

AI-Driven Identification of High-Value Samples: Multi-Modal Screening for Rare and Non-Typical Cases in Clinical Diagnostics

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Introduction

High-volume clinical laboratories frequently struggle with the manual identification of rare (R) and non-typical (NT) specimens (e.g., early MDS, subtle parasitic infections) which hold the highest value for translational research. The conventional, time-intensive review process often subjects specimen triage to delays and high inter-observer variability.

Objectives

To develop and validate a Multi-Modal AI Diagnostic Assistant (AI-DA) that intelligently fuses diverse data streams to autonomously identify and flag R/NT samples, serving as a standardized "Research Accelerator" for laboratory hematologists.

Methods

The Dymind AI-DA utilizes a fusion architecture integrating vision and language models. The system employs: 1) A Vision Model for Optical Character Recognition (OCR) on physical IVD reports, extracting key numerical test results; and 2) A Large Language Model (LLM) fine-tuned on medical texts to process unstructured patient complaints and history. The system's key advantage is its robustness in handling unstructured and optional inputs (e.g., clinical notes or patient symptoms may be provided alone). The system input encompasses a comprehensive panel of IVD test results (hematology, coagulation, clinical chemistry, immunoassay, flow cytometry, etc.), patient symptoms, and captured image data (e.g., blood smear photos or report scans). Output includes a Research Value Score (RVS), a detailed clinical analysis of the sample, and suggested further testing, in addition to an interpretive comment detailing suspected pathology. Validation will compare the AI-DA output against the consensus diagnosis of senior hematopathologists on a cohort of expert-confirmed R/NT cases.

Results

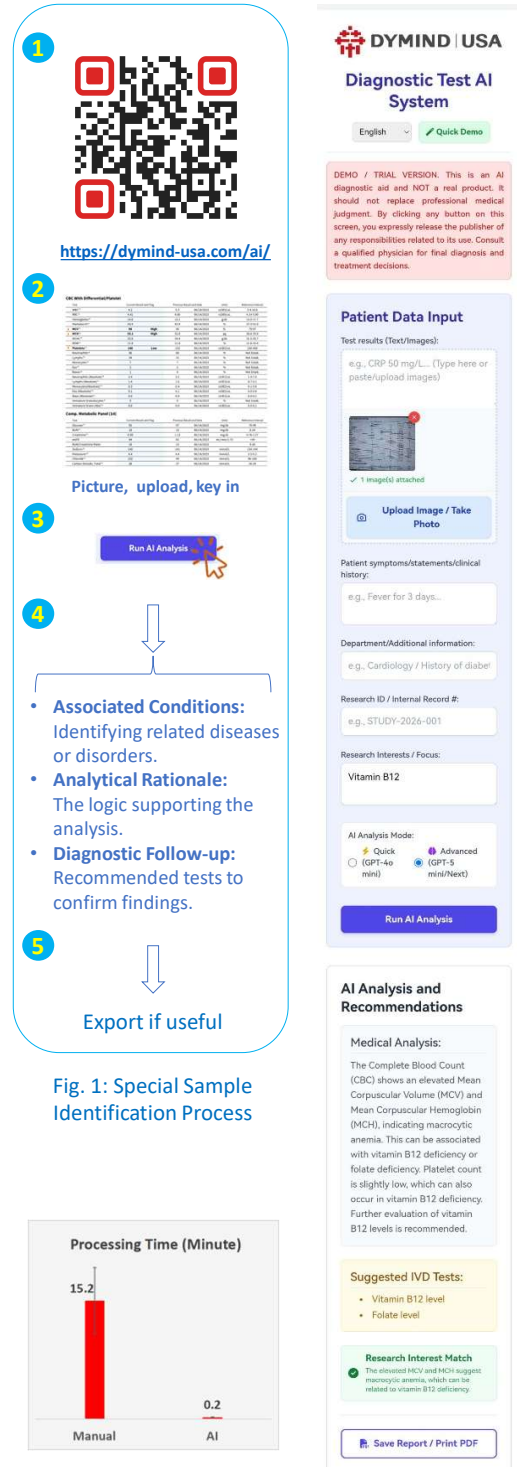
Preliminary internal testing indicates high performance in flagging subtle morphological shifts relevant to hematologic malignancies. The system is designed to achieve a sensitivity and specificity exceeding 90% in identifying R/NT research samples. Furthermore, the integration of the AI-DA is projected to reduce the mean time for initial identification and triage of R/NT specimens from over 15 minutes (manual) to under 20 seconds per case, significantly increasing research throughput efficiency.

Conclusions & Discussions

The Dymind AI-DA offers a standardized, high-efficiency tool for the proactive identification of high-value research specimens. By leveraging multi-modal data fusion, this technology dramatically accelerates the translational research process, allowing hematologists to focus on high-impact scientific inquiry and collaborative clinical trials.

References

- El-Sisi, A. B., et al. (2025). Artificial intelligence in hematology: Advances, challenges, and prospects. *Blood*, 146(19), 2283-2295.
- Caruso, C., et al. (2025). Multimodal foundation models for clinical diagnostics: Integrating vision and language in laboratory medicine. *Nature Genetics*, 57(3), 412-425.



1 <https://dymind-usa.com/ai/>

2 Picture, upload, key in

3 Run AI Analysis

4 Associated Conditions: Identifying related diseases or disorders.
Analytical Rationale: The logic supporting the analysis.
Diagnostic Follow-up: Recommended tests to confirm findings.

5 Export if useful

Fig. 1: Special Sample Identification Process

Processing Time (Minute)

Method	Processing Time (Minute)
Manual	15.2
AI	0.2

Fig. 2: Process Time Comparison

Fig. 3: Sample Report