.15PM-2.45PM   Madhura Amdekar (Let's Talk Science!)
Risk of social colours in an agamid lizard: implications for the   e
evolution of dynamic signals 📑

2.45PM-2.50PM   Pooja Nathan (Lights Out!)
A baffling case of tool use in insects

2.50PM-3.05PM   Caleb Daniel (Let's Talk Science!)
How are Spiny Tailed Lizards coping with Anthropogenic
stresses?

3.05PM-4.00PM   Break + Poster Session ☕ 📊

4.00PM-5.30PM   Kavita Isvaran,Krishnapriya Tamma, Hari Sridhar (Discussion)
Discussion on good practice in authorship

MORNING | 9.30AM-12.20PM

9:30AM-10.00AM   Raghavendra Gadagkar (Let's Talk Science!)
Towards the Physiology of Social Behaviour in the Primitively Eusocial Wasp *Ropalidia marginata* 📄

10.00AM-10.05AM   Pritha Kundu (Lights Out!)
Fishy Movement

10.05AM-10.20AM   Nitin Saxena (Let's Talk Science!)
Tracing the pattern of evolution of cooperative breeding in birds. 📄

10.20AM-10.35AM   Vignesh Venkateswaran (Let's Talk Science!)
Simple mathematical intuition to characterize movement across ephemeral resources. 📄

10.35AM-11.00AM   Break ☕

11.00AM-11.30AM   Satyajeet Gupta (Let's Talk Science!)
Hitchhiker's quest for a ride and a mate. 📄

11.30AM-11.45AM   Mridula Nandakumar (Let's Talk Science!)
Variations in the immune genes of Himalayan birds 📄

11.45AM-11.50AM   Akshata Bhat , Kanika Rawat (Lights Out!)
Cormorants: Wing-spreading Behaviour

11.50AM-12.20PM   Kunal Arekar (Let's Talk Science!)
Did the langur population in western Himalaya undergo a recent bottleneck? 📄

12.20PM-2.00PM   Lunch and Photo Session 🍴 📷

AFTERNOON | 2.00PM–5.20PM

2.00PM-2.15PM   Praveen Karanth (Let's Talk Science!)
Everything in print ain't gospel! 📑

2.15PM-2.45PM   Ananya Jana (Let's Talk Science!)
Nuclear evidence for the evolutionary history of *Antilope cervicapra*. 📑

2.45PM-2.50PM   Shatarupa Sarkar, Subhasmita Patro (Lights Out!)
Jumper's Delight, Designer's Paradise

2.50PM-3.05PM   Mihir Sule (Let's Talk Science!)
Deciphering the Sousa spp. taxonomic complex across populations along the coast of India to understand the role of space and time on speciation. 📑

3.05PM-4.00PM   Break +Poster ☕ 📊

4.00PM-4.30PM   Kesang Bhutia (Let's Talk Science!)
Species Distribution Modelling for Endemic and Rare Species of Western Ghats, India: A comparative study using MaxEnt and Ensemble Model 📑

4.30PM-4.35PM   Shuaib Palathingal, Avik Banerjee (Lights Out!)
The minefield: A minidocumentary on Antlion

4.35PM-5.05PM   Arkamitra Vishnu (Let's Talk Science!)
Fungal diversity within ant shelters (domatia) of the endemic ant-plant *Humboldtia brunonis* (Fabaceae). 📑

Day 3

9:30AM-10.00AM Nitika Sharma (Let's Talk Science!)
Food distribution on the nest of the paper wasp *Ropalidia marginata* 📄

10.00AM-10.15AM Sambita Modak (Let's Talk Science!)
Nutrition and age-dependent male investment in signaling and remating in the tree cricket *Oecanthus henryi*

10.15AM-10.35AM Break ☕

10.35AM-11.05AM Jitesh Jhawar (Let's Talk Science!)
Inferring the rules of interactions in fish. 📄

11.05AM-11.10AM Satyajeet Gupta (Behind The Scenes)
Eureka moments: Keep looking as small things matter

11.10AM-11.40PM Anne Heloise Theo (Let's Talk Science!)
Patterns of grouping propensity in Mixed-species groups of fish.

