

Brain Cancer Detection Using Radiogenomics-Based Insights

Charney Shane*

Developmental Genomics Section, National Human Genome Research Institute, Bethesda, USA

Introduction

Using a variety of methods, including tumor segmentation, classification, detection, and risk analysis, the process of determining the underlying cause and characteristics of brain tumors is known as brain tumor characterization (BTC). A significant component of the characterization of a brain tumor is the identification of the molecular signature of various useful genomes whose alteration causes the tumor. In an artificial intelligence (AI) environment, the radiomics approach extracts quantitative radiomics features from radiological images for disease characterization. The combined study of "radiomics and genomics" has been referred to as "radiogenomics" when a higher level of disease characteristics, such as genetic information and mutation status, are taken into consideration. A brain tumor is a disease that kills people, and as the number of deaths around the world rises, the threat to human life gets harder to avoid. Cancer of the brain and nervous system is the tenth leading cause of death, affecting adult men, women, and children. People, families, communities, and healthcare systems continue to bear enormous physical, emotional, and financial burdens as the global burden of brain cancer continues to rise. Standard diagnosis and treatment are not readily available to a large number of patients in nations with subpar or nonexistent healthcare support systems. Depending on the size, type, location, and grade of the tumor, traditional treatments for brain tumors include chemotherapy, radiation therapy, surgery, and biopsy. In addition to these more conventional approaches to treatment, medical imaging techniques have been producing exceptional outcomes for the treatment. Medical image modalities such as magnetic resonance imaging (MRI), computed tomography (CT), cranial ultrasound imaging, and positron emission tomography (PET) have been used to detect neurological disorders and brain tumors. However, MRI is the most desirable option due to its soft tissue characteristics and radiation-free nature. CT is another medical image modality. On the other hand, the radiologist must manually examine the medical image to find features of the tumor that are characteristic of the disease. Their performance varies depending on the radiologist's experience.

Description

Artificial intelligence (AI) technologies such as machine learning (ML) and deep learning (DL) have demonstrated benefits in disease detection and classification [1]. Several ML methods have been developed for cancer diagnosis, including brain, liver, thyroid, tumour vascularity in breast cancer, ovarian, skin, diabetes, heart disease, and coronary artery disease [2]. These ML techniques have performed well; however, the feature extraction techniques are ad hoc, resulting in ML results that vary. Deep learning (DL) methods have recently emerged and have demonstrated several medical imaging

applications, including brain cancer, carotid wall segmentation, COVID lesion detection, lung segmentation, and coronary/carotid plaque classification.

Machine learning (ML) and deep learning (DL) are two AI technologies that have demonstrated advantages in disease classification [1]. Brain, liver, thyroid, tumor vascularity in breast cancer, ovarian, skin, diabetes, heart disease, and coronary artery disease are just some of the cancers for which ML methods have been developed [2]. These ML methods have been effective; However, the ad hoc methods for feature extraction produce diverse ML outcomes. Several medical imaging applications, such as the detection of COVID lesions, lung segmentation, and coronary/carotid plaque classification, have been demonstrated using recently developed deep learning (DL) techniques.

Although these DL methods are unquestionably superior to ML, their implementation is extremely challenging due to the high cost of training time [3]. With a higher level of automation, new methods like transfer learning (TL) and hybrid deep learning (HDL) have reduced training time for brain tumor classification, detection, and segmentation. Using a variety of feature extraction techniques, these AI technologies have been able to segment and classify disease characteristics from medical images of tissue-based diseases. Consequently, brain cancer diagnosis is elevated to a new level when AI and radiography are combined [4]. Brain tumors can be classified, detected, and segmented using the AI paradigm, which has proven effective in terms of early detection, high-quality treatment, and survivability. However, these classification and segmentation techniques must perform even better in order to achieve a higher diagnosis rate [5]. During the classification and segmentation of brain tumors, the detection of genomics information can improve diagnosis because genetic mutation is the primary cause of brain cancer. Healthy cells become cancerous when their genes are altered when they are exposed to substances from the outside. Consequently, genetic mutation should be identified as the primary cause of brain tumors during diagnosis.

Conclusion

Radiological medical images can reveal the genomic assessment and state of the genetic mutation on various genes and cell proteins, which are the disease's molecular characteristics. We begin with brain tumor biology to comprehend the underlying process of brain tumors and the genomics mutation process in glia brain cells in the proposed review for brain tumor characterization using radiomics and genomics features. The process of mutation, gene status, and the essential genetics that are crucial to brain tumors are all discussed. In addition, the genetic mutation-based classification and grading system for various brain tumors has been tabulated to provide comprehensive information regarding the tumor's characterization.

References

1. Rambaut, Andrew, Edward C. Holmes, Áine O'Toole and Verity Hill, et al. "A dynamic nomenclature proposal for SARS-CoV-2 lineages to assist genomic epidemiology." *Nat Microbiol* 5 (2020): 1403-1407.
2. Plitnick, Jonathan, Sara Griesemer, Erica Lasek-Nesselquist and Navjot Singh, et al. "Whole-genome sequencing of SARS-CoV-2: Assessment of the Ion Torrent AmpliSeq panel and comparison with the Illumina MiSeq ARTIC Protocol." *J Clin Microbiol* 59 (2021): e00649-21.
3. Tyson, John R, Phillip James, David Stoddart and Natalie Sparks, et al. "Improvements to the ARTIC multiplex PCR method for SARS-CoV-2 genome sequencing using nanopore." *bioRxiv* (2020).
4. Charre, Caroline, Christophe Ginevra, Marina Sabatier and Hadrien Regue,

*Address for Correspondence: Charney Shane, Developmental Genomics Section, National Human Genome Research Institute, Bethesda, USA, E-mail: shanechar9895@gmail.com

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- et al. "Evaluation of NGS-based approaches for SARS-CoV-2 whole genome characterisation." *Virus Evol* 6 (2020): veaa075.
5. Bolger, Anthony M, Marc Lohse and Bjoern Usadel. "Trimmomatic: A flexible trimmer for Illumina Sequence Data." *Bioinformatics* 30 (2014): 2114-2120.

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