

Towards automated screening of Gram stained slides by combining a slide scanning platform and deep learning analysis methods

S. Hänselmann, S. Degenhardt, H. Mannsperger
MetaSystems Hard & Software GmbH, Altlussheim, Germany



Class	Precision	Recall	f1-Score	Support
Background	0.98	0.98	0.98	1496
Gram+ Diplococci	0.86	0.91	0.88	184
Gram+ Clusters	0.97	0.97	0.97	557
Gram+ Chains	1	0.97	0.98	464
Gram- Rods	0.96	0.98	0.97	699
avg/sum	0.97	0.97	0.97	3400

Table 1: Classification accuracies for the test data set for the different classes

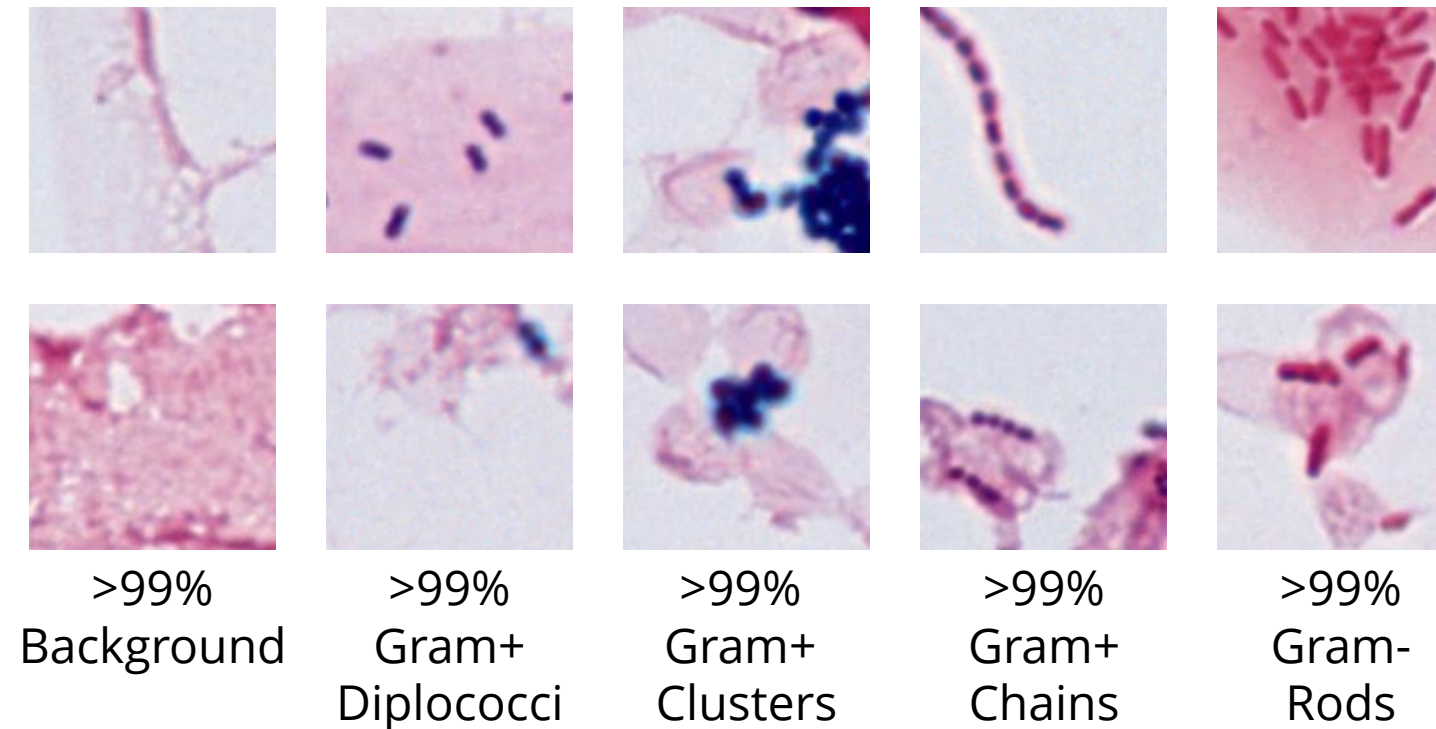


Image 1: Examples of predicted class probabilities

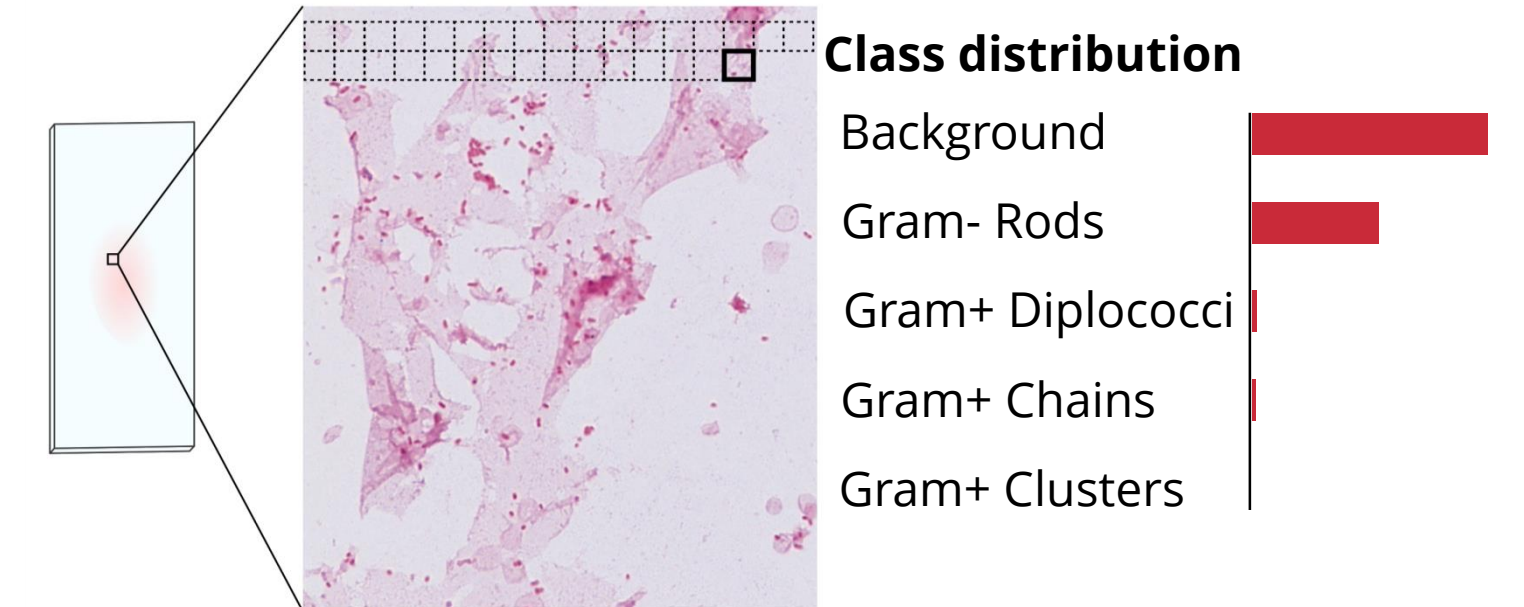


Image 2: Generation of a class distribution as result of the screening process

Background

Automated digital imaging of Gram stained slides promises to improve the diagnostic workflow with respect to ease of case review, information sharing, and documentation. On-screen review of digital images replaces tedious manual microscopy and provides considerable practical and ergonomic benefits by itself. As published recently, deep learning techniques can potentially support interpretation of digital Gram images¹⁾. To match the growing demand for workload reduction and efficiency increase in the review process of Gram stained slides we have integrated deep learning-based object classification using convolutional neural networks (CNN) with our automated scanning platform Metafer to create a unique Gram slide screening environment.

¹⁾ Smith et al. (<https://doi.org/10.1128/JCM.01521-17>)

