

St. Xavier's College (Autonomous), Kolkata

**Comparative Study of Environmental Microbiological  
Content Based Image Analysis Models**

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# Introduction

Environmental microbiology is a dynamic field that explores the intricate relationships between microorganisms and their environments, emphasizing their roles in biogeochemical cycles, ecosystem functioning, and environmental health. Microorganisms, including bacteria, archaea, fungi, and viruses, are ubiquitous in various habitats—ranging from soils and oceans to extreme environments—and are crucial for nutrient cycling, biodegradation, and the maintenance of ecosystem balance. These can break down pollutants, including oil spills, heavy metals, and plastics. By understanding how these microbes behave, we can harness them to clean up contaminated environments, known as bioindicators. For example, lichens and byrophytes (mosses and liverworts) can be used to assess air pollution. They have a high surface area to volume ratio, which helps them accumulate contaminants from air. Owing to the current stage of global warming and climate change, identifying and understanding new microbes might be the key to addressing these critical issues effectively.

Traditionally, environmental microbiological researchers identify a new EM by conducting a myriad of biochemical tests, and checking references or asking experts. These approaches are known to be very time-consuming as well as labour-intensive. The search effectiveness as well as the classification process can be improved considerably with a *Content-based Image Analysis* (CBIA) system.

EM classification is a necessary step in scientific research processes to understand the different characteristics, habits and operating conditions of different EMs. Microorganisms possess huge morphological similarities that sometimes it becomes exhaustive to classify them. These approaches are known to be very time consuming as well as labour-intensive. To make the process of classification less exhaustive, an automatic machine learning image recognition tool with less human intervention can be developed. The search effectiveness as well as the classification process can be improved considerably with a *Content-based Image Analysis* (CBIA) system.

A CBIA model automatically extracts features even from very complex EM images, and can classify images based on low-level visual features (e.g., color, shape, texture, and spatial layout) very quickly. This EM-CBIA system acts as a powerful tool to assist with automating image analysis, identifying microbes and even monitoring environmental health. There are mainly two tasks to be tackled for this— image retrieval and evaluation of the retrieved images. The retrieval process takes input images of microorganisms and performs *image segmentation* on them. These segmented images are passed through different algorithms to *extract different features* and ultimately make predictions based on what the *fusion* of these features signify, as a single category features is never sufficient to accurately classify EMs. Our main focus is on classification and interpretation using various feature extractors and neural network models and perform a comparative study to determine the most efficient system without required a huge dataset and high computing power.

## Related Work

There have been very few EM-CBIA models in the existing literature so far, although CBIA is a well researched topic with many existing methodologies. However, they all may not be suitable for the study of EM. There are certain relevant feature extraction and classification methods that exist for different types of microorganisms.

The Zou et al. group have done a series of EM-CBIA models using this structure. They proposed a novel Content-Based Image Retrieval (CBIA) system for Environmental Microbiology (EM) to improve the efficiency of microorganism information retrieval. Their system takes a microorganism image as input, applies image segmentation to isolate the microorganism’s shape, and then extracts features using a contour-based descriptor called Internal Structure Histogram (ISH). By calculating Euclidean distances between ISHs, the system measures similarities between microorganism images. Experimental results, evaluated using Average Precision (AP), demonstrate the system’s effectiveness and potential in enhancing EM image search processes. (Y. L. Zou et al. 2015)

(Li, Shirahama, and Grzegorzek 2014) explored the classification of microorganisms using *Content-Based Image Analysis* (CBIA) by employing a framework that leverages both texture and shape features for improved accuracy. This paper demonstrates the application of CBIA to microorganism classification by integrating

multiple visual descriptors, including shape and texture. Their research group at the University of Siegen has consistently contributed to advancing CBIA techniques for microorganisms.

Expanding on this, (Y. Zou et al. 2017) proposed a double-stage optimization-based fusion method for content-based image retrieval (CBIA) of microorganisms. Their system combines multiple image features and optimizes fusion strategies to further enhance retrieval accuracy. While effective, this approach mainly focuses on improving the feature fusion process, leaving room for exploring new feature extraction techniques.

In another study, (Li, Shirahama, and Grzegorzec 2015) applied content-based image analysis to aid environmental microbiology. Their research highlights the potential of CBIA to assist in the identification and classification of microorganisms by utilizing advanced pattern recognition techniques. However, the study emphasizes traditional visual descriptors and does not fully explore the use of deep learning, which has become increasingly popular in modern CBIA systems (P. Rani and Sharma 2021).

## Role

My role in this project is to monitor the literature survey and carefully review research papers, documentations, and citations concerning CBIA methods. I will concentrate on learning how the inner layers of the various models we plan to utilize function, particularly U-Net, through examining their architectures and implementation aspects. From this understanding, I will set up and tune the different classifier models to deliver the optimal output.

Once the various models have been created and are ready to be demonstrated, I will implement the backend of the prototype application.

## Requirements and Technology Used

To develop our CBIA system structure, we will be using these primary modules and frameworks to develop the general model:

### 1. Hardware Requirements

High-performance GPU is preferred for fast and better training performance (e.g., NVIDIA RTX 3090, A100) Multi-core CPU (Intel i3 minimum) for preprocessing and feature extraction tasks. RAM: At least 8GB (32GB recommended) is required. It is possible to work with low RAM as our dataset is not that huge.

Storage: SSD with at least 500GB to store image datasets and model checkpoints.

### 2. Software & Framework Requirements

Operating System: Ubuntu 20.04+ (preferred) / Windows 10+ with WSL support.

Programming Language: Python 3.8+

Deep Learning Frameworks: TensorFlow / Keras (for segmentation, feature extraction)

Image Processing & Feature Extraction:

- OpenCV, PIL (for preprocessing)
- Scikit-image (for morphological feature extraction)
- NumPy, SciPy (for numerical computations)

### 4. Functional Requirements

Dataset: We have used EMDS-6, an open source collection of 21 classes of different EMs which was also used by (P. Zhao and Grzegorzec 2022). Those images have been augmented in four different orientations as a part of bias mitigation.

Preprocessing Module: Image resizing, denoising, and enhancement using CLAHE, Gaussian blur Standardization & normalization (to match deep learning model input)

Feature Extraction & Similarity Search:

- Morphological features (shape, texture)
- Deep feature embeddings (ResNet, Autoencoders)
- Distance metrics (Cosine, Euclidean, Hamming) for efficient retrieval

## 5. Classification Requirements

- Confusion matrix
- Evaluation metrics (F1 score, IoU, DICE coefficient, misclassification rate, precision, recall)
- K-Fold cross validation for bias mitigation

## References

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