Automatically Tumor Recognition using Histopathological Tissue Scans

Mantas Kundrotas*

Department of Diagnostic Pathology, Oita University, Oita 879-5593, Japan

Introduction

The most recent advances in artificial intelligence development, particularly machine learning (ML), enable the development of automated technologies that can eliminate or at least reduce human errors in analysing health data. To this day, pathologists analyse slides of histopathologic tissues stained with hematoxylin and eosin under the microscope due to the ethics of AI use in pathology and laboratory medicine; by law, it cannot be substituted and must go under visual observation, as pathologists are fully accountable for the result. A large number of automated systems, on the other hand, could solve complex problems that require an extremely fast response, accuracy, or work on tasks that require both a fast and accurate response at the same time [1].

Description

Today, histology has become an essential tool in medical research and diagnosis, allowing clinicians to examine tissue samples to identify diseases and disorders at the cellular level. In this article, we will explore the different types of tissues, their structure and function, and the techniques used to study them. Epithelial tissue covers the surfaces of the body, including the skin and the lining of organs and cavities. This tissue provides a protective barrier against physical, chemical, and biological factors, preventing injury and infection. There are several types of epithelial tissue, including simple squamous, simple cuboidal, simple columnar, pseudostratified columnar and stratified squamous. The structure and function of each type of epithelial tissue depend on its location in the body and the specific functions it performs [2].

Accurate tumour identification, especially at an early stage, necessitates extensive expert knowledge, so cancerous tissue is frequently identified only after experiencing its side effects. Our study's main goal was to improve our ability to find more accurate ML methods and techniques that can lead to the detection of tumour damaged tissues in histopathological WSIs. According to the results of our experiments, there was a 1% AUC difference between the training and test datasets. Over several training iterations, the U-Net model was able to nearly double the model size while increasing accuracy from 0.95491 to 0.95515 AUC. When properly trained, convolutional models performed well on groups of varying sizes [3].

Because of the possibility of faster and more accurate results, the medical field, particularly image analysis for histopathology and cancer research, could have a significant impact. In recent years, technological advancements have revolutionised the health system, allowing it to use digitised imaging to review patient data via computer systems and applications. Because of the growing number of image analysis applications and large image compression tools, digital content can be easily stored without losing quality and reshared among health professionals. Unfortunately, transitioning from glass to digital analysis necessitates the purchase of new expensive hardware, a large amount of memory, and specially trained technicians.

***Address for Correspondence:** Mantas Kundrotas, Department of Diagnostic Pathology, Oita University, Oita 879-5593, Japan, E-mail: mantaskundrotas@gmail.com*

A cancer, also known as a tumor, is a cluster of abnormal cells that are altered, unregulated, and proliferate indefinitely. It causes terminal illnesses. Tumors are classified into three types: benign, premalignant, and malignant. Because benign tumours are noninvasive, they are considered less dangerous and harmful; however, certain cases indicate that they can become malignant. Malignant tumours typically grow quickly, penetrating and destroying healthy tissues before spreading to distant organs and metastasizing. Magnetic resonance imaging (MRI), computed tomography, Single-Photon-Emission Computed Tomography (SPECT), and other medical imaging technologies are used to determine the exact type, location, and level of threat that cancer-damaged tissue has [4-6].

Conclusion

These models were extremely adaptable, allowing the model's size and architecture to be experimentally tailored to the type of task. Using the M-model in several training iterations, we were able to nearly double the model size while increasing the accuracy from 0.95491 to 0.95515 AUC. Third, convolutional models perform well on groups of varying sizes when properly trained. The TTA method improved the result to 0.96870, and the multi-model ensemble improved it to 0.96977. Fourth, using special analysis methods, it was possible to identify and correct the models' flaws. After discovering that excessive and inappropriate image augmentation was detrimental to learning, a simple adjustment to the image processing parameters was enough to nearly double the AUC.

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Conflict of Interest

There are no conflicts of interest by author.

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