1 The monodomain model

The monodomain equations are given by

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

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

$$\mathbf{n} \cdot (\mathbf{M} \nabla v) = 0, \qquad \mathbf{x} \in \delta H,$$
(2)

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

with $v(\mathbf{x},t)$ the transmembrane potential (in mV), H the domain, δH the boundary of H, **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 $\mu F/(mm^2)$). 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 repository [9] for an overview of different types of models.

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

$$\mathbf{M} = \frac{\lambda}{1+\lambda} \mathbf{M}_i,\tag{4}$$

with $\mathbf{M}_e = \lambda \mathbf{M}_i$. Here, \mathbf{M}_e and \mathbf{M}_i are the extracellular and intracellular conductivities (in mm²/ms), divided by the product of the membrane capacitance (in $\mu F/(mm^2)$) and the cell membrane area-to-volume ratio (in 1/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].

$\mathbf{2}$ ${f A}$ basic test case

For our test case, we take a square of 5 mm \times 5 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 splittingsolver module from the cbcbeat Python package [10] with the default parameter values and default initial conditions for v and s. The splittingsolver solves the monodomain PDE system and its coupled cell membrame dynamics ODE system separately, using the operator splitting scheme as described in [3]. We take typical values $\sigma_l = 0.1$

¹This electrophysiology solver package is based on the FEniCS Project software [7] and the dolfin-adjoint software [8]

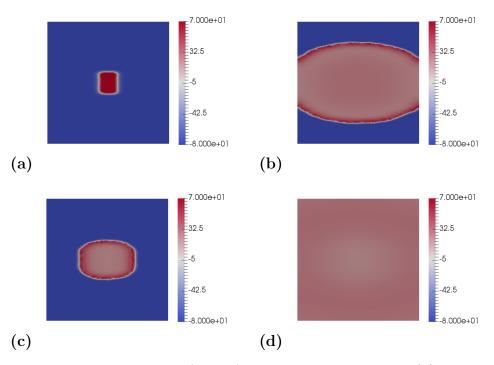


Figure 1: Heat maps of v (in mV) of our basic test case at (a) t = 5ms, (b) t = 15ms, (c) t = 40ms and (d) t = 80ms.

and $\sigma_t = 0.02$ (in mS/mm) for the longitudinal and tangential conductivity respectively and take $C_m = 0.2$ for the membrane capacitance (in μ F/(mm²)) and $\beta = 200$ for the cell membrane area-to-volume ratio (in 1/mm) [4], data from [5, 6]. We apply a stimulus of 10 mV/ms over 1 mm² in the centre of the square from t = 0 to t = 3 ms. In Figure 1, we show a heat map of v at v = 0, 15, 40 and 80 ms. In Figure 2, we show a heat map of v = 0 to the same times. This variable is one of the 37 state variables v = 0 to the Grandi cell model and measures the intracellular calcium concentration [1]. In Figures 3 and 4, we plotted v = 0 and v = 0

3 The inverse problem

It is possible to obtain measurements u_{obs} of the transmembrane potential and measurements c_{obs} of the intracellular calcium concentration Ca_sl over the whole domain H at discrete points in time. With those measurements, we can estimate the value of the parameters in our model, using an adjoint-

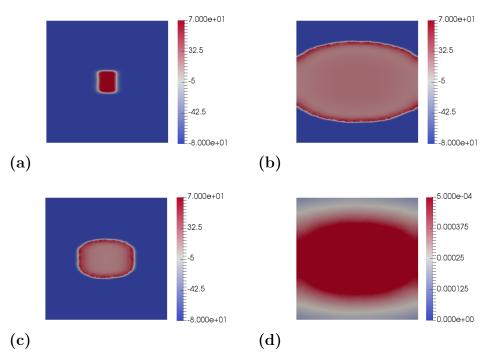


Figure 2: Heat maps of Ca_sl of our basic test case at (a) t = 5 ms, (b) t = 15 ms, (c) t = 40 ms and (d) t = 80 ms.

