AI in Archaeology & Bioanthropology

SYMPOSIUM

2025

Book of Abstracts

M1 ARCHAEOLOGY, SCIENCES FOR ARCHAEOLOGY

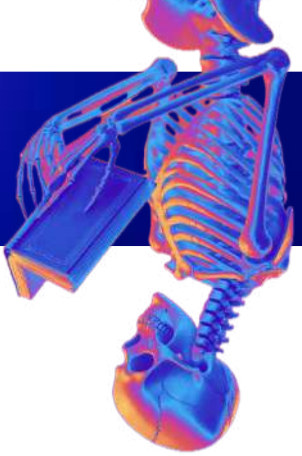


TABLE OF CONTENTS

WELCOME WORD

THE M1 STUDENTS OF THE MASTER ARCHAEOLOGY, SCIENCES FOR ARCHAEOLOGY (ASA) OF THE COURSES BIOLOGICAL ANTHROPOLOGY (AB) AND ARCHAEOTHANATOLOGY (AT) ARE DELIGHTED TO WELCOME YOU TO THE **9TH EDITION OF THE SYMPOSIUM**, AS PART OF THE TEACHING UNIT "FONCTIONNEMENT ET VALORISATION DE LA RECHERCHE". THIS UE DEVELOPED BY PRISCILLA BAYLE AND CHRISTINE COUTURE AIMS TO OFFER STUDENTS A FIRST EDUCATIONAL IMMERSION IN THE WORLD OF SCIENTIFIC RESEARCH, THROUGH A SUPERVISED PRODUCTION OF AN ABSTRACT AND AN INDIVIDUAL POSTER, AS WELL AS THE ORGANIZATION OF THE EVENT ITSELF.

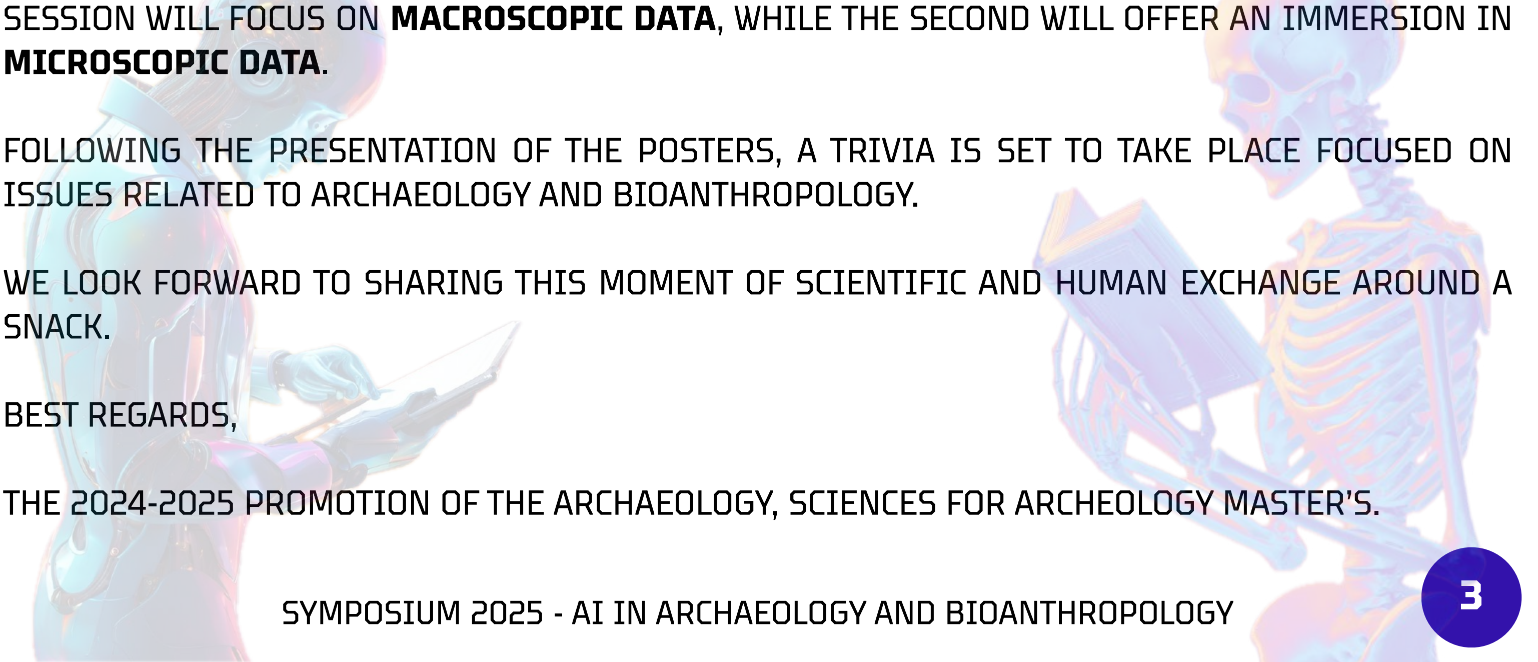
THIS YEAR'S SYMPOSIUM EXPOSES THE "**ACTUAL AND POTENTIAL USES OF AI IN ARCHAEOLOGICAL SCIENCES**". THUS, THE THEME COMPLETELY RELATES TO THE WORLD'S CURRENT SITUATION WHERE AI USE IS INCREASINGLY PRESENT.AS YOU MOVE ACROSS THE POSTERS, TERMS SUCH AS AI, DEEP LEARNING OR MACHINE LEARNING WILL BE CURRENT TERMS YOU'LL SEE.WE THINK A BRIEF DEFINITION OF THESE WORDS COULD BE USEFUL.

ARTIFICIAL INTELLIGENCE (AI) : A SET OF THEORIES AND TECHNIQUES DEVELOPING COMPLEX COMPUTER PROGRAMS CAPABLE OF SIMULATING CERTAIN TRAITS OF HUMAN INTELLIGENCE (REASONING, LEARNING...).

MACHINE LEARNING : A SUBSET OF ARTIFICIAL INTELLIGENCE (AI). THIS TECHNOLOGY AIMS TO TEACH MACHINES TO LEARN FROM DATA AND IMPROVE WITH EXPERIENCE, INSTEAD OF BEING EXPLICITLY PROGRAMMED TO DO SO.

