commentary

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Diagnostic Evaluations and Artificial Intelligence Models

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Description

The incidence and mortality rates of cervical cancer have both significantly decreased as a result of routine screening. Retrospective review of cytology and HPV test results with cervical biopsy diagnosis is essential for validating and adapting these algorithms to changing technologies, demographics, and optimal clinical practices because selection of appropriate screening modalities depends on well-validated clinical decision algorithms. Due to the overwhelming number of specimens, however, manual categorization of the free-text biopsy diagnosis into discrete categories is extremely laborious, which may result in significant error and bias. Computer-based classification tasks have seen significant progress thanks to advances in natural language processing and machine learning, particularly in the last ten years. For the purpose of developing a supervised classifier that is capable of assigning precise biopsy categories to free-text biopsy interpretations while maintaining high concordance with manually annotated data, we use an effective version of an NLP framework called Fast-Text^{TM} and an annotated cervical biopsy dataset to accomplish this. After a referee review by an experienced pathologist, we examine cases in which the machine-learning classifier disagrees with previous annotations. With a concordance of 97.7%, we also demonstrate that the classifier is robust on an untrained external dataset. In conclusion, we discuss the advantages and drawbacks of this strategy and demonstrate how NLP can be applied to a real-world task of pathology classification. In the field of digital pathology, transfer learning has been the most common method due to a lack of annotated pathological images. Pre-trained neural networks based on the ImageNet database are frequently used to extract "off-the-shelf" features, predicting tissue types, molecular characteristics, clinical outcomes, and other outcomes with great success. We conjecture that calibrating the pre-prepared models utilizing histopathological pictures could additionally further develop highlight extraction, and downstream forecast execution. In a two-step process, we fine-tuned a pre-trained Xception model using one million annotated H&E image patches for colorectal cancer (CRC).

Cancer Prediction for Gene Expression and Mutation

The Image-pretrained model and the finely tuned Xception model's features were compared using the following methods: (1) tissue classification using the same image type used for fine-tuning for H&E images from CRC; (2) expectation of invulnerable related quality articulation, and for lung adenocarcinoma. The model's performance was evaluated using five-fold cross validation. 50 times were spent on each experiment. For both cross-cancer prediction for gene expression and mutation at the patient level and for same-cancer tissue classification, where similar images from the same cancer are used for fine-tuning, we demonstrated that fine-tuning the pretrained ImageNet neural networks with histopathology images can produce higher quality features and better prediction performance. Tissue microarray Immuno-Histochemistry (IHC) data can be accurately assessed using digital pathology. However, it is still essential to validate the data against pathologist manual interpretation and evaluate the comparability of the data obtained by various software applications. In this study, we benchmarked the results against pathologist manual scores by comparing the IHC quantification of five clinical breast cancer biomarkers-Estrogen Receptor (ER), Progesterone Receptor (PR), Human Epidermal Growth Factor Receptor 2, Epidermal Growth Factor Receptor, and Cytokeratin 5/6 (CK5/6). In diagnostic pathology, the study of whole cells is called cytology. Cryptologic preparations, in contrast to standard histologic thinly sliced specimens, are prepared from whole cells where cells typically cluster and aggregate. As a result, when viewed through a microscope, cytology preparations typically exhibit large areas of defocus because they are significantly thicker than histologic slides. Pathologists must constantly manipulate the focal plane to view a diagnostic aggregate of cells in focus together, which makes it difficult to accurately assess the entire cellular aggregate and, consequently, to make a diagnosis. In addition, it is extremely challenging to acquire digital images of cytology preparations that are uniformly focused and useful for applications like artificial intelligence models and remote diagnostic evaluations. Acquiring digital images at multiple focal planes across the slide is currently the most common approach to this problem. However, this method necessitates a significant amount of storage space, complex and expensive scanning systems, and a lengthy scanning time. Standard microscopes can use this technology, which we believe can improve diagnostic accuracy as well as the ease and speed with which difficult specimens can be diagnosed. While cytology slides are the focus of this article, we anticipate that applications in histology will benefit greatly from this technology. The issue of remote rapid evaluation of cytology preparations is also addressed by this method. Lastly,

we believe that this method is an important step forward in the application of machine learning to cytology specimens because it resolves the focus heterogeneity issues in standard digital images. Digital pathology represents a brand-new development phase in the field of patho-morphological diagnostics. During the COVID-19 pandemic, this issue received the most attention.

Non-Concurrent Counsel, and Mechanization of Business Processes

The upsides of digitization of diagnostics incorporate the chance of remote work of a pathologist, distant non-concurrent counsel, and mechanization of business processes. They speed up the diagnosis process and improve diagnostic quality. Digital cancer diagnostics can offer a lot more than just these advantages. Our personal experiences working at Russia's first digital path morphological laboratory, UNIM, are the basis for this article. The economics of the process, the importance of integration with LIS and MIS, errors and the principles of their solution, payback, and every stage of laboratory work will be considered in detail. Additionally, all advantages and disadvantages of digitization, peculiarities of using technology, differences from the conventional approach to diagnostics, and differences from the conventional approach will be discussed. From diagnosis and archiving to logistics and registration. We will present a comprehensive analysis of statistics and observations on how to organize processes in a fully digital laboratory because all data has been digitized over several years. The high cost-effectiveness of the platform and approach, which enabled us to compete successfully in the market, is an important aspect of our experience. The survey of physicians' attitudes toward digital pathology's findings will also be presented. The uPath HER2 Dual ISH Image Analysis for Breast algorithm was developed to assist pathologists in determining the HER2 gene status of breast cancer specimens. This study sought to contrast manual read scoring with uPath HER2 DISH image analysis for VENTANA HER2 DISH-stained breast carcinoma specimens using the Ground Truth (GT) gene status as a reference. 220 Formalin-Fixed, Paraffin-Embedded (FFPE) breast cancer cases were examined by three reader pathologists using both manual and uPath HER2 DISH IA techniques. The GT gene status determined by a panel of pathologists was compared to the scoring results from computer-assisted scores (IA) and manual read scores (MR). The distinctions in understanding paces of HER2 quality status between manual, PC helped, and GT quality not set in stone. Overall, our data support the uPath HER2 DISH IA's use as an aid for pathologists in routine breast cancer diagnosis because it is comparable to manual scoring.