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This is a brief summary of the methods used in TOPPCAT

T1 Map Sub:

The general equation for signal intensity at a given flip angle

 $S(\alpha) = S_0(1 - e^{-TR/T1}))\sin(\alpha)/(1 - \cos(\alpha)e^{-TR/T1})$, where TR is the repetition time, α is the flip angle, and S_0 is the equilibrium longitudinal magnetization, can be rewritten as $S(\alpha)/\sin(\alpha) = mS(\alpha)/\tan(\alpha) + S_0(1 - m)$, where $m = e^{-TR/T1}$. For each pixel location, the plug-in performs a linear least-squares fit for the slope m and the intercept $S_0(1 - m)$, considering $S(\alpha)/\tan(\alpha)$ as abscissa and $S(\alpha)/\sin(\alpha)$ as ordinate for each flip angle acquired, then solves for T1 and S_0 [1]. This method has been shown to be efficient and reasonably accurate in a recent evaluation [2].

Start Patlak:

In the first step, the plug-in calculates the T1 relaxation rate R1(t) at each pixel over time from changes in the signal intensity relative to baseline (S(t)-S(0)) using the formula

$$R1(t) = -1/TR \ln \frac{1 - \left(\frac{S(t) - S(0)}{S_0 \sin \alpha} + \frac{1 - m}{1 - (m \cdot \cos \alpha)}\right)}{1 - \cos \alpha \left(\frac{S(t) - S(0)}{S_0 \sin \alpha} + \frac{1 - m}{1 - (m \cdot \cos \alpha)}\right)}$$

(adapted from [3]) where α and TR are the flip angle and repetition time of the dynamic MR sequence. The user provides both S₀ and T1 maps, with m calculated as above from the latter. The baseline relaxation rate R1(0) is calculated by averaging the dynamic images obtained before contrast arrival, and the concentration of gadolinium is calculated from the change in R1: C(t) = (R1(t) - R1(0))/\Re1, where $\Re1$ is 4.39 s⁻¹mM⁻¹ for gadolinium [3].

In the second step, K^{trans} and vascular volume maps are calculated using Patlak analysis. Patlak analysis is a relative simple method that attempts to separate contrast agent distribution due to permeability effects from those due to increased vascularity [4]. K^{trans} of gadolinium derived using this method have correlated well with ¹⁴C-sucrose transfer constants in a model of rat cerebral ischemia [5]. The equation for the Tofts-Kermode model [4] for contrast agent distribution modified [6] to take into account the presence of separate extracellular and intravascular compartments is

$$\mathbf{C}_{t}(t) = \mathbf{K}^{\text{trans}} \int_{0}^{t} \mathbf{C}_{p}(\tau) e^{\frac{\mathbf{K} \text{trans}}{\text{ve}}(t-\tau)} d\tau + \mathbf{v}_{p} \cdot \mathbf{C}_{p}(t)$$

where v_e is the fractional volume of the extracellular extravascular volume, $C_t(t)$ is the tissue concentration over time, and $C_p(t)$ is the plasma concentration over time. Patlak analysis assumes that the value of the exponential term is unity because either the back diffusion rate K^{trans}/v_e is small, t- τ is small, or both. If this is the case, division of the entire equation by $C_p(t)$ yields a linear equation, if $\int C_p(\tau) d\tau / C_p(t)$ is considered the ordinate and $C_t(t)/C_p(t)$ is considered the abscissa for each time point. The plug-in uses the least squares method to solve this equation for the slope K^{trans} and the intercept v_p . A concentration time curve chosen from a region of interest in a vascular structure, adjusted for capillary hematocrit (user-supplied), is used as a surrogate for $C_p(t)$.

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