CPEG

2nd Crossing the Palaeontological-Ecological Gap

Online, 5th-9th September 2021

Hosted by the Museum für Naturkunde, Berlin

Abstract Book

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Plenary talks

Interrogating ecological patterns and processes across timescales

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I will discuss recent work from my lab examining patterns of niche change, diversity gradients, and extinction selectivity from both an ecological and paleoecological perspective. The first part of my talk will use the exceptional fossil record of planktonic foraminifera to examine changes in biodiversity gradients on timescales that are usually difficult to interrogate with either paleontological or modern data. The second part of my talk will focus on patterns of extinction selectivity in the past and future, and what we can learn from applying models of dispersal to evaluate how species respond to climate change.

A recommender systems approach to the fossil record

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Machine-learned recommender systems are behind most of online life today from personalisation of news, ads or dates to selection of study programmes or fastest routes. The setup of recommender systems closely relates to species distribution modelling if we consider a task of recommending animals for localities. Just like fossil data, user preference data are highly fragmented and uncertainties are asymmetric with presences being more certain than absences. Machine learning techniques for recommender systems are tailored to work with such uncertainties and offer an interesting take on species distribution modelling. In this talk I will discuss how to frame analysis of fossil ecosystems as a recommender systems task and show how existing techniques for data with implicit feedback can be leveraged for analysing past ecosystems. I will show how such techniques can be used for identifying functional companionships of taxa, assessing completeness and consistency of species lists at localities, as well as estimating relative abundances solely from species lists. I will illustrate the potential of recommender systems approaches for palaeontological analyses with a case study of Middle Miocene mammalian fossil localities in Europe.

Consequences of selection and biotic interactions for macroevolution

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Macroevolutionary patterns discernible from the fossil record include originations and extinctions of lineages and the distributions of their morphological traits in space and time. These patterns, as revealed by fossilized organisms, are necessarily the consequences of selection, drift and constraints, given physical and biological backdrops. While links between short-term ecological interactions plus generation-to-generation selective pressures with longer-term macroevolutionary and/or paleontological patterns are assumed, they are seldom elucidated with empirical data. This impedes the development of more realistic, nuanced and/or useful theoretical, mathematical and/or statistical models for linking micro- and macroevolution, as well as ecology and paleoecology. In this presentation, I discuss how we have begun to alleviate some of this impediment: by accumulating new data and developing novel models from multiple vantage points for cheilostome bryozoans. Cheilostomes, a fossil-rich and widespread marine clade, are still ecologically important and taxonomically diverse in contemporary waters. I will give examples of how selection gradients and competitive interactions might be approximated in the fossil record, and what relationships these might have to typical macroevolutionary patterns presented for fossil clades.

Paleoecology reveals dynamic landscapes: the case for conserving for change

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To establish the most effective conservation strategies, we must understand the ecological dynamics of the systems that we are trying to conserve. But we do not know the extent to which plants and animals shift their ranges in response to changing climates. Using the fossil pollen and mammal records, we explore how rapidly biomes transition in response to changing climates and to what extent human impacts prevent species from tracking their preferred climate. We have found that plants and animals will need to traverse broad landscapes at unprecedented rates to track climate as it changes, and I have identified strategic regions to target for facilitating this connectivity. However, we also have found that not all species exhibit the same human tolerance or climate fidelity (i.e., some species' ranges are less affected by climate than others). My lab and I found that 67% of mammals have shifted their climatic niche, mostly in the last 500 years. Interestingly many small mammals have actually expanded their climatic niches into agricultural and urban landscapes, suggesting that humans facilitate their survival. Whereas most large mammals have been extirpated from human-impacted landscapes. We are now working to identify the climate fidelity that plant and animal taxa have exhibited over the last 20,000 years. Our goal is to identify the types of species whose climate tracking we must prioritize as we identify efficient and effective connectivity strategies.

Integrating paleobiology and macroecology to inform current and future megafauna-based rewilding

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During the last 100,000 years, approximately 50% of terrestrial mammal species with body mass ≥10 kg (megafauna s.l.) have been in lost, in an extinction event linked to the global expansion of Homo sapiens. Hereby, current faunas in much of the world are megafauna-poor and deviate from the norm across the last 30-40 million years. There are likely strong functional consequences, but these are poorly understood, as are their consequences for nature management and restoration efforts. Here, I will address these questions through an integrative macroecological-paleobiological approach, with a focus on large herbivores given their potential importance for ecosystem functioning and their important, sometimes controversial role in conservation and ecosystem restoration (notably trophic rewilding).

Session 1: Biogeography

Climatic constraints on the latitudinal distribution and biogeographic history of dinosaurs

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During the Jurassic–Cretaceous (201–66 million years ago), dinosaurs dominated every available terrestrial niche, with an almost ubiquitous distribution, from Antarctica to the Arctic Circle. However, fundamental spatial segregations were present between the three main dinosaurian subgroups, with pole-to-pole distributions of ornithischians and theropods, and a lower latitudinal occupation and polar absence for sauropods. Whether sampling biases or environmental agents were the primary drivers of these perceived patterns is still open to debate. We investigated biogeographic patterns, sampling coverage, and climatic suitability in Jurassic–Cretaceous dinosaurs, combining climate predictions from General Circulation Models and spatial subsampling techniques on distributional data of dinosaur occurrences. Climatic suitability for the main dinosaur subgroups was evaluated by building taxon-specific habitat suitability models and spatially projecting climatic envelopes based on thermal and humidity values matching dinosaur occurrences worldwide. Uniquely among dinosaurs, sauropods occupied climatic niches characterized by higher temperatures both in the cold and warm intervals, with high predicted climatic suitability for equatorial and tropical areas, and lower or absent suitable areas in the latitudinal extremes. Our findings might explain the high abundance of sauropods in the southern continents and their proportional rarity elsewhere during the Cretaceous, in addition to explaining some intriguing biogeographic patterns for this clade, such as the timings of higher latitude dispersal. This hitherto enigmatic pattern of sauropod biogeography potentially links their thermal biology to their distributional and paleodiversity patterns.

South American freshwater fish diversity shaped by Andean uplift since the Late Cretaceous

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South America is home to the highest freshwater fish biodiversity on Earth. The hotspot of species richness is located in the western Amazon Basin, and richness decreases downstream along the Amazon River towards the mouth at the Atlantic coast, which contradicts the positive relationship between stream size and biodiversity that is commonly observed in river systems across the world. We investigate the role of river rerouting events caused by Andean mountain building and repeated episodes of flooding in western Amazonia in shaping the modern-day richness pattern of freshwater fishes in South America. To this end, we combine a reconstruction of river networks following Andean surface uplift since 80 million years ago with a mechanistic biological model simulating dispersal, allopatric speciation and extinction over the dynamic landscape of rivers and lakes. We show that the numerous small river rerouting events in western Amazonia resulting from mountain building produced highly dynamic riverine habitats that caused high diversification rates, shaping the exceptional present-day richness of this region. The history of marine incursions and lakes, including the Miocene Pebas megawetland system in western Amazonia, played a secondary role. This study is a major step towards the understanding of the processes involved in the interactions between the solid Earth, landscapes, and life of extraordinary biodiverse South America.

Biome specialization enhances diversification in swallowtail butterflies

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A major task in macroevolutionary research is to test hypothesis linking shifts in climate with diversification patterns (i.e., speciation and extinction rates). For example, it is generally thought that biome specialists (those species restricted to a single biome) have higher speciation and extinction rates than generalists, as the former are more prone to population fragmentation and genetic divergence due to environmental forcing. This and other related predictions are encapsulated under the resource-use hypothesis, which has been tested both using fossil and living species data. However, previous work has been mainly focused on vertebrate clades, especially mammals. Thus, little is known about the universality of such predictions in other key groups such as insects, preventing us from understanding the impact of climate shifts in a significant part of the global biota. In this work, we test some of the predictions derived from the resource-use hypothesis in swallowtail butterflies (family Papilionidae) by estimating the degree of biome specialization of each species, and testing for its correlation with species-level diversifcation rates estimated from the most complete Papilionidae time-calibrated phylogeny to date. We found a higher prevalence of biome specialists than expected under null models, which also showed higher diversification rates than biome generalists, and the proportion of specialists in climatically extreme biomes was higher than in transitional biomes. In this work we demonstrate, for the first time for an invertebrate group, that biome specialization provides higher diversifications rates among swallowtail butterflies.

Marine plankton latitudinal diversity patterns since the last ice age

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Understanding the response of marine ecosystems to climate change requires knowledge of processes that operate over long time-scales. Over the last decades, many studies have generated sedimentary time-series of marine microplankton assemblage composition across the last deglaciation. These time-series were used mainly to reconstruct ocean temperature but their potential to reveal the long-term biotic response to climatic forcing has been rarely explored. Here, we compiled abundance data of planktonic foraminifera species from the North Atlantic Ocean covering the past 24,000 years (with an average temporal resolution of at least 600 years) to study plankton response to temperature change. We determine the compositional change of the planktonic foraminifera community by principal components analyses, quantify temporal compositional turnover, and analyse spatio-temporal patterns in the rates of biodiversity change. We find that the current latitudinal diversity gradient results from a complex transformation of plankton biogeography since the last deglaciation, which started with the onset of global warming around 17,000 years ago. However, compositional change continued during the climatically stable Holocene, indicating that the plankton response to temperature change is less predictable since the early Holocene. The biotic response we observe was largest in the mid-latitudes and was dominated by species' range expansion rather than contraction, and new communities with no analogues in the glacial ocean emerged during the Holocene. In summary, our study shows that plankton response to global warming is a complex process and not always directly related to temperature change. These findings may have implications for the predictions of how current plankton communities will respond to ongoing climate change.

Diversity dynamics through deep time: overcoming the hurdle of spatiotemporal sampling bias

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Analysing large-scale diversity trends through geological time has been a staple of palaeontological enquiry for over 70 years. The quality and quantity of data underpinning such analyses has grown and the methods used to mitigate variation in sampling intensity through time have become ever more sophisticated. It is increasingly apparent, however, that variation in the geographical distribution of palaeontological data continues to distort relative and absolute diversity trends, even when temporal variation in sampling intensity is accounted for. While methods to address this issue have been proposed, they all produce point-wise diversity estimates from spatially-standardised subsamples and cannot provide the temporally continuous datasets needed for the calculation of speciation, extinction and preservation rates – the variables which ultimately determined true past diversity and its manifestation in the geological record. To overcome these hurdles, I present an alternative approach to accounting for spatial sampling bias, employing the geometry of ocean basins as *a priori* biogeographic regions and natural sampling units to provide temporally continuous datasets that can be standardised by a number of different geographic extent metrics, in particular minimum spanning tree length and longitude-latitude extent. I then apply Bayesian methods which account for temporal sampling bias within these standardised regional samples, where the resultant diversity trends show no relationship to geographic extent and may be considered to reflect the true signal through time. I showcase this approach using the Triassic marine fossil record, highlighting individual biogeographic histories and the coordinated diversity changes which reflect emergent global events, including the Permo-Triassic and Triassic-Jurassic mass extinctions and the Carnian Pluvial Episode.

The impact of the Permian and Triassic biotic crises on spatial patterns of origination and extinction in marine invertebrates

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The Permian and Triassic (~300–200 Mya) represent an interesting time in Earth history, characterised by an icehouse-greenhouse transition, followed by large-scale volcanic episodes and extreme greenhouse temperatures, resulting in biotic crises at the end of the Capitanian (Middle Permian) and the most severe known mass extinction event at the Permian-Triassic boundary. Two theories have been put forward to describe the spatial distribution of extinctions during the end-Permian event: (a) rising temperatures in the already-warm equatorial regions rendered them uninhabitably hot, driving poleward migration and/or high rates of extinction at low latitudes, and (b) rising temperatures in the cooler polar regions meant the loss of niche-suitable habitat for cool-adapted organisms, driving high rates of extinction at high latitudes. We built simulations to test whether proportions of origination and extinction could be reliably reconstructed from the fossil record for spatially divided occurrence datasets. Using these methods, we estimated origination and extinction by latitude throughout the Permian and Triassic using a global database of fossil ammonoid, brachiopod and bivalve occurrences. These results were then used to examine whether one or both of the aforementioned mechanisms took place during the end-Capitanian and end-Permian extinctions and subsequent recoveries, and whether similar or different dynamics could be observed between the benthic and pelagic clades.

Fossil evidence for marine dispersal in an iconic example of vicariance

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While the importance of fossils in biogeographic inference has been recognized since the early days of evolutionary biology, the impact of palaeontological relative to neontological data for the reconstruction of the biogeographic history of extant clades remains mostly unexplored. Bonytongue fishes (Osteoglossomorpha)—popularly seen as an example of continental vicariance caused by the progressive breakup of Pangaea —represent an ideal study case in this respect, as their fossil record is relatively abundant and geographically widespread. While living species are restricted to freshwater settings in mostly tropical environments, several fossil bonytongues are known from marine deposits worldwide, making this group particularly fitting to study freshwater-to-marine ecological transitions in a biogeographical context. We inferred ancestral geographic ranges and environments using phylogenetic models of biogeographic evolution applied on a total-evidence phylogeny of 32 fossil and 61 extant bonytongue species. Trait-based dispersal models—where freshwater/marine ecology is treated as a binary trait affecting dispersal ability—strongly support a marine origin for osteoglossid bonytongues (arapaima, arowanas and relatives). Extant osteoglossids likely derive from marine ancestors that dispersed globally and entered freshwater environments multiple times independently. Extinction of all marine forms and survival of few freshwater lineages in tropical regions resulted in the disjunct geographic distribution we observe today. Therefore, the current distribution of bonytongues and apparent agreement with patterns of continental fragmentation represents an instance of pseudo-congruence. Ignoring fossil taxa in the biogeographic analysis results in a completely different scenario that largely corresponds to continental vicariance. Our study provides a striking case of how fossil data can overthrow biogeographic and ecological patterns that are apparent from the examination of extant species alone, and highlights the perils of ignoring palaeontological evidence when inferring ancestral conditions for living organisms.

Palaeobiogeography of Neogene European chondrichthyans

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Despite the rich fossil record of Neogene (23 to 2.6 Ma) chondrichthyans (chimaeras, sharks, rays and skates) from Europe, little is known about the macroevolutionary processes that generated their current geographical distribution. We compiled a database of 4,368 Neogene occurrences on genus level from four European regions (Atlantic, Mediterranean, North Sea and Paratethys) based on a comprehensive literature review (including journal articles, unpublished thesis, conference abstracts and books) complemented with data from Paleobiology Database and from museum online collections databases. In order to reconstruct biogeographic patterns of European chondrichthyans from the Neogene to the Recent, we estimated the proportion of Neogene genera still living in each region today. Records from the Paratethys were compared against the present-day Mediterranean occurrences. Our results show that 27% of genera that inhabited the marine environments of Europe during the Neogene are now globally extinct. This proportion is higher in comparison to that reported for chondrichthyan faunas from temperate South America (3%) and tropical America (13%). Regionally, the proportion of extinct genera was much higher (40-56%), but there were no significant differences between European regions. Biogeographic dynamics of each region likely reflect the impact of palaeoenvironmental conditions (*e.g.*, warm and cold episodes) that occurred at different spatial scales across Europe and the globe. However, the role of ecological and life-history traits of each genus should be tested in the future. Therefore, our analysis only can provide first steps to synthesize and understand palaeobiogeographic patterns of chondrichthyans from the Neogene of Europe. Thus, additional palaeontological and ecological studies are needed to provide data for further refinements of the present analyses.

Using the abundance and climatic niche of fossil microvertebrates for paleoclimatic reconstruction

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Ecological features are quite susceptible to environmental modifications, and among those, demography being the first affected during events of climate change. Vertebrate paleoclimatic reconstructions have never used the species abundance as a functional trait (ecometric) to infer past climates. We used both the current relationship between abundance and Distance to the Niche Centroid approach (DNC), and the relationship between the DNC with the mean annual temperature (MAT) and annual precipitation (AP). Those analyses were assayed within the distribution range of the volcano rabbit (*Romerolagus diazi*) and the Yucatan small-eared shrew (*Cryptotis mayensis*) to reconstruct the mean annual temperature (MAT) and annual precipitation (AP) for two Late Pleistocene Mexican paleontological localities. We used the minimum number or individuals (MNI) to account for relative abundance and calculated the past-DNC with species present information. We used the relationship between the past-DNC with the values of MAT and AP to reconstruct the climate shifts through different stratigraphic levels during the Quaternary in Valsequillo, Puebla and Loltún Cave, Yucatán, México. Our results indicate that today the highest abundance of species distribution range is closer to its climatic niche centroid, and the paleoclimatic reconstruction shows that during the late Pleistocene the MAT was cooler and the AP was highest than their present values, while climatic conditions change during the Holocene. Our results match with paleoclimatic values inferred with fossil pollen near by the study sites.

