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Chemical species recognition in an adaptive radiation of Hawaiian spiders

The mechanisms by which reproductive isolation evolves and is maintained in adaptive radiations is central to fundamental processes such as reinforcement, sensory drive, and hybridization. Particularly important are situations where ecologically distinct incipient sister species co-occur geographically, resulting in frequent encounters between diverging species and necessitating finely tuned recognition mechanisms for species to maintain reproductive isolation. This is seen in adaptive radiations of *Anolis* lizards, cichlid fish, and Hawaiian *Drosophila*. In these systems however, much of the work has been done within the domain of human perception – visual and auditory cues. Chemical cues are one of the most ancient and widespread modalities of communication, yet their importance in species recognition and reproductive isolation remains to be studied in the context of adaptive radiations. This study focuses on the role of chemical species recognition cues in reproductive isolation and speciation within a well-studied adaptive radiation of Hawaiian *Tetragnatha* spiders in which ecologically distinct sister species co-occur, and visual and auditory cues appear to play little or no role in species recognition prior to mating. Our work is the first to demonstrate the use of chemical species recognition cues in an adaptive radiation of spiders and highlights how chemosensory cues may serve as the initial axis for diversification during the process of species formation.

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Phylogenetic instability in a clade of the conifer family Podocarpaceae (Order Araucariales)

The Podocarpaceae constitute the second most diverse conifer family in the world, with ca. 198 extant species within 18 genera. Recent molecular phylogenetic analyses of the Podocarpaceae retrieve two main clades for the family: a tropical clade that encompasses nearly 80% of its extant species diversity, contained within 11 genera, and a prumnopityoid clade with the remaining 20%, within 7 genera. The intergeneric relationships within the tropical clade have remained relatively stable among different studies. However, this has not been the case for the genera of the prumnopityoid clade, where different studies retrieve different groupings of taxa. Therefore, our objectives were (1) to build a molecular matrix integrating a large number of available DNA sequences, (2) to test the topological differences among the results of different partitioned data analyses, and (3) to try to identify the main possible causes of the mentioned phylogenetic instability of the prumnopityoids. Some of the hypothesized causes for the reported instability of this group are long branch attraction (LBA), rapid radiations in deep time (too short branches), conflicting evidence provided by different partitions of the data, and lack of information (missing data) of the sampled taxa. We built a DNA matrix for the family with 11 molecular markers (11044 DNA characters, 26.5% informative) from nucleus and chloroplast.

Our taxon sampling includes 158 species and 8 subspecies of the Podocarpaceae, 35 Araucariaceae species, and *Cryptomeria japonica* (Cupressaceae) for rooting. The strict consensus of the most parsimonious trees recovers the monophyly of all the genera within Podocarpaceae, and that of the large clades recovered in previous studies. Also, within the prumnopityoid clade we recover a previously defined scale-leaved clade. Different partitions of the matrix result in a diverse pool of contrasting topologies for the prumnopityoid clade, suggesting that there is conflicting evidence provided by different data partitions.

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A biogeographic event model under a dynamic geography

Although plate tectonics is an important cornerstone in modern phylogenetic biogeography, it is currently used either as subjective dispersal parameter between poorly predefined areas, or as a post-hoc inference after the analysis.

Here, a new phylogenetic biogeography method is presented. The method is (1) based on cladogenetic (vicariance, full copy sympatry, point sympatry, and jump dispersal), and anagenetic events (dispersal, extinction); (2) it is explicitly geographic, using a geographic data model (a raster) and ranges of any size in both terminals and internal nodes, instead of predefined areas; (3) the geography is dynamic, so the position of each pixel is estimated using an explicit tectonic model, which might include paleogeographic data (emerged land, epicontinental seas, glacial ice sheets). Implementation details, an empirical example, and potential expansions are also discussed.

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Microbial phylogenetic macroecology: a pioneering necessity

In ecology, only recently researchers have incorporated historical constraints represented as phylogenies in their analyses motivated by the fact that species interact within the community based on their traits, and traits have an evolutionary history. For uncultured microorganisms, trait information is often scarce, and ecological and taxonomic scales are hard to define. However microbial ecologists frequently use phylogenetic methods to assess: where and when most of the microbiological diversity accumulates and how it is structured, and how community similarity is distributed along environmental gradients. I will discuss with examples how the field of microbial ecology pioneered the use of phylogenetic approaches, and the reasons why incorporating phylogenies into microbial macroecology allows large-scale ecological questions to be addressed in an evolutionary context.

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Down the rabbit-hole: origins and co-evolution of obligate bacterial symbioses in plant-sap feeding insects (Hemiptera)

The Auchenorrhyncha (Hemiptera) established obligate symbioses with bacteria ~300 million years ago [MYA]. Specific bacteria provide essential nutrition (e.g., amino acids and

vitamins) absent in their hosts' plant-sap diets. However, symbionts lose ~90% of their genes due to their permanent intracellular lifestyle. In order to function, bacteria require significant resources from their hosts. Yet symbiont origins, and the host-derived mechanisms that support them, have remained poorly understood for many insect groups. Although the Auchenorrhyncha split early during its diversification (>250 MYA) into the Fulgoroidea (planthoppers) and Cicadomorpha (leafhoppers and cicadas), phylogenomics reveal that many descendent species share two ancient symbiont lineages, Sulcia and a Betaproteobacteria (e.g., described as Nasuia in leafhoppers, Vidania in planthoppers, and Zinderia in spittlebugs). In each case, bacterial partners collaboratively provide their hosts with the 10 essential amino acids that all animals require. However, in leafhoppers, Sulcia and Nasuia have two of the smallest and most degraded bacterial genomes known. Thus, to individually prop up each bacterium, leafhoppers evolved distinct and precise mechanisms of support. Leafhopper hosts differentially express thousands of genes in symbiont-containing organs to meet the specific needs of each symbiont, including metabolite provisioning and support of essential cellular processes. Many of these genetic mechanisms are derived from the evolution of novel functional traits via horizontally transferred genes to the host genome, reassigned mitochondrial support genes, and gene-family duplications. Single gene phylogenies have helped determine the origin and evolutionary fate of these genes.

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Wrangling 3D data for next-generation morphology

3D data from tomographic imaging are increasingly important to all kinds of morphological studies. Though vertebrate biologists have relied upon CT scanning for decades, studies of terrestrial arthropods are experiencing a renaissance amid recent advances in 3D imaging. The world of purpose-built tools for visualizing and using 3D image data can be intimidating for researchers new to the field. I will present a workflow for processing, enhancing, manipulating, and segmenting data from micro-CT scanning using only free and open source software, and discuss two applications of these data in my research: gathering 3D morphometric measurements for a phylogenetic comparative study in a group of extant carabid beetles and studying the morphology of a group of extinct carabid beetles from Cretaceous Burmese amber.

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The role of host phylogeny in shaping the diversity of bee fly (Bombyliidae) microbiomes

A growing interest in the field of evolutionary biology has been the study of host-associated microorganisms. Studies have shown that these microbial communities can influence a host's behaviour, development and even speciation. Bombyliidae, or bee flies, are a large family of ~5,000 species. These pollinating flies have a virtually cosmopolitan distribution, with a large amount of diversity found in arid and semi-arid regions. Bee fly larvae are parasitoids of other insects and are an ideal group to study parasitoid evolution within the Diptera as the family includes species that exhibit ecto-, endo- and hyperparasitic life histories. Given the diverse parasitic life histories, this study sets out to understand how host phylogeny and ecology influence the resident microbial communities. Thirty-four samples were collected representing seven subfamilies, 17 genera of Bombyliidae and two samples representing the sister-group

Mythicomyiidae. Bacterial communities of each specimen were characterised using 16s rRNA gene sequencing. Preliminary results indicate that the composition and diversity of resident microbial communities are shaped by both host phylogeny and ecology. These results provide a baseline understanding of the resident bacterial communities across the Bombyliidae, which will help with future studies in understanding how bacterial communities influence host selection and diversification within the Bombyliidae.

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Improvements on PASOS: analysis with reduced sampling of specimens using interpolation functions and calculation of morphological disparity along ontogenetic trajectories

We have recently published a method for the phylogenetic analysis of shape ontogenies described by landmarks configurations (PASOS; Catalano, Segura & Vera Candioti 2019). The method considers parsimony as optimality criterion to define the ancestral shapes along the ancestral ontogenies for internal nodes of the tree and also to determine changes in developmental timing (i.e. heterochronic changes). In its original implementation, PASOS requires a complete sampling along the ontogenies, what precludes its use in cases with poor samplings of specimens. We present here a modification of the original approach to deal with ontogenies that present a few specimens sampled for each species. The ontogenetic trajectories are now completed interpolating shapes using an approach based on weighting moving averages. The new approach has shown to work efficiently in real datasets. We also show how PASOS can be employed to determine the morphological disparity associated to changes in developmental timing.

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A biodiversity hotspot heats up: molecular and morphological evidence of hidden diversity within the African galaxias, *Galaxias zebratus*

The Cape Fold Ecoregion (CFE) located at the southern tip of Africa is renowned for its high plant diversity and endemism that is unrivalled by other Mediterranean-type ecosystems in the world. Although the CFE's vertebrate diversity is much lower, the region is a hotspot of high endemism for stream fishes. The application of molecular techniques has stimulated renewed interest in the systematics of stream fishes in the CFE. Previous and ongoing DNA-based studies are shedding more light of the diversity and evolutionary history of these animals. The present study integrated molecular and morphological data to explore the extent to which the current taxonomy conceals hidden diversity within the African galaxias, *Galaxias zebratus*, in the CFE. Phylogenetic reconstructions based on the mitochondrial COI and cyt b sequences revealed at least 12 deeply divergent lineages within *G. zebratus*. Morphological analysis allowed separation of five of these lineages which are herein recognized as distinct species. Our results supports the notion that the continued recognition of several stream fishes within the CFE and other adjacent regions as having widespread geographic ranges reflects the lack of systematic knowledge and contributes to the biodiversity crisis in southern Africa.

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Morphological and molecular data set contradiction - fossils decide?