11.40PM-12.00PM Feedback

Diversity within lookalikes: Exploring the Indian *Indotyphlops*

Pragyadeep Roy

Guides: Chinta Sidharthan and Prof. Praveen Karanth

Scolecophidia (blindsnakes) is a paraphyletic infraorder, comprising five families - Anomalepididae, Leptotyphlopidae, Typhlopidae, Gerrhopilidae and Xenotyphlopidae. Typhlopidae is the largest family of the five, comprising 18 genera and over 257 species. However, only 3 (Indotyphlops, Argyrophis and Grypotyphlops) out of 18 genera are found in India. In addition to these, another Scolecophidian genus, Gerrhopilus (family: Gerrhopilidae), is also found in the subcontinent. This study is aimed at understanding the cryptic diversity and distribution patterns within the blindsnake genus Indotyphlops, across peninsular India. Molecular data has been used to reconstruct phylogenetic relationships within samples collected from various parts of peninsular India. For the purpose of the study, Cytochrome b, a mitochondrial marker, has been selected and sequences of the marker have been generated from 51 snakes. Morphological patterns will be compared against the existing morphological descriptions of type specimens from literature, to identify the species from the various clades retrieved from the phylogenetic trees. Although 8 species have been reported in earlier studies, morphological differences are negligibly perceivable among individuals of different species. Hence, it is paramount to understand the cryptic diversity within the genus. Therefore, an integrative species delimitation would also be carried out to understand the true diversity of species in the genus and its distribution.

Late Quaternary Paleoecological Reconstruction of Sandynallah Based on Multiproxy Analysis of Peat Deposits.

Sarath P K

Understanding the ecological history of a region is essential in integrating conservation actions and predicting the future responses to global change. Humans have extensively altered the global environment, changing the ecosystem structure and disrupting the equilibrium between climate and vegetation. Vegetation shifts in the past of tropical montane forest-grassland ecosystem mosaic in Nilgiris is well documented using stable isotope studies and palynology. In this study we reconstructed the paleofire records to understand fire-vegetation relationship and also to establish role of human in altering the stability of the ecosystem mosaic. Peat samples from Sandynallah basin was used to reconstruct, fire history based on charcoal records, fungal spores to understand levels of herbivory and lipid biomarkers to understand the human interferences. Macro and microcharcoal record indicated a local fire event ~3500 calyr BP along with abundance in coprophilous fungal spores, indicating herbivory. Various biomarker signatures indicated dry arid conditions with increased $nC31$ signatures, during the period and a characteristic shift towards grassland ecosystem. The late-Holocene fire event sample also shows signatures of human and bovine faecal contamination. Fire event recorded in our samples coincides with the C3 to C4 shift recorded in the previous studies from the region. Fire is an important disturbance event influencing the vegetation and climate of the region. Paleoecological reconstruction from the region shows that fire as a tool to manage landscapes played an integral role in human-environment interactions in the past.

Flock formation and species interactions in mixed-species bird flocks

Priti Bangal

Mixed-species bird flocks (flocks, hereafter) are social groups of two or more species formed for foraging and anti-predatory benefits. Recent studies have shown that flocks are composed of species more similar than expected by chance. However, the dynamic assembly of flocks or the process of flock formation has not been studied given the challenges in observing mixed-flocks as they assemble. Mixed-species flocks comprise a large part of the bird community in many forests across the world. Interactions within these flocks are therefore likely to have community consequences for the avifauna of a given region. We ask how flock heterogeneity changes as flocks get larger during formation and if the species pool size was not a constraint, would flock composition be driven by species similarity. Flock communities often have some species that are more important for the formation, maintenance and cohesion in mixed-species flocks. They can be thought of as within-trophic keystones in flocks, often known as nuclear species. Intraspecifically gregarious species are known to be nuclear in mixed-species flocks. We examine species roles in flock formation and ask what characters make these species important in mixed-species flocks. We find that flock assembly is a process based on phenotypic similarity and phenotypic clumping in large communities with small flocks is greater than clumping in small communities. We do not find evidence for importance of a particular trait in the gregarious species in flocks. We however expect that important species exhibit the 'average trait' in flocks as compared to other non-nuclear species therefore maintaining similarity with other flock participants. Through this study we attempt to integrate the role of behavioural interactions in the community assembly of birds.