Past and present ecologies, panarchy and possible peatland futures

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In this paper, I frame the dynamic history of a highly modified raised mire in the north east of England as an ever evolving and changing number of adaptive cycles, confering both resilience and potential for transformation to one of the most important lowland peatland sites in Britain. The concept of ecosystems as panarchies – a series of interconnected adaptive cycles conveying information and materials across different scales of time and space – is compatible with the framework of Ecosystem Restoration. Both disregard the traditional model of succession whereby there is a single end-point of a linear process of development, and instead embrace the dynamicity of ecosystems and knowledge of past states as a guide to future potential states. Starting approximately 10,000 years ago, we follow the progress of the Humberhead Levels through a phase of experimentation and restructuring at the tail-end of the Devensian glacial period, followed by a phase of growth and accumulation fed by positive feedbacks from the development of peat, waterlogged conditions and the arrival and spread of keystone Sphagnum. The process briefly pauses when relatively stable and resilient oligotrophic peatland emerges before being released into new cycles of reorganisation and growth when people embark on centuries of drainage, cutting and compartmentalisation of what had been a single massif, thereby introducing new levels of complexity. The progress of the Humberhead Levels can be tracked through its multiple adaptive cycles by observation of change in palaeoecological and ecological data; this study focuses on changes in the beetle fauna of the Humberhead Levels from 10,000 years ago to the present day, and finds that evaluating beetle assemblage data from the present day alongside palaeoecological data can provide useful insights into the current position of compartments in their adaptive cycles, their likely trajectories, and what land managers can do to influence those trajectories.

The role of western Indian pleurotomariid gastropods in changing migration patterns of the family during the Cenozoic

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The Family Pleurotomariidae Swainson, 1840 is the only family under the superfamily Pleurotomariodea Swainson, 1840 to have survived the end-Cretaceous mass extinction. Although there are numerous taxonomic studies done on these gastropods, very few have studied their paleobiogeographic distributions. Herein, a detailed study on the paleobiogeographic distributions of the family is done to understand their global migration patterns during the Cenozoic. In this study, we deduced several migration pathways for different pleurotomariid genera during different Cenozoic time intervals. However, the biogeographic distribution is seen quite widespread with long gaps in record in-between two nearest localities which sometimes make it difficult to decipher the actual migration pathways for these gastropods. The study further reveals that the Mediterranean (Tethys) Region remained the nucleus of the pleurotomariid distribution during the Paleogene and the early Neogene with additional presence recorded in the Western Pacific Region (e.g., in Japan, Philippines and Taiwan), Australia-New Zealand in the east and North American Region in the west. The paleogeographic position of the Indian subcontinent, especially the western India, is very important to understand the biogeographic migration pathways of marine fauna between the Mediterranean and the Western Pacific regions as it serves as the junction point between the two regions during the Paleogene and early Neogene. Although there are numerous reports of the pleurotomariids from the Mesozoic, only a few handful pleurotomariid species under two genera, *Perotrochus* Fischer, 1885 and *Entemnotrochus,* Fischer, 1885 are reported from the Early Eocene–Early Miocene marine deposits of the western India. The study reveals that these pleurotomariids from the western India are the missing links to the long questionable migration pathways between the Mediterranean and the Western Pacific regions during Paleogene and early Neogene.

Considering how scale, biases in taxon sample, and evolutionary hotspots influence patterns of size evolution in fishes globally

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In the process of designing research in evolutionary biology, paleontology and macroecology, one is faced with decisions regarding which scale to study (including which specific clades and/or regions to choose), which taxa to sample, and what phylogeny to use in the analyses (e.g. molecular trees vs. supertrees). While testing for repeatable patterns in size evolution between fundamental aquatic habitats in nearly all fish species globally, I considered questions such as: 1. how should I select and display results from multiple scales; 2: how might underappreciated biases in the taxon sample influence the macroevolutionary/macroecological conclusions drawn; and 3. whether "hotspots" for the phenomenon of interest provide representative results relative to "non-hotspots". With regard to each of these points, I found that: 1. simple visualization could clearly illustrate how my size phenomenon of interest was maintained across multiple scales; 2. the specific taxa included within molecular phylogenies of fishes (i.e. those most often chosen for studies) are size biased (i.e. larger) relative to a more complete sample of taxa (which could be included within analyses using supertrees), reinforcing that size biases, and many other forms of bias (e.g. towards specific anatomical/ecological traits or regions) are likely commonplace, and where possible, efforts to document and correct for these biases (potentially using supertrees or 'bias aware subsampling' of the available data) could be of great benefit; and 3. that "hotspots" for the phenomenon of interest, which represent most obvious candidates for study by researchers for the phenomenon of interest, may more commonly show unusual dynamics relative to "non-hotspots".

Session 2: Community ecology and Biotic interactions

Shifts in ecological resources recorded in a 1-Ma-long drill core from the southern Kenya Rift explain Pleistocene mammalian faunal turnover and novel hominin behaviors

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Climate change is widely assumed to be the major explanation for faunal turnover and hominin evolution. Yet, how climate change affects evolutionary processes is not comprehensively understood while ecological drivers of evolutionary change are rarely investigated for the Quaternary. A massive turnover in mammal species is recorded in the southern Kenya Rift between 500 and 320 ka, during which a water-dependent fauna dominated by large grazers was replaced by a community of species with smaller body masses, less water dependence and broader feeding strategies. Large grazing megaherbivores with body masses over 900 kg were permanently lost from the region, while extant mammal species with less than 23 kg body mass became more prominent. Contemporaneous with this taxonomic and adaptive turnover was the replacement of the Acheulean by Middle Stone Age technology as recorded in the Olorgesailie basin. To investigate the environmental context of these significant changes we recovered a 139 m long drill core from the Koora basin south of Olorgesailie, which covers the past 1 Ma. By studying past freshwater availability, woody cover, grassland composition and hydroclimate using ecological indicators such as stable isotopes and diatom and phytolith indices, we document major ecological disruptions that affected the region during the critical interval between 500 and 300 ka. Our data reveal a stable resource base in terms of vegetation and freshwater availability prior to ~400 ka was supplanted by a long period of fluctuating and less predictable resource landscapes. These shifts are attributed to a combination of and interactions between ecological, geological and climatic factors. This talk will focus on the ecological cascades caused by these landscape changes and their relevance for initiating the faunal turnover and novel hominin behaviors.

Worms on film: The colonization of anoxic, matground-dominated sedimentary environments during the Early Cambrian

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Burrowing organisms play a key role in controlling the physio-chemical conditions within marine sediments. In modern marine environments these organisms mix oxygen into, and redistribute material, within the sediments. In the Proterozoic, seafloor sediments were largely oxygen-deficient, with an abundance of biofilms and microbial mats. However, the late Proterozoic–early Cambrian fossil record shows a rapid increase of infaunal trace fossil diversity, reflecting the evolution of burrowing metazoans, and indicating that the earliest bioturbators were tolerant of hypoxic conditions. Our investigation of early Phanerozoic metazoan-microbial interactions has focused on the Cambro-Ordovician successions of Bell Island, Newfoundland, where the destruction of Proterozoic-like microbial matgrounds can be linked to the presence of dense assemblages of simple, near-surface, trace fossils. Matground break-up within these successions was followed by colonization by deeper-tier trace makers. These field observations indicate that the colonization of microbially dominated, early Phanerozoic marine sediments was initiated by small, probably opportunistic animals which were capable of creating oxygenated near burrow sedimentary microenvironments. This would have engineered settings amenable to larger, more oxygen-dependent metazoans. We have also investigated the burrow morphologies and activity of modern burrowing organisms in oxygen-deficient laboratory sediments, mimicking the conditions present in Precambrian sediments. This allowed us to assess which burrowing behaviors different vermiform animals employ in Proterozoic-like sedimentary environments. Initial results indicate that opportunistic deposit-feeding animals, such as oligochaetes, are able to produce more extensive and deeper burrows in anoxic sediments than other infauna. The results from both the geological investigation into the successions of Bell Island and the lab-based experiments imply that the colonization of early Cambrian infaunal marine ecosystems may have been initiated by near-surface and likely opportunistic meiofaunal to small macrofaunal trace makers.

The changing effect of biotic interactions on communities under human disturbance

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The effect of biotic interactions on the spatial distributions and coexistence of species is of broad interest in both ecology and paleoecology, but differences in the form, abundance, and collection of interaction data make it difficult to draw parallels across disciplines. New models coupled with quantitative methods such as co-occurrence analysis are changing the way we study interactions on a broad spatial scale. These methods have been applied in paleoecology where direct evidence of interactions is scarce, but they are also applicable to ecological systems, where direct monitoring of interactions is nonetheless beset by logistical hurdles and sampling inconsistencies. As an example, we use a hierarchical Bayesian model to assess modern Neotropical bird and bat assemblages, asking whether spatial patterns of co-occurrence among species pairs that compete for food resources differ between intact and anthropogenically altered habitats. The model uses only occurrence and functional data that could be collected for many fossil assemblages. We find that on average, competing species pairs of both taxa are more spatially segregated in altered habitats than they are in intact habitats. The shift is not driven by compositional differences but by assemblage-level changes in biotic interactions. Our results suggest that altered habitats fail to support diverse competitive interactions by fostering competitive exclusion, reversing the pattern of coexistence observed in the wild. This and previous investigations using fossil data support the conclusion that interactions have profound effects on community composition, and that subtle shifts in interaction dynamics when assemblages are subjected to disturbance may therefore have far-reaching consequences at a variety of spatiotemporal scales.

Climate and ecosystem productivity control the functional role of omnivores in food webs

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Omnivory, the feeding of organisms on multiple trophic levels, is a pervasive phenomenon that controls nutrient cycling in food webs and enhances food web stability. However, it is unresolved how changing climate and primary productivity affect the trophic position and functional role of omnivores in food webs. Here we combine two lines of evidence based on macroecological and palaeontological data to show that the trophic position of omnivores is jointly controlled by temperature and primary productivity. A macroecological analysis shows that, across their geographic ranges, extant bears—the largest terrestrial omnivores—are carnivores in cold and unproductive and herbivores in warm and productive environments. In line with this, stable isotope analyses reveal that the European brown bear was a carnivore during the Last Glacial Period but became an herbivore during the Holocene. The macroecological and palaeoecological approaches yield a coherent pattern, suggesting that the trophic position of omnivores as observed today across large spatial scales is a consequence of long-term trophic adaptation to regional climate and primary productivity. Our results indicate that climate and primary productivity control the trophic niche and functional role of omnivores in ecosystems.

Phanerozoic prevalence of parasitism and marine metazoan diversity: Dilution versus amplification

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Growing evidence suggests that biodiversity mediates parasite prevalence. The dilution hypothesis suggests a negative correlation between biodiversity and disease prevalence, while other studies suggest a positive correlation and therefore amplification of disease prevalence with host biodiversity on larger scales. We compiled the first global database on prevalence and occurrences marine parasitism throughout the Phanerozoic and assess the relationship with biodiversity to test the amplification and dilution hypotheses. Median prevalence values by Era are 5% for the Paleozoic, 4% for the Mesozoic, and significantly increasing to 21% for the Cenozoic. We calculated Period-level shareholder quorum sub-sampled (SQS) estimates of mean diversity, origination rates, and extinction rates for the 10 most abundant host classes in the Paleobiology Database to compare to both occurrences of parasitism and parasite prevalence values. Generalized linear models (GLM) of parasite occurrences and SQS diversity measures support both the amplification (all taxa pooled, brachiopods, crinoids and blastoids, and bivalves) and dilution hypotheses (cnidarians, and echinoids). GLMs of prevalence and SQS diversity measures support the amplification hypothesis (all taxa pooled and bivalves). Though likely scale-dependent, parasitism has escalated through the Phanerozoic and clear patterns are emerging that offer support for both amplification and dilution of disease with biodiversity in the history of life.

The influence of stoloniferous reproduction on intra-specific competition in Ediacaran macrofossil assemblages

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Reproductive traits are key to an organism's capacity to adapt and evolve, but little is known about the influence of reproductive modes on selection pressures within the first animal communities, those found within the Ediacaran time period ~580–560 Ma. Previous analyses of Ediacaran communities from Newfoundland (Canada) and Charnwood Forest (UK) found that inter-specific resource competition was rare, and weak where present. Independent spatial analyses predicted stoloniferous reproduction within some Ediacaran populations, which has been corroborated by fossil specimens suggesting that filamentous stolons facilitate persistent connectivity even between large specimens. These latter results offer a possible explanation for the observed low resource competition, whereby physical connection of proportions of Ediacaran populations via stolons enabled resource sharing, thus reducing intra-specific competition. Stoloniferous reproduction leaves distinct spatial signatures, in the form of isotropic clusters (uniform directionality) and constrained dispersal clusters. The presence and strength of intra-specific competition, dispersal cluster size and anisotropy were quantified using spatial point process analyses (SPPA) from 20 taxa populations across 9 Avalonian communities, and compared with 6 deep sea sponge and coral communities. General linear models found that the strength of intra-specific competition was significantly correlated with anisotropy and cluster size in Avalonian communities, while the density of modern fauna was the strongest predictive variable for modern deep-water benthic populations. SPPA models of Avalonian intra-specific competition showed that when individuals were modelled as sharing resources (through their stoloniferous connections), this reduced intra-specific competition and increased the spatial scales of such intra-specific competition. This study demonstrates how reproductive mode has a significant impact on intra-specific competition, reducing the presence and strength of such competition. The rarity and weakness of intra-specific competition suggests that these first animal communities may have had reduced selection pressures, slowing evolutionary rates in these early animal communities.

An evidence of carrying capacity in the biodiversity dynamics of Coccolithophorids

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One of the central goals of palaeobiology is the identification of the mechanisms leading to the emergence of biodiversity dynamics. However, too little is known about the relative importance of biotic and abiotic environmental controls on biodiversity dynamics at large temporal scale. Comparing the relative importance of biotic and abiotic components between taxa is a major challenge for the identification of general regulatory processes of the biosphere. To address this question, we focused our analyses on Coccolithophorids using the Neptune DataBase. The use of fossil occurrence databases allows us to build accurate time series computed using recent subsampling and rate estimator methods. Our analyses rather aim to highlight large-scale patterns in a multifactorial approach by analyzing causal relationships between seven time series representing both biotic and abiotic factors: standing diversity, extinction rate, origination rate, temperature, $\delta^{13}C$ (surrogate of productivity), $^{87}Sr/^{86}Sr$, and $\delta^{34}S$ (surrogates of nutrient input). We tested causal linkages from each potential driving factor on diversity and rates using Convergent Cross-Maping with a sliding window to detect global and local effects. We were able to find that the diversity dynamics of coccolithophorids is driven mainly by biotic factors more than abiotic ones. More specifically, there is a strong evidence of diversity dependence of both the extinction and the origination rates. Abiotic factors only act during major crises episodes. Our results are consistent with the existence of carrying capacity modulated by abiotic factors.

A common language and tools for multidimensional analyses in ecology and palaeontology?

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Multidimensional analyses of traits are now common in ecology and evolution and are based on trait spaces in which each dimension summarizes the observed trait combinations (a morphospace or an ecospace). Observations of interest will typically occupy a subset of this space, and researchers will calculate one or more measures to quantify how organisms inhabit that space. In macroevolution and ecology these measures are called disparity or dissimilarity metrics (or space occupancy measures). Researchers use these measures to investigate how space occupancy changes through time, in relation to other groups of organisms, or in response to global environmental changes. However, the mathematical and biological meaning of most space occupancy measures is vague with the majority of widely-used measures lacking formal description. Furthermore, although the objectives between ecology and evolution are globally the same, there is often little to no overlap in the literature between fields resulting in precious knowledge and time being lost. Working with ecologists and evolutionary biologists we propose a broad classification of space occupancy measures into three categories that capture changes in size, density, or position. We also propose tools and guidelines helping workers to decide which measurement is best suited to answer which biological question. By providing these guidelines and a common vocabulary for space occupancy analysis, we hope to help bridging the gap in multidimensional research between ecology and evolution.

Time-averaging of ecological signals in the vertebrate skeletal record of a modern African ecosystem

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Paleontological data used for tracking vertebrate biodiversity and paleoecology through time usually can only be resolved to temporal bins of 10^3-10^7 yrs, greatly exceeding neo-ecological time scales of 10^{-1}-10^2 yrs. These differences in temporal scale interact with spatial scale and affect comparisons of modern and fossil biodiversity data (e.g., taxonomic richness), potentially recording different ecological processes (e.g., local versus regional controls on diversity). Data from modern death assemblages can help bridge such gaps and build understanding of temporal scaling relationships that can be applied to the fossil record. A long-term study of modern vertebrate remains in Amboseli National Park, Kenya shows how data from 40+ years of attritional deaths in a tropical setting samples living biodiversity. For taxa >15kg, time-averaged data from multiple censuses show high fidelity between the live and bone data sets in species abundances and ecological guild (diet) representation, including for partially buried bones. Drought-induced mass mortality of over 11,000 individuals (primarily grazers) in 2009 introduced a pulse of relatively complete bones into the time-averaged sample but had minimal impact on relative abundances of the 15 common herbivores. Modeling of species-time-area relationships (STAR) using the Amboseli bone data found that species richness scales positively with both time and area, but with a negative interaction between the two. It is hypothesized that increasing area and time are alternative ways of uncovering the species pool, such that increased time-averaging results in a more spatially averaged ecological signal. The STAR model provides a framework for extrapolating and comparing richness between small-scale modern and larger-scale fossil communities. Modeling further suggests that modern and fossil biodiversity data stress different aspects of community assembly processes, with modern samples weighted towards recording local-scale processes (e.g., species habitat preferences, interspecific interactions), while paleontological samples are primarily shaped by regional-scale processes (e.g., dispersal, speciation, extinction).

