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BOOK OF ABSTRACTS

HFSP Frontier Workshop

BRIDGING FOSSIL RECORDS AND MODERN SCIENCE: INTEGRATIVE APPROACHES TO EVOLUTION

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Interpreting structure-function relations through computational and mechanical intelligence

Parvez Alam, The University of Edinburgh, UK

In this talk, I will discuss opportunities in which computational and mechanical intelligence can be used to understand colour, movement, and functional performance in extinct animal species. Our recent advances in open-source AI-based geometrical pattern recognition, colour quantification, and mechanical prediction, now enable analyses on high resolution datasets across variable length scales, providing new insights into morphological diversity and function. Complementing our computational tools, mechanical intelligence provides a pathway by which means we can reconstruct movement, load-bearing behaviour, and functional performance in organisms lacking preserved soft tissues. Principles drawn from robotics and particularly necrobotics are transferrable, enabling new opportunities for paleobiological inference. Using some of our early examples such as *Pak Biawak*, I will illustrate how these approaches could be used to generate hypotheses about gait, stability, and environmental interaction in extinct species. Together, computational and mechanical intelligence create a conjoint framework that can be used to interpret structure-function relationships in ancient organisms, transforming fossilised structures into dynamic, testable models to elucidate biological performance.

Exploring the relationship between symmetry, size, and topological diversity in animal evolution with a bio-inspired cellular automaton

Miguel Brun-Usan, Andalusian Center for Developmental Biology, Spain
The ALIS team (Adaptable Living Systems); Centre for the integration of Paleobiology (CIPb), Spain. María José Jiménez-Rodríguez, University of Seville, Spain. Belén Medrano-Garfía, University of Seville, Spain. Fernando Casares, Andalusian Center for Developmental Biology, Spain

The morphogenetic processes underlying the origin of animal phyla remain a major unresolved question in paleobiology. Without a quantitative understanding of these processes, it is difficult to explain why animal body plans are so limited in number, so morphologically discrete, and so evolutionarily conserved. Despite extensive morphological diversification within phyla, animal architectures occupy a restricted and discontinuous morphospace, and the mechanisms underlying this pattern remain unclear.

To address this paleobiological conundrum, we explore how fundamental properties of multicellular organization (body size, symmetry, and internal topology, understood as the number and spatial arrangement of internal cavities such as coeloms and guts), interact to constrain the accessible morphospace of animal body plans. To this end, we developed a bio-inspired cellular automaton on a hexagonal lattice that generates large ensembles of *in silico* multicellular organisms ("hexazoans"), whose internal organization emerges from simple, developmentally inspired rules of epithelial-mesenchymal interactions. The resulting generative morphospaces, independent of historical and selective contingencies, are quantified using topological data analysis (TDA), allowing direct comparison between simulated morphologies and representative taxa from extant animal phyla.

Preliminary results suggest that, beyond well-known adaptive constraints (such as surface-to-volume ratios), previously unrecognized architectural trade-offs between symmetry, size, and topology may have played a key role in shaping the diversity and stability of animal body plans.

Beyond Fossils: Bridging Fields for Deeper Palaeobiological Insights

Anusuya Chinsamy-Turan, University of Cape Town, South Africa

Despite millions of years of fossilisation, the microscopic structure of fossil bones remains intact. Remarkably, within the fossilised tissues, key aspects of the life history of the animal are archived. Here, I will present highlights of my research on fossil bone microstructure to show how this has led to a better understanding of the biology of extinct animals such as, nonavian dinosaurs, Mesozoic birds and nonmammalian therapsids. Using case studies, I will demonstrate how collaborations across scientific disciplines, and the use of cross cutting methodologies such as finite element analyses, porosity modelling, biomechanical testing etc., have permitted deeper insight into the adaptation and functioning of skeletal structures of both extant and extinct animals. Additionally, I will briefly outline my approaches to communicating my research to the wider public and I will highlight my current research exploring how palaeosciences is communicated globally.

Bits, bobs and biomechanics: Reconstructing the feeding, anatomy and materials of massive sharks from limited samples

Mason Dean, City University of Hong Kong, China

Amar Surapaneni, City University of Hong Kong, China; Mike Schindler, City University of Hong Kong, China; Aurora Li, University College London, UK; Frederik Mollen, Liege University, Belgium; Dave Cade, Stanford University, USA; Tim Persoons, Trinity College Dublin, Ireland; Daniel Baum, Zuse Institute Berlin, Germany; Jeremy Goldbogen, Stanford University, USA; Sean Hanna, University College London, UK.

