DSC-MRI first-pass curve fitting and modelling is improved with a novel cosine-based function

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Introduction First-pass contrast-time curves from DSC-MRI data can be characterized by fitting a suitable function to the data, from which summary parameters (bolus arrival time, time-to-peak, maximum peak value, etc.) can be derived [1]. In this application the fitting procedure is essentially a de-noising operation, in that the summary measures could in principle be (noisily) estimated from the data themselves. A less widely used application is to fit a model to the data that includes specific parameters describing the tissue properties (mean transit time, blood volume and blood flow), in a similar manner to the methodology routinely used to fit DCE-MRI data [2]. In both applications the success of the technique depends on how well the model function describes such data. In this abstract we propose a new model to describe DSC-MRI first-pass data and demonstrate that it gives improved fits to clinical DSC-MRI data compared with two established models.

A gamma-variate function of the form $At^{\alpha-1}\exp(-\mu t)/\Gamma(\alpha)$ is widely used for fitting first-pass contrast changes in DSC-MRI data [3]. Less often used is a log-normal function of the form $At^{-1}\exp(-(\ln(t)-\mu)^2/(2\sigma^2))$ [4], which is empirically motivated and has no physical interpretation. First-pass curves arise after a bolus injection of contrast into a peripheral vein, after which the contrast passes through the right-heart, the lungs and the left-heart before it arrives at the brain or other tissues. The transit times of these regions will not be identically distributed or have the same mean value, which means that the commonly cited interpretation of the gamma-variate model as a series of α mixing chambers with equal exponentially distributed transit times [5] is unsatisfactory.

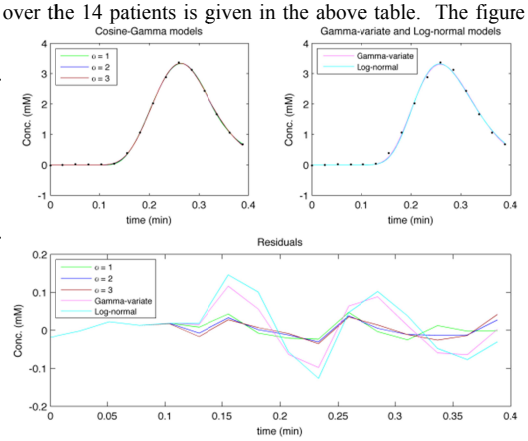
We propose a new model to describe DSC-MRI data that is based on the convolution between a raised-cosine function (of the form $A(1-\cos(\kappa t))$ for $0< t < 2\pi/\kappa$), and a gamma-variate. The idea behind this is that the gamma-variate is appropriate for describing transit times through regions that operate as simple mixing chambers (e.g. the heart), while a more symmetric function (the raised-cosine function) is potentially better suited to modeling transit times through tissues containing a vascular network (e.g. the lungs). Other symmetric functions (e.g. a Gaussian) are feasible and perhaps more theoretically plausible, but the raised-cosine has the advantage that it is symmetric, has a finite duration in time and the convolution can be analytically solved giving a function that can be easily and quickly evaluated.

Method The gamma-variate function, the log-normal function and three cosine-based models with α = 1, 2 and 3 were evaluated by comparing how well they fit DSC-MRI data. Since all these models have the same number of unknown parameters it is sufficient to compare the residual sum of squared errors (RSS) from least-squares fitting. We also compare the execution time, number of iterations for the fitting to converge, and the execution time per evaluation of the model function.

Data Acquisition and Processing Fourteen patients with advanced glioblastoma multiforme (GBM) were imaged at DSC-MRI with a Philips Achieva 3T and the following parameters: multi-slice FE-EPI with 45 echoes and SENSE factor 2, TR/TE = 1554/40 ms, flip-angle = 75°, 25×4mm axial slices, 96^2 acquisition matrix, 224^2 mm FOV, 40 dynamic points at 1.5 sec/volume. Magnevist contrast agent was used at a dose of 0.2ml/kg, delivered at 3ml/sec using a power injector, and signal changes were converted to concentration changes assuming exponential signal dependence and a relaxivity of 4.4 mM/ms. From each data set a slice through the cerebral ventricles was selected and an ROI drawn to include the whole brain, excluding the ventricles and any pathology. A cut-off time was manually selected to remove recirculation data leaving only the first pass curve, which was fitted pixel-wise using all five models. A delay parameter was included in the model to account for variations in the arrival time of the contrast. Fitting was implemented in IDL (Research Systems Inc, Boulder, Colorado) running in Windows XP under VMware Fusion 3.1.3 on a Mac Pro 2.26 GHz Quad-Core Intel Xeon.

	Cos-Gamma α = 1	Cos-Gamma α = 2	Cos-Gamma α = 3	Gamma-variate	Log-Normal
Formula	$A\exp(-\mu t)\otimes(1-\cos(\kappa t))$	$At\exp(-\mu t)\otimes(1-\cos(\kappa t))$	$At^2\exp(-\mu t)\otimes(1-\cos(\kappa t))$	$At^{\alpha-1}\exp(-\mu t)/\Gamma(\alpha)$	$At^{-1}\exp(-(\ln(t)-\mu)^2/(2\sigma^2))$
RSS	0.6596	0.6434	0.6644	1.1834	0.7611
Mean execution time/pixel (ms)	130	54	360	74	58
Mean iterations per pixel	436	143	705	220	209
Mean ex. time per iteration (ms)	0.32	0.38	0.51	0.34	0.27

Results and Discussion The mean over pixels of the RSS was reported for each patient and the mean over the 14 patients is given in the above table. The figure shows an example fit to the mean curve from one patient. The cosine and non-cosine models have been plotted on separate axes to better show their fit accuracy. The residuals plot indicates the improvement in the fit of the cosine-based models, and their similarity with each other. These figures are representative of the patterns seen in the whole data set.



Overall the three cosine-based models have very similar errors: α = 2 is slightly better than α = 1 and 3, although a paired t-test is not significant for all comparisons between these models. This implies that there is little to be gained by including α as a fit parameter with these models, and that restricting α to integer values has little impact. The execution time per iteration of the cosine-based models is longer for larger α (due to the number of terms in the formula with the convolution written out), although the number of iterations per pixel means that this pattern is not seen in the overall execution time. Overall, the model with α = 2 is preferred among the cosine-based models due to its fitting accuracy and more importantly, its execution time.

The cosine-based models have lower errors than the gamma-variate and log-normal models, and all comparisons between the cosine and non-cosine models are significant ($p<0.05$). In particular the mean errors for the Gamma-variate model are 84% larger than the Cos-Gamma α = 2 mode1, ($p = 0.016$) and for the Log-Normal model they are 18% larger ($p = 0.0098$).

Conclusions In this study we have presented a novel model for describing DSC-MRI first-pass data that gives improved fitting accuracy and speed (for α = 2) relative to two established models. Further work is needed to establish if the components of the model correspond to the transit of contrast through different vascular components (mixing chambers/capillary beds) and therefore if the model parameters derived have a direct physical interpretation.

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