Machine Learning-Based Quantitative Evaluation of Histological Disease Severity in Ulcerative Colitis

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STUDY BACKGROUND

Emerging evidence supports the adoption of histologic improvement as a therapeutic goal and clinical trial endpoint for patients with ulcerative colitis (UC), including reports that show relapse has been associated with residual histologic disease activity in patients who achieved endoscopic endpoints¹⁻³.

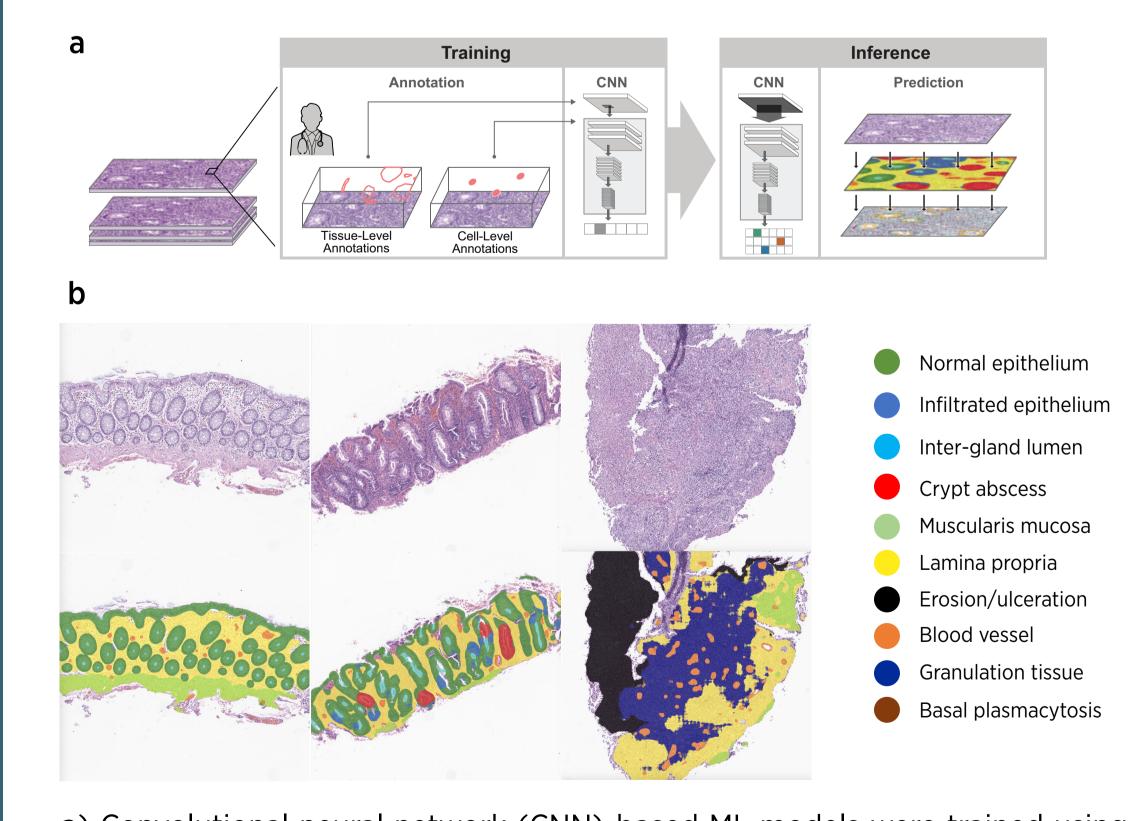
Here we show sensitive and reproducible machine learning (ML)-based pixel-level identification and quantification of histological features of UC, correlation with expert manual pathologist scoring of disease severity, and use of model-derived histological features for prediction of UC disease severity scores.

PATHAI UC MODELS Normal epithelium Infiltrated epithelium PathAl UC Crypt abscess Epithelial non goblet models showing model Muscularis mucosa Intraepithelial lymphocyte predictions of relevant Lamina propria Lymphocyte non intraepithelial histological features. a) Erosion/ulceration Plasma cell Blood vessel Cell-level overlay. b) Eosinophil Granulation tissue Tissue-level overlay. Neutrophil Basal plasmacytosis Goblet cell cytoplasm Blood vessel lumen Tissue-level overlay **Cell-level overlay**

MODEL DEVELOPMENT

- Machine learning models, based on convolutional neural networks, were trained to predict histologic features and generate quantitative, slide-level read-outs using 637 whole-slide images (WSI) of hematoxylin and eosin (H&E) stained biopsies covering the spectrum of disease severity in UC (Fig. 1a).
- Models were trained using >130k region- and point-based annotations provided by the PathAl network of board-certified pathologists, indicating relevant tissue (e.g., erosion/ulceration, crypt abscesses, epithelium with neutrophil infiltration, normal epithelium, granulation tissue, basal plasmacytosis) and cell (e.g., neutrophils, plasma cells, lymphocytes, and eosinophils) features (Figs. 1,2).