DEEP LEARNING : A SUBSET OF MACHINE LEARNING (ML), WHERE ARTIFICIAL NEURAL NETWORKS (ALGORITHMS DESIGNED TO WORK LIKE THE HUMAN BRAIN) LEARN FROM LARGE AMOUNTS OF DATA.

THE SYMPOSIUM'S 9TH EDITION WILL TAKE PLACE ON **THURSDAY, APRIL 17, 2025 FROM 2:00 PM TO 5:00 PM IN ROOM TD2 OF THE B7 BUILDING**. TWO SESSIONS WILL BE PRESENTED, THE FIRST SESSION WILL FOCUS ON **MACROSCOPIC DATA**, WHILE THE SECOND WILL OFFER AN IMMERSION IN **MICROSCOPIC DATA**.



FOLLOWING THE PRESENTATION OF THE POSTERS, A TRIVIA IS SET TO TAKE PLACE FOCUSED ON ISSUES RELATED TO ARCHAEOLOGY AND BIOANTHROPOLOGY.

WE LOOK FORWARD TO SHARING THIS MOMENT OF SCIENTIFIC AND HUMAN EXCHANGE AROUND A SNACK.

BEST REGARDS,

THE 2024-2025 PROMOTION OF THE ARCHAEOLOGY, SCIENCES FOR ARCHEOLOGY MASTER'S.

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PROGRAM

2:00 PM : WELCOME

2:15 PM : OPENING SPEECH, PRESENTATION OF THIS YEAR'S TOPIC AND SUBTOPICS

2:30 PM TO 4:00 PM : POSTER SESSION

SUBTOPIC 1 – MACROSCOPIC : RECONSTRUCTION AND MORPHOLOGICAL IDENTIFICATION

SALOMÉ BIRAUD - VIRTUAL CRANIAL RECONSTRUCTION IN INCOMPLETE OR DISTORTED PALEOANTHROPOLOGICAL REMAINS AND ITS COMPLEMENTATION WITH IA

FLORENCE LAMOTTE - USING AI TO SIMULATE LOCOMOTOR REPERTOIRES: TOWARDS AN APPLICATION IN AUSTRALOPITHECINES

CORALY LOUIS - THE USE OF ARTIFICIAL INTELLIGENCE TO IMPROVE POST-MORTEM IDENTIFICATION OF SEVERELY DECOMPOSED BODIES BY OVERCOMING THE LIMITATIONS OF TRADITIONAL FORENSIC METHODS

JOSUÉ LOUYA - TOOL ANALYSIS USED IN PREHISTORY THROUGH THE STUDY OF ENTHESES PRESENT ON FIRST METACARPAL, AND POTENTIAL PERSPECTIVES ENABLED BY AI

SEYEDEH PEGA MADANI - APPLICATION OF ARTIFICIAL INTELLIGENCE IN CRANIAL RECONSTRUCTION AND ITS IMPLICATIONS IN GENETIC DISEASE RESEARCH

ARI OTSUKA - SEX AND GENDER IN BIOARCHAEOLOGY, AI SEX DETERMINATION: BIAS AND CRITICS

LOLA RUSPINI - FROM FRAGMENTS TO INDIVIDUALS: USING AI FOR ASSOCIATION AND DISCRIMINATION OF HUMAN REMAINS IN ARCHAEOLOGY

PROGRAM

SUBTOPIC 2 – MICROSCOPIC : TRACING HUMAN FOOTSTEPS IN BIOLOGICAL ANTHROPOLOGY; THE USE OF AI IN MICROSCOPIC STUDIES

CLOÉ CATILLON - RECONSTRUCTING THE KINSHIP RELATIONS OF AVAR COMMUNITIES USING ARCHAEOLOGY, ARCHAEOGENETICS, AND SOCIAL ANTHROPOLOGY

CLOÉ DARNE CLAVARON - NEOLITHIC EPIDEMICS : POTENTIAL USE OF AI FOR PATHOGEN IDENTIFICATION

ALESSIA DE LUCA - THE USE OF ARTIFICIAL INTELLIGENCE IN PATHOGEN IDENTIFICATION

CHARLES DUBOIS - ENHANCING GEOGRAPHIC ORIGIN ASSESSMENTS IN ARCHAEOLOGY : MACHINE LEARNING AND MULTI-ISOTOPE ISOSCAPES, AN OVERVIEW

SARA HERVADA - APPLICATION OF AI FOR VICTIM IDENTIFICATION IN FORENSIC GENETICS

LÉANE LEXTRAIT - ARTIFICIAL INTELLIGENCE IN THE FIELD OF ANCIENT METAGENOMICS THROUGH HUMAN ORAL AND GUT MICROBIOMES: ADVANCEMENTS AND CHALLENGES

3:45 PM : CLOSING SPEECH

4:00 PM TO 5:00 PM : WORKSHOP, IT WILL BE AN OPPORTUNITY FOR YOU TO TEST YOUR KNOWLEDGE IN ARCHAEOLOGY/ NEW TECHNOLOGIES, SOME ANSWERS MAY SURPRISE YOU...

