Model selection in high temporal resolution DCE-MRI of breast tumors

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Purpose

An accurate assessment of tumor blood flow and permeability can be important for the treatment of breast cancer patients. High temporal resolution T1 weighted DCE MRI in combination with a deconvolution analysis has been shown to provide model independent quantitative blood flow values [1]. In order to extract trustworthy permeability information from the same data, a model based analysis is required. Several models can be of interest. In this study, we have used the Akaike information criterion (AIC) to investigate which of these models fits the high temporal resolution data best, balancing goodness-of-fit and number of parameters.

Methods

In vivo perfusion measurements were performed in 21 women with histologically proven breast tumors (5 benign, 16 malignant) on a 1.5 T scanner (Philips Intera). The routine MR mammography protocol was applied first. At the slice position where the tumor enhanced maximally, a prebolus protocol was applied using the 2ml/s injection of a prebolus of 1ml and a main bolus of 10-20ml of Gd-DTPA solution. The axial single slice dynamic inversion-prepared TFE time course covered 140s at a temporal resolution of 0.3s. Image post-processing was performed on a personal computer using the software PMI written in-house in IDL [2]. ROIs were placed manually over the central part of the aorta and the region within the breast lesion with highest enhancement. The signals were converted to relative enhancement. The tumor ROI data were fitted to three kinetic models: the full 4-parameter 2-compartment exchange model (2CXM) [3] and the 3-parameter modified Tofts (mTofts) [4] and uptake (2CUM) [5] models. Fit parameters included arterial delay and were constrained to positive values. The appropriateness of the models for fitting each tumor time course was compared on the basis of their respective Akaike weight (=probability for a model to be the best one among the models considered, according to the AIC [6]).

Results

The results are summarized in Fig. 1. Although the Akaike weights depend strongly on the individual tumors, in about 70% of cases one model is at least twice as likely as the next to be the best. On average, a benign tumor time course is best fitted by the 2CUM, while malignant tumors tend to favour the 2CXM. Redundant parameters that often lead to unphysical estimates are successfully eliminated using the AIC (Fig. 2).

Discussion/Conclusion

The values obtained for the extraction flow and other parameters depend strongly on the model. The AIC can help in automatically selecting the most appropriate model. The selection result is not simply a function of the two categories malignant/benign, but is influenced by the individual characteristics of each tumor. It also reflects the known limitations of the models and data: (1) a well-resolved sharp arterial transit is not modelled correctly using mTofts, (2) the relatively short time window does not allow accurate estimation of large interstitial volumes.

References

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[4] Tofts: JMRI, **7**, 91 (1997) [5] de Bazelaire et al.: Eur. Radiol., **15**, 2497 (2005) [6] Glatting et al.: Med. Phys., **34**, 4285 (2007)

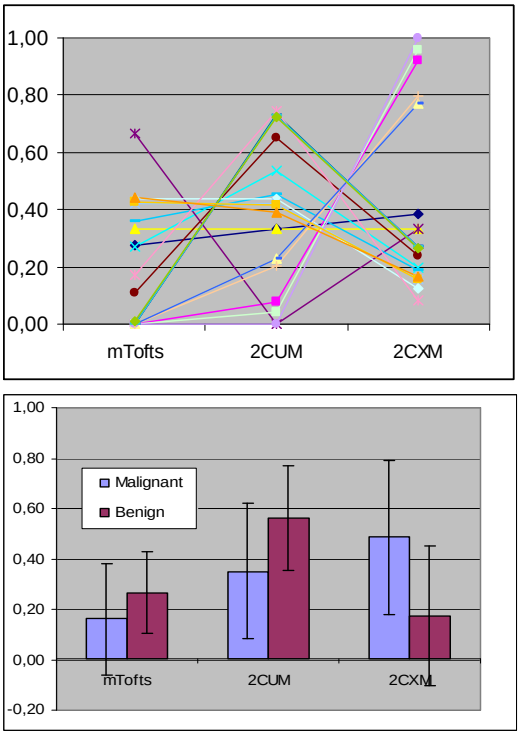

Fig. 1: Akaike weights for the three models: individual tumors (top), mean weights in benign and malignant tumors (bottom). The error bars correspond to 1 SD.

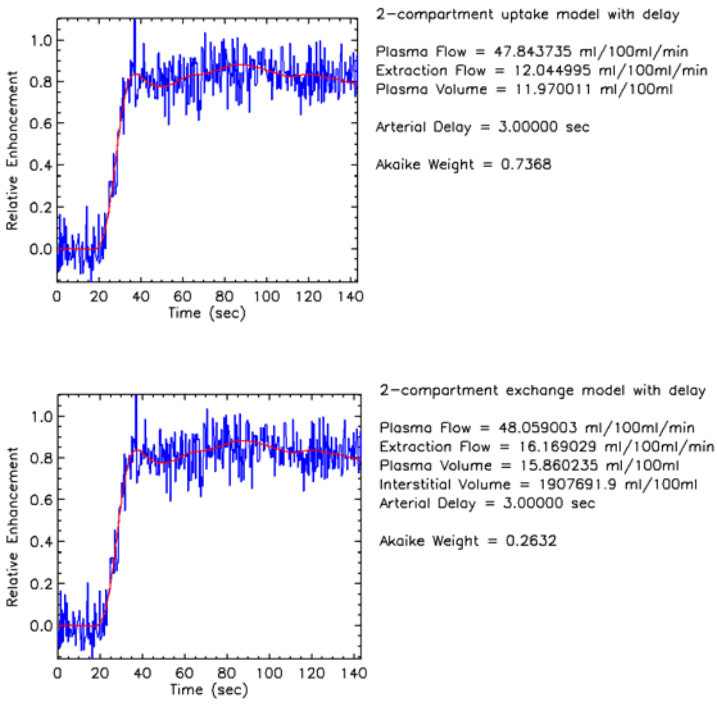

Fig. 2: Extra parameter introduced by 2CXM (bottom) is redundant, in agreement with much higher Akaike weight for 2CUM (top). The Akaike weight for mTofts was negligible in this case.