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MegaQuant: Fully Integrated Deep-Learning Workflow in QuPath - Application to the Detection of Megakaryocytes in Human Bone Marrow

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Introduction

Megakaryocytes (MKs), precursors of platelets, can be altered by clinical conditions and their assessment is of diagnostic value. When evaluated on H&E images, they are challenging to segment due to their complex shape. Here, we propose a fully integrated workflow implemented within QuPath, leveraging existing deep-learning tools to segment and quantify MKs.

Material and methods

First, we rely on the image management platform Omero to organize our datasets and annotations with seamless access in QuPath by multiple users. QuPath facilitates the annotation of ground truth data, which was done both manually and using a foundation model, Segment Anything Model (SAM). This ground truth annotation (n=984 SAM annotated MKs used for the training, and n=483 for CellPose validation) was validated by a pathologist and used to train a customized Cellpose model, with iterative refinement between annotations and detections. Subsequently, StarDist was adapted to detect nuclear regions within the Cellpose-detected MK regions.

Results and discussion

The CellPose model detects MKs of different morphological features. Applied to 37-H&E trephine images with 2 training and 1 validation tile each, it provides morphometric parameters for every MK. SAM significantly accelerated annotation. Our workflow provided insights into the morphological heterogeneity, characteristics, and spatial distribution of MKs based solely on H&E images.

Conclusion

We believe that this fully integrated workflow within one platform, QuPath, could facilitate the adoption of MegaQuant in a clinical context and enable integration of MK quantitative information within diagnostic pathology reports. Moreover, it paves the way for a public MK-specific CellPose model for broader use in QuPath and Python applications.

Key words: Computational Pathology, Hematology, QuPath, CellPose, Omero, StarDist