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A mathematical modelling tool for predicting survival of individual patients following resection of glioblastoma: a proof of principle

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The prediction of the outcome of individual patients with glioblastoma would be of great significance for monitoring responses to therapy. We hypothesise that, although a large number of genetic-metabolic abnormalities occur upstream, there are two 'final common pathways' dominating glioblastoma growth – net rates of proliferation (ρ) and dispersal (D). These rates can be estimated from features of pretreatment MR images and can be applied in a mathematical model to predict tumour growth, impact of extent of tumour resection and patient survival. Only the pre-operative gadolinium-enhanced T1-weighted (T1-Gd) and T2-weighted (T2) volume data from 70 patients with previously untreated glioblastoma were used to derive a ratio D/ρ for each patient. We developed a 'virtual control' for each patient with the same size tumour at the time of diagnosis, the same ratio of net invasion to proliferation (D/ρ) and the same extent of resection. The median durations of survival and the shapes of the survival curves of actual and 'virtual' patients subjected to biopsy or subtotal resection (STR) superimpose exactly. For those actually receiving gross total resection (GTR), as shown by post-operative CT, the actual survival curve lies between the 'virtual' results predicted for 100 and 125% resection of the T1-Gd volume. The concordance between predicted (virtual) and actual survivals suggests that the mathematical model is realistic enough to allow precise definition of the effectiveness of individualised treatments and their site(s) of action on proliferation (ρ) and/or dispersal (D) of the tumour cells without knowledge of any other clinical or pathological information.

Keywords: glioblastoma; invasion; MRI; mathematical model; proliferation; resection

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