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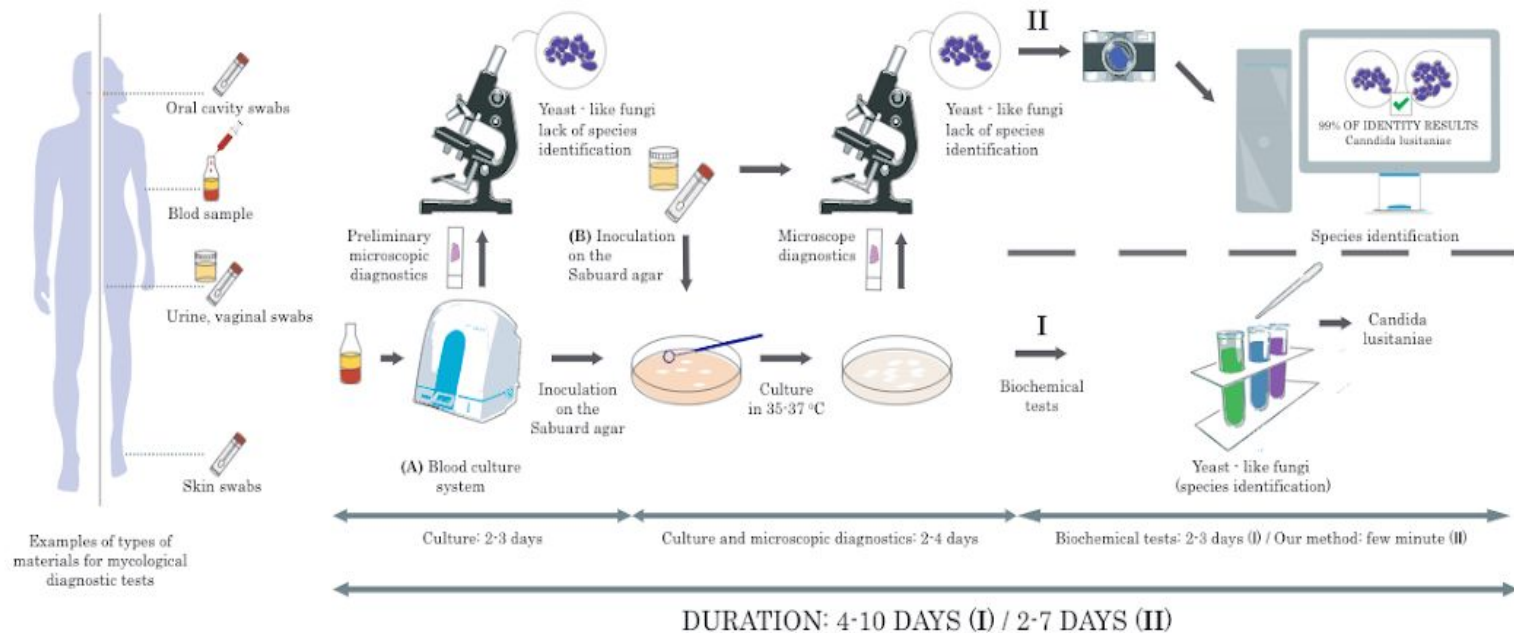
Deep learning approach to describe and classify fungi microscopic images

Medical Imaging with Deep Learning 2020

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Motivation

- We use a machine learning approach to classify microscopic images of fungi species.
- It can make the last stage of biochemical identification redundant, shorten the identification process by 2-3 days, and reduce the cost of the diagnosis.



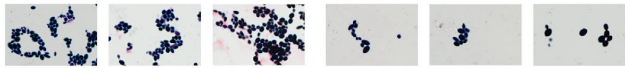
Problem description

- Images of resolution $3600 \times 5760 \times 3$.
- Small dataset (180 images).
- 9 fungi species.
- 2 preparations per fungal strain.
- Gram staining.



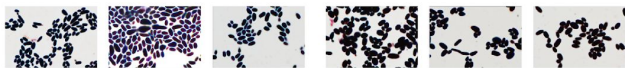
(a) *Candida albicans* (CA)

(b) *Candida glabrata* (CG)



(c) *Candida lusitanae* (CL)

(d) *Cryptococcus neoformans* (CN)



(e) *Candida parapsilosis* (CP)

(f) *Candida tropicalis* (CT)



(g) *Maalasezia furfur* (MF)