A comparison of forest biomass estimation using vegetation indices (such as NVDI/ EVI) and textural indices: A case study from a rainfall gradient of Mudumalai Tiger Reserve, Tamil Nadu

Ankur Shringi

Large-scale regional forest biomass is often estimated using reflectance-based vegetation indices (such as NDVI/EVI) obtained through satellite imagery. This approach involves three main steps. First, estimation of biomass at the plot level; second, correlating plot-level biomass values with their corresponding pixels' vegetation indices; and third, interpolating biomass for the entire region using a correlation between these indices and the plot biomass. The accuracy and efficacy of the second and third approaches largely depend on how well satellite-based vegetation indices can capture actual biomass information.

In the last decade or so, the availability of very high-resolution optical imagery (sub 3 meters/pixel) has made it possible to explore an alternative approach to the vegetation indices-based biomass estimation. This approach uses textural information visually created by light and shadow patterns of canopy trees instead of reflectance ratios of frequency bands as traditionally used in the vegetation indices calculation. This has a few advantages compared to the traditional approach. First, unlike NDVI, the correlation between textural indices does not saturate at high biomass density; second, very high-resolution imagery makes it possible to consider smaller plot size and proper alignment with the corresponding pixel in satellite imagery. However, these techniques are not fully established and have been attempted largely in tropical rainforest areas. In this study, an attempt has been made to test this technique in a rainfall gradient of Mudumalai Tiger Reserve, facilitating a continuous transition from dry thorn to wet evergreen forest. Furthermore, the availability of ground data from 20 long-term monitoring plots, as well as high-resolution satellite imagery, makes it a suitable study site for testing this approach.

In this talk, I will present a preliminary comparison of biomass estimation of the study region using the texture-based approach and approaches based on vegetation indices.

Environmental effects on species synchrony in grassland ecosystems

Dilip Naidu

Understanding the response of grassland community dynamics to environmental fluctuations is central to develop conservation strategies. Community dynamics in a grassland ecosystem are determined by collective response of individual species to both intrinsic (competition, facilitation) and extrinsic (temperature, precipitation) factors. Correlated species response (synchrony) in a community means a decrease in variation of species population densities. Any increase in synchrony indicates higher probability of species extinction. We analysed species abundance data from 12 North American grasslands, spread over different climatic zones for a time period ranging between 20-60 years. Contrary to our expectations, we found that variance in species abundance increased with synchrony. However, when we segregated the effect of intrinsic and extrinsic factors, variation indeed decreased with increase in synchrony for extrinsic factors but remained variable for intrinsic factors. This suggests species extinction may be strongly related to environmental conditions, though this can be masked by intrinsic factors. Peaks in synchrony were observed during drought years, whereas synchrony decreased in wet years. We also found that there was a lag between the occurrence of extreme events (dry and wet years) and change in synchrony. These results provide insights into complex community dynamics which can be used for monitoring grassland ecosystems.

When the going gets hot, the hot gets going

Maria Thaker

Movement strategies of animals have been well studied as a function of ecological drivers (e.g., forage selection and avoiding predation) rather than physiological requirements (e.g., thermoregulation). Thermal stress is a major concern for large mammals, especially for savanna elephants *(Loxodonta africana),* which have amongst the greatest challenge for heat dissipation in hot and arid environments. Therefore, elephants must make decisions about where and how fast to move to reduce thermal stress. We tracked 14 herds of elephant in Kruger National Park (KNP), South Africa, for 2 years, using GPS collars with inbuilt temperature sensors to examine the influence of temperature on movement strategies, particularly when accessing water. We first confirmed that collar-mounted temperature loggers captured hourly variation in relative ambient temperatures across the landscape, and thus, could be used to predict elephant movement strategies at fine spatio-temporal scales. We found that elephants moved slower in more densely wooded areas, but unexpectedly, moved faster at higher temperatures, especially in the wet season compared to the dry season. Notably, this speed of movement was highest when elephants were approaching and leaving water sources. Visits to water showed a periodic shuttling pattern, with a peak return rate of 10-30 hours, wherein elephants were closest to water during the hotter times of the day, and spent longer at water sources in the dry season compared to the wet season. When elephants left water, they showed low fidelity to the same water source, and travelled farther in the dry season than in the wet season. In KNP, where water is easily accessible, and the risk of poaching is low, we found that elephants use short, high-speed bursts of movement to get to water at hotter times of day. This strategy not only provides the benefit of predation risk avoidance, but also allows them to use water to thermoregulate. We demonstrate that ambient temperature is an important predictor of movement and water use across the landscape, with elephants responding facultatively to a "landscape of thermal stress".

