

IS IT POSSIBLE TO AUTOMATE MICROSCOPIC PLANKTON SPECIES IDENTIFICATION USING AI?

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Abstract: With the development of artificial intelligence and the trend towards automation of various subtasks, there is a need to automate microscopic plankton species identification. Some solutions already exist with relatively modest capabilities. This study examines the results hitherto achieved in this area, the potential goals to be achieved and the way how current AI systems can be applied to this task.

Key words: AI, large language models, machine learning, plankton identification, taxonomy

INTRODUCTION

Ecology, as a scientific discipline, investigates supra-individual levels of biological organisation, employing statistical analyses, mathematical modelling, and hypothesis testing. Nonetheless, its foundation rests upon precise observation. In plankton ecology, species-level identification within individual water or surface samples is essential, necessitating both qualitative and quantitative analysis. The identification process is labour-intensive, requiring not only significant time investment for sample collection and preparation but also expert-level taxonomic knowledge, often acquired through extensive training. As noted by KARBSTEIN *et al.* (2024), KUSUMAWARDANI *et al.* (2019), trained taxonomist him/herself is a rare and endangered species. This raises the critical question of whether species-level identification is indispensable (KARBSTEIN *et al.* 2024), particularly considering the evolving nature of species concepts and the transformation of morphology-based species definitions (KARBSTEIN *et al.* 2024).

In practice, several approaches can avoid species-level identification. Functional group classification, for instance, is notably more cost-effective and less complex (SALMASO *et al.* 2015). Alternatively, species proportions can be inferred from pigment composition using spectral analysers or through detailed individual analysis with flow cytometry (LABRIGHLI *et al.* 2022). Genetic and genomic techniques also offer potential for automation, although integration with morphology-based taxonomy remains incomplete (KARBSTEIN *et al.* 2024).

Despite these alternatives, traditional taxonomy remains vital for long-term and in-depth ecological studies due to its compatibility with historical datasets. Microscopic preparations, a cornerstone of this method, allow for retrospective verification and consistent species identification in line with taxonomic standards. Although taxonomic classifications evolve, referencing established taxonomic keys allows for database revisions and ensures continuity (HAJNAL 2006, HAJNAL and PADISÁK 2008). This methodological consistency has facilitated century-long studies of Lake Balaton’s water quality (HAJNAL and PADISÁK 2008), exemplifying the enduring value of precise identification.

Consequently, abandoning microscopic taxonomy entirely is not advisable. The pertinent question arises: to what extent can this process be automated, and how can artificial intelligence (AI) contribute? Although advancements in AI inspire optimism, scepticism persists among experts due to current limitations (GIERING *et al.* 2022). In macrophyte studies, detection accuracy has reached 80–90% across several hundred species, yielding promising, albeit hobby-level, results (HABIB *et al.* 2024). In contrast, automated plankton identification remains significantly less accurate (Table 1).

This research thus investigates the feasibility and potential of automating microscopic plankton identification using AI technologies. It does not aim to summarise existing literature – comprehensive reviews are already available (EEROLA *et al.* 2024, LABRIGHLI *et al.* 2022) – but rather to assess the challenges,

Table 1. Results in taxonomic identification of phytoplankton or diatom samples.

Year	Classification output	Estimated level	Acc	Methods	Reference
2007	22	genus	88%	Feature extraction + SVM	SOSIK and OLSON (2007)
2020	2	phylum	84%	Feature extraction with + machine learning (RF, SVM)	RIVAS-VILLAR <i>et al.</i> (2021)
2020	4	species, morphotype	88%	Feature extraction + machine learning (SVM)	RIVAS-VILLAR <i>et al.</i> (2021)
2021	2	genus	78%	VGG-16 CNN	RACHMAN <i>et al.</i> (2022)
2021	4	genus	79%	VGG-16 CNN	RACHMAN <i>et al.</i> (2022)
2021	6	genus	54%	VGG-16 CNN	RACHMAN <i>et al.</i> (2022)
2023	29	marine phytoplankton, ordo	95%	photo + fluoro-electro-chemical features + KNN or NN	CHEN <i>et al.</i> (2023)
2024	15	phylum, not only plankton	96.50%	ResNet50 CNN	HABIB <i>et al.</i> (2024)
2024	4	species	85%	Faster-RCNN	FIGUEROA <i>et al.</i> (2024)

explore prospective methodologies, and analyse the initial outcomes of existing solutions in the context of rapid technological progress. Ultimately, such developments could enable high-resolution spatiotemporal data acquisition that integrates seamlessly with long-standing scientific records.

