

**Texture analysis- and support vector machine-assisted diffusional kurtosis  
imaging may allow in vivo gliomas grading and IDH-mutation status prediction:  
a preliminary study**

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## Supplement

### Methods – Diffusion kurtosis imaging

The DWI signal intensity,  $S$ , can be regarded as a function of the b-value, which for a Stejskal-Tanner sequence is defined by

$$b \equiv (\gamma\delta g)^2 \left( \Delta - \frac{\delta}{3} \right) \quad (1)$$

where  $g$  is the proton gyromagnetic ratio,  $\gamma$  is the amplitude of the diffusion sensitizing magnetic field gradient pulses,  $\delta$  is the duration of the gradient pulses, and  $D$  is the time interval between the centres of the gradient pulses. According to the Taylor series<sup>1,2</sup>

$$\ln[S(b)] = \ln(S_0) - bD_{app} + O(b^2) \quad (2)$$

where  $D_{app}$  is the ‘apparent’ diffusion coefficient and  $S_0$  (three lines)  $S(0)$ . Notably, it is assumed that both  $D$  and  $\delta$  are fixed so that  $b$  is varied by changing  $g$ . In the short pulse duration limit  $\delta \rightarrow 0$ ,  $D_{app}$  approaches the true diffusion coefficient  $D$  for a diffusion time  $t = \delta$ . Generally, if we assume the dependence on  $\delta$  is small, we have the approximation

$$\ln[S(b)] \approx \ln(S_0) - bD(t) \quad (3)$$

The DKI model is based on the eqn (2) but includes explicitly the  $O(b^2)$  term. The eqn (2) is expressed as

$$\ln[S(b)] = \ln(S_0) - bD_{app} + \frac{1}{6}b^2D_{app}^2K_{app} + O(b^3) \quad (4)$$

corresponding to a cumulant expansion for the diffusion MR signal, where  $K_{app}$  is the apparent diffusional kurtosis (unitless, equals 0 in the setting of completely Gaussian diffusion), which approaches the true kurtosis  $K$  in the limit of short pulse durations and contains specific information on the non-Gaussian diffusion behaviour<sup>3-5</sup>. The parameter  $D_{app}$  is the diffusion coefficient that is corrected to account for the observed non-Gaussian behaviour. The DKI extension of eqn (3) is

$$\ln[S(b)] \approx \ln(S_0) - bD(t) + \frac{1}{6}[bD(t)]^2K(t) \quad (5)$$

where b-values are regarded sufficiently small so that the  $O(b^3)$  term of eqn (4) is negligible. With this approximation, one can estimate both  $D$  and  $K$  by fitting to diffusion-weighted signal intensity data with three or more b-values in any gradient direction. The DKI model is parameterized by the diffusion tensor (DT) and kurtosis tensor (KT) from which several rotationally invariant scalar measures (e.g mean, axial, and radial diffusivity as well as fractional anisotropy (FA); and axial, radial, and mean kurtoses) <sup>6-8</sup>. The interpretability of these metrics is influenced by the estimation accuracy of the tensors. Thus, any hampering factor (incl. noise, motion, and artifacts) can introduce errors that may propagate to render physically and/or biologically implausible tensor estimates <sup>9</sup>. In this work, directionally-averaged  $K_{app}$  (later referred to as  $MK$ ) were calculated using were estimated using unconstrained nonlinear least squares, which has been previously reported and demonstrated tissue-specific geometry for different brain regions <sup>7</sup>.

## Methods – Support Vector Machine (SVM)

In general, an SVM is a binary pattern recognition technique. The aim of SVM is to construct a hyperplane (e.g., decision boundary) that best separates the two groups by maximising a margin between the groups. Prediction of an unseen sample is performed by identifying which side of the hyperplane the data lies.