Risk of social colours in an agamid lizard: implications for the evolution of dynamic signals

Madhura S. Amdekar, Maria Thaker

The conflicting forces of sexual and natural selection are typically invoked to explain variation in colour patterns of animals. While the benefits of conspicuous colours for social signalling are well documented, there is relatively limited empirical evidence for the ecological cost of colours. We examined the riskiness of colours on *Psammophilus dorsalis*, a species in which males exhibit distinct colour states on their dorsal and lateral regions during social interactions. We first measured the conspicuousness of colour states of males and females against natural substrates, and then quantified predation risk of colours using wax/polymer lizard models in the wild. The black expressed by males during courtship interactions was the most conspicuous, while the yellow and orange male dorsal colours and female brown colours were less conspicuous. In addition, models bearing black experienced the highest predator attacks. Thus, social colours are not only conspicuous, but also risky for males. Positioning conspicuous colours on lateral body regions and using physiological colours to shift in and out of conspicuous states seem to be effective evolutionary solutions to balance social signalling benefits from predation costs.

Towards the Physiology of Social Behaviour in the Primitively Eusocial Wasp *Ropalidiamarginata*

Raghavendra Gadagkar

Over the past many years my research group has advanced our understanding of the proximate and ultimate mechanisms of social behaviour in the primitively eusocial wasp *Ropalidia marginata*. In many cases our understanding of social behaviour is now ready for further investigation into the physiological causes and consequences of the behavioural strategies used by the wasps. In this talk I will briefly describe two such behavioural phenomena, namely, reproductive and non-reproductive division of labour, and explain how physiology can now help us make further progress. I will conclude with a brief description of the expected roles of Juvenile Hormone, Ecdysone and other molecules in potentially modulating these behavioural phenomena. My goal will be to inspire colleagues interested in physiology to collaborate with us in studying this fascinating social wasp species.

Tracing the pattern of evolution of cooperative breeding in birds

Nitin Saxena

Among the vast repertoire of fascinating and at times puzzling behaviours shown by living organisms, lies cooperative breeding. Cooperative breeding is where one or more members of the same species help the parents in raising their offspring. Such behaviour may cost the helper their own time, energy and chance to mate and breed. This leaves us with the puzzle as to why such behaviour would evolve. While the cost and benefits of such behaviour have been studied in detail, not much attention has been paid to the pattern of evolution of cooperative breeding. Having a better understanding of such patterns can help arrive at the processes that could drive the evolution of this behaviour. We aim to use the large dataset of avian phylogeny and information on breeding behaviour, together with phylogenetic comparative methods, to understand the pattern of evolution of cooperative breeding in birds.

Simple mathematical intuition to characterize movement across ephemeral resources

Vignesh Venkateswaran

Figs and wasps are key-stone communities providing innumerable ecosystem services. Fig wasp communities are symbiotically and obligately dependent on host plants. They disperse from natal trees to new trees for oviposition resources. The special urn-shaped fig inflorescences serve as resources for colonization by fig wasps. The dynamics of wasp release and wasp colonization are controlled by the flowering phenology of fig trees. Further, without pollination, host-plants abort their figs. So far, the performance of fig wasp communities in these complex phenology-driven resource landscapes has only been deduced through cumbersome simulations. This talk will describe an analytical approximation to successfully deduce minimum resource requirements for the persistence of any fig wasp species in a community given the knowledge of a few simple parameters on host plant phenology and timing of wasp arrival.

Hitchhiker's quest for a ride and a mate

Satyajeet Gupta

Phoresy is a phenomenon in which the phoretic organism (traveller or hitchhiker) actively seeks out its vehicle (carrier or host) for dispersal or migration. This intimate relationship might arise and evolve due to passenger's mobility constraints and ephemeral nature of the developmental substratum. The life cycle of a phoretic organism starts with the development of a phoretic stage upon encountering an unsuitable habitat. It further seeks and recognizes its host, latches on to it and disembarks at a suitable substratum where it mates, lays eggs and carries out its further development. The two most important aspects in this entire phoretic life cycle are vehicle recognition and mate finding. The first aspect makes sure of its successful dispersal while the second aspect enables it to propagate and eventually colonize the new substratum. To understand and explore these two behaviours of the phoretic organisms, we use the fig–fig wasp–nematode model system. Here, the fig and fig wasp are in a mutualistic relationship whereas the associated nematode community show a phoretic association with the fig wasp. Both the wasp and nematodes use figs as their developmental substratum. Under this study, we investigated whether these nematodes are able to differentiate between different physiological conditions of the vehicle (live vs. dead; low infestation vs. high infestation) and its involved mechanisms. Further, we looked at mate signalling in these phoretic nematodes i.e. which sex sends out signals during mating period, its nature (chemical) and its effect on conspecifics and heterospecifics.

