Comparison of blood flow measurements using 2-compartment model and deconvolution based analysis of T1-weighted DCE MRI of breast tumors

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Introduction: An accurate assessment of the Tumor Blood Flow (TBF) can become crucial in deciding the best management for breast cancer patients. Earlier studies have demonstrated the feasibility of quantifying blood flow in human breast tumors using prebolus DCE-MRI time courses covering a limited time window at high temporal resolution, combined with deconvolution analysis [1, 2]. Alternatively, these time courses can be efficiently fitted by a 2-compartment uptake model (2CUM), generating both blood flow and permeability [3, 4]. In this study, the aim is to compare the model-free blood flow values derived with deconvolution analysis against those derived with a 2-compartment uptake model (2CUM).

Materials & Methods: In vivo perfusion measurements were performed in 22 women with histologically proven breast tumors on a 1.5 T scanner (Philips Intera). The routine MR mammography protocol was applied first. The slice where the tumor enhanced maximally was identified on these data. At that slice position, 10 minutes later prebolus protocol was applied. 1ml of Gd-DTPA solution at 2ml/s was injected at the beginning of a dynamic axial single slice inversion-prepared (IR prepared) TFE acquisition. At the 400th dynamic, a high dose (10 / 20ml) of contrast agent is injected at 2ml/s and a further 400 dynamics were acquired. Other parameters of this sequence include: TR/TE/FA 4.9 ms /2.4 ms /12°, non-slice-selective 180° prepulse, inversion time: 196 ms, 128x90 matrix reconstructed at 256x256, FOV 425 mm, slice thickness 6 mm and temporal resolution 0.3s. Image post-processing was performed on a personal computer using the software PMI 0.3 [5]. Regions of interest (ROI) were placed manually in aorta and the region within the breast lesion with highest enhancement. The signals were converted to relative enhancement (RE). From the prebolus curve, AIFs were reconstructed by time-shifting and adding the prebolus response curve until the relevant high dose is reached [6]. The 10 ml or 20ml RE time course from the tumor ROI was then deconvolved with the reconstructed AIF using standard-form Tikhonov regularization and an optimized minimization scheme for the L-curve criterion [5]. Finally, the deconvolution TBF was calculated as the maximum of the impulse response function (IRF) [7]. The tumor ROI data was also fitted to the 2-compartment uptake (2CUM) model. The mean TBF values thus generated were compared with the deconvolution based TBF values.

Results: A malignant tumor RE time course with its fit using 2CUM is shown along with the corresponding IRF (Figure 1). Deconvolution based TBF showed a significant positive correlation with 2CUM derived TBF (Pearson $r = 0.977$ $p < 0.05$) (Figure 2). The mean TBF values of malignant breast tumors derived with deconvolution analysis and with modeling were 16 ± 7 and 22 ± 12 ml/100ml/min respectively. The difference with modeling was more marked in hypervascular malignant tumors.

Conclusion: We have shown that: 1) Deconvolution and model based approaches in breast tumors result in blood flow values that are well correlated. 2) Deconvolution based TBF values are systematically lower than the model based values. This difference is consistent with the results reported in brain [5, 8].

References

[1] Makkat et al. [2008] Radiology 2008 249:471-482. [2] Makkat et al. [2008] Proc.ESMRMB 25; 549.
[3] Sourbron S [2007ISMRM workshop: Cerebral perfusion and brain function Brazil[4] de Bazelaire et al. [2005] Eur. Radiol,. 15, 2497
[5] Sourbron et al. [2007] Phys Med Biol;52(2):429-47 [6] Kostler et al. [2004] Magn Reson Med;52:296-299
[7] Makkat et al. [2007] J Magn Reson Imaging;25:1159-67 [8] Sourbron et al. [2007] Phys Med Biol;52(22): 6761-78

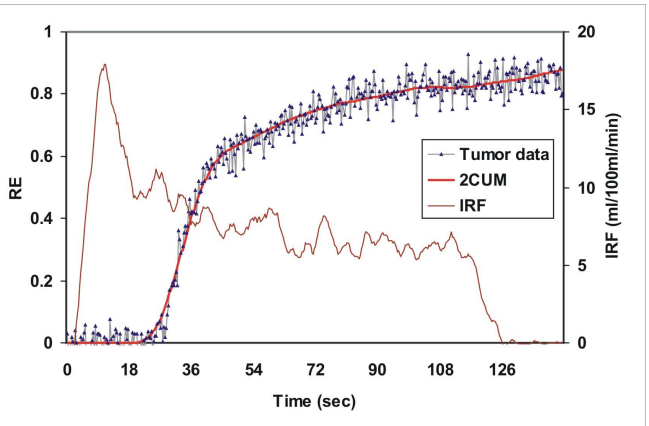

Figure.1: Malignant tumor data and corresponding 2CUM fit scaled on the left axis. IRF is scaled on the right axis.

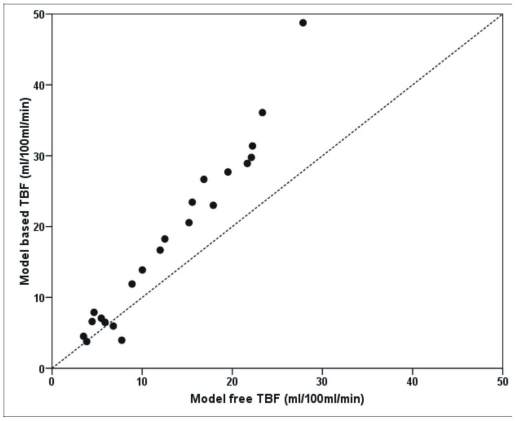

Figure.2: Comparison of ROI based TBF calculated with a model free deconvolution analysis (x axis) and the two-compartment model (y axis). Dotted line is line of identity.