MicroMatch: A Content-Based Macroscopic Microbial Image Retrieval Module

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ABSTRACT

Identifying microorganisms is essential for investigating the chemical substances they produce, which have potential applications in biotechnology and pharmaceuticals. Artificial intelligence, particularly machine learning and Content-Based Image Retrieval (CBIR), provides means to make this task more efficient by improving accuracy and reducing operational costs. While supervised learning models for classification are trained to predict taxonomic groups, such as genus and/or species, with high predictive performance from microbial image collections, CBIR supports domain experts by retrieving visually similar samples from these databases, contributing to more reliable decision-making with respect to recognition. This paper presents MicroMatch, a prototype computational module for CBIR of microorganisms cultivated in Petri dishes. We describe the tool herein, covering image acquisition with a customized low-cost device and extending to the design of a similarity search framework that integrates an indexing structure and a matching engine tailored to the specific characteristics of the aforementioned multimedia data type. Through an intuitive interface, MicroMatch promises to accelerate microbial biodiscovery.

KEYWORDS

image search, feature extraction, dimensionality reduction, multidimensional indexing, information retrieval

1 INTRODUCTION

Microorganisms are living beings invisible to the naked eye, such as bacteria and fungi, that inhabit all ecosystems on Earth, from soil, water, and air to plant and animal hosts, including humans. Current estimates suggest that researchers have already described approximately 10 million strains, which corresponds to only 0.001% of the total inferred diversity [5]. Based on these data, projections indicate that microbial species outnumber the human population, evidencing the vast scale of global biodiversity.

Although a fraction of microorganisms is pathogenic and poses risks to human health, such as *Mycobacterium tuberculosis*, also known as Koch's bacillus and the causative agent of tuberculosis, a substantial number of strains produce chemical substances of interest to both science and industry, particularly in biotechnological and medical applications [1, 8, 10, 11]. A notable example in pharmaceuticals is the fungus of the genus *Penicillium*, which is responsible for the synthesis of penicillin, the first antibiotic widely used in modern medicine.

Given the scientific and technological importance of microorganisms, correct species identification is essential in clinical and microbiology laboratories. This task provides an initial understanding of the strains' characteristics and enables inferences about the natural compounds that may be associated with them [4]. In this context, artificial intelligence-driven tools, especially machine learning in the deep learning modality, have shown promise for automating microbial biodiscovery, whether through multimedia data classification methods [2, 7, 8, 10, 11, 13] and/or Content-Based Image Retrieval (CBIR) approaches [6, 9, 12, 14–17]. Such technologies, when combined with images of cultures grown on solid media, contribute to improving identification accuracy while reducing analysis time, operational costs, and dependence on highly specialized labor [8].

Regarding classification, models trained on macroscopic images of microorganisms, annotated according to Linnaean taxonomy, are capable of predicting, at the culture or colony level, the taxa linked to a given sample. CBIR systems, in turn, allow microbiology experts to search for labeled images and retrieve those that exhibit the highest visual similarity to a certain query, thereby leveraging domain knowledge to support automated recognition primarily. This strategy can be applied independently or specifically triggered when the classifier yields low confidence in its output.

In light of the aforementioned scenario, this work introduces MicroMatch, a CBIR tool for Petri dish images developed to assist professionals in identifying these microscopic organisms. Designed in collaboration with domain experts, the prototype computational module will soon be adapted for integration into the web system for microbial biodiscovery, AI4Micro. Both are connected to an image database of microorganisms grown on solid media. To the best of our knowledge, this is the first repository of taxonomically annotated macroscopic microbial images, which our research group is currently supplying. We have been acquiring these images employing a custom-built device, following a protocol that spans from cultivation to the segmentation of cultures and/or colonies,

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particularly conceived to enhance computer vision tasks [8]. This approach promotes the continuous expansion of both the database and the MicroMatch tool itself, enabling it to accommodate the broad spectrum of strains that have already been cataloged, as well as those yet to be discovered.

The remainder of this paper is structured as follows: Section 2 presents the proposed computational module, MicroMatch, together with the related image acquisition process, CBIR framework, and user interface. Section 3 discusses the system's impact and future perspectives, and Section 4 outlines the concluding remarks.

2 PROPOSED TOOL

We organize the description of the prototype computational module, MicroMatch, into three sections: (i) image acquisition (Section 2.1), (ii) CBIR framework (Section 2.2), and (iii) user interface (Section 2.3). Together, these components provide a clear and systematic overview of the proposed solution.