The filter elements (gill rakers) of basking shark species have remained unmistakable structures in the fossil record for >40 million years. This suggests that extinct basking sharks—like the modern species—also fed by gaping their mouths to filter plankton. Yet, we know surprisingly little about the ecologies of these ocean giants and how their filters work, due to the difficulty studying wild sharks and the rarity of well-preserved specimens. We addressed this challenge collaboratively—uniting biomaterials, robotics, biologging and architectural design—integrating from animal behavior down to the filter's structural building blocks. First, we constructed a bio-realistic skeletal model of feeding sharks, integrating anatomy from museum and beached specimens; bio-logging videos and photogrammetry; and diverse multi-scale imaging. The resultant poseable “digital puppet” captures the coordinated motion of joints as controllable parameters, reproducing—digitally and in 3D—how animals deploy their filters into flow. High-resolution imaging and materials characterization showed gill rakers' geometries create architectures with distinct behaviors in flow, imparting an emergent stiffness gradient to the filter, with thousands of arrayed rakers. We discovered rakers are not keratin (as thought) but exceptionally modified denticles, adapted for flexibility and stiffness, with the highest aspect ratio of any dental structure in nature (e.g. teeth, tusks). Particle image velocimetry of rakers and artificial mimics (with varied morphologies, tested at multiple flow speeds) clarified filtration mechanics: accumulation of simulated plankton under certain conditions suggests basking sharks swim at optimal speeds for feeding and that a small architectural feature—only appreciated when rakers are arrayed together—is critical to efficiently transport food and reduce filter clogging. The hierarchical design and performance of basking shark filters show how even microarchitecture can profoundly affect biomechanics, with adaptation of both material and geometry in evolution enabling novel dietary niches. The findings show the value of interdisciplinary approaches for studying large and elusive wildlife, offer inspiration for advanced filtration tools, and support reconstruction of ecologies from limited fossil evidence.

Unearthing the diversity and 300-million-year evolution of phloem in ferns

Zishan Fu, University of Edinburgh, UK

Rafael Cruz, University of Edinburgh, UK & University of São Paulo, Brazil; Kaare H. Jensen, Technical University of Denmark, Denmark; Alexander J. Hetherington, University of Edinburgh, Royal Botanic Garden Edinburgh & National Museums Scotland, UK.

Phloem is vital for vascular plants because of its fundamental role in transporting photosynthate and comprehensive roles in signalling. Despite its importance, the evolution of phloem remains poorly understood. This is because phloem is rarely preserved in fossils and poorly studied across vascular plant diversity including major groups such as ferns. Therefore, my research aims to uncover the diversity and evolution of the sieve elements (SEs) anatomy, the structure of conducting cells in phloem. Utilising histology and advanced microscopy, I am examining phloem structure in 26 extant and eight extinct ferns, making over 18,000 measurements of SE anatomy. We report high diversity in extant fern phloem, and that SE radius preserves a strong phylogenetic signal. SE radius is similar in closely related taxa despite differences in leaf and vascular characteristics. We also detect clear scaling relationships between SE radius and leaf and vascular characteristics in leptosporangiates. Integrating fossils, we recognise a trend of decreasing SE radius and total conducting area through geological time. Combining with mathematical modelling of phloem conductivity, we predict this decrease likely had a major functional impact by reducing phloem conductivity in the highly diverse eupolypod ferns, which diversified into angiosperm-dominated ecosystems.

The Speed of Life: A Deep Time Perspective

Anjali Goswami, Natural History Museum, UK

Why is evolution seemingly a story of fits and starts, with long periods of relative stability interrupted by rapid transitions? What allows some species to survive and quickly exploit new opportunities, while others are consigned to the fossil record? Why do some groups diversify into thousands of species, while others potter along at small numbers for millions of years? Why do the same forms evolve over and over again in different groups, at different times, and in different places, while many hypothetical forms never evolve at all? Why, in essence, has life on Earth evolved the way that it has?

Using a wealth of fossil data, I will walk through our work piecing together the changing tempos of evolution across different animal groups. I will further delve into how the latest technology, especially imaging and AI, is allowing scientists to gain new insights from old bones and making it possible for the first time to gather and analyse rich data on form from thousands of species. From reconstructing the ecology of groups that have been extinct for hundreds of millions of years to better predicting health outcomes for domesticated species that we keep in our homes, these new approaches are expanding our understanding of past, present, and future life on Earth like never before.

