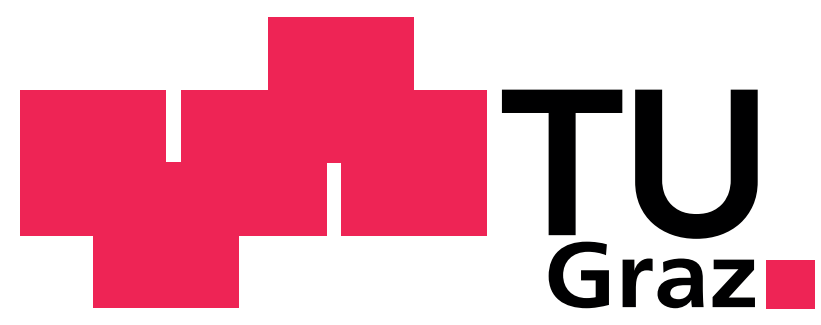


REAL-TIME INTERACTION WITH AN ELECTROPHYSIOLOGICAL CANCER CELL MODEL



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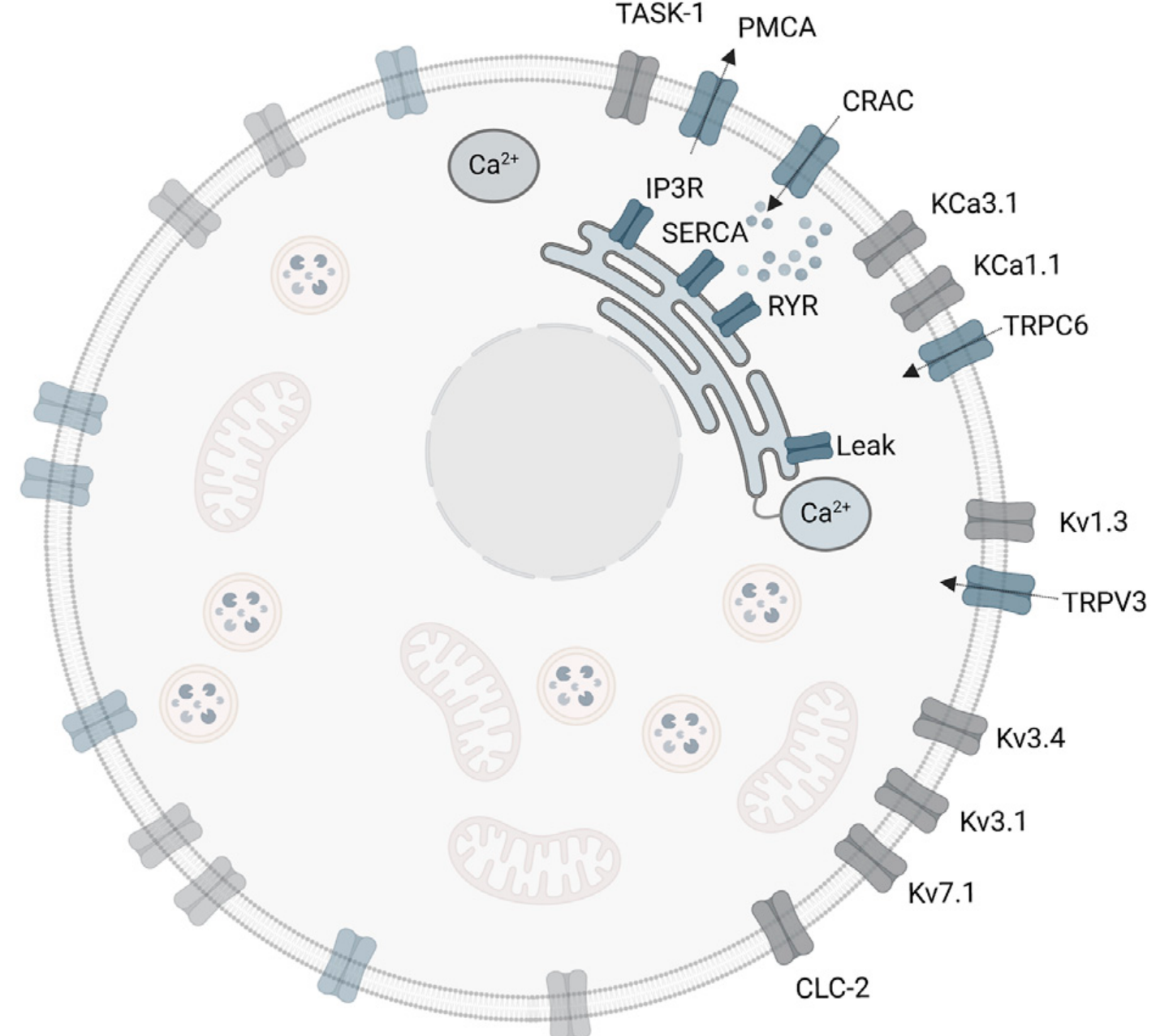
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INTRODUCTION

We improve on the A549 electrophysiological cancer cell model introduced in [1, 2], combining numerical methods with an efficient implementation to reduce simulation time to a level where it is feasible for live interaction.



Schematic depiction of the cell, source: [2]

We accelerated the simulation with adaptive timestepping and a highly efficient implementation in the Rust programming language. The corresponding inverse problem is expressed as a quadratic program, solving it within milliseconds. We introduce a visualisation approach of the entire model: a live simulation dashboard available online, running directly in the browser.

