Real-time Automatic Resolution Adaption (AURA) for dynamic contrast-enhanced MRI

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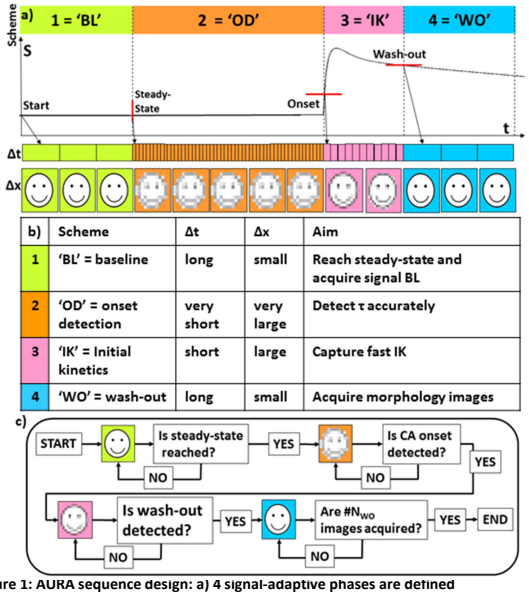
Introduction:

In dynamic contrast-enhanced (DCE) MRI, pharmacokinetic modelling (PK) is used to quantify tissue physiology. For fitting accuracy, high temporal resolution is needed whilst high spatial resolution yields morphological information. However, both are not compatible. Studies[1,2] have shown that acquiring images at high temporal resolution during the fast initial kinetics (IK) and high spatial resolution during slower wash-out (WO) improves the diagnostic performance. In these studies, temporal resolution changes at fixed time points. However, it is not *a priori* known at which time the IK phase starts and at when the WO begins. This may lead to information loss. If the onset time is missed, fitting accuracy decreases. If the peak is missed, CA is partly washed-out in high spatial resolution images. In a previous study, real-time automatic contrast agent (CA) bolus detection in vessels was introduced[3]. In this work, this concept is extended to an automatic resolution adaption (AURA) sequence. Acquired dynamic data are analyzed in real-time to find the onset and beginning of the WO and consequently temporal resolution is automatically adapted by alteration of spatial resolution. In this study, the AURA sequence is validated using a perfusion phantom. Furthermore, the model fitting performance of the AURA sequence is compared to that of a fast sequence (**f**) with low temporal/high spatial resolution and a slow sequence (**s**) with high temporal/low spatial resolution.



b)	Scheme	Δt	Δx	Aim
1	'BL' = baseline	long	small	Reach steady-state and acquire signal BL
2	'OD' = onset detection	very short	very large	Detect τ accurately
3	'IK' = Initial kinetics	short	large	Capture fast IK
4	'WO' = wash-out	long	small	Acquire morphology images

Figure 1: AURA sequence design: a) 4 signal-adaptive phases are defined with b) characteristic spatial/temporal resolutions. c) Real-time feedback mechanism

Methods:

The AURA sequence design, based on a T1-weighted 2D GRE sequence, is described in figure 1. Four schemes of characteristic signal-adaptive spatial/temporal resolutions are defined (a, b). A real-time feedback mechanism evaluates acquired dynamic data for predefined signal-dependent switch criteria. The result of this analysis determines the resolution of the next image (c). Phantom data are acquired, for which the contrast-enhanced signal time curves are described by the gamma variate function[4]:

$$\Gamma(t) = \varepsilon \text{ for } t \le \tau \text{ and } \Gamma(t) = \varepsilon + (\Gamma_{max} - \varepsilon) e^{\alpha\left(1-\frac{(t-\tau)}{(t_{max}-\tau)}\right)} \left(\frac{(t-\tau)}{(t_{max}-\tau)}\right)^{\alpha} \text{ for } t > \tau.$$

The switch criteria for the phantom are defined based on the *k*-space center signal as shown in figure 2. The experiment is repeated acquiring 1 slice using the AURA, the **f** and **s** sequence. PK maps of the **s** sequence are calculated by fitting Γ(t) and are assumed to be the ground truth (GT). To mimic a multi-slice acquisition of 25 slices, all three datasets are temporally under-sampled by a factor of 25. PK maps are generated for the under-sampled data and joint histograms of the resulting maps with the GT are calculated. For each joint histogram, Pearson's correlation coefficient r is calculated. Furthermore, morphological images near the mean signal peak are investigated.