²⁾ We would like to thank Drs. I Burckhardt and S. Zimmermann from the Department for Infectious Diseases Medical Microbiology and Hygiene, University Heidelberg for providing Gram stained samples.

Materials/Methods

Twelve Gram stained slides²⁾ from positive blood cultures were scanned automatically with the Metafer slide scanning system (MetaSystems) using a 40x oil immersion objective (Zeiss) and a high-resolution camera (CC 4c, MetaSystems). A prescan automatically identified suitable fields of view based on color intensity and contrast in order to avoid empty or overstained areas. From each field of view, image-tiles of 144 pixels by 144 pixels were extracted in a grid-like manner. A CNN was trained to categorize each tile into one of 5 classes: 0) empty/background, 1) Gram-positive diplococci, 2) Gram-positive clusters, 3) Gram-positive chains, 4) Gram-negative rods. Training success was evaluated based on a test set of 3,400 previously unseen tiles.

Results

After training, the CNN achieved an overall classification accuracy of 97.1% for all categorization classes for the 3,400 test tiles. When applied in a blind test to 12 new slides, the CNN correctly detected the respective categorization class as confirmed independently by two experts after manual review. Using a budget graphics card with 768 cores, a Metafer scanning system can scan and classify one slide in around 3 minutes.

Conclusions

Automated slide scanning and classification of Gram stains by deep learning will save working time and improve the adequacy of primary positive blood culture diagnostics.