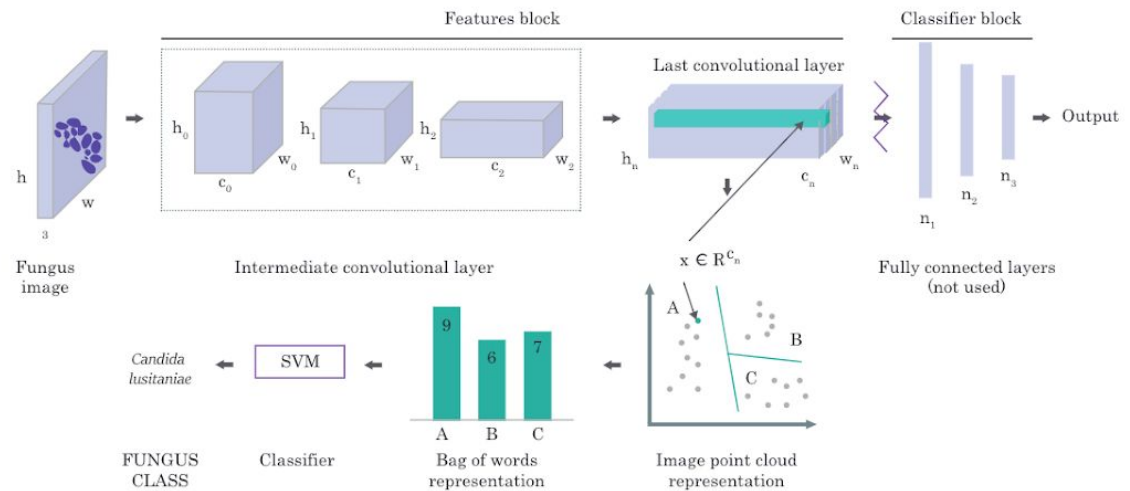
(h) *Saccharomyces boulardii* (SB)



(i) *Saccharomyces cerevisiae* (SC)

Methodology

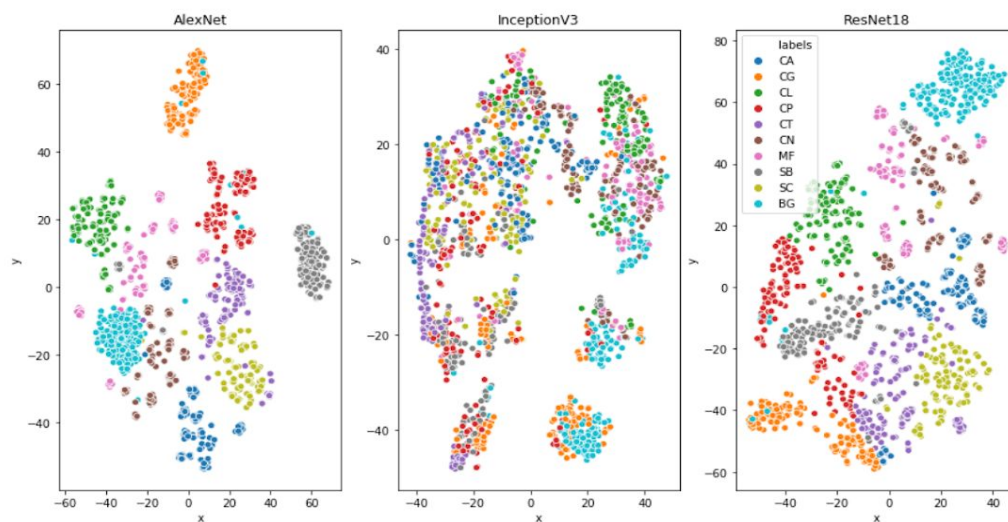
- We combine deep neural networks and bag-of-words approaches to identify fungi species causing common fungal infections.
- Each of the images is preprocessed with contrast stretching, and thresholding segmentation is used to differentiate between background and



Experiments and results

- Image patches of size 500x500 pixels are first represented with features obtained using a pre-trained convolutional part of selected neural networks (AlexNet, InceptionV3, ResNet18). Then, this representation is coded using the Fisher Vector.
- We compared the results for patch-based and scan-based classification of our method to fine-tuned neural networks (scan-based classification is obtained by patch-based voting).
- We projected the features obtained from NNs using T-SNE and observe that the representation from AlexNet is the most descriptive.

Method	Patch-based	Scan-based
AlexNet	71.6 ± 2.4	77.3 ± 4.2
InceptionV3	69.9 ± 1.9	65.9 ± 4.9
ResNet18	75.9 ± 2.6	78.3 ± 5.4
Fisher vector with AlexNet	82.4 ± 0.2	93.9 ± 3.9
Fisher vector with InceptionV3	41.3 ± 1.9	55.0 ± 5.6
Fisher vector with ResNet18	71.3 ± 1.5	88.3 ± 2.7



Interpreting the results

- We analyze classifier certainty by investigating the distance of patches' representations from the classifier hyperplane.
- Our method has the potential to be successfully used by microbiologists in their daily practice.