SESSION ONE

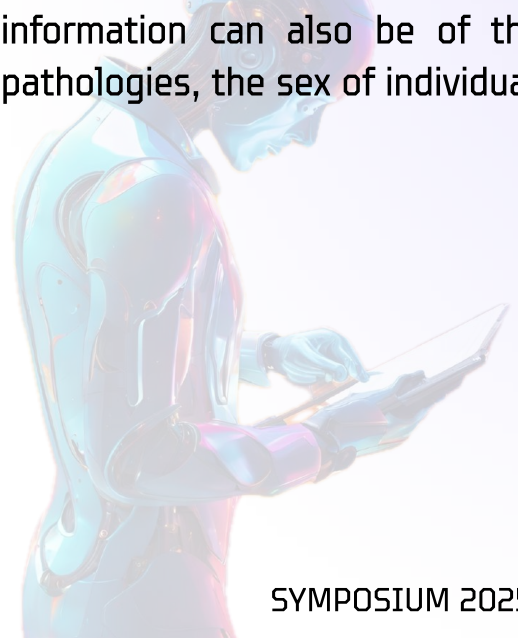
MACROSCOPIC

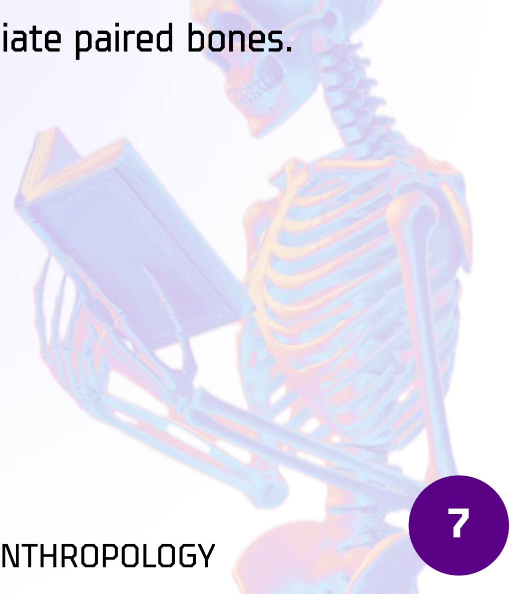
RECONSTRUCTION AND MORPHOLOGICAL IDENTIFICATION

The posters associated with this subtopic will be the **odd numbers** in the poster session !

IN THIS FIRST SESSION WE WILL SEE HOW THE ASSOCIATION BETWEEN **MACROSCOPIC DATA** AND **AI** CAN PROVIDE US WITH A LOT OF INFORMATION IN **BIOANTHROPOLOGY**.

This information can help us to answer some questions that are in the order of **reconstruction**, whether it is to decipher the gait that our distant ancestors could have, to visualize the missing parts of a skull, or in forensic context, to regain the appearance that an individual could have despite the fact that his face is no longer recognizable. This information can also be of the order of **identification**, whether it is that of cranial pathologies, the sex of individuals, their activities, or to associate paired bones.





Virtual cranial reconstruction in incomplete or distorted paleoanthropological remains and its complementation with IA

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Keywords : cranium remains, virtual reconstruction, geometric morphometrics, AI

The discovery of paleoanthropological remains leads to systematic restoration processes, and reconstructive techniques might be applied to them later on. The uncovered remains are frequently incomplete, fragmented or taphonomically distorted, adding a layer of difficulty for the subsequent analyses conducted on them. That is why reconstructing them is sometimes necessary.

New noninvasive methods based on data obtained by high-resolution models tomography scans, combined with geometric morphometrics, are used to obtain 2D and 3D images. These methods allow deepened analyses and virtual manipulation of the fragments, for instance cranial remains, diminishing the danger of damaging the original specimens.

Besides, this approach allows estimating missing or distorted parts by mirror-imaging or deformation on the basis of well preserved fragments to extrapolate at best a complete specimen [1; 2; 4; 3; 5]. 3D imagery can also help to figure out misinterpretations from many physical casts and ancient cranial restorations, influenced by the sculptor's vision and preconceptions, such as the Zhoukoudian skull reconstruction [1; 5; 6]. Some virtual cranial reconstructions are also biased by the assumptions that are being made before the final results, like the perfect symmetry of the cranium or the complete closure of cranial sutures for immature people like Le Moustier 2 [4].

In addition, the virtual aspect of the new methods allows application on immature cranium and to better understand the development of specific morphological characteristics, such as the many found Neanderthal immature specimens [4]. Furthermore, 3D reconstruction can provide functional insights on Early hominin evolution [2] with a correct and partially complete specimen. It also permits the reassessment of ancient cranial restoration like the Ceprano calvarium [6].

These new methods can be improved by the potential help of AI about the different data, using machine- or deep-learning to contrast or validate the confidence level regarding virtual cranial reconstruction. In fact, AI by pipeline of machine-learning is currently being used in the field of medicine for medical cranial reconstruction ; thus, these methods might be very useful in our field in the future [7].

Acknowledgements :

I would like to thank my tutor, **Diego Lopez Onaindia**, who has helped and guided me for this project. I am grateful for his support and his very enriching feedback. I would also like to thank Nicolas Vanderesse for his recommandations, my classmates for their involvement in the preparation of the symposium, but especially Priscilla Bayle for the opportunity she gave us.

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Using AI to simulate Locomotor Repertoires: Towards an application in Australopithecines

Generating Simulations through Musculoskeletal Models and Kinematics based on Fossil Data

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Keywords : Australopithecines, Biomechanics, Bipedalism, Kinematic, Musculoskeletal model

The acquisition of habitual bipedal locomotion is a key feature of hominin evolution. However, the gait of Pliocene hominins, such as Australopithecus afarensis, likely differed from that of modern humans. Understanding these locomotor patterns requires computational approaches that integrate both anatomical [1] and kinematic [2,3] data. Current musculoskeletal models, developed primarily for humans and non-human primates [3], provide insights into biomechanics, but their application to fossil hominins remains limited due to uncertainties in anatomical reconstruction and movement variability [4]. Here, we explore how AI-driven simulations can be applied to generate and analyze locomotor repertoires in early hominins, using musculoskeletal models and kinematic analysis.

A musculoskeletal model was developed, based on fossil skeletal landmarks and comparative anatomical data from modern humans and non-human primates. The kinematic analysis incorporated different sources of experimental locomotor data, such as those from a bipedally-trained macaque [5,6], chimpanzees [7], and modern humans [1,7], to hypothesize on fossil biomechanical constraints. These datasets allowed the estimation of potential gait patterns for Australopithecus afarensis.

The results highlight key differences in locomotor mechanics between species. Non-human primates' bipedalism is defined by limited heel-strike mechanics, higher joint work during swing phase, and less efficient energy transfer than humans. In contrast, A. afarensis exhibits structural adaptations—such as a robust calcaneus and inferred utilization of the inverted pendulum mechanism—suggesting a more human-like gait but with distinct kinematic constraints. [4,5,7]

Despite these advances, fossil reconstructions introduce uncertainties, and intra-specific anatomical and locomotor variability in primates hardens direct comparisons [4]. Additionally, not all kinematic and muscle force data are available in the literature, requiring labor-intensive frame-by-frame analyses. AI approaches offer a solution by automating data processing, improving accuracy, and enabling broader comparative studies. [8] Future developments should refine musculoskeletal modelling, integrate more adapted Ground Reaction Forces (GRF), and expand datasets to better capture the locomotor diversity of early hominins.[5]

Acknowledgments :

I would like to express my sincere gratitude to **Quentin Cosnefroy** for his review, valuable advice, and significant involvement in the research process, including resource selection and detailed explanations of the topic. I also thank Coraly Louis for her careful corrections and insightful suggestions as a reviewer. Finally, I am grateful to Catherine Poutiers-Peytureau for her help in improving the English language of this work.