From imaging to function: insights into the past by looking at the present

Anthony Herrel, Muséum National d'Histoire Naturelle, France

Modern imaging techniques such as CT scanning in synchrotron scanning can provide unprecedented insights into bone structure and function of extinct and extant animals alike. However, to infer ecology or life style biomechanical models linking bone structure and function to movements and whole-organism performance are essential. To create such models comparative anatomical data on both soft and hard tissues are essential but soft tissue anatomy is only rarely preserved in the fossil record. Even in extant organisms quantitative data on soft tissues are often scarce. Together with in vivo data on motion and forces biomechanical models can be validated for extant taxa and then applied to extinct organisms. In the present talk I will give an overview of some of the large comparative data sets I and my collaborators have been gathering on soft and hard tissue using both imaging as well as direct dissection. The application of these data to questions of ecology and function in extinct organisms will be illustrated and limitations to these approaches will be highlighted.

Identification of core shell matrix proteins in molluscs and their preservation potential in fossil shell

Kazuki Hirota, The University of Tokyo, Japan

Taro Yoshimura, The University Museum, The University of Tokyo, Japan; Takenori Sasaki, The University Museum, The University of Tokyo, Japan; Davin H.E. Setiamarga, University of Vienna, Austria

Molluscs emerged during the Cambrian explosion with biomineralized shells that protected their soft bodies from predators. These rigid protective structures contributed to the remarkable diversification of molluscs, resulting in an abundant fossil record throughout Earth history. However, molecular paleontological research on molluscan shells remains limited, despite the presence of organic shell matrix components, including proteins and polysaccharides. To address this gap, we investigated the organic components preserved within molluscan shells to better understand the evolution of biomineralized structures. Specifically, we examined which shell matrix proteins (SMPs) are evolutionarily conserved across molluscs and whether ancient proteins can be preserved in fossil shells.

We conducted a comparative analysis of molluscan SMPs using proteomic data from 14 species and identified 11 core SMPs conserved across molluscs. These shared SMPs accounted for only approximately 30% of the total SMP repertoire, indicating that the majority of SMP families are lineage-specific. Phylogenetic analyses further revealed lineage-specific expansions of all core SMPs. We also investigated the preservation of organic components in fossil bivalve shells (*Batissa sitakaraensis*) dating to approximately 3,800 years ago. To evaluate the preservation of endogenous organic components, we combined multiple analytical approaches, including scanning electron microscopy (SEM), energy-dispersive X-ray spectroscopy (EDS), and bicinchoninic acid (BCA) protein assays. These analyses provided evidence for the preservation of several organic components within the fossil shells, suggesting that shells preserved under favorable conditions may retain ancient shell matrix proteins suitable for future paleoproteomic analyses. Our findings provide a valuable framework for assessing the preservation of shell-associated biomolecules in fossil shells and provide a basis for future shell paleoproteomic analyses.

New digitization and visualization approaches help reveal great transformations in vertebrate evolution

Casey M Holliday, University of Missouri, USA

Partha Mitra, Cold Spring Harbor Laboratory, USA; Sarah Bottjer, University of Southern California, USA; Janine Ziermann-Canabarro, Howard University, USA; Carol Ward, University of Missouri, USA; Alec Wilken, University of Missouri, USA.

Exploring the mechanisms and patterns that drive vertebrate evolution continues to be a major objective in the biological sciences. To gain a deeper understanding of significant evolutionary transformations –such as the transition from dinosaurs to birds, the development of the mammalian middle ear and temporomandibular joint, or the emergence of human grasping capabilities—advanced quantitative methods are required to bridge the gap between neontological and paleontological data. High resolution contrast imaging of adult human and primate hands reveals 3D architecture of intrinsic hand muscles and their moments about joints of our thumb. We can visualize the sensory nerves of bird beaks or deep protractor muscles of the palate which maintain neuromuscular control of characteristic avian cranial kinesis. We can demonstrate vestigial connections between pterygoideus muscles, the TMJ articular disc, and their insertions onto the malleus in developing mammals.

A primary difficulty lies in the integrated characterization of bone and soft tissues across scales, from microscopic cellular structures to entire organisms.

To address this challenge, we present a multi-modal framework including DiceCT, MRI, and serial section histology, enabling tissue visualization at sub-cellular resolution within the context of complete anatomical structures such as whole heads. The whole-head histological approach is new, and utilizes tape-transfer assisted serial section histology. This methodology greatly reduces the geometrical section-to-section distortions inherent in conventional histological processing and permits assembly of 3D histological atlases. It is able to deal with hard as well soft tissues at the same time, which is not possible using tissue clearing based fluorescent imaging approaches.

Acquiring these datasets is only a first step—analysis of the large multi-scale imaging data sets pose significant challenges, and without advanced methods to address these challenges the full potential of the data cannot be met. We utilize computational methods and human-in-the-loop machine learning to automate analysis and annotation. We demonstrate this approach through three case studies: primate limb biomechanics, avian craniofacial evolution, and mammal head development. For the latter cases, integrated histology and imaging provide unprecedented, comprehensive views of the musculoskeletal system, central and peripheral nervous system, and other organ systems in the head.

