

MyData: A Comprehensive Database of Mycetoma Tissue Microscopic Images for Histopathological Analysis

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Abstract

Mycetoma is a chronic and neglected inflammatory disease prevalent in tropical and subtropical regions. It can lead to severe disability and social stigma. The disease is classified into two types based on the causative microorganisms: eumycetoma (fungal) and actinomycetoma (bacterial). Effective treatment strategies depend on accurately identifying the causative agents. Current identification methods include molecular, cytological, and histopathological techniques, as well as grain culturing. Among these, histopathological techniques are considered optimal for use in endemic areas, but they require expert pathologists for accurate identification, which can be challenging in rural areas lacking such expertise. The advent of digital pathology and automated image analysis algorithms offers a potential solution. This report introduces a novel dataset designed for the automated detection and classification of mycetoma using histopathological images. It includes the first database of microscopic images of mycetoma tissue, detailing the entire pipeline from species distribution and patient sampling to acquisition protocols through histological procedures. The dataset consists of images from 142 patients, totalling 864 images, each annotated with binary masks indicating the presence of grains, facilitating both detection and segmentation tasks.

Keywords

Mycetoma, histopathology diagnosis, Microscopic images, Image Analysis, Classification, Segmentation.

Article informations

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1. Background

Mycetoma is a significantly neglected tropical disease characterised by chronic, disabling subcutaneous granulomatous inflammation. It is caused by a variety of microorganisms, leading to its classification into two types: eumycetoma, caused by fungi, and actinomycetoma, caused by bacteria (WHO, 2024). The most common species responsible for eumycetoma is *Madurella mycetomatis* (*M. mycetomatis*). In contrast, common species for actinomycetoma include *Streptomyces somaliensis* (*S. somaliensis*), *Actinomadura madurae* (*A. madurae*), *Actinomadura pelletieri* (*A. pelletieri*), and *Nocardia brasiliensis* (*N. brasiliensis*) (van de Sande, 2013; van de Sande et al.,

2014b; Zijlstra et al., 2016; Hay et al., 2021).

Mycetoma occurs worldwide, but the overall global burden of the disease is still unclear. The infection is predominantly reported from tropical and subtropical regions, with most cases occurring in the so-called "Mycetoma belt" (WHO, 2024). The highest prevalence has been reported in Sudan, India, and Mexico. Sudan is considered the mycetoma epicenter, with the Mycetoma Research Centre (MRC) at the University of Khartoum, a WHO Collaborating Centre on Mycetoma, reporting 355 new cases annually (Fahal et al., 2015). However, this number likely underestimates the actual number of cases, as it only includes patients who were able to access medical care at the MRC. Young adults, especially males aged 20 to 40 in remote



rural areas, are the most vulnerable to mycetoma infection (WHO, 2024; Fahal et al., 2015). Women are less likely to be infected than men, with a ratio of 1:3. (Fahal, 2004; Fahal et al., 2015). The disease predominantly affects field labourers, agriculturalists, and herdsmen (Fahal, 2004). The lower extremities and hands are the most commonly infected areas (van de Sande, 2013; Fahal, 2004). In endemic areas, the initial diagnosis of mycetoma is often made clinically through physical examinations, though this can be challenging and inaccurate (van de Sande et al., 2014b; Emmanuel et al., 2018). To determine the appropriate treatment, further investigations to identify the causative agents are essential. Accurate identification is critical for effective treatment and minimising complications (Hay et al., 2021), typically requiring the use of laboratory-based diagnostic tools (Ahmed et al., 2017; Emmanuel et al., 2018). Histopathological techniques are considered an efficient, cost-effective, and time-saving method for diagnosing mycetoma in these regions (van de Sande et al., 2014a).

Over the past decades, medical image analysis models, particularly those utilising deep learning, have become a crucial approach in the medical field. However, no model has been developed specifically for diagnosing mycetoma, likely due to the neglect of this condition in both health and computational research. A dedicated database is needed to facilitate the development of a mycetoma image analysis model. Therefore, we created **MyData**, the first database of histopathological microscopic images of mycetoma, following specific and consistent standards. This database aims to serve as a valuable resource for developing AI-based diagnostic tools, enhancing diagnostic accuracy, and improving patient outcomes. MyData can be used by the scientific community to model and analyses mycetoma histological characteristics, providing insights to develop more effective diagnostic parameters and strategies.