Environmental change and body size evolution in Neogene large mammals

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Body size is an overarching trait of taxa, related to virtually all aspects of their life history and their relationships with the environment. Therefore, body size variation reflects key processes of evolution and ecology across a wide range of organisms, and studying the spatial and temporal variation of body size among taxa can help illuminate how communities, regional assemblages, and the global biota have been assembled through ecological and evolutionary mechanisms. Here, we analyse the Neogene fossil record to identify drivers of body size evolution in terrestrial mammals, comparing the relative importance of environmental factors whose change coincided during the Neogene. We first develop a new method for estimating body size of Proboscidea from incomplete skeletons. Probosideans show consistent trends of increasing sizes through time across Eurasia and Africa. These trends are similar to those of other mammalian orders from previous studies, and tracked global warming and cooling events, which suggests selection of larger sizes due to harshening terrestrial environments. We then use a combined dataset of five mammalian orders to relate body size evolution to mammalian ecology, specifically their dietary preference, which directly reflects how the animals interact with their environment. We found that the body size patterns differ among dietary groups and between Europe and North America, suggesting a bigger role of habitat change than the change of climatic condition *per se* in driving body size evolution. Specifically, large herbivores increased in body size through time in North America, but maintained earlier sizes in Europe. This continental difference reflects the more stable Neogene biome distribution in Europe, and highlights the importance of ecogeographic approaches for understanding body size evolution.

Contribution of calcium isotope geochemistry to the study of diet in present and fossil elasmobranchs, case of Megalodon.

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Previously based on the analysis of stomach contents, the study of shark diet and trophic position has gained momentum with the development of isotope geochemistry tools in recent years. These tools open new perspectives for the study of present-day species but also fossil species whose behavior remains poorly known from an ecological point of view. Recent analyses have shown a correlation between the calcium isotopic composition (δ^{44}Ca) of tooth enamel and the trophic position of the studied taxa. Here, we present a study based on changes in the calcium isotope composition of tooth enamel from three living shark species: the bluntnose sixgill shark (*Hexanchus griseus*), the mako shark (*Isurus oxyrinchus*) and the great white shark (*Carcharodon carcharias*) during various growth stages. The results obtained in these sharks, which can reach several meters in length, show isotopic variability reflecting the change in trophic level correlated with ontogeny and/or spatial distribution of populations of the same species as well, but also highlight changes in the exploitation of food resources and scavenging phases in certain taxa. This characterization of calcium isotopic variability within several present-day species with different diets open the way to a better understanding of the ecology of extinct species like the famous Meg, *O. (megaselachus) megalodon*. A preliminary analysis of its ancient trophic level through time revealed a more complex signal than expected for this giant predator of Cenozoic seas.

3D model of *Otodus megalodon* body reveal movement and feeding ecology

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Given its low preservation potential, the entire body of the extinct giant shark *Otodus megalodon* remains an enigma. We use an exceptionally-preserved vertebral column to create a 3D model of this individual's body and estimate length (15.93 m), mass (61,500 kg), swimming speed (1.39 m/s), stomach volume (9,600 L), gape size (1.81 m), energy requirement (98,100 kcal/day) and encounter rate of putative prey. Comparisons against contemporaneous taxa indicate that while an individual of this size would have been slower than some smaller sharks, it would have also been able to swim long distances. Although small prey would have been found daily and provided calories beyond its daily requirements, prey the size of modern apex predators could have been entirely eaten and found frequently enough to provide excess energy to sustain prolonged migrations without further feeding. Thus, a preference for large prey could have been a strategy used by adult *O. megalodon* individuals to both avoid competition with more agile sharks, and to fuel movement across oceans. The extinction of this cosmopolitan, highly mobile super-predator likely impacted global nutrient transfer and trophic food webs.

Multi-scale causal analysis of biotic and abiotic drivers of Cenozoic mammalian evolution

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The animal tree of life is a very specific structure, generated and pruned by distinct multi-scale processes over hundreds of millions of years. Evolution is driven by both stochastic events (e.g. tectonic or volcanic activity, abrupt climate transitions), quasi-periodic environmental forcing driven by variations of Earth's orbital parameters, and biotic interactions (competition, speciation, restructuring of trophic networks). Attempts to disentangle relative importance of biotic and abiotic forcing range from the Red Queen hypothesis emphasising the impact of competition, to models claiming that environmental changes and related mass extinctions are the most relevant. We will present our analysis of the drivers of Cenozoic land mammal evolution, based on high resolution time series data and methods of causal inference. Our preliminary results shed light on causal relations between physical environmental change, internal biotic interactions, and macroevolutionary dynamics, yielding a quantitative description of the "spectrum" of evolutionary responses at various temporal and phylogenetic scales.

Foraminiferal assemblage along the shallow transect on the Kveithola Trough (NW Barents Sea): an actuopaleontological approach

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The distribution of the benthic foraminiferal assemblage along the shallow transect on the Kveithola Trough (NW Barents Sea), characterized by peculiar geo-morphological and environmental conditions, is the object of this work. Quantitative data of the living (Cell Tracker Green labelled) and dead benthic foraminiferal communities in terms of density, biodiversity and vertical distribution is reported, together with the environmental features (e.g., currents, oxygenation, sediment grain size and organic carbon content). The results of our study highlight differences between living (CTG) and dead assemblages in terms of density, biodiversity, and taxonomic composition. The living (CTG) foraminiferal fauna is dominated by *Pullenia bulloides*, *Globobulimina auriculata*, *Nonionellina labradorica*, *Reophax fusiformis*, *Micrometula* sp. and *Cylindrogullmia*-like while in the dead assemblage the main species are *Cassidulina neoteretis*, *Cassidulina reniforme* and *Cibicidoides lobatulus*. The living fauna, representing a snapshot of recent environmental conditions, shows that this area is subject to seasonal variations related to circulation changes and organic matter burial in sediments, to which the biota adapts quickly. Conversely, the dead foraminiferal assemblage shows no significant traceable environmental changes in the Kveithola Trough area occurred during the last *ca.* 100 years. The bias between the living and dead assemblages could be mainly related to taphonomic process induced by the different oceanographic settings and environmental conditions: dissolution of calcareous tests, loss of fragile organic-cemented agglutinated tests and also, the rapid degradation after dead of organic test species. For these reasons, we suggest that it is important to understand the differences between living and dead benthic foraminiferal assemblages and the factors that contribute to their distribution to obtain an accurate interpretation in ecological and palaeoecological studies.

Ecological data analysis of Ediacaran fossiliferous surfaces in the Bonavista Peninsula of Newfoundland

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The Ediacaran macrobiota is an assortment of morphologically diverse soft-bodied fossils with a global distribution found in strata spanning 575–541 Mya. The fossiliferous surfaces in the Bonavista Peninsula of Newfoundland (Canada) bear some of the oldest deep-marine Ediacaran communities of the Avalon assemblage (ca. 575– 560 Ma). Although some of their taxonomic affinities remain uncertain, these Avalonian fossils pose a great opportunity to study the paleoecology of Late Neoproterozoic communities. The population structure of two surfaces in the Catalina Dome region was studied, which mainly consist of rangeomorph taxa, including quantitative morphometry and size-frequency distribution analysis. The number of size modes corresponding to population groups were determined according to Bayesian Information Criterion (BIC). Moreover, the preserved fossil orientation of several morphometrically distinct classes of numerous taxa was analyzed in relation to paleocurrent orientation to shed light on the paleoecology of the two fossil surfaces. Morphometric methods and population analysis are pivotal tools in modern paleontology to resolve taxonomic inconsistencies, study morphological disparity, and reveal community structure.

Recurrence plots reveal the 'sloshing bucket'-like ostracod paleocommunity dynamics in the mid-Silurian of Baltica

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The Silurian period (443.8 - 419.2 Myrs BP) is characterized by a hierarchy of high-magnitude extinction events which were first detected in the fossil record of nektonic graptolites and nektobenthic conodonts. These extinction and turnover events currently are tied to the high magnitude cooling events, and associated global sea level regressions. The effects of these events are essentially unknown for the shelly benthos – the major part of the known fossil record. Here we present the detailed high-resolution (~ 20 Ka) record of ostracod paleocommunity change in the vicinity of the Mulde event (mid- Homerian, early Silurian) from the south-eastern part of the Baltica (Lithuania). The paleoecological dynamics were studied using compositional recurrence plots, which are filtered distance matrices of ordered observables which present patterns of similarity (recurrence) and difference (non-recurrence) between pairs of ordered points. The analysis revealed that ostracode paleocommunities experienced a series of sudden transitions which are coherent with the 4th and 5th order hierarchically modulated sea level cycles, which are presumably related to the 400 Ka and 100-130 Ka Milankovitch eccentricity cycles. The paleocommunity compositions between these transitions were extremely similar, forming hierarchical checkerboard-like fractal pattern. Apparently the magnitude and significance of transitions was dependant on the interference of different order climatic cycles. The revealed pattern could be explained by the 'sloshing bucket' hypothesis proposed by Niles Eldredge, which states that the transitions in ecosystems are governed by the perturbations in the physical realm. The degree of irreversibility in these transitions is directly positively related to the magnitudes of external perturbations, which appears to be the case in the studied mid- Silurian ostracods.

Integrating community turnover from modern and fossil data

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Studies in ecology and paleoecology draw on similar theory and data. These inherent similarities provide a unique opportunity to evaluate hypotheses over long periods of time, extending from the present to millions of years in the past. To realize this potential, however, differences in assumptions and uncertainties between disciplines must be evaluated to ensure data are comparable and reliable. One of the most challenging differences between ecological and paleontological data is variation in temporal resolution. Whereas temporal uncertainty in ecological datasets is typically minimal, paleoecological datasets rely on age models with substantial uncertainty and their temporal resolution is influenced by taphonomic processes such as time averaging. Taphonomic processes also mix the environmental, spatial, and temporal variation in species composition among fossil assemblages, complicating comparisons between modern and fossil data. Here, we explore these challenges in the framework of understanding past and present biodiversity change using existing large ecological and paleontological data compilations. We present preliminary results on community turnover at different temporal scales and discuss how the fossil record can be used to constrain our understanding of current biodiversity change.

Projecting community trophic structures for the last 120,000 years

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The study of past patterns of community and ecosystem shifts is pivotal to anticipate critical changes in the future. However, the fossil record is too sparse to enable continuous reconstructions of community dynamics in deep time. Here we used a machine learning approach rooted in the principles of food web biogeography to hindcast the dynamics of community trophic structures in time slices of 1k and 2k years during the Pleistocene (0 to 120ka). Our hindcasts generate hypotheses of how trophic communities might have changed through time. They indicate that climate might have led to a significant redistribution of trophic structures in the last 26,000 years, particularly at higher latitudes. Comparison of hindcasts against observational evidence in the fossil record demonstrates that models can recover past trends of community stasis and transition, although there is still room for improvement by coupling climate dynamics with biotic interactions, chiefly those arising from human expansion. As such, it is an approach that is potentially useful to generate hypotheses about past community dynamics independently of the quality of the fossil record.

Next generation IBMs shed light on the paleoecological interactions of Late Cretaceous dinosaurs

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The end-Cretaceous mass extinction (66Ma) is one of the most important biotic events in the history of the Earth. A series of drastic environmental disturbances spread among ecosystems around the world, and this led to the reorganization of biotic communities and the extinction of species at the very end of the Cretaceous. Of pivotal importance is to understand the drivers of species composition, turnover, and evolution in these communities. By using Weaver, a Next-Generation Individual-Based Model platform and data from several up-to-date literature sources, we have created a virtual late Cretaceous ecosystem where dinosaur individuals are born, search for food, interact with each other (both intra- and interspecifically; e.g., in food webs); and grow and reproduce with genetically-based multidimensional trait variation. Populations are tracked through space and through both ecological and (micro)evolutionary time scales, by analyzing hundreds of thousands of output data points. To introduce this novel platform, we simulated interacting predator-prey populations of two Late Cretaceous dinosaurs from North America (the large theropod *Tyrannosaurus* and the herbivore hadrosaurids). Animals grew, reproduced and interacted according to the information available from the literature: ecosystem productivity, individual growth curves, predator-prey body mass ratios, mixoterm metabolic rates, ingestion rates, predator-prey body-size dependent speed ratios, assimilation efficiencies and home ranges. Our simulations allowed, among other things, to estimate how many individuals of each species and of what size-age classes can be present in ecosystems of different sizes or productivities, and what are the most relevant traits responding at micro-evolutionary time scales. We also document size-age class shifts in herbivore populations from *T. rex* predation pressure and whether alternative *T. rex* prey (including cannibalism and scavenging) could affect the persistence of both populations over ecological time. We conclude that Next-Generation IBMs open new and exciting collaboration possibilities among ecologists, paleontologists, and computer scientists.

Session 3: Functional ecology

Carbon and strontium isotope ratios shed new light on the paleobiology and collapse of *Theropithecus*, a primate experiment in graminivory

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The rise and spread of tropical grasslands was a signal event in the Cenozoic, causing many ungulates to evolve adaptations to a diet of graminoid (grass) tissues, or graminivory. In parallel, a lineage of monkeys (*Theropithecus*) is distinguished among primates for its large size and commitment to graminivory, a trait expressed by species throughout the Plio-Pleistocene fossil record and *T. gelada*, the sole surviving species today. An open question concerns the behavioral mechanics of how fossil species of *Theropithecus* handled graminoid tissues. They might have exhibited preference, selecting tissues within a given tuft, or they might have practiced indiscriminate bulk- feeding in a manner similar to some large grazing ungulates. To differentiate between these handling behaviors, we used time- and graminivore-calibrated carbon stable isotope values to show progressive reliance on high-throughput bulk-feeding graminivory. Variation in this behavior explained a significant amount of variation in body mass through time, and we describe these covarying traits, which peaked during the Pleistocene of Africa, as evolutionary traps. To support this characterization, we report evidence of temporal increases in strontium isotope variability among North African theropiths, a result suggesting greater lifetime travel and energetic costs in response to diminishing food resources, a probable factor in the extinction of *Theropithecus oswaldi*, the largest monkey that ever lived.

Do the small-ranged species of mammals diversify slower?

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The relationship between range size and diversification potential of species is a cornerstone of many macro-evolutionary theories, such as neutral theory of ecology or taxon cycles theory. It is typically assumed that the small-ranged species have lower rates of net diversification, due to slower speciation and faster extinction. This assumption is, at least seemingly, at odds with practical observations that recent small-ranged species are often less evolutionary distinct than large-ranged species. Moreover, the closely related small-ranged species often form spatially localized hotspots of neo-endemism, claimed to be the cradles of biodiversity. The research of range size evolution is complicated due to confounding associations between range size and other processes structuring the data. In case of paleontological studies, it is notably the correlation between range size and probability of fossilization. In the studies using recent data and molecular phylogenies, the major problem is that the range size evolves not only anagenetically (range expansion or contraction), but also cladogenetically (range size change between mother and daughter species during speciation). Here we use a model of range size evolution covering both these processes to explore relationship between range sizes and the rates of diversification in terrestrial placental mammals. We show that in general, small-ranged species indeed diversify slower, as theoretically expected. In closer look, this pattern is however reversed in some large mammalian taxa, such as Chiroptera (bats), Carnivora (carnivores) or Eulipotyphla (insectivores). Moreover, our results suggest that both range size evolution and diversification are strongly influenced by idiosyncratic geographical settings, that can locally invert the global pattern and create hotspots of small-ranged species with high future diversification potential. We conclude that, while the range size is an important factor influencing species diversification, its effect in real-world systems is strongly modulated by other factors, such as insularity, latitude or dispersal capacity of species.

