LLM-augmented taxonomy for >4500 palaeopalynology genera

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Abstract

Large Language Models (LLMs), being text-based, are ideal types of artificial intelligence to consider the complexities of palaeontological taxonomy because palaeontology depends on published textual descriptions as the primary, authoritative record of a taxon. This paper describes (1) the preparation of palynological (the study of organic-walled microfossils) taxonomic text contained within the >4500 genera of the Jansonius and Hills palaeopalynological catalogue (JHC) for an LLM-augmented taxonomy system (LATS), (2) the efficiency and accuracy of the LATS, and (3) examples of possible further uses of the LATS beyond aids to identification. The conversion of the JHC into a LATS is typical of the challenges of making so called 'long tail' data suitable for AI development and can involve considerable manual checking. Principles of development include (1) 'inclusion', that is, making sure that the LATS as far as possible includes rather than excludes candidate genera; (2) the principle of 'assistance' rather than supplantation so that the LATS is intended as an aid to taxonomy, not a replacement for a human taxonomist; and (3) the principle of 'non-intervention' whereby no alterations to original authoritative genus descriptions or diagnoses are applied. Training for the

dataset involved 500 Question/Answer pairs generated for the JHC by specialists, as well as additional synthetic QA pairs which, combined, were used to supervised-fine tune the LLM.

The LATS functions through Retrieval Augmented Generation and returns candidate genera with statistical measures of match against the prompt(s). Access to full descriptions of genera extracted from the JHC and to scans of the original catalogue cards allow the taxonomist to use their own judgment in final identification. The LATS produces generally good results but there are two types of limitations or shortcomings: those that emanate from the JHC (and palaeopalynological taxonomy itself), and those that emanate from the working of the LATS. Limitations due to the JHC include (1) poor potential for discrimination between some genera because of poor original descriptions which have not been subsequently emended, (2) numerous candidate genus names that may be synonyms, and (3) invalid candidate genera, i.e. that were illegitimately published. Limitations that emanate from the working of the LATS include evidence of bias against finely described genera.

As well as providing a LATS to aid a palynologist through the stages of identification, the information and 'understanding' that the underlying system has of a large area of palaeopalynological taxonomy means that the system could be put to more general uses for example in the identification of genus names that are likely synonyms, and investigation of the distribution of genera (or taxa) in 'morphological space'.

The development of the LATS described here has implications for other palaeontological groups in terms of the text basis of their taxonomy (for example variable quality of descriptions and inconsistency in terminology), and their suitability for development of other LLM-assisted taxonomic aids.

Introduction

Palaeontological and palaeopalynological taxonomy aims to classify fossil organisms, provide stable names for unambiguous communication, and organize diversity by placing fossils into hierarchical groups (species, genera, families, etc.) that reflect evolutionary relationships. The determination of a specimen to a taxon requires reference to literature, type specimens, illustrations and photographs.

Early taxonomic keys (e.g. Lamarck 1778) were used as aids to determination and used dichotomous processes that allow the user to choose between opposing pairs of morphological characters; and keys continue to be used for example in botany and zoology (e.g. ZoologyTalks: https://www.zoologytalks.com/types-of-taxonomic-keys/). Text-based palynological keys have been published in archaeological studies (e.g. Hubbard 1992), and in palaeopalynology (e.g. Steemans and Wellman 2018), and several modern pollen identification keys exist: for example, Das et al. (2025) constructed a taxonomic key for Papilionoideae (Fabaceae) from Northeast India. The use of artificial intelligence in identification keys is rare (Yu et al. 2024), an exception being Liu et al. (1994) who constructed a dual-step identification tool with a Knowledge-Based System (KBS) and an image analysis subsystem, which extracted graphic information from foraminifera chambers and suture images in addition to previous shape analysis based on Fourier analysis and edge detection.

Various forms of artificial intelligence have also been used to aid palynomorph identification using image recognition (e.g. Zhang et al. 2004, Rodriguez-Damian et al. 2006, Mander et al. 2013, Kong et al. 2016, Niu et al. 2024, von Allmen et al. 2024) based on learning from very large numbers of high-resolution images of specimens whose taxonomic status were validated by experts, though not by direct reference to authoritative text-based diagnoses or descriptions of taxa. Thus, the expert validations are placed between the user and the first-principle taxonomic information. Though they may supply accurate determinations within that framework, their taxonomic decisions are not visible to the user, and their methods do not offer pedagogic value or insight into processes of taxonomic decision-making.

Large Language Models (LLMs), being text-based, are ideal types of artificial intelligence to consider the complexities of palaeontological taxonomy because palaeontology depends on published textual descriptions as the primary, authoritative record of a taxon (ICZN 1999; Turland et al. 2025). An LLM-augmented taxonomic key was developed for a small dataset of around 70 spore species from the Carboniferous-Permian of the Arabian Plate (Stephenson et al. 2025) as a pilot project. This allowed users to make choices amongst a fixed set of options and then allowed free text prompts to refine the search. Because of the small size and limited applicability of the system, it was not released publicly.

Considering these developments, we investigated the possibility of constructing an LLM based system that would respond to simple descriptive prompts rather than requiring a series of dichotomous or polytomous choices. LLMs 'learn' from extensive text datasets, including books, articles, and websites which helps them recognize patterns in language, grammar, meaning, and context (e.g. Patil & Gudivada 2024). Transformers enable models to weight different words and phrases based on their relationships within a sentence. Text is broken down into smaller units (tokens), which the model processes to predict the most likely next words in a sentence or generate full responses. LLMs generate text by predicting the most statistically probable sequence of words based on their training (Bender and Koller 2020). When applied to palynological identification scenarios, LLMs are also expected to bring several distinct advantages:

1. Unlike many areas of modern biology that can rely on genetics, living specimens, or high-resolution imaging, palaeontology depends on published textual descriptions as the primary, authoritative record of a taxon (e.g. Gravendyck et al. 2021). Under the rules of zoological and botanical nomenclature (ICZN 1999; Turland et al. 2025), a species becomes valid only when it is described in text. Text provides the diagnosis (what makes the taxon unique), the description (its full morphological characterisation), the type

designation (holotype, lectotype, etc.), and the comparisons with similar taxa. All these elements must be written, published, and permanent. Even high-quality plates or photographs cannot capture subtle morphological distinctions and variability, describe internal structures not visible externally, or explain reasoning behind taxonomic decisions. In this sense, text provides the conceptual framework that the images support. Text allows reproducibility and comparison because future researchers must be able to compare new specimens to the original description, evaluate whether a fossil belongs to an existing species, and identify synonyms. Large Language Models (LLMs), being text-based, are therefore ideal types of artificial intelligence to consider the complexities of palaeontological taxonomy because palaeontology depends on published textual descriptions as the primary, authoritative record of a taxon.

2. Human-like interaction and interpretability: unlike image-based identification apps for botany (for example those on an iPhone such as PictureThis®) which function without human interaction in decision making (i.e. they are black-boxes), LLMs can show reasoning and generate human-readable explanations and responses, enabling more interpretation of classification decisions. It also allows the interpretation of morphological details that may not be discerned from a photograph. This capability supports greater transparency and user trust in AI-assisted identification systems.
3. LLMs exhibit strong language comprehension abilities, allowing them to capture subtle semantic distinctions (e.g. Rogers et al. 2021). This is particularly beneficial in identification tasks where subtle differentiation between similar taxa is required, thereby addressing persistent challenges such as ambiguous terminology, short or inadequate descriptions, or continuous variability between taxa.
4. LLMs possess broad world knowledge, including foundational understanding in many scientific domains allowing extraneous knowledge to be brought into taxonomic decision making, for example translation of Latin-based terminology.

