A Model-Driven Registration Framework for DCE-MRI

Erik A. Hanson, Department of Mathematics, University of Bergen
Constantin Heck, Institute of Mathematics and Image Computing, University of Lübeck

PURPOSE

The process of acquiring filtration related measurements from DCE-MRI of the kidney requires a series of processing steps. In this work we combine two closely related steps, the image registration (motion correction) and the pharmacokinetic modelling. The DCE-MRI data is generally sampled in 4D (3D + time) and proper alignment of the spatial volumes over time is required in order to express meaningful time series on voxel level. The combination of the processes allows the pharmacokinetic model to guide the registration resulting in an improved motion correction [1, 2]. We present a model-driven registration, using regularized parametermaps, SSD distance measure and a coupled optimization yielding robust parameterestimation and registration.

METHODS

Given a 4D image $f(x,t)$ with $x \in \Omega$, $t \in [0,T]$ and $\Omega \subseteq \mathbb{R}^3$, image registration can be formulated as the search for a deformation $y : \mathbb{R}^3 \to \mathbb{R}^3$ maximising the similarity between $f(y(x),t)$ and a motion-free reference image $g(x)$ for all $t \in [0,T]$. In this work, we assumed that the deformation is rigid and hence $y = y(x,u)$ for some parameter vector $u \in \mathbb{R}^5$. We also assumed that the time-series of a voxel at spatial location x_i can be described adequately by a model $M(p(x_i),C_A(\cdot),t)$, where $p(x_i) = (p_1(x_i),\ldots,p_m(x_i))^\top$ is a vector of unknown pharmacokinetic parameters and $C_A(\cdot)$ is the Arterial Input Function. In order to compute the model fit and the the deformation in a joint approach, we added a time variation to our static reference image and expressed it as $g(x,t) = M(p(x),C_A(\cdot),t)$. This yields the following optimization problem

$$J(y,p) = \int_{[0,T]} \int_\Omega (f(y(x,u),t)) - M(p(x),C_A(\cdot),t))^2 \, dxdt + \sum_{k=1}^m \alpha_k \|\nabla p_k(x)\|^2 \tag{1}$$

such that $p_k(x) \geq 0, \forall k \in \{1,\ldots,m\}$.

As pharmacokinetic model we applied the two-compartment Patlak-Ruthland Model, yielding $M(p,C_A(\cdot),t) = p_1 C_A(t) + p_2 \int_0^t C_A(s)ds$. In order to increase stability we added the positivity constraints, the diffusive regularization on the parametermaps and implemented our method in a multilevel framework. The minimisation was performed as a Non-linear Least squares problem and solved using a constrained multi-level Gauss Newton method. The real data was from a DCE-MRI study of glomerular filtration [3].

SNR	μ_{def}	σ_{def}	RE_{p1}	RE_{p2}
8	0.32	0.23	0.09	0.08
10	0.26	0.20	0.07	0.07
∞	0.05	0.03	0.01	0.03

Figure 1: Results for registration of the simulated data (38x85, 21 timepoints) at different SNR levels. Here SNR is with respect to the mean signal, μ_{def}, σ_{def} are the mean and the standard deviation of the maximal errors of all deformations (in pixel), and RE_{p1},RE_{p2} are the relative errors of the parametermaps. For regularization we chose $\alpha_1 = \alpha_2 = 10$.

RESULTS

We evaluated our method on real and simulated DCE-MRI data. In the simulation, we used the Patlak-Model to generate a phantom dataset, added noise and a random spatial deformation to the uptake curves. We further employed our algorithm to reconstruct the phantom and the parameter maps for different noise levels. Results from the experiments on synthetic data can be found in Figure 1 and in Figure 2, while an example of real dat registration is found in Figure 3.

DISCUSSION

The introduced model can be interpreted in two ways. On the one hand it can be regarded as a registration problem to adjusting reference images. On the other hand one can see it as a standard voxelwise parameter fit with the option of not only adjusting the model parameters but also switching to timecourses of different locations to correct for motion. Experiments showed that there is a risk of underestimation in the deformation terms of the model. This will happen in situations where the model parameters don't co-align (are shifted with e few voxels) and in that way simulate motion. This effect can be reduced by right regularization of the parameter maps.
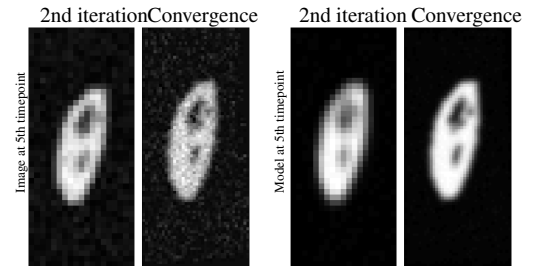

Figure 2: Registration of moving kidney phantom. Left panel: Transformed image, f (5th time point) at the 2nd iteration and convergence. Right panel: Model M (5th time point) at the 2th iteration and convergence. The difference in resolution is due to the multilevel implementation.
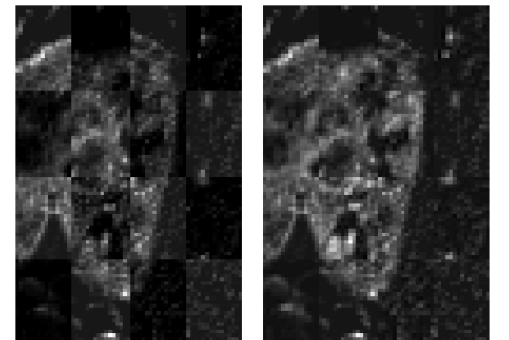
CONCLUSION

The proposed method showed promising results for parametric 4D image registration. The framework also opens several possibilities for further work including registration using more advanced compartment models (e.g Tofts or Sourbron model) as well as extension to a wider range of deformable and nonparametric registration schemes.

References

[1] Buonaccorsi et al., "Tracer Kinetic Model–Driven Registration for Dynamic Contrast-Enhanced MRI Time-Series Data", Magn Reson Med, 2007

[2] Bhushan et al., "Motion Correction and Parameter Estimation in dceMRI Sequences: Application to Colorectal Cancer", Proceedings of MICCAI, 2011

[3] Hodneland et al., "In vivo estimation of glomerular filtration in the kidney using DCE-MRI", Proceedings of ISPA 2011

Figure 3: Checkerboard image of unregistered (left) and registrated (right) DCE-MRI image of the kidney.