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POSTER ABSTRACTS

803.EMERGING TOOLS, TECHNIQUES AND ARTIFICIAL INTELLIGENCE IN HEMATOLOGY

Automated Cytomorphological Analysis of Bone Marrow Samples: A Proof-of-Principle Study for AI-Based Classification on a Real-Life Data Set of 979 Unselected Cases

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BACKGROUND: Cytomorphological analysis of bone marrow (BM) samples is a cornerstone of hematological diagnostics. It requires microscopical cell counting by a human specialist, resulting in a differential cell count and a morphological description/diagnosis. The process is susceptible to interobserver variability and may be limited by the areas examined.
AIM: Clinical implementation of AI-based recognition of pathological patterns in BM smears to support cytomorphological diagnostics.
METHODS: We evaluated unselected BM samples over a three-week period (n= 979), including cases with various hematological diseases. We analyzed both shipped unstained slides (n=522, 53%) and smears prepared in-house from BM aspirates (n=457, 47%) with variable shipping time (0-10d, median = 1d), reflecting diagnostic reality in an international reference laboratory. After conventional cytomorphological assessment, each sample was further analyzed by immunophenotyping, cytogenetics, FISH or molecular genetics, according to diagnostic guidelines. BM slides were then scanned using a Metasystems Metafer System (Altlussheim, GER), yielding up to 52 fields of view (FOVs) (2048x1496px each). Cells were automatically identified, segmented, and imaged resulting in 2636 cells per case on average (range = 0 - 10,072, SD = 2164), which were classified into 24 distinct cell classes using an AI-classifier based on the ResNext-architecture. After eliminating 107 samples (10.9%) due to insufficient scanning/sample quality or low cell counts (<100), 872 samples were further analyzed. We defined 7 relevant pathological patterns extractable from human differential counts which served as ground truth for comparison with AI-based classifications: elevated blast fraction (three-tiered, ≥5%, ≥10%, ≥20%), eosinophilia (≥ 20%), plasmacytosis (≥10%), lymphocytosis (≥20%) and monocytosis (≥5%). For each case, we calculated the median prediction probability (MPP) for each pathological pattern, based on the sum of single cell predictions for pattern-specific cell type and cell fraction (Figure 1).
RESULTS: Out of 872 analyzed cases, 341 cases showed one pathological pattern (39.1%), 85 cases showed two patterns (9.7%), and 8 showed three patterns (0.9%) as ground truth. MPP for the pathological patterns were: 0.60 for blasts ≥20% (indicating acute leukemia), 0.52 for blasts ≥10% (e.g. suggesting MDS-IB2), 0.61 for blasts ≥5% (e.g. suggesting MDS-IB1), 0.90 for Eosinophilia (suggesting ML-Eo, HES), 0.87 for plasmacytosis (suggesting plasma cell myeloma), 0.87 for lymphocytosis (suggesting lymphoma) and 0.79 for monocytosis (suggesting MDS or CMML). In cases presenting a blast fraction ≥20% (ground truth) and an MPP for blasts below the median of 0.61, MPP for lymphocytosis and monocytosis was substantially higher (0.81 and 0.71 respectively). This points to the known challenge of differentiating these 3 cell types in AI-supported as well as in human cell classification. Of note, pathological patterns of high clinical relevance (i.e. elevated blast fractions) had consistently low MPP in true negative cases (0.03 for blasts ≥20%, 0.07 for blasts ≥10%, 0.15 for blasts ≥5%).
CONCLUSION: We successfully implemented automated scanning and AI-based recognition of pathological patterns in a high-throughput routine workflow on unselected BM smears with variable pathologies, preanalytical parameters and quality. AI detected 7 relevant pathological patterns extracted from human differentials at acceptable prediction probability, even if present concurrently. Confusion of mononuclear cells was noted and requires further optimization of image acquisition and AI-based quality control (e.g., upstream binary classifiers or pre-selection of FOVs) to enhance robustness. This preliminary study proves the technical feasibility of AI-based recognition of pathological BM patterns, to support human investigators in decision making for further diagnostic processes.

Disclosures Kornauth: *MLL Munich Leukemia Laboratory:* Current Employment. **Lupperger:** *MLL Munich Leukemia Laboratory:* Current Employment. **Kern:** *MLL Munich Leukemia Laboratory:* Current Employment, Other: Equity Ownership. **Haferlach:** *MLL Munich Leukemia Laboratory:* Current Employment, Other: Equity Ownership. **Haferlach:** *MLL Munich Leukemia*

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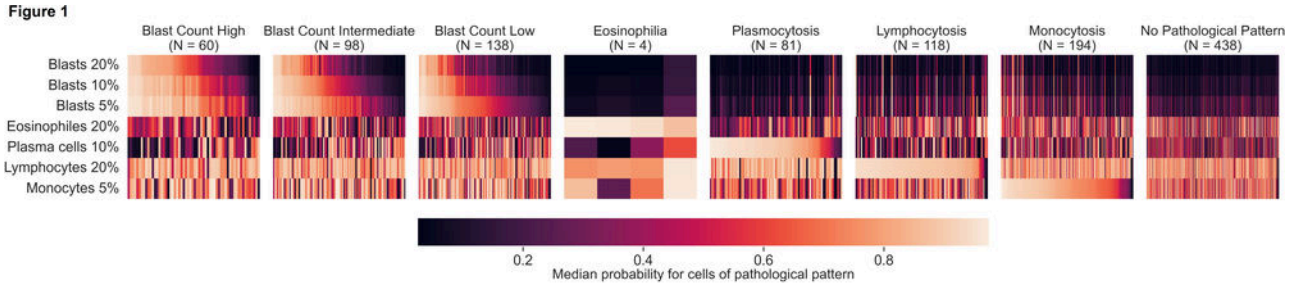

Figure 1

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