Figure 1. Machine Learning Model Training and Predictions

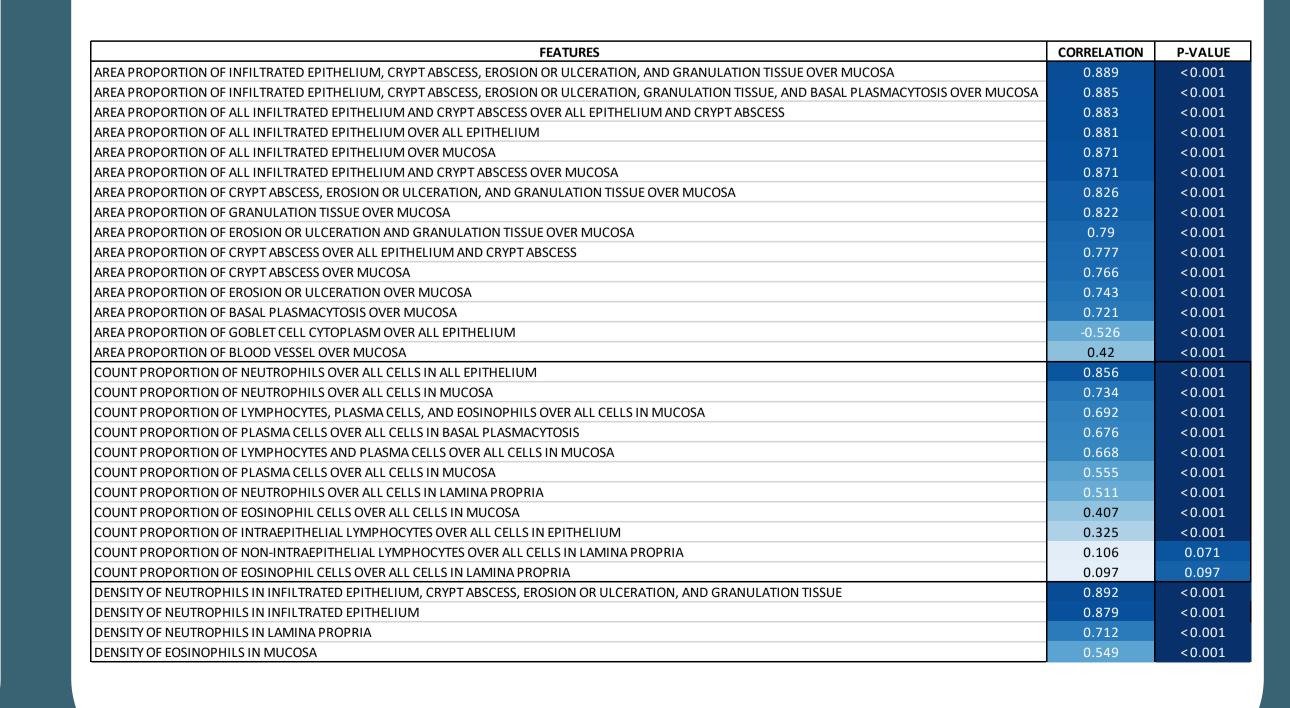


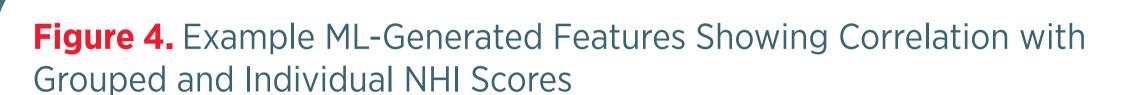
a) Convolutional neural network (CNN)-based ML models were trained using manual annotations provided by pathologists identifying histological features relevant to UC. Inference of study samples generates tissue- and cell-level predictions. b) Representative fields (4x magnification) from biopsies with corresponding ML overlays: left panel, normal biopsy NHI 0; middle panel, moderate chronic active colitis NHI 3; right panel, severe chronic active colitis NHI 4.