In this communication, Section 1 introduces the work, while Section 2 discusses the epidemiological distribution of mycetoma causative agents. Section 3 details the study population, including sample selection and diagnosis. Section 4 outlines the histopathological process pipeline and the preparation of microscopic images, which is the main focus of this work. A comprehensive description of the proposed mycetoma database, along with a summary of the data and labels, is presented next. The final section concludes the paper.

2. The distribution of Mycetoma Causative Agents and Organisms

To introduce the mycetoma database, it is crucial to outline the epidemiological distribution of mycetoma causative agents to ensure the database accurately represents myc-

toma cases globally.

Approximately 40% of mycetoma cases worldwide are caused by eumycetoma (van de Sande, 2013; DNDi). However, eumycetoma is more prevalent in certain regions, such as central and eastern African countries, while actinomycetoma is more common in the Americas and the Middle and Far East (Emery and Denning, 2020). Additionally, the distribution of eumycetoma and actinomycetoma can vary within the same region and between neighbouring countries, Figure 1. For instance, most countries report mixed cases of both types, but some countries have a higher proportion of one type. In Sudan, for example, 73% of cases are eumycetoma, whereas in India, this percentage drops to 42%, and in Mexico, only 3% of cases are eumycetoma (Emery and Denning, 2020).

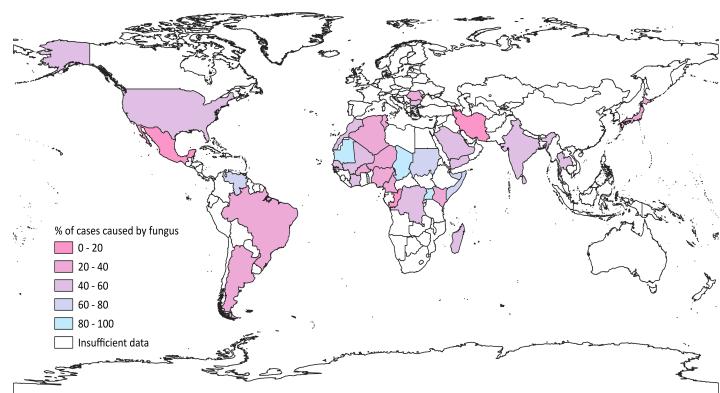


Figure 1: Prevalence of eumycetoma and actinomycetoma (Emery and Denning, 2020)

While the pathogens causing mycetoma are either fungal or bacterial, overall mycetoma can be caused by up to 70 different causative organisms (WHO, 2024). Globally, the prevalence of these agents has been documented (van de Sande, 2013), most recently (Emery and Denning, 2020). In this study, *Madurella mycetomatis* (MM) and *Nocardia* species were the predominant causative organisms, likely due to the study focused on qualitative rather than quantitative data. Given the uneven distribution of mycetoma types even within individual countries, the mapping performed in this study provides a notable overview of the distribution of mycetoma-causative organisms. In general, the most common causative organisms include *Madurella mycetomatis* (MM), *Actinomadura madurae* (AMM), *Streptomyces somaliensis* (SS), *Actinomadura pelletieri* (AMP), *Nocardia brasiliensis*, and *Nocardia asteroides*. However, *Nocardia* species are more prevalent in South America and Asia and less common in Europe and Africa (van de Sande, 2013).

The MyData database sample was collected at the MRC, so the types of mycetoma represented reflect the geographical distribution in Sudan, where eumycetoma is more prevalent. The database includes organisms such as *Madurella*

mycetomatis (MM), *Actinomadura madurae* (AMM), *Streptomyces somaliensis* (SS), and *Actinomadura pelletieri* (AMP). However, it does not include *Nocardia* species, as they are rarely observed in Sudan. While the inclusion of specific mycetoma organisms in our database does not impact treatment options, it can influence the prognosis of the disease. This information may be useful for purposes beyond developing AI models for identifying causative agents.