2.1 Image Acquisition

Our research group captured and annotated images of microorganisms in Petri dishes using a low-cost, height-adjustable stand device that incorporates a digital camera and an LED light pad. We also developed a collection protocol, specifically designed to boost computer vision tasks, that specifies the procedures from cultivation to microbial image preprocessing and the segmentation of pure cultures and their colonies [8]. Figure 1 shows our custom-built apparatus and a simulated view of the capture interface in operation.

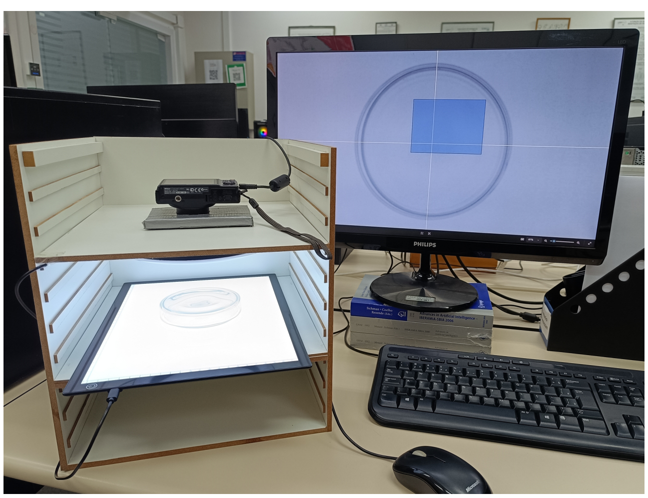
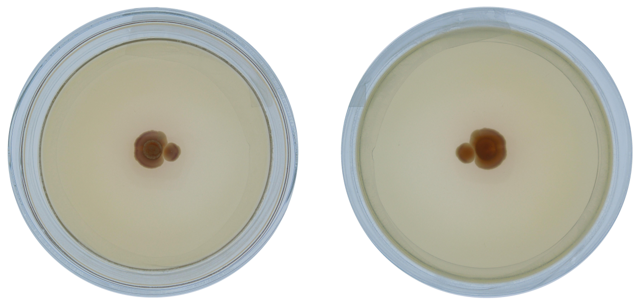


Figure 1: Device for high-resolution image acquisition of microorganisms grown on solid media.

We inoculated each strain in triplicate and captured images of the corresponding cultures at equidistant time intervals along the microbial growth curve, from the appearance of the first colony to its decline. For each replicate, we photographed both the front and back sides of the Petri dish. Finally, we labeled all records taxonomically according to the Linnaean system, following the hierarchy: Kingdom → Phylum → Class → Order → Family → Genus → Species. Figure 2 illustrates two representative images of *Streptomyces rubrisoli*, whose taxonomic classification is: Bacteria → Actinomycetota → Actinomycetia → Kitasatosporales → Streptomycetaceae → Streptomyces → *S. rubrisoli*.



(a) Front **(b) Back**

Figure 2: Macroscopic images from our database, depicting the front and back views of a Petri dish with the actinobacterium *S. rubrisoli* (strain AM24).

2.2 CBIR Framework

Figure 3 portrays the two phases of the CBIR architecture that compose the proposed tool. In the first phase, shown in the upper part of Figure 3, we prepare our database as described in Section 2.1. We resize all images to 224×224 pixels, normalize RGB channels to the range $[0, 1]$, and standardize them to ensure compatibility with the pre-trained Vision Transformer (ViT) model [3]. ViT extracts visual descriptors from each image, generating a 768-dimensional feature vector. We then apply the Uniform Manifold Approximation and Projection (UMAP) method, configured with cosine distance, to reduce the dimensionality of these vectors, thereby improving computational efficiency. This step compresses the representations from 768 to 32 dimensions. Finally, based on the reduced features, we construct an indexing structure with the Ball Tree algorithm, which builds a hierarchy of hyperspherical regions to optimize distance-based queries among feature vectors.

