Automatic segmentation and classification of fungal-infected tissue using Deep Learning

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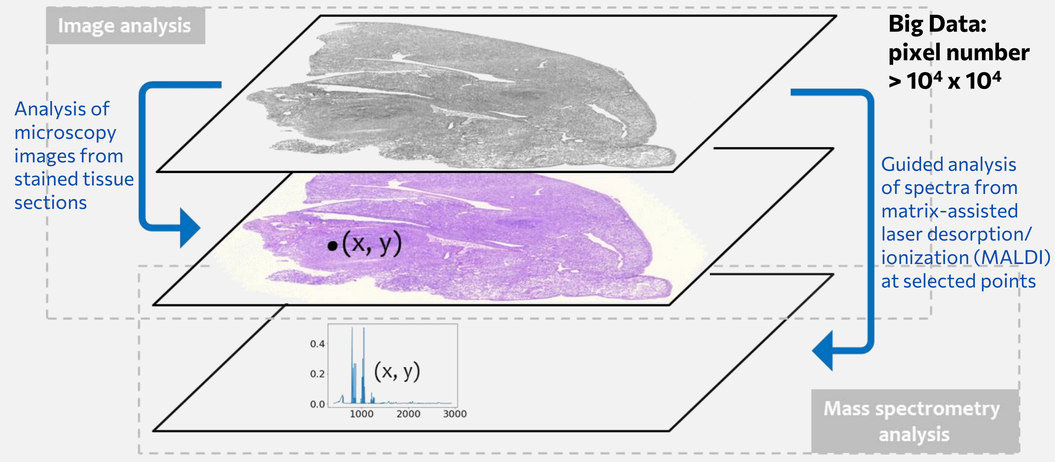
Medical background

- Increasing number of patients with invasive fungal infections (2.5 million per year worldwide)
- High mortality rate of 40% - 60%
- Challenging diagnosis which is based on morphological features of histochemicaly stained tissue sections
- Improvement of diagnosis and identification of fungal genus for a better therapy decision, by combining of:

Histopathological evaluation & spectral classification

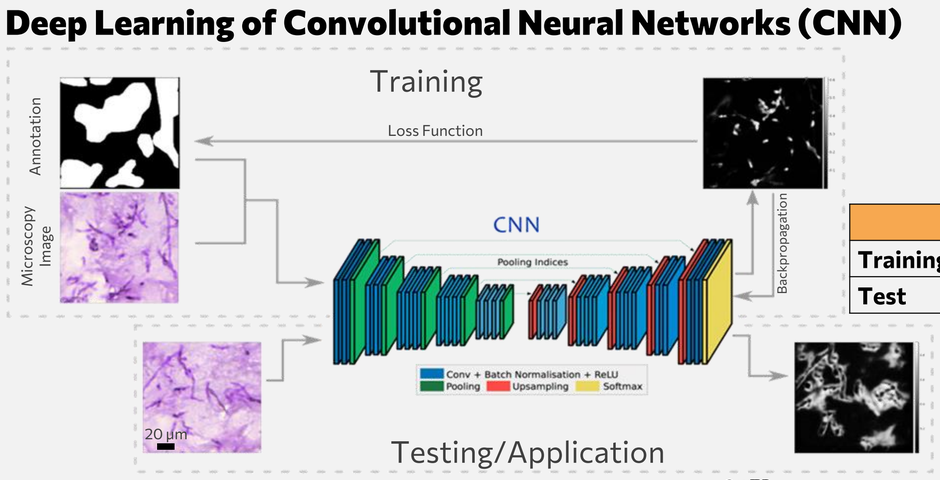
Study design

- Combine optical image analysis with MALDI [1] to detect fungal infected regions
- Learn one segmentation model for multiple staining methods:
  - Gomori (Gömöri trichrome stain)
  - PAS (Periodic acid-Schiff reaction)
- Classify mass spectrum (MS) according to respective fungus species



Optical image segmentation

Deep Learning of Convolutional Neural Networks (CNN)