3. MyData Population

3.1 Sample collection and Selection criteria

The initial MyData database comprised 180 patients with clinically confirmed mycetoma infection, who were either seen at the MRC or identified through field surveys in Sudan. Surgical biopsies were collected from patients with various mycetoma types, durations, and clinical presentations. Thirty-eight patients were excluded from the study because their biopsies lacked grains, which are essential for a conclusive diagnosis of mycetoma, even if clinical symptoms are present. As a result, the MyData database includes samples from 142 patients with confirmed mycetoma infection. These patients were randomly selected from cases seen over the past five years to ensure homogeneity and diagnostic accuracy, regardless of age, sex, or race. Samples were selected to balance the eumycetoma and actinomycetoma classes, but the genus and species were not considered for the selection criteria. A summary of the MyData database population is provided in Table 1.

Table 1: The demographic of the studied population.

Characteristic	Category	Number
Age in years	10 – 70	
Sex	Male	89
	Female	53
Type	Eumycetoma	80
	Actinomycetoma	62
Site of infection	Hands	40
	Feet	68
	Others	34
Duration in years	< 1	18
	> 1 – 5	69
	> 5 – 10	46
	> 10	9
Lesion size	Small (< 5 cm in diameter)	35
	Moderate (5–10 cm)	59
	Massive (> 10 cm in diameter)	48

3.2 Sample diagnosis

Specialised microbiologists at the MRC conducted grain culture techniques to identify the mycetoma causative agents. We reviewed all histological tissue blocks along with their

corresponding culture diagnoses to check for any misdiagnosis or incorrect identification of the causative agents. Any samples with conflicting diagnoses were excluded from the database.

Next, we examined all data on the genera and species responsible for mycetoma. Since fungal species are often misidentified using culture techniques (van de Sande, 2013), we identified actinomycetoma at the species level and eumycetoma at the genus level. For some eumycetoma samples, we used molecular techniques to achieve species-level identification.

All the actinomycetoma samples in our database were identified as either *Actinomadura madurae* (AMM), *Streptomyces somaliensis* (SS), or *Actinomadura pelletieri* (AMP). They were determined using both grain culture and histopathological examination. For our eumycetoma data, 32 patients were assessed using both grain culture and histopathology and were classified as *Madurella* species (Mspp), *Aspergillus* species (Aspp), or *Fusarium* species (Fspp). For an additional 48 patients, a molecular technique was used to determine whether they were *Madurella* mycetomatis positive (MM+) or not (MM-). A summary of this data is provided in Table 2.

Table 2: The distribution of study samples.

Causative Agent	Species	No. Patients
Eumycetoma	<i>Madurella</i> spp. (Mspp)	22
	MM+	29
	MM-	19
	<i>Aspergillus</i> spp. (Aspp)	8
	<i>Fusarium</i> spp. (Fspp)	2
Actinomycetoma	<i>Actinomadura pelletieri</i> (AMP)	9
	<i>Actinomadura madurae</i> (AMM)	9
	<i>Streptomyces somaliensis</i> (SS)	44

4. Histopathology and Slides Preparation

This section outlines the essential steps involved in preparing tissue slides for histopathological examination, Figure 2.

The process begins with collecting tissue samples from the site of investigation through surgery or biopsies, adhering to standard histological procedures. The preparation process involves three key steps (Suvarna et al., 2018):

1. **Tissue collection and Fixation:** Tissue was obtained via fine needle aspiration, tru-cut needle biopsy, or surgical biopsy. Larger biopsies provided more material for a comprehensive examination. The collected tissue was immersed in a fixative solution to prevent degradation and inhibit microorganism growth.
2. **Embedding and Sectioning:** The tissue was embedded in a supportive material, typically paraffin wax,

to create solid blocks. These blocks were then sliced into thin sections, usually $(3-5)\mu\text{m}$ thickness, using a microtome. The sections were placed in a heated water bath to melt the paraffin and smooth out wrinkles before being mounted on glass microscope slides for preservation and enhanced visual clarity.

3. Staining: To improve contrast and aid in identifying regions of interest (ROIs), the tissue sections were stained. Haematoxylin and Eosin (H&E) stain, the most commonly used histological stain, was used.