Effect of pathogen pressure on Toll-like receptor gene family variations in Western Himalayan birds

Mridula Nandakumar and Farah Ishtiaq

The Toll-like receptor (TLR) gene family is an integral component of innate immunity, the first line of defense in the immune system, and is critical in recognizing molecular patterns in pathogens to trigger an immune response. Variations in these genes have been shown to be associated with numerous infections and can account for variability in disease susceptibility and response. Studies in different organisms also show that TLR genes are good indicators of selection, with variations that aid in better immune response being positively selected. The gene family is evolutionarily conserved across different taxa, with the bird TLR repertoire comprising of10 genes which recognize distinct antigens. In this study, we are looking at how pathogen pressure shapes variation in TLR genes to combat infection. Migratory birds endure significant energetic costs, parasite pressure and physiological changes during their seasonal movements. Birds that are elevational migrants are exposed to a higher pathogenic burden as compared to sedentary birds, as pathogenic pressure decreases with altitude. We expect that birds present at lower elevations and exposed to a higher pathogen pressure will be positively selected for TLR gene variations, as opposed to variations in neutral loci such as microsatellites. To test this, we are using a broad spectrum of elevational migrant and resident birds in the western Himalayas and compare the variations across an elevational gradient in response to pathogen-mediated selection.

Did the langur population in western Himalaya undergo a recent bottleneck?

Kunal Arekar

Himalayan langur (*Semnopithecus* spp.) is the northern most population of the widely distributed northern type Hanuman langur (*Semnopithecus* cf. *entellus*). It is distributed across the Himalayan range from Pakistan to Bhutan covering an altitudinal range from 600m to 4270m asl. A recent study on the population genetic structure of Himalayan langurs in Nepal indicated that the Himalayan rivers served as barriers to gene flow between different populations of these langurs. However, this study did not use any samples from the Indian Himalayan region. Additionally, it is well known that past climatic events also play an important role in shaping the population genetic structure, evolutionary history and distribution of a species. Himalayas have experienced major climatic fluctuations in the past and it contains unique climatic and geographic features. To better understand the role of geography and past climate in shaping langur population structure, we undertook extensive sampling in India. Our data was then combined with above mentioned study to derive a comprehensive picture of Himalayan langur population structure. Our analysis using mitochondrial cytochrome *b* gene, showed very low levels of divergence among the samples from western Himalaya (Indian region).The haplotype network analysis showed a distinct cluster for western sequences with low variations. Phylogenetically the western sequences are nested within the Nepal clade. Importantly, western populations do not exhibit evidence of river valley mediated population structure. This suggests that there might be recent expansion into the western Himalaya possibly after a bottleneck event. Thus past climate rather than geography might have shaped Himalayan langur population genetic structure in the west. Further analysis using nuclear markers will help us understand the population genetic structure of these langurs in the Himalaya. Furthermore, species distribution modelling (SDM) using current and past climatic data and Bayesian skyline analysis will help us understand the effect of climate on langur distribution and their demographic history. This is particularly pertinent given previous SDM analysis suggested that langur population moved southwards towards warmer climates during the last glaciation period.

Everything in print ain't gospel

Praveen Karanth

One of the first steps in a scientific endeavour is literature search, wherein we review past studies undertaken on a particular topic of interest. This review is then used as basis for testing existing hypothesis or formulate new / revised hypothesis. However, it must be noted that we often take published material as irrefutable fact! i.e., we assume that anything that is 'written' must be accepted as is. Blindly accepting the conclusions of a paper is very dangerous and is counter to healthy growth of science. In this talk I will discuss a few examples from my research career and elsewhere that hopefully drives home this important point.

