# Multiparametric MRI Towards a Predictive Model to Differentiate Solitary Brain Metastasis from Glioblastoma Multiforme

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**Target audience:** MR scientists, Neuroradiologists and Neuro-oncologists

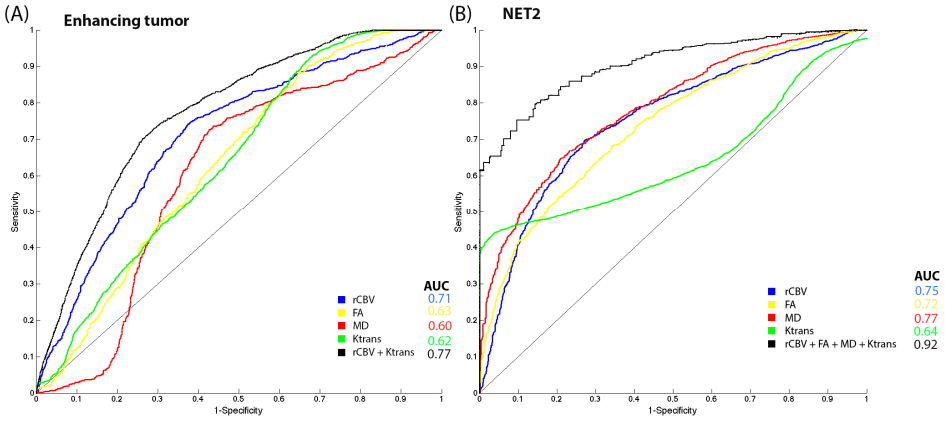
**Purpose**: Solitary brain metastasis (MET) and glioblastoma multiforme (GBM) can appear similar on conventional MRI and therefore reliable imaging differentiation between MET and GBM can be important for medical staging, surgical planning, and therapeutic decision making[1]. The purpose of this study was to identify MR perfusion and diffusion-weighted biomarkers that can differentiate MET from GBM, using voxel-based analysis.

**Methods**: In this retrospective study, patients were included if they met the following criteria: underwent resection of a solitary enhancing brain tumor and had preoperative 3.0T MRI encompassing following imaging sequences: diffusion tensor imaging (DTI): [single-shot spin-echo EPI; TR/TE, 5500/82 msec; FOV: 22 $cm^2$; matrix 128 mm; slices 40 x 3 mm; GRAPPA x 3; diffusion gradients along 20 non-collinear directions with a b-value of 1000 s/mm²]; dynamic contrast-enhanced (DCE): [3D radial volumetric interpolated examination (VIBE) sequence; TR/TE: 3.6/1.7 msec; FA: 12º; FOV: 22 $cm^2$; 328 radial views in 8 rotations (42 views/rotation) with 'stack-of-stars' scheme; K-space weighted image contrast echo-sharing[2] with resultant temporal resolution of 4.5 sec], and dynamic susceptibility contrast (DSC) perfusion: [gradient-EPI sequence; TR/TE: 1450/22 msec; FA 90º; FOV: 22$cm^2$; matrix 128 mm; slices 30 x 4 mm; GRAPPA x3; 60 dynamic frames]. The contrast injected for DCE served as pre-bolus dose for the subsequent DSC-leakage correction. The arterial input function was selected automatically and multi-parametric perfusion maps were calculated using an extended toft model[3] for DCE and block-circulant singular value decomposition technique[4] for DSC. Using coregistered images, voxel-based FA, MD, $K^{trans}$ and rCBV values were obtained in the enhancing tumor and non-enhancing peritumoral T2 hyperintense region (NET2). Data were analyzed by logistic regression and analysis of variance. Receiver operating characteristic (ROC) analysis was performed to determine the optimal parameter(s) and threshold(s) for predicting GBM vs. MET.

**Results:** Twenty-three patients (14 M, age: 32-78 y/o) met inclusion criteria. Pathology revealed 13 GBMs and 10 METs. In the enhancing tumor, rCBV, Ktrans, and FA were significantly higher ($p<0.0001$) in GBM than in MET, whereas MD was significantly lower ($p<0.0001$) in GBM than in MET. In the NET2, rCBV and FA were significantly higher ($p<0.0001$) in GBM than in MET, but MD and Ktrans were significantly lower ($p<0.0001$) in GBM compared to MET. The best discriminative power was obtained in NET2 (not in enhancing tumor) from a combination of rCBV > 0.78, FA > 0.12, MD < 1700 x $10^{-6}$ $mm^{2/s}$, and $K^{trans}$ < 0.25 $^{1/min}$, resulting in an AUC of 0.92 superior to any individual or combination of other classifiers (**Figure**).

**Discussion:** In distinguishing GBM from solitary MET using the described imaging model, special attention should be given to NET2 rather than enhancing tumor. In addition although all described imaging biomarkers are statistically different between MET and GBM, we showed improved predictive power using multiparametric analysis superior to any individual classifiers.

**Conclusions**: Described multiparametric MRI model can distinguish GBM from MET by using a combination of rCBV, $K^{trans}$, FA, and ADC in NET2 with an AUC of 0.92.

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