



Introduction

- Pharmacokinetic analysis of dceMRI has shown potential as a tool to predict and assess tumour treatment response
- Quantitative PK analysis can reveal more information from tumour micro-vasculature and increase the reproducibility of dceMRI studies
- It requires the estimation of the pre-contrast relaxation time (T_{10}) to convert signal intensity to contrast agent (CA) concentration curves
- T_{10} maps may be computed from a sequence of Spoiled Gradient Echo (SPGR) volumes with variable flip angles
- This method for T_{10} estimation assumes that no motion is present during the SPGR acquisitions

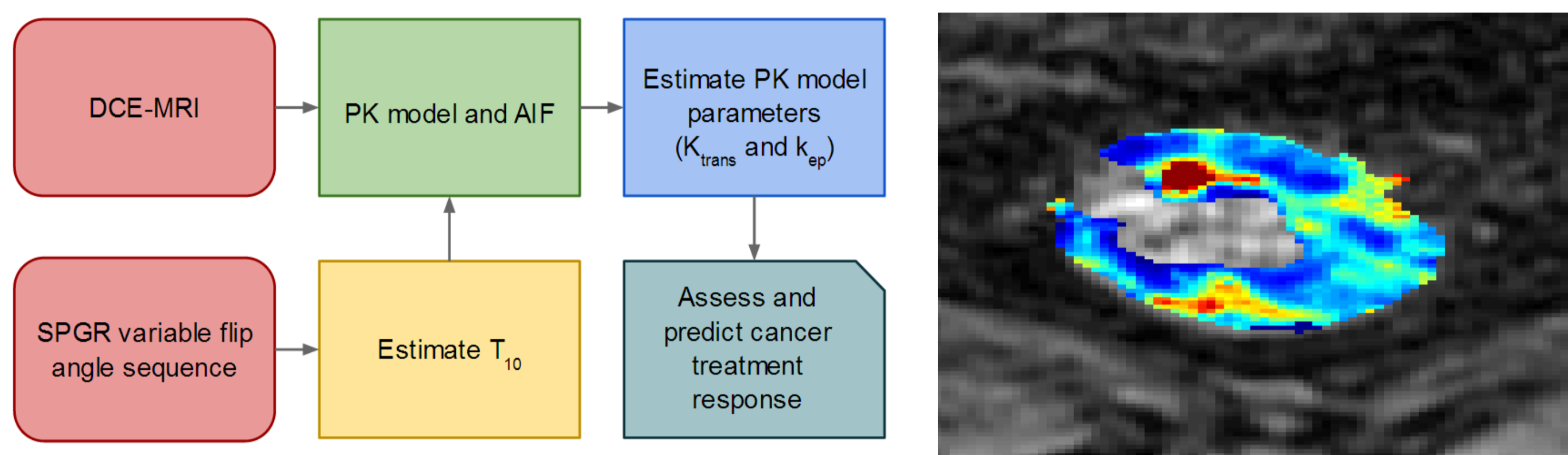


Fig. 1: PK model parameter estimation in dceMRI studies

Fig. 2: K_{trans} map of colorectal tumour

Aim

Evaluate the effects of motion within variable flip angle SPGR sequences on T_{10} and subsequent PK model parameter (K_{trans} and k_{ep}) estimation

T10 Estimation

- Signal intensity in SPGR acquisitions relate to the relaxation time and equilibrium magnetization (T_1 and M) by [1]:

$$S = M \sin(\alpha) \left[\frac{1 - \exp(-TR/T_1)}{1 - \cos(\alpha)\exp(-TR/T_1)} \right]$$

where α is the flip angle and TR the repetition time

- T_{10} and M_0 maps can be obtained from a sequence of variable flip angles by fitting the signal intensities curves over the several volumes