Modern insights into the blackbuck lineage: Nuclear evidence for resolving evolutionary history

Ananya Jana[1], Praveen Karanth[1]

Evolutionary relationships between members of the Antilopinae sub-family have been debated over the years. This clade is currently accepted to consist of 4 genera viz., *Gazella, Nanger, Eudorcas*and the monotypic genus *Antilope*, that includes *Antilope cervicapra*(the blackbuck). Most studies have focused on the mitochondrial genome or morphological data to study their inter-relationships. However, mito-nuclear discordance has been increasingly observed in multiple model systems, resulting in conflicting genetic signals. In this study we used 12 nuclear markers to understand the phylogenetic relationships between the true antelopes (Antilopinae) and make inferences regarding their evolution, particularly with respect to the lineage leading to the blackbucks. We utilized both morphological and genetic evidences to re-consider the taxonomic categorization of the blackbucks. Our second objective was to elucidate the timeline of diversification of the blackbuck lineage and whether it corresponded to the expansion of grasslands in India. The phylogenetic tress built using multiple coalescent and concatenated methods all supported the paraphyly of the genus *Gazella*, with *Antilope* nested within. The Indian gazelle or chinkara, which shows a range overlap in certain regions, is not the sister species to blackbucks and denotes a far younger radiation. We calibrated a larger bovid phylogeny using known fossil records and established the diversification of the *Antilope* lineage from its sister species at ~2 Mya, a more recent period than previously accepted. Although shifts in global climatic conditions in the late Miocene are well known, the study shows that the *Antilope* lineage underwent diversification only in the Pleistocene. It also highlights the evolutionary significance of the arid zone, an often-ignored landscape in India, as it does not belong to bio-diversity hotspots like the Western Ghats. Finally, our biogeographic analysis places the Saharo-Arabian realm as the region of origin for *Antilope*.

Understanding the phylogeny and biogeography of the Humpback dolphin (*Sousa* spp.) in peninsular India

Mihir Sule

The talk discusses the proposed topic for my PhD, and aims to resolve the genetic and taxonomic identity of the *Sousa* spp. complex in India, using non-invasive sampling, to determine if the population(s) is continuous or fragmented and if so, estimate gene flow across the populations. The morphologically different forms of humpback dolphins observed along the Indian coastline will be assessed to examine if these 'morphotypes' also exhibit generic differences. These data will be compared with existing datasets for the genus across their distribution to examine how the Indian animals place in the global phylogeny. Understanding of the genetic diversity of the population(s) will shed light on the allelic richness and expected heterozygosity, connectivity and effective population size of the sampled population and help identify fragmented populations that may require conservation intervention.

Species Distribution Modelling for Endemic and Rare Species of Western Ghats, India: A comparative study using MaxEnt and Ensemble Model

Kesang Bhutia

Species distribution models have been widely used to identify localities where a species is likely to occur due to its similarity with areas where they were found, thus acting as invaluable tools in mapping and conservation of endemic species. Western Ghats in India harbours large number of endemic plants. In this study, we modelled the potential distribution of 153 endemic woody species of Western Ghats. For modeling of these species, we used MaxEnt and ensemble method of modeling using SSDM package in R software. For the metric of comparison of the two approaches, AUC and True skill statistics (TSS) values were selected. Both models had very high AUC values for all the species; however TSS value for Maxent showed lots of variation with varying sample sizes. Ensemble, on the other hand performed well in terms of both AUC and TSS. Thus, it was concluded that ensemble model was better of the two approaches. The selection of environmental predictors also plays an extremely important role in the prediction. A two-step approach was followed for selection of predictors for the final modeling. In the first step correlation method was used to remove highly correlated environmental predictors. In the second step, MaxEnt modeling was carried out using these predictors and the predictors whose contribution was very low were removed. It was found that getting rid of variables low contributing variables improved the prediction capabilities of both the models. Our result also showed that species richness and the number of both the endemics and the threatened species are high towards the southern part of Palghat Gap.

Fungal diversity within ant shelters (domatia) of the endemic ant-plant *Humboldtiabrunonis*(Fabaceae).