The second phase of the framework corresponds to the image search and retrieval process, illustrated in the lower part of Figure 3. The user provides a query image, which undergoes the same preprocessing sequence applied to the database: resizing, normalization, standardization, feature extraction with ViT, and dimensionality reduction via UMAP, resulting in a 32-dimensional feature vector. The system then employs the k-Nearest Neighbors (kNN) algorithm—with k defined by the user—to compute similarity between the query vector and the indexed representations using cosine distance. Finally, it retrieves the k most similar records and displays them to the user for inspection

The design of the adopted CBIR architecture originated from the feasibility analysis reported in [6] and was later refined and consolidated in [9], based on the characteristics of our image collection and an empirical assessment of the system's components. In those earlier studies, we tested several feature extractors, including EfficientNet, ResNet50, and Swin Transformer, and identified ViT

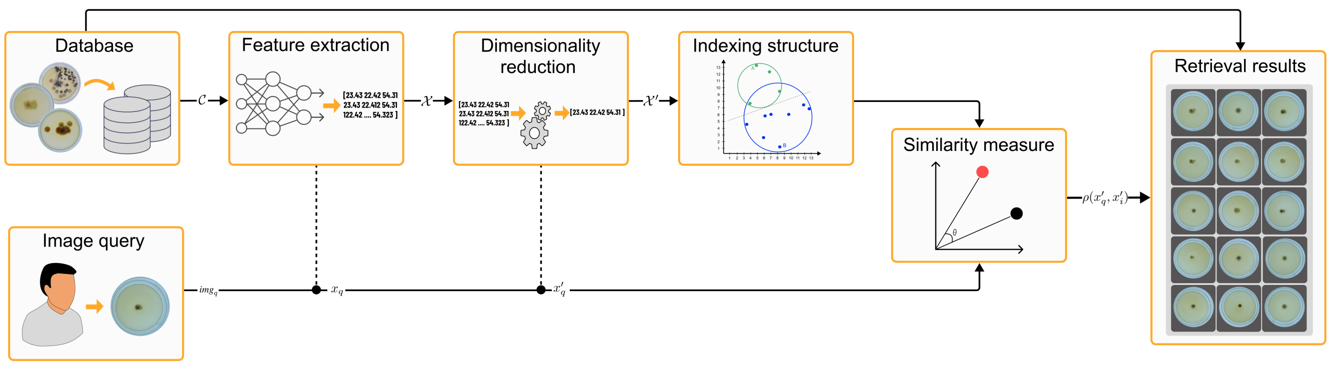


Figure 3: MicroMatch CBIR system. The upper part comprises the indexing phase, where database images undergo feature extraction, dimensionality reduction, and multidimensional indexing. The lower part covers the query phase, where a user image follows the same steps to compute similarity and retrieve the k most similar records.

as the pre-trained model that achieved the best performance. We also examined different UMAP configurations, indexing structures, and similarity measures. The final framework reached a Mean Average Precision (MAP) of up to 85.14% in experiments involving 24 actinobacteria species, with an average query time of less than 0.0054 seconds for $k = 15$.

We implemented the MicroMatch CBIR architecture in Python[1], employing the VSCode environment[2] and the following libraries: `PyTorch`[3] for ViT instantiation, `scikit-learn`[4] for Ball Tree indexing and kNN search, and `umap-learn`[5] for dimensionality reduction.

2.3 User Interface

Figure 4 shows the MicroMatch user interface, which connects to the CBIR system (Section 2.2) that accesses the microbial database (Section 2.1). We designed it to be functional and straightforward, enhancing usability. The interface consists of two main panels: the search panel (on the left) and the results panel (on the right). In the search panel, users upload a query image and configure the search parameters, such as the number of similar images to retrieve (k in kNN), the restriction of the search to a specific subset of the database, the microbial growth-curve interval to consider, and the Petri dish side (front, back, or both). We specified these configurable parameters together with domain experts to optimize microorganism recognition.

The results panel portrays the k images most similar to the query. The tool arranges them in columns, with up to five per column, and automatically distributes them into rows as needed. It ranks the results from left to right and top to bottom, placing the most similar image in the upper-left corner, followed by the others in descending order of similarity. When the number of images exceeds the visible area, a vertical scroll bar allows users to browse all results. Each image is highlighted with an orange border, as