Historically fossil evidence was seen as the only way to understand evolutionary history. This approach lost ground when the importance of obtaining phylogenetic hypotheses based on character evidence became clear. We have studied the evolution of four clicking elateroid beetle families, Cerophytidae, Elateridae, Eucnemidae and Throscidae as reflected in fossil record. Three of the families have been shown to be monophyletic with morphological data sets, one, Elateridae however not. The same holds for results based on molecular data sets. The molecular studies imply also that the clicking mechanism of Elateridae has evolved independently and later than in the other three families. We have had the opportunity to study substantial numbers of fossil clicking elateroid beetles belonging to all these families from Baltic Amber (40-50 mya), Burmese Amber (99 mya) and Cretaceous (125 mya) and Jurassic (165 mya) Chinese deposits. The results favor those of the earlier morphological analyses. The fossil evidence does not support the idea of multiple origins of the clicking mechanism nor does it support the idea of a young Elateridae clade. It appears that the contradiction between the results is based on biased sampling. On the basis of the fossil record this bias may have interesting evolutionary implications.

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Phylogeny, speciation & environmental change through deep time

Climate change has long been identified as a driver of diversity turnover on macroevolutionary scales. Current rates of extinction, partly resulting from anthropogenic climate change, are rapidly approaching those seen in the 'big five' extinction events of the geological past, with the present biodiversity crisis now being heralded as the sixth. However, in order to predict the probable effects of current and future climate change it is vital that we understand past processes and trends.

A promising new strategy is to use the geological record and palaeontology to inform our understanding of present day change. My research utilises these types of macroevolutionary data in combination with phylogenies and numerical palaeobiological modelling to better understand biotic responses to environmental change. I have a particular focus on how key factors such as ecology, geography and climate have interacted to shape the history of life on Earth; and whether our knowledge of past interactions can help us to predict the impact of ongoing anthropogenic climate change.

Here, I will present three examples from my recent work; 1) temperature as a driver of speciation through deep time, 2) ecological transitions and their effect on speciation, and 3) disentangling the effects of biotic and abiotic drivers. With these I will demonstrate how we can use the geological past and the fossil record to inform our understanding of the complex interactions between biodiversity and the environment through time.

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Shaping our taxonomic legacy through openly sharing primary biodiversity data in taxonomic revisions

Taxonomy has a long tradition of describing earth's biodiversity. For the past 20 years or so, taxonomic revisions have become available in PDF format, which is regarded by most practicing taxonomists to be a good means of digital dissemination. However, a PDF document is nothing more than a text document that can be transferred easily for viewing among researchers and computer platforms. In today's world, traditional taxonomic techniques need to be met with novel tools to make data dissemination a reality, make species hypotheses more robust, and open the field up to rigorous scientific testing. Here, I argue that high-quality taxonomic output is not just the publication of detailed species descriptions and re-descriptions, precise taxon delimitations, easy-to-use identification keys, and comprehensively undertaken and illustrated revisions. Rather, high-quality taxonomic output embraces digital workflows and data standards to disseminate captured and published data in structured, machine-readable formats to data repositories so as to make all data openly accessible. Imagine that a taxonomist today has every original description and every subsequent re-description of a species at her/his fingertips online, has every specimen photograph produced by a previous reviser digitally available in the original resolution, and can take advantage of existing, openly accessible data and resources produced by peers in digital format in the past. When we as taxonomists provide such data, the future of biodiversity discovery will accelerate and our own taxonomic legacy will be enhanced. Cybertaxonomic tools provide methods to accomplish this goal and their use and implementation are here summarized in the context of revisionary taxonomy from the standpoint of a publishing taxonomist. While many of the tools have been around for some time now, very few taxonomists embrace and utilize these tools in their publications. This presentation will provide information on what kind of data can and should be openly shared (e.g., specimen occurrence data, digital images, names, descriptions, authors) and outline best practices utilizing globally unique identifiers for specimens and data. Data standards and the best-suited data repositories such as the Global Biodiversity Information Facility (GBIF) and Zenodo, with its Biodiversity Literature Repository, and the Plazi TreatmentBank, an emerging species portal, are discussed to illustrate retrospective and prospective data capture of taxonomic revisions.

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Unifying the global phylogeny and environmental distribution of ammonia-oxidizing archaea based on amoA genes

Ammonia-oxidizing archaea (AOA) of the phylum Thaumarchaeota represent a highly diverse group of organisms that is ubiquitous and abundant in nature, and play a major role in global nitrogen cycling. Environmental AOA have been intensively studied, often in comparison to ammonia-oxidizing bacteria, and mainly based on analysis of amoA genes (encoding ammonia monooxygenase subunit A). As a result, amoA became the most sequenced marker gene involved in biogeochemical cycles, with the archaeal orthologue comprising approximately

56% (~58,000 sequences) of all amoA gene sequences in public databases. However, associations between ecological, functional and phylogenetic patterns of AOA have been difficult to relate between studies, and their global phylogenetic breadth and coherence have remained ambiguous, mainly due to the lack of robust and comprehensive phylogenetic frameworks. Moreover, previous patterns were mainly inferred on subjective phylogenetic levels in different phylogenies and often based on polyphyletic or unsupported clades, being thus prone to generate biased and inconsistent categorical assumptions.

Here, based on extensive data curation and phylogenetic analyses of available archaeal amoA gene sequences (33,378 curated sequences), we defined a highly resolved, phylogeny-guided taxonomy that provides a classification system spanning multiple levels. Importantly, we detected a large number of chimeras among publicly available sequences, which particularly deteriorate tree topology and likely constituted a critical factor underlying the low resolution of other amoA gene phylogenies. Moreover, we performed a meta-analysis of the environmental distribution and frequency of amoA gene diversity, and uncovered global patterns that challenge many earlier generalizations. Particularly, we show that: (i) the global detection frequency of AOA is extremely uneven across their phylogenetic diversity, with few clades dominating AOA diversity in most ecosystems; (ii) AOA exhibit distinct environmental distribution patterns across variable phylogenetic levels, with both broad and narrow clades being either cosmopolitan or habitat-specific; (iii) current generalized knowledge of AOA is limited to strains and genomes that do not represent either the predominant or most specialized clades in nature, including those in broad environments with global ecological significance, namely soils and oceans; (iv) the functional role of the most prevalent environmental AOA clade remains unclear; and (v) archaeal amoA genes harbor molecular signatures that possibly reflect phenotypic traits of AOA. Additionally, we implemented our curated database and novel taxonomy as publicly available reference databases for automatic sequence classification with several popular bioinformatic tools, and provided interactive displays that integrate the taxonomy with the global environmental distribution and molecular signatures of amoA genes.

Our work synthesizes information from a decade of research on AOA and provides the first integrative framework to test hypotheses and interpret studies of environmental AOA in a global context, as well as to guide further cultivation and (meta)genomic efforts.

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Phylogenetic inference and the misplaced premise of substitution rates

Three competing ‘methods’ have traditionally been endorsed for inferring phylogenetic hypotheses: parsimony, likelihood, and Bayesianism. The latter two have been flaunted as superior because they take into account rates of sequence evolution, whereas ‘parsimony’ is said not to consider rates because evolutionary ‘models’ or theories are ignored. This presentation seeks to answer the question, ‘Can rates of sequence substitution be justified on its own accord in inferences of explanatory hypotheses?’ Answering this question requires addressing four interconnected issues: 1) the aim of scientific inquiry, 2) the nature of why-questions, 3) inferences of explanatory hypotheses as answers to why-questions, and 4) acknowledging that neither parsimony, likelihood, nor Bayesianism are inferential actions leading to explanatory hypotheses. The aim of scientific inquiry, which extends to all of biological systematics, is to acquire causal understanding of effects. Observation statements of organismal characters lead to

implicit or explicit why-questions. Those questions, which are conveyed in data matrices, assume the truth of observation statements, which is contrary to subsequently invoking substitution rates within inferences to phylogenetic hypotheses. Inferences of explanatory hypotheses, as reactions to observations of differentially-shared characters, are abductive in form, such that some version of an evolutionary theory(ies) is/are included or implied by necessity. These inferences cannot be distinguished as ‘parsimony,’ ‘likelihood,’ or ‘Bayesian;’ they are all abductive. It is then shown that if rates of sequence evolution are to be considered, it must be done prior to, rather than within abduction, further establishing that the parsimony-likelihood-Bayesian decision process is lacking in foundation. The question then becomes whether or not it is even realistic to attempt to rename selected, putatively-shared nucleotides per the background assumption of rates of substitution, much less attempt to explain such modified observation statements. There appear to be no available epistemic grounds for renaming shared characters to accommodate rates. This, coupled with problems associated with downward causation described by Fitzhugh (2016, *Acta Biotheoretica* 64(2): 133–160), largely obviate opportunities to causally account for sequence data via phylogenetic hypotheses.

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Phylogeny of the ribbon flies (Diptera: Schizophora: Odiniidae), with a discussion on homology of the male terminalia sclerites in the family

Oдиниidae is a small family of acalytratae flies with 71 described species for the world distributed in 16 genera. The family received relatively large attention in the last 10 years, with a catalog for the species of the world, description of new species and new genera, key to the genera etc. Nevertheless, a global understanding of the group is still wanting and the homology of different sclerites of the male terminalia remains unclear. Willi Hennig divided the group into two subfamilies, Oдиниinae and Traginopinae, and tried to understand the phylogenetic relationships between these two subfamilies including seven genera of the family, including a Baltic amber Eocene fossil. Several other genera were described in Oдиниidae more recently and no other studies were carried out on the phylogenetic relationships between the genera of the family. Moreover, genera as *Schildomyia* and *Odinia* present diagnoses composed only of symplesiomorphies. This study investigates the relationships between the genera of Oдиниidae. A data matrix—consisting of 84 morphological characters from 37 terminal taxa, representing 13 of the 16 genera of Oдиниidae, three genera of Agromyzidae, and two genera of Clusiidae—was analyzed under the principle of parsimony using TNT under equal weight and implied weight. Both analysis produced a single most parsimonious tree. Oдиниidae was recovered as monophyletic, supported by the presence of two surstylar lobes and the absence of an ejaculatory apodema as synapomorphies. It also recovered both subfamilies traditionally proposed in the literature, but *Pradomyia* Gaimari and *Coganodinia* Gaimari, previously allocated in the Traginopinae, were recovered as belonging to the Oдиниinae. Oдиниinae is supported mainly by the presence of the prescutellum. Traginopinae is supported especially by the posterior ocellus not aligned with the inner vertical setae. *Odinia* was not recovered as monophyletic, but it was possible to identify two lineages previously proposed in the literature: a clade with reticulated wing and a clade with spots only on the transversal veins. Two major clades were particularly well supported in the Traginopinae: (*Inpaeuma* + *Helgreelia* Gaimari) and (((*Traginops* + *Neotraginops*) + New genus A) + *Paratraginops*). The surstylar lobes strongly fused to the

epandrium is a shared synapomorphy of (*Inpauema* + *Helgreelia*). The other major clade is supported by the presence of a prominent ocellar tubercle. A discussion is developed on problems of homology of male terminalia sclerites.