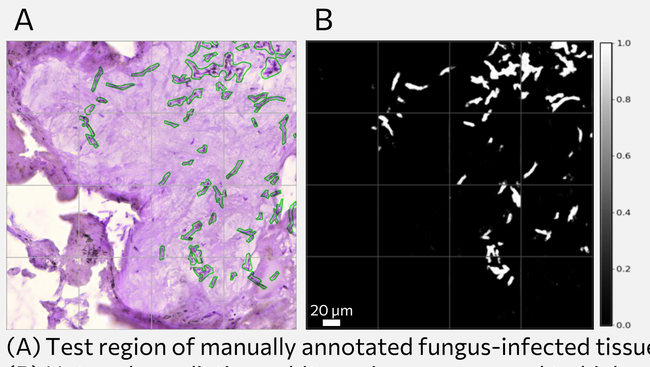


images:

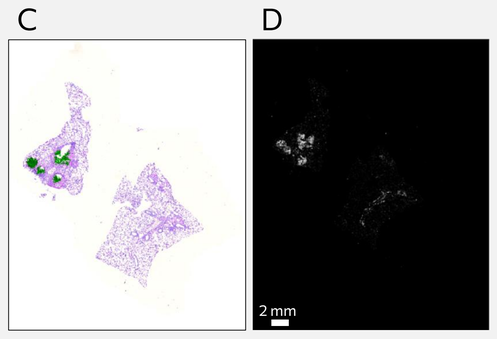
	Gomori	PAS
Training	2322	2850
Test	410	503

Network – metric-value on test images: $Dice\ Coefficient(DC) = \frac{2x\ TP}{2\ TP+FP+FN} = 0.93$