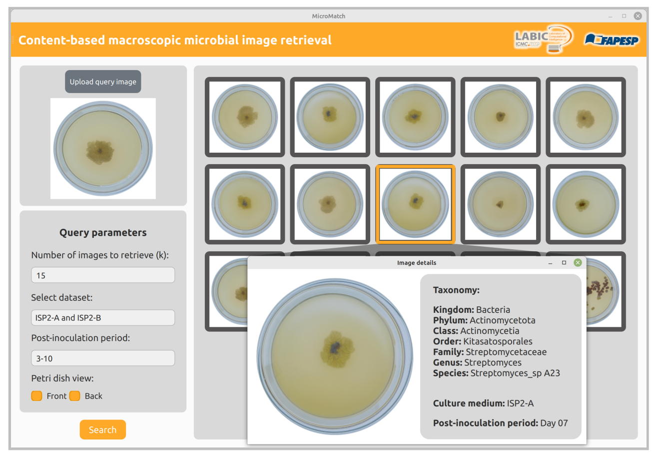


Figure 4: MicroMatch user interface displaying the search panel (on the left) and the results panel (on the right). Clicking a retrieved image opens a pop-up window that exhibits its metadata and an enlarged version of the image.

illustrated in Figure 4. By clicking one, users open a pop-up window that enlarges the selected sample and displays its metadata, which includes the Linnaean taxonomy up to the species level, the time point along the growth curve, and the Petri dish perspective. The window also features a zoom-in tool that enables users to examine the microorganism's morphology in greater detail.

We developed the user interface in Python, employing the `PySide` library[6], which provides Python bindings for the `Qt` framework[7]—a technology widely used to build modern and responsive desktop applications. The interface connects directly to the CBIR system, also implemented in Python. Since the tool remains an internal prototype, it does not yet have a defined usage license.

[1]https://www.python.org.
[2]https://code.visualstudio.com.
[3]https://pytorch.org.
[4]https://scikit-learn.org.
[5]https://umap-learn.readthedocs.io.
[6]https://pypi.org/project/PySide6.
[7]https://www.qt.io.

3 IMPACT AND PERSPECTIVES

The main contribution of the MicroMatch module lies in providing a decision-support mechanism that aids life science professionals in identifying the microorganism under analysis. Its usefulness becomes evident in two situations: (i) when the module retrieves images highly similar to the query, thereby facilitating species recognition; and (ii) when it returns markedly dissimilar images, which may suggest that the organism belongs to a species not yet cataloged in the database—or possibly to a previously unknown one.

In the future, we plan to integrate the module into a broader web platform, AI4Micro, which will combine multiple components designed to automate microbial biodiscovery. Figure 5 depicts the planned system architecture, including an "Identification" module that automatically classifies microorganisms through machine learning models. The "Retrieval" module, described in this work, will assist in cases where classifiers exhibit low confidence in their predictions and will also enable scientists and domain experts to visually explore the database. Additional modules will oversee the continuous expansion of the repository, ensure the quality of newly added data, and foster collaborations with national and international research groups contributing macroscopic microbial images and related analyses.

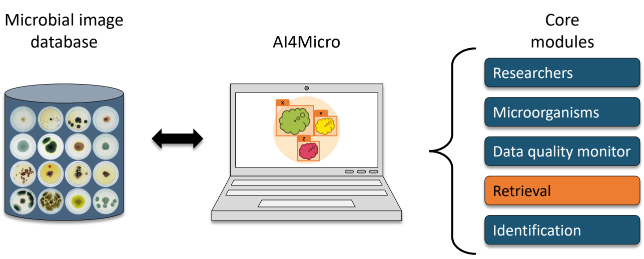


Figure 5: Web platform structure and planned modules.

AI4Micro adopts a client–server architecture. The front-end, built with React[8] and Bootstrap[9], interacts with RESTful APIs provided by a FastAPI[10] back-end that manages the business logic. MongoDB[11] stores user data, images, and other system records.

4 CONCLUDING REMARKS

This paper reported on a prototype for CBIR of microorganisms grown on solid media. The solution encompassed the entire pipeline—from image acquisition under controlled laboratory conditions using a customized, low-cost device developed in-house to the implementation of a CBIR framework configured through experimental evaluations and tailored to the specific characteristics of the collected images. These components converged in a prototype computational module that provided an intuitive interface for expert users. This study is part of a broader set of initiatives aimed at automating microbial biodiscovery.

As future work, we plan to enhance the tool's performance by incorporating a re-ranking component into the CBIR architecture outlined in Figure 3, exploring strategies such as k-reciprocal re-ranking, supervised re-ranking, and cluster-based re-ranking. We also intend to identify an optimal set of handcrafted image descriptors and compare its effectiveness with that of ViT, which is currently adopted as the system's feature extractor.

[8]https://react.dev.
[9]https://getbootstrap.com.
[10]https://fastapi.tiangolo.com.
[11]https://www.mongodb.com.

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