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The use of artificial intelligence to improve post-mortem identification of severely decomposed bodies by overcoming the limitations of traditional forensic methods

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Keywords : Forensic, AI, Facial recognition, Taphonomy, Identification, Post-mortem

AI is revolutionising forensic science by offering new and innovative solutions for identifying deceased individuals, analysing the cause of death and enabling the reconstruction of crime scenes. In the near future, the use of AI for post-mortem identification will be complementing traditional methods such as dental analysis, fingerprints and DNA, which are not always available.

Research has shown that facial creases persist after death and can be exploited for identification [1]. Using photogrammetry software, the study has enabled the identification of 20 facial creases, including two new creases not documented in the literature [1]. AI-assisted 3D analysis and deep learning algorithms could be applied to automate this process, improving accuracy and speed.

Another study of Michalski et al. [2] used automated facial recognition to identify victims of mass disasters. The method was based on the evaluation of a facial recognition algorithm (cognitec FaceVACS- engine SDK 9.7) on a large set of post-mortem and ante-mortem data. A structured protocol was proposed by Wilkinson et al. [2] comparing post-mortem and ante-mortem facials images on 29 forensic cases, with an overall accuracy rate of 85%, indicating potential effectiveness in forensic science and forensic anthropology. The best results were obtained when several good quality ante-mortem images were available. This protocol is not based on AI, but could incorporate it in the future [3].

In forensic anthropology, AI has also been used to determine the identity of unidentified human remains, estimate age and identify ancestry using morphometric measurements. Machine learning is also been tested on the interpretation of peri-mortem trauma and burnt remains [4]. In forensic pathology, AI makes it easier to identify causes of death such as drowning by recognising diatoms, overcoming the limitations of traditional analyses [4].

Despite its potential, AI faces several challenges, notably its need for vast datasets, post-mortem variations with taphonomy, and ethical issues such as data protection and algorithmic biases [5]. For example, in Michalski et al.'s [2] study, ethical and legal issues were not addressed in depth. Future studies should focus on improving image capture processes and looking more closely at the ethical and legal aspects.

Acknowledgements :

I would particularly like to thank my referee **Eline Schotsmans**, for her time, patience and precious help with my references research and the development of my topic for the symposium.

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Tool analysis used in prehistory through the study of entheses present on first metacarpal, and potential perspectives enabled by AI

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Key words : Musculo-skeletal stress markers (MSM), enthesopathy, morphometry, metacarpal 1, stone tools use

Do the activities carried out by past populations leave traces on their bones? To answer this question, the study of entheses, which are musculoskeletal stress markers (MSM) located at muscle or ligament insertion sites and resulting from repeated microtrauma on the bone, is particularly relevant for analyzing activity related skeletal stress [1]. Here, we will look at the stress on the muscles required for tool use, by studying a paper which analyzed the entheses present on metacarpal I (MTC 1) [2].

The study material consisted of MTC 1 from Australopithecus (n=3), the archaic indeterminate hominin SK 84, H. naledi (n=1), H. neandertalensis (n=5), fossil (n=6) and recent (n=15) H. sapiens, Gorilla gorilla (n=7), Pan troglodytes (n=9), and Pongo (n=9). Entheses were identified and delineated according to the VERA (Validated Entheses-based Reconstruction of Activity) protocol on thumb muscles: Opponens pollicis (OP), Abductor pollicis longus (APL), and First dorsal interosseous (DI1), these last two muscles play an important role during precisions grip [3]. The VERA protocol is mainly based on the analysis of the elevation (including projection and depression) of entheses present on 3D models of bones, quantifying it precisely using various filters that can be applied via Meshlab software. This provides a precise delineation of entheses, enabling geometric morphometric to be applied for multivariate analyses of their 3D shape [4].

The results reveal a clear distinction between non-human apes and recent hominins (H. sapiens and H.neandertalensis) in terms of enthesis size compared with thumb size, suggesting differences in muscle recruitment associated for these two groups. Unlike A. africanus, the proportional size of the entheses of A. afarensis and A. sediba is closer to those of recent hominins than to those of non-human apes. The same applies to H. naledi and SK 84, the latter even falling within the variability of recent hominins. This would confirm that the Lomekwian industry [5] could well have been made by Australopithecus [2].

Artificial intelligence, particularly deep learning, presents a promising avenue for optimizing this type of analysis. While some studies have successfully combined geometric morphometrics and AI for different research purposes [6], this approach could offer an interesting perspective for the study of entheses and MSM.

Acknowledgments :

I would like to thank **Arthur Gicqueau**, for accepting to be my referent and for accompanying me throughout this project by giving me valuable advice and always being accessible. I would also like to thank Priscilla Bayle for the opportunity she gave us to do this formative work and Christine Couture for listening to the presentation of our projects. Finally, I would like to thank all my colleagues who participated in this symposium and made it possible for it to take place.

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Application of Artificial Intelligence in Cranial Reconstruction and its Implications in Genetic Disease Research

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Keywords : Autoimplant, Generative Adversarial Networks , Cranioplasty , Neural Networks

Reconstruction of 3D images of the skull helps scientists study ancient human remains and contributes to the understanding of genetic diseases by identifying structural abnormalities and providing a more detailed analysis of morphological changes that may have affected early human populations.

Techniques such as CT scanning allow for the identification of skeletal markers that are not easily visible through traditional examinations, facilitating the study of conditions like craniosynostosis.

Cranioplasty is a surgical procedure in which cranial implants, or prostheses, are used to repair skull defects caused by trauma, congenital defects, or tumor resection Skull. Reconstruction or Autoimplant encompasses a range of techniques aimed at rebuilding or restoring the skull .[1]

The process begins with data acquisition where images of a defective skull are acquired from the patient using CT imaging. Skull segmentation extracts the skull from a CT images.[4]

Among various deep learning techniques, GANs can be used as a deep learning approach for volumetric shape completion, generating realistic reconstructions of missing skull portions and enhancing implant prediction accuracy.