By employing a spectrum of advanced computational methods including differential geometry and machine-vision algorithms, we show how these tools accelerate the work of human experts and are crucial in deriving the full value of such data.

Diffeomorphic mapping allows cross-modal, cross-scale integration of volumetric imaging data using CT/MRI with 3D histological volumes. Machine-vision assisted auto-segmentation of the image data greatly facilitates human experts in annotating the 2D and 3D imaging data. Together, these three case studies showcase how emerging computational methods illustrate the potential of this approach for 3D anatomical visualization, analysis, and modern evolutionary biology.

Reconstruction of extinct bush-cricket calls based on fossilised wings reveals ultrasonic communication in the Jurassic

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A salient feature of biodiverse habitats is the acoustic landscape, which reveals key animal interactions and their ecologies. Very little is known about the acoustic landscape of long-gone environments, such as the Jurassic forests. The sounds made by dinosaurs and other charismatic vertebrates are not definitively known because their vocal organs rarely preserve well in fossils. Unlike tetrapod vocal cords, the sound-producing organs present in the sclerotised cuticle of some arthropods do fossilise well. For example, the stridulatory structures (file, plectrum) can be observed and measured in the fossilised forewings of male katydids and allies. These fossils incorporate a fingerprint of the acoustic signals they generated, offering a unique window into the soundscapes of the past. Call frequencies can be inferred from fossilised wings using phylogenetically informed predictions, yet the reconstruction of wing vibrations and the songs' temporal patterns from fossil material remains elusive. Integrating phylogenetics, biomechanics, numerical simulations, and an AI-based approach, 20 ensiferan fossils (representing nine species) from a single location (Jiulongshan Formation, Inner Mongolia, China) were studied to recreate the acoustic landscape of the Middle Jurassic. These early singing insects produced pure-tone calls, an adaptation to avoid localisation by eavesdropping predators. These species also exhibited rich diversity in their calling song frequencies and call repertoires, facilitated by specialised file morphologies and variation in wing size. While most species communicated using low frequencies, one species likely broadcast ultrasounds (>20 kHz). These findings support the hypothesis that ultrasonic communication in insects was established long before the emergence of bats, which appeared as fossil records in the Eocene. Analysis of mammalian hearing thresholds through time unveils potential undocumented coevolutionary pressures and constraints exerted by eavesdropping predators, prior to the evolution of echolocating bats. The arms race between ensiferan singing and auditory capabilities of early mammals likely constituted one of the key selective pressures driving Jurassic insect song diversity and the evolution of both mammalian and insect hearing systems.

Uncovering the developmental basis of adaptations in extinct and not yet extinct species

Jukka Jernvall, University of Helsinki, Finland

We humans tend to measure things that we can detect. Be it from fossil or living species, the most widely used morphological measurements are size and shape. Especially shape measures use landmarks, marking specific features that make comparisons of wide range of species possible. With the advent of fast-throughput, three-dimensional data acquisition methods, it is now possible to experiment and mine different kinds of morphological measures. Topographic methods capturing aspects of shape allow the linking of morphology to the process of development. Rather than similarities in shapes, topographic measures capture similarities in the process. Tooth enamel is the most highly mineralized tissue in mammals, and principally responsible for the excellent fossil record of mammalian evolution. The uneven distribution of enamel across the occlusal surface often contributes to variation in tooth shape, making landmark-based analyses difficult. I will use extinct and living bears as an example to show how the analyses of dental topography allow the linking of ecology, evolution and development, thereby providing new opportunities for integrative studies.

The benefits and challenges of digitizing the human fossil record

Tracy Kivell, Max Planck Institute for Evolutionary Anthropology, Germany

Micro-tomographic CT (microCT) scanning of fossils provides the ability to visualize and digitally quantify external shape and to reveal internal structures that are otherwise inaccessible. Importantly, microCT data also offer digital “replicas” of priceless fossils for curatorial institutions and facilitates, in theory, global accessibility for scientific study, teaching and public engagement. Although the field of palaeoanthropology—the study of human evolution—has historically struggled to provide access to fossils and to openly share data, this is now improving. In this talk, I will present a brief overview of the ways in which we use microCT data to extract novel information about behavior, age, and species from the internal bone and dental structures of hominin (humans and their extinct ancestors) fossils, primarily from East and South Africa. I will also discuss the challenges and benefits of generating and sharing such large data at local curatorial institutions, and some examples of solutions, such as the Human Fossil Record online archive, that allow institutions to retain curatorial control and credit, maintain their physical collections, and further scientific inquiry.