The purpose of this paper is to describe the preparation of palynological taxonomic text for an LLM-augmented taxonomy system (LATS) of more than 4500 genera, the efficiency and accuracy of the LATS, and potential further uses of the LATS beyond identification. The LATS is intended for open and free use for all scientists and provides a guide to determination rather than acting as an ultimate arbiter of genus determination.

Preparation of the data

Background

Much data generated by geoscientists is still not accessible to other geoscientists or to artificial intelligence tools (Stephenson et al. 2020). This is a problem for geoscience and other observational sciences which often rely on mixed qualitative and quantitative data that is part of the so-called 'long tail' (e.g. Sinha et al. 2013) – the unstructured and heterogeneous datasets of geological surveys, university research groups, and individual scientists. Palynological taxonomic datasets are often similar: they may have been collected and compiled from the peer-reviewed literature, developed separately from the peer-reviewed literature, or exist only as separate records (diagnoses/descriptions) in the peer-reviewed literature, often behind a paywall. This often hinders palynological taxonomic study and determination of species and genera, because of the size of datasets, their heterogeneity in terms of language, terminology, precision and comprehensibility - and in the case of paywalled information - their inaccessibility.

An example of a large openly available palaeopalynological database is the Jansonius and Hills Catalogue (JHC; 1976 and subsequent updates) of fossil spore and pollen genera. The JHC was created as a series of physical cards - originally one card per genus – and contains more than 4500 spore (fungi, plants and algae) and pollen genera from the Phanerozoic Eon spanning the last 540 million years. This database was created by Calgary palynologists J. Jansonius and L. V. Hills and provides original authorial (i.e., sourced from the peer-reviewed literature) descriptions and diagnoses for these genera, details of the source publications and authors, descriptions of genus type species, and often subsequent genus descriptions, including formal emendations. Taken as a whole, the catalogue is a useful resource which has no other equivalent in palaeopalynology. The physical cards of the JHC were scanned into the form of a PDF in the early 2000s, and are freely accessible online at the Calgary University Library website (https://openlibrary.org/books/OL22388791M/Genera_file_of_fossil_spores_and_pollen). Permission was granted from the Jansonius family and the University of Calgary to proceed with the development. The first 78 pages of the PDF consists of an introduction, genus lists, corrigenda and addenda, and p. 79-5676 are the genera files.

The AI assisted key of Stephenson et al. (2025) was developed for a small dataset, and 'chain of thought' logical steps were embedded in the system through structuring of the learning material (for example in providing sequenced choice stages linked to hierarchical aspects of taxonomy). The approach to the development of a LATS for JHC was different because of the difficulties of pre-structuring such a large dataset of very heterogeneous palynomorph types (fungal spores, vascular plant spores, angiosperm and gymnosperm pollen, algal and other spores). For this LATS, the Retrieval-Augmented Generation (RAG) technique was adapted to search for the best matches based on users' descriptions, incorporating, if necessary, iterative sequences of prompts. (Lewis et al. 2020)

Guiding principles during preparations of materials

A number of principles were decided on before development, these included inclusion, assistance, and non-intervention.

Principle of inclusion

Any taxonomic key or identification system attempts to narrow down possible 'candidates' using information provided by the user (the user's 'prompts'). Many early guides used dichotomous keys, which are classification tools that allow the user to choose between opposing pairs of morphological characters necessitating the rejection of groups of taxa at each point of choice (e.g. Lamarck 1778). In the present system which uses a Retrieval, Augmentation, and Generation (RAG) method, the quality of the initial prompt - in terms of accuracy and detail -determines the numbers of candidate taxa, and the quality of the match between the prompt (the description of the observed specimen) and the candidates. However, both methods of input potentially exclude candidate taxa, if a mistake on the part of the user is made early on. Thus, the system is designed as much as possible to allow a user to backtrack if necessary, and to include rather than exclude candidate taxa; in other words, if in doubt, the system includes rather than excludes candidate genera.

This principle is extended to taxa that are invalid (not published legally in line with ICBN rules). Many of the genera in JHC are invalid in that for example, a holotype was not designated. The system however includes any relevant invalid genera (identified by Jansonius and Hills or identified subsequently) within its candidate lists following a prompt. The genus is noted as invalid but is included for completeness. It is sometimes the case that invalid genera are later validated (for example by designating a holotype) because they are considered useful. Thus, in keeping with JHC, the system is inclusive in the spirit of helping to keep taxonomy transparent.

Principle of assistance

The LATS is intended as an aid to taxonomy, not a replacement for a human taxonomist. The principle followed in the design is that the LATS provides relevant information to allow the taxonomist to make an informed determination. The use of the LATS encourages transparency in that the system provides information at every step; and through regular use, has pedagogic value in that it illustrates how palynological taxonomy proceeds. This contrasts with image recognition systems that essentially recognise visual patterns and do not consider the authoritative text.

Principle of non-intervention

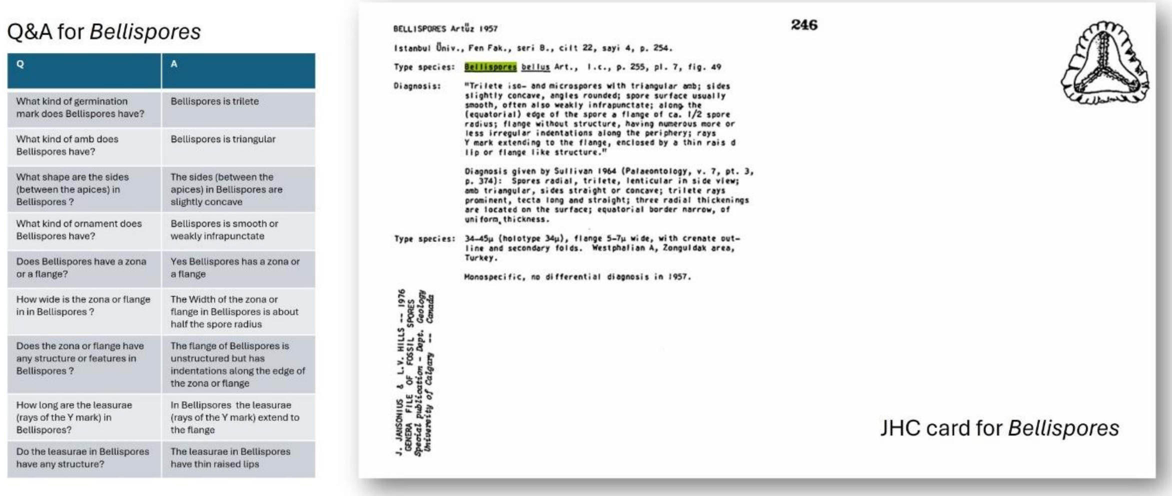
The database developed by Jansonius and Hills is unaltered in the LATS. Although it is possible that improvements to diagnoses (for example making them clearer or more precise) would improve the LATS's discrimination capability, this would involve decisions made by the creators of the LATS, which would be interventionist. Further use of the LATS and the system that underlies it could bring about improvement and rationalisations in palaeopalynological taxonomy (for example by identifying possible synonyms, see later section) but this would have to be done as a community, perhaps at some future date.