Generative Adversarial Networks (GANs) is a type of deep learning consisting of two neural networks called the "Generator" and the "Discriminator." These two networks compete against each other to generate new data that are indistinguishable from real data. The Generator network tries to create new data that resembles real data, while the Discriminator network determines if the data is real (taken from the real dataset) or fake (created by the Generator network).

The GAN method has been explored in several studies to repair skull defects and was able to handle more complex defects. For example, Kodym et al. integrated Generative Adversarial Networks (GANs) with Convolutional Neural Networks (CNNs) and demonstrated improved performances in reconstructing skull defects.[2]

AI-powered algorithms, particularly Convolutional Neural Networks (CNNs), offer the ability to handle high-resolution 3D medical data more efficiently and accurately.[2]

The application of Generative Adversarial Networks (GANs) in skull reconstruction has demonstrated significant potential in handling complex defects and improving the accuracy of 3D cranial restoration.

Acknowledgments :

I would like to express my sincere gratitude to my supervisor, Priscilla Bayle, for her invaluable guidance and continuous support throughout this research. Her insights and expertise have been instrumental in shaping this work.
I am also deeply grateful to **Yann Heuzé** for his assistance in selecting the research topic, finding relevant sources, and refining the abstract. His support has been essential to the development of this study.
Finally, I appreciate the resources and academic environment provided by University of Bordeaux, which have contributed significantly to this research.

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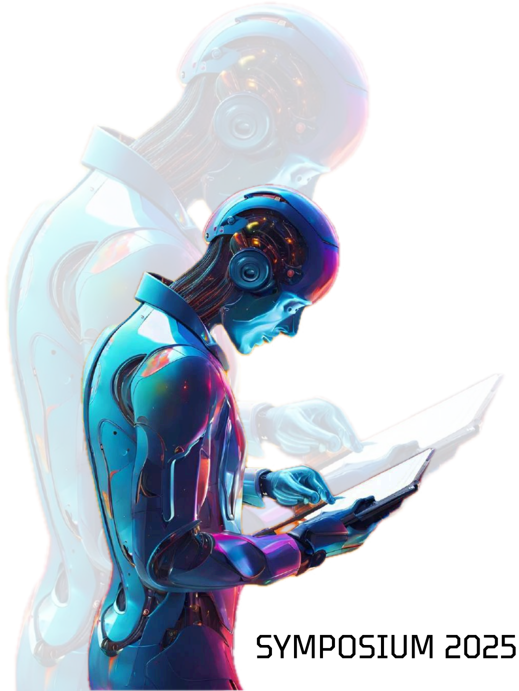

Sex and Gender in Bioarchaeology, AI Sex Determination: Bias and Critics

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Keywords : Sex determination, Gender Archaeology, Bioarchaeology, Bicategorization.

In bioarchaeological analysis, whether gender is studied or not, one of the first steps is usually to determine the biological sex of the individuals. Various methods are used, such as morphological characteristics of dimorphic bones or genetic testing[3][4][5]. This categorization is accepted as objective and is either equated to gender or used as a reference to test the gender against. How could AI (Artificial Intelligence) technology be used to estimate the biological sex and what would be the consequences?

Very recently, new AI-based sex determination methods have been developed. They present multiple appeals: their ability to overcome the subjective side of some morphological approaches, the use of bones considered not to be very dimorphic but often preserved and the quick process of large datasets. As there are numerous methods on a diversity of bones, only one study will be further developed here. An AI based on mimicking the human brain (artificial neural network) was trained on images of human modern skull from medical sources with known sex. It learned without any human input how to categorize the skull in the two predefined boxes, male and female. When tested on images not used to train the AI, they achieved an overall accuracy of 95%.[2]

However, this type of AI analysis has weaknesses, it requires large sets of training data and is a "black box", meaning it is difficult to know how the decision was made [2]. Furthermore, it risks minimizing the variability of both sex and gender by constraining the individuals to a binary system. For example, the agnostophobia of AI, the fear or reluctance of not knowing [6], could wrongly categorize individuals with ambiguous morphological characteristics, and raise the question of intersex individuals. Moreover, the equivalence of gender and sex as well as their independence should be questioned, they are both affected by social and cultural constructs. Researchers have been confronted to the plurality of their definitions, sex can be understood as hormonal, chromosomic, gonadic (etc...) which can sometimes contradict with each other [1][7].

Gender archaeology should be based upon the understanding of intersectionality and the context to apprehend the complexity of past societies.

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From Fragments to Individuals: Using AI for Association and Discrimination of Human Remains in Archaeology

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Keyswords : artificial intelligence, pair-matching, deep-learning, computational archaeology, bones association

Knowing which bones belong to which individual in a large collection of disconnected bones might be a tricky question, especially when those bones are fragmented. Recent advances in Artificial Intelligence (AI) could significantly help archaeologists and bio-anthropologists on this task, as it may allow for automated association of human remains based on their morphology.

For now, AI is semi-potent in placing landmarks on images' important features [1] thanks to deep-learning methods, but it still needs a human check-up to avoid any errors. This speciality is called computational anatomy [2], and could allow researchers to simplify anthropometry (the systematic study of human measurements [3]). The medical field has some of the most complete skeletal anatomy databases, and it could be useful for training such systems. Also, there are AI models, called Convolutional Neural Networks (CNN) that are potent in image processing and recognition [1], as well as detecting major features. This is key for the placement of landmarks.

AI has already been put to use in the archaeological and forensic fields, especially for pair-matching remains of mingled skeletons [4]. This work focuses on the association of similar-looking bones thanks to AI and 3D models. On the opposite hand, there also exists a statistical method for osteometric sorting [5] (pair-matching of long bones antimeres). This approach is based on Quadratic Discriminant Analysis, and separates bones that could potentially be falsely paired with one another. This method only needs the measurements of the bones, which could be provided by computational anatomy. Both methods, association and discrimination, seem to have great accuracy.

A research direction that we didn't take into consideration in this work would be how to pair fragmented bones. An option could be cortical bone analysis [6, 7], but this method needs development.