From dry land to the open ocean: Opportunities and constraints in whales and ichthyosaurs

Lene Liebe Delsett, Norwegian Center for Paleontology, Norway
Faure-Brac, M. G., Natural History Museum, University of Oslo, Norway; Sai, V. S., University of Edinburgh, UK; Alam, P., University of Edinburgh, UK; Chinsamy-Turan, A., University of Cape Town, South Africa.

Over the last 300 million years, between 30 and 60 amniote lineages have become aquatic. It is often stated that they “return to water”, but these animals entered a new habitat altogether, as their reproduction, locomotion and physiology were thoroughly adapted to life on land before moving partly or completely into water. These transitions represent unique opportunities to understand morphological adaptations during habitat shifts, knowledge that is needed in a rapidly changing world. Here, we use whales and ichthyosaurs, among the few lineages that experienced the most extreme such shift, from land to open oceans, to answer what prerequisites, constraints and opportunities unfold in these transitions. We target bone microstructure at two levels: microanatomy and histology, as such data reflect biomechanical forces and physiology and are preserved across time, enabling comparisons between modern and extinct faunas. Recently excavated ichthyosaur fossils and newly stranded whales can then be compared to museum specimens collected two hundred years ago, using a combination of modern and classical tools for analysis. To map locomotory shifts after transition to water, and from coastal areas to open ocean, we analyze vertebral microanatomy using CT data, thin sections and porosity modelling. We find spine stiffening and caudal fluke enlargement in both groups, but also unexpected diversity and more complex patterns, especially in their early evolution. Secondly, we ask whether ichthyosaurs were endothermic and ever evolved corresponding adaptations for ontogeny and growth to whales. Our results indicate instances of deep physiological convergences, but also phylogenetic and developmental constraints.

Towards an integrated understanding of melanin evolution in vertebrate animals: progress in the analysis of fossils and modern analogues

Maria McNamara, University College Cork, Ireland

Melanins are a chemically heterogeneous family of indole-based polymers that are fundamental to life on Earth. They are the most common pigments in vertebrate animals, where they occur as membrane-bound organelles – melanosomes – in many body tissues and in all major vertebrate groups. This wide anatomical and taxonomic distribution reflects varied biological functions. The roles of melanin in visual communication are widely known, but melanin also underpins critical roles in physiology, especially metal homeostasis, photoprotection, oxidant scavenging and immunity. The evolution of this remarkable suite of functions is of increasing interest, and growing evidence for melanin in fossil vertebrates offers the potential to integrate data from extant vertebrates with the fossil record, for a more complete understanding of melanin evolution. Over the last ten years, my work has focussed on the characterization of key melanosome attributes, including geometry, organic chemistry, and metallome, across the entire vertebrate phylogenetic tree, in order to identify which attributes inform on important aspects of biology, including anatomy, ecology, physiology and phylogeny. Complementary analysis of vertebrate fossils from the Carboniferous to Miocene, plus a rigorous programme of fossilization experiments, has shed light on which biologically important melanosome parameters survive in fossils, and under which conditions. These empirical data provide an essential taphonomic framework that allows the fidelity of fossil data to be assessed. Integration of high-fidelity fossil data with our modern dataset on melanosome attributes validates aspects of our evolutionary models, constraining the timing of important evolutionary events, and revealing cryptic events not evident in the modern vertebrate dataset. Despite these advances in knowledge, barriers to progress remain, but these can be overcome by targeted coverage of phylogenetic trees, rigorous characterisation of melanosome attributes, refinement of analytical methods, and a better understanding of melanin preservation in the fossil record.

Reverse-engineering the locomotion of a stem amniote – insights from a multidisciplinary approach.

John Nyakatura, University of Berlin, Germany

Reconstructing the locomotion of key vertebrate fossils provides crucial insights into their palaeobiology and helps illuminate major transitions in vertebrate evolution. Yet inferring locomotor behaviour from fossils remains challenging due to incomplete preservation and the absence of a direct, one-to-one relationship between form and function. *Orobates pabsti* from the Bromacker quarry in Thuringia, central Germany, represents a diadectid—likely the fossil sister taxon to crown amniotes—and is preserved as an exceptionally complete articulated skeleton. The same locality has yielded hundreds of tetrapod trackways, several of which have been attributed to *Orobates*, offering a rare combination of body fossil and corresponding trace fossil evidence. This unique dataset enabled a comprehensive, multi-modal reconstruction of *Orobates* locomotion using both experimental and computer-aided approaches in the framework of “virtual palaeontology.” Beginning with a broad range of plausible postures and gaits, we progressively narrowed the solution space by excluding unlikely locomotor patterns based on quantitative anatomical, kinematic, and biomechanical constraints. The reconstruction integrates analyses of skeletal morphology, joint mobility, and simulated trackway fitting; comparative X-ray motion analysis of extant tetrapods; and the development of a bio-inspired walking robot (OroBOT). Together, these lines of evidence indicate that *Orobates* employed a more advanced, mechanically efficient terrestrial gait than traditionally assumed for early tetrapods. This suggests that relatively sophisticated terrestrial locomotion evolved prior to the diversification of crown amniotes.

