

Computational Pathology and the Understanding of Disease

Computational Pathology

Computational pathology encompasses a range of approaches, all of which share the application of computational analysis to the study and diagnosis of disease. With increasing generation of whole slide images from tissue sections mounted on glass slides, there is a rapidly increasing resource of images derived from tissues that can be used for a wide range of analyses. These range from direct viewing for diagnostic purposes, with the consequent change from image viewing with light microscope to computer screen [1], to advanced computational investigation of these digitized images, employing artificial intelligence to derive increasingly complex information from tissue images. This is addressed in a recent paper in the Journal by Colling *et al*, who set out a roadmap for the development of software tools for approved clinical use [2].

The hardware required to generate whole slide images is increasingly available and the use of whole slide images for routine diagnostic pathology is becoming increasingly common. This ready availability of whole slide images raises many issues, from the ethics of using such images for research through the use of digital images to add quantitation to diagnostic assessment, to the stratification of images based solely on computational assessment. In another recent paper in the Journal, the current position of computational pathology is reviewed and summarized by Abels *et al* [3]. In addition to providing a very useful glossary of terms, they discuss the various issues facing the implementation of computational pathology approaches in diagnostic and research practice. This has wide applicability and clarifies the notion that computational pathology will affect everyone involved in tissue-based diagnostics and/or research. This includes the whole spectrum of tissue analysis, from regular diagnosis based on H&E-stained sections [4,5] and immunohistochemistry [6], through individual research projects [7] to clinical trials [8], where pathology review, for example, is increasingly performed on whole slide images.

As the technology is adopted, it is crucial that standards are defined and implemented to ensure that the quality of diagnosis and research based on whole slide images is 'non-inferior' to that using glass slides [9,10]. Moreover, the introduction of ancillary analyses, for example assessment of immunostaining [6] or measurement of tissue structures, requires rigorous quality control to ensure that clinical

application is evidence-based. This is particularly important as data accrue to show that computational analysis can, for example, identify molecular abnormalities such as microsatellite instability directly from tissue morphology [11]. The availability of annotated digital image resources such as those provided by The Cancer Genome Atlas, which are accompanied by clinicopathological and genomic/epigenomic/proteomic data [12], will help clinical and research communities to identify, test and verify algorithms.

Call for Papers

Given the rapidly increasing importance of computational pathology to the study and diagnosis of disease, *The Journal of Pathology* invites submissions of primary research that uses computational methods to investigate disease processes. We are interested in receiving submissions that address any aspect of computational pathology in this context. Examples include, but are not restricted to:

- Novel computational approaches to the investigation of disease in tissues
- Application of computational techniques to understanding disease mechanisms
- Validation of computational approaches for the identification of molecular abnormalities in tissues

Manuscripts should ideally offer clinically relevant findings and/or mechanistic insights. Timely reviews and perspectives will also be welcomed.

Correctly formatted manuscripts will be fast-tracked and expertly peer-reviewed, aiming for a final decision within 10 working days. We would anticipate that initial online publication would occur within 7 days of acceptance. Once published, each article will be made free to view online, facilitating dissemination within the community.

In your covering letter, please mention that the submission is a response to the "Computational Pathology Call". Please note that the manuscript must contain full details of the hardware and software used in the analyses either in the main manuscript or as supplementary material.

We look forward to receiving your manuscript via <http://mc.manuscriptcentral.com/jpath>

Key words - computational pathology; deep learning; machine learning; artificial intelligence; digital pathology; whole slide images; clinical trials; disease mechanisms

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