# **Enhancing NASH Fibrosis Staging with Virtual Staining and Deep Ordinal Regression: A Graph Convolutional Network Approach**

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# Abstract

- **Summary of Objectives**: This project explores the integration of virtual staining and Al-based deep learning models, particularly graph convolutional networks (GCNs), to improve the accuracy and consistency of staging fibrosis in Nonalcoholic Steatohepatitis (NASH) patients.
- **Key Findings**: The combined approach of virtual staining and GCN-based ordinal regression provides a standardized, efficient method for staging NASH fibrosis, with potential for clinical integration and enhanced diagnostic accuracy.

# Introduction

## Liver Fibrosis and NASH:

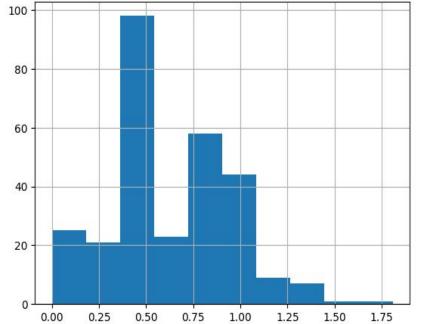
- Liver fibrosis is the excessive accumulation of connective tissue in response to chronic liver injury, common in conditions like NASH.
- NASH is a severe form of nonalcoholic fatty liver disease that can lead to cirrhosis and liver cancer if not accurately diagnosed and managed.

# Current Challenges:

- Traditional fibrosis staging relies on histopathological analysis, which is subjective and prone to variability among pathologists.
- There is a need for more objective, reproducible methods to ensure accurate diagnosis and treatment planning.
- Pathologist Variability:
- Traditional methods for staging fibrosis rely on subjective interpretation by pathologists, leading to considerable variability in results, particularly in cases with ambiguous features.

# Virtual Staining:

- An AI-driven technique that converts unstained tissue images into virtually stained ones. providing a consistent and scalable alternative to traditional methods.
- This method is especially useful in preprocessing large datasets for training AI models.



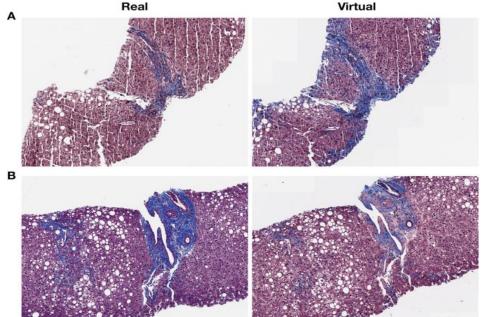


Figure 1: Histogram illustrating the distribution and disagreement among pathologists when classifying fibrosis stages in liver biopsy cases.

Figure 2: Comparison of Traditional vs. Virtual Staining

### **Data Collection and Sources**

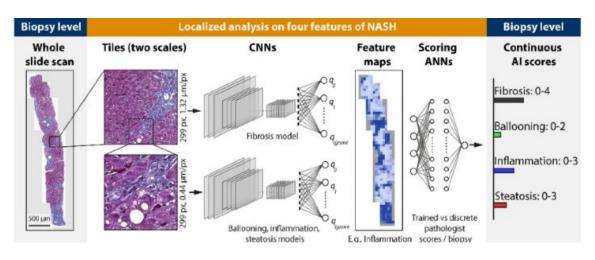
#### Virtual Staining

- subsequent analysis.

#### Al Model Development

### Feature Extraction with CNNs:

- Ordinal Regression for Staging:
  - order of progression





# Methods

 Data Origin: The study utilized liver biopsy images and clinical serology data from NASH patients, provided by Dartmouth-Hitchcock Medical Center. This comprehensive dataset includes annotated fibrosis stages and relevant clinical markers like liver function tests and inflammatory indicators.

• **Purpose**: Virtual staining was applied to convert raw biopsy images into high-quality stained equivalents using deep learning, ensuring consistency and eliminating variability associated with manual staining. Process: AI models trained on paired stained/unstained images were used, creating standardized inputs for

> **Task:** A convolutional neural network (CNN) extracted critical features from the virtually stained images, identifying patterns such as texture and cellular morphology.

> Integration: Clinical serology data was incorporated alongside image features, enhancing the model's ability to predict fibrosis stages by considering systemic disease markers.

