T_1 and T_2 mapping in cardiac MRI

The longitudinal relaxation time constant, T_1, reflects the loss in magnetisation of the nuclear spin magnetisation vector $\mathbf{M}$ parallel to the magnetic field $\mathbf{B_0}$: $\mathrm{M_z(t)} = \mathrm{M_{z,eq}} - \left[\mathrm{M_{z,eq}} - \mathrm{M_z}(0)\right]e^{-\mathrm{t}/\mathrm{T_1}}$. On the other hand, the T_2 relaxation time constant reflects the loss in magnetisation of the nuclear spin magnetisation vector $\mathbf{M}$ perpendicular to the magnetic field $\mathbf{B_0}$: $\mathrm{M_{xy}(t)} = \mathrm{M_{xy}}(0)e^{-\mathrm{t}/\mathrm{T_2}}$.

T_1 and T_2 of the myocardium is altered in various diseases because of changes in the local molecular environment, which result in altering the water content (Kellman and Hansen, 2014). For example, elevated T_1 values have been reported in a number of myocardium conditions, such as cardiac amyloidosis, diffuse fibrosis, myocardial infraction and so on. In fact T_1 tissue characterisation enables the identification of fibrosis and subsequently the differentiation between ischemic and non-ischemic cardiomyopathies (Ferreira et al., 2014). On the other hand, T_2 relaxation time is sensitive to the inflammation and myocardial edema. Therefore, T_1 and T_2 mapping techniques can provide useful biomarkers and quantitative prediction measurements.

In T_1 mapping, a series of images acquired with different T_1 weighting is generated. Modified Look-Locker inversion recovery (MOLLI) pulse sequence allows for pixel-wise accurate in-vivo T_1 mapping of myocardium within a single breath hold (Kellman and Hansen, 2014; Messroghli et al., 2004). However, with MOLLI sequences we measure the apparent recovery time, $\mathrm{T_1^*}$. Subsequently, T_1 can be approximated after a three parameter fitting, $\mathrm{S(t)} = \mathrm{A} - \mathrm{B}e^{-\mathrm{t}/\mathrm{T_1^*}}$, based on the Look-Locker correction: $T_1 \approx \mathrm{T_1^*}(B/A - 1)$. In order to recover the initial sign of the MR signal, we repeat a phase sensitive detection (PSIR) based fitting with an increasing number of image intensity values switched to negative (Messroghli et al., 2004). Finally, we choose the configuration with the smaller fitting error. This method is less sensitive to initial parameters' value than a direct magnitude fit but it results in a four-parameter fit that includes three parameters for the curve fitting and a parameter for the zero-crossing (Kellman and Hansen, 2014).

The Levenberg-Marquard method in mapping T_1 and T_2.

We use the Levenberg-Marquardt (LM) method in mapping T_1 and T_2 in vivo. The Levenberg-Marquardt method is a standard technique to solve nonlinear least squares problems [Gavin 2011]. Due to its application to a broad range of problems, increasing its efficiency and accuracy is under intensive investigation (Prado et al., 2015).

Here, we are interested in fitting a non-linear function $\hat{y}(t; \mathbf{p})$ of an independent variable t and a parameters vector **p** of length n to a set of m data points (t_i, y_i). The minimisation algorithm aims to minimise the sum of the weighted squares of the errors between the measured data $y(t_i)$ and the curve fitting function $\hat{y}(t_i)$. This cost function provides a scalar-valued goodness of fit measure called the chi-squared error criterion:

$$c^2(\boldsymbol{p}) = \big(\mathbf{y} - \hat{\mathbf{y}}(\mathbf{p})\big)^{\mathrm{T}}\mathbf{W}\big(\mathbf{y} - \hat{\mathbf{y}}(\mathbf{p})\big)$$

W is set to the measurement error covariance matrix.

LM is an iterative method that aims to minimise the chi-square error with respect to the parameters. It can be thought and implemented as a combination of the steepest descent and the Gauss-Newton method (Lourakis, 2005). Therefore, the update relationship takes the form:

$$\left[\mathbf{J}^{\mathrm{T}}\mathbf{W}\mathbf{J} + \lambda \mathrm{diag}\left(\mathbf{J}^{\mathrm{T}}\mathbf{W}\mathbf{J}\right)\right]\mathbf{h} = \mathbf{J}^{\mathrm{T}}\mathbf{W}(\mathbf{y} - \hat{\mathbf{y}})$$

$\mathbf{J}$ is the Jacobian matrix and $\mathbf{h}$ is the parameter update. When the solution is far from the global optimum then the algorithm behaves like a gradient descent method (λ value increases), which is slow but it is guaranteed to converge. On the other hand, when the solution is close to the optimum then the algorithm behaves like the Gauss-Newton method (λ value decreases), which assumes that the objective function is approximately quadratic and it converges much faster than gradient descent methods. An update $\mathbf{h} + \mathbf{p}$ of the parameter vector is accepted as sufficiently better than $\mathbf{p}$ according to the metric ρ (Gavin, 2016):

$$\rho_k(\mathbf{h}) = \frac{c^2(\mathbf{p}) - c^2(\mathbf{h}+\mathbf{p})}{\mathbf{h}^{\mathrm{T}}\left(\lambda \mathrm{diag}(\mathbf{J}^{\mathrm{T}}\mathbf{W}\mathbf{J})\mathbf{h} + \mathbf{J}^{\mathrm{T}}\mathbf{W}\left(\mathbf{y} - \hat{\mathbf{y}}(\mathbf{p})\right)\right)}$$

If $\rho_k(\mathbf{h}) > \epsilon_0$ then λ is reduced by a factor, otherwise λ is increased by a factor.

The LM algorithm stores both the Jacobian matrix $\mathbf{J}$ as well as the approximation Hessian matrix $\mathbf{J}^{\mathrm{T}}\mathbf{W}\mathbf{J}$ and thus it trades more memory for more robust algorithm.

Our implementation incorporates the Broyden's rank-one update. According to this method the whole Jacobian is only estimated in every $2 \times n$ iterations or when the chi-square error increases. In every other iteration, the Broyden's equation is applied to estimate a rank-one update:

$$\mathbf{J_k} = \mathbf{J_{k-1}} + (\nabla\hat{\mathbf{y}} - \mathbf{J_{k-1}}\mathbf{h})\mathbf{h}^{\mathrm{T}}/(\mathbf{h}^{\mathrm{T}}\mathbf{h})$$

We use an LDL Cholesky factorization based solver to obtain the updating vector at each iteration of the algorithm. The Cholesky factorisation is the fastest exact solver for linear equation systems since it takes into advantage the symmetry of the matrix. Although, SVD is more robust, in this case the Cholesky factorisation is adequate since the matrix is at least semi-definite [Prado2015]. Furthermore, it is 26 times faster than SVD and twice as fast as LU.

Convergence is achieved if one of the following criteria are met:

- Convergence in the gradient: $\max\left|\mathbf{J}^{\mathrm{T}}\mathbf{W}(\mathbf{y} - \hat{\mathbf{y}})\right| < \epsilon_1$
- Convergence in parameters: $\max|h_i/p_i| < \epsilon_2$
- Convergence in chi-squared error: $c^2/(m - n + 1) < \epsilon_3$

If convergence is not achieved, then fitting is terminated when the number of iterations exceeds a pre-specified limit.

This algorithm has been implemented in C++ based on the Eigen template library for linear algebra (Benoît Jacob, 2013).

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