Challenges

The first challenge is the quality and non-standard format of the PDF resulting from the scan of the original JHC cards. The text was originally manually typed onto cards in the 1970s and 80s and some of the typed letters are not clear which causes problems for machine recognition. An example is that the machine does not distinguish always between the typed letter "O" and number "0", with the result that the names of genera and their characteristics are sometimes obscured. Similar mistakes occur with recognition of line breaks, non-standard symbols and letters, or letters with umlauts, for example. Correction of these mistakes can be a long, laborious process involving manual checking of OCR (Optical Character Recognition) results.

A second issue is that the quality of original descriptions and diagnoses of genera transferred from the literature into JHC is very variable. There are some excellent comprehensive descriptions and diagnoses of genera erected in the later years of the rapid expansion of palaeopalynology in the 1960s and 1970s, particularly when the science was being taken up by the oil industry. However, many early genus descriptions and diagnoses are very short and sketchy, partly because at the time of their composition, palynology was a young science, and few other genera had been recognised and low levels of detail in descriptions and diagnoses were the norm. Jansonius and Hills also correctly recognised that some genera have been invalidly published, so some names appearing in the JHC are superfluous. Jansonius and Hills often dealt with descriptions and diagnoses in foreign languages by translating them (many are translated from Russian). The variability in diagnosis/description leads to other difficulties of bias and an inability of the system to distinguish genera. This is discussed in a later section.

Inconsistent use of terminology is a third issue. This inconsistency occurs in several forms, for example synonyms for the same ornament element type (verrucae/warts; see e.g. Punt et al. 2007), or more commonly multiple slightly different versions of descriptive terms (spines or spinae; bacula or baculae). Palynological terminology has also developed near parallel systems (e.g. exoexine/intexine, nexine/sexine; cavate/camerate; e.g. Punt et al. 2007) often due to different usage in the different international 'schools' of palynology, and different terminology developed for different time periods (e.g. the Palaeozoic and Cenozoic; Stephenson 2016). Elements of LLM training can alleviate these problems through the creation of 'question-and-answer pairs' because they help the LLM to learn the meanings of terms, their interchangeability and their variability, and how to generate relevant, structured, and context-aware responses (e.g. Wei et al. 2022). For the JHC, two kinds of question-and-answer pairs were developed. The first were structured QA pairs directly anchored in the original diagnosis or description as supplied in the JHC; in other words, the answers to the questions can be found directly within the text. A set of Q&A pairs for the spore genus *Bellispores* is shown in Fig. 1. Most questions are simple: 'Question; What kind of germination mark does *Bellispores* have?', 'Answer; *Bellispores* has a trilete mark'; and the answers can be found directly in the corresponding card/record (Fig. 1). QA pairs must also include similarly anchored compound questions (requiring integration of multiple information), and counterintuitive questions (testing the model's error-correction ability, e.g. 'Is *Bellispores* monolete?'). The simple, compound and counterintuitive QA pairs are used to 'supervised fine tune' the model to expand the word lists for the genera.


Q&A for *Bellispores*

Q	A
What kind of germination mark does Bellispores have?	Bellispores is trilete
What kind of amb does Bellispores have?	Bellispores is triangular
What shape are the sides (between the apices) in Bellispores ?	The sides (between the apices) in Bellispores are slightly concave
What kind of ornament does Bellispores have?	Bellispores is smooth or weakly infrapunctate
Does Bellispores have a zona or a flange?	Yes Bellispores has a zona or a flange
How wide is the zona or flange in in Bellispores ?	The Width of the zona or flange in Bellispores is about half the spore radius
Does the zona or flange have any structure or features in Bellispores ?	The flange of Bellispores is unstructured but has indentations along the edge of the zona or flange
How long are the leasurae (rays of the Y mark) in Bellispores?	In Bellipsores the leasurae (rays of the Y mark) extend to the flange
Do the leasurae in Bellispores have any structure?	The leasurae in Bellispores have thin raised lips

BELLISPORES Artüz 1957 246

Istanbul Üniv., Fen Fak., seri B., cilt 22, sayi 4, p. 254.

Type species: Bellispores bellus Art., l.c., p. 255, pl. 7, fig. 49

Diagnosis: "Trilete iso- and microspores with triangular amb; sides slightly concave, angles rounded; spore surface usually smooth, often also weakly infrapunctate; along the (equatorial) edge of the spore a flange of ca. 1/2 spore radius; flange without structure, having numerous more or less irregular indentations along the periphery; rays Y mark extending to the flange, enclosed by a thin rais d lip or flange like structure."

Diagnosis given by Sullivan 1964 (Palaeontology, v. 7, pt. 3, p. 374): Spores radial, trilete, lenticular in side view; amb triangular, sides straight or concave; trilete rays prominent, tecta long and straight; three radial thickenings are located on the surface; equatorial border narrow, of uniform thickness.

Type species: 34-45μ (holotype 34μ), flange 5-7μ wide, with crenate outline and secondary folds. Westphalian A, Zonguldak area, Turkey.

Monospecific, no differential diagnosis in 1957.

J. JANSONIUS & L.V. HILLS -- 1976
GENERA FILE OF FOSSIL SPORES
Special publication - Dept. Geology
University of Calgary -- Canada

JHC card for *Bellispores*

Fig. 1. A series of QA pairs for the spore genus *Bellispores*

The second type of QA pairs is known as 'incorporate' (e.g. Ouyang et al. 2022); these cover areas of palaeopalynology, for example, basic principles and terminology outside the immediate learning materials, so outside the original diagnosis or description as supplied in JHC. They include questions like 'What are the characteristics of zonate spores?' and 'Describe all the features of monolete spores.' The incorporate QA pairs are similarly used to supervised-fine tune (SFT) the LLM in the broader knowledge of palynology, resulting in improved understanding and interpretation of taxonomic terminology in the genera descriptions.

The embedding model was trained as follows: 1894 more incorporate QA pairs were generated based on the 206 incorporate QA pairs provided by specialists with the GPT-5 model. These generated QA pairs did not alter the meanings in the original question and answer pair but changed the order and manner of the word usage. These QA pairs were then proofread by specialists to make sure that no mistakes were made. For genus-related QA pairs, the LLM learned the patterns of QA pairs created by specialists and generated 18 QA pairs in total for each genus. (6 simple QA pairs, 6 compound QA pairs and 6 counterintuitive QA pairs) Some genera in the JHC have no diagnosis (e.g. *nomina nuda*) and were removed so 69299 QA pairs were used for training.

Among these 2100 incorporate and 69299 genus-related QA pairs, 1000 QA pairs were randomly selected as the test set and Mean Reciprocal Rank (MRR) and Recall were used as evaluation criteria. MRR indicates the quality of the position of the first relevant result in the retrieval ranking under a single query, which can be considered as a measure of the accuracy of the embedding model in semantic understanding. Recall, usually Top-K recall, measures the proportion of all relevant results that are retrieved and included in the Top-K ranking under a single query.