These procedures were conducted at the microscopy facility of the University of Tours and according to standard protocols at Bretonneau Hospital in Tours, France. The prepared sections were then imaged using an optical light microscope to capture detailed microscopic images to document the grain morphology and the host tissue reaction and components.



Figure 2: Comprehensive View of Histopathology Process

5. Preparation of Microscopic Images in MyData

5.1 Mycetoma Tissue Images Acquisition

The tissue slides from the tissue blocks of 142 patients were handled with a unique reproducible acquisition protocol to ensure a uniform database. Microscopic images were captured in RGB color space using a Nikon Eclipse 80i digital microscope (Figure 3) according to the conditions given in Table 3. For each patient, a variety of grains were examined, with an average of six grains per patient. While the histopathological tissue slide screening aimed to capture one grain per field (Figure 4a), some slides contained adjacent grains, leading to multiple grains appearing



Figure 3: Digital Microscope

Table 3: The distribution of study samples.

Parameter	Value
Brightness control	Knob 5/10 ND8 On ND32 On
Field diaphragm	Highest level
Magnification	10 \times
Dimension and Quality	800 \times 600
Colour	Enhance and white auto
Field diaphragm knob	Highest level
Filter	6
NCB11 Filter	Off

in a single image (Figure 4b). In these instances, only one grain per image was included in the image.

5.2 Ground-truth Segmentation of Mycetoma Grains

For histopathological diagnosis, it is crucial to identify grains within the tissue to determine the causative agents and provide appropriate treatment. Consequently, mycetoma grains are considered the Regions of Interest (ROIs) in the tissue images. Manual segmentation of these grains was essential to create a comprehensive and accurate database of mycetoma tissue grains and their annotations. This database can then be utilised for computational tasks related to histopathological tissue diagnosis.

Grains from the histopathological microscopic images of mycetoma-infected tissues were manually segmented using ImageJ software. This task was performed by an expert from the MRC with a strong background in image processing, ensuring high-quality and accurate annotations. Each image in the dataset was annotated by labelling pixels as

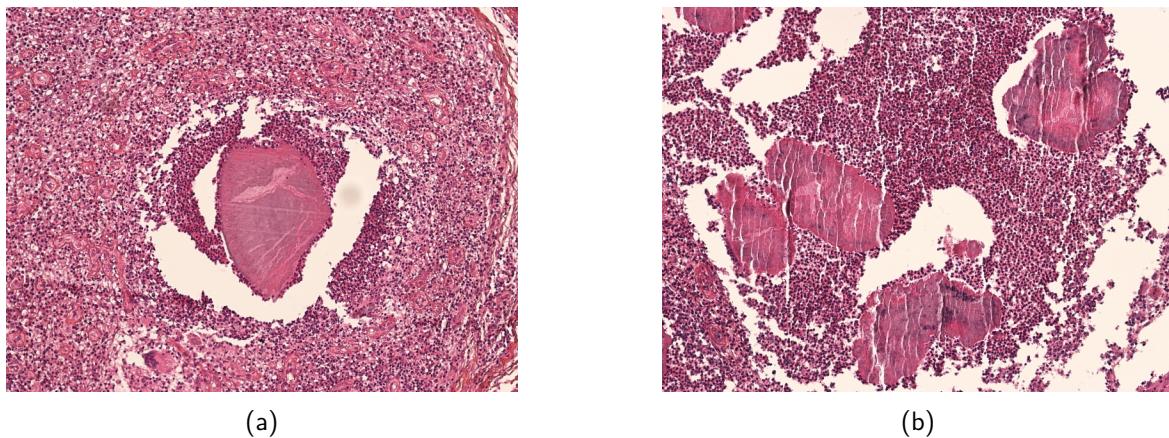


Figure 4: Mycetoma Microscopic Images. (a): Single grain. (b): Multiple grains.

either ROI or background, with pixels labelled as 1 representing the ROI and those labelled as 0 representing the background. These original images and their annotations are used for training and validating AI models.