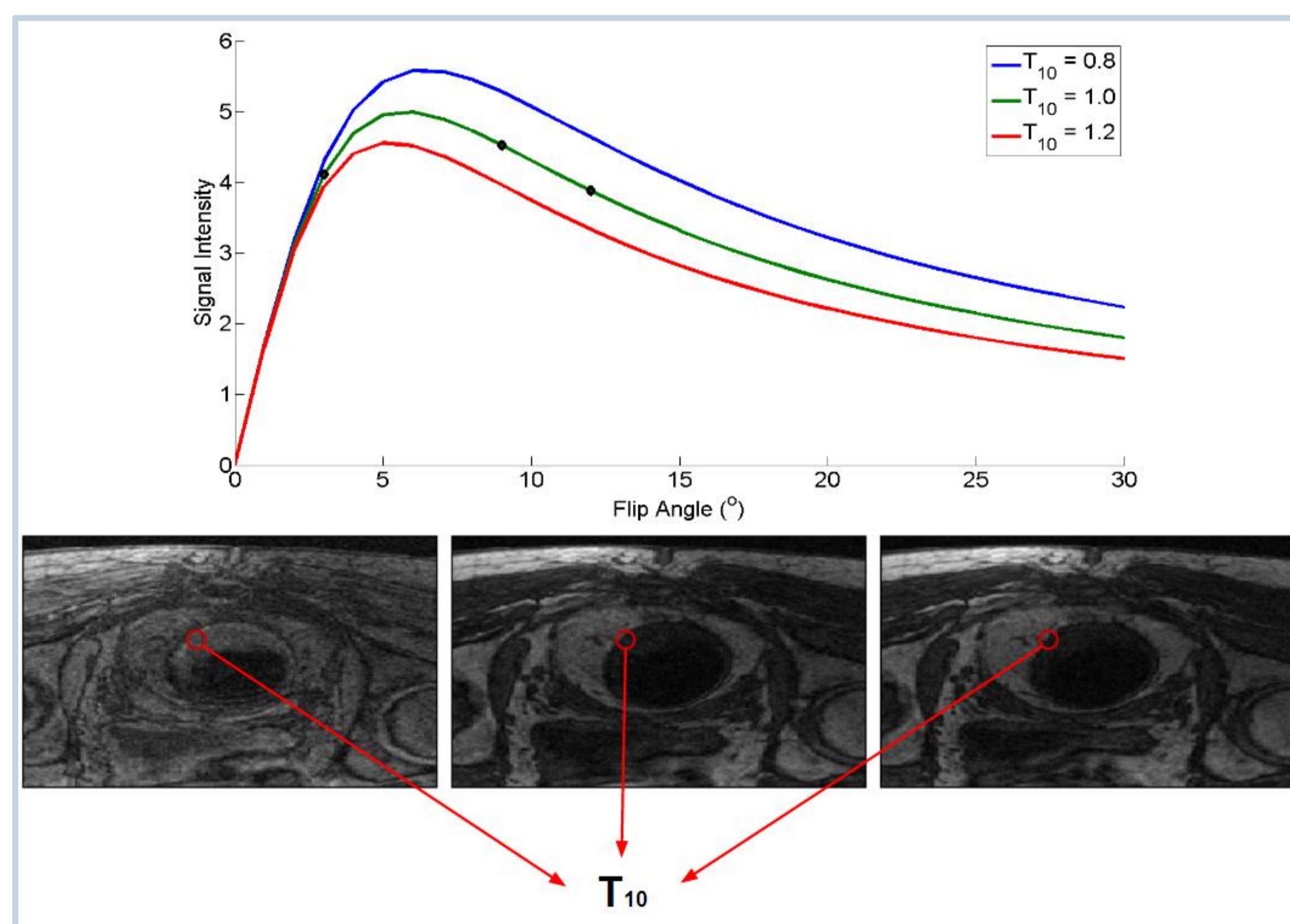


Fig. 3: T_{10} estimation by fitting the signal intensity curve over three variable flip angle SPGR acquisitions

PK Modelling

- The CA enhancement on the extravascular extracellular space can be modelled by the Tofts model [2]:

$$C_e(t) = K_{trans} C_p(t) \otimes \exp(-k_{ep}t)$$

- C_p is the arterial input function (AIF). We used the Orton AIF [3], a population model
- The CA causes a shortening of the relaxation time which then relates to change in the dceMRI intensities:

$$\frac{1}{T_1} = \frac{1}{T_{10}} + r_1 C_e$$

- K_{trans} and k_{ep} are the desired model parameter estimated by fitting them to the dceMRI signal enhancement curves

Estimating motion in flip angle sequences

- 21 colorectal SPGR sequences with 3 or 4 acquisitions volumes each (3° , 9° , 12° and/or 15° flip angles)
- Rigid registration using Groupwise Normalized Mutual Information [4] was applied to each sequence
- The mean displacement found by the registration provided an estimation of the motion present within these acquisitions:

	Mean	Std Dev	Min	Max
Recovered Motion	0.43mm	0.34mm	0.00mm	0.90mm

Evaluating the effects of simulated motion on T10 estimation

- 21 T_{10} and M_0 maps were computed from clinical data and considered as ground truth data
- These maps were used to generate synthetic SPGR variable flip angle sequences
- Random B-Splines free-form deformation [5] was applied to the volumes within these sequences
- \hat{T}_{10} was estimated from the motion corrupted sequences and compared to the ground truth maps