Criteria	MRR		Recall	
Top-K	Before SFT	After SFT	Before SFT	After SFT
Top 1	0.514	0.901	0.514	0.901
Top 10	0.625	0.935	0.846	0.984
Top 100	0.630	0.936	0.943	0.994

Table 1. embedding model performance on semantics of palynological knowledge and professional terminology before and after supervised fine tuning. MRR = Mean Reciprocal Rank; SFT = Supervised Fine Tuning.

Based on the results (Table 1), it is clear that the embedding model better understands the semantics of palynological knowledge and professional terminologies after supervised fine tuning. This improves the evaluation of semantic similarities between user input and diagnosis.

Model construction

There are three major steps in the LATS: (1) understand users' input (prompt) and provide reasonable matches; (2) provide a ranked list of candidates based on the calculated similarity scores between users' prompt and genera diagnoses; and (3) provide tips to improve users' prompts and a suggested refined query or prompt (Fig. 2.). Note that reasonable matches in

Step 1 are generated purely with the LLM and can be minorly varied given identical input. While the list of candidates in Step 2 is provided based on statistical analysis, comparing the user input only with diagnosis at genus level, the LATS would first transfer user input to vectors based on the embedding model, then use cosine similarity to calculate the semantic similarity. (Salton et al. 1975, Deerwester et al. 1990)

$$cos\theta = \frac{\vec{A} \cdot \vec{B}}{\|\vec{A}\| \times \|\vec{B}\|},$$

where the numerator is the dot product of vectors $\vec{A}$ and $\vec{B}$; the denominator is the product of the L2 norms of vectors $\vec{A}$ and $\vec{B}$. Namely, the candidate list would remain the same given identical user input. A threshold is then set to include as many similar taxa as possible, rather than eliminating possibilities, and users can choose to show the top 5, top 10, or top 20 genera only. At this point an 'approximate string matching' or 'fuzzy' search is also possible (Ukkonen 1985, Bast and Celikik 2013). This is a search method that finds results not identical to the query but similar or closely related to it. It tolerates typos, misspellings, missing/extra characters, or minor formatting differences—unlike exact search, which only returns perfect matches.

The LATS is built with the GeoGPT 72B model, which is trained on an open-source LLM Qwen-72B from Alibaba Group (Yang et al. 2025). The training process for the GeoGPT models consists of three key stages.:

1. Continual Pre-training (CPT)： The continual pre-training stage utilizes a variety of datasets, including open access papers/books, and geoscience-related materials from Wikipedia and Common Crawl that grant rights for non-commercial LLM modeling training and model output sharing. This extensive corpus is used to ensure a solid foundation in geoscience literature (Gururangan et al. 2020).

2. Multi-stage Supervised Fine-tuning (MSFT): The fine-tuning process is divided into three stages to refine the model's performance, using curated open-source QA pairs, the filtered Tulu-v3 dataset, geoscience-related QA data and long-context data. (Ouyang et al. 2022)

3. Direct Preference Optimization (DPO): The final stage, direct preference optimization, involves refining the model based on prompts paired with preferred answers. This ensures that the model's responses align more closely with user expectations and preferences. (Rafailov et al. 2023)

These processes ensure that the GeoGPT model is trained on a wide range of geoscience data, fine-tuned for specific tasks, and optimized for user preferences. All the data used for training comes from open-access publications with permission to train non-commercial LLM and share model output. (GeoGPT User Manual 2026).

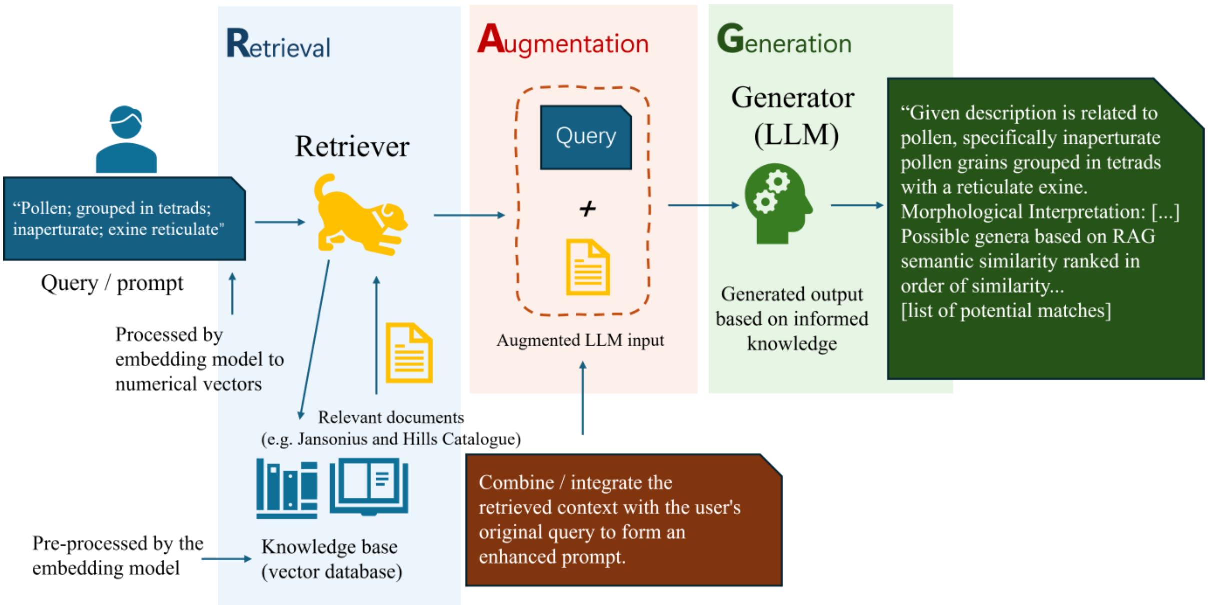


Fig. 2. RAG workflow for LATS.

The essence of the embedding model is to convert discrete and unstructured text into fixed-dimensional continuous dense vectors (embedding vectors), enabling machines to achieve semantic-level understanding, matching, and interaction through vector similarity calculations.

(Reimers and Gurevych, 2019). The embedding model for this LATS is the BAAI General Embedding large v1.5 (BGE-large-en v1.5) (Zhang et al. 2023, Chen et al. 2024). The BGE model is a universal open-source embedding model that is commonly used in the open-source community. The model adopts RetroMAE (Retrieval-oriented Language Models Via Masked Auto-Encoder) pre-training technology and the large-scale contrastive learning training strategy, and has been specially optimized for the problem of similarity distribution. (Xiao et al. 2022) In version 1.5, it significantly improved the rationality of the similarity score distribution and improved the ability to retrieve candidate genera. In the future development plan, the embedding model will be trained using the QA pairs provided by palynological experts and explanations of professional terms, enabling the LATS to possess palynological expertise, thereby better understanding the user input and providing better matching of candidate genera.

Finally, a measure was taken to determine whether the prompt is related to spores, pollen, or other palynomorphs (e.g. dinoflagellate cysts, chitinozoans, acritarchs). If irrelevant, the LATS would clearly state that the description is not related to palynology and suggest how to describe morphological features relevant to spores, pollen, or other palynomorphs (e.g. shape, size, ornamentation, aperture type, etc.). Then immediately end the response. If there were multiple rounds of input, the LATS would consider all user inputs and generate matching results based on all historical inputs. Additionally, users are allowed to edit previous input and re-generate answers from any historical round. After the re-generation, the system will retain all outputs from previous rounds but clear the subsequent generation of the edited round and start generating again based on the new input. Meanwhile, the system also provides a history record module, through which users can access the historical records along with the corresponding generated output.