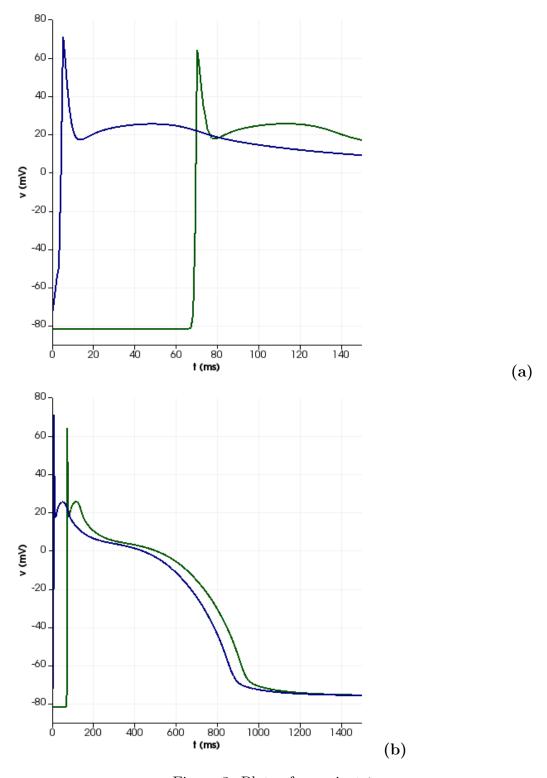


Figure 3: Plots of v against t.

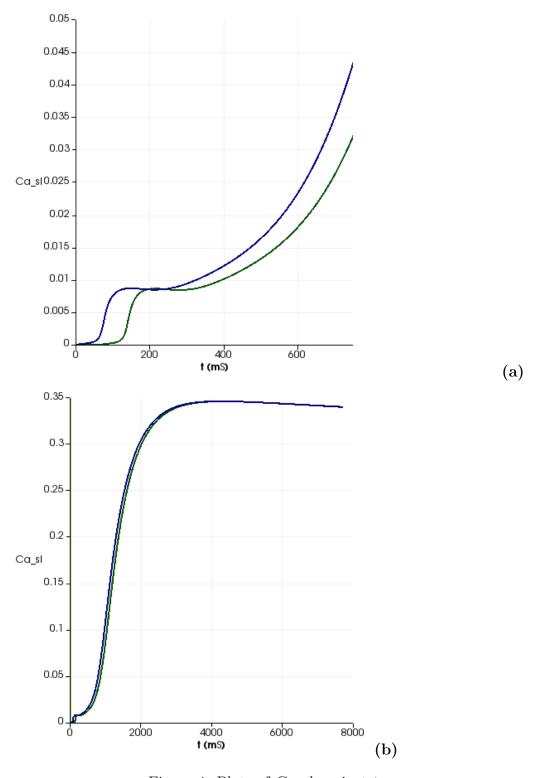


Figure 4: Plots of Ca_sl against t.

based approach.² Here, as an example, we will try to estimate the values of the σ_l parameter from the Grandi cell model. We can formulate this problem as an optimisation problem: find σ_l , such that the functional

$$\mathcal{J}(v, c, \sigma_l) = \frac{1}{N} \sum_{i=1}^{N} ||v - v_{\text{obs}}(t_i)||_{L^2(H)}^2 + ||c - c_{\text{obs}}(t_i)||_{L^2(H)}^2,$$
 (5)

is minimized, subject to the requirements that v, c and σ_l satisfy the state system of equations (1)-(3) and initial conditions $v(\mathbf{x},0) = v_0(\mathbf{x})$ and $\mathbf{s}(\mathbf{x},0) = v_0(\mathbf{x})$ $\mathbf{s}_0(\mathbf{x})$. Here, N are the number of measurements in time and t_i , $i=1,\ldots N$ the respective moments in time. Using cbcbeat and the dolfin-adjoint software on which it is based, we can automatically compute the total derivative of \mathcal{J} with respect to the optimization parameter σ_l . We can then use the scipy optimisation algorithm minimize() -which uses the limited memory BroydenFletcherGoldfarbShanno (BFGS) method with bound support - to find an optimal value for σ_l . We first generated some fake observed data fir $\sigma_l = 0.15$, from t = 0.0 to t = 5.0 ms, with a timestep dt = 0.5 ms. With $\sigma_l = 0.10$ as initial guess, the minimize() algorithm returned $\sigma_l = 0.150004$ after six iterations. Similarly, we can optimize for other parameters, such as σ_t , or g_Na , g_CaL , g_K1 or g_K2 from the Grandi cell model. With $\sigma_t = 0.01$ as initial guess and fake data created for $\sigma_t = 0.02$, the minimize() algorithm converged to $\sigma_t = 0.020005$ after five iterations. Optimizing for both σ_l and σ_t , with the same initial guesses and synthetic data, gave convergence in eight iterations. The value of the functional at each iteration step was consecutively 38.6, 11.7, 10.0, 3.19, 0.89, 0.023, 0.00063, 0.0000084 and 0.0000098. We also looked at synthetic spatially varying σ_l and σ_t ...

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²See, for example, [2] for an introductory text in adjoint-based optimization methods.

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