MATERIALS AND METHODS

This study is grounded in a comprehensive review of the current literature on AI-assisted plankton identification. Although not a systematic review, it critically evaluates existing systems. Relevant publications were identified using search terms such as “plankton/phytoplankton/diatom identification AI/Artificial Intelligence” and “plankton/phytoplankton/diatom taxonomy AI/Artificial Intelligence”, yielding 17 pertinent sources. This paper addresses the following research questions: (1) What are the ideal requirements for an automated system? (2) What levels of accuracy are achievable? (3) What results have been documented? (4) Which AI technologies show the greatest promise?

RESULTS

Requirements

Figure 1 illustrates a methodological block scheme for taxonomic identification. Phytoplankton sampling is readily automatable, with robotic vessels and flow-cell systems (e.g., VPR, SIPPER, KRIP, FlowCytobot) enabling individual imaging (CHEN *et al.* 2023, SOSA-TREJO *et al.* 2023, SOSIK and OLSON 2007). These devices can function in situ or in laboratory settings. While sampling from submerged substrates is technically feasible using robotic systems, such solutions

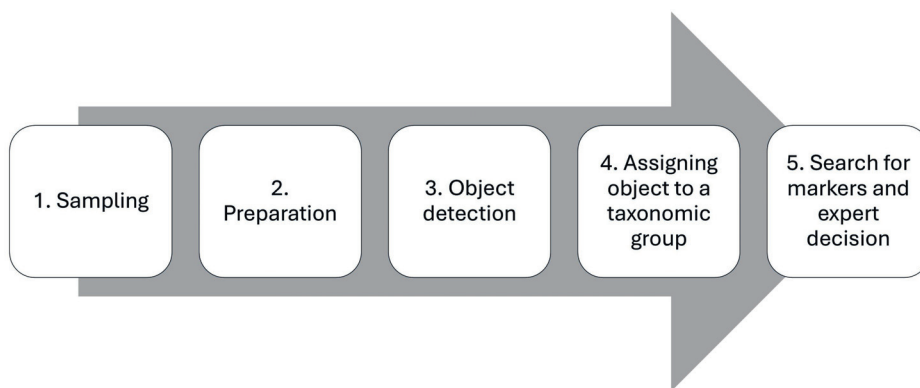


Fig. 1. Block scheme of the taxonomic identification made by human expert.

are rare and economically impractical, potentially compromising comprehensive environmental assessments.

Sample preparation remains a laboratory-intensive task that can be partially or fully automated using robotic assistance (WOLF *et al.* 2024). However, the key challenge lies in automating microscopic identification, which is in the focus of this study.

Over the past two decades, efforts to replicate expert-level taxonomic identification via automation have shaped current system requirements. The manual process involves object detection, organism delineation, taxonomic marker identification, and hierarchical classification based on observed markers (RIVAS-VILLAR *et al.* 2021). Although replicating this exact process algorithmically is complex, scientific fidelity warrants such an approach.

The goal is to achieve human accuracy. According to experience, trained taxonomists' self-coherence is 85–95%, which is approximately the top accuracy of human work (KELLY *et al.* 2007). Its reason is that phytoplankton and diatoms are the so-called Taxonomically Complex Groups (TCGs) (KARBSTEIN *et al.* 2024), on the other hand, this is the psychological consequence of boring and fatigue microscopic workloads (RIVAS-VILLAR *et al.* 2021).

An optimal system should emulate a generalist taxonomist, capable of identifying diverse species across multiple habitats. It must be self-reflective, adjusting identification resolution based on input data and its internal knowledge. Unlike conventional AI algorithms, it should recognise and abstain from classifying unfamiliar specimens.

Achieved results

Despite their importance, current automated systems fall short of these ideals. Existing models often specialise in limited taxa and lack adaptability or interpretability (Table 2). Early applications extracted manually selected image features for classification via support vector machines (SVM), random forests (RF), or k-nearest neighbours (KNN) algorithms (RIVAS-VILLAR *et al.* 2021). Several solutions use a two-step approach, in the first step they try to separate plankton individuals from other objects, followed by the collection of features and the determination. Although the features were not stamps corresponding to the original markers, it can be stated that they were generally well interpretable and were features based on the conscious decision of the system developer.

The advent of deep learning, particularly convolutional neural networks (CNNs), such as VGG, ResNet50, and Faster-RCNN, significantly enhanced identification accuracy. However, these models continued to suffer from poor interpretability and methodological inconsistency (EEROLA *et al.* 2024, FIGUEROA *et al.* 2024, RACHMAN *et al.* 2022, SOSA-TREJO *et al.* 2023).