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Assessing the impact of morphology on phylogenetic analyses of combined data in bryophytes

The bryophytes constitute a morphologically diverse group of taxa comprising the earliest lineages of embryophytes (i.e., land plants) sister to vascular plants. In the last decades, phylogenetic analyses of sequence-level data have radically modified the systematic schemes within bryophytes and revealed a widespread pattern of conflict with morphology-based classifications. Data conflict between morphology and molecular data in bryophytes has become widely accepted. Yet, a comprehensive evaluation of character conflict has not been performed in the context of combined matrices. In this study, an extensive assessment of the impact of morphology on bryophyte phylogeny is conducted in the framework of a total-evidence approach using 10 published matrices. The analysed matrices spanned a wide range of bryophyte groups, taxonomic levels, gene sampling and number of morphological characters and taxa. Data conflict was addressed by measuring: (i) the topological congruence between individual partitions, (ii) changes in support values of the combined data relative to the molecular partition and (iii) clade stability. The association between these measures and the number of morphological characters per taxon (character/taxon ratio) and the proportion of non-fixed characters (i.e., polymorphism and missing data) was explored. In the individual partition analyses, the number of morphological characters and the proportion of non-fixed characters correlated positively with the topological congruence. However, upon merging data, only the proportion of non-fixed data remained positively associated with support values and clade stability. The number of morphological characters, in contrast, led to negative or ambiguous responses, respectively. Several instances of taxon-specific responses were found as well, where certain datasets departed considerably from the general pattern. Hence data conflict should be carefully explored in different taxonomic groups. Overall, the results indicate that, despite the existence of character conflict between morphological and molecular data, the addition of morphology may still contribute to the inference of phylogenetic relationships of bryophytes. For example, the presence of non-fixed morphological character, usually considered a main conundrum in bryophyte systematics, influenced positively the phylogenetic inference. Our findings suggest that merely comparing (a) morphology-based classifications with molecular phylogenies or (b) the outcome from individual data partitions can misestimate data conflict. These findings imply that combined data analyses may provide conservative assessments of data conflict and, eventually, lead to a more accurate designation of morphological diagnosis.

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Quantitative analysis of phylogenetic informativeness, signal and noise in ultraconserved elements within Percomorpha and Neoaves

My talk aims to explore the ability of UCEs to resolve clade relationships within the vertebrate tree of life, specifically percomorph fishes and neoaves birds. To do so, I will explain how I used phylogenetic informativeness and phylogenetic signal to noise ratios in order to calculate the ability of a marker to resolve deep clade relationships. I will also describe the automated pipeline we designed in order to calculate these statistical measures for each of the nucleotides in thousands of UCEs. UCE cores and their respective flanking regions are large and spread out across the entire genome. Thus the approaches and findings described here are the first to analyze UCEs at a fine scale (per nucleotide) and the first to assess this phylogenetic marker type using these methods. Work described during this talk has been previously published as Genome-wide ultraconserved elements exhibit higher phylogenetic informativeness than traditional gene markers in percomorph fishes. Gilbert PS, Chang J, Pan C, Sobel EM, Sinsheimer JS, Faircloth BC, Alfaro ME. *Mol Phylogenet Evol.* 2015 Nov; 92:140-6. doi: 10.1016/j.ympev.2015.05.027 and Filtering nucleotide sites by phylogenetic signal to noise ratio increases confidence in the Neoaves phylogeny generated from ultraconserved elements Gilbert PS, Wu J, Simon MW, Sinsheimer JS, Alfaro ME. *Mol Phylogenet Evol.* 2018 Sep; 126:116-128. doi: 10.1016/j.ympev.2018.03.033.

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Microbial roles in the biosynthesis and diversity of ground beetle (Coleoptera: Carabidae) chemical defenses

Ground beetles (Coleoptera: Carabidae) are among the most prolific chemists in the animal world, using a homologous gland system to collectively produce over 250 compounds representing at least 19 distinct chemical classes. However the genetic basis and evolutionary history of carabid chemical biosynthesis remains almost completely unknown. Here we investigated the hypothesis that bacteria contribute to the biosynthetic diversity of their ground beetle hosts. Based on 16S surveys of bacterial and archaeal communities residing in over 200 species of ground beetles, we evaluated how patterns of carabid microbial biodiversity correspond to three different models of microbial community-level diversification. These include null models that predict stochastic community assembly across beetle host species, phyllosymbiosis models predicting concordance between host phylogenetic history and microbial community similarity, and a chemical correspondence model that predicts that pairwise microbial differences are commensurate with pairwise chemical differences. We describe evidence that all three models are operating to a degree, as well as results suggesting that several small subsets of bacterial taxa are consistently associated with host defensive chemistry, suggesting a potential role in biosynthesis.

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Comparative Cladistics: identifying causes for differences in results for alternative morphological datasets

No matter the utility or dominance of molecular data in the phylogenetic analysis of Recent organisms and those few young fossils preserving DNA, the remainder of the tree of life

is constructed on the analysis of morphological character data, and those analyses differ in two key regards that make comparison of results extremely challenging. First, the taxonomic scope of analyses based on morphological data varies to a much greater degree, because data rarely comes from single individuals in a limited set of extant taxa but rather a still growing array of fossil taxa that can be incorporated or excluded. Second, scoring of morphological character data is much harder to automate, often causing differences in formulation of characters and character states, as well as individual matrix scorings. As a result, new matrices generating different phylogenetic results are routinely presented with little or no discussion of the reasons underlying different results—altered terminal taxa, characters, or character state scores. A decade ago, Sereno (2009) made a plea to formalize the structure of morphological characters and to quantify with simple comparative ratios differences between competing analyses. To date, no programs facilitating comparisons have emerged. This presentation will discuss methods (implemented in TNT) to determine the differences in datasets that are responsible for producing differences in results, both in terms of monophyly of groups, and in terms of the degree of support for different groups. Even an apparently simple task such as this presents several challenges, both conceptual and computational.

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Likelihood approximations of implied weights parsimony can be selected over the Mk model by the Akaike information criterion

A likelihood method that approximates the behavior of implied weighting is described. This approach provides a likelihood perspective on several aspects of implied weighting, such as guidance for the choice of concavity values, a justification to use different concavities for different numbers of taxa, and a natural basis for extended implied weighting. In this approach, the number of free parameters in the estimation depends on C , the number of characters (in contrast with the standard Mk model, which estimates $2T-3$ parameters for T taxa). Depending on the characteristics of the dataset, the likelihood obtained with this approach may in some cases be similar or superior to that of the Mk model, but with fewer parameters being adjusted. Because of that tradeoff, testing against the Mk model by means of the Akaike Information Criterion on a set of 182 morphological datasets indicated many cases (36) where the likelihood approximation to implied weighting is the best method, from an information-theoretic point of view. Given that it is expected to produce (almost) the same results as this ML approximation, implied weighting can therefore be seen as a valid alternative to the Mk model often used for morphological datasets, on the basis of a criterion for model fit widely advocated by likelihoodists.

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Character analysis in phylogenetics – Conceptualization, ancestral states and evolutionary transformation

Phylogenetic systematics sensu Hennig exceeds the mere search for cladograms as depiction of phylogenetic relationships. The discipline is explanatory in nature and includes the analysis of characters (both molecular and morphological) and evolutionary transformation of

character states in a historical context. The multilayered process of character analysis plays an important role in each step of phylogenetic work ranging from the conceptualization of putative evolutionary entities, i.e. character states and characters, to the derivation of evolutionary scenarios of character evolution. Character analysis happens before and after the inference of the phylogenetic hypothesis. The conceptualization of characters and character states including homology assessment marks the basis for the phylogenetic analysis, whereas the reconstruction of ancestral character states happens afterwards. Ancestral state reconstruction provides the framework for the construction of hypotheses on evolutionary transformations. In this talk, processes of morphological character analysis that are leading to an evolutionary narrative are explored and illustrated using examples from evolutionary morphology. It will be shown, that "mapping" morphological characters on molecular based cladograms may be deficient but is of heuristic value as part of a research cycle (Kluge, 1997). An ultimate explanation (sensu Mayr, 1961) of observed features is based on but not restricted to the sequence of character state transformations and includes a multidisciplinary approach. In the course of reciprocal illumination, integrative character analysis can in turn provide new perspectives for character conceptualizations for tree inference.