Operation of the system

The LATS has a simple interface with a box for the user to type in a description as a prompt (Fig. 2).

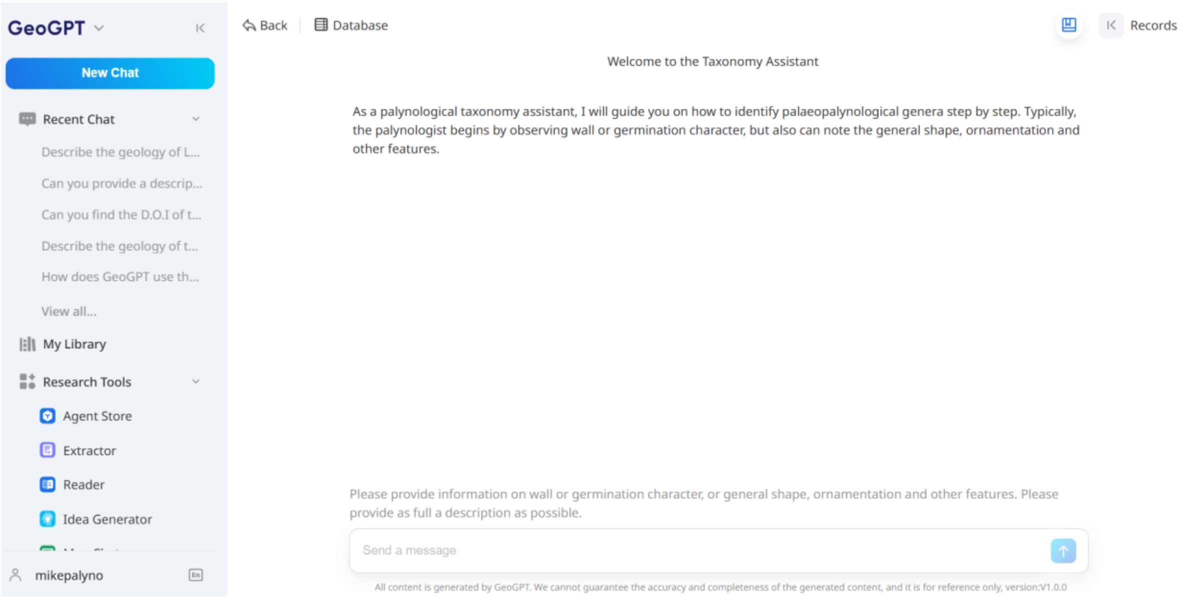


Fig. 3. Box for prompt

If a description such as 'Pollen; grouped in tetrads; inaperturate; exine reticulate' is entered, the LATS provides first a morphological interpretation of the user's description (Fig. 3). The purpose of this section is for the user to check that the LATS understands the prompt, for example the prompt mentions 'grouped in tetrads' and the LATS states that 'the pollen grains are arranged in tetrads which means they are found in groups of four'; similarly, the LATS confirms the meaning of 'inaperturate'. At this point, if the LATS does not understand the prompt, it will be clear to the user who can backtrack and enter a slightly different prompt, perhaps with alternative terms.

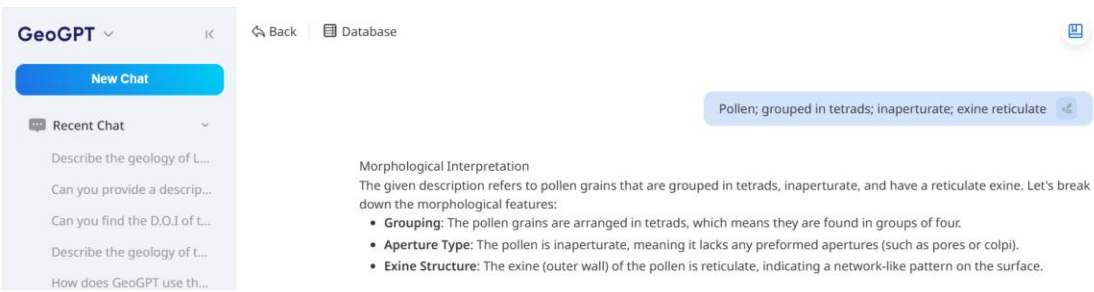


Fig. 4. Morphological interpretation of the user's description

Following this stage the LATS produces the best five matches for the genera (Fig. 4) in relation to the prompt description. These are not in order of level of fit. The LATS provides the name of the candidate genus, details of the genus and the rationale for the selection.

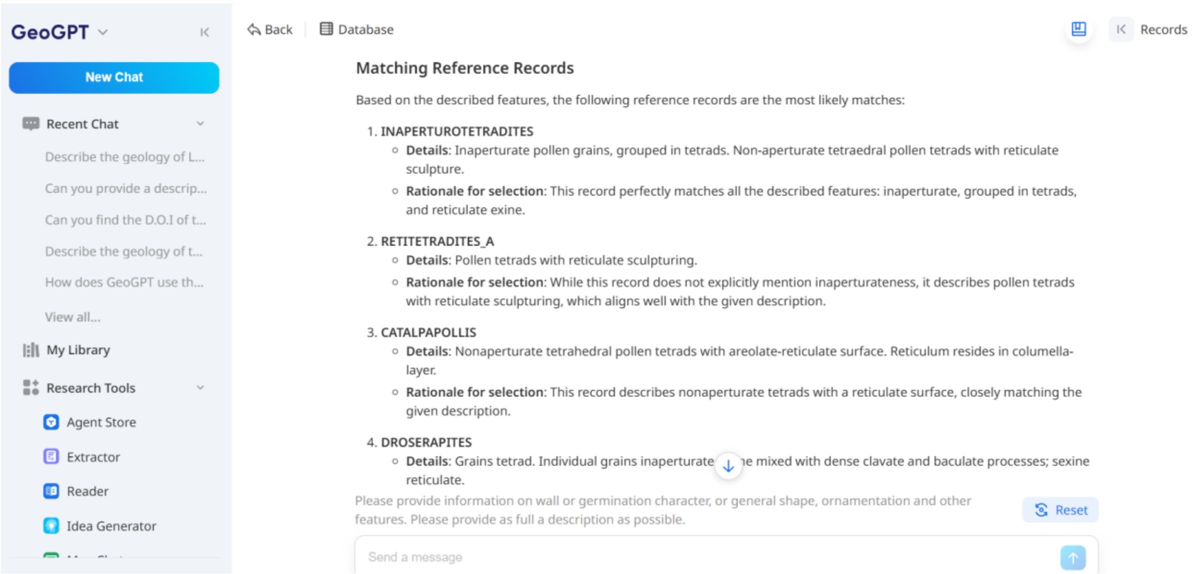


Fig. 5. Best five matches

Below this, is a broader assessment of semantic similarity (Fig. 5), with candidate taxa ranked in order of statistical similarity. This assessment provides the wider context of possible genera. At either this stage or the previous stage the description/diagnoses of the candidate taxa can be consulted, and the original scans of JHC can also be consulted through clicking the 'Database' icon or the genus candidate names. Many JHC cards contain simple line drawings of the main features of genera.

