AUTOMATIC DEEP LEARNING MODELS FOR GASTROINTESTINAL TUMOR DIAGNOSIS AND PROGNOSIS USING HEMATOXYLIN AND EOSIN SLIDES

Lianlian Wu

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Deep learning models trained on 134 whole-slide images predicted five gastrointestinal tumor biomarkers from H&E staining with AUCs of 0.90–0.96, and AI-generated IHC reports achieved 84.8–100% concordance with real IHC across biomarkers in a three-pathologist reader study.

KEY POINTS

- Five biomarker prediction models (anti-P40, CK-pan, Desmin, P53, Ki-67) achieved sensitivity 75.44–92.40%, specificity 86.04–89.35%, and AUC 0.90–0.96 on independent whole-slide image validation sets.
- In a reader study with 30 cases, AI-generated IHC pathology reports showed 100% accuracy for Desmin (66/66), 98.3% for Pan-CK (59/60) and P53 (59/60), 96.7% for P40 (29/30), and 84.8% for T-stage (56/66) compared with real IHC reports.
- AI-predicted Ki-67 percentage differed from expert pathologists' assessments by 7.00% ±3.69%, with no statistically significant difference (t=0.253, P=0.800).
- The pipeline used HEMnet neural network to align IHC and H&E whole-slide images, pathologist-reviewed annotations to correct mismatched tiles, then trained models to predict positive tiles from 415,463 H&E patches.
- The authors state the models may alleviate IHC staining burden and have potential to aid patient grading and treatment decisions in gastrointestinal tumor pathology.

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