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Transcriptomes, chalcidoid wasps and conflicting phylogenetic signals

Chalcidoidea (Hymenoptera) are a megadiverse superfamily of wasps with an astounding variation in morphology and biology. Most species are parasitoids and thus important natural enemies of insects in terrestrial ecosystems. Previous studies have not recovered strongly supported relationships along the backbone of the chalcidoid phylogeny. In this study we explored a transcriptome-based phylogeny of Chalcidoidea, and found that the poorly resolved relationships could only be marginally improved by adding more genes and taxa, proof-checking for errors of homology and contamination, and decreasing missing data. Results of concatenation analyses were consistent in supporting the following topology:

Mymaridae+(Trichogrammatidae+remaining Chalcidoidea). Considering the lifestyle of these two early lineages, this result indicates that egg parasitism might represent the ground plan biology of Chalcidoidea. However, coalescent approaches provided a different hypothesis, unless the data were filtered for loci that included more taxa and higher average bootstrap support. At the deeper nodes, the results uncover a wide spectrum of gene discordance in the transcriptomic markers and identified a strong signal of functional bias in genes supporting alternative phylogenies that might indicate ancient adaptive introgression. Thus, the basal nodes of the phylogeny may be incorrectly biased by support from different functional gene complexes. More shallow nodes showed similar gene discordance, but without strong functional bias.

Understanding and identifying mechanisms that result in gene tree discordance may be beneficial and even essential to sorting out the backbone relationships, especially for a group that has gone through an extremely rapid radiation.

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Global cooling & the rise of modern grasslands: Revealing cause & effect of environmental change on insect diversification dynamics

Utilising geo-historical environmental data to disentangle cause and effect in complex natural systems is a major goal in our quest to better understand how climate change has shaped life on Earth. Global temperature is known to drive biotic change over macro-evolutionary time-scales but the mechanisms by which it acts are often unclear. Here, we model speciation rates for Orthoptera within a phylogenetic framework and use this to demonstrate that global cooling is strongly correlated with increased speciation rates. Transfer Entropy analyses reveal the presence of one or more additional processes that are required to explain the information transfer from global temperature to Orthoptera speciation. We identify the rise of C4 grasslands as one such mechanism operating from the Miocene onwards. We therefore demonstrate the value of the geological record in increasing our understanding of climate change on macro-evolutionary and macro-ecological processes.

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Enhanced mitogenome annotation and phylogenetic analysis of Cestoda

The mtDNA is the source of molecular markers in a great variety of studies, including in phylogenetic systematics. With the advancement of high-throughput DNA sequencing technologies, the mtDNA is becoming increasingly accessible even for neglected organisms such as cestodes. However, before we can make the most extensive use of its informational content in phylogenetics, the mtDNA sequence must be adequately coded into evidence. That is to say that we must conceive matrices of putatively homologous characters, often derived from appropriated DNA annotation. Unfortunately, despite the availability of numerous bioinformatic strategies for sequence annotation, the error rate of gene calling in non-model organisms tends to increase. These errors can result from the absence of reference sequences to support homology-based inferences or inadequate use of parameter sets in some software available to date. Here we show how a widely used annotation software will fail to annotate the mitogenome of cestodes and present a novel tool that improves annotations by reducing error rate from over 50% to less than 10%. To illustrate the impact of different annotations in phylogenetic inference, we perform several cladistic analysis on data annotated mitogenomes from different procedures. Finally, we discuss how our work serves to demonstrate the significance of bridging the gap between basic research in non-model organisms and applied bioinformatics.

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Evolution of gain and loss of antimicrobial resistance genes in *Escherichia coli*

Antimicrobial resistance (AMR) in pathogenic strains of bacteria, such as *Escherichia coli* (*E. coli*), adversely affects personal and public health. In this study, we examine competing hypotheses for the evolution of AMR: 1) “genetic capitalism” in which genes that confer

antibiotic resistance are gained and not often lost in bacterial lineages, and 2) “stabilizing selection” in which genes that confer antibiotic resistance are gained and lost in balance in bacterial lineages. To test these hypotheses, we assembled a dataset that includes annotations for 409 AMR genes and a phylogenetic tree based on genome-wide single nucleotide polymorphisms from 29,255 *E. coli* isolates from the National Center for Biotechnology Information (NCBI) Pathogen Detection database. We used the “change” command in TNT to count the number of times each of the 409 AMR genes were gained and lost across the tree. We show that a large fraction of AMR genes fit the hypothesis for genetic capitalism and few AMR genes fit the hypothesis for stabilizing selection. The result that many AMR genes are under genetic capitalism reflects that strong positive selective forces, primarily induced by human industrialization of antibiotics, outweigh the energetic costs to the bacterial lineages for carrying the AMR genes. Given current conditions, we expect genetic capitalism to further drive bacterial lineages to resist antibiotics. We will discuss possible solutions.

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Eclecticism in cladistics: Convergence among opposing optimality criteria may be a hoax

Currently, most authors gave up on justifying the choice of a single optimality criterion in phylogenetics. Instead, they frequently apply as many methods as feasible as an unofficial means to tackle the question of the uncertainty inherent to tree reconstruction. For example, we reviewed recent volumes of the journal *Molecular Phylogenetics and Evolution* (volumes 94–115) and observed that 311 of 545 articles used this informal strategy (i.e., more than one method). However, only two articles attempted to justify this approach, both stating that convergence provides some measure of robustness. Neither offered any references or supporting evidence for that claim. This should not be surprising since older but similar reviews have noticed a comparable pattern. Nevertheless, we interpret this pattern differently. While others have asserted that the frequent convergence in the literature (which in our case is reported in 295 of 311 publications) is an indication of the futility of comparing methods, we hypothesize it could be an indication of publication bias. Using 100 empirical cladograms, we simulated nine alignments per tree and performed 100 tree search experiments per dataset using parsimony, maximum likelihood, and posterior probability. We designed alignment simulations to improve the retention index in comparison to the original matrix and facilitate convergence. Still, the vast majority of results were divergent by measures of the match-split distance of unrooted binary trees. These results suggest that convergence may be rare and that it is a poor indicator of the distance between the results and the original tree. Furthermore, we analyzed our data under the light of Bayesian theory to argue that the comparison of opposing optimality criteria can, at least under certain experimental conditions, increase the false discovery rate in phylogenetics.

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Ancestral state reconstructions of *Xylella fastidiosa*-host plant relationships

Xylella fastidiosa is an insect transmitted bacterial plant pathogen found across the Americas and more recently, in southern Europe. *X. fastidiosa* is typically considered to be a

generalist because as a species, it can infect plants in at least 563 plant species belonging to 82 botanical families. This broad host specificity that *X. fastidiosa* exhibits globally contrasts with increased plant host specificity for individual strains. Understanding the molecular underpinnings of plant host specificity in *X. fastidiosa* is vital for predicting host shifts and epidemics. While there are multiple genetic determinants of host range in *X. fastidiosa*, there should still be detectable genomic evidence of the unique relationships between *X. fastidiosa* and its hosts. The objective of this project is to use phylogenetic relationships to predict the ancestral plant hosts of *X. fastidiosa*. We used genomic data to construct maximum likelihood (ML) phylogenetic trees of subsets of the core and accessory genomes at varied clade depths. With those trees, we ran ML ancestral state reconstructions of plant host at several taxonomic scales (species, genus, and multi-order clade). While some genomic regions were not historically informative in terms of predicting ancestral host state, others predicted high likelihoods of particular ancestral plant hosts at particular nodes. In future work, these same historically predictive genome regions could be used to identify genetic underpinnings of host specificity and be integrated into modeling potential host jumps and host range changes of individual strains of *X. fastidiosa*.

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Save the trees: informing conservation planning with multiple facets of phylodiversity

To protect biodiversity in a systematic fashion, we must first define what it is. While it is typically defined as species richness, redefining biodiversity as branches of the phylogenetic tree can help us better prioritize which taxa to protect. Phylogenies contain information about the genomic, ecological, and evolutionary characteristics of lineages that can allow us to more efficiently protect biological diversity by identifying species and communities with complementary characteristics. I will discuss the three facets of phylogenetic diversity—divergence, diversification, and survival—and their connections to alternative conservation goals. Then I'll describe a case study in systematic conservation planning focused on the full flora of California, in which we compare and contrast future land conservation priorities under each phylodiversity facet. This analysis is based on a phylogenetic tree and geographic range models representing over 7000 plant taxa in this world biodiversity hotspot, in addition to data on land protection status and landscape ecological intactness. Our results identify a number of critical future conservation targets that are priorities under all three diversity facets, but also strong geographic distinctions among each facet. The results suggest that conservation practitioners (as well as ecologists and biogeographers) would do well to consider phylogeny and its multiple dimensions when performing spatial analyses of biodiversity.

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Exploring data manipulation strategies in phylogenomic analysis of assassin bugs (Insecta: Hemiptera: Heteroptera: Reduvidae)

Reduvidae (Hemiptera: Heteroptera), or the assassin bugs, are one of the morphologically and ecologically most diverse lineages of hemimetabolous insects, with around 7000 described species, 2 families and 26 subfamilies. Although the published phylogenies show

support for the monophyly of Reduvidae, Reduviidae, and several subfamily- and tribal-level clades, a substantial number of pressing issues remain unresolved. Most of the datasets have been using limited molecular data (nuclear ribosomal genes) or were based solely on morphological features. To address these shortcomings, a larger dataset was put together that utilized data from RNA sequencing, low-coverage whole genome sequencing, and hybrid enrichment for selected nuclear loci. In my talk I will show preliminary results that emerge from the analysis of the new data, and how different data processing techniques impact the results.

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Using NGS barcodes for investigating Avian Lice diversity and co-extinction in Singapore (Insecta: Phthiraptera),

Avian lice (Insecta: Phthiraptera) are interesting because they allow for the study of co-evolution and co-extinction with their bird hosts. However, very little is known about their diversity in Southeast Asia because they are poorly sampled and studied. Here, I obtained ca. 1500 lice from 101 bird carcasses belonging to 38 species. I then optimized methods for efficient barcoding of the lice. I settled on DNA extraction with hotSHOT because it is non-destructive, fast, and still yields usable DNA for a large proportion of the specimens. The extracted DNA was used to generate >400 NGS barcodes that allowed for sorting the specimens into putative species. I find strong molecular and morphological evidence for >40 species of avian lice. The number of lice species per bird species varies from 0-3 and the lice species appear very host-specific with only two species being found across multiple closely-related hosts. One potential method for host shifts are blood-sucking hippoboscids that I find to frequently carry phoretic bird lice. In addition to a broad survey, I also collected data on how the different lice species partition the body of Pink-necked Green Pigeons (*Treron vernans*) into different habitats. *Columbicola elbeli* is a long and thin louse that resides on the pigeon's wings between the feather barbs while *Coloceras* sp. and *Hohorstiella* sp. are round-bodied lice that reside on the pigeon's body. My next step will be placing the lice species onto the tree-of-life in order to study trait evolution, host-parasite co-evolution, and co-extinction.