Unravelling the diverse locomotor repertoire of early primates using ankle bone morphology

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A substantial reorganization of the primate body plan marks the transition between archaic primates and Euprimates or primates of modern aspect (adapiforms and omomyiforms). To explain the adaptive morphological innovations of crown primates, several ecological scenarios have been suggested, either agreeing to a locomotor behaviour that was either cheirogaleid-like (similar to that of mouse and dwarf lemurs), vertical clinger and leaper (as observed in tarsiers and bushbabies) or lorisid-like (visual predators like extant lorises and pottos). In this study, we assessed the shape of a tarsal bone, the navicular, by means of a 3D geometric morphometric approach, assembling an extensive dataset describing navicular shape and quantified locomotor behaviour of most extant genera of lemuriforms, lorisiforms, tarsiiforms and platyrrhines. Our results demonstrate that navicular shape strongly correlates with locomotor behaviour, thus allowing the use of this bone, usually set apart in favour of other elements of the tarsus such as the calcaneus and the astragalus, to infer the locomotor repertoire of extinct primates. In addition, we reconstructed the locomotor behaviour of several early representatives of the major euprimate lineages, demonstrating that they already showed a moderate diversity in their locomotor repertoire. Body size appears to have channelled such locomotor diversification, allowing some groups of early primates to depart from the ancestral euprimate condition. Overall, this study brings forward that Euprimates suffered a rapid ecological diversification early in their history, allowing them to exploit different arboreal niches.

The hidden legacy of megafaunal extinction: Loss of functional diversity and resilience over the Late Quaternary at Hall's Cave

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Functional traits mediate the interactions of species among themselves and with their environment, providing a link between diversity and ecosystem function. Critically, the loss of biodiversity can jeopardize the functionality of ecosystems. Much focus is on predicting the impacts of current and future species loss, however, modern ecosystems have undergone biodiversity decline throughout the Late Quaternary, starting with the Pleistocene megafaunal extinctions. Thus, the fossil record offers the opportunity to investigate the long-term legacy of biodiversity erosion, and how this cumulatively is affecting modern ecosystems. Here, we investigated changes in functional diversity and redundancy of a local mammal community at Hall's Cave, a site in central Texas with a continuous record from 21,000 years ago to the present. Additionally, we included several common introduced species to the modern community to test whether they restore some lost ecological function. We used eight functional traits (mass, diet, arboreality, cursoriality, soil disturbance, group size, activity period, migratory) that collectively describe a species' ecological role and influence on ecosystem processes to construct multidimensional functional space. We characterized the change in functional richness, range, and distribution of the Hall's Cave community as well as the degree of functional redundancy over time. We found that declines in functional diversity were greater than expected given the decrease in species richness, implying lost taxa contributed higher than average distinct ecological function. Functional distances between remaining species increased through time leading to lowered functional redundancy in younger communities. However, recently introduced taxa increased functional diversity to levels similar to the Holocene and partially restored functional space occupied by Late Pleistocene fauna. Our local-scale analysis demonstrates how prolonged biodiversity erosion not only leads to functionally depauperate communities, but critically lowers ecological resilience to future disturbance.

Late Quaternary biotic homogenization of North American mammalian faunas

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The global-scale ecological impacts of humans have accelerated over the last several hundred years. One conspicuous consequence of human-driven extinctions and introductions is biotic homogenization – the increasing similarity of species composition among ecological communities across space. Over time scales of years to decades, ecologists have documented patterns of biological homogenization for extant groups including birds, fishes, mammals, and plants, in terrestrial and aquatic settings. However, these short-term data do not provide a complete picture of biodiversity change nor 'human free' ecological scenarios against which recent changes can be measured. We quantify biotic homogenization of North American mammalian assemblages during the late Pleistocene through Holocene (~30,000 ybp to recent), a timespan that encompasses the arrival of humans (~16,000–14,000 ybp). From ~15,000 ybp to recent, assemblages became significantly more homogenous (>100% increase in Jaccard Similarity), a pattern that cannot be explained by changes in fossil record sampling. The change we observe is equivalent to what one would observe if the subtropical mammalian faunas of central Mexico became homogenized to the same extent as Arctic Alaskan faunas, which are currently more than twice as similar over comparable distances. Homogenization was most pronounced among mammals larger than 1 kg and occurred in two phases. The first phase followed the megafauna extinction at ~11,700 ybp. The second, more rapid phase began during early agricultural intensification (~2,000–1,000 ybp). We show that North American ecosystems have been homogenizing for millennia, potentially extending human impacts in North America back to ~15,000 years, which likely had consequences for community resilience and ecosystem functioning.

Linking deep- and shallow-time paleoecology: the need for ecologically relevant traits

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Our empirical understanding of palaeoecology is only as good as our records. Measuring the right variable, whilst considering both regional and local palaeoenvironment, is important to ensure records reflect sample palaeoecology. Using planktonic foraminifera from the Middle Eocene we show that analytical protocols can bias inferences of diversity when the geographical setting is dismissed. Furthermore, we demonstrate that inferring function of protists living ~40 million years ago is hindered by the measurement of readily available traits such as size and shape. Using effective diversity numbers (Hill numbers) we measured diversity at two size fractions (>63 μm and >180 μm) in planktonic foraminifera during the gradual cooling and transient warming of the middle Eocene in the Northwest Atlantic Ocean, ~700 km east southeast of Newfoundland. Using non-parametric generalized additive models, we show overall reduced diversity and greater sensitivity to transient abiotic forcing in the larger size fraction (>180 μm). Thus, the larger size fraction does not represent the diversity of the region and if used in isolation could overestimate the impact of the Middle Eocene Climatic Optimum (MECO). Despite substantial palaeoceanographic changes, that we find to be concentrated in the thermocline and subthermocline, the thermocline dwelling genus *Subbotina* dominates diversity at both size fractions. To understand this group's survival, we measure functional traits (geochemical and morphological) of *Subbotina* individuals at six time intervals across the middle Eocene. We find that the success of *Subbotina* is linked to trait plasticity and thus a wider ecological niche than previously thought for this group aiding survival through palaeoceanographic fluctuations. In addition, we find that geochemical traits, whist more expensive to extract, provide greater insights into planktonic foraminifera palaeoenvironment suggesting we should seek to leverage new technologies that provide the greater ecological insights rather than measuring traditional taxonomic traits loosely related to ecological function.

Investigating fallback dietary habits among hominins: perspectives from controlled feeding experiments on domestic pigs

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Robust craniodental morphologies among early hominins, especially in the genus *Paranthropus*, have traditionally been associated with dietary specialization on hard and brittle foods. However, studies focusing on dental dietary proxies, such as dental microwear textures (DMT) and enamel stable carbon isotopes, have challenged the hypothesis of durophagy for *Paranthropus*. Besides, the consumption of fallback foods, rather than preferred ones, has received considerable attention to track niche partitioning between early hominins and to explain the selection of such phenotypes. Therefore, it is necessary to establish an experimental baseline to track such subtle variations in dietary habits. This project aims to test whether craniodental proxies of controlled-fed pigs reflect the consumption of low to moderate proportions of resources that mimic potential fallback foods targeted by early hominins. We conducted several trials on juvenile domestic pigs. They were fed on various proportions of foods with different isotopic compositions and physical properties, including plant and animal matter. Focusing on different dietary proxies, this project has the potential to provide new insights on their capabilities to track subtle variations in dietary habits within early hominins, and on the influence of such ecological needs on the selection of craniodental phenotypes. We present here results obtained on three dietary proxies representing different timescales: mandibular morphology, dental topography and DMT. Pigs were fed daily with similar overall diet but supplemented with different types of seeds (barley seeds, corn kernels or in-shell hazelnuts). Results show that pigs exhibit significant variations in each considered proxy depending on the type of seed consumed. These findings are promising to track subtle dietary variations among early hominins, which have probably played a key role not only in niche partitioning but also in the selection of craniodental phenotypes.

Ecometric modelling of the relationship between turtle body size distributions and climate

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Large body size of fossil turtles has previously been considered an indicator of warm paleotemperatures, but the relationships between turtle body size and climate have not been quantified. To determine the precision with which climate can be estimated using on the turtle fossil record, we employed ecometric modelling to predict temperature and precipitation based on the distribution of turtle body sizes. Ecometrics, the analysis of functional relationships between traits and environmental parameters at the community level, can be used to develop new paleoenvironmental proxies or to predict trait changes with future climate change. We built maximum likelihood models and linear models for the relationship between temperature and precipitation metrics and modern turtle communities, using BIOCLIM variables, species size data, and the global geographic distributions of modern turtle species, their body sizes, and climate data drawn from the Global Biodiversity Information Facility, range maps from the Turtle Taxonomy Working Group, and Species Distribution Models (SDMs) projecting species ranges based on their climatic niches, which accounts for anthropogenic range extirpations. Incorporating SDMs into these ecometric models significantly improved maximum likelihood models' accuracy in contrast to models using raw occurrence data. Results show that turtle body size distributions are not strong predictors for individual climate variables, with prediction anomalies at modern test points spanning most of the range of temperature and precipitation variation between sites. Models trained at continental scales predict climate variables based on local communities on each continent better than models trained on the global dataset, indicating that there are disparate regional patterns in turtle community assembly with regards to body size. Application of these ecometric models to a variety of Neogene and Pleistocene turtle communities from East Africa produces estimates that, although imprecise, can be used alongside independent paleoclimate proxies to better understand links between faunal and environmental changes.

Capturing functional ecology from ichthyoliths: what isolated microfossil fish teeth and dermal scales can reveal about ancient vertebrate ecology

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Isolated microfossil fish teeth and shark dermal scales (denticles) preserved in sediments (ichthyoliths) provide one of the highest resolution records of vertebrate evolution in the paleontological record. However, these isolated microfossils are found independently of full-body fossils that can provide taxonomic or ecological context about the fish that produced them, making ichthyoliths a challenge to interpret in an ecological or taxonomic context. Despite this limitation, both teeth and scales play significant functional roles in the ecology and life history of fish and sharks. For example, teeth are used in prey capture and handling, and thus the size, shape, and placement of teeth in the fish's jaw are all impacted by the type of diet and lifestyle that the fish leads. Similarly, denticles form a dense coating along the body of most shark species, providing an interface between the shark and its environment, such as protection from physical abrasion, drag reduction while swimming. Here we present results from a series of ongoing morphological studies of bony fish teeth and shark dermal scales and discuss broad-scale morphological links between ichthyolith morphology and function. These characteristics can be used to reconstruct the paleoecology of an ichthyolith assemblage, providing a unique and robust way to reconstruct marine vertebrate community ecology, as well as provide a window into the evolution of ecological roles of these diverse and important groups of marine predators through geological time.

Understanding the 3D morphology of the Ediacaran rangeomorph *Fractofusus misrai* from Mistaken Point, Newfoundland

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The Ediacaran rangeomorph organism *Fractofusus misrai* is the most commonly occurring fossil at Newfoundland's Mistaken Point. It is also one of the best-preserved taxa found there, with highly detailed impressions of its lower surface recorded as a result of its having lived a reclining epifaunal lifestyle on the Ediacaran seafloor. There is considerable variety in outline among the specimens of *F. misrai* preserved on Mistaken Point's E Surface: while most have a symmetrical spindle-like shape, some possess curves or kinks; rare individuals demonstrate irregular 'tousling'. This variability represents a combination of factors, including changes in growth direction and/or specimen orientation as well as taphonomic influences. Study of these atypical specimens, which demonstrate features not seen in the more common spindle-shaped *F. misrai* fossils, has provided us with a better understanding of the three-dimensional morphology as well as the palaeobiology of this complex organism. *F. misrai* possessed two parallel rows of primary order rangeomorph units that emerged from a longitudinal central axis. Each of these primary units consisted of a series of self-similar secondary units; these smaller secondary unit branches often bifurcated, producing multiple secondary branch tips at the distal edge of the primary branches. Fine branching details and marginal morphology can vary between specimens, suggesting that these primary and secondary branches possessed some degree of mobility or flexibility. It is here inferred that the rangeomorph units were thin and emerged from the midline in contact with the seafloor, curling upwards away from the sediment surface along the distal edges of the organism.

Using paleontological trait data to evaluate temporal dynamics of ecosystem services

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Trait-based approaches have emerged as powerful tools for conservation scientists to evaluate the provisioning of ecosystem services (ES). Traits are not restricted to single taxa (i.e., they are taxon-free), enabling comparisons among communities composed of different taxa. Taxon-free approaches are well-suited for making comparisons across timescales, particularly as communities, and the ES imparted by the distribution of traits in them, shift under changing environmental conditions (e.g., climate change; habitat fragmentation). Trait-based approaches enable the inclusion of data from the past (e.g., geohistorical record), which can help provide an important but often absent temporal perspective in assessments of ES capacity. Particularly when used opportunistically with other sources of temporal data (e.g., aerial photographs, census records, traditional ecological knowledge), the paleotrait-based approach can be used in ES assessment to account for the effects of long-acting processes and past management actions, evaluate synergies and tradeoffs, and establish appropriate baselines. Leveraging studies of modern organisms, paleotraits can be directly or indirectly applied to evaluate ES capacity through time using the geohistorical record. Applied directly, a distribution of traits in a community can be quantified and related to a particular ES. Alternatively, an indirect approach allows for the inclusion of a much broader set of data and requires an additional inferential step: a trait is quantified and related to a particular ecosystem state, which is then used to estimate ES capacity. The resulting information can be incorporated into existing decision support tools for ES management. In this presentation, we develop a case for this paleotrait approach, illustrated with examples, with the goal of expanding the set of tools used in assessments of ES capacity.

Southern Ocean diatom size dynamics and the end-Eocene paleoproductivity

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The size structure of phytoplankton communities has a strong influence on food web dynamics and carbon cycling in the ocean. Within phytoplankton, diatoms are a major group contributing significantly to the biological carbon pump and the regulation of atmospheric carbon. Changes in ocean temperature, chemistry, and circulation can alter the size structure of diatom communities, which in turn can have cascading effects on food web structure and organic carbon export. The Eocene-Oligocene transition (EOT, ~33.9) marked the largest climate shift in the Cenozoic cooling. Examining changes in diatom size across the EOT offers the opportunity to illuminate the relationship and feedback between climate and diatom community size structure. However, data on size dynamics of deep-time diatom communities so far is mainly based on literature compilation rather than actual measurements of specimens. Here we present a new size dataset (over 5000 specimens) from the Atlantic Sector of the Southern Ocean that we compare with new geochemical proxies (e.g., $\delta18O$, $\delta15N$, biological-Barium accumulation rates). Initial analyses show a strong coupling between pelagic diatom size and paleoproductivity, suggesting a significant contribution of diatoms to export productivity, and thus to the biological carbon pump. This result therefore seems to corroborate the hypothesis of a significant role of diatoms in the end-Eocene climatic events. This signal furthers our understanding of the intricate dynamics between climate, paleoproductivity, and diatom ecology.

Nature, red in one and zero: simulating the evolution of predators

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Predatory species can be found in ecosystems all over the world and from throughout the Phanerozoic. Evidence for protistan predators stretches back even further. However, predation is more abundant in some times and places than in others and, while hypotheses about the processes that control food-chain length have been established for some time, these hypotheses can be difficult to test because of the timescales involved and because predictor variables are often not independent. Observational studies have thus been able to establish correlations between predation and environmental parameters, but not to clearly demonstrate any causal links. We have employed high-speed eco-evolutionary simulations to investigate the impact of environmental variables on the evolution and persistence of predators within ecosystems. Preliminary results confirm theoretical predictions that predation should be absent in ecosystems where either a) there has not been sufficient time to it evolve, or b) there is not sufficient productivity to support stable populations of predators. Further exploration of results from our simulations has the potential to shed light on how food-chain length is influenced by other variables, such as environmental disturbance, and could provide insights into the ecology of unusual ecosystems, such as the Ediacaran biota or modern deep marine settings.

Dental microwear texture analysis of deer from Combe Grenal (Dordogne, France): a new insight into the paleoenvironmental variations during the Middle Paleolithic

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Red deer (*Cervus elaphus*) and reindeer (*Rangifer tarandus*) constituted major components of the European Middle Paleolithic faunas, and hence a key resource for hominid populations. In paleoenvironmental reconstructions, red deer and reindeer occurrences are typically considered as a tree-cover indicator and an open landscape marker, respectively. However, insights into the ecology of extant deer uncover a wide variety of feeding behaviors and occupied habitats. Exploring the feeding behavior of extinct eurytopic cervids constitutes a key to better apprehend paleoenvironments and their variations through time. By reflecting what has eaten an animal during the last few days or weeks of its life, dental microwear textures of herbivores constitute a bridge between a population and its environment. Here we analyzed, via Dental Microwear Texture Analysis (DMTA-SSFA), the diet of 202 *R. tarandus* and 116 *C. elaphus* preyed by the Neanderthal populations that occupied Combe Grenal. This site is one of the most important Mousterian archaeo-sequences in southwestern France (spanning MIS 6 to 3), characterized by an abundance of faunal remains (>12,000 remains) and ample variation in the lithic industries. Results illustrate the diversity of the food categories the two taxa were able to consume around Combe Grenal. The fact that both deer are eurytopic allows us to consider their feeding behavior as a good indicator of paleoenvironmental variations through time. DMTA-SSFA provide a more complex picture of Combe Grenal local paleoenvironmental variations than previously thought. These variations are discussed and contrasted with changes already documented in the sequence in hunted prey and Neanderthal productions (lithic industries and pigment use). Identifying and understanding ecological adaptations in fossil populations in response to environmental and climatic changes is a relevant approach to better understand the current adaptations of species to the climatic changes they are currently facing.

