Lay Summary

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Multi-modal computational interrogation of the molecular-morphological intersection in brain tumours

Prof Silvia Marino and Dr Thomas Millner, Blizard Institute, Queen Mary University of London

Brain tumours called gliomas are the most common primary tumours, with glioblastoma being the form of glioma with the worst outcomes. Glioblastomas spread invasively meaning they cannot be completely removed by surgery. They also don't respond very well to other conventional treatments, such as chemotherapy and radiotherapy.

Epigenetics is the study of the way genes are switched on and off without changing the DNA sequence itself. Every cell in your body has the same DNA, but every cell does not express each gene equally – resulting in many types of cell with very different functions.

Epigenetic alterations are known to play a role in almost all disease processes, including brain tumours. The epigenetic alteration that we will study is DNA methylation. Analysis of DNA methylation together with examination of tumours under a microscope (which is called histology) are important aspects of brain tumour diagnosis.

This project will apply the latest computational and artificial intelligence (AI) techniques to data collected from brain tumours during this diagnostic process. It is based on work developed at Queen Mary University of London. We will use novel computational methods to examine DNA methylation data to find out more about this process in brain tumours and how it may be abnormal.

We will also use AI to integrate data collected from histology and DNA methylation changes. This will help us describe how DNA methylation affects the way brain tumours develop and grow in patients. We hope to predict patient outcomes better and to identify new targets for treatment in gliomas by exploring this complex data with the latest computational tools available.