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Facing long-branch anxiety and outgroup prejudice in the phylogenomic analysis of Flaviviridae

The ongoing and severe threat of viruses of the family Flaviviridae, especially *Flavivirus* (e.g., dengue, West Nile, yellow fever, and Zika viruses), to public health demand a greater understanding of how they evolve, emerge and spread for the development of countermeasures. Central to this understanding is an updated phylogeny of the family. Unfortunately, most trees focus on specific genera, ignore outgroups, and rely on midpoint rooting. It is possible that this approach is due to the lack of fully annotated genomes within the family. The family has genera with slightly different gene content, which impedes genome analysis without partitioning. Moreover, some authors have expressed the concern that the inclusion of outgroups could lead to long-branch distortions. To tackle these problems, we developed an annotation pipeline for genomes of Flaviviridae. We recovered 100% of the genes in 77 reference genomes, with an

annotation efficiency of 97% in the remaining 41 genomes. The annotation and combined analysis of genomes of *Flavivirus*, *Hepacivirus*, *Pegivirus*, and *Pestivirus* enhance the results of the phylogeny under various optimality criteria (parsimony, maximum likelihood, and posterior probability). The updated phylogeny of Flaviviridae provides insight into the close relationship between dengue virus and zika virus. We provide a novel classification of viruses such as the Tamana bat virus and soybean cyst nematode virus 5. We present strategies to test for long-branch distortions. Ours is the first comprehensive phylogeny of Flaviviridae and serves as an empirical example of the importance of outgroup sampling and adequate character partitioning.

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The significance of differences between molecular phylogenies and the fossil record when trying to infer the diversity dynamics of the living biota

Paleontologically, the present represents a time of staggering preservation, with an almost inconceivable scope of data, from soft tissue and behavioral data to the vast richness of the genome. But the present is also peculiar, being almost claustrophobically static, with data from essentially one time slice, the last frame of a vast unfolding drama. Nonetheless, neontological phylogenies, current biogeographic patterns, nested patterns of evolutionary innovation, etc., enable inferences to be made about that past, so the fact of the unfolding drama is of itself no surprise. But historical conclusions are limited to inferences, not direct observation.

Neontologically, the fossil record represents a time machine, enabling us to directly observe how phenotypes, species richness, geographic ranges, etc., have changed over time. But to a neontologist the past is disappointingly devoid of data, with limited phenotypic data, only an idiosyncratic subset of species preserved, incomplete geographic ranges, and, beyond a few hundred thousand years, no genomic data.

Yet there are morphologies, geographic, and biodiversity patterns that are completely unexpected if one only had a knowledge of the living, and the histories revealed by taking the time machine can have an unexpected complexity compared to those inferred from just neontological data. Here I explore the consequences of the differences between the neontological and paleontological data when trying to infer the diversity dynamics of the living biota.

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Integrative species delimitation in Nearctic ambush bugs (Heteroptera: Reduviidae: Phymatinae): Insights from molecules, geometric morphometrics, and ecological associations

Biodiversity cannot be accurately assessed without a resolved understanding of species boundaries. Species delimitation, the process of identifying species-level diversity and defining tangible boundaries between taxa, is central to this understanding and a fundamental component of evolutionary biology. Defining species as consistently and objectively as possible is crucial when classifying polymorphic taxa in which boundaries are less apparent. Ambush bugs, *Phymata* Latreille (Hemiptera: Reduviidae), are sit-and-wait predators of flower-visiting insects including pollinators. Broad species distribution ranges, intraspecific polymorphism, sexual

dimorphism, and subtle interspecific differences all contribute to making species delimitation especially difficult in this group that is used as a model to study interactions between sexual dimorphism and sexual selection. Recent phylogenetic research on Phymatinae has revealed that several widespread species are actually para- or polyphyletic. We here build on this research, integrating geometric morphometrics, molecular species delimitation approaches, and host plant association data for a comprehensive dataset with respect to both taxon and character sampling with the goal of teasing apart evolutionary lineages and delimiting species of Nearctic *Phymata* (Latreille). While molecular-based species delimitation analyses suggested a variety of species hypotheses, likely a result of striking discordance between mitochondrial and nuclear ribosomal genes, when combined with geometric morphometric data, we were able to confidently delimit several of these problematic taxa. In addition, geometric morphometric analysis of pronotal shape revealed undocumented morphological patterns that appear useful in diagnosing many of the surveyed taxa. Results from this study provide an objective foundation for the much-needed taxonomic revision of the most ubiquitous ambush bugs in North America.

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Tackling open-ended taxa – large-scale species discovery and phylogenetics of South-east Asian Insects

In 2011, the President of the Royal Society, Robert May, wrote that ... [we] are astonishingly ignorant about how many species are alive on Earth today, and even more ignorant about how many we can lose [and] yet still maintain ecosystem services that humanity ultimately depends upon. (PLoS Biol 9: e1001130). He pointed out that it is embarrassing that species estimates for the planet differ by more than one order of magnitude (3–100 million) and calculated that it would take ca 500 years to complete species discovery at the current rate (15,000/ year). This assessment remains valid today, but what used to be an academic issue has morphed into a significant environmental problem: there is now evidence for a global decline in insect species and populations, but biologists lack tools and data because the species diversity had not been tackled. We are therefore now developing low-cost and simple DNA-based methods for pre-sorting large numbers of specimens into putative species. Each specimen is individually barcoded using tagged amplicon sequencing (<20cents/specimens) and the NGS barcodes are used to group the specimens into putative species. We have used the technique to sort ca. 150,000 specimens from Singapore into ca. 7000 species. For some taxa, we also build species-rich trees based on mitochondrial genomes and 28S rDNA which are obtained through a mixture of tagged amplicon sequencing and genome skimming for one specimen per putative species. We again develop scalable techniques that can be applied to large numbers of species.

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Ecological traits mediated diversification patterns in squirrels (Sciuridae, Rodentia) in response to climatic shifts during the Cenozoic

We used phylogenetic comparative methods to test previously proposed hypotheses relating diversification rates with different extrinsic and intrinsic factors: biomic specialization, presence in mountain ranges, biogeographic occupancy and lifestyle adaptations. The high diversity and variety of adaptations of squirrels makes them a suitable group for assessing the combined contribution of intrinsic and extrinsic factors in shaping diversification patterns. We reconstructed the most complete phylogeny of squirrels to the moment, including almost 80% of the modern species representing 59 of the 60 genera, and applied multiple and binary state-dependent diversification models to test differences in diversification rates among groups. Furthermore, we reconstructed ancestral states for each factor. For all the traits tested, our results support differences in diversification rates among groups. These rates were higher in biome specialist species, which are more dependent upon their resources and thus suffer more the effects of the environmental change. We also found higher diversification rates in squirrels inhabiting mountain ranges, probably due to the higher isolation that these species undergone in a climatic change event due to the altitudinal gradient. The species present in the Nearctic biogeographic realm also showed higher diversification rates, maybe as a result of the high biomic heterogeneity and the numerous mountain ranges of the Neartic. Terrestriality may have also promoted diversification in squirrels, because they were able to occupy open environments that emerged during the Miocene. Finally, ancestral reconstructions suggested that cold and warm periods had a differential effect on squirrel diversification depending on their lifestyle and biomic preferences. During periods of global warming, short events of climatic cooling promoted speciation of species specialized in warm biomes, those inhabiting mountain ranges and those with arboreal habits (most of which belong to the tribe Callosciurini). On the other hand, global warming events during global cold periods promoted speciation of species specialized in cold biomes and of species with terrestrial habits (most of which belong to the tribe Marmotini).

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The logic of the data matrix in phylogenetic analysis

Phylogenetic analysis inherently consists of two phases. First a data matrix is assembled, then a phylogenetic tree is inferred from that matrix. The first phase of phylogenetic analysis is the more important of the two; but paradoxically, by far the largest proportion of effort in phylogenetic theory and method development has been directed at the second phase.

My goal is to examine each of the logical elements in the assembly of the data matrix: the rows (what are OTUs?), the columns (what are characters?), and the individual entries (what are character states?). There is a reciprocal relationship among the three elements of the matrix; OTUs need to be constructed from semaphoronts using character evidence, and characters need to be discovered and evaluated, in part through consideration of their states.

The same principles of character analysis apply regardless of the data type (e.g., morphology or molecules). A good taxonomic character has the following characteristics: (1) It must be homologous across OTUs. (2) It must show greater variation among OTU's than within; i.e., each must be a system of at least two discrete transformational homologs, or character states. (3) This variation must be heritable and independent of other characters. Application of these principles of character analysis will be discussed using examples from morphological data, DNA sequences, and genome structural comparisons.

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Advances on the phylogeny of the Neotropical wastebasket scorpion genus *Tityus* (Scorpiones: Buthidae): a total evidence approach

Tityus Koch, 1837 is a Neotropical scorpion genus widely distributed, venomous, and with a confusing taxonomy. With over 200 described species, *Tityus* constitutes the most diverse genus of the Order Scorpiones. However, the internal phylogenetic relationships of *Tityus* have not been rigorously tested, and there is no previous total evidence analysis of this genus. In order to test the phylogenetic relationships of *Tityus*: 86 in-group terminals (~51 *Tityus* species), 33 out-group terminals (eight genera and 25 species), five gene markers (12S, 16S, 18S, 28S, and COI), and 62 morphological characters were analyzed in a total evidence analysis framework, using maximum parsimony as optimality criterion. The parsimony analysis under equal weights was performed using POY with dynamic homology for non-coding markers and using static homology for protein-coding markers and morphological characters. A strict consensus tree with the Goodman-Bremer support values was calculated. In the strict consensus tree, the genus *Tityus* and the subgenus *Tityus* (*Archaeotityus*) were recovered as monophyletic. However, *Tityus* (*Caribetityus*) was recovered as paraphyletic, and *Tityus* (*Atreus*) and *Tityus* (*Tityus*) were recovered as polyphyletic. Empirical implications of these phylogenetic hypotheses are discussed and compared with previous works.