Energetic equivalence, isotaphonomy, and productivity loss as a driver of megafaunal extinction in the African fossil Record

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Body mass estimates were generated using published dental metrics for over 5400 specimens of African fossil large mammals from the late Miocene to late Pleistocene. These were used to examine paleocommunity energetic scaling through the relationships of taxonomic diversity, specimen abundance, and the proportion of biomass occupied by each size category. Preliminary results indicate that paleocommunity size-abundance distributions follow the predictions of energetic equivalence (Damuth's Rule, loosely) in showing an even distribution of biomass across log-size categories between 100 and 10,000 kg. The consistency of this pattern implies, surprisingly, that size-abundance distributions in the fossil record could be iso-taphonomic at the broad scale, whether examined at the size of single assemblages or as aggregate communities by time bin. Additionally, in line with predictions of energetic equivalence, we show how decreasing the total biomass available in a community results in a disproportionate loss of larger taxa (even while maintaining energetic equivalence). This supports the idea that global decreases in productivity could have been a main driver of Pleistocene megafaunal extinction, while also explaining Pleistocene losses in diversity across mammals of all sizes.

Extinction risk in Plio-Pleistocene Mediterranean bivalves

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Following the Mid Pliocene Warm Period (~3.0 Ma ago), Mediterranean Sea biodiversity experienced a sharp decline, which has been linked to the onset of the Northern Hemisphere Glaciation. Among bivalves, around 50% of Pliocene species became extinct, while the remaining 50% still lives in the Mediterranean today. What factors drove extinction of one species and success of another? A species-level dataset of 1350 occurrences of three bivalve families (Pectinidae, Veneridae, Lucinidae) was assembled from literature data, with information, for each species, on: age (Zanclean-Calabrian; 5.22-0.77 Ma); geographic location (spanning the Mediterranean Sea and the North Atlantic); and paleoenvironment (brackish-water, shoreface, inner-outer shelf, slope-bathyal). We analyzed per-family changes in species richness through time, and using non parametric statistics, we tested whether abundance, habitat specialization, and geographic range, considered among the principal factors controlling extinction risk in ancient and modern seas, explained species survival or extinction. For all bivalve families, species loss in shoreface settings seems to predate changes at shelf depth, suggesting that shallower communities were the first to respond to climate perturbation. For all bivalve families, abundance and habitat specialization are good predictors of extinction, as extinct species were significantly rarer than extant species and occur in a lower number of environments. Surprisingly, there is no statistical difference between geographic range size of extant and extinct species, which would suggest that broad geographic range did not play a role in species survival. This is in contradiction with evidence that most Pliocene species that still lives in the Mediterranean are eurythermal, and today live both in the Mediterranean and in the North Atlantic. This is probably due to the poorly documented Plio-Pleistocene fossil record in the North Atlantic, limited to occurrences in Portugal, the Azores and Canary islands, United Kingdom and Belgium.

Integrating fossils and genomics to reconstruct the decline of the threatened Mountain Dragon, *Rankinia diemensis*

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Many Australian reptile species are increasingly threatened by human-induced climate change. Quaternary fossils of endangered taxa combined with neontological data provide a holistic perspective on how environmental change impacts extinction risk. However, the taxonomic assignment of many fossil Australian herpetofauna is problematic since osteological apomorphies for most lower taxonomic groups are missing and cryptic diversity is prevalent. Here, using geometric morphometrics, we taxonomically assign isolated maxillae of Australian agamids and use this dataset to identify fossils of a threatened agamid lizard, *Rankinia diemensis*. We combine this approach with population genomics and species distribution modelling, to identify links between extinction risk and Quaternary climate change in this species. *R. diemensis* is distributed in temperate southeastern Australia, including Tasmania, with Quaternary sea-level changes playing a major role in shaping this species distribution. We identify Late Pleistocene to Holocene fossil *R. diemensis* from South Australia, outside of the modern range of the species. These results are consistent with a larger area of hindcasted suitable habitat during the LGM, and subsequent range contractions as suggested by species distribution modelling. Our results show lower genomic diversity in remnant lowland populations, which experienced environmental change towards less suitable habitat since the LGM. In contrast, populations of the eastern Victorian Alps show high genomic diversity and deeper coalescent histories. This indicates a disruption of the western range, local extinctions of this species during the late Pleistocene to Holocene and a refugial role of the eastern Victorian Alps during warm and wet interglacial periods. Predictions of future habitat suitability indicate further climate related habitat contractions, with western Victoria as most vulnerable to human induced threats. Our study shows the tremendous potential of Quaternary fossils to inform conservation of reptiles and provides a methodological framework for future research.

How predictable are mass extinction events?

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Recent extinction rates show that we are in the midst of a human-induced biodiversity crisis that threatens to rival the mass extinction events of the geological past. Many modern extinction drivers are shared with past mass extinction events, e.g., rapid climate change, habitat loss, pollution, and invasive species. These apparent consistencies present a key question; can we predict extinction risk during past mass extinction events, and can ancient biotic crises be used as analogues for a modern biodiversity crisis? To investigate if mass extinctions are predictable, we applied a functional trait-based model of extinction risk using a machine learning algorithm (gradient boosting on decision trees) for the three most catastrophic and recent mass extinction events: the end-Permian, end-Triassic and end-Cretaceous. We used the trait-based models to predict extinction selectivity across each individual mass extinction event and then used the selectivity patterns obtained from each event in an attempt to predict extinction selectivity across the other mass extinctions. Our analyses show that despite some similarities in extinction selectivity patterns between ancient crises, that the selectivity of mass extinction events is not universally predictable. This lack of predictability is attributed to the evolution of marine ecosystems during the post-Permian radiation and Mesozoic Marine Revolution, which caused shifts in community structure, clade representation, functional diversity, functional evenness, and Earth system changes too. Furthermore, given the large shifts in marine ecosystem community structure over the Cenozoic our results suggest that past mass extinction events are unlikely to serve as robust analogues of extinction risk during a future mass extinction event.

Primary and secondary extinction across a Mesozoic hyperthermal extinction event

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In order to fully understand ecosystem collapse across mass extinction events, it is essential to consider extinction dynamics within a trophic community framework. As palaeobiologists, we often make the assumption that all taxa that went extinct at times of mass extinction did so in response to severe abiotic stress. However, ecological theory suggests that many victims of past extinction events did not become extinct as a direct effect of abiotic stress, but probably did so in response to cascading secondary effects brought about by the loss of prey resources and changing competition dynamics. Here, we present a case study of using trophic network models to assess the impact of extinction cascades in response to the early Toarcian extinction event. Food webs were reconstructed for pre- and post-extinction ecosystems from the Cleveland Basin of NE England. Secondary extinction cascades were simulated across the extinction event in order to assess ecosystem robustness to informed and random primary extinction events. Model outputs were then compared to empirical post-extinction food webs to determine the likely abiotic driver of ecosystem collapse. Results show benthic organisms with high metabolic demands were selected against which fits well with an anoxia primary kill mechanism.

Thermal extinction selectivity patterns during global warming events

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Anthropogenic global warming is expected to raise regional extinction risk following the stress responses of warm-water organisms, especially coral reefs, while cold-water organisms may also suffer from decreases in suitable habitat. Empirical data on widespread extinctions can only really be sourced from the fossil record, with interpretations complicated by sampling heterogeneity and timescale mismatches. Previous studies of regional extinction selectivity have used the paleolatitude of marine genus occurrences but trends under global warming events have been inconsistent, potentially because latitude is a complicated proxy for seawater temperature and other abiotic variables. Here we assess marine extinction selectivity of marine animals based directly on regional temperatures sourced from climate models. We assess whether thermal selectivity trends deviate under hyperthermal conditions and how patterns associate with environmental and sampling parameters. We find that sampling patterns have an important influence on observed extinction selectivity but cannot account for some of the trends observed at hyperthermal events, including raised extinction risk for cold-water genera. The modern distribution of organism thermal preferences makes these findings particularly important.

Modeling the immediate environmental consequences of the Chicxulub impact: Severe cooling and short peak ocean productivity

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66 million years ago the impact of a large asteroid near Chicxulub, Mexico, severely disrupted the Earth system and played a key-role in the end-Cretaceous mass extinction. However, understanding the immediate environmental consequences of the Chicxulub impact is difficult due to the limited temporal resolution of the geological record. Climate modeling provides an excellent tool to fill this gap and can help understand short-term ecological processes during paleontological events. Therefore, we investigate the combined effect of sulfate aerosols, carbon dioxide and dust from the Chicxulub impact on the oceans and the marine biosphere in the decades to centuries following the impact using a coupled ocean-atmosphere model including ocean biogeochemistry. We find strong surface cooling, a brief algal bloom triggered by nutrients originating from both the deep ocean and the iron-rich projectile, and moderate surface ocean acidification. Comparison of the modeling results with high-resolution proxy data for the centuries to millennia after the impact suggests a release of significant amounts of carbon from the terrestrial biosphere. We conclude that the Chicxulub impact caused a combination of abrupt and severe changes which triggered the end-Cretaceous mass extinction.

Short-term impact of diet on dental mesowear: New insights from dental topography and a controlled feeding experiment on domestic pigs

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Disentangling the complex interplay between environmental change and the diet of vertebrates requires dietary estimates working at multiple temporal scales. Mesowear i.e., the macroscopic effect of diet on dental wear, is a prominent estimate of pluri-annual dietary variation in extant and extinct mammals. Still, how subtle changes in diet might affect dental mesowear in the short term has yet to be thoroughly investigated. We looked at mesowear on the recently erupted upper and lower first molars, and the moderately worn fourth decidual premolars of 6-to-10 months-old domestic pigs (*Sus domesticus*). Trials were conducted on four groups of five individuals: the control group only fed on mixed cereal and soy flours, while the three other groups were supplemented with 30% barley grain, 20% corn kernels plus 20% corn flour, and 30 hazelnuts per day for 1 month before the end of the trial. We precisely describe mesowear using dental topography to measure tooth complexity, slope and curvature, as well as the curvature of low-slope areas i.e., the most worn areas. Comparison of the means between dietary groups was done using Dunn's post-hoc analysis of a one-way ANOVA on ranks. The effect of diet on mesowear was also assessed using linear models with wear as the explanatory variable. As expected, the complexity, slope and curvature of the tooth decreased as it wore out. However, both complexity and curvature were significantly lower in the premolars of hazelnut-fed pigs ($p < 0.05$). In addition, the curvature of worn areas increased in all groups but the barley-fed pigs, in which it remained stable ($p < 0.001$). These findings are promising not only for inferring the seasonal diet of extinct vertebrates, but also to study dietary variation in mammals from present-day ecosystems, some of which are difficult to observe.

Reproduction and Autoecology of an Ediacaran Rangeomorph

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The fossil record of the Ediacaran of Avalonia is dominated by the soft-bodied Rangeomorpha, an extinct poorly understood clade with disputed phylogenetic affinities. The Rangeomorpha present a unique Bauplan, characterized by an almost fractal branching, that may have evolved to harbour symbionts. The rangeomorphs of Avalonia are preserved impressions on surfaces underlying volcanic ashes in deep marine settings. New descriptions of some of the Rangeomorpha interpret their mode of life as being epifaunal or quasi-infaunal rather than erect in the water column. This new interpretation requires reconsideration of ecological models to account for adaptative traits that the rangeomorph could have evolved in response to sediment accumulation. Asexual budding has been documented in modern day cnidarians as a response to environmental distress (such as starvation or smothering) and as a secondary reproductive strategy. Exceptionally preserved *Culmofrons plumosa* Laflamme 2012, from the Catalina Dome, Newfoundland, reveal possible reproductive structures. The inferred reproductive structures are composed of bundles of three branches on the lower surface of the organism—at the distal portion of certain secondary order branches—but which do not follow the otherwise regular growth pattern. The bundles of branches may comprise the beginning of a new individual produced by asexual budding, which is the first described occurrence of an asexual reproductive strategy in the Rangeomorpha. Asexual reproductive strategies involving budding typically require a reduced genetic makeup, as they do not involve specialized reproductive organs, and allow for an efficient dispersal of already developed juveniles, which could potentially undergo a planktonic stage before settling. If correctly interpreted as reproductive modules, the structures here described may offer a viable life strategy for immotile organisms that were likely subject to periodic burials. This would represent a distinct phase on the lifecycle of the Rangeomorpha and has significant bearing on ecological considerations of the clade.

Biogeochemistry at the crossroads between environment and ecology: use of oxygen isotopes to track environment preference variation in fossil crocodilians

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The Shungura Formation of the Lower Omo Valley (southwestern Ethiopia, dated between 3.6 Ma and ~1.0 Ma) recorded major environmental change occurred during the Plio-Pleistocene (aridification, landscape opening, intensification of seasonality, change in hydrography). In these conditions, the continuous persistence of several crocodilian species, throughout the time interval and different environments, is explained either by their adaptation to habitats that remain available despite global change, or by their adjustment to new habitats over time. As for extant crocodilians, we suspect that past species were able to occupy a wide range of freshwater habitats, so that the diversity of habitats they occupied documents at least a significant part of available aquatic environments. We used stable isotope geochemistry (oxygen) recorded in crocodilian teeth to describe the environment(s) occupied by the fossilized specimens from different levels across the Shungura series. Indeed, the isotopic oxygen composition of each tooth is known to be mainly dependent on that of the water ingested during dental formation (nearly during a year). The ingested water corresponds to the water of the environment, which is itself closely related to the isotopic composition of local and upstream rainwaters, as well as evaporation conditions. The distribution and range of part of the signal indicate the diversity, nature, and conditions of the occupied aquatic environments. The use of this approach on the fossil crocodilians from various horizons of the Shungura Formation shows they occupied different environments, and alternately wide or narrow range of habitats over time. Comparison with independent information on past environmental contexts of different levels strengthen these conclusions.

A Mammoth buffet: resolving extinct herbivores community structure through high-resolution coprolite analysis

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During the Pleistocene, the Arctic harboured a diverse community of cold-adapted herbivores that disappeared over the course of the last 20,000 years. The mechanism that allowed the coexistence of a high biomass of different herbivore species (including *Mammuthus primigenius*, *Coelodonta antiquitatis*, *Bison priscus*, *Equus sp.*, *Rangifer tarandus*) in an environment supposedly low in plant diversity and productivity is still a subject of debate. According to niche theory, coexistence between herbivore species is promoted by dietary specialization, with different species feeding preferentially on specific food items. However, due to low taxonomic resolution, isotopic studies based on fossil bones give us conflicting results on the degree of overlap of Arctic herbivore diets. To better understand how extinct herbivores from the same region partitioned their diet, I will analyze a unique set of 60 coprolites (sub-fossil feces) from Yakutia, Siberia, dating back to the Late Pleistocene. I will use a multiproxy approach combining both traditional (macrofossils, pollen, starch grains) and cutting-edge (ancient DNA) paleoecological tools to achieve a high-resolution environmental and dietary reconstruction. The unprecedented number of samples from the same region coupled with the use of complementary dietary proxies will allow me to reconstruct the diet of extinct Arctic herbivores with greater accuracy than any other previous work on the subject, shedding light on the mechanisms that allowed their coexistence and potentially informing the reasons behind their final demise.

Ice Age giants at the end of the world: chronology and extinction of Gomphotheres in Chile, South America.

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Gomphotheres (Order Proboscidea) are among the largest members of the late Pleistocene mammal assemblage that became extinct in South America at the end of the last Ice Age. The Gomphothere fossil record in South America shows a broad distribution with the genus Cuvieronius restricted to the Andean highlands and Notiomastodon present in the lowlands of almost every country in the continent. Given their size and broad distribution, they possibly had a great impact in the ecosystems they inhabited. Here we present and analyze the radiocarbon chronology of Gomphotheres from Chile, giving some insights into their late Pleistocene distribution, their relation to the presence of humans and their extinction. The dataset is composed by 26 radiocarbon dates, many of which are new and unpublished. The radiocarbon record covers a geographic band between 31°- 42° S showing a late Pleistocene distribution encompassing a long latitudinal gradient and different environments. According to this dataset, Gomphotheres where present in Chile up to sometime between 11,500-10,800 cal yr BP, with last appearance dates present in the southern portion of the distribution. The archaeological record for the presence of humans overlaps for about 4,000 years with the temporal range indicated by the chronology for Gomphotheres. Using summed probability distribution (SPD) analyses of calibrated 14C dates as a proxy of ancient demography, we can observe how the major decline, before extinction, in the faunas (including the record for Gomphotheres) coincides with a temporally discrete increase in humans. These demographic events, as well as the extinction of faunas in the area, happened at a time of important changes in vegetation and climate experienced in the western Pacific coast of South America during the last glacial termination.