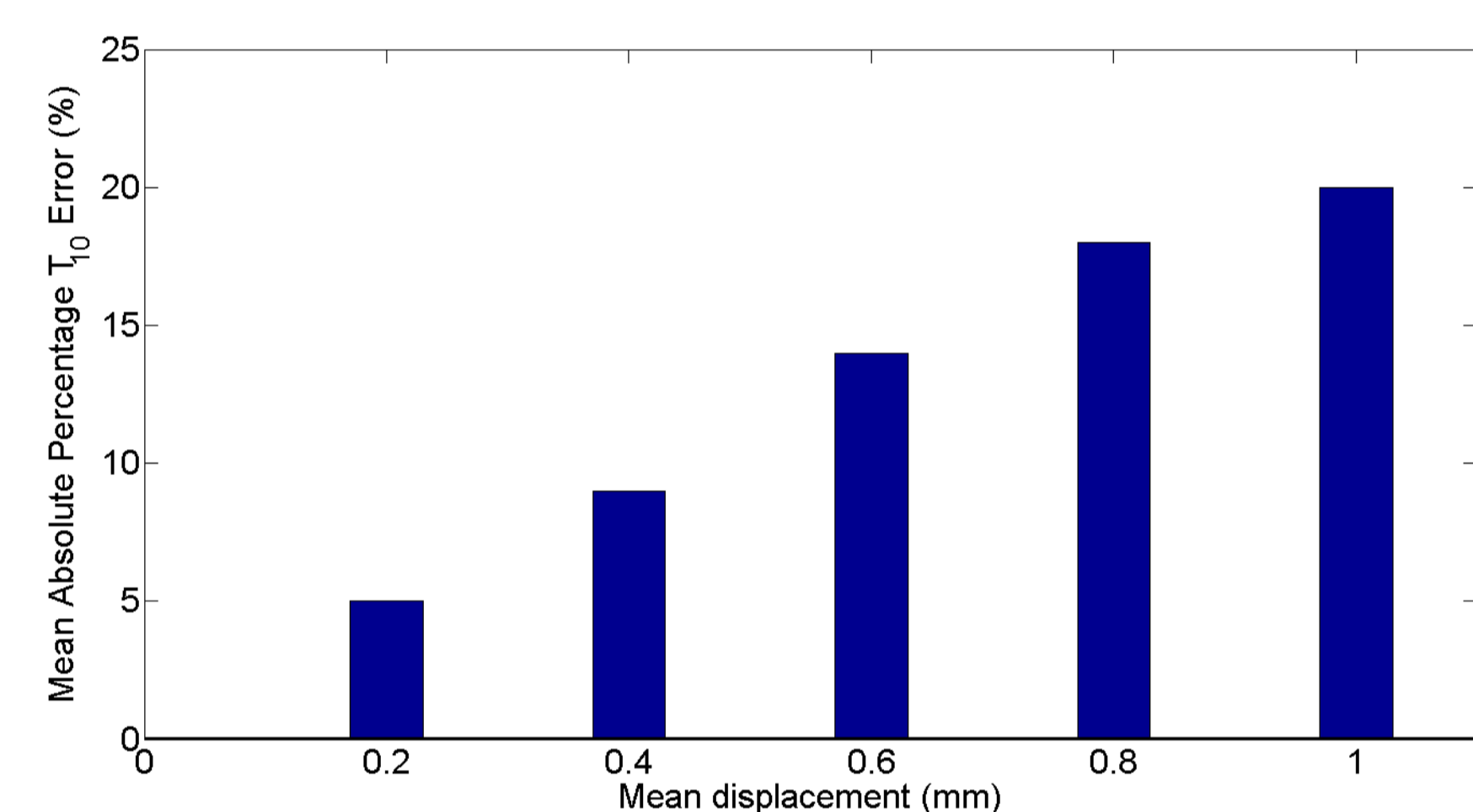


Fig. 4: Mean absolute percentage T_{10} estimation error caused by increasing levels of motion within the variable flip angle sequences

Evaluating the effects of inaccurate T10 on PK parameter estimation

- dceMRI signal intensity curves were generated using the Tofts model and the Orton AIF with $T_{10}=1.0s$ and a range of PK model parameters
- \hat{K}_{trans} and \hat{k}_{ep} were estimated from the signal intensity curves using inaccurate \hat{T}_{10} parameters and compared to the ground truth

