Original Investigation | Neurology

Convolutional Neural Networks Efficacy in Identifying MGMT Methylation Status in Brain Tumors: A Systematic Review

Omar Mohannad Mohammad Mansoor[1,] Abdallah Mohammed Abdallah Sayegh[2,] Sudqi Samer Sudqi Alshunnar[2,] Dara Hassan Ali[3]

Alexandria University Faculty of Medicine, Alexandria, Egypt[1,] MD, An-Najah National University Faculty of Medicine and Health Sciences, Department of Biomedical Sciences, Nablus, Palestine[2,] (MBChB), · International Baccalaureate, Jerusalem, Israel[3]

Key Points

Question:
Can CNNs accurately determine MGMT methylation status in brain tumors non-invasively?
How effective are CNNs compared to traditional invasive methods?
What limitations affect the implementation of CNN-based MGMT detection?

Findings:
CNNs achieved high accuracy (80%–95%) in MGMT methylation detection.
Studies confirm CNNs as a viable non-invasive alternative to traditional biopsy methods.
Variability in CNN models, lack of standardization, and data size limitations impact reliability.
Accuracy drops to moderate levels (60%–80%) under suboptimal conditions.

Meaning:
CNNs offer a promising non-invasive method for MGMT status identification in brain tumors.
Their implementation requires sufficient computational resources and standardized models.
Further studies and optimization are needed to improve consistency and clinical adoption.

Abstract

Importance:
Chemotherapy, specifically temozolomide is a type of treatment is that conducted for individuals with primary brain tumors- gliomas and glioblastomas. Through the attachment of a guanine DNA, chemotherapy induces apoptosis on cancer cells. O-6-methylguanine-DNA-methyltransferase (MGMT) is a promoter enzyme which mediates DNA damage, it is acknowledged as a component in the ineffectiveness of chemotherapy, therefore, it has been recognized as an important prognostic indicator and a predictor of chemotherapy response. Hence, patients with a methylated MGMT have better prognosis and extended survival rate. Convolutional Neural Networks, a type of deep-learning machines that are able to interpret visual data were questioned on their effectiveness to detect MGMT methylation status via imaging.

Objective:
This abstract's objective is to examine the efficacy of CNNs in determining MGMT methylation status in patients with primary brain tumors- Gliomas or Glioblastomas, non-invasively.

Evidence Review:
This study utilized MeSH terms and conducted its search in PubMed, the search items were: Neural networks, glioblastoma and gliomas. The total number of studies identified were 342, they were filtered to only include those who have the word 'MGMT', leaving 13 studies. Lastly, two were excluded due to faults in data collection, and being beyond the scope of the abstract.

Findings:
A number of studies achieved excellent results from 80% to 95% accuracy using CNNs, including: (Zlochower et al., 2020), (Chang et al., 2018), (Chen et al., 2020), and (Zhong et al., 2022), highlighting that CNNs can be used as a non-invasive tool to identify MGMT methylation status, and being more effective than invasive methods (Chelliah et al., 2024). However, there were several limitations, including the large variability between CNN modules, lack of standardization, and need of large data-sets. Those limitations do not only affect the implementation of CNNs, but also their results, dropping the accuracy to moderate (60% to 80%) as seen in (Saxena et al., 2023), (Han & Kamdar, 2018), (Faghani et al., 2023), and (Schmitz et al., 2024).

Conclusion:
CNNs can be used as a non-invasive tool to detect MGMT methylation status under physician oversight, although, only in hospitals with adequate resources to counter mentioned limitations.

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Article Information

Corresponding Author: Omar Mohannad Mohammad Mansoor, Alexandria University Faculty of Medicine, Alexandria, Egypt.