Shifts in food web architecture and niche occupancy across the end-Cretaceous mass extinction

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The end-Cretaceous mass extinction was a global cataclysm that largely devastated Earth ecosystems, leading non-avian dinosaurs, along with many other groups, to vanish after a 10-km-wide bolide impacted in the Yucatan Peninsula 66 million years ago. The effect of food web restructuring and expansion of new ecological spaces on terminal Cretaceous ecosystems and the subsequent biotic radiation during the earliest Palaeocene have been fiercely debated for several decades. We compiled a new dataset for multiple vertebrate clades from Campanian (83.6-72.1 Ma), Maastrichtian (72.1-66.0 Ma) and Danian (66.0-61.6 Ma) terrestrial and freshwater environments across the Western Interior of North America. Following the utilisation of standardisation techniques to mediate for taphonomical biases and the sampling heterogeneity of the fossil record, we applied partial correlation networks and niche decomposition models to explicitly reconstruct the disruptions in trophic relationships and long-term trajectories in ecospace occupancy that shaped the evolution of North American ecosystems through the latest Cretaceous and early Cenozoic. In tandem, these flexible modelling approaches support the dramatic removal of the large-bodied preeminent herbivore guild during the Maastrichtian, leading to a potential destabilisation of the trophic webs of which they were part. We also provide multiple lines of evidence for a measurable ecospace occupancy change in small tetrapods, especially in the ground-dwelling mammal guild. Such relaxation of ecological limits likely helped these clades to exploit novel niche opportunities and expand their physical space towards less marginal habitats, suggesting that competitive release was probably a strong driving mechanism of the explosive evolution and diversification of surviving lineages in post-extinction ecosystems, particularly mammals. Overall, we inferred disrupting events for interaction networks and probable trajectories of among-clade niche evolution before and after the extinction pulse that caused the abrupt demise of the "age of dinosaurs" and the onset of the "age of mammals".

Climatic range of modern fossilizable phytoplankton

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Phytoplankton as a whole is responsible for half of global primary productivity. Marine diatoms and calcareous nannoplankton in particular have a strong control on the marine carbon cycle. Both also have an extensive fossil record with an almost complete taxonomical coverage. Given the difficulty to monitor marine single-celled eukaryotic populations and thus estimates their extinction risk in the current context of anthropogenic climate change, micropaleontology offers us a rare occasion to understand and estimate their capacity to mitigate climatic fluctuations. In this study, we compiled the age range of several hundred species of living diatoms and calcareous nannofossils, and translated them, using the benthic oxygen isotope stack of Westerhold et al. 2020, into global mean temperature ranges that each species lived through. It reveals a tipping point around +3.5°C above preindustrial global mean temperature after which 60 to 80% of the compiled species of both diatoms and calcareous nannofossils will enter a climatic *terra incognita*, i. e. a temperature range that they never encountered before and to which they are likely not adapted for. Comparing these data with current estimates of global mean temperatures projected for 2300 under various RCP scenarii (IPCC Representative Concentration Pathways) places that tipping point between RCP4.5 and RCP6.0 (both scenarii imply a reduction of anthropogenic carbon release before 2100). Preliminary, more nuanced regional patterns of sea surface temperature species ranges will also be discussed, with a special emphasis on polar species.

Bivalve assemblages as palaeoecological markers at the onset of the OAE2 event

(Bohemian Cretaceous Basin, Czech Republic)

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The locality of Pecínov is located approximately 30 km west of Prague, on the south-western margin of the Bohemian Cretaceous Basin. The well-exposed succession of Cenomanian through the Lower Turonian strata contains one of the most complex record of the Ocean Anoxic Event 2 (OAE2) in Central Europe. The rich molluscan fauna from the locality has been thoroughly studied, however the bivalve association and its potential to paleoenvironmental reconstructions has received very little attention until now. This research provides an updated taxonomic investigation according to the modern systematics of the bivalves. The assemblage from the locality (with the exception of inoceramids, which have already been described in the past) is divided into guilds based on their ecospace utilization (e.g. tiering, life habit, and feeding category). Additionally, the statistical evaluation, population analysis and subsequent paleoecology interpretations (e.g. bathymetry, salinity, temperature, oxic and energy condition) are newly introduced. In total, over 350 specimens have been studied and assigned to 20 genera within 15 families and 9 orders. The bivalve association is strongly dominated by infaunal suspension feeders, followed by semi-infaunal suspension feeders. Epifaunal suspension feeders as well as infaunal deposit feeders are also present but comparatively rare. This indicates nutrient rich environment with water energy level sufficiently high to keep organic matter in suspension with a very small amount of organic matter in the sediment. The near absence of free-living epifaunal bivalves was probably caused by the very fine, muddy substrate. The population analysis as well as taphonomy of the shells suggest an environment significantly influenced by waves and/or currents. The assemblage is considered to be deposited at the onset of the OAE2 (just below the peak of anoxy, within M. geslinianum Zone – S. gracile/E. septemseriatum Subzones), during the normal, shallow marine conditions.

Simulating large grazers with a physiological model

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Large, terrestrial herbivores (megafauna) once shaped Pleistocene ecosystems in the northern hemisphere but are now either extinct or diminished to insignificance. One way to further our understanding of past vegetation–herbivore ecology is mechanistic modeling. I will present a modeling framework that simulates potential population densities of grazing megafauna. It uses simple theoretical relationships and physiological parameters derived from modern analogs and paleontology. It is coupled with a dynamic global vegetation model and designed with flexibility and modularity in mind. A major modeling goal is to identify the consequences of uncertainty in parameter estimates and theoretical assumptions. Narrowing the highlighted ecological and paleontological knowledge gaps can improve mechanistic models of large herbivores in past and present.

Lepidophagy in the Triassic coelacanth *Piveteauia*

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Lepidophagy is a piscine feeding strategy that involves removing and eating the scales of other fish. Although difficult to digest, scales are a nutritious food. More than ten living fish families have independently evolved a lepidophagous lifestyle. Several lines of evidence suggest that the Triassic coelacanth *Piveteauia madagascariensis* was a lepidophage. The posterior half of the angular is greatly elevated, and the gular plate is massive, implying a powerful clipping bite force. *Piveteauia* is small compared to other Triassic coelacanths from Madagascar. Its body is elongate and the fins are relatively small, as is the case for modern lepidophages such as the scale-eating pupfish (*Cyprinodon desquamator*). Enigmatic phosphatic spherical bodies occur in the abdomen of *Piveteauia*, the remains of objects that (according to Gael Clement) were "relatively hard and resistant to decay." The spherical bodies are interpreted here as the partially digested remains of ingested scales, most likely the tough scales of other species of fish or scales of the aquatic procolophonid reptile *Barasaurus*. Finally, the unusual morphology of the *Piveteauia* sclerotic ring suggests an adaptation for minimizing eye injuries during feeding. *Piveteauia's* eyes are reinforced by a thick sclerotic ring, a morphology comparable to that seen in predatory placoderms such as *Dunkleosteus*. Each ossicle in *Piveteauia* bears a medial crease, a morphology unknown in other vertebrates. This crease imparts to each ossicle an ability to flex inward, and thus functions as a shock absorber on impact.

Mass spawnings of the arthropod *Isoxys volucris* reveal a seasonal signature to the early Cambrian Sirius Passet Lagerstätte, North Greenland

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Localities with Burgess Shale-type preservation of soft-bodied animals offer some of the best windows for understanding Cambrian ecosystems. They are largely a consequence of fossiliferous 'event beds'—rapid burial events that mixes the present living animal community and its accumulated carcasses/moults with transported elements to various degrees. However, these event beds are often separated by prolonged periods of poorer preservation ranging from decades to millennia. They may therefore provide filtered, and hence biased, time-averaged pictures of otherwise dynamic communities. We show here that the early Cambrian Sirius Passet Lagerstätte, North Greenland, captures in situ benthic and accompanying pelagic communities in frequent event beds with limited time-averaging. We use distinct bed-by-bed size populations of the ubiquitous arthropod Isoxys volucris to show that the thin amalgamated beds of Sirius Passet record seasonal (intra-annual?) variation. Surface counts (N=674) and length measurements (N=391) of I. volucris on 20 bedding surfaces in an 8 cm thick succession reveal a bimodal size distribution with two surfaces (separated by 5.7 cm/15 beds) exhibiting disproportionally high abundances of juvenile specimens, interpreted as results of mass spawnings. The discrete size differences of I. volucris assemblages, together with high taphonomic quality of other fossils, suggest limited time-averaging (decay) between the event beds, with the former possibly reflecting seasonal population dynamics. The surmised seasonality matches extant arthropod spawning patterns, such as krill, and suggests an adaptation to seasonal fluctuations in nutrient availability mirroring those in modern ecosystems. The extraordinary richness in both diversity and quantity in Sirius Passet, along with these particularly frequent depositional events, provide a uniquely resolved window on the Cambrian marine ecosystem.

Session 5: Conservation ecology and Biodiversity

The sixth mass extinction outpaces the fifth one in freshwater ecosystems

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Biodiversity decline is one of humankind's major challenges today. Because of the magnitude of the already observed and future predicted change, many scientists consider the current biodiversity crisis an incipient "sixth mass extinction". The current crisis resembles the previous, fifth mass extinction event at the Cretaceous–Paleogene (K–Pg) boundary 66 million years ago in terms of the rapidity of the change – an asteroid impact paired with extreme weather conditions in the successive months/years vs. anthropogenic impact and climate change. The fifth mass extinction is well understood for terrestrial and marine biota, but little data are available on freshwater biota. Freshwater vertebrate faunas seem to experience a much lesser decline of 10–22% (compared to the global average of 76%). However, vertebrates make up only a minor proportion of freshwater biota, and no comprehensive data are available for invertebrates. We estimated speciation and extinction rates for a large dataset spanning the fossil record of freshwater gastropods of Europe, with 3,122 species from 24,759 fossil occurrences from Jurassic to Pleistocene deposits. To compare the impact of the sixth versus the fifth mass extinction, we predicted future extinction rates and species loss based on conservation statuses of the extant European freshwater gastropod fauna. The results were alarming. While our reconstructions show that already the fifth mass extinction has been dramatically underestimated – 92.5% of the gastropod species go extinct and the extinction rate is an order of magnitude higher than the background rate – the predictions for the future are much worse. Our estimates suggest that a third of the modern European gastropod fauna may be lost within 100 years. The estimated extinction rate is approximately a thousand times higher than for the fifth mass extinction event. Our results once more highlight the devasting prospects for Earth's biota and the need for immediate action.

Improving the performance of species distribution models in new spatial-temporal domains: A trophic rewilding case study

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Bridging the divide between paleontology and ecology requires applying knowledge obtained in one spatial-temporal domain to another, possibly very distant domain. Species distribution models (SDMs), which correlate a species' occurrence with environmental conditions, are often used in just such a setting, for predicting environmental suitability or probability of occurrence in new geographic regions, or in the differing climates of the past or future. This is certainly the case in SDM studies assessing species' potential as candidates for *trophic rewilding*, a restoration strategy in which species are (re)introduced to reestablish local ecosystem structure and function. African (*Loxodonta*) and Asian (*Elephas maximus*) elephants are important ecosystem engineers, and have been nominated for rewilding on several continents. How might elephants fare in different biogeographic realms, in present and future climates? In this work, we develop SDMs for these species, to address (1) obtaining an accurate estimate of an SDM's predictive performance in new spatial-temporal domains, and (2) preparing an SDM likely to generalize well to such new settings. We assess model performance using both random and spatial cross-validation (CV), the latter accounting for spatial structure in the training datasets and yielding more reasonable estimates of model performance in new domains. Furthermore, we use forward feature selection (FFS), assessed by spatial CV, to select predictors most likely to deliver spatial-temporal generalizability. However, predictors selected via spatial CV show no systematic improvement in dissimilarity/extrapolation metrics in new biogeographic realms or climate scenarios. This suggests spatial CV/FFS may not be the final solution to optimizing SDMs for use in new domains. These results, however useful, are complex, and contingent on the flexibility of the selected model, the spatial structure of predictors and response, the blocking of the spatial CV, and other mitigating factors.

Quaternary carbonate factories of the Mediterranean Sea: a case study from the Northern Apennines

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Crustose coralline algae are shallow bio-engineers able to develop both stable structures (algal build-ups or reefs) with a topographic relief, and mobile sediments (rhodoliths), in the form of gravel particles of different shape which form complete coverage of the seafloor (bed). The Mediterranean shelves presently host biogenic carbonate production dominated by crustose coralline algae, both algal build-ups and rhodolith beds, as well as it did in the past, as reconstructed in the limestone bodies outcropping in the whole area and dating back to the Pliocene and Quaternary. Several records of Plio-Quaternary build-ups and rhodalgal carbonates have been reported in literature for Italy, and most of them are concentrated in the southern part, whereas they are rare in the northern regions. Here probably, the sediment load from rivers, present-day as well as in the past, is much higher, affecting the development of such biogenic carbonates, and this suggests that over the long time scale, high sedimentation rates hindered the development of such deposits. Despite this, we focus on some rare and local records of algal biogenic carbonates from the Pleistocene stratigraphic successions outcropping along Enza and Stirone rivers (Northern Apennines, Italy). These marine deposits formed during the final phase of the Apennine orogenesis, at the southern edge of a paleo-basin, now corresponding to the *Pianura Padana*. We analyzed the paleo-biodiversity and the main structural and morphological features associated to such deposits, with the aim of understand why in a unfavorable paleogeographic context, we recorded such active carbonate factory. This will contribute to the knowledge of the environmental control in the development of such type of habitats and organisms, which are presently listed in international treatises for the protection of the biodiversity and the marine environment.

Providing Earth system modeling for studying ecological dynamics in deep time

(with a focus on the Mesozoic Era)

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Understanding past ecosystem dynamics frequently demands information about climate conditions and their changes in the considered spatial and temporal context, which can be difficult to extract from empirical records alone. Climate models can provide this context and can thus help to bridge the gap between paleoclimate, paleontology and ecology. Here, we give an overview over recent and ongoing work on modeling Mesozoic (~252 – 66 Ma) climate states and dynamics. This includes the long-term climate evolution over geologic timescales, as well as effects of orbital cycles and perturbations by e.g. volcanism. The CLIMBER-3α and CLIMBER-X Earth System Models are employed for these investigations. Besides physical processes in the atmosphere, ocean and sea and land ice, the models are also able to simulate aspects of vegetation dynamics and marine and terrestrial biogeochemical cycles. Extensive climate model output data has already been provided alongside published work and can be readily (but cautiously) used as a resource for paleoecological research. However, we would like to further contribute Earth System modeling expertise and data to deep time ecosystem and biodiversity research projects and exchange with the paleo-community. We show a few examples in which we have tentatively evaluated model results against assumed thermal niches of some Mesozoic forms of life (e.g. scleractinian corals), and we reflect on potential ways to link such modeling and paleontological/ecological research. Although we focus on the Mesozoic era here, our interests and techniques are not limited to this.

Incorporating recent fossil data in a multi-temporal framework markedly improves predictive power and transferability of ecological niche models

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Ecological niche models, when used correctly, offer powerful insights into biotic interactions, climate change sensitivity, and extinction risk and can inform conservation plans for species threatened by climate change. However, species' ecological niches are dynamic through time, and models based on a single time period are often insufficient to accurately quantify both pattern and process in distributional ecology. These inaccuracies can result in mis-characterizing fundamental niche axes for a given species and predicting unsuitable environments as suitable and *vice versa*. Here, I investigate limitations of models based on a single snapshot in time using a dataset of Late Quaternary felids ranging from extant *Lynx* and *Puma* to the extinct American lion and saber-toothed cat *Smilodon*. I show that incorporating recent fossil data from the terminal Pleistocene and Holocene markedly improves our understanding of species fundamental niches. These improved ecological niche models can then be used to better inform processes such as species' interactions, spatio-temporal demographic trends, and potential mechanisms of allopatric speciation. Incorporating a multi-temporal approach not only improves sample size for data-deficient/rare taxa, such as apex carnivores, but expands the suite of environments that these species could experience. This permits better approximation of physiological tolerances, particularly improving correlative models such as Maxent. I further present an open access R-based niche modelling framework for incorporating occurrences across multiple time periods. I ultimately demonstrate that the recent fossil record can offer unique insights to niche dynamics on broad temporal scales for which modern data alone are insufficient. Ultimately, deeper paleontological-neontological intersectionality can markedly enhance insights into both paleo-macroecology and biogeography.