Arkamitra Vishnu

Humboldtia brunonis (Fabaceae), an endemic ant-plant of the Indian Western Ghats dominates the rainforest understory and produces extrafloral nectaries on young expanding leaves and floral bud bracts for its resident ants. Some plants produce a hollow domatium in their stem internodes that provides shelter to 16 ant species such as *Vombisidrishum boldticola* (obligatory ant species of *Humboldtia brunonis*). The domatia are also occupied by several other invertebrates, most prominently by the arboreal earthworm *Perionyxpullus*. We have found that the ants can use fungi in two distinctive ways inside the domatia: i) building a disc-shaped carton to form a partition when they share the domatium with earthworms, and ii) maintaining a group of fungi in the inner wall of domatia, probably as a food source. Preliminary microscopic, pure cultural isolation and molecular data revealed that these two fungal communities represent two fungal clades, i.e. the carton clade (used for the structural component of the partition) and the domatia clade (maintained by the ants in the inner wall of the domatia) in this system. We hypothesized that, when there is earthworm present in the same domatium, the ants are probably maintaining a specific group of fungi in the domatia wall by constructing a carton separation using a different group of fungi. By using a DNA metabarcoding approach (Oxford Nanopore and Illumina MiSeq platform) and targeting fungal ITS region, we characterised the community profile of these two fungal clades. OTU abundance for both clades indicates that the ants have clear preference for specific fungal group as probable food source in the domatia wall while they use a diverse group of fungi in carton. Our study shows a possible tripartite symbiosis in this ant-plant system involving ants, the plant and fungi as a first example from the Indian subcontinent.

Spatial organization of food distribution on the nests of the primitively eusocial paper wasp *Ropalidia marginata*

Nitika Sharma and Raghavendra Gadagkar

Workers on the nests of social insects forego direct reproduction to gain indirect fitness by cooperatively raising the reproductive's brood. A major task of the workers is to forage and feed the larvae on the nest. Using the primitively eusocial wasp *Ropalidia marginata*, here we investigated how workers choose which larvae to feed and in what order; the larvae themselves being randomly distributed on the nest surface. We used the analogy of the travelling salesman problem and the Hamiltonian path to investigate whether wasps optimized their feeding routes. While feeding several larvae in one feeding bout, we find that adults adopt a route that is shorter than expected by chance alone. We also found that workers did not feed any particular larvae preferentially and that the sequence in which larvae were fed was independent of the development stage of the larvae. Instead, in each feeding bout, all wasps that fed larvae did so by spatially spreading their feeding efforts and minimizing repetitive feedings of the same larvae by different individuals. Nevertheless, the larvae closer to the centre of the colony were fed significantly more frequently than larvae at the periphery. Such variation in rates of larval feeding can influence their future fates; previous work has shown that well-fed larvae develop into adults that are more likely to become egg-layers while poorly-fed larvae develop into adults more likely to become non egg-layers.

Emergent group level patterns are explained by simple pairwise interactions in fish

Jitesh Jhawar

Collective behaviour in animals is a fascinating phenomenon observed across many taxa. A wide variety of collective behaviour like schooling, flocking, milling is observed in nature. Although we understand that such behaviours often emerge from simple local rules of interaction between individuals, the mapping between individual and collective behaviour is still unclear. To address this, we study fish schooling dynamics by conducting experiments to investigate individual and group behaviour. First, we record the movement of fish groups of different sizes and quantify group dynamics by calculating instantaneous group polarization (i.e. alignment of individuals in the group). From the polarization dynamics, we reconstruct the underlying dynamical equation governing group movement. Next, we develop de novo a mathematical model of collective behaviour that has just two rules at the individual level: A) spontaneous switching and B) pairwise switching of directions (feedback reactions). Our reconstruction of fish school dynamics reveals that group polarization decreases gradually with increasing group size. Remarkably, our de novo mathematical model reproduces this observed trend and captures the underlying dynamical equation. Thus, this simple model is different from other known models of collective behaviour that do not completely capture patterns observed here. Thus, our study maps individual and collective behaviour in fish by suggesting that emergent group-level phenomena arise through potentially simple pairwise individual interactions.

SCIENCE ON CANVAS

PRESENTER	POSTER TITLE
Bharti Dharapuram	Predictions of coastal connectivity from larval dispersal simulations
M. C. Shilpa	Mate choice in the primitively eusocial wasp Ropalidiamarginata
Nitin Saxena	Role of phylogenetic features in ancestral character state reconstruction
Priya Iyer	Partial paternity and sex roles in parenting: what is the link?
Ratna Karatgi	Response of male peninsular rock agamas to different levels of threat
Sambita Modak	Nutrition-dependent male investment in signaling and remating in the tree cricketOecanthushenryi
Satyajeet Gupta	Cost of hitchhikers on a mutualism
Thresiamma Varghese	Social Bees and wasps of the Indian Institute of Science campus
Vignesh Venkateswaran	Analytically characterising fig wasp resource landscapes