

# Ca e e -Med a ed Me a f Ce a Ca c f T a e A d a

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## Regulation of SR $Ca^{2+}$ release

A crucial element in modeling EC coupling is the mechanism which regulates  $Ca^{2+}$  release. In the Hofferaw model, it was assumed that the amount of  $Ca^{2+}$  release is a phenomenological nonlinear function of the  $Ca^{2+}$  load which becomes steep for high loads (8). The origin of this nonlinear relationship, however, is not well understood. Calcium release from the SR is regulated by the ryanodine receptors (RyRs), which open up on a rise in the cytosolic  $Ca^{2+}$  concentration (14). There is a growing body of experimental evidence showing that  $Ca^{2+}$  regulates the sensitivity of the RyRs to the interaction of auxiliary proteins (triadin-1/junctin, TAJ) with the  $Ca^{2+}$  release channel (C<sub>2</sub>N) (e.g., (15-17)). In particular, Gorka

the equations and model parameters is given in the Appendix. In Elementary  $Ca^{2+}$  release kinetics we describe the intracellular compartments and the various currents in our model. In Cell Architecture we briefly describe the geometry of ventricular myocytes, which we use to realistically implement our spatially extended model. Finally, in the subsections Lumina Gating and Lumina Buffering we present a new mathematical formulation of  $Ca^{2+}$ -mediated lumina gating and buffering that takes into account the transition from monomeric to dimeric forms of  $Ca^{2+}$  with increasing lumina free  $Ca^{2+}$  concentration.

## Excitation-contraction coupling in the cardiac myocyte

Excitation-contraction coupling, the process by which cardiac myocytes transform the membrane depolarization signal into cell contraction, is a complex process that spans multiple scales (44,45). Calcium ions ( $Ca^{2+}$ ) enter the cell upon membrane depolarization, triggering discrete  $Ca^{2+}$  release events at the elementary  $Ca^{2+}$  stores of the cell, an intracellular store whose primary function is the sequestration and release of intracellular  $Ca^{2+}$ . These  $Ca^{2+}$  sparks (46,47) are highly localized in space ( $\sim 1 \mu m$ ) and time ( $\sim 20 ms$ ). The sarcoplasmic reticulum is a sac-like structure which forms a spatially dense network of interconnected tubules and cisternae. The tubular network is usually referred to as network (N), while the cisternae are referred to as junctional (J). These cisternae are localized in close proximity to the tubules, cell membrane invaginations that form a dense structure in ventricular myocytes (48). The cisternae are usually called dyads, and the space between a dyad and the sarcolemma is referred to as the

number of LCC channels varied would result in a more heterogeneous  $I_{Ca}$  current amplitude, since different numbers of channels could open within some narrow time





$$k_{41} = \tau_u^{-1}. \quad (9)$$

where  $\tau_u$  and  $\tau$  are the characteristic unbinding (slow) and binding (fast) times, and  $B_{C-N}^0 = 400 \mu M$  is the normal  $C-N$  concentration and guarantees that  $k_{14} \rightarrow \tau^{-1}$  for low  $C_N$ . We will choose these constants based on experimentally measured spark restitution curves. The transition rate from the open  $C-N$  unbound to the open  $C-N$  bound state is taken to be the same as the one from the closed  $C-N$  unbound to the closed  $C-N$  bound state,  $k_{23} = k_{14}$ . Finally, to satisfy detailed balance,  $k_{12}k_{23}k_{34}k_{41} = k_{14}k_{43}k_{32}k_{21}$ , we set the transition rate from the open  $C-N$  bound to the open  $C-N$  unbound to be

$$k_{32} = k_{41}k_{12}/k_{43}. \quad (10)$$

The value of the parameters can be found later in a  $\mu e 10$  and further details can be found in the Appendix.

We will model each diad as having 100 channels. Each channel evolves stochastically, independent of the other channels in the diad. However, to avoid keeping track of the  $\sim 20,000 \times 100$  channels in the molecule, we only keep

track in each diad of the number of channels that are in each of the four states. As described in the Appendix, these numbers can be updated in each time-step in a way that is equivalent to individually evolving each channel. Therefore we are able to speed up the simulations a factor of  $\sim 20$  (from 100  $\mu s$  and four L-type channels to the number of channels per state and four L-type channels).

