AI-BASED BLAST CELL QUANTIFICATION IN MYELOPYSPLASTIC NEOPLASMS AND COMPARISON WITH ESTABLISHED METHODS

Z Kasmani, L Brandes, T Fletcher, K Sirinukunwattana, D Royston

Introduction and context:

Blast cells (CD34+ve) are immature cells that normally reside in the bone marrow. Accurate blast-cell quantification is central to the diagnosis, classification and monitoring of myeloid neoplasms.

Blast cell numbers are currently estimated by a combination of established methods: Bone marrow aspirate cytology, bone marrow trephine biopsy and flow cytometry. These methods only estimate blast cell numbers or are subjective (user dependent).

Aim of AI tool:

Provide accurate and objective blast cell counts in a highly reproducible way by removing user variability.

Potentially useful as a screening tool or to aid task prioritisation in busy pathology laboratories.

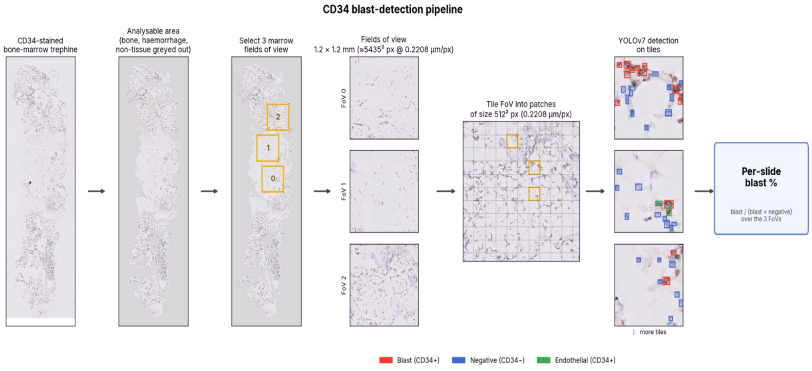
Methodology:

Refine database of reported and digitised histopathology slides for patients across Oxfordshire, Buckinghamshire and Berkshire with myeloid neoplasms

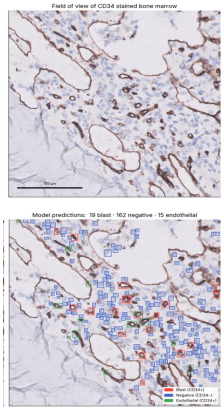
Extract and clean data for blast cell counts across all reported modalities from electronic patient records

Development and training of an AI model to estimate blast cell count, using trained pathologists to manually annotate digital slides

Compare AI model to other modalities, using bone marrow aspirate as the 'gold standard'

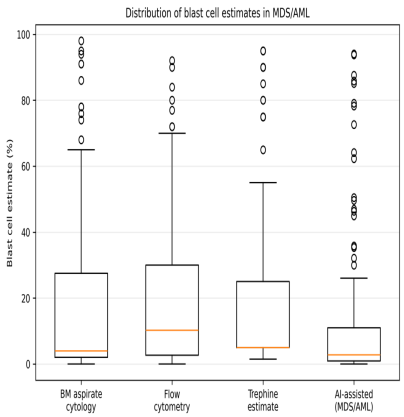


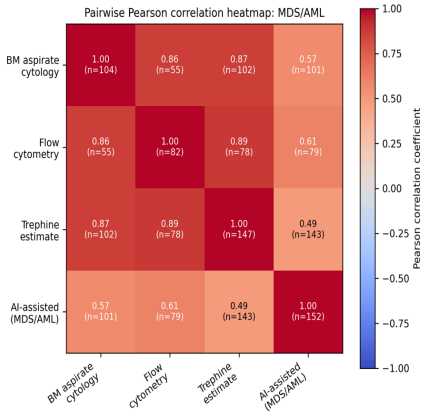
Steps in the CD34 pipeline: 1) CD34 stained bone marrow trephines. 2) Segmentation models run to segment tissue and remove haemorrhage and bone areas. 3) From the resulting analysable area (tissue - bone - haemorrhage), random selection of three fields of view (FoV) for analysis. 4) Tile the FoVs into smaller patches for analysis. 5) For each patch, run a trained inference model, which segments and classifies CD34 negative cells, endothelial cells and blast cells. From the model predictions, compute the blast percentage across the three FoVs which represent the blast cell average percentage across the whole slide.



Expanded image to show FOV model analysis

Preliminary Results:





Blast cell counts were not available across all modalities for each patient, preventing comparison with equal numbers. Total results in each modality: Bone marrow aspirate (104), Flow cytometry (82), Trephine biopsy (147) and AI assisted (152).

The AI-assisted tool was able to provide blast cell estimates between 0 and 1 (the other modalities were not), meaning this method had a lower mean and median

The correlation between bone marrow aspirate cytology and flow cytometry was 0.86; with trephine estimation it was 0.87; and with AI-assisted blast estimation it was 0.57.

Discussion:

Analysis demonstrates that blast-estimation methods are associated but not interchangeable. Flow cytometry and trephine estimation generally tracked bone marrow aspirate cytology more closely than the AI-assisted methods, however only 55 samples were compared in this category due to missing data.

Random FOV analysis may produce inaccurate estimates of total blast numbers due uneven blast cell populations across the histology slide.

Assigning standard quantitative values to qualitative description of blast cell numbers on trephine biopsies may reduce correlation to the AI model. As an example, 'no increase in blasts' was assigned a value of '5%' when the true value may be significantly less.

Next steps:

Immediate:

Further cleaning of data to represent clinically relevant blast cell thresholds, particularly when numbers are <5%, as this may alter statistical correlation.

Review cases where there is a significant discrepancy between the AI method and the other modalities to establish possible cause.

Long-term:

Testing of final, refined model on new histology slides with expert peer review of outcomes.

Trial integration of model into clinical workflow, aiming to reduce observer variability and aid task prioritisation.