Refining ecometric analyses to better integrate paleontology with ecology

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Functional traits describe how organisms interact with their local environments, and trait-environment alignment is essential for ecosystem function. Ecometric analyses examine community-level functional trait-environment relationships. A powerful research strategy is to evaluate ecometric relationships through time to establish how these relationships shift as conditions change. Certain functional traits, such as locomotor morphology and dental characters, are frequently preserved in the fossil record and strongly relate to environmental conditions. Thus, they provide a 'common currency' to work across temporal, spatial, and taxonomic scales. We can learn a lot about mammals and their interactions with both past and future environments using ecometrics, but first we need to refine our understanding of how to best assess these trait-environment relationships. We discuss the utility of ecometric analyses for evaluating how expanding human footprints affect trait-environment relationships. As first steps, we refine the methodologies and the traits used in these ecometric analyses. We have investigated different estimation methods used in ecometric studies and found that maximum likelihood consistently produced the most accurate estimates of environment from community-level functional traits. We also extended the taxonomic scope over which an ecometric trait can be applied. Calcaneal gear ratio is known to be related to ecoregion and vegetation cover in carnivoran communities, and we showed that this relationship holds for artiodactyl communities. Interestingly, this trait is functionally opposite in carnivorans and artiodactyls, yet it is related to the same environmental variables, making it useful for integrating ecometric studies. Using this expanded toolset for evaluating ecometrics, we have begun applying these methods to fossil sites to investigate the timing and synchronicity of trait shifts as environments change and anthropogenic impacts arise. Overall, ecometrics is an emerging and highly informative field that can use trait-environment relationships to develop long-term understanding of faunal responses and support conservation of mammalian communities.

Mammal species occupy different climates following the expansion of human impacts

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Human occupation of the globe has expanded substantially since the last glaciation, especially across temperate areas with easy access to water sources. Human-mediated landscape transformation can exclude mammal species from their former habitats. Thus, we anticipate a change in the realized niches of mammal species as increased human occupancy forces them to shift within their fundamental niches. In our study, we collected modern and fossil species occurrences from 11,700 ybp to the present for 46 North American mammal species covering six taxonomic orders. We inferred temperature and precipitation for each location using paleoclimate simulations (CCSM3). We calculated niche overlap between multiple past time intervals and the present to identify whether the realized niches of these mammals did indeed shift through time. We also estimated the environmental niches of modern habitat types with varying severity of human impacts and calculated their niche overlap with mammal species' niches at each time interval. Our results suggest that human impacts have altered the ranges of climatic conditions North American mammals inhabit. Sixty-seven percent of the studied mammals have significantly different niches today than they did before the onset of the Industrial Revolution. Mammalian climatic niches change the most in the portion that overlaps with human-impacted landscapes. Large-bodied dietary specialists are being extirpated from climates in human-impacted areas; whereas smaller, generalist mammals are being facilitated, colonizing climates now occupied by urban and agricultural landscapes. Importantly, the climates where we find mammals today do not necessarily represent their natural habitats. This disagreement between modern and historical niches has critical implications for niche-based conservation models. Integrating fossil and modern data has the potential to make better predictions about species distributions to conserve biodiversity going forward. Without mitigation, as we move further into the Anthropocene, we can anticipate a low standing biodiversity dominated by small, generalist mammals.

Late Pleistocene fossils recontextualize the ecology of introduced turkeys in California

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Managing invasive species is a central challenge in conservation biology given funding constraints and the potential for unanticipated ecological consequences. New techniques that bring Quaternary fossil records and zooarchaeological assemblages into such discussions reveal that many introduced species have unexpected histories and may represent ecological or taxonomic substitutes for extirpated or extinct species lost historically or in the Late Pleistocene. Wild turkeys (*Meleagris gallopavo*) are a non-native, potentially invasive species in California introduced in the 1900s as a game animal. However, they are congeneric with the California turkey (*Meleagris californica*), an endemic species that went extinct at the end of the Pleistocene. Previous research has suggested a role of changing precipitation patterns in driving the extinction of the native California turkey, and it is conspicuously absent from archaeological middens. To assess these two closely related species' potential ecological overlap and thus provide a currently unaccounted for baseline of turkey ecology in California, a species distribution model (SDM) for *Meleagris californica* was developed based on bioclimatic data and fossil localities from the Last Glacial Maximum. This model was then projected into current landscapes using present-day climatic data as a counterfactual of this extinct species distribution as if it never went extinct. This projection was then compared to an SDM for extant *Meleagris gallopavo* generated using present-day observations from citizen science datasets. Quantitative indices of model overlap and variable importance strongly suggest that *Meleagris gallopavo* in California today largely occupies geographic and environmental spaces similar to those used by *Meleagris californica*. Future analyses using various techniques, including morphological and stable isotope analyses, may be needed to crystallize the precise ecological effects of *Meleagris gallopavo* in California and confirm the species' role as an ecological substitute.

Integrative taxonomy of the bushbuck species complex (*Tragelaphus scriptus*):
Combining molecular and morphological systematics

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The bushbuck (*Tragelaphus scriptus*) is a generalist antelope adapted to a large geographic range covering almost the entirety of sub-Saharan Africa. It is the most widely distributed wild ungulate in Africa, and local adaptations have produced in it much variation in body size, horn length, and coat pattern. Recent taxonomic work has suggested that the African bushbuck might be better classified as two or more species: Molecular studies have shown a deep mitochondrial divergence between north-western (Scriptus) and south-eastern (Sylvaticus) bushbuck populations, while morphological assessment has suggested dividing the bushbuck into as many as 8 species and 32 subspecies. Molecular and morphological approaches have to date not been brought together in a single integrative study. We combined complete mitogenome sequencing and three-dimensional geometric morphometrics to assess correlation between genetic and morphological divergence among 44 individuals from different regions of the total species range. By analysing the same cranial specimens with both morphological and molecular methods, we compared the genetic and phenotypic variation of the *Tragelaphus scriptus* species complex in a biogeographic context and assessed whether consistent morphological changes can be seen that match the apparently deep genetic isolation of the bushbuck's different geographic populations. Although mean body size differed between males (but not females) of the Scriptus and Sylvaticus lineages, size-shape allometry was conserved across all groups, and morphological variation due to sexual dimorphism was greater than within-sex variation across lineages. Despite a mitochondrial lineage divergence of nearly 3 million years, we found only small differences in cranial morphology and a significant but weak relationship between phenotypic and genetic distances. Thus, our study helps resolve the taxonomy of the African bushbuck, supporting its classification as a single species.

Assessing biodiversity of ancient plant ecosystems: opportunities, constraints, and a case study

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Palaeobotanical and palynological studies provide the primary data sources to study diversity and evolution dynamics of vegetation in the geological past. However, a major issue in assessing ancient plant biodiversity is an artificial taxonomic knowledge on fossil plants, as fragmented and isolated plant organs are classified as form taxa and whole-plant concepts are widely missing. One of the most important tools to assess the biodiversity research potential of fossil floral assemblages is taphonomy. Taphonomical studies shed light on the discrepancy between the true diversity and the fossil record of an ancient vegetation community. Most assemblages are allochthonous, with plant fossils that have been subjected to varying degrees of fragmentation, transportation and time averaging. The highest potential to study true diversity patterns in the fossil record is given for autochthonous floras, which have been rapidly buried at their places of growth. One of these so-called T^0 assemblages is the Chemnitz Fossil Forest, a 291 Ma old forest ecosystem that grew under seasonal palaeoclimatic conditions and was buried by pyroclastics of a nearby volcanic eruption in a geological instant. Fossil plants were preserved three-dimensionally, whereas some of them remained anchored in the substrate or show organ connections of roots, stems, foliage, and reproductive organs. Even though the potential for studying α-biodiversity of this fossil assemblage is high, careful and comprehensive taxonomic studies are required, with a focus on whole-plant concepts. The talk presents the current state of research and provides insights to the puzzling process of reconstructing this 291 Ma old habitat.

Relationships between reef proliferation and reef diversity over geological time scales

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Understanding mechanisms that regulate reef building and biodiversity in reef ecosystems is imperative to understanding global declines in coral reefs. The relationship between biodiversity and the development of reefs is presently not well established, although the assumption of ecologists is that reef declines increase the extinction of reef corals. Paleontological studies have demonstrated that while there is a statistically significant cross-correlation between reef diversity and reef proliferation, there are important exceptions with high reef production with a limited species pool of reef builders. Here, we assess the relationship between reef proliferation and diversity at Phanerozoic scales, testing the hypothesis that high diversity enhances reef building. Using fossil occurrence data from the Paleobiology Database (PBDB), and reef attributes from the PaleoReefs Database (PARED), we study over 20,000 Phanerozoic observations of tropical reef building species to understand the relationship between alpha, beta and gamma diversity, and reef proliferation, in roughly equal ten-million-year bins. We measure proliferation as a combination of reef thickness, reef volume, reef count, and geographic range in each time bin. Preliminary analysis of raw data, corrected for autocorrelation, shows a statistically significant linear relationship between the number of reefs present in each time bin with sampled-in-bin alpha, beta, and gamma diversity of reef builders. A similar relationship is observed between diversity metrics and the geographic range of reefs in each time bin. Initial results indicate that during the Phanerozoic, high biodiversity promoted reef building, and the global spatial extent of reef systems, but the size of individual reefs was unrelated to the number of reef building species present.

Ecological census implications, site description, and systematic paleontology of Boomerang Cave, a vertebrate assemblage In Cache County, Utah, U.S.A.

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Deposits of vertebrate remains are increasingly recognized as a powerful tool for censusing wildlife populations, supplementing traditional zoological survey techniques (e.g., trapping, camera traps, aerial census) by providing observations spanning larger temporal scales. We describe a late Quaternary paleontological assemblage from Boomerang Cave in the Bear River Range of Cache County, northern Utah, U.S.A., at an elevation of 2231 m. The site is a limestone cave with a >45 m vertical entrance forming a natural trap alongside multiple other vertical chambers, each containing vertebrate fossils. We analyze 1228 surface-collected specimens from six main chambers within the cave: a single specimen is fully lithified and likely dates to the Pleistocene, whereas most specimens are not mineralized and likely date to the past several centuries. Many are well-preserved due to the stable, cool cave environment, low disturbance, and protective coatings of carbonate. We identified a minimum of 23 non-overlapping taxa (22 mammals, one bird), comprising seven of the eight functional groups of mammals in the region. Of particular importance is the cave's diverse carnivoran assemblage, preserving at least nine taxa. We also record the first extant or fossil occurrence of *Sorex merriami* from the region. Our dataset was compared to mammalian museum specimen data from VertNet from the Bear River Range and data collected by trapping in the vicinity of the cave. We find that traditional census methods under-sample taxonomic and functional diversity. This is particularly apparent for Carnivora, which are rare in zoological assemblages but well-sampled in the Boomerang Cave assemblage. We attribute this to the more random nature of natural trap cave deposition removing accumulation biases due to size and/or diet. This supports the importance of skeletal deposits for censusing of terrestrial ecosystems.

A fossil of forest hog from Rusinga Island (Kenya) and the ecology of extant and extinct African Suidae

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The recent evolutionary history of many African taxa remains obscured partly due to the scarcity of fossils in the latest part of the Pleistocene. One evident example is that of African forest hogs (genus *Hylochoerus*). Forest hogs are, together with warthogs, the evolutionary end-product of a well-documented African Plio-Pleistocene suid radiation. Contrary to warthogs and various extinct suids, which developed highly derived craniodental adaptations to grazing diets as a response to the expansion of C4-grasslands, forest hogs became adapted to mixed diets and to living in Afro-tropical forest environments. *Hylochoerus* likely evolved from a population related to the eastern African Pleistocene species *Kolpochoerus majus*, but the only securely dated and well-identified fossils of *Hylochoerus* are those of the Kibish Formation ~0.1 Ma. Here, we redescribe a partial right lower third molar of *Hylochoerus* from Rusinga Island dated to ~50-36 ka, which was previously attributed to *Kolpochoerus*. The crowns are mesiodistally compressed and arranged in relatively tall columnar pillars that resemble those of extant forest hogs. Using micro computed tomography, we show that the hypsodonty index (HI) that the Rusinga third molar crown was as tall as those of extant *Hylochoerus* (HI = 1.8-2.0). Stable carbon isotope analyses, including previously unpublished data on extant *Hylochoerus*, suggest that the diet of the Rusinga specimen (δ^{13}C = -17.0 ‰) was isotopically similar to that of extant forest hogs (δ^{13}C average = -17.6 ‰). This is the most negative carbon isotope value of any mammal in the African Neogene-Quaternary fossil record. Furthermore, this value contrasts strikingly with those of other fossil large herbivores at Rusinga (δ^{13}C average = -0.7 ‰.). The presence of forest hogs in this site suggests that the Late Pleistocene paleoenvironments were more heterogeneous than previously considered and may have included closed-canopy woodland in the highlands of Rusinga.

At the crossroads of conservation palaeobiology: How World Heritage fossil sites contribute to the future by promoting the past.

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The World Heritage listed Naracoorte Caves, situated in the Limestone Coast region in Southeastern South Australia, contains the richest accumulation of Pleistocene mammal fossil remains in Australia. The caves contain vertebrate fossils from over 130 species of extinct and extant vertebrate fauna in well dated sedimentary deposits covering the last 530,000 years. These deposits span important temporal events including the megafaunal extinction approximately 45,000 years ago and several glacial/interglacial cycles. As a major tourist drawcard for the region and the site of ongoing palaeontological research, it serves to inform visitors about the geological processes that form caves and the ecological changes over time. Since European settlement, around 175 years ago, the region has undergone extensive landscape modification and has suffered significant biodiversity loss and large-scale decline in critical weight range (35 g to 5.5kg) mammals. As a biodiversity hotspot it is also an area in need of effective conservation planning, management and implementation. Naracoorte Caves, as a globally recognized fossil site, is well placed to deliver an impactful and engaging ecological conservation message delivered at the crossing of the past and future, and of science and the general public. In this presentation we look at the factors present at the Naracoorte Caves that exemplify it as an effective site for bridging the palaeoecological-ecological gap and facilitating outreach to the general public.

Session 6: Responses to climate change

Taking the long view: the importance of historical and ecological perspective in our understanding of the effects of climate change on phenological synchrony

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Climatic conditions frequently serve as cues to trigger developmental and life history stages. A species' phenology—the timing of these stages—is therefore an obvious phenotypic trait liable to be influenced by climate change. Often, these climatic cues are indirect indications of changes in the biotic as well as the abiotic environment. For insectivorous birds, for example, the onset of spring, which triggers egg-laying, signifies not only more favourable weather conditions but also the impending maximum availability of insect food for their offspring: such taxa are said to be phenologically synchronised. Here, I will discuss the synchronised phenology of spring feeding caterpillars (particularly the winter moth *Operophtera brumata*) and their host-plants. Recent work emphasises the severe fitness consequences which these caterpillars suffer if they do not precisely match the phenology of their host trees. Where climate change occurs and the phenology of each trophic level responds differently, there is therefore the potential for significant detrimental effects to the consumer, which then ripple through the food chain. However, previous studies tend to take a very restricted view of the ecology of these caterpillars and typically focus on their interaction with a single host-plant species. Using host-plant assays, I will show the highly generalist nature of the diet of these species and the complexity of their trophic environment. I will examine the phenological cues they employ, intraspecific variation in their cue requirements, and the intrinsic variation in the spring environment which they must tolerate. Viewed across a geological timescale, it is clear that these species cope with a highly variable adaptive landscape, and that their phenological and ecological adaptations reflect this. This suggests, I will argue, that they are perhaps more robust to future climate change than has been thought, highlighting the importance of historical and ecological context in phenological research.

Evolutionary dynamics of the Southern Ocean diatoms across the Eocene-Oligocene transition

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Modern diatom communities are a critical agent for the long-term regulation of atmospheric CO2 via biological ocean carbon pump. Global warming can irreversibly alter this diatom-climate system since modern communities consist of mainly cold-water adapted species. The Eocene-Oligocene transition (EOT, 33.9 Ma) marks a taxonomical reorganization in the evolutionary history of marine diatoms and the onset of the modern diatom-based biological carbon pump in the Southern Ocean (SO): it thus provides a realm to investigate the nature of the diatom-climate interactions. Whereas reported diversity increase across the EOT suggests that diatoms contributed to the end-Eocene climatic events, data so far are mostly reliant on the synthesis of biodiversity-incomplete biostratigraphic literature. Here we present new diatom diversity data of the Southern Ocean that allow us to examine the role of the diatom communities at the end-Eocene climatic events. Our results show that the SO diatoms experienced a substantial increase in origination rates shortly before the EO boundary (~ 34 Ma), suggesting that, together with increased overall diversity, diatom evolution and early Oligocene cooling events pertain to each other. We discuss this link under the light of high-resolution paleoproductivity proxies and highlight the co-evolution of paleoceanographic dynamics and diatom macroevolutionary trends, with a particular focus on the response characteristics of diatoms under climatic perturbations.