SEM-EBSD for studying biomineralisation in extant molluscs: experimental insights and potential for integrating fossil evidence

Kanmani Chandra Rajan, City University of Hong Kong, China

Biomineralisation, the process by which molluscs make shells, evolved independently but convergently. The convergence suggests shared biophysical and biochemical constraints could lead to similar responses with environmental changes. Biomineralisation is sensitive to temperature, pH, seawater saturation state (Ω), and trace elements – environmental factors that leave quantifiable crystallographic signatures in shells. Scanning Electron Microscopy – Electron Backscatter Diffraction (SEM-EBSD), a tool originally used by material scientists, is now widely used for studying the crystallography of biomineralised structures. SEM-EBSD is employed to understand the effect of environmental factors on the degree of control of biomineralisation, particularly in the context of climate change. Several studies on extant molluscs show that biological control shifts from strong crystallographic preferred orientation to weaker, more random orientation under future climate change scenarios (warming and ocean acidification). My research on *Magallana hongkongensis* biomineralisation under ocean acidification (OA) shows a different pattern. These Hong Kong oyster species show resilience to crystallographic changes and maintain strong preferred crystallographic orientation in their shells, even under extreme OA (pH 7.4, ~2300 μ atm CO₂), demonstrating that different species could respond differently to environmental change. This species-specific resilience raises a critical question: do other molluscs show similar resilience, or have different lineages diverged in their crystallographic responses? To effectively predict how biomineralisation will be affected in future climate scenarios, and understand the evolution of biomineralisation, it is crucial to integrate evidence from fossils of past climate events. In this talk, drawing from my experimental OA research on oyster biomineralisation and other published studies on fossils, I will present how SEM-EBSD can help answer two interconnected questions:

Complexity Begets Simplicity: Self-Supervised Learning for Palaeontological Images with Few or No Labels

Niall Rodgers, University of Edinburgh, UK

Palaeontology has seen widespread and growing use of machine learning to classify and analyse large datasets of fossil images. However, palaeontology is a challenging field in which to apply machine learning. Datasets may be small or unlabelled, images may be complex and different from standard datasets and palaeontologists may lack specialist training and access to large computational resources. We show how these challenges can be addressed by utilising recent developments in self-supervised learning (SSL). Using a frozen DINOv3 feature extractor and a simple linear classifier, with reduced data, we can achieve comparable results to literature benchmarks using Convolutional Neural Networks (CNNs), the previous standard, when classifying fossil tracks, pollen, radiolaria, foraminifera and a dataset of diverse fossil images. Moreover, the rich feature vectors generated by the model can be used for few-shot learning, unsupervised clustering and quantification of disparity. Using state-of-the-art self-supervised methods, sourced directly from high-level Python packages, increases accessibility by reducing code, compute and data required. It also maintains accuracy, while increasing reproducibility by reducing parameters and allowing simple future-proof model agnostic pipelines which may become the new standard approach in palaeontology. We also hint towards further developments in easily accessible large pre-trained models which could be useful for paleontological data.

New insights into the evolution of early land plants using computational image analysis

Ana Julia Sagasti, University of Edinburgh, UK

C. Jill Harrison, University of Bristol, UK; Rieko Fujinami, Kyoto University, Japan; Tom Beeckman, Ghent University and VIB Center for Plant Systems Biology, Belgium; Alexander J. Hetherington, University of Edinburgh, National Museums Scotland and Royal Botanic Garden Edinburgh, UK.