The performance of any AI model depends on the precision of our manual segmentation. Therefore, this process is carried out meticulously to outline the grain borders accurately, avoiding the inclusion of other tissue components or inflammatory cells unless they are part of the grain itself. Additionally, the annotated grains must encompass the entire grain area, even if there were background or visible fractures within the grain. Figure 5 displays sample microscopic images along with their annotated grains.

6. MyData: Mycetoma Histology Microscopic Images Database

The database contains a total of 864 microscopic tissue images from 142 patients. It is composed of 471 eumycetoma and 393 actinomycetoma images. The images are in JPEG format, while the ground truth annotations are in TIFF format. Table 4 gives the summary of database images.

Table 4: Summary of images in MyData considering the mycetoma organisms.

Causative Agent	No. Images	Species	No. Images
Eumycetoma	471	Madurella spp. (Mspp)	149
		MM+	167
		MM-	110
		Aspergillus spp. (Aspp)	36
		Fusarium spp. (Fspp)	9
Actinomycetoma	393	Actinomadura pelletieri (AMP)	57
		Actinomadura madurae (AMM)	62
		Streptomyces somaliensis (SS)	274

6.1 Images conditions

Technical and human errors:

The tissue samples were collected, labelled, prepared, and

diagnosed by laboratory technicians and pathologists. Following collection, samples were processed and examined using histopathological techniques and grain culture, with results compared to verify accuracy. Any discrepancies led to the removal of samples from the database, and labels and results were double-checked to minimise errors.

A challenge in mycetoma histopathological diagnosis is the complete or partial disappearance of grains in tissue slides, even though they are present in the tissue blocks. The sectioning or mounting process often causes this issue. The solid or rigid texture of mycetoma grains can lead to improper sectioning due to the thinness of the slides. To address this, we prepared two slides for each patient sample to maximize the chance of grain presence.

Folding and dissociation of sections in slides is a common problem in classical histology processing. Therefore, we accepted this as a normal condition in mycetoma tissue processing. Slides with folds were treated as regular slides and included in the database. From the two prepared slides, we selected the one that contained the grain and had a better appearance in terms of folding and tissue separation.

6.2 Exclusion and inclusion criteria of samples in MyData

Considering the conditions mentioned, the following criteria were defined for including and excluding images:

- For each patient, all grains in the tissue slide are included regardless of size and shape.
- If a grain is larger than the image size but fits the field, the visible part is included (Figure 6a).
- Partially folded grains (Figure 6b) are included; completely folded grains are excluded.
- Tissue sections showing dissociation due to tissue reaction or processing (Figure 6c) are included.