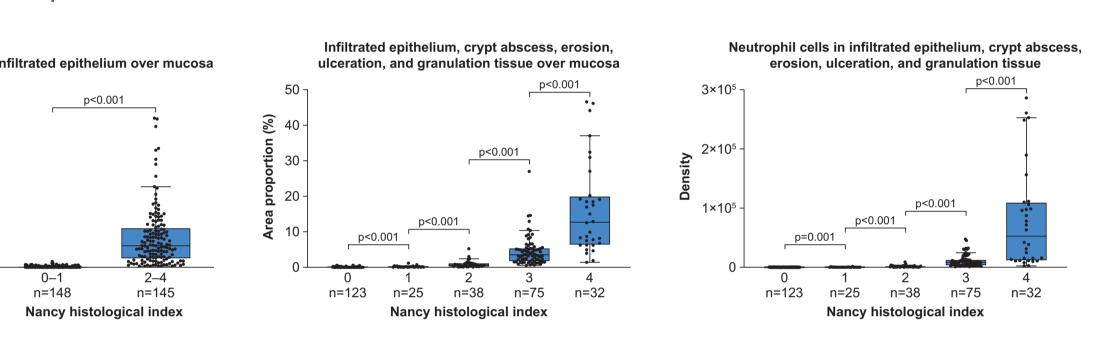
ML MODEL AND PATHOLOGIST CORRELATION

- The models were applied to the validation set of 147 H&E images, and correlation with consensus expert manual pathologist scoring of UC (Nancy Histology Index, NHI) was evaluated. The NHI is a scoring system that measures disease severity in UC with ordinal scores from 0 to 4, where higher scores indicate more severe disease.
- ML-based model predictions were used to generate quantitative "human-interpretable features" (HIFs) measuring tissue area proportions, cell counts, and cell densities.
- ML model-generated HIFs were correlated to manual pathologist NHI scores using Spearman correlation (Figs. 3,4). Manual scoring was done by a group of 5 Gl-specialized pathologists, and consensus was defined as agreement among 3 out of the 5 pathologists. Slides that did not achieve consensus were excluded (7 slides).

Figure 3. ML-Generated Feature Correlation with Pathologist NHI Scores



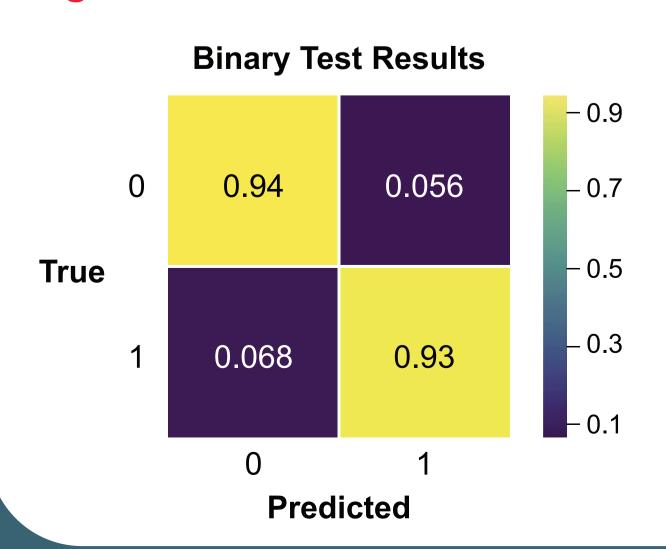




PREDICTION OF UC DISEASE SEVERITY SCORES

- Multivariate analysis was performed to predict the NHI using 16 selected histologic features. The best model, random forest classifier, was selected based on the performance of 5-fold cross validation measure by weighted kappa and yielded a weighted kappa of k=0.93 and Spearman correlation of r=0.93 (p<0.001).
- Multivariate analysis was also performed to predict cases with active disease (binary prediction of chronic active colitis NHI 2-4 vs chronic inactive colitis and normal NHI 0-1). The random forest classifier model yielded an accuracy of 0.94 (weighted kappa k=0.87 and Spearman correlation r=0.87, p<0.001) (Fig. 5).

Figure 5. Prediction of UC NHI Scores



Confusion matrix for binarized prediction of chronic active colitis NHI 2-4 vs. chronic inactive colitis and normal NHI 0-1, produced by the random forest classifier trained using 16 model-derived histological features as input.

CONCLUSIONS

- ML model predictions show high correlation with pathologist scoring of UC histological features and assessment of disease severity.
- Model-derived histological features can be used to predict slide-level NHI scores. These quantitative features can potentially be correlated with endoscopic findings, specific treatment response, or patient outcomes.
- This highlights the potential of a robust and reproducible ML-based image analysis for quantitative characterization of UC histology to better guide management decisions.

CONTACT

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