Segmentation results

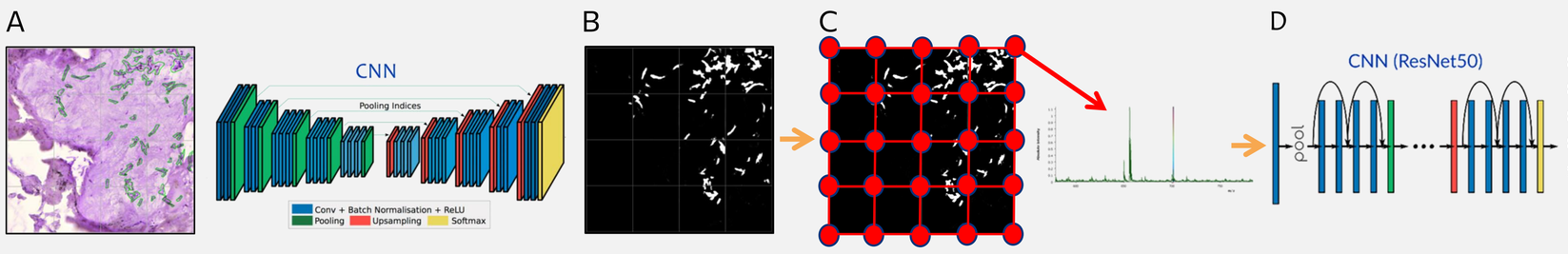


Network inference



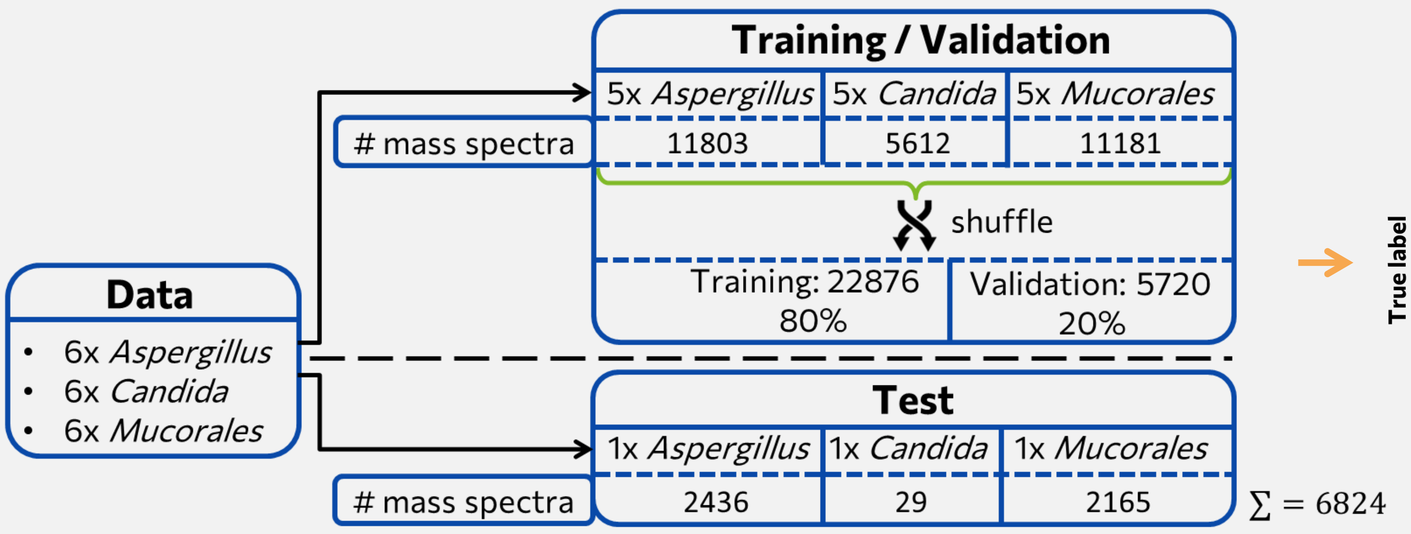
(A) Test region of manually annotated fungus-infected tissue
(B) Network prediction: white regions correspond to high probability *P* of fungal-infected tissue Scalebar: *P(fungal-infected tissue)*
(C) Complete tissue sample: green regions represent the annotated fungus
(D) Network for the entire sample image using the SegNet [2] CNN

Correlative analysis: Microscopy images and MALDI imaging

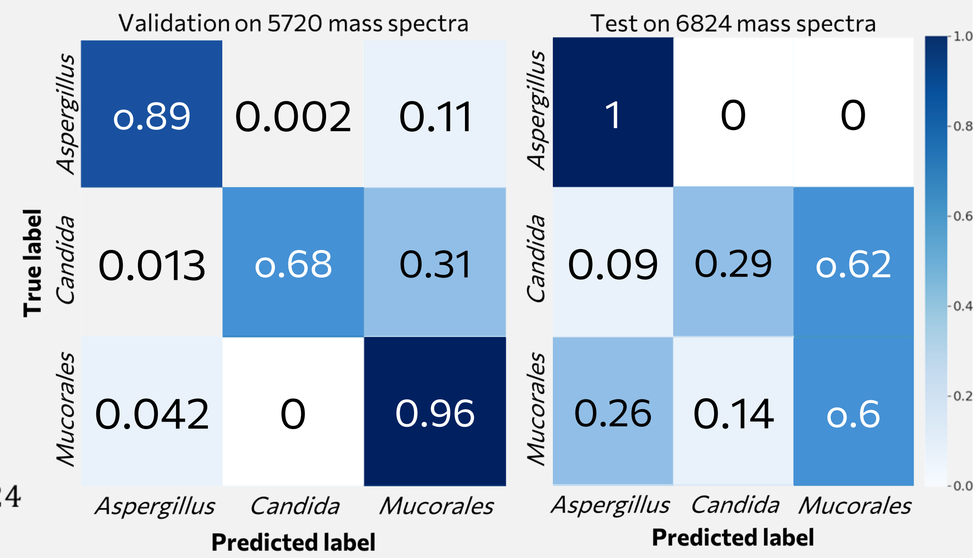


(A) Using of manual annotations and
(B) output of Segmentation CNN as labels
(C) Use CNN prediction as seed points for spectral classification
(D) Apply second CNN on spectra data of the same infected tissue section with previously segmented ROIs

Classification of fungal genus based on mass spectra



Preliminary results of ResNet50 model



Conclusion: While it is possible to detect fungal infected tissue on optical histopathology images independent of various environmental conditions such as the fungal genus, organ, or staining method used, it is challenging to identify the corresponding fungal genus in spectral data on test images that the network has never seen before. We use here several advanced techniques to overcome this problem and provide a novel translational clinical approach. CNN provide the ability to learn features in a data-driven manner, while techniques exist to visualize where these networks are actually looking during the underlying decision process of each sample. The use of this inverse mapping may allow us to identify the molecular fingerprint for the fungal genus in this study.

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References
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[2] Badrinarayanan *et al.* 2016. *IEEE Trans Pattern Anal Mach Intell.* 39: 2481-2495