The Lower Devonian Rhynie chert (Scotland, UK) contains the oldest in situ preserved terrestrial ecosystem and represents a unique window into the early evolution of land plants. The siliceous geothermal activity led to the exceptional anatomical preservation of plants and microorganisms. Species from the Rhynie chert hold key phylogenetic positions, providing insight into the origin and early evolution of plant innovation and development. Taking advantage of these unique fossils, we present advances in two projects focused on *Aglaophyton majus* and *Rhynia gwynne-vaughanii*. By combining Fluorescence Lifetime Imaging Microscopy (FLIM) and Confocal Laser Scanning Microscopy (CLSM) with AI-assisted cell segmentation algorithms, we have been able to tridimensionally reconstruct the structure of the shoot apical meristems (SAM) of these species. The SAM is a localized region of tissue which, by cell division, adds new cells to a plant resulting in an increase in length of the stem. Our new reconstructions provide insight into the evolutionary steps on the evolution of SAMs by identifying differences in the structure of the meristems of these species. In our second project, we leverage the extraction of large fragments of axes to quantify stomata and epidermal patterning in these leafless species. Using light images of the extracted axes, we created unwrapped models of the epidermal surface and positional coordinates for stomata to test density and distribution. Our results show that stomata are distributed around the full cylindrical surface of axes and aligned with the growth direction. Moreover, stomatal density is highly variable within species, significantly lower than previous estimates and much lower than in modern leaves, and lacks a correlation with axis diameter. We then built on the cellpose cyto3 model for cell segmentation by training it with a dataset of epidermal images of *A. majus* and *R. gwynne-vaughanii* to extract cell areas and shape descriptors. Our statistical analysis of cell size and shape confirms the presence of subsidiary cell-like cells in both species. This combined evidence suggest that a robust and complex epidermal patterning mechanism was present in *A. majus* and *R. gwynne-vaughanii*. Our work shows the potential of AI-assisted segmentation tools for the study of fossils and how it can provide essential insights and help us address key questions in the evolutionary history of plants.

The challenges of data sustainability: Lessons from the Global Biodata Coalition

Philippe Sanseau, Global Biodata Coalition

Abstract: Open biodata is foundational to life sciences research, innovation, biotechnology, and AI-enabled discovery. Its economic impact and scientific value are well established and have been quantified multiple times, yet the infrastructure supporting biodata resources remains vulnerable and lacks resilience. Several structural challenges underpin this observation. To address those, the Global Biodata Coalition (GBC) was established offering a forum for funders across the world to discuss and identify solutions. In addition, the GBC is exploring with pilots concrete approaches to address sustainability and offering relevant analyses to inform funders decisions. The overall and ambitious vision is to achieve a globally coordinated, resilient, and sustainable biodata ecosystem that supports open life sciences research and meets the scientific needs of users. In this presentation, I will discuss what have been the learnings so far, the changes for the GBC in 2026 and its future priorities.

Morphological Data Analysis of Natural Objects

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Abstract: Morphological variation preserved in the fossil record provides a unique window into evolutionary history, adaptation, and diversification across deep time. Statistical shape analysis has emerged as a powerful framework for quantifying, comparing, and modeling biological form while accounting for variation within and among populations. Recent advances in this field have expanded shape analysis beyond traditional landmark-based methods to include the analysis of curves, surfaces, and complex anatomical structures. This talk will provide an overview of modern statistical shape analysis, highlighting developments in geometric representations of morphology, shape registration and alignment, statistical modeling of shape variability, and the simulation of morphological forms. Particular emphasis will be placed on methods that enable rigorous comparisons of objects despite differences in size, orientation, preservation, and incomplete anatomical information. Potential applications to paleontology include quantifying morphological disparity, reconstructing evolutionary trajectories, identifying taxonomic relationships, studying functional adaptation, and investigating macroevolutionary patterns across geological timescales. By integrating geometry, statistics, and computational modeling, these approaches provide new opportunities to extract biological and evolutionary insights from fossil morphology and to better understand the relationship between form, function, and evolutionary change.

Windows to the past: the functional evolution of trilobite eyes

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The evolution of vision revolutionised how animals interact with their environment. However, studying vision and its interactions with evolutionary processes typically relies on inferences from living species because eyes often fossilise poorly. Trilobite eyes are a rare exception as their lenses are made of calcite. Trilobites first appeared during the Cambrian explosion (~520 mya) and became the most speciose animals on Earth, representing the oldest preserved eyes and providing an unparalleled record of eye evolution over >270 million years. The relationships between trilobite vision, evolution, and ecology have been subject to much discussion, but large-scale comparative approaches have been historically challenging due to the painstaking nature of data acquisition from hundreds or thousands of lenses in 3D. The recent revolution in the digital analysis of compound eye structure offers a fresh route to tackling these questions, but has not yet been applied to trilobites. As part of a new HFSP-funded project, we will integrate palaeobiological, functional morphology, and biomimetic engineering approaches to reconstruct how trilobite eyes saw their ancient ocean habitats, how they were shaped over geological time, and how they interacted with processes such as speciation and extinction. This approach will unlock the longstanding mysteries of trilobite vision, generating new insights to how the first complex eyes saw the world over half a billion years ago.

