Reconstructing the one-compartment tracer-kinetic field with diffusion and convection

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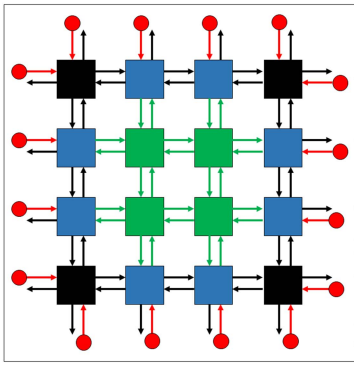

Figure 1. Forward and inverse problems illustrated for a 4x4 voxel system. In the forward problem, the input functions are given (red circles), as well as the values of all transfer constants (arrows). The concentrations in all 16 voxels (squares) are calculated as a function of time. In the inverse problem, the concentrations in all voxels are given and the inner transfer constants (green arrows) are reconstructed by treating the outer voxels (blue) as input functions.

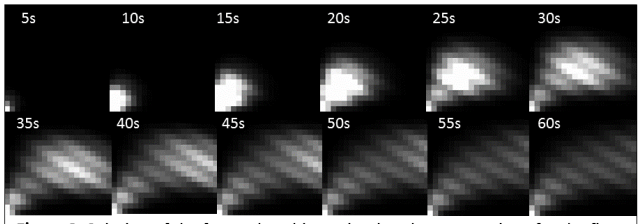

Figure 2. Solution of the forward problem: simulated concentrations for the first 60s in steps of 5s.

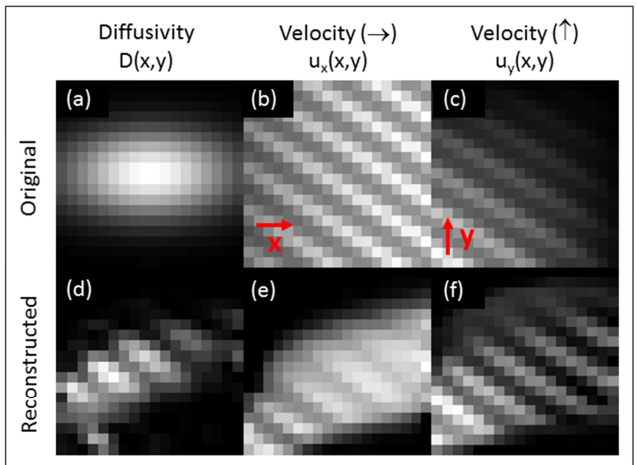

Figure 3. Solution of the inverse problem: original fields (a,b,c) and reconstructions (d,e,f) for diffusivity (a,d), x-velocity (b,e) and y-velocity (c,f).

TARGET AUDIENCE: Physicists

OBJECTIVES: A tracer-kinetic field theory has been proposed for DCE- and DSC-MRI that models the spatial transport of indicator, potentially reducing systematic errors and providing new physiological information [1,2]. However, it is currently unclear whether all model parameters are identifiable without additional constraints. Here this question is investigated in 2D for the simplest field model describing a single compartment with diffusion and convection.

THEORY: A one-compartment field model is defined by a divergence-free flow field $\mathbf{f}(\mathbf{r})$ (ml/min/cm^2), a diffusivity $D(\mathbf{r})$ (cm^2/min), and a volume fraction $v(\mathbf{r})$. After suitable space discretisation (fig 1) this reduces to a multi-compartment model where each voxel is a compartment and neighbouring voxels (i,j) exchange indicator with non-negative transfer constants K_{ij} and K_{ji} [2]. Given a measurement of (K_{ij}, K_{ji}) on a surface normal to the x-axis, the diffusivity D_{ij} and the x-component u_{ij} of the velocity $\mathbf{u} = \mathbf{f}/v$ at the surface can be derived as $u_{ij} = (K_{ij}-K_{ji})*\Delta x$ and $D_{ij} = \min(K_{ij}, K_{ji}) *\Delta x^2$.

METHODS: A square field of view with side L=40cm was simulated with $v(x,y)=0.7+0.2*\sin(2\pi(3x+5y)/L)$, $f_y(x,y)=(y/L-1)*(x/L-1)$, $f_x(0,y)=0.5$ and $D(x,y)=\exp(-((x/L-0.5)/0.4)^2 - ((y/L-0.5)/0.2)^2)$. A population-average input function was injected at (x,y)=(0,0) for 60s. The space was discretised with 2cm voxels, and the time step Δt was equal to the smallest voxel mean transit time of 0.48s.

The forward problem (fig 1) was solved by iterating the matrix equation $\mathbf{C}(t+\Delta t) = \mathbf{C}(t) + \Delta t\mathbf{K}\mathbf{C}(t) + \Delta t\mathbf{K}_a\mathbf{C}_a(t)$, where $\mathbf{C}(t)$ is a vector with all concentrations, $\mathbf{C}_a(t)$ is a vector of input functions, $\mathbf{K}_a$ depends on the K_{ij} entering the slice, $\mathbf{K}$ depends on all other K_{ij}. The inverse problem was solved by rewriting this equation as $\mathbf{C}(t+\Delta t) - \mathbf{C}(t) = \mathbf{C}^*(t)\mathbf{K}$, where $\mathbf{C}(t)$ is a vector of inner concentrations only, $\mathbf{K}$ is a vector of K_{ij} into- or out of inner voxels, and $\mathbf{C}^*(t)$ depends on all concentrations. This defines a linear system $\mathbf{B}(t) = \mathbf{A}(t)\mathbf{K}$ for each t, which can summarised into one sparse system $\mathbf{B}=\mathbf{A}\mathbf{K}$. The system is solved iteratively for $\mathbf{K}$ with a gradient descent method and initial $\mathbf{K}=\mathbf{0}$. At each iteration, the solution is projected onto the constraints $K_{ij} > 0$ and $\Sigma_j K_{ij} < 1/\Delta t$.

RESULTS: Figure 2 shows the solution of the forward problem at time steps of 5s (Δt was 0.48s). The bolus enters in the lower left corner and leaves at the upper right, dispersing in the process. The sinusoidal imprint of $v(\mathbf{r})$ is clearly seen. Very little indicator reaches the bottom right or top left corner within the 60s acquisition. Figure 3 shows the reconstruction for the three scalar fields in comparison to the exact field. The fields are undetermined in areas where no indicator enters, leading to values of zero in those regions. In other regions the basic structure of the original fields can be observed, but the reconstruction is generally inaccurate.

CONCLUSION: In a simulation without data error (noise, undersampling, artefacts) or model error (tracer-kinetic model, signal model), one would expect a very good reconstruction in well-perfused areas. This is not the case, suggesting that multiple solutions exist and/or the algorithm has not converged. Therefore an improved algorithm is required to identify the global optimum, or additional constraints must be imposed to reduce the size of the solution space.

REFERENCES [1] M. Pellerin, TE Yankeelov and M Lepage. Incorporating contrast agent diffusion into the analysis of DCE-MRI data. MRM 2007; 58: 1124-34 **[2]** S. Sourbron. A tracer-kinetic field theory for medical imaging. IEEE TMI 2014; 33(4): 935-946.