

1 The monodomain model

The monodomain equations are given by

$$\frac{\partial \mathbf{s}}{\partial t} = \mathbf{F}(\mathbf{s}, v), \quad \mathbf{x} \in H, \quad (1)$$

$$\frac{\partial v}{\partial t} + I_{ion}(v, \mathbf{s}) = \nabla \cdot (\mathbf{M} \nabla v) + I_s, \quad \mathbf{x} \in H, \quad (2)$$

$$\mathbf{n} \cdot (\mathbf{M} \nabla v) = 0, \quad \mathbf{x} \in \delta H, \quad (3)$$

with $v(\mathbf{x}, t)$ the transmembrane potential (in mV), H the domain, δH the boundary of H , \mathbf{n} the outward pointing normal of the boundary, and with I_s the prescribed input current (in mV/ms) and I_{ion} the ionic current across the membrane (in mV/ms), both scaled by the cell membrane capacitance (in $\mu\text{F}/(\text{mm}^2)$). Equation (1) is a system of ODE's that models the membrane dynamics. There exist many different cell membrane dynamics models with varying degrees of complexity that can be used to specify I_{ion} , $\mathbf{F}(\mathbf{s}, v)$ and the state variables $\mathbf{s}(\mathbf{x}, t)$, see the CellML repository¹ for an overview of different types of models.

Finally, \mathbf{M} is a conductivity tensor (in mm^2/ms), that satisfies

$$\mathbf{M} = \frac{\lambda}{1 + \lambda} \mathbf{M}_i, \quad (4)$$

with $\mathbf{M}_e = \lambda \mathbf{M}_i$. Here, \mathbf{M}_e and \mathbf{M}_i are the extracellular and intracellular conductivities (in mm^2/ms), divided by the product of the membrane capacitance (in $\mu\text{F}/(\text{mm}^2)$) and the cell membrane area-to-volume ratio (in $1/\text{mm}$). By assuming that there exists a λ such that $\mathbf{M}_e = \lambda \mathbf{M}_i$ the monodomain equations can be derived from the more complicated bidomain equations [3].

2 A basic test case

For our test case, we take a square of $10 \text{ mm} \times 10 \text{ mm}$ as our domain H . We will use the Grandi cell model to model the membrane kinetics [1]. We solve our test case with the cbcbeat splittingsolver with the default parameter values and default initial conditions for v and s . We take $M_i = 2$, $M_e = 1$, so that $M = 2/3$. After 0.5 ms, we apply a stimulus during 10 ms of 250 mV/ms over 1 mm^2 in the centre of the square.

¹models.cellml.org/electrophysiology

3 The inverse problem

Now assume we have measurements Φ of the transmembrane potential over time at some subdomain $\tilde{H} \subset H$. Using those measurements, we would like to estimate the conductivity tensor \mathbf{M} . We can formulate this problem as an optimisation problem: find \mathbf{M} , such that the functional

$$\mathcal{J}(v, \mathbf{M}) = \frac{1}{2} \int_0^T \int_{\tilde{H}} (v - \Phi)^2 \, d\mathbf{x} dt + \frac{\alpha}{2} \mathcal{R}(\mathbf{M}), \quad (5)$$

is minimized, subject to the requirements that v and \mathbf{M} satisfy the state system of equations (1)-(3) and initial conditions $v(\mathbf{x}, 0) = v_0(\mathbf{x})$ and $\mathbf{s}(\mathbf{x}, 0) = \mathbf{s}_0(\mathbf{x})$. Here, \mathcal{R} is a regularization term, and α a regularization parameter. To find a minimum for our functional \mathcal{J} , we will need to determine its total derivative with respect to the optimization parameter $\mathbf{M} = (M_1, M_2)$. Assuming that $M_1 = M_2 = M$, we obtain:

$$\frac{D\mathcal{J}}{DM} = \frac{\partial \mathcal{J}}{\partial v} \frac{\partial v}{\partial M} + \frac{\partial \mathcal{J}}{\partial M} = \int_0^T \int_{\tilde{H}} (v - \Phi) \frac{\partial v}{\partial M} \, d\mathbf{x} dt + \frac{\alpha}{2} \frac{\partial \mathcal{R}}{\partial M}. \quad (6)$$

References

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- [3] Sundnes, J., Nielsen, B., Mardal, K., Cai, X., Lines, G., & Tveito, A. (2006). On the Computational Complexity of the Bidomain and the Monodomain Models of Electrophysiology. *Annals of Biomedical Engineering*, 34(7), 1088-1097.
- [4] Yang, H., & Venziani, A. (2015). Estimation of cardiac conductivities in ventricular tissue by a variational approach. *Inverse Problems*, 31(11), 115001.