In the coming years, AI use in biological anthropology will likely lead to the automation of a variety of tasks, whether it is association, discrimination or recognition, hence enabling a more accurate and thorough analysis of isolated human remains discovered in archaeological contexts.

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SESSION TWO

MICROSCOPIC

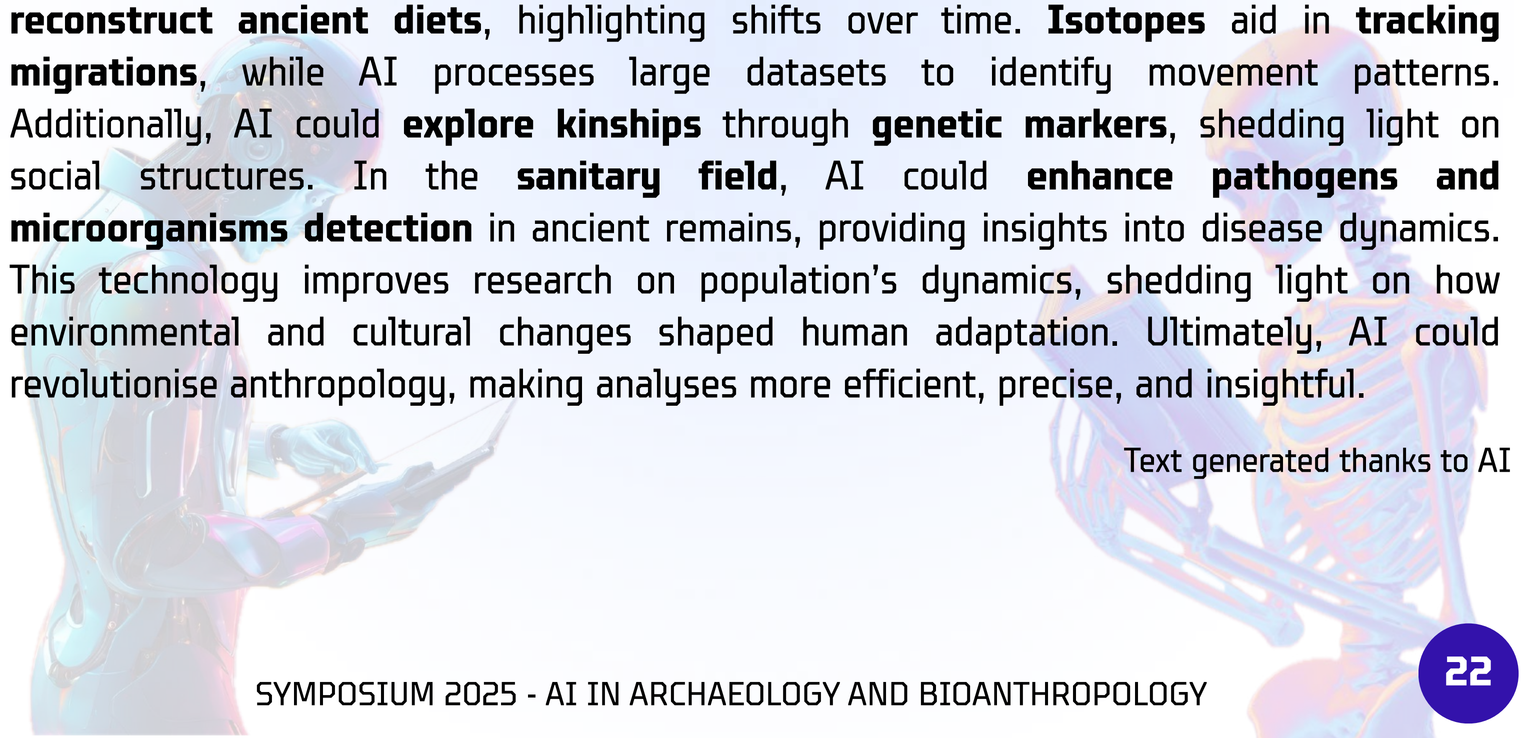
TRACING HUMAN FOOTSTEPS IN BIOLOGICAL ANTHROPOLOGY; THE USE OF AI IN MICROSCOPIC STUDIES

The posters associated with this subtopic will be the **even numbers** in the poster session !

IN THIS SECOND SESSION WE WILL SEE HOW THE ASSOCIATION BETWEEN **MICROSCOPIC DATA** AND **AI** CAN PROVIDE US WITH A LOT OF INFORMATION IN **BIOANTHROPOLOGY**.

Integrating AI in biological anthropology and archaeology offers significant potential to deepen our understanding of past and present populations. By **analysing DNA**, AI helps **reconstruct ancient diets**, highlighting shifts over time. **Isotopes** aid in **tracking migrations**, while AI processes large datasets to identify movement patterns. Additionally, AI could **explore kinships** through **genetic markers**, shedding light on social structures. In the **sanitary field**, AI could **enhance pathogens and microorganisms detection** in ancient remains, providing insights into disease dynamics. This technology improves research on population’s dynamics, shedding light on how environmental and cultural changes shaped human adaptation. Ultimately, AI could revolutionise anthropology, making analyses more efficient, precise, and insightful.

Text generated thanks to AI



Reconstructing the kinship relations of Avar communities using archaeology, archaeogenetics, and social anthropology

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Keywords : Avar, archaeogenetics, biological relatedness, Carpathian Basin, steppe ancestry

Previous studies have stated that the Avars were a nomadic population likely descending from Eurasian steppe populations who settled in the Carpathian Basin during the late 6th century CE [4], and that their empire thrived until the early 9th century, when it fell to the Franks. As to get a better understanding of social organisation in Avar communities, newly published works integrate archaeological, genetics, and anthropological data.

Archaeological evidence from over 600 excavated settlements and burial sites reveals a hierarchical society: high-status individuals were buried with gold and silver adorned weaponry, belts, and insignia, and smaller burial clusters with animal remains suggest cultural links to eastern Eurasian steppe populations [3]. Genomic data from 66 ancient individuals, spanning both pre-Avar (4th–5th century) and Avar (7th–8th century) periods, provide key insights into their ancestry and mobility patterns. An analysis of nuclear DNA confirms that Avar elites had predominantly Northeast Asian genetic profiles, distinct from the preceding West Eurasian populations [3].