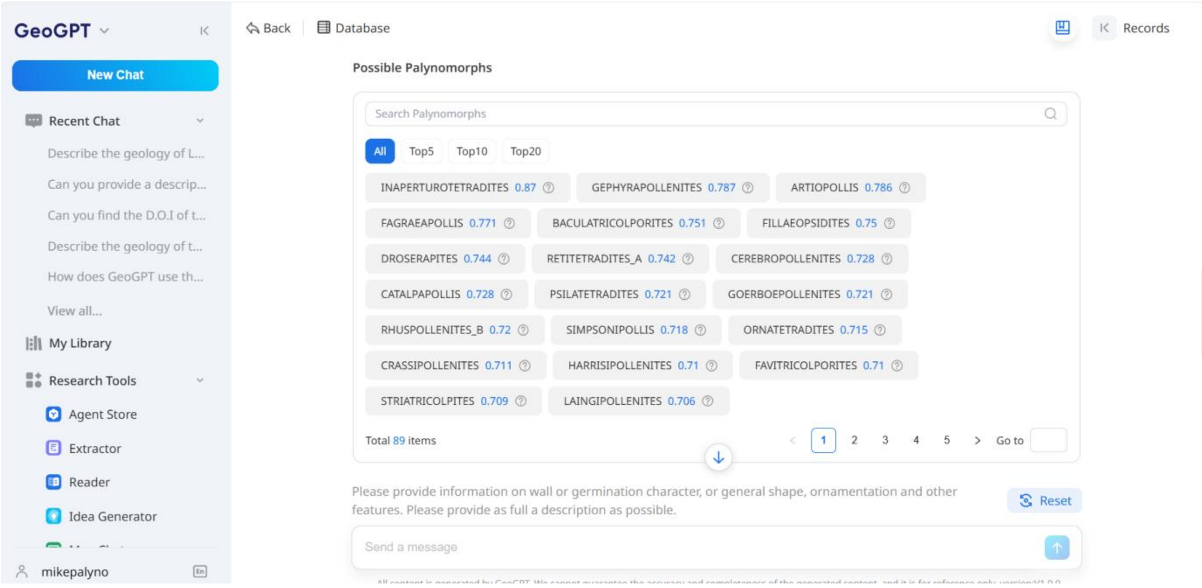


Fig. 6. Broader assessment of semantic similarity

For a detailed rationale for the match as well as areas where there is a mismatch, an assessment is also available for each candidate genus (Fig. 6)

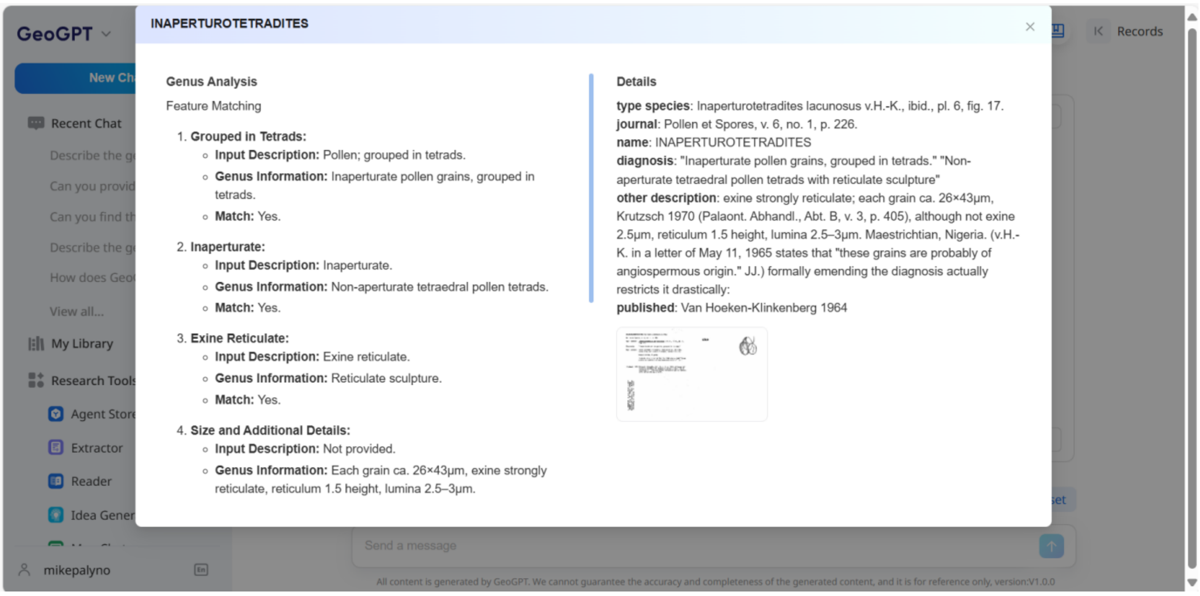


Fig. 7. Detailed rationale including reasons for match and mismatch for each candidate genus

The LATS also provides tips to improve the prompt and a suggested refined query or prompt (Fig. 7).

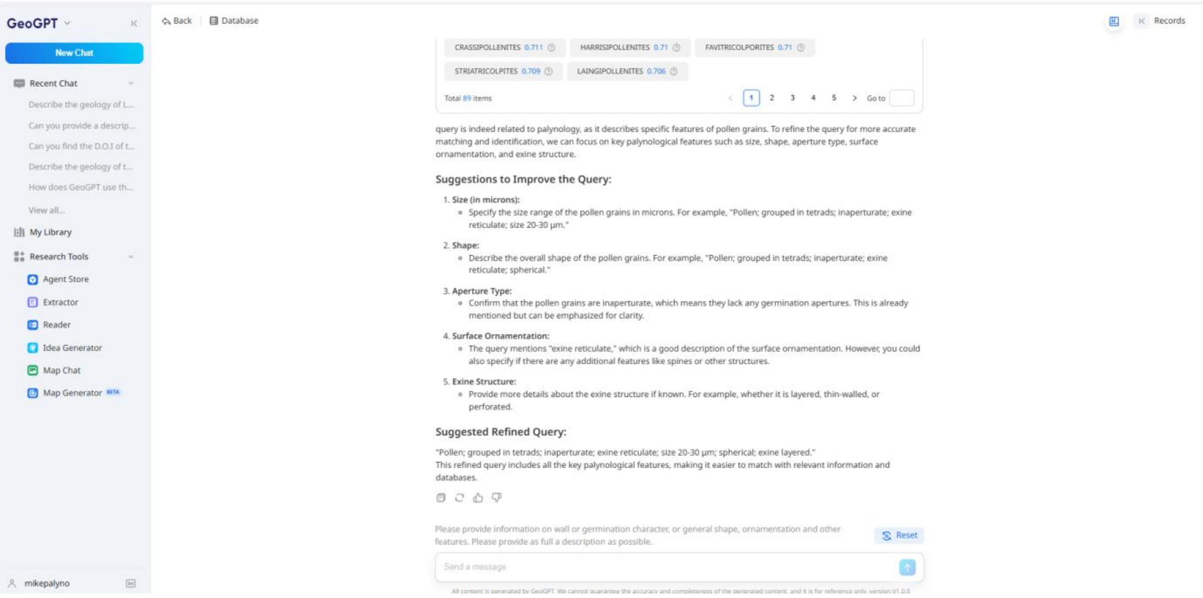


Fig. 8. Tips to improve user's prompt and a suggested refined query or prompt

Limitations of the system

There are two types of limitation or shortcoming: those the emanate from JHC itself, and those that emanate from the system.