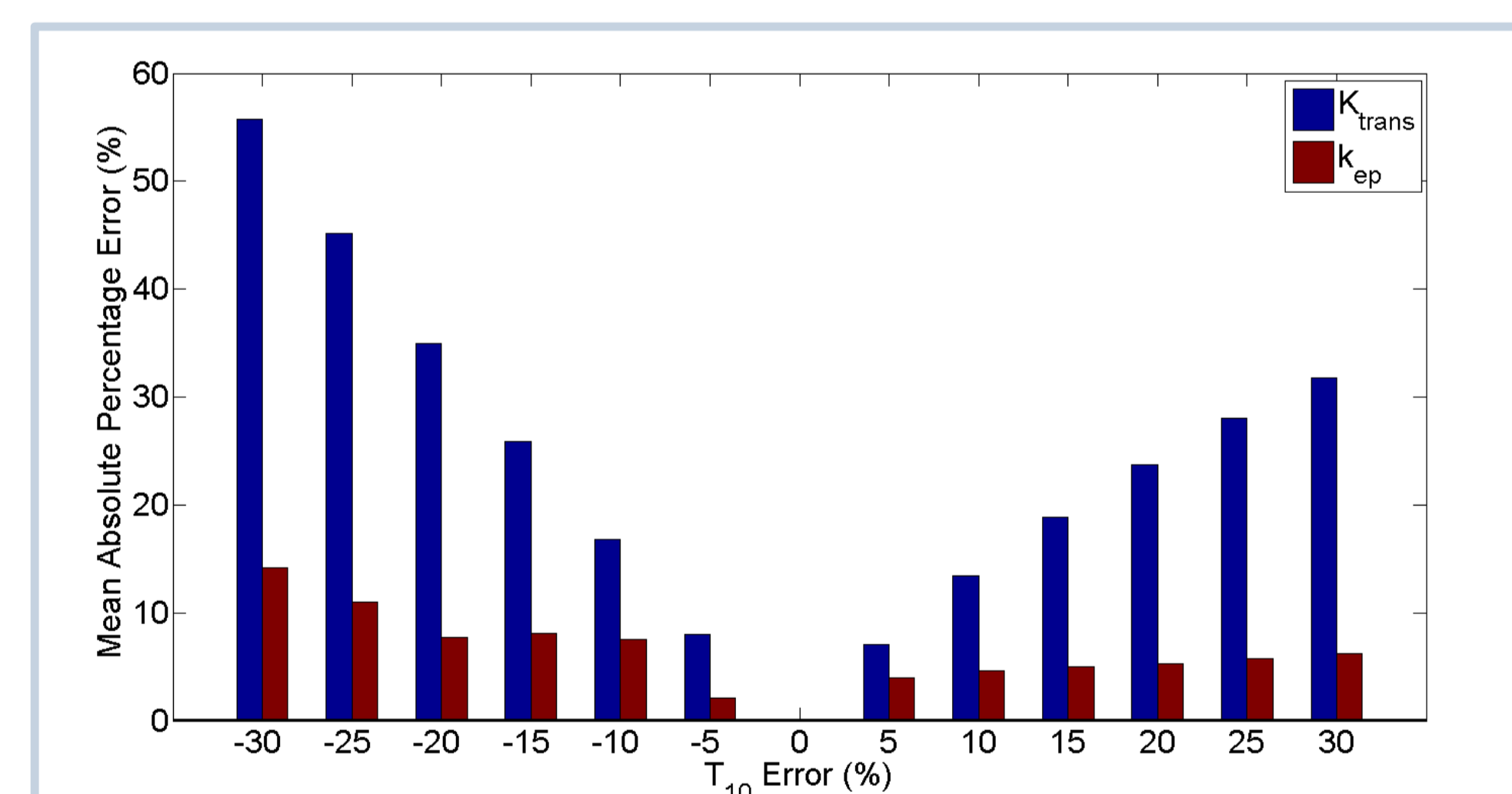


Fig. 5: Average K_{trans} and k_{ep} errors for different levels of T_{10} deviation

Summary

- Errors in T_{10} estimation are propagated and amplified to subsequent K_{trans} estimation
- k_{ep} is much more robust to T_{10} deviations
- An average displacement of 0.43mm was observed between volumes in variable flip angle SPGR sequences, and this motion is expected to cause 10% T_{10} estimation error leading to 16% mean K_{trans} estimation error

Acknowledgements

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