The physiological dimension of the Cambrian efflorescence

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The Cambrian efflorescence, often inaptly termed the “Cambrian explosion”, was a 10 MY long proliferation of novel forms of animal life emerging roughly 540 MY ago. The Cambrian efflorescence marking the beginning of the Cambrian period, when the major animal phyla were established. The emerging life forms of the Cambrian efflorescence saw the proliferation of hard body parts, development of coherent nervous and sensory systems, new forms of mobility, and other innovations. Various reasons have been given for the origins of this remarkable event, most involving response of life to “top down” drivers of evolution, including global changes in ocean acidity, or changing levels of atmospheric oxygen. These explanations do not account for life’s novel form of agency. I lay out an alternative argument that puts the real origin of the animals at the Ediacaran period, roughly 100 million years prior to the Cambrian efflorescence. The novel event there was the invention of the epithelium among the Ediacaran biota, and the novel forms of physiology and form that epithelia enable. These include new forms of partitioning internal environments, the ability to generate internal hydrostatic pressures, new ways to fold and nest epithelia and produce novel body forms. This physiology-based model also introduces a form of agency into evolutionary thinking that is absent from the common “top down” models for the Cambrian efflorescence, and from the prevailing Darwinian conception of evolution. Using the novel forms of form and function that originated with the Ediacaran biota, I outline a model for purposeful evolution that relies on the largely misunderstood and widely trivialized concept of homeostasis.

Monsters of the apocalypse: fossil teratology reveals how brine-driven metal pollution shaped the global Palaeozoic oceans

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The middle Palaeozoic palaeobiodiversity record is riddled by several large extinction events that decimated various clades of marine organisms, and that were accompanied by large disruptions of the oceanic carbon cycle, recorded as marked stable carbon isotope excursions. Despite this strongly held linkage with the C-cycle, the fundamental cause-and-effect relationships that underpin these events have long remained obscure. Here, we present a synthesis of our palaeontological (chitinozoan, conodont), geochemical (Sr-isotopes, trace element geochemistry of microfossils, pyrite-grains and whole rock) and ore-mineralogical data of exhalative (sedex) Zn-Pb deposits. We accumulated these integrated paleobiological-geochemical data over decades of research, across various events, timescales and palaeogeographic areas. Taken together, these independent lines of evidence indicate that repeated venting of metalliferous hydrothermal brines into the ocean is the most parsimonious explanation for these ancient extinction events. One of the milestones during this revelation has been the discovery of peak occurrences of severely malformed organic-walled fossil plankton at the onsets of the extinction events. These deformities were metal-induced and can serve as palaeo-biomonitoring, testifying to the primary nature of the geochemical signatures. Combined, our research identifies metal pollution events of the ancient global ocean, that served as kill-mechanisms during marked episodes of steep palaeobiodiversity decline, and that left behind strongly metal-enriched horizons in the Palaeozoic record.

Expanding engagement through specimen digitization, 3D modeling, AR technology, and 3D printing of Hong Kong Biodiversity Museum Specimens

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Museum specimen digitization is a rapidly growing practice, with considerable potential for cataloguing, research, and public access to museum collections. The Hong Kong Biodiversity Museum (HKBM) boasts Hong Kong's largest natural history collection, >55,000 specimens across the taxonomic spectrum, from plants to insects to vertebrates. However, constraints to space, funding, and manpower, pose challenges to sharing our resources. In a joint project, we are building a digital collection to expand collection accessibility and create new avenues for public interaction and anatomy education, using a diversity of approaches for interacting with 3D data. We have produced more than 30 CT/microCT scans of dry specimens, primarily skulls, and utilized open-source software (e.g. 3D Slicer, Blender) to create 3D prints for hands-on experience. From our data, for example, we generate up-scaled 3D-printed models to interactively teach CityU anatomy students cranial nerve pathways. Partnering with local start-up OAO and Scan the World (STW), we use their scanning and visualization platforms (e.g. OAO's GIMII app) to generate and annotate models of taxidermy, skeletal and wet dissected specimens. GIMII's AR capabilities and STW's 3D engine give museum guests and students opportunities to explore items that cannot be easily physically displayed (e.g. the museum's largest specimens), with STW's browser-based platform allowing integrated annotation, commenting, and LLM-powered interaction to support multi-user, fully navigable, 3D-scanned environments with drag-and-drop model placement. We discuss how digitization is allowing the museum to modernize, reach a broader audience and transcend limitations, outlining expansion of resources in classes and museum exhibitions.



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