Limitations due to JHC

The JHC contains genus names that are (1) poorly described, because they were originally poorly described in the relevant peer-reviewed paper or report, and their descriptions or diagnoses have never been improved, (2) invalid, (3) are described in translations into English from original diagnoses, introducing an element of interpretation on the part of the translator, (4) acknowledged and unacknowledged synonyms, and (5) homonyms. Jansonius and Hill's aims were to document as completely as possible the array of genera that a palaeopalynologist has at his/her disposal. Regular users of the PDF of JHC are aware of these characteristics, and aware that information in JHC is not sufficient to distinguish certain genera - or that certain useful genera are technically invalid. This often means that it is impossible using the information provided to make a satisfactory determination. This is not the fault of JHC, but of the taxonomy of palaeopalynology itself, which grew rapidly from a relatively small database in the early 19th Century to a growing science in 1960s and 70s, particularly as its use in economic biostratigraphy became important (e.g. McGowran 2005). Thus, the LATS does not provide any better levels of discrimination between some genera but simply offers the same potential for determination as study of the JHC. Here a few examples are examined and discussed in detail.

Valid but 'redundant' genera

Amongst the many genera of the JHC are those that are valid but rarely 'used'. This is often the case with genera that have been described early in the growth of palaeopalynology as a discipline. Their diagnosis or description may be rather short often because - to the original describing palynologist - there appeared to be few similar genera to discriminate. An explanation for their low usage maybe that later palaeopalynologists preferred to use genera that seemed more appropriate with more circumscribed morphological variation. Another explanation for this 'redundancy' relates to the siloed expertise of palaeopalynologists in a certain Period (for example the Permian), and a particular group of genera become associated with that system which become habitually used by 'Permian palynologists' even though suitable genera may be available in the Mesozoic (for example the Triassic).

An example is the genus *Cingulatizonites* Mädler 1964, from the Upper Rhaetian of Germany (Upper Triassic). Its diagnosis (translated from the German) is: *'Trilete miospores, amb subcircular to rounded triangular; cingulum present, thinning wedge shaped towards the equatorial margin, and grading into a narrow zona; cingulum smooth and structureless, which differentiates the genus from* Densosporites' (Mädler 1964). A palaeopalynologist working in a Carboniferous succession observing a spore with '…cingulum present, thinning wedge shaped towards the equatorial margin…' might expect to find the genus *Cingulizonates* (first erected by Dybova & Jachowicz 1957 from the Upper Carboniferous) among the higher-matching LATS candidates but will also find *Cingulatizonites* which is never used in the Carboniferous, even though its circumscription is suitable for many spores that might be assigned to *Cingulizonates*.

Invalid genera

As discussed above, the JHC includes genera that are invalid under ICBN rules, as well as genera originally considered invalid but then made valid through, for example, the designation of a holotype by a later author (see e.g. McNeil 2014). All this information, when available in JHC, is also included in the LATS. Thus, a prompt will potentially provide these kinds of genera. Though this could be considered a limitation, the LATS allows the palynologist to see a full range of candidate genera without exclusion. As stated in the principle of 'assistance' above, the purpose of the LATS is to assist the palynologist in his/her determination, rather than supplant the palynologist's role.

Near-synonyms

A related challenge is that as with JHC, the LATS, following a prompt, may return candidates which are very close morphologically. As discussed later in this paper, conceptual 'morphological space' appears to be crowded in some areas of palynological taxonomy, particularly where small differences in morphology are considered important for biostratigraphy, for example in the Palaeozoic of the Middle East and the Mesozoic of the North Sea. Thus, prompts with low discriminative potential may supply many, very similar genera. In these, the judgment of to the user is required to discriminate amongst the list of candidates.

Limitations due to system operation

Bias

The LATS considers similarity that is expressed through text and returns candidate genera based on statistical matches. The most challenging aspect of this is that genera with short descriptions or diagnoses, which encompass a wide theoretical range of morphology, are very likely to appear in a candidate list. On the other hand, those that are described with detailed textual terms that enable discrimination, will appear in candidate lists but not with a high level of statistical similarity. In mathematical terms this can be explained simply: based on a one-word input from a user, the statistical distance of a 10-word diagnosis is larger than that of a 2-

word diagnosis, although they are semantically similar, which leads to a higher similarity score for the genus with a 2-word diagnosis.Thus, it could be said that the LATS is biased against genera with a diagnosis/description with a high discriminative potential.

Without altering the detail of diagnosis/description (which would contravene the principle of non-intervention above) the best solution to such bias is to allow the palynologist access to all the candidate taxa as in the principle of inclusion above, and to allow swift access to the original descriptions and diagnoses. This ensures that the palynologist makes the final determination with all the relevant material at his/her disposal.

Further uses of the LATS

As well as the providing a LATS to aid a palynologist through the stages of identification, allowing him/her to make the best judgements on determination with the best supporting information, the information and 'understanding' that the underlying system has over a large area of palaeopalynological taxonomy means that LATS could be put to more general uses. Two examples follow.

Synonyms

In the early years of palaeopalynology many genera were named quickly, locally, sometimes with limited access to global literature; and often without comparison to previously described material (e.g. Fensome 1990, Traverse 1988). This led to a proliferation of synonyms; two (or more) different names referring to the same taxon. Synonymy affects the accuracy of biodiversity estimates, biostratigraphic correlation, macroevolutionary and palaeobiogeography analyses, and the stability of scientific communication (e.g. Patterson et al. 2010). Because of the 'understanding' that the LATS has of palaeopalynological taxonomy, it is capable of detecting potential synonyms and indicating the priority of the name, the senior synonym, which is the earliest validly published scientific name for a taxon.

An example is the Genus *Tethysispora* Vijaya and Tiwari (in Vijaya et al. 1988) whose diagnosis, when input as a prompt to the LATS produces candidate genera with high semantic similarity such as *Vallatisporites* Hacquebard 1957 and *Gondisporites* Bharadwaj 1962. If the user found that there were grounds for suspecting synonymy, then *Vallatisporites* Hacquebard 1957 would take priority.

Distribution of genera (or taxa) in 'morphological space'

The morphological range of palynomorphs could be seen as occurring in multidimensional space with dimensions like width, height, density of ornaments, and size of ornaments.

By creating a feature table (Table 2), all JHC diagnoses can be reorganized or parsed so that the embedding model can convert the elements of descriptions into fixed-dimensional embedding vectors. Furthermore, an unsupervised learning approach, such as principal component analysis (PCA) or *K*-means clustering can be adapted to investigate genera in morphological space. (Jolliffe 2005, Hartigan and Wong 1979)

Features	Description of Feature
Wall layer number	This taxonomic character concerns the number of wall layers
Cameration or cavation	This taxonomic character concerns the presence and extent of space or cavity between wall layers
Ornament type	This taxonomic character concerns the type of ornament of the surface of the palynomorph or within its wall
Shape (amb)	This taxonomic character concerns the outline of a pollen grain or spore seen in polar view
Cingulum or zona	This taxonomic character concerns the presence of an equatorial extension of the palynomorph wall: thick (cingulum), thin (zona)

Table 2. Spore characters

As an example, a table of features of spores of this type enables *Tethysispora* to be categorized (Table 3).