#### Graph Construction and GCN Application:

Graph Representation: Tissue regions were modeled as a graph, with nodes representing areas of interest and edges denoting spatial relationships.

GCN Role: A graph convolutional network (GCN) processed these graphs, integrating the spatial and clinical data to improve staging accuracy.

Reasoning: The model applied deep ordinal regression to predict fibrosis stages, respecting the natural

Training: The model was trained using cross-validation and data augmentation techniques to enhance robustness, with metrics like mean squared error and Cohen's kappa used for evaluation.

> Figure 3: Illustrates how each of these components—virtual staining, CNNs, GCNs, and ordinal regression—work together to produce accurate and reliable fibrosis stage predictions.

# RESULTS

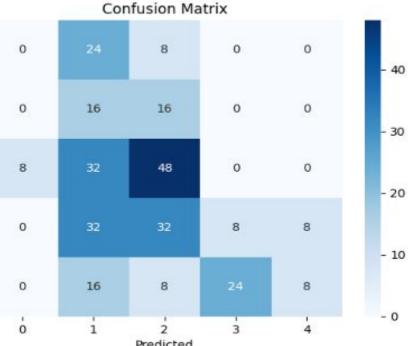
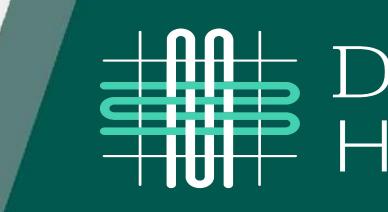


Figure 4: Confusion matrix displaying the performance of the AI model in predicting fibrosis stages. The matrix shows how well the model's predictions align with the actual classifications, highlighting areas of strength and potential improvement.



# RESULTS

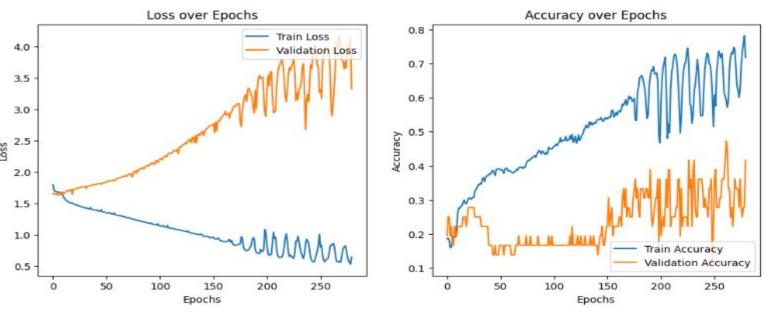


Figure 5: Plots showing the loss and accuracy of the model over training epochs. The loss plot (left) illustrates the model's convergence during training, while the accuracy plot (right) shows how the model's performance improved over time.

# Conclusion

## Key Takeaways:

- standardize and improve the accuracy of NASH fibrosis staging.
- This method reduces subjectivity, provides reproducible results, and has the potential to significantly impact clinical workflows.

## Clinical Relevance:

variability in fibrosis staging, and improve patient outcomes.

## Model Refinement:

- accuracy
- predictive power

## Scalability:

- application.

#### research Support:

- supported the research.

Levy, J.J., Azizgolshani, N., Andersen, M.J. et al. A large-scale internal validation study of unsupervised virtual trichrome staining technologies on nonalcoholic steatohepatitis liver biopsies. Mod Pathol 34, 808-822 (2021). https://doi.org/10.1038/s41379-020-00718-1

Rivenson, Y., Wang, H., Wei, Z., de Haan, K., Zhang, Y., Wu, Y., ... & Ozcan, A. (2021). Virtual histological staining of unlabelled tissue-autofluorescence images via deep learning. Modern Pathology, 34(11), 1717-1728. https://doi.org/10.1038/s41379-020-00718-1

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• The combination of virtual staining and AI-based GCN models offers a promising approach to

• Integrating this approach into clinical practice could streamline the diagnostic process, reduce

• Continuous learning and feedback from clinical use will be crucial for further improving model

Incorporating additional data types (e.g., genetic or serological data) could enhance the model's

• Expanding the use of this model to other forms of liver disease and fibrosis could generalize its

• Developing a user-friendly interface for clinical use will be essential for widespread adoption.

Acknowledge the contributions of the data sources, collaborators, and any funding agencies that

Mention the institutions or laboratories involved in the development and validation of the model.

# References