

# Evolving Trends and Measurement Challenges for Genomic Etiology in Next Generation Digital Pathology

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## Introduction

Any form of disease diagnostics that includes computer assistance is referred to as digital pathology. This includes, but is not limited to, automated histological image capture (and associated metadata), computer-assisted image analysis and instrument calibration, AI-based diagnosis and classification, and the acquisition, analysis, and interpretation of other modalities such as molecular pathology. The acquisition of images of molecular features such as specific tagged proteins or RNA or full metabolic, proteomic, or transcriptomic imaging is referred to as molecular pathology. Digital pathology methods, like histopathology, can be applied to molecular pathology imaging. Digitizing the pathology process creates virtual records that can be linked to historical pathologies and can improve clinical efficiency by lowering the cost and time between biopsy and diagnosis. Obtaining the most information in pathology is critical to enabling personalised medicine. Previous research has shown that performing whole-slide imaging (WSI) and digitally analysing the results improves efficiency. This is a straightforward case of utilising existing pathology workflows and digitising data where possible. Furthermore, machine learning (ML) and artificial intelligence (AI) can be used to classify and diagnose digital slides. This has the potential to reduce inter-operative variability while also improving diagnostic accuracy and saving time.

## Description

Rapid sharing of information across the entire world (telepathology) can also be accomplished by digitising the information contained in a histology slide. This could allow expert pathologists to review samples obtained in remote locations far from the pathologist's office, or even on smart phones. This can also be used for crowdsourcing efforts to gather information from multiple pathologists, as well as for training new pathologists. Standard approaches are insufficient in some diseases to accurately diagnose and thus select appropriate treatment regimens. As a result, novel approaches such as molecular pathology are required. Metabolic imaging [1-3], for example, can measure complex intra- and inter-tumor heterogeneity. Pathologists can use visualisation tools and machine learning to help them interpret whole-slide images. On the most basic level, this is a platform for interactive viewing and manual annotation of histological slides, similar to what a pathologist would see through a microscope. AI and machine learning advancements can provide pathologists with a wealth of additional information and tools. Some tools, for example, can perform unsupervised or supervised segmentation, which can then be refined by a pathologist, or can perform tasks like nuclear segmentation and calculate distances between nuclei.

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Date of Submission: 07 July, 2022, Manuscript No. jcsb-22-78950; Editor assigned: 09 July, 2022, Pre QC No. P-78950; Reviewed: 23 July, 2022, QC No. Q-78950; Revised: 28 July, 2022, Manuscript No. R-78950; Published: 02 August, 2022, DOI: 10.37421/0974-7230.2022.15.423

This reduces the time required to manually draw annotations, which is especially useful in very complex and detailed tissue architectures like calculating multiple nuclei distances. This, however, introduces another source of uncertainty into the decision-making process. Some software packages allow a pathologist to annotate the various tissue types on a slide before classifying the rest of the slide or other slides. The key feature of any visualisation tool for digital pathology is that it must be simple for pathologists to use in order for digital pathology to be adopted in a clinical setting [4,5]. One of the most difficult challenges in digital pathology classification is obtaining sufficient labelled data for either training or performance evaluation when using supervised methods.

## Conclusion

Manual annotation by a pathologist is time-consuming and thus expensive. Large resources are available for cases such as glioblastoma and breast carcinoma, but this is more difficult for less common diseases. In cases where data is scarce, data augmentation via image transformation can be used to artificially increase the size of available training data; however, this approach does not always capture the full variability observed in larger training datasets. One advantage of digital pathology, as previously stated, is the ability to crowdsource annotations to multiple experts, which can alleviate this problem. In addition to pathologist input for training data, validation of results via expert comparison is required to evaluate classification accuracy in digital pathology, as well as to manually review regions and tissues that show discrepancies. Explainable AI for digital pathology is one of the most significant recent developments. Explainable AI not only provides a classification diagnosis, but also determines the underlying factors. This enables a pathologist to comprehend and analyse the underlying reason for the classification process in order to aid in diagnosis and determine confidence in the diagnosis.

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How to cite this article: Flores, Bradley. "Evolving Trends and Measurement Challenges for Genomic Etiology in Next Generation Digital Pathology." *J Comput Sci Syst Biol* 15 (2022): 423.