Genus name	Wall layer number and arrangement	Cameration or cavation	Ornament type	Shape (amb)	Cingulum or zona
Tethysispora	Exine two-layere	Cavity equatorially, distally and partly proximally within the central body, surrounding the inner body	Small, 1–2µm regular to irregular coni; broad-based to mammoid-shaped spines with elongated, curved detachable apices also seen in some processes; processes generally sparse on distal polar region but becoming bigger and denser towards body equator; sometimes mammoid process also present along the equator of body. Ornamentation crowded on the equatorial region of the body imparting a denser appearance to the zona-base and projecting out prominently below the zona	triangular to broadly subtriangular	zona

Table 3. Features of *Tethysispora* Vijaya and Tiwari (in Vijaya et al. 1988)

A 2D-visualization for all JHC genera using PCA is shown in Fig. 9, including the candidate synonyms *Tethysispora*, *Indotriradites* and *Vallatisporites* indicating the small statistical distances between the genera.

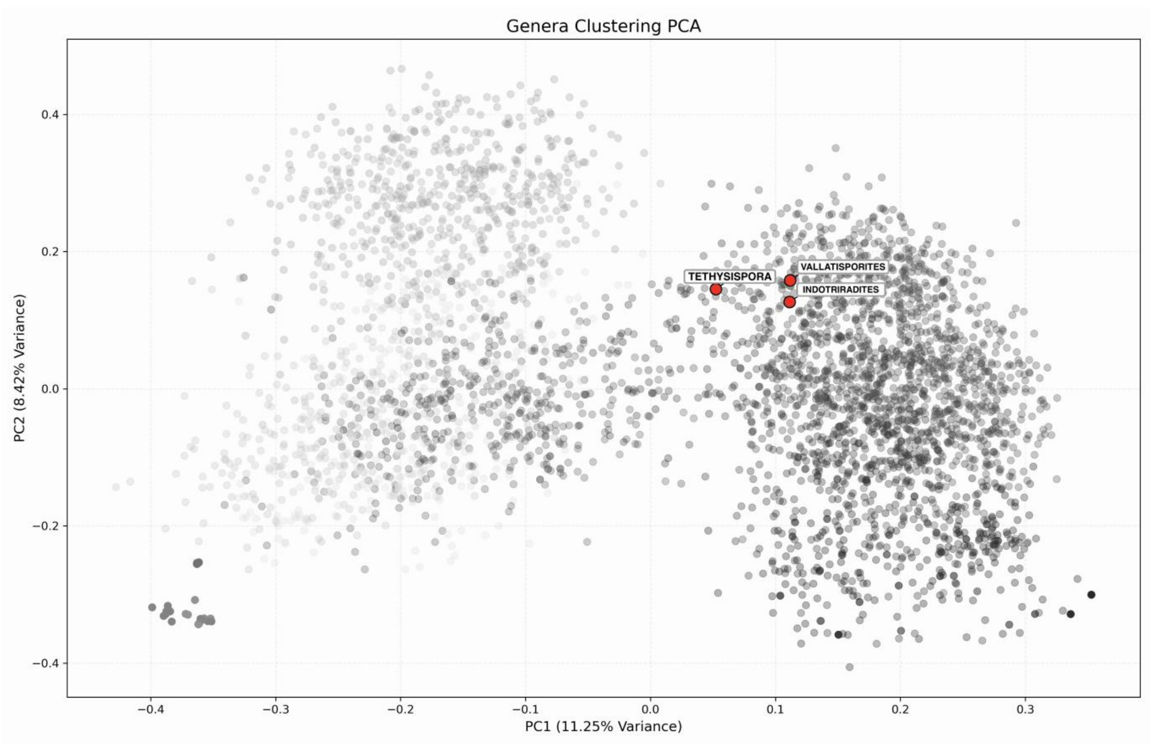


Fig. 9. 2D-visualized morphological variation amongst JHC diagnosis with marked genera

Implications for LATS in other parts of palaeontology

The use of artificial intelligence is likely to increase in palaeontological taxonomy. Perhaps the most rapid development is in image recognition based on learning from very large numbers of high-resolution images of specimens without direct reference to authoritative text-based diagnoses or descriptions of taxa (e.g. Niu et al. 2024). Though valuable, this method places expert validations between the user and the first-principle taxonomic information. Thus, a LATS has a special role in providing direct access to authoritative text-based diagnoses or descriptions of taxa and we believe should be encouraged as a useful aid to professional taxonomists and as a pedagogic tool for educators.

Many of the challenges and opportunities illustrated in this study of the conversion of a palaeopalynological dataset into LATS will be similar for other fossil groups. Much palaeontological taxonomic information is disparate and varies in quality and detail or may be unavailable to many as it is locked behind a paywall. In palaeontological groups with a long history of research, for example the brachiopods, the original peer-reviewed literature also contains variation in the meaning and use of morphological terms (e.g. Williams et al. 1965).

The Treatise of Invertebrate Paleontology, published from 1953 by the Geological Society of America and the University of Kansas provides more consistent detail. It comprises 55 volumes, written by more than 300 palaeontologists, and is subdivided into a number of sections each dealing with a different invertebrate animal phylum. An example is the Treatise Section Part H Brachiopoda (Revised) (Williams et al. 1999-2007), a revised version of earlier brachiopod volumes (Williams et al. 1965), which is one of the most complete and recently updated sections of the Treatise. The work of many brachiopod specialists allowed the provision of condensed, rationalised descriptions and diagnoses of 4192 genera, and offer consistent morphological terminology. However, complete original (authorial) diagnoses and descriptions are not provided (though are referenced).

The methodology used in this study may be of value to other scientists working palaeontological taxonomy.

Conclusions

Large Language Models (LLMs), being text-based, are ideal types of artificial intelligence to aid in palaeontological taxonomic determination because published textual descriptions are the ultimate, authority in taxonomy. This paper describes some of the preparation required to develop a database for LLM development.

The Jansonius and Hills palaeopalynological catalogue (JHC) is a unique record of taxonomic data in palaeopalynology in that it provides original authorial diagnoses and descriptions on which to train the LLM augmented taxonomic key (LATS), thus providing authoritative 'first principle' taxonomic information.

The LATS functions through Retrieval Augmented Generation (RAG) and returns candidate genera with statistical measures of match against the prompt(s) or users' descriptions.

The advantages of the use of the LATS include rapid access to statistically relevant candidate genera, including the authorial diagnoses and descriptions, which allows the taxonomist to make efficient and accurate determinations. The LATS also supplies information on the structures and methods of taxonomy and thus has pedagogic value, as well as broader research value in the theory and concepts of taxonomy.

The development of the LATS described here has implications for other palaeontological groups in terms of the text basis of their taxonomy (for example variable quality of descriptions and inconsistency in terminology), and their suitability for development of other LLM-assisted taxonomic aids or keys.

Acknowledgements

We acknowledge the help of the University of Calgary and the permission of the Jansonius family in the development of this project.

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