Reconstruction of cardiac images in limited data MRI

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Image acquisition in MR is time consuming because of the need to sample all of k-space. If the object being imaged is dynamic and its motion periodic, such as the heart, then the data is collected in a gated manner. This is essentially a time average over many periods of motion of the object. The images are then reconstructed and finally segmented. The quality of the segmentation is dependant on the quality of the reconstruction. In the case of limited data MR, the reconstruction is an ill-posed problem. To overcome this dependance, a method which combines segmentation and reconstruction is proposed. The proposed method directly segments the object from the background using limited MR measurements.

A combined model is used to approximate the intensity of the image and the shape of the object. If the image is considered to be sufficiently smooth, it can be represented by weights of basis functions on a regular grid:

$$B_j(\mathbf{r}) = B_0(\mathbf{r} + \mathbf{r}_j) = B_0(\mathbf{r}) * \delta(r - r_j)\,, \tag{1}$$

where B_0 is the central basis function. Some choices for basis functions can be found in [1]. In this particular case B_0 is based on the Kaiser Bessel window function [2]. The combined mapping from the parameter space P to the measurement space Y is a mapping $y = Z(p) = F(G(p)), p \in P, y \in Y$. The problem of calculating the optimal parameters is a least squares linear problem and the following functional requires minimisation:

$$\Phi(p) = ||g - Z(p)||_2^2\,, \tag{2}$$

where $g \in Y$ is the measured data and $Z : P \to Y$ is the combined mapping.

Having reconstructed the intensity of the image, the segmentation problem is to find an explicit jump around the object of interest. The boundary of the shape is defined using trigonometric functions [3]. The mapping Z becomes non-linear in this case and the problem requires an iterative solution. This is typically solved using the Levenberg - Marquardt method, which updates the solution estimate:

$$p^{k+1} = p^k + (J^*(p^k)J(p^k) + \lambda I)^{-1} J^*(p^k)[g - Z(p^k)]\,, \tag{3}$$

where matrix J is the linearisation of the forward model Z and λ is a regularisation parameter. The matrix J has been calculated in [4]:

$$J = \begin{cases} F\left[\int_{s_1}^{s_2} \dot{y}(s)\theta_n(s)\,ds\right] & n \in \gamma^x \\ -F\left[\int_{s_1}^{s_2} \dot{x}(s)\theta_n(s)\,ds\right] & n \in \gamma^y \end{cases}\,, \tag{4}$$

where $\gamma^x, \gamma^y \in P$ are the weights of the trigonometric functions θ_n, s_1, s_2 are the intersection points of the boundary with each pixel and $\dot{x}(s), \dot{y}(s)$ are normals to the curve.

In a proof of concept experiment the method was applied to fully reconstructed cardiac images. Radial undersampling was simulated by using only five profiles, each consisting out of 185 samples.

References

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