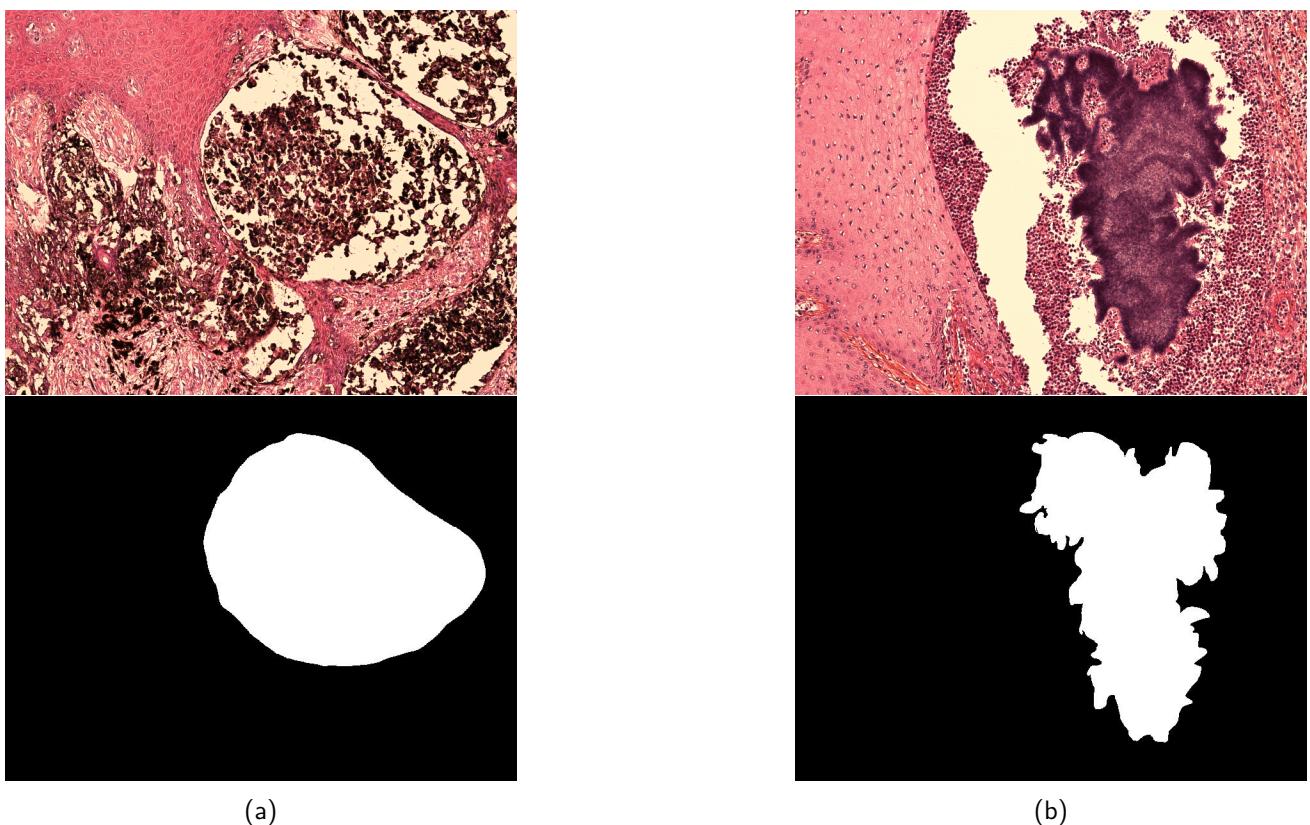


Figure 5: Mycetoma Microscopic Images and its annotated grain. (a): Eumycetoma with fracture grain. (b): Actinomycetoma grain.

6.3 Labelling

Labels were defined considering patient ID to avoid statistical bias. Eumycetoma (fungus) and actinomycetoma (bacteria) are denoted as FM and BM, respectively. The naming format is main-type_patient-ID_grain-number. Ground-truth segmentation for grains adds a “_mask” suffix to the grain image name. For example, *FM3_4* means it is an eumycetoma sample from patient 3, grain 4. The segmentation for *FM3_4* is named *FM3_4_mask*.

7. Conclusion

This report describes the creation of MyData, the first database of mycetoma histopathological microscopic images. It includes detailed information on the samples used to compile the database. MyData is a comprehensive collection containing 864 microscopic tissue images with segmented ground-truth grain images from 142 patients. The database includes 80 eumycetoma and 62 actinomycetoma samples, representing four of the five most common mycetoma species worldwide. This makes MyData an important initial step toward developing a broader and larger database with various species from around the world, especially given the specific preparation and acquisition protocols provided. MyData paves the way for global collaboration by encouraging laboratories worldwide to collect new samples. It

also supports the creation of databases for different types of mycetoma images, such as X-rays and ultrasounds. We are open to collaboration and the exchange of knowledge, skills, and expertise to further advance this field. Additionally, we provided guidelines and optimised protocols for image preparation and acquisition. Following these guidelines offers numerous benefits, such as maintaining consistency, improving quality assurance, reducing errors, enhancing productivity, and preserving the integrity of the data.

Initially, the MyData database was collected and prepared to develop a diagnostic model for mycetoma. Recognising its potential value to the scientific community, we later decided to publish the database. The collected samples reflect the epidemiological distribution of mycetoma in Sudan, the epicenter of this disease. Given that mycetoma is a neglected disease, we believe the MyData database is highly suitable for publication. The database size is sufficient and comparable to the total infected population, and it includes the most common causative organisms in Europe and Africa, as well as less common ones in South America and Asia.