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Characters of chaetotaxy in Collembola: concepts, challenges and perspectives

Springtails (Hexapoda: Collembola) have a relatively simple body, with restricted morphological variability among phylogenetically related genera and species, which makes taxonomic and comparative studies based on morphological data challenging. From this limited set of morphological characters, chaetotaxy—the distribution and presence of bristles and sensilla in different parts of the body—have been the main source of information for differentiation of collembolan taxa, due to their high number of bristles and their variability. Despite the frequent use of chaetotaxic characters in traditional taxonomic studies, three main character coding remain complicated in order to use their information in phylogenetic analyses: 1) What criteria should be used to propose hypotheses of homology between bristles?; 2) What should we consider as a character, each individual bristle or a group of bristles? 3) How to detect biological dependence and infer character delimitation regarding sets of bristles? In this talk I will discuss the current scenario of the use of chaetotaxy in comparative phylogenetic studies of Collembola, its main challenges, and perspectives of improvement of such technique.

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A likelihoodist view on characters, model parsimony, and principled phylogenetic analysis in paleobiology

Paleobiological researchers have long debated over the most effective and consistent approaches for reconstructing evolutionary relationships between extinct taxa using

morphological traits. Despite challenges from more general approaches, such as stratocladistics, traditional cladistics, which seeks to reconstruct patterns in concordance between cladograms and matrices of discrete characters, has long been the ‘standard’ approach to phylogenetic reconstruction among fossil taxa. However, during the past several years, the proliferation of probabilistic approaches to phylogenetic inference from morphology have reignited debates over both the use of trait models and the incorporation of temporal data using parametric models of stratigraphic preservation and lineage diversification. In this talk, I will describe my work in developing a new set of parametric approaches to phylogenetic reconstruction in paleobiology that incorporate sources of data unconventional to paleobiology: quantitative traits and stratigraphic ranges. Treatment of character data as quantitative can improve existing parametric approaches by 1) increasing objectivity in the treatment of biological variation 2) facilitating use of continuous trait models that rely upon simpler assumptions than commonly used discrete trait models. Despite these clear benefits to parametric phylogenetics, quantitative traits have previously been adopted by traditional cladistics alone. Nevertheless, their use can improve the philosophical congruence between likelihoodist and cladistic approaches in several key ways. Stratigraphic information can also improve parametric and cladistic phylogenetic inference among fossil lineages by enabling the examination of hypotheses of direct ancestry. Although direct ancestry has previously been regarded as controversial, recent work has suggested that traditional approaches can generate misleading phylogenetic results when direct ancestors are present, such as are expected between taxa that occur at different intervals in the fossil record. I will explain my attempts at examining these issues from a likelihoodist standpoint, while being guided by the principles of total-evidence, model parsimony, and model adequacy. Although my approaches are operationally and conceptually distinct from both existing cladistic and parametric Bayesian approaches, I will demonstrate their association with both schools while highlighting their utility in revealing important insights in important paleoanthropological and paleobiological study systems.

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Investigating the semi-social beetle *Odontotaenius disjunctus* as a model for microbial chemical ecology studies

Some insects, e.g. ants and beetles, are known to be associated with diverse microbes. Among these, actinomycetes have been studied closely, due to their remarkable specialized metabolism that is expressed in vitro, encompassing a range of biological activities, e.g. antibacterial, antifungal and anthelmintic. However, the detection of these molecules in situ is challenging. Therefore, a question that still remains is whether or not these compounds are present in the environment and if so, can we define their ecological role? We are currently investigating *Odontotaenius disjunctus*, a Passalidae semi-social beetle, as a model for studying chemical ecology within an insect-microbe association. *O. disjunctus*, that inhabits decaying wood across the Eastern US, has shown to harbor a diverse microbiome within its gut, however, little is known about the diversity within the beetle colony. Here we are interested in investigating the chemical and biological diversity of the colony, with specific interest in actinomycetes. We subjected frass from 22 colonies across 11 US states to isolation of bacteria and metabolomic analysis. The culturable actinomycete community proved to be diverse across the different colonies, and several microbes produced diverse bioactive specialized metabolites

in vitro. By using the combination of detailed untargeted and targeted metabolomic analysis of the frass and isolated microbes, we were able to detect several analogs of three groups of antibiotics: the nonribosomal peptides actinomycins, the polyketides nactins, and angucyclinones. Interestingly, the actinomycin producer *Streptomyces padanus* was the only actinomycete isolated from almost all states. *S. padanus* also produces the antifungal polyketides Filipin III and Fungichromin. When tested together, Actinomycin D and Filipin III showed synergistic effect against the entomopathogenic fungus *Metarhizium anisopliae*. All together, we demonstrated that the microbiome associated with this insect host is diverse and contributes to the chemical composition of the beetle's environment. Therefore, *O. disjunctus* can be used as a model to investigate the chemical ecology of specialized metabolites in the context of insect-microbes associations. Beyond this, the prevalence of *S. padanus* from the same environment across large geographic distances provides a unique opportunity to study the evolution of microbial specialized metabolism in the context of symbioses.

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Combining transcriptomes, genomes, and target capture data to investigate the deep nodes of the Bembidiini (Coleoptera: Carabidae) phylogeny

Bembidiini is a diverse tribe of small ground beetles containing over 1,200 species primarily distributed throughout temperate habitats world-wide. Despite their small size, they are predaceous, preying on other small arthropods near the margins of ponds, lakes, and streams. Their size and diversity have made them a particularly challenging group for systematic study, and many more species likely remain undescribed and undiscovered. Although recent molecular work using Sanger-sequencing has untangled some of the shallow relationships within the group, the backbone of the Bembidiini phylogeny remains uncertain. We present a phylogeny of over 5,000 loci from 50 species of Bembidiini assembled from three sources of next-generation sequencing (NGS) data: transcriptomes, genomes, and target capture. This effort represents the first major genomic-scale study of the tribe, and includes several species known only from museum specimens. We also present a new pipeline which we employed for rapidly prototyping exonic loci for target capture. This pipeline, written in python, uses a single de novo genome assembly and a collection of homologous loci to identify and extract putative single-copy exons suitable for designing target capture probes. Our work greatly clarifies the deep relationships within Bembidiini, and the resulting NGS data and analysis pipeline will serve as a useful starting point for further research into the evolution of Carabidae.

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Potential for powered flight development in microraptorine dromaeosaurids, bird-like 'raptor' dinosaurs from the Cretaceous period

The evolution of birds from non-flying theropod dinosaurs is a fantastic example of flight evolution and has been studied for over 150 years. Unfortunately, a deeper understanding of early theropod flight has been frustrated by gaps in the fossil record and by disagreements on the relationships between birds (avialans) and their closest theropod relatives. This presentation focuses on the implications a new, larger, more resolved evolutionary hypothesis has on the

potential that powered flight developed in microraptorine dromaeosaurids, a subclade of early diverging ‘raptor’ theropods from the Cretaceous of East Asia and North America.

Recently, a larger, more resolved evolutionary hypothesis of coelurosaur theropods - carnivorous dinosaurs including *T. rex* as well as early birds and their closest relatives - was produced by an automated analysis pipeline tailored for large morphological datasets. This corroborates the basic composition of the Paraves – a clade of bird-like dinosaurs that groups dromaeosaurids + troodontids (Deinonychosauria) as the sister taxon to birds. The hypothesis also supports the recovery of the controversial Late Jurassic anchiornithid paravians as the earliest diverging subclade of birds. These results have important implications on the sequence of flight-related evolutionary changes that occurred along the theropod lineage to modern birds. This includes the potential of flight in non-avian paravians that have not traditionally been thought of as flying animals, such as the early diverging microraptorine dromaeosaurids.

Microraptorinae includes the tiny species *Microraptor* which possesses potentially flight-relevant anatomy like asymmetrically-vaned feathers on their long arms and legs as well as the potential for non-powered flight as indicated by physical, computer and equation-based aerodynamic modelling.

Tianyuraptor is the largest and earliest diverging microraptorine with another relatively large-bodied microraptorine, *Zhenyuanlong*, recently recovered as the next earliest diverging microraptorine for the first time. In the context of the revised microraptorine portion of the phylogeny, forelimb length and body size, traits traditionally important in considering flight in birds, both appear to decrease along the microraptorine lineage. Ancestral state reconstruction analysis of wing loading and specific lift, proxies for powered flight capability in modern birds, identifies *Microraptor* as having the potential for powered flight. Taken together, the context provided by the new phylogeny raises the possibility that the potential for powered flight decreased along the microraptorine lineage. This has motivated intensive on-going study of the dozens of known microraptorine specimens, including laser-based imaging of otherwise invisible aerodynamically-related preserved soft tissues. The way these new data will be used to refine the aerodynamic modelling needed to further interrogate this new hypothesis of microraptorine powered flight development will be discussed.

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How functional morphology informs character analysis

The transformation of the units of description, i.e. morphemes, into character states and characters, a process we call character conceptualization, is the first and crucial step in character analysis. Cladistic analyses require the independence of characters, which, however, is rarely tested. Because form and function are logically dependent and functional processes are in many cases the result of the functions of various forms, we ask how analyses of functional processes might inform character conceptualizations, particularly concerning the dependence of characters. Various examples from crustaceans will be given.

