Computer Vision in Hematological Malignancies

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Background
Following excellent results in pathology and radiology, deep learning -based image analysis is increasingly applied to support routine diagnostics. However, there is an unmet need in hematology for automated machine vision to speed up and standardize routine diagnostics. Moreover, the full potential of May-Grünwald-Giemsa (MGG) and hematoxylin-eosin (H&E)-stained bone marrow (BM) samples in describing the clinical course of hematological diseases has likely not been unveiled.

Methods
In study I (Brück et al, 2021), 236 MDS, 87 MDS/MPN, and 11 control BM biopsies were stained with H&E and digitized with a slide scanner. Clinical data, cytogenetics profiles and results of a clinical targeted myeloid sequencing panel were collected. Morphological features were extracted with convolutional neural networks and used to predict genetic and cytogenetic aberrations, survival and patient demographics with multivariate regression models.
In study II, we digitize routine clinical MGG-stained samples with a two-phase strategy (10x and 100x) using an automated slide scanner. Digital images are transferred to a clinical database and automatically labelled with essential clinical information. From images, white blood cells are detected and classified with a regional convolutional neural network. Moreover, images are automatically classified by their clinical urgency.

Results
In study I, we could predict the occurrence of *TET2* [area under the receiver operating curve (AUROC) = 0.94] and spliceosome mutations (0.89) as well as chromosome 7 monosomy (0.89). We found that the probability of a mutation correlated with its variant allele frequency emphasizing the algorithms' ability to identify relevant morphologic patterns.
In study II, we show how 400 slides can be digitized weekly achieving a digital slide archive of 12 000 samples as of October 2021. Moreover, we achieved over 0.90 classification accuracy for multiple white blood cell types.

Conclusions
Image analysis of BM samples represent an understudied and promising avenue that can possibly help to improve our understanding of hematological diseases and automate diagnostics, disease monitoring and treatment response prediction.

Keywords
Computer vision, MGG, H&E, bone marrow, machine learning