Using MyData, we developed and evaluated a machine learning model to analyze histopathological microscopic images of mycetoma grains and classify the disease as either eumycetoma or actinomycetoma. The model, which

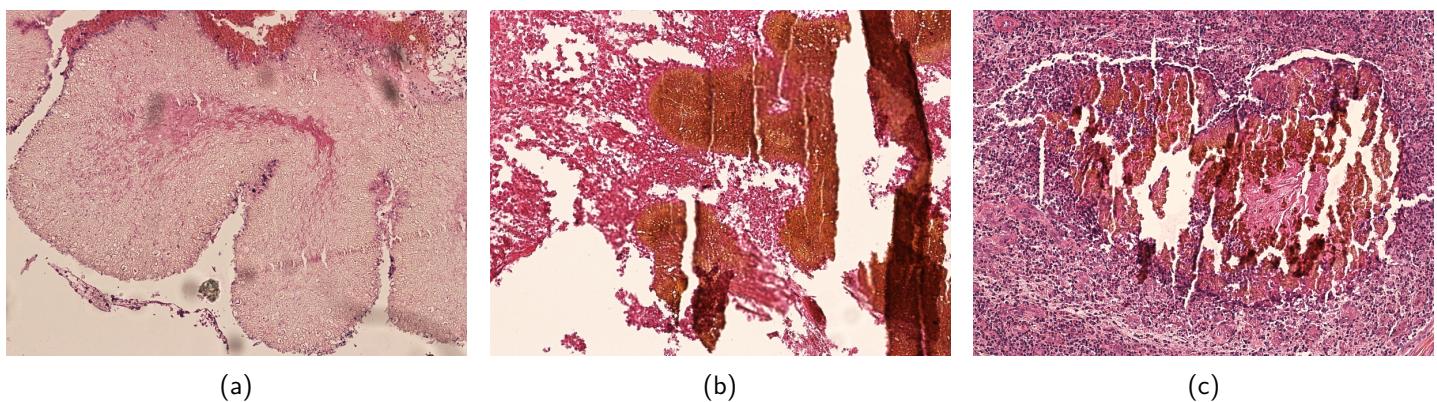


Figure 6: Example of the images included in the database

employs radiomics and partial least squares, achieved an accuracy of 91.89% (Omar Ali et al., 2024). This illustrates the potential applications of the dataset in advancing diagnostic tools for mycetoma.

As the first database of mycetoma histopathological microscopic images, MyData represents a significant advancement. It provides a solid foundation for future research and can be expanded and refined in subsequent versions to further enhance its utility and comprehensiveness. In future work, we plan to assess inter- and intra-rater variability to strengthen the annotations further. This assessment will help evaluate the consistency and reliability of the annotations, ensuring the database's robustness for ongoing and future research.

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Ethical Standards

This study received approval from the Soba University Hospital Institutional Review Board Committee in Khartoum, Sudan (No. SUH 05/01/2019). Clinical data were collected from patients treated at the Mycetoma Research Center (MRC). Prior to collecting surgical biopsies, written informed consent was obtained from each patient. These biopsies were taken from patients who visited the MRC over the past five years, representing a range of mycetoma

types, durations, and clinical presentations.

Conflicts of Interest

We declare we do not have conflicts of interest.

Data availability

MyData is publicly hosted in two permanent non-commercial repositories; AFRICAI repository (Omar Ali, Hyam and mAlcetoma Team, 2024) and Zenodo (Omar Ali and mAlcetoma Team, 2024). Access to the dataset is restricted and requires submission of a formal request through the hosting repositories. The dataset is released under the Creative Commons Attribution (CC BY 4.0) license, allowing reuse, redistribution, and adaptation with appropriate attribution. It adhere to the FAIR data principles and follow the guidance outlined in AFRICAI Imaging Repository (Starmans and Tsirikoglou, 2024) for proper data uploading and backup procedures.

Potential Use Cases

This dataset is intended to support AI and medical imaging research, particularly in the areas of automated histopathological image analysis, mycetoma grain segmentation, and mycetoma type classification. Potential use cases include benchmarking deep learning and machine learning models for segmentation and classification, developing AI-assisted diagnostic tools for neglected tropical diseases, and advancing research in digital pathology for low-resource clinical settings.

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