A crucial feature of the model described above is that the transition rate from the  $C-N$  unbound to the  $C-N$  bound states depends dynamically on the minimum  $Ca^{2+}$  concentration through the dependence of the monomer concentration  $[M]$  on  $C_N$ . In Fig. 2 b we plot the fraction of monomers  $\hat{M}$

of C-N bond channels increases. These channels have a lower open probability, and therefore the spark terminates shortly thereafter. Subsequently, the J<sub>Ca</sub> falls, and eventually the luminal Ca<sup>2+</sup> concentration becomes high enough that the concentration of monomers decreases. C-N unbinds from the J<sub>Ca</sub> complex of the channels, and the dead









of Fig. 7 we plot the averaged cytosolic  $Ca^{2+}$  concentration  $C_i$  (Eq. 1) as a function of time for a pacing period of  $T = 220$  ms. In the bottom panel we show the cytosolic  $Ca^{2+}$  concentration  $C_i$  as a function of time for a transversal line of dendrites across the molecule, indicated in the vertical axis. This panel shows that, even though there is a well-defined whole cell  $Ca^{2+}$   $C_A$ , individual dendrites do not necessarily reflect this, since, in the time interval shown, there are some dendrites that are in the state with large  $C_i$ , some that are never in that state, and some that are irregular, examples of which are indicated with the horizontal arrows and marked as a, b, and c, respectively. The vertical arrows in the top panel indicate the time of pacing. In Fig. 8 a we show the maximum values of the averaged  $Ca^{2+}$  cytosolic concentration during steady state pacing for different pacing periods. A bifurcation to  $C_A$  appears when the pacing period is decreased at  $<$



development of a ternans. Inserting these expressions in Eqs. 22 and linearizing, we obtain

$$\begin{pmatrix} \delta l_{n+1} \\ \delta f_{n+1} \end{pmatrix} = \begin{pmatrix} 1 - \partial_t R & 1 + \partial_t U \\ \partial_t g & 1 - \partial_t R e^{-t/\tau_u} \end{pmatrix} \begin{pmatrix} \delta l_n \\ \delta f_n \end{pmatrix}, \quad (23)$$

where the derivatives are evaluated at the values  $l, f$ . The condition for alternating growth of the perturbations is that the eigenvalue of the matrix in Eq. 23 with the largest magnitude is  $< 1$  (for a ternans, this eigenvalue is negative). This condition results in that a ternans develops when

$$1 + \partial_t U - \partial_t R - 1 + \partial_t R \partial_t g e^{-t/\tau_u} > 1. \quad (24)$$

This equation is the key to understanding the relative contributions of steepness, release-load relationships, uptake, and recovery of C<sub>2</sub>N<sub>2</sub>-bound channels. If we can neglect C<sub>2</sub>N<sub>2</sub>-mediated effects,  $\partial_t R = 0$ ,  $\partial_t g = 0$ , or  $\tau_u \ll T$



operator of  $C_N$  activity, which allows us to investigate the role of  $C_N$  in promoting  $C_A$ . In Fig. 11 c we show the ma -



number of available channels, and vice versa. However, when the uptake is enough to reduce or eliminate the dependence of the diastolic content on the number of available channels in the previous beat, one can observe C/A without significant alternations in diastolic  $Ca^{2+}$  content as in Fig. 8 c.

Another important feature of our model is that, for the first time, it simulates a realistic number ( $\sim 20,000$ ) of diffusively coupled, biologically detailed elementary release units, where each unit has a realistic ( $\sim 100$ ) number of





Diff. f. f. i. a. i. ace. b. e. b. e

prohibitive, since diffusive coupling between adjacent C's requires the simultaneous processing of neighboring dynamics. To reduce the computation time to reasonable levels, we do not simulate each individual channel in a given C, but rather keep track of the number of channels in a given C that are in each state. The number of states in the  $n^{\text{th}}$  dendrite in the open C-N-ounod (3), open C-N-ounod (2), and closed C-N-ounod (1) are denoted  $x_3^{(n)}$ ,  $x_2^{(n)}$ , and  $x_1^{(n)}$ , respectively (the number of C's in the closed C-N-ounod state is  $x_4^{(n)} = 100 - x_1^{(n)} - x_2^{(n)} - x_3^{(n)}$ ). Henceforth we will omit the superscript  $(n)$ . The release current  $I_r$  depends only on the fraction of states in the open states  $P_o = (x_2 + x_3)/100$ , rather than on which particular channels are in each state. Therefore, at each time step we only need to compute the number of channels that make transitions from one state to another. Since we have the probabilities for the transition of an individual channel, the distribution of the number of channels making a transition from state  $j$  can be obtained from a multinomial distribution with the number of trials being the number of C's in state  $j$  and the probabilities of success being the probabilities of transition to another state given the expressions in Eqs. 55. We remark that, so far, this is an elegant mathematical formulation of the process that requires, for the large number of channels we consider, less computational effort. Further approximations allow us to increase the efficiency of the simulation. In practice, the probabilities of transition per unit time are small and we can treat transitions to different states as independent. For example, if at time  $t$  there are  $x_1$  channels in the closed unbound state, the probability that  $x_{12}$  of these channels makes a transition to the open unbound state and  $x_{14}$  channels make a transition to the closed bound state in the time interval  $[t, t + \Delta t)$  is

$$\begin{aligned}
 p(x_1, x_{12}, x_{14}) &= M(x_1, k_{12}\Delta t, k_{14}\Delta t), \\
 &\approx B(x_1, k
 \end{aligned}
 \tag{56}$$

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