Computational Diagnostic Method of the Organisms Causing Mycetoma Based on Histology

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INTRODUCTION

The Disease

- Mycetoma is a subcutaneous infection that leads to massive deformities and disabilities.⁽¹⁾
- Mycetoma by bacterial caused (Actinomycetoma AM) or fungal (Eumycetoma



• Tropical and subtropical regions (**The Mycetoma belt**)

Laboratory Diagnosis

- Identification of causative agents relies on the analysis of grains that develop in infected tissues.
- Grain culture is a core tool but it is time consuming.

EM).

• The treatment of mycetoma depends on the accurate identification of the causative agents.^(1,2)





Aim of Our Project

- Molecular techniques provide authenticated results, it is expensive.
- Cytological and Histopathological are rapid, cheap and commonly used in rural areas.
- HISTOPATHOLOGY is considered to be an efficient, cost and time-effective tool for mycetoma diagnosis in endemic areas.^(2,3)

To develop an automated diagnostic method that could reduce the need for expert pathologists in non-

specialized clinical centres to perform *histological analysis*.

MATERIAL AND METHOD

Dataset

- Tissue biopsies of **142 mycetoma** patients with **80** EM and **62** patients with AM.
- Tissue sections were stained with Haematoxylin and Eosin stain (H&E).
- Images were captured in RGB colour space with a magnification of **10×.**
- *Nikon Eclipse 80i* microscope was used for acquisition.
- The dataset contained a total of **864** tissue grain microscopic grain images.



Classification/Diagnosis

• Using **RADIOMICS** in conjunction with **Partial least squares** discrimination analysis (PLS-DA), we proposed a model to discriminate between AM and EM effectively.



- To further increase the automatization of the method we proposed a **CNN model for** grain segmentation.
- Our proposed model is a reduced version of Unet with small number of weights in each layer.



RADIOMICS

RESULTS

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Manual Segmentation

- manually segmented grains, our • From achieved method mycetoma type identification with an accuracy of **91.8**%.
- ♦ EM AM
- This is comparable to the score obtained by experts $(92.4\%)^{(4)}$.
- The model is assessed against manual





CNN Segmentation

- The network achieved a DICE index of 0.7626 and 94.9% accuracy on segmentation task.
- The segmentation is assessed to classify the mycetoma agents by using radiomic model.
- The diagnosis accuracy was 88% for the integrated automated segmentation and radiomics model.

Prediction **Ground Truth** Image







CONCLUSION

- The different effective diagnostic tools currently used for mycetoma diagnosis require expert physicians and/or expensive hardware equipment.
- In this work, we introduced a novel, simple, low-cost computational method that could be integrated into routine histopathological diagnosis procedures in endemic areas. The proposed method uses radiomics in conjunction with PLS-DA to effectively discriminate between actinomycetoma and eumycetoma.
- With the manually segmented grains, our model has a performance similar to experts. The accuracy is slightly decreased but remains close with auto-segmented grains.
- Further work will aim at better avoiding false positive grain segmentation to increase the robustness of the automated approach.

References

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