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***Begonia balangcodiae* sp. nov. from northern Luzon, the Philippines and its natural hybrid with *B. crispipila*, *B. kapangan* nothosp. nov., the first report of natural hybridization in sect. Petermannia**

The pantropically distributed *Begonia* (Begoniaceae) is one of the most species-rich genera. Philippines is one of the diversity centers of Southeast Asian *Begonia*. In our 2012 field survey, three species of *Begonia* section Petermannia were collected in Barangay Sagubo, Municipality of Kapangan, Province of Benguet in the northern Luzon Island, Philippines. Our study on literatures and herbarium specimens suggests that these collections consist of *B. crispipila*, an unknown new species hereby we named *B. balangcodiae*, and the natural hybrid between them. Molecular analyses confirm that the former contributed the maternal genome while the latter provided the paternal genome. We name the natural hybrid *B. kapangan*, which is the first natural hybrid reported in sect. Petermannia. Our studies of *Begonia* biodiversity help bring attention the Philippine flora that need immediate preservation, conservation and protection.

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Phylogenomics of the tasty clade and genomic resources for comparative studies of decapod crustaceans

Comprising over 15000 living species, decapods (crabs, shrimp and lobsters) are the most recognizable crustaceans, representing a considerable global food source. In decapod systematics morphological and Sanger sequence data have yet to produce a consensus for higher-level relationships. We leveraged a new anchored hybrid enrichment kit for decapod phylogenetics designed from genomic and transcriptomic sequences that captured new high-throughput sequence data from 94 species, including 58 of 179 extant decapod families, and 11 of 12 major lineages. The enrichment kit yields 410 loci (greater than 86 Kbp) conserved across all lineages of Decapoda, more clade-specific data than any prior study. Phylogenetic analyses recover a robust decapod tree of life strongly supporting the monophyly of all infraorders, and monophyly of each of the reptant, ‘lobster’ and ‘crab’ groups, with some results supporting pleocyemate monophyly. Crown decapods are hypothesized to have diverged in the Late Ordovician with most lineages arising in the Triassic–Jurassic, suggesting a cryptic Paleozoic history. New insights into decapod relationships provide a phylogenomic window into morphology and behaviour, and a basis to rapidly and cheaply expand sampling in this economically and ecologically significant invertebrate clade.

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Divergence and support among slightly suboptimal likelihood gene trees

Contemporary phylogenomic studies frequently incorporate two-step coalescent analyses wherein the first step is to infer individual-gene trees, generally using maximum likelihood implemented in the popular programs PhyML and RAxML. Four concerns with this approach are that these programs only present a single fully resolved gene tree to the user despite potential for ambiguous support, insufficient phylogenetic signal to fully resolve each gene tree, inexact

computer arithmetic affecting the reported likelihood of gene trees, and an exclusive focus on the most likely tree while ignoring trees that are only slightly suboptimal or within the error tolerance. Taken together, these four concerns with inferring individual-gene trees using PhyML or RAxML are sufficient for users to be suspicious of the resulting (perhaps over-resolved) topologies and (perhaps unjustifiably high) bootstrap support for individual clades. Furthermore, these gene-tree artifacts might be negatively determinate to the downstream coalescent analyses. In this study we sought to help address the fundamental question: how frequently do these concerns apply in practice to contemporary phylogenomic studies wherein the study authors typically do not explicitly address any of them? We did so by focusing on the following six questions by using RAxML. First, are the few search replicates that are frequently applied in phylogenomic studies that infer individual gene trees sufficient to find the optimal tree? Second, how much variation is there among slightly suboptimal trees relative to the best-reported tree? Third, how frequently do two existing measures (minimum branch length, SH-like aLRT) identify clades that are present in the fully resolved best-reported tree but otherwise dubious? Fourth, does the bootstrap indicate that clades which are not resolved amongst slightly suboptimal trees are well supported? Fifth, how does increasing the precision by which RAxML optimizes model-parameter values affect the best-reported trees? Sixth, how do answers to the first five questions differ when implementing the GTRGAMMA vs. GTRCAT models in RAxML?

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The evolution and biogeography of drought resistance in oaks

Aridity gradients are major drivers of functional trait variation and diversification in plants globally. Yet, phylogenetically explicit tests of aridification as an evolutionary driver remain uncommon, limiting our ability to mechanistically tie trait variation to biogeographic history. Using the ecologically diverse northern hemisphere tree genus *Quercus*, we investigated the evolution of xylem hydraulic properties along a fully resolved phylogeny of the study species, testing the hypothesis that hydraulic traits in these long-lived woody trees have responded to long-term aridification.

For all 20 *Quercus* species occurring in the California Floristic Province, representing three monophyletic and broadly sympatric clades, we measured xylem vulnerability to embolism from natural populations. At phylogenetic levels of variation we tested for conservatism in xylem vulnerability and used phylogenetic regression to understand connections between xylem vulnerability and aridity. At phylogeographic levels we investigated whether xylem vulnerability is locally adapted in one focal species and explored which biogeographic range edges are most linked to xylem vulnerability across species.

We found a phylogenetically independent and replicated signal of decreased xylem vulnerability in species with more arid distributions, highlighting the evolutionary association of xylem traits with climate and supporting the hypothesis that xylem vulnerability to embolism is a key trait influencing contemporary distributions of woody angiosperms. These findings change the paradigm of which traits we think are important for determining species biogeographic patterns, placing xylem vulnerability to embolism firmly at the fore. Further we postulate that evolving high embolism resistance allowed the Californian oaks to diversify into xeric

environments, and possibly played a role in the radiation of *Quercus* into Mexico the region with the highest species diversity.

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Phylogenomic heterogeneity and attempts to identify noise and signal in evolution

Before the wide-spread availability of large genomic datasets, researchers worked under the assumption that recalcitrant nodes would be resolved with the collection of more data. The development of new sequencing technologies made large datasets a reality, though recalcitrant nodes remain. The last decade of genomic sequencing and phylogenetic reconstruction has demonstrated that with the collection of more data has come an increase in the heterogeneity underlying those data. In this presentation, I will discuss some of the sources of heterogeneity and how we might distinguish signal from noise. I will also argue that, instead of discarding conflict, phylogenetic conflict serves to present a more complete picture of the processes underlying lineage diversification.

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Homology in the age of phylogenomics

Homology is arguably the most central concept in phylogenetic biology. Molecular systematists have traditionally paid diligent attention to the homology statements that are implied by their sequence alignments, but manual gene-by-gene curation has gone by the wayside in the phylogenomics era. Here, we show that a variety of phylogenomic data sets are compromised by homology errors that negatively impact the integrity of these data. We also outline multiple approaches to efficiently screen for and detect homology errors in phylogenomic data. Application of these screening approaches shows that some phylogenomic data sets are replete with homology errors including alignments of different exons to each other, alignments of introns to exons, and alignments of paralogous sequences to each other. The extent of these homology errors weakens the conclusions of these studies. Despite advances in automated phylogenomic pipelines, the sometimes tedious work of systematics is still required to guard against pervasive homology errors. This conclusion is underscored by recent studies that show that just a few outlier genes can impact phylogenetic results at short, closely spaced internodes that are deep in the Tree of Life. The view that widespread DNA sequence alignment errors are not a major concern for rigorous systematic research is not tenable. If a primary goal of phylogenomics is to resolve the most challenging phylogenetic problems with the abundant sequence data that are now available, researchers must employ effective procedures to screen for and correct homology errors prior to performing phylogenetic and other downstream analyses.

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Unraveling Ross' classification of Anisembiidae (Embioptera)

The Southamerican family Anisembiidae appears as a monophyletic group in the first to the last published cladistic analyses of the Embioptera Order. However, half of the genera

described by Edward S. Ross – the specialist of order - appear as paraphyletic or polyphyletic groups (e.g. *Bulbocerca*, *Dactylocerca*, *Pelorembia*, *Stenembia*). The Anisembiidae, had - at the end of the 90 - a handful of genera (4-5) and around 40 species. Between 2001 and 2004, Ross published six compendia on Embioptera in the journal Occ. Paper of California Academy. One of them is a review of the family Anisembiidae, where he describes about 70 new species and 15 new genera (half of them monotypic), as well as groups like tribes and subfamilies. In this compendium is clear the conflict between the specialist's point of view and the basic principle in systematics: achieve a stable classification; taxonomic groups should be supported by the evidence. As a result of this particular interpretation of the systematics, there are new genera grouping autapomorphic species of other well known genera and, geography as a criterion to define genera (e.g. the genus *Mesembia* exclusive for Cuba). Therefore, in this work we propose to analyze the whole group (around 110 species) and try to untangle Ross' classification in a phylogenetic context.

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Biogeographic and diversification patterns of squamate reptiles across North Africa and Arabia

Desert areas comprise an important part of the world's land surface. In spite of their harsh conditions, deserts can harbor a high diversity of fauna and flora. This offers the opportunity of investigating how the geographic and climatic history of these areas have affected the evolutionary history of their biodiversity. In this study, we focus on some of the largest arid regions of the world, the north of Africa and the Arabian Peninsula, to study large-scale biogeographic and diversification patterns of squamate reptiles, one of the most successful groups inhabiting the deserts. Evolutionary history has been explored and discussed independently for several groups of reptiles from north Africa and the Arabian Peninsula, but a study integrating a large number of groups is still lacking. Here, we assemble a comprehensive dataset including most of the squamate genera present both in Africa and Arabia with the objective of investigating large-scale biogeographic and diversification patterns in a comparative framework. We reconstruct phylogenetic relationships among 550 species with 5 mitochondrial and 6 nuclear loci, and estimate divergence times with eleven calibration points, including fossils and biogeographic events. With this broad dataset, we are able to reconstruct and compare the evolutionary history of 22 genera of squamate reptiles across north Africa and Arabia. By applying statistical biogeographic models, we can associate diversification dynamics with paleogeographic events affecting these regions. As a result, we can describe the effect of the Afro-Arabian geologic and climatic history on the diversity and evolution of desert-dwelling squamates.