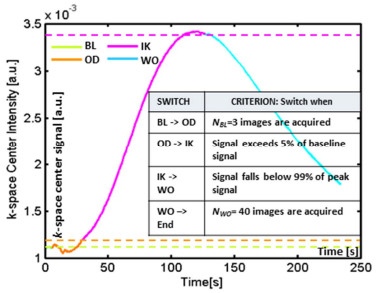


Figure 2: Pre-defined switch criteria for the perfusion phantom

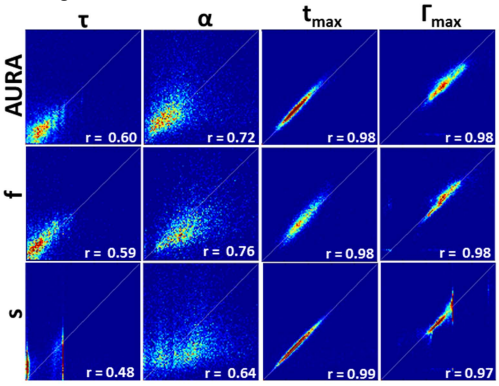


Figure 3: Joint histograms between resulting and ground truth PK maps

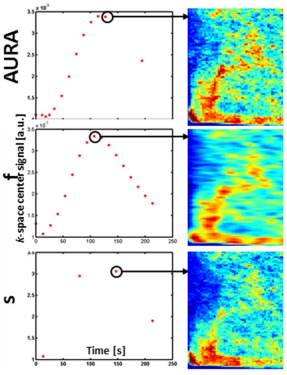


Figure 4: Morphological images close to the mean signal peak

Results:

The chosen switch criteria worked for the perfusion phantom. The joint histograms of the parameter maps for τ, α, t_{max} and Γ_{max} are shown in figure 3. For AURA and **f**, the results are comparable for all parameters. Comparing **s** to AURA, r is lower for τ and α and large systematic errors are visible for τ, α and Γ_{max}. t_{max} of **s** is comparable to that of AURA. Morphological images close to the contrast agent (CA) peak are shown in figure 4. AURA provides a high spatial resolution image shortly after the peak, whilst for **s**, the peak is missed and less CA is present. **f** provides an image close to the peak, however at low spatial resolution.

Summary & Discussion:

An 'intelligent' AURA sequence is developed for DCE MRI, which automatically adapts the resolution to signal changes. By that, comparable fitting accuracy to a fast sequence is achieved and high spatial resolution images located reliably close to the mean signal peak are provided. The *k*-space center intensity based criteria worked robustly for the phantom. *In vivo*, more sophisticated bolus tracking methods would be needed, for example to handle enhancing areas outside the region of interest. The employed adaption is global and is optimized for the mean signal, but may be suboptimal for single voxels. In this study, a gamma-variate function is used as a model. In reality, tissue signal is better modeled using multi-compartment models[5] in which the wash-out is slower. In this case, the wash-out can be exploited further to acquire high spatial resolution images. In the next steps, sophisticated acceleration techniques for the fast sequence should be implemented. Additionally, to better optimize tempo-spatial requirements, the adaption could be extended to arbitrary resolutions.

References: 1) Pinker K, et al.Invest Radiol.2009;44:553-558.2) Jansen, et al. Phys Med Biol.2010;55:473-485.3) Ho VB, et al.J Magn Reson Imaging.1999;10(3):276-88.4) Chan A, et al.IEEE.2004;1067-1070.5) Tofts PS, et al.Magn Reson Med.1991;17:357-267