Table 2. Multimodal Large Language Models (LLM) for combined text and image processing capabilities.

Model	Developer	Main attributes	Year
GPT-4V (Vision)	OpenAI	Combined interpretation of images and texts (<i>e.g.</i> graph reading, visual QA)	2023
Flamingo	DeepMind	Multimodal transformer, fine-tuned for image-text-based interactions	2022
BLIP / BLIP-2	Salesforce	Image-based question-answer, image description generation	2022–2023
MiniGPT-4	Open-source (Vision encoder + LLM)	Multimodal system modelled after GPT-4	2023
Kosmos-1	Microsoft	Multimodal large model: joint interpretation of text, image and OCR	2023

Macrophyte recognition, in contrast, has advanced rapidly since-2017. With competitions like Kaggle driving development and massive image datasets fueling training, detection accuracy surpassed 90% for hundreds of plant categories (BAMBIL *et al.* 2020, HABIB *et al.* 2024, IBRAHIM *et al.* 2023, LABRIGHLI *et al.* 2022, XIE *et al.* 2024). In contrast, plankton-focused efforts suffer from a paucity of annotated image datasets, underscoring the need for the development of large-scale image repository.

Possible current and future AI solutions

Recent AI innovations offer promising avenues for plankton identification. YOLO (You Only Look Once), a real-time object detection framework, integrates detection, classification, and post-processing into a single convolutional pass, enhancing speed and accuracy (REDMON *et al.* 2016). It generalizes well across diverse image contexts, reducing background noise and increasing adaptability.

Generative Pre-trained Transformers (GPTs), although originally language models, now include visual processing capabilities. While adept at interpreting scientific texts and simple image features, they lack the structured knowledge base and logical reasoning required for taxonomic decision-making (OPENAI *et al.* (2024).

Deep metric learning, exemplified by FaceNet, maps similar objects into proximal regions of an embedding space, distinguishing even closely related images with resilience to lighting or orientation changes (YAN *et al.* 2024). Siamese networks extend this approach, enabling interpretable comparisons between image pairs and elucidating determinant differences (FEDELE *et al.* 2024).

Future improvements may arise from integrating GPT architectures with fuzzy logic systems, enabling more human-like, non-monotonic inference. Such

models could bridge the gap between linguistic processing and taxonomic logic, enhancing AI explainability and decision transparency (Novák 2011).

DISCUSSION

This review has outlined the requirements for a scientifically robust plankton identification system. While these criteria are idealized, they are essential for compatibility with existing taxonomic databases. Currently, no AI solution fully replicates the expert-driven workflow, and image feature extraction from descriptive text remains a significant limitation.

Experts agree that creating a large, well-annotated, and diverse image database is critical for both system development and validation. While multimodal LLMs, such as GPT show potential, they must be integrated with logical and model-based reasoning systems to meet scientific standards.

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Összefoglaló: A mesterséges intelligencia és a különböző feladatok automatizálásának sikerre felveti a kérdést bizonyos tudományos vizsgálatok, ez esetben a mikroszkópi alga határozás automatizálhatóságát illetően. Részeredmények már születtek ezen a területen, melyeket jelen publikáció összefoglal és értékel. Megállapítható, hogy a makrofitonok határozásában a mesterséges intelligencia alapú megoldások már jó amatőr szintre jutottak, az úgynevezett taxonómiai komplex csoportok esetében azonban igen csekélyek az eredmények. Néhány nemzetség és néhány faj meghatározására képesek a rendszerek elfogadható biztonsággal. Fontos lépés ezen a területen a feladat specifikációja, vagyis össze kell gyűjteni egy human szakértővel egyenértékűnek tartott rendszer ismerveit. A jelenleg alkalmazott mesterséges intelligencia módszerek néhány fontos algoritmusát elemeztem ezen ismervek alapján, külön kitértem a multimodális nagy nyelvi modellek alkalmazhatóságára. Megállapítható, hogy a manapság alkalmazott algoritmusok önmagukban nem fognak ezen a területen áttörést hozni, hanem a különböző módszerek kombinációja, amelyek a képfelismerést egy komplex tudásbázis kiépítésével egészítik ki. A végeredmény megvalósításához és teszteléséhez szükséges egy nagyméretű annotált kép gyűjtemény építése, de ez önmagában nem elegendő, hanem a taxonómiai tudás modellezésére is szükség van a sikerhez.

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