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Gene tree incongruence is a major predictor of the differences between parsimony and maximum likelihood in phylogenomics

In previous studies we found a high congruence between the results of Maximum Parsimony (MP) and Maximum Likelihood (ML) for 149 phylogenomic datasets (average of 3.5

SPR-moves; 49% of the resulting trees from MP and ML were identical or differed in one SPR-move), with those differences generally not affecting the main conclusions discussed in the original studies. In addition, we found that most of the incongruence between MP and ML was related to poorly supported nodes. Furthermore, in preliminary analyses we observed an association between branch lengths/missing data and the differences between the results of both methods. In this study we performed a more detailed evaluation of the incongruence between MP and ML, exploring other characteristics that can be related to the MP-ML incongruence, and improving the statistical comparisons. We evaluated whether the amount of incongruence between MP and ML was related to the taxonomic ranks to which the terminal taxa belong and whether the incongruent nodes present specific locations in the trees (basal vs. terminal). Finally, using a multiple linear regression approach we assessed whether there was a relationship between the MP-ML incongruence and the incongruence among gene trees. We found that gene tree incongruence was significantly associated to the MP-ML incongruence, showing that incongruent nodes are in general those that were recovered in a low percentage of the gene trees. We did not observe a significant relationship between the taxonomic ranks and the MP-ML incongruence. The same occurs with the location of the incongruent nodes, where we found no specific trend. The results obtained in the present study indicate that gene tree incongruence is an important explaining factor of the MP-ML incongruence. However, our findings evidenced that explaining the incongruence between parsimony and likelihood in phylogenomic inference requires taking into account several factors in an integrative approach.

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Incorporating functional genomics into UCE phylogenomics

Ultraconserved genomic elements (UCEs), have long been treated as independent loci in phylogenetic analyses. The identification pipeline for UCE probes is agnostic to genetic identity, only selecting loci that are highly conserved, single copy, without repeats, and of a particular length. Here we characterize the most widely used sets of UCE makers in phylogenomic studies and demonstrate the subsequent effect on gene and species tree reconstruction. We examined 4 different sets of UCE markers from 5 different studies including birds, mammals, fish, Hymenoptera (ants, wasps and bees) and Coleoptera (beetles). We found that within vertebrate lineages UCEs are mostly intronic and intergenic, while in invertebrates, the majority are in exons. Of genes captured by UCEs, we find many are represented by 2 or more UCEs that represent non-overlapping segments of a single locus. We considered these UCEs to be non-independent, and merged all UCEs that belonged to a particular gene, and constructed gene and species trees, with RAxML and ASTRAL-III. Average bootstrap support values for merged UCE gene trees were significantly improved across all vertebrate and invertebrate datasets. The average bootstrap support for the subsequent species trees improved as well. Increased loci length appears to drive this increase in bootstrap support values. Also, we found no difference in average bootstrap support values for gene trees based on intergenic UCEs versus those based on UCEs found within genes. This modest degree of UCE characterization and curation impacts downstream analyses and demonstrates the advantages of incorporating basic functional genomics into phylogenomics analyses. I will also present on other novel genomic data sources and their applicability for phylogenomic reconstruction.

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Untangling extant biodiversity in Hydroporini

Aquatic beetles can be characterized based on the habitats where they live, with a main division between species living in standing water or species living in running waters. Both habitat types present differences based on their physical and chemical characteristics, leading to different ecological dynamics at geological scale, in essentially long-term habitat stability. Small standing water environments, where aquatic beetles are usually found, are usually filled up by sediments in decades, whilst running water environments are stable and they are connected with the drainage network, even when they sometimes dry up seasonally. Some studies had shown that one of the consequences of living in one kind or the other is a difference in range size linked to their dispersal capabilities, with standing water species having broader geographical ranges than running water species. It has been hypothesizing that dispersal abilities may affect gene flow and turnover, but there is a lack of knowledge of how these differences affect long-term diversification.

Hydroporini is a speciose tribe containing ca. 680 species living in both habitats, making them an ideal group to study diversification. We built a phylogeny of Hydroporini combining 5 genes obtained with sanger sequences plus 69 mitochondrial genomes. In total, 473 terminals representing species were used. Ecological data were obtained by bibliographic revision plus own collected information in the field. Phylogeny and habitat type evolution were reconstructed using Bayesian inference. Diversification rates were calculated using Bayesian Analysis of Macroevolutionary Mixtures (BAMM) and method of moments (MM). Preliminary results suggest that the most recent common ancestor of Hydroporini was reconstructed with a preference for running water, with multiple shifts to standing waters. We also found several significant diversification shifts across the phylogeny, and a clear pattern of gradual accelerated speciation.

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Advances in methods for large-scale multi-locus species tree estimation

The estimation of species trees from multi-locus datasets is a basic step in biological research. However, heterogeneity between loci resulting from biological processes such as incomplete lineage sorting and horizontal gene transfer make standard approaches (such as concatenation using maximum likelihood) statistically inconsistent. In this talk, I will present very recent work on species tree estimation from multi-locus data sets when gene trees can differ from the species tree due to incomplete lineage sorting, focusing on both empirical (e.g., performance on data) and theoretical performance (e.g., statistical consistency). I will also present new (unpublished) techniques for improving the scalability of these methods to large data sets. Much of this talk is based on joint work with Siavash Mirarab (UCSD), Erin Molloy (Illinois), Mike Nute (Illinois), Sébastien Roch (Wisconsin), and Pranjal Vachaspati (Illinois).

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Integrating phylogenomic and morphological data to revise the true bug classification (Hemiptera: Dipsocoromorpha and Reduvidae)

Building and revising phylogenetic classifications based on monophyly and diagnosability is at the core of systematic research. Ideally, diagnostic characters are derived from explicitly coded and analyzed morphological datasets. Concatenated molecular and morphological datasets have therefore long been used to infer phylogenetic relationships and to revise existing classifications. Although the importance of morphology in the phylogenomic era continues to be stressed, many recently published insect phylogenies are based exclusively on molecular data. We here explore avenues to integrate morphological and molecular datasets, using either concatenated datasets or ancestral state reconstructions, and based on examples from different groups of true bugs.

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Algorithmic information as phylogenetic optimality criterion

Algorithmic (Kolmogorov) information is presented as an optimality criterion for phylogenetic analysis. Though uncomputable, heuristic methods are presented for the calculation of upper bounds on the information content of a phylogenetic hypothesis. This approach generates natural weighting functions for a diversity of phylogenetic graph types and character change scenarios. An example is presented demonstrating the approach.

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Phylogeny, ecology, and patterns of diversity

In this talk, I will present recent research from my lab group at the interface of phylogeny and ecology. I will emphasize our studies on patterns of species diversity, including patterns of richness among clades and among regions. In the first part, I will use phylogeny-based approaches to show that much of the variation in species richness among clades is explained by variation in diversification rates (i.e. speciation minus extinction, or how quickly clades accumulate richness). I will then show that ecological traits seem to be especially important for explaining these patterns of diversification and richness. Intriguingly, traits related to species interactions and other aspects of local-scale ecology (e.g. microhabitat) appear to be especially important at deeper phylogenetic scales in many groups (e.g. across animal phyla, vertebrates, and insects). In the second part, I will focus on patterns of species richness among regions and habitats, and how these diversity patterns can potentially be explained by variation in: (a) rates of diversification of lineages in each region or habitat, (b) the frequency of colonization of each region or habitat, and/or (c) the timing of colonization, with regions or habitats that have been colonized longer potentially having higher species richness. Phylogenetic analyses reveal that patterns of species diversity among regions within clades (e.g. families) are often explained primarily by differences in the timing of colonization of each region. On the other hand, richness patterns at deeper time scales and/or larger spatial scales may be explained by differences in

diversification rates. Surprisingly, patterns of relative richness among clades at local sites also seem to be explained primarily by variation in diversification rates. Finally, I will discuss some of our work on patterns of niche evolution, including their potential relevance to studies of climate change.

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Weaponising philosophy

Philosophy of science and science have a complex relationship. Many scientists make philosophical points, usually to assert the scientific correctness or a lack of it, of various programs. Many philosophers have asserted much the same of philosophies of science. How might philosophy aid, or impede, systematics? In the end, it gets down to inferences. What do we know and how do we know it. Is philosophy a tool, and if so, is it weaponised? And should philosophers believe scientists?

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Methodological plurality and the future of cladistics

How many methods of tree reconstruction/estimation do you include in a publication or proposal? Some early papers dismissed the practice of using multiple method agreement as a support measure in phylogenetics and others relegated methodological plurality to be meaningful only as a modestly effective sensitivity analysis. In practice, however, methodological pluralism is a dominant approach in current phylogenetic research. The use of several methods to generate phylogenetic trees using the same dataset in a given publication is widespread, for some people even expected. Clarification of the purpose intended when the methodological plurality approach is used and the actions to take based on the resulting agreement or disagreement among methods are very rarely discussed. Discussion on this topic has been hindered by a lack of reference to the ontological and epistemological foundations for the methods. Potentially insoluble ontological differences like this exist in our field. Such differences have been particularly significant to the Hennig Society and in some cases led to misconceptions like the notion that Cladistics equals parsimony or that the Society's role is waning in the face of the many contemporary methods emerging. Such a dire assessment is rejected and I endorse the view that the Society has an exceptionally important, timely, and unique role to promote and advance phylogenetics. I present thoughts and ideas for discussion on ways that the Hennig Society might expand its relevance.

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Building a species-rich tree-of-life for Diptera with NGS barcodes, multiplexed tagged amplicons, and mitogenomic genome skimming

Species-rich trees are important for robust evolutionary hypotheses testing, obtaining phylogenetic diversity measures for habitats and understanding the processes underlying community assembly. However, obtaining species-rich trees for species-rich groups such as arthropods is challenging and can be prohibitively expensive if large amounts of data are

collected for each species. Here, we use a three-pronged approach for overcoming these challenges. We developed techniques for obtaining species-rich trees based on ~20,000-bp of DNA data (mitogenome, 28S rDNA) for <\$15 per species. NGS barcodes are first used for sorting thousands of specimens into putative species. Subsequently, we utilize multiplexed tagged amplicon sequencing applied to one specimen per putative species for obtaining full length 28S rDNA and baits for the mitogenomes. Lastly, we use genome skimming for obtaining mitogenome scaffolds. Here, we used these techniques to place >900 Singaporean Diptera species on the tree-of-life. Using the barcodes and other genetic data, we also compare the species diversity and distributions of different habitats in Singapore. We find that mangroves are unexpectedly species-rich and have high beta-diversity.