Kinship reconstruction using ancient DNA from four cemeteries in Hungary uncovered 298 closely related individuals, revealing a strictly patrilineal descent system [3]. These pedigrees span up to nine generations, demonstrating a social structure based on male lineage continuity, patrilocality, and female exogamy. Furthermore, the absence of genetic inbreeding indicates that Avar society maintained detailed memory of ancestry, while network analysis suggests that social cohesion was reinforced through strategic marital alliances [5]. The Avars exhibited flexible reproductive strategies, including polygyny and levirate unions, practices common among steppe pastoralists and despite political and cultural shifts, these kinship structures remained stable throughout the Avar period [5].

One of the largest cemeteries analyzed (at Rákóczifalva, in the Transtisza region TT, east of the river Tisza and the Danube) experienced a community replacement in the mid-7th century, coinciding with shifts in burial customs and dietary practices. However, genetic continuity suggests that these changes were sociopolitical rather than demographic [2].

These studies provide the most detailed reconstruction of Avar kinship to date, confirming the arrival of entire steppe-descended communities and their persistence in the Carpathian Basin. By combining archaeogenetics with archaeological and anthropological data, these studies reveal the Avars' complex social networks, their adaptive kinship strategies, and their long-term integration into the European landscape.

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Neolithic epidemics: potential use of AI for pathogen identification

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Keywords : Neolithic, epidemic, plague, pathogen, AI

The Neolithic is an important period of transition for humankind. This era is characterised by the development of agriculture, a shift in the subsistence strategies, more densely populated communities and expanding trading networks [5]. With this new way of life, Neolithic societies were likely exposed to new pathogens that could have caused epidemics [6]. Studies suggest that a demographic decline observed in Neolithic populations throughout various parts of Europe, may be linked to the spread of various pathogens such as Yersinia pestis [4].

Modern genetic techniques, particularly ancient DNA sequencing, help us better understand epidemic dynamics and how they spread. Nowadays, partial or complete pathogen genomes can be retrieved from archaeological sources such as teeth or petrous bones [5]. AI is already used in clinical settings to identify a pathogen signature in individuals or clusters and consequently predict the disease trajectory on the rest of the population. Similarly, AI could be leveraged to facilitate pathogen identification in ancient DNA samples. By developing deep-learning models, AI could help identify ancient microbial species by learning the patterns in genetic sequences [1].

To fully understand how societies reacted to these phenomena, the study of burial practices is essential. Periods of rapid mortality increase are sometimes reflected in mortuary sites, where a high number of individuals (particularly young individuals were buried) as well as evidence of mass or unusual burials [2]. Nevertheless we can't always attribute this mass burials to epidemic episodes. Sometimes, the conditions of the remains don't allow us to retrieve ancient DNA. As such we can't determine if a disease surge took place.

When combined with evidence of pathogens linked to specific diseases (such as those found across Scandinavia) we can ultimately support present theories about disease frequency, such as Yersinia pestis or Mycobacterium tuberculosis [3,6], and their geographical distribution.

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The Use of Artificial Intelligence in Pathogen Identification

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Keys words : AI, paleomicrobiology, pathogen, ancient DNA, human evolution

NGS (Next Generation Sequencing) has revolutionized pathogen identification by improving accuracy and speed. AI (artificial intelligence), based on deep and machine learning, precisely identifies pathogens. However, its application in archeology is still unexplored. This raises the question : how would AI contribute to pathogen identification and have other benefits in archaeological context ?

In clinical studies, the use of AI enhances accuracy and speed by using pre-existing experimental data of known organisms to identify structural similarities in genomes of lesser-known pathogens [1][2]. Furthermore, we were able to develop deep-learning models that identify and structurally characterize protein-protein interaction to help understand pathogenicity mechanisms, by looking into residue-residue co-evolution and protein structure prediction [2][4]. Thus, the application of these methods in archaeology have provided valuable information on past bacterial commensals and pathogens deepening our knowledge about ancient human life and infections. As an example, HOPS (Heuristic Operations for Pathogen Screening) , an automated bacterial screening pipeline for ancient DNA sequences, is a versatile tool to identify bacterial candidates [3].

Moreover, NGS is currently used to produce phylogenomic reconstruction of pathogens, by analyzing a large amount of data which can be a long process. AI accelerates the research by automatizing the analysis [1]. In archaeology we commonly use NGS like HOPS and Kraken2 to identify pathogens, by sequencing their genomes and finding their taxa.[3][5]. The understanding of the phylogenetic relationship between mutated microorganisms is a way to track human migration [5][2].

Despite its potential, AI faces several challenges like the need of big datasets that can lead to bias if their quality is low [1], and the risk of contamination is elevated [2]. To minimize such environmental contamination and accurately authenticate ancient DNA, many rules were established like the use of a dedicated ancient DNA laboratory [6]. However, AI also has downsides, it requires 3 times more computer resources to function at its best [4] than NGS, making it quite expensive and environmentally catastrophic.

Future developments of AI in archaeology can be possible by adapting the protocols, they should focus on creating models of pathogens evolution and its impact on our genome.

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Enhancing Geographic Origin Assessments in Archaeology : Machine Learning and Multi-Isotope Isoscapes, an overview

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Keywords : Isoscapes – AI in Archaeology – Ancient human mobility – Multi-isotope analysis – Predictive isoscape modeling

Isotopic analysis of archaeological remains has long been used to study past human migrations. By incorporating multi-isotope isoscapes, machine learning enhances the precision of geographic origin estimations, providing deeper insights into ancient human mobility.

Machine learning is a powerful method for enhancing the accuracy and spatial resolution of isoscapes, especially in cases where isotopic data are incomplete or scarce [1]. An isoscape is a geospatial model representing the geographic distribution of isotopic variations across a given region . Isotopic isoscape maps are widely used in fields such as geology, ecology and anthropology, to trace the origins of materials, animals and human remains. By integrating diverse datasets, machine learning algorithms optimize the prediction of isotopic distributions across landscapes, even in areas with limited available data. The models generated through machine learning uncover correlations between isotopic variations and environmental factors such as geology, climate and hydrology, allowing the generation of high-precision isoscapes [2].