Assessing the impact of climate change on the structural integrity of benthic foraminifera during the Palaeocene Eocene Thermal Maximum – implications for future climate change

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Benthic foraminifera are a group of calcifying marine organisms that play a significant role in global carbonate production. These organisms, however, are under increasing threat from climate change. As environmental conditions change, the morphology of benthic foraminifera is known to be affected. Subsequently, changes in morphology may lead to the production of weakened forms, leaving benthic foraminifera more susceptible to breakage through predation or exposure to wave action Finite Element Analysis (FEA) is a useful mathematical technique that allows us to assess structural integrity within biological organisms. Here, simple finite element models are used to assess how the morphology of benthic foraminifera is affected during periods of climate change and how they impact overall structural integrity. Assessment of these morphological changes focused on the creation of simple 3-D geometric models, based on 2-D images, that can easily be altered. To assess the reliability of these models, they were compared to biologically accurate 3-D geometric models of benthic foraminifera which were generated from computed tomography (CT) scans. The results showed that the simple models were capable of distinguishing differences in mechanical robustness between different morphologies. These simple models were then altered in alignment with morphological changes observed in the fossil record of the Palaeocene Eocene Thermal Maximum (PETM), a rapid warming event used as a geological analogue to future climate change. The results show that species-specific morphological changes that occurred across the PETM, such as decreases in overall body size and percentage calcite, led to a weakening of structural integrity. This suggests that, under future climate change, certain species of benthic foraminifera may produce mechanically weaker tests, making it harder to withstand predation and wave erosion. This could, in turn, lead to a lower diversity and abundance of benthic foraminifera.

Functional stasis of mammalian communities across the PETM

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The Paleocene-Eocene transition in North America was marked by a rapid global warming event of 5° to 8°C (PETM; ~56 Ma) that followed an abrupt carbon isotope excursion lasting 21 ky or less. The PETM saw a significant shift in the composition of North American floral communities as well as immigration of the Perissodactyla, Artiodactyla, and Primates into North America from Eurasia, which led to significant body size change. However, a previous study found little to no change in the phylogenetic and functional components of North American PETM mammal diversity. It did not, however, include data on the abiotic environment or mammal traits relating to diet and locomotion. We assembled a database of 121 mammal species from the Bighorn Basin, Wyoming including their associated body sizes, inferred diets, and limb postures alongside a database of 73 floral localities as proxies for the abiotic environment. For each mammal species, we determined their abiotic preferences based on the floral communities with which they co-occurred. For each North American Land Mammal Age (NALMA), we then calculated dispersion in traits and environmental preference. We found little to no change in trait dispersion across the PETM, aligning with previous work. But we found that species occurring during the PETM showed higher environmental preference dispersion, suggesting that mammal species more finely partitioned the available abiotic space. These results indicate the persistence of a stable mammalian functional community structure despite considerable taxonomic turnover as well as decoupling of Eltonian (morphological) and Grinnellian (environmental) niche occupation.

Taphonomy and site formation history of vertebrate-bearing breccia in the caves of Sumatra

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In complex tropical cave environments, conventional dating methods are susceptible to significant risk of time- or habitat-averaging due to natural 'mixing' of vertebrate remains. Thus, I have formed a novel multi-method study to establish the dominant factors responsible for fossil accumulation and preservation in karstic breccia from Sumatran caves. A digital imaging survey combined with a micro-contextual study reveals the internal composition of fossiliferous deposits from Lida Ajer, Ngalau Gupin and Ngalau Sampit cave in the Padang Highlands of western Sumatra that would otherwise have been disregarded or destroyed using standard excavation methods. Thermal neutron imaging of karst breccia gives a three-dimensional view of spatial location and temporal sequence of sediment layers and inclusions within the breccia laid down during formation, revealing several rapid depositional phases of water and sediment gravity flow. Micromorphological analysis exposes the internal geometry and situation of incorporated components, revealing several further taphonomic agents including carnivore occupation, water action and calcite precipitation. This research successfully reconstructs the complex taphonomic history of fossil assemblages in the caves of Sumatra and the diagenesis of the sediments in which they are held. This contextual approach could be reconstructed to resolve mechanisms of site formation, depositional history, and faunal accumulation in further tropical cave sites. These data has the potential to establish stratigraphic provenance and temporal positions of fossil-bearing deposits in complex depositional environments across Southeast Asia.

Increase of marine provinciality over the last 250 million years was governed more by climate change than plate tectonics

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Amidst long-term fluctuations of the abiotic environment, the degree to which life organises into distinct biogeographic provinces provinciality can reveal the key drivers of biodiversity. Our understanding of present-day biogeography implies that changes in the distribution of continents across climatic zones have predictable effects on habitat distribution, dispersal barriers and the evolution of provinciality. To assess provinciality through the Phanerozoic, here we (a) simulate provinces based on palaeogeographic reconstructions and global climate models and (b) contrast them with empirically derived provinces that we define using network analysis of fossil occurrences. Simulated and empirical pattern match reasonably well and consistently suggest a >15% increase in provinciality since the Mesozoic era. Although both factors played a role, the simulations imply that the effect of the latitudinal temperature gradient has been twice as important in determining marine provinciality as continental configuration.

Diversity-productivity relationship in past 21,000 years: the evidence from North American woody species pollen data

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The energy available to species (environmental productivity) is considered as a universal correlate of species richness. Nevertheless, as most species-productivity studies are only contemporary or cover relatively short temporal gradients, the question of whether and when richness tracks changes in productivity remains unresolved despite its importance for predicting future diversity dynamics. We explored temporal fluctuation in pollen type richness of woody species ('richness') in the USA and Canada and climate since 21,000 years before present ('yr BP') in 1000-year time steps. We used reconstructed paleoclimate (temperature and precipitation) to calculate productivity according to the Miami model. We tested for the slope and strength of 1) the site-specific relationships between richness and productivity time series and 2) the spatial richness-productivity relationships in 1000-year time-bins. Richness increased with increasing productivity during the period of rapid climate change in the Early Holocene/Late Pleistocene (10,000-21,000 yr BP) but not in the climatically stable Holocene (1000-9000 yr BP). Conversely, when focusing on spatial relationships in particular time bins, richness increased with increasing productivity in the Mid/Late Holocene, but not in the Early Holocene/Late Pleistocene. Nevertheless, differences occurred between the Western and Eastern parts of the continent; in the West, this relationship remained strong over the Holocene until 13,000 yr BP whereas, in the East, this relationship was weak and non-significant overall. There is a mismatch between the temporal and spatial richness-productivity relationship. In the period of fast climate change, richness track change in climate well, but the spatial richness-productivity relationship is poor. The strong spatial relationship between richness and productivity formed under climatically stable Mid/Late Holocene when the temporal richness-productivity relationship weakened.

Planktonic foraminifera conserved environmental niches across 700,000 years of glacial–interglacial climate change

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Abiotic niche lability reduces extinction risk by allowing species to adapt to changing environmental conditions *in situ*. Species with static niches, in contrast, must keep pace with the velocity of climate change as they migrate to track suitable habitat. The rate and frequency of niche lability have been studied on human scales (months to decades) and geological scales (millions of years), but lability on intermediate (millennia) timescales remains largely uninvestigated. Here, we quantified abiotic niche lability at 8-ka resolution across the last 700 ka of glacial–interglacial fluctuations, using the exceptionally well-known fossil record of planktonic foraminifera coupled with Atmosphere–Ocean Global Circulation Model reconstructions of palaeoclimate. We developed a new R package ('kerneval') to characterize niches as continuous probability distribution functions while accounting for sampling bias, and to compare kernel densities in a quantitative way. We tracked foraminiferal niches through time along the univariate axis of mean annual temperature, measured both at the sea surface and from species' depth habitats. Species' temperature preferences were uncoupled from the global temperature regime, undermining a hypothesis of local adaptation to changing environmental conditions. Furthermore, intraspecific niches were equally similar through time, regardless of climate change magnitude on short timescales (8 ka) and across contrasts of glacial and interglacial extremes. Evolutionary trait models fitted to time series of occupied temperature values supported widespread niche stasis above randomly wandering or directional change. Ecotype explained little variation in species-level differences in niche lability after accounting for evolutionary relatedness. Together, these results suggest that warming and ocean acidification over the next hundreds to thousands of years could redistribute and reduce populations of foraminifera and other calcifying plankton, which are primary components of marine food webs and biogeochemical cycles.

Consistency in reef assemblages through the Holocene shows diversity persisting in a turbid reef

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Singapore reefs are increasingly threatened by the urbanization and development of coastlines where many reef communities used to be found. Yet, the modern reefs that remain are still characterized by high diversity despite the extreme turbidity conditions, with sedimentation thought to have increased with the rising anthropogenic stressors. With limited knowledge on what past reefs of Singapore were like before reef surveys began in the 1980s, we used a percussion reef coring approach for obtaining multiple cores from intertidal flats adjacent to the southern offshore islands to examine radiocarbon-dated assemblages of Holocene reefs. We found evidence of coral reef growth from 7000 years BP, punctuated across time, with past assemblages reminiscent of today's reefs. Similar reef communities were found, with much of the assemblage comprising massive and submassive forms, though foliose species were not as common in the past. Our work sheds light on what the past reef communities of Singapore were like, and by comparing them to modern reef assemblages, we could distinguish anthropogenic and natural variations in reef communities through the Holocene.

The size trait toolbox: new perspectives on community structure response to climate change in calcifying marine phytoplankton

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Species responses to future ocean change will drive substantial restructuring of modern marine phytoplankton communities, triggering a range of ecological and biogeochemical impacts. Marine ecologists increasingly use trait-based approaches to understand these processes that link environmental drivers of species physiology to community structure. Cell size is the master functional trait, associated with virtually all aspects of physiology and species' ability to utilize and transform carbon and other elements that influence elemental cycles and trophic energy transfer. Our understanding of phytoplankton community structure under warmer climate states can be greatly advanced by exploring species and community size structure recorded in the exceptional fossil record of mineralized phytoplankton assemblages. However, fossil size records for calcifying phytoplankton – the coccolithophores - remain elusive, as their exoskeleton (coccosphere) rarely remains intact and typically disaggregating into its individual component plates (coccoliths). Recent efforts to find intact fossil coccospheres in sediments have provided direct records of cell size that newly enable species and community size structure, biomass and calcite production to be reconstructed from more traditional morphometric and assemblage data. Here, we present first-look 'snapshots' of coccolithophore community size structure through the 'warm' icehouse background state of the Oligocene, 34 to 23 million years ago, at a new high latitude South Pacific Ocean site (IODP Expedition 378, Site U1553). Oligocene communities at Site U1553 are dominated by *Chiasmolithus*, *Reticulofenestra*, and *Cyclicargolithus*, typical of high latitude assemblages at this time, that exhibit large and very large cell size distributions. Community size structure and biomass partitioning are therefore skewed toward large size classes (>15 to 20 μm) throughout the Oligocene, overwhelming contributions from smaller species. As this project progresses, interactions between available environmental resources, the ecological strategies of different lineages, and evolving community composition will be explored to better understand the role of functional trait trade-offs in coccolithophore ecology.

The clam before the storm – what bivalves can tell us about climate change

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Bivalves are an environmentally important group of Molluscs found worldwide. These shelled filter feeders are involved in reef building and stabilizing shorelines. They are economically important in the seafood trade. Their carbonate shells have good preservation potential, and consequently bivalves have a strong fossil record. Bivalve growth patterns are sensitive to environmental conditions. These show clear responses to environmental stressors predicted by climate change models. The stressors investigated were temperature, salinity, hypoxic events and ocean acidification. Metabolism and shell building are directly affected by climate stressors, however there are also complex relationships where combinations of these changes act in an additive or dampening manner. Meta-analysis was used to determine the family level response to temperature, pH, hypoxia and salinity and combinations of these changes. The effect-size was used to predict an extinction threat level for each family. Using data from WoRMs (World Register of Marine Species) and the PDBD (Palaeobiology Database), extinction rate for each family of Bivalvia was calculated across the end-Cretaceous mass extinction. Generalised linear modelling could then predict whether vulnerability to climate change is correlated with extinction rate, when adjusted for phylogenetic and spatial signal. Preliminary results of an 18 month project are presented here.

Climate change and its effect on mammalian diversity in the Cenozoic of South America

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In the shadow of rapid global climate change, the preservation of today's biodiversity is a major concern. Although the responses of species to climate change can be modelled, only the fossil record provides empirical evidence on the long-term link between climate and biodiversity, including its underlying mechanisms. While significant advances have been made to unravel North American biodiversity patterns, this is not the case for other continents such as South America, that is characterised by a unique geomorphological and palaeogeographical evolution throughout the Cenozoic (the last 66 million years), including the continent's extended isolation and Andean orogeny. This contributed to the evolution of an exceptional endemic fossil fauna and flora, of which only remnants exist today. We focus on South American terrestrial eutherian mammals, which include the endemic notoungulates and xenarthrans. We developed a comprehensive dataset built and standardised within the Paleobiology Database, comprising approximately 6500 occurrences of 700 genera. We apply two main analytical techniques to reconstruct Cenozoic palaeobiodiversity through time that account for the effects of spatiotemporal fossil sampling bias: Shareholder Quorum Subsampling and PyRate. We identified diversity peaks in the Oligocene, early Miocene and Pleistocene, and dips in the late Eocene, middle Miocene and late Pliocene, although the late Eocene trough is characterized by extremely low preservation rates. Preservation is disproportionately high in the Pleistocene, and while subsampling shows a diversity increase during that interval, PyRate shows a diversity increase followed by an decrease towards recent times. Temporal variation in diversity is not correlated with fluctuations in global palaeotemperature proxies. Although this suggests no role for climate in constraining South American diversity dynamics, it might instead indicate the unsuitability of global climate reconstructions for assessing regional patterns.

Bison responses to Late Quaternary climate change in North America

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North American bison have demonstrated remarkable resilience to thousands of years of environmental variability including climate change, biome expansions and contractions, and predation. Bison endured the Late Quaternary mass extinction event that eliminated 70% of North American megaherbivores, and subsequently rose to dominance across mid-latitude North America throughout the Holocene. The importance of bison to indigenous cultures and to the coevolution of North American grassland ecosystems is widely acknowledged, but there has been little research documenting how bison populations shifted in time and space following the Last Glacial Maximum c. 21,000 years ago. Our understanding of large herbivore adaptations to changing environmental conditions over long time periods is similarly limited. To address these challenges, we employed a species distribution modeling approach to characterize abundance and distribution dynamics of bison since the Last Glacial Maximum through the Holocene. Our findings indicate that Late Quaternary changes in the distribution and abundance of bison were influenced directly by large-scale trends in the climate system and indirectly through biophysical and environmental changes. Our results suggest that bison distribution and morphology was strongly influenced by warming temperatures at the Pleistocene-Holocene transition and that bison abundance during the Holocene was largely driven by regional hydroclimatic variability.

Radiocarbon dating of individual foram tests show that alleged Lessepsian species are of Holocene age

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The Lessepsian invasion – the largest marine biological invasion – followed the opening of the Suez Canal in 1869 (81 years BP). This time coincided with an acceleration in natural history exploration and description, but the eastern sectors of the Mediterranean Sea lagged behind. Baseline information on pre-Lessepsian ecosystem states is thus scarce. This knowledge gap has rarely been considered by invasion scientists: every new finding of species belonging to tropical clades has been assumed to be a Lessepsian invader. We here question this assumption by radiocarbon dating seven individual tests of miliolids – imperforated calcareous foraminifera – belonging to five alleged non-indigenous species. The tests were found in two sediment cores collected at 30 and 40 m depth off Ashqelon, on the Mediterranean Israeli shelf. All foraminiferal tests proved to be of Holocene age, with a median calibrated age spanning between 749 and 8285 years BP. Therefore, these foraminiferal species are not introduced, but native species. They are all circumtropical or Indo-Pacific and in the Mediterranean distributed mostly in the eastern sectors. Two hypotheses can explain our results: these species are Tethyan relicts that survived the Messinian salinity crisis (5.97–5.33 Ma) and the glacial periods of the Pleistocene in the Eastern Mediterranean, which may have never desiccated completely during the Messinian crisis and which may have worked as a warm-water refugium in the Pleistocene; or they entered the Mediterranean Sea from the Red Sea more recently but before the opening of the Suez Canal, for example during the Last Interglacial (MIS5e) high-stand (125,000 years BP) when the Isthmus of Suez was likely flooded allowing exchanges between the Mediterranean and the Indo-Pacific fauna. The longer temporal perspective enabled by the Holocene record sheds new light on the invasion process, its rates and environmental correlates.

Deep-time climate legacies affect origination rates of marine genera

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Biodiversity dynamics are shaped by a complex interplay between current conditions and historic legacy. While a simple relationship is often used to link evolution with temperature, short-term climate change likely interacts with previous temperature trends when influencing the pace of origination. Such palaeoclimate interactions have been demonstrated for extinction risk but the effect on evolutionary dynamics is untested. Using a dynamic modeling framework, we analyzed the differential origination response of major Phanerozoic marine fossil groups after palaeoclimate interactions. We found a substantial effect of these interactions on origination rates, where the effect remains consistent through time and all studied groups. Building on a potential model for the causal relationship between palaeoclimate interactions and origination rates, we identified conditional dependencies and tested them using a continental fragmentation index. This proxy for available habitat space in the continental shelve indicated that palaeoclimate interactions act through sea level changes, leading to allopatric speciation and hence an increased origination rate. Our results demonstrate that biodiversity is controlled by a complex array of ecological and evolutionary factors, with mutual interactions. Explicitly integrating these effects within a dynamic modeling framework leads to an improved discernment of origination patterns in the fossil record.

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