Theoretically, given a training set consisting  $N$  subjects  $(\mathbf{x}_i, y_i)$ ,  $i=1, \dots, N$ ; where  $\mathbf{x}_i$  constitutes a feature vector of each subject (e.g., the extracted biomarkers from DKI images), and  $y_i$  represents a subject's group label (e.g., -1 or 1), SVM finds the optimal hyperplane  $\mathbf{w}^\top \mathbf{x} + b = 0$  by solving the following optimization problem:

$$\begin{aligned} \min_{\mathbf{w}, \xi} \quad & \frac{1}{2} \|\mathbf{w}\|^2 + C \sum_{i=1}^N \xi_i \\ \text{s.t.} \quad & y_i(\mathbf{w}^\top \mathbf{x}_i + b) \geq 1 - \xi_i, \quad i = 1, \dots, N \\ \text{s.t.} \quad & \xi_i \geq 0, \quad i = 1, \dots, N \end{aligned} \tag{1}$$

where  $C$  is a parameter controlling the trade-off between model complexity and training errors;  $\xi_i$  ( $i=1, \dots, N$ ) are slack variables, which penalises each misclassified subjects as a function of distance from the hyperplane.

Formula (1) can be solved by optimizing the following dual form:

$$\begin{aligned} \max_{\alpha} \quad & \sum_{i=1}^N \alpha_i - \frac{1}{2} \sum_{i,j=1}^N y_i y_j \alpha_i \alpha_j \langle \mathbf{x}_i, \mathbf{x}_j \rangle \\ \text{s.t.} \quad & 0 \leq \alpha_i \leq C, \quad i = 1, \dots, N \\ \text{s.t.} \quad & \sum_{i=1}^N \alpha_i y_i = 0 \end{aligned} \tag{2}$$

where  $\alpha_i$  is the Lagrange dual variable. A full derivation of the mathematics involved in SVMs can be found in [1]. For non-linear separable data, SVM uses a kernel  $\langle \mathbf{x}_i, \mathbf{x}_j \rangle$  to map the data into a higher dimensional space where the data can be linearly separated by a hyperplane. One common choice for the kernel is the radial basis function (RBF):

$$\langle \mathbf{x}_i, \mathbf{x}_j \rangle = \exp(-\gamma \|\mathbf{x}_i - \mathbf{x}_j\|^2), \quad \gamma > 0 \quad (3)$$

where  $\gamma$  is a free parameter controlling the width of the Gaussian kernel.

Once the SVM has identified the optimal hyperplane from the training data, the unseen test data  $\mathbf{x}$  can then be classified based the sign of the decision function:

$$f(\mathbf{x}) = \text{sgn}\left(\sum_{i=1}^N \alpha_i y_i \langle \mathbf{x}_i, \mathbf{x} \rangle + b\right) \quad (4)$$

### *Methods – Handling class imbalance*

The training phase of SVM is sensitive to class imbalance, an issue which occurs when one group has more subjects than the other. In this case the major group will overwhelm the correct training of the classifier, making the label of major group more likely to be predicted during testing. In our case, both tasks have imbalance data (e.g., 23 WHO grade 2 vs. 14 WHO grade 3 and 26 mutants vs. 11 wild-type). We addressed this problem by replacing the free parameter  $C$  with  $C_p$  and  $C_n$  for positive and negative classes respectively. Formula (1) then becomes:

$$\begin{aligned}
& \min_{\mathbf{w}, \xi^+, \xi^-} \quad \frac{1}{2} \|\mathbf{w}\|^2 + C_p \sum_{i=1}^{N^+} \xi_i^+ + C_n \sum_{i=1}^{N^-} \xi_i^- \\
& s.t. \quad \mathbf{w}^\top \mathbf{x}_i^+ + b \geq 1 - \xi_i^+, \\
& s.t. \quad -\mathbf{w}^\top \mathbf{x}_i^- - b \geq 1 - \xi_i^-, \\
& s.t. \quad \xi_i^+ \geq 0, \quad \xi_i^- \geq 0
\end{aligned} \tag{5}$$

where  $x_{i+}$ ,  $x_{i-}$  are positive and negative training examples in the training set;  $N_+$  and  $N_-$  are the numbers of such examples;  $\xi_{i+}$ ,  $i=1, \dots, N_+$  and  $\xi_{i-}$  are slack variables;  $C_p$  and  $C_n$  are set as  $C_p = (N_+ + N_-)/(2N_+) \times C_0$  and as  $C_n = (N_+ + N_-)/(2N_-) \times C_0$ .  $C_0$  was found by grid search.

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