When applied to multi-isotope frameworks — specifically Strontium (87Sr/86S), Oxygen (δ18O) and Sulfur (δ34S) in this case study — machine learning provides a more robust tool for provenance analyses [3]. Strontium isotopes reflect the geological composition of a region and are commonly used to determine whether an individual was local or non-local to a given area. Oxygen isotopes, largely influenced by climatic and hydrologic conditions, provide insights into water sources consumed by past populations, making them valuable for reconstructing mobility patterns. Sulfur isotopes, influenced by factors such as the proximity to marine environments, offer further insight into geographic origin and ecological conditions [4]. By analyzing and modeling the complex interactions between these isotopic signatures, machine learning enhances the precision of geographic origin assessments.

In archaeological research, this method, highlighted by the present poster, significantly advances the reconstruction of past human mobility by refining geographic provenance estimation based on isotopic signatures preserved in skeletal and dental remains. [5]

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Application of AI for Victim Identification in Forensic Genetics

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Keywords : “Artificial Intelligence”, “Human identification”, “Genetics”, “ Disaster Victim Identification (DVI)”, “Forensic”

Artificial Intelligence (AI) is rapidly becoming a powerful tool across various disciplines, including forensic genetics. It is particularly valuable in Disaster Victim Identification (DVI), providing rapid and automated solutions that are crucial in emergency scenarios [1]. DVI compares post-mortem DNA samples with ante-mortem references from personal items or relatives [2].

Beyond DVI, AI plays an expanding role in forensic genetics as scientific research demonstrates. AI assists in haplogroup analysis, refines STR profiling and improves DNA classification by correcting errors and interpreting allele peaks more accurately [3]. Machine learning (ML) models enhance genetic relatedness predictions [4], with some achieving high accuracy levels. Others may prove useful in distinguishing different DNA profiles within mixed samples. Systems like the ParaDNA intelligence network and other artificial neural networks have demonstrated the ability to interpret DNA profiles with up to 99% reliability. Rapid DNA technology, such as the ANDE system [5], generates STR profiles in under two hours, significantly improving response times in mass disasters [6][7].

Additionally, AI-powered genetic genealogy is emerging as a powerful forensic tool, integrating DNA analysis with genealogical research to identify unknown individuals [8]. It relies on single nucleotide polymorphisms (SNPs) for more precise ancestry tracing, expanding forensic identification capabilities. Public databases such as GEDmatch facilitate DNA comparisons, enabling law enforcement to establish familial connections and solve cases where traditional methods have failed.

Despite its potential, IA in forensic genetics faces challenges. For instance, biases in training data can lead to misidentification. Ensuring algorithm transparency and fairness requires training AI on bigger and more diverse datasets and implementing counterfactual fairness to prevent demographic disparities. Additionally, researchers must be aware of each system’s limitations and select the most suitable machine learning model for their specific objectives. At last, AI is transforming forensic genetics by enhancing speed, accuracy, and efficiency in DVI and criminal investigations. While AI significantly improves forensic investigations, continuous validation and ethical oversight are essential to ensure its responsible and effective use. As AI continues to evolve, further research will be crucial in unlocking its full potential in forensic applications.

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Artificial Intelligence in the field of ancient metagenomics through human oral and gut microbiomes: advancements and challenges

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Key words : metagenomic, human microbiome, taxonomic classification, artificial intelligence, deep learning

Lately, studies about ancient human microbiomes have been multiplying, giving many insights on past societies and their health, diet, and epidemic outbreaks. For example, researchers discovered that during the Iron Age people were producing and consuming beer [1], and that the dietary shifts introduced by the Neolithic transition resulted in an increased abundance of oral pathogens [2]. The oral microbiome is easily accessible through teeth and dental calculus, which is less sensitive to taphonomy and better conserved through time as compared to other human remains [3]. On the other hand, the gut microbiome is studied using coprolites, fecal remains fossilized due to unusual and extraordinary conditions that must occur for its conservation [4].

Metagenomic analyses conducted on these types of samples still present significant challenges, such as the slow process of building reference databases and the extensive storage space required for their use. Another major issue concerns coprolites. The large number of elements they contain makes them the most suitable material for studying ancient diets, however, they are rare compared to the ubiquity of teeth [5]. These current issues lead to the question of whether artificial intelligence (AI) could offer some solutions. Two tools using convolutional neural networks, which are important for pattern recognition, and classification, have come to light in recent years, G2S and DL-TODA [6]. These tools have been trained on NCBI reference sequences identified in oral and stool samples for G2S [3], and complete bacterial genomes from microbial species found in oral and soil samples for DL-TODA [7].

The results demonstrate that DL-TODA improves the accuracy of taxonomic classification. In addition, DL-TODA reduces analysis duration by removing the database construction step [7]. Furthermore, G2S predicts taxonomic abundance, at the family rank, of the gut microbiome based on the taxonomic composition of oral samples [3].

The emergence of these AIs tools provides improvements in the analysis of modern samples, but they could be also applied to ancient microbiomes with modifications. Overall, these AI tools could improve ancient metagenomic analyses, by increasing the accuracy of taxonomic classification, and predicting ancient gut microbiome composition from oral samples, which would constitute major advancements in the field.

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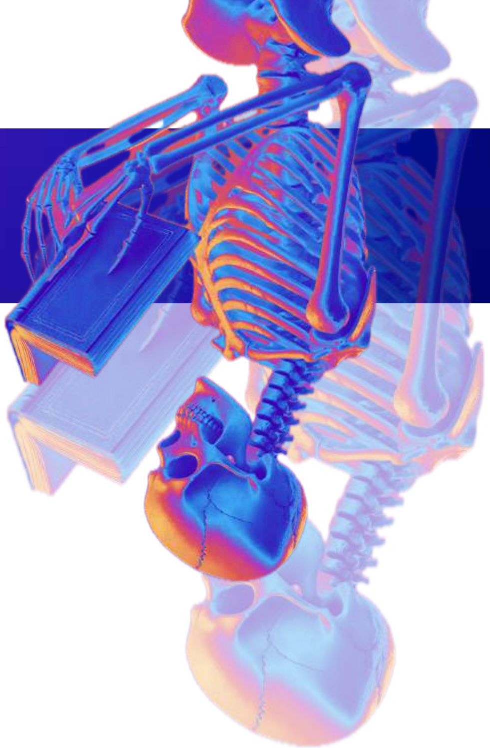

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