The algorithm involved AI models for tissue area segmentation and cell detection, calculating CPS by identifying tumor cells within the tumor area and immune cells in both the tumor and surrounding areas. The model's performance was validated on 114 PD-L1 stained WSIs from five cancer types. A consensus CPS classification (≥1 or <1) was determined if at least two of three pathologists agreed. Pathologists re-evaluated WSIs with AI assistance in cases of discrepancies.

Results: Among the 114 WSIs, 122 (90.4%) were consistently classified by all three pathologists. The CPS ≥1 and <1 subgroups included 60 (52.6%) and 54 (47.4%) cases, respectively. The overall percent agreement (OPA) between the AI model and the pathologists' consensus was 84.4%, with a range of 78.3% (liver) to 91.3% (biliary tract). AI-assisted re-evaluation led to an increased unanimous agreement level of 91.2% (104 cases), and the OPA between the AI model and pathologists' consensus rose, ranging from 82.6% (liver) to 100.0% (pancreas).

Conclusions: The AI-powered PD-L1 CPS analyzer demonstrated comparable performance to pathologists in evaluating CPS in gastrointestinal cancers. Additionally, AI assistance improved the concordance among pathologists in CPS interpretation.

G2-05

Clinical application :
Gastrointestinal and hepatobiliary

Identifying the ASH/MASH Spectrum in Liver Biopsies Using Weakly Supervising

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Background: The clear distinction between the pathological properties of metabolic dysfunction-associated steatohepatitis (MASH) and alcoholic steatohepatitis (ASH) is considered challenging due to their histological similarity and overlap. Identifying the coexistence and severity of each disease is difficult because the typical labeling process selects only one of two diseases, meaning that labeling ASH implies non-MASH, which is technically limiting with the identification of a new spectrum of MetALD (ASH+MASH). Algorithms need modification to identify the coexistence and to accurately locate a patient within the ASH/MASH spectrum using weak supervision.

Methods: We obtained 308 H&E-stained liver biopsy slides from patients diagnosed with ASH (n=150) or MASH (n=158) at Mayo Clinic in Rochester, US, based on clinical presentation. A convolution neural network (CNN), trained on the patches used mutually exclusive labeling, followed by analysis of coexistence and positive unlabeled (PU) labeling under weak supervision. In the context of weak supervision, labeling a slide as ASH does not necessarily imply the absence of MASH, and vice versa.

Results: Our CNN achieved an AUROC of 0.859 for patch classification and a slide prediction accuracy of 0.857. During evaluation, we identified 20 ASH slides that the model classified as having both ASH and MASH. We modified the training to identify their coexistence. Consequently, the number of misclassified MASH slides in the testing data decreased from 40 to 20 out of 95, supporting the identified 20 ASH slides may exhibit both ASH and MASH properties. The results employed with weak supervision further identified the coexistence of ASH and MASH in the two-dimensional embed-

ding of neural network outputs (Fig. 1).

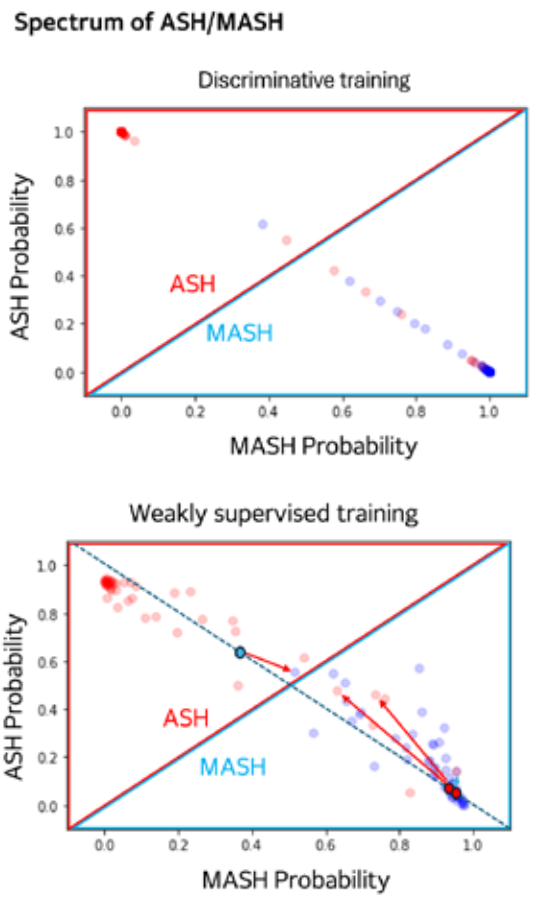

Figure 1. Results of conventional discriminative and weakly supervised training. Compared to conventional discriminative training, weakly supervised learning demonstrates a clearer spread of data across the spectrum between ASH and NASH. It alleviates some instances of extreme misclassification.

Conclusions: Our CNN-based experiment demonstrated the coexistence of ASH and MASH in patients labeled with only one, achieving 0.915 prediction accuracy for slide level classification after considering the coexistence. PU learning with weak supervision and its output spectrum confirmed the coexistence.

Keywords: Alcoholic steatohepatitis, Metabolic dysfunction-associated steatohepatitis, Weakly supervised learning, End-to-end classification, Patch-based classification

G2-06

Clinical application :
Gastrointestinal and hepatobiliary

Automated NASH CRN Scoring Pipeline Through Lesion Segmentation for Alcohol-Associated Liver Disease

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Background: The prevalence of alocohol-associated liver disease is increasing. The diagnosis usually relies on invasive and non-invasive methods, including liver biopsies. The quantification of disease activity of ALD relies on scores derived from the NAFLD activity score NAS based on NASH-CRN scoring system. However, there are significant inconsistencies in SLB scoring among human experts, which are considered a major issue. In addition, most machine learning (ML) NAS scores relies on NAFLD cases and are not sufficiently reproducible in ASH. An automated pipeline using artificial intelligence that provides a consistent NAS score for patient with ALD is imperative.

Methods: We obtained 120 H&E-stained liver biopsy images from patients with ASH at the Mayo Clinic (Rochester, MN, USA). Annotations of steatosis, lobular inflammation and ballooning areas have been provided by QRITIVE and verified by a gastrointestinal pathologist. NAS scores have been collected from pathology reports. A fully convolu-