MODEL

The whole cell current $I : T \rightarrow \mathbb{R}$ over time $t \in T \subset \mathbb{R}^+$ is the sum of all individual channel contributions $I_k, k \in \{1, \dots, M\}$ over $M \in \mathbb{N}$ channel types

$$I(t) := \sum_{k=1}^M N_k I_k(t) = \sum_{k=1}^M N_k g_k p_{o,k} (V(t) - E_k) .$$

At each time step, the next state $\mathbf{s}_{k,n+1} \in [0, 1]^{N_{s,k}}$ of the k -th channel type is obtained by

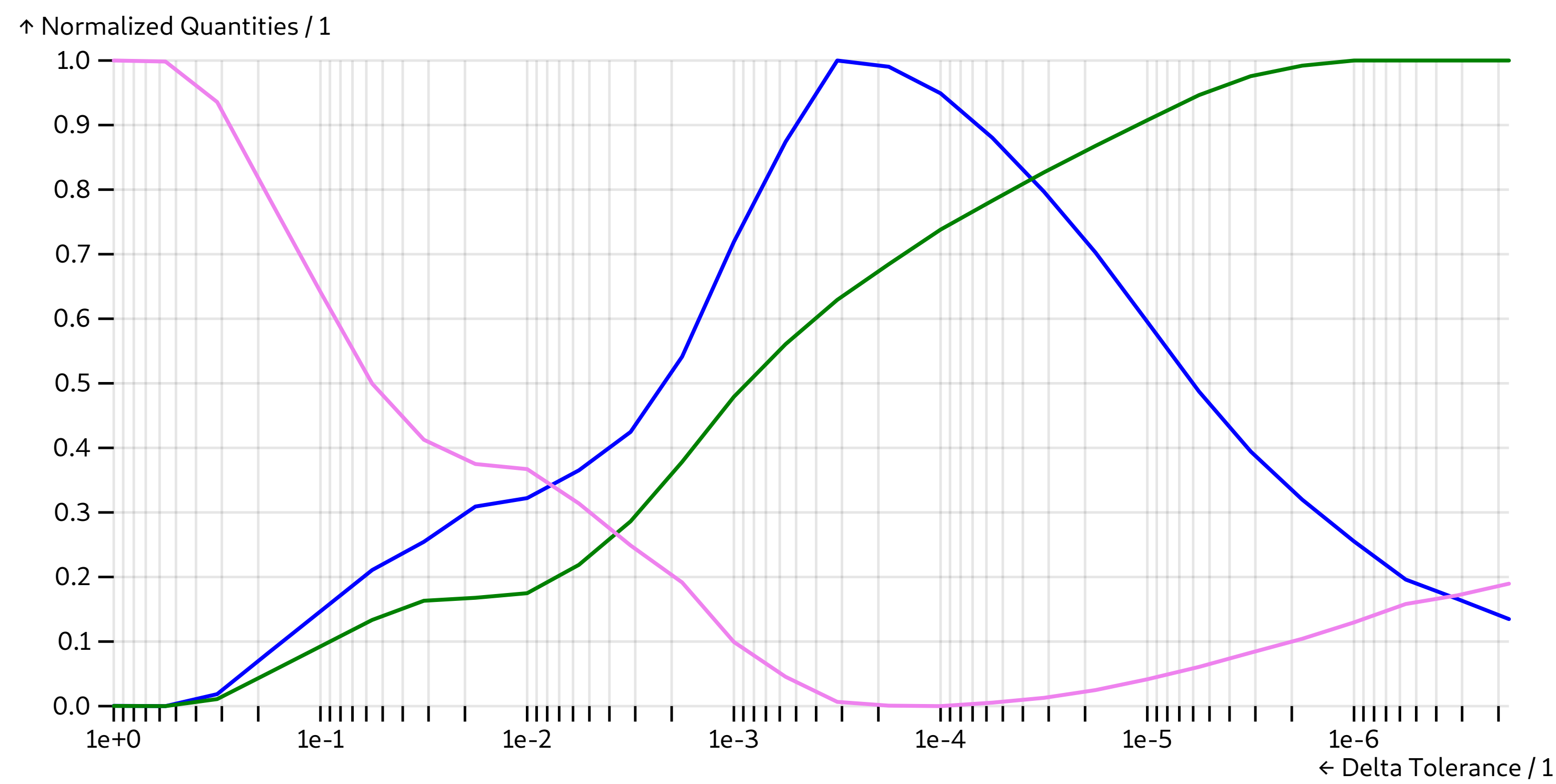
$$\mathbf{s}_{k,n+1} = H_k(V(t_n), \mathbf{C}(t_n), t_n) \mathbf{s}_{k,n}, \quad \text{with} \quad t_n := \sum_{i=0}^n (\Delta t)_i .$$

ADAPTIVE TIMESTEPPING

In order to accelerate the simulation in areas where there is little change to the dynamics, we choose an adaptive step size $(\Delta t)_n$ based on

$$(\Delta t)_{n+1} = (\Delta t)_n \left(\frac{\Delta^{\text{tol}}}{\sum_{k=1}^M N_k \|\mathbf{s}_{k,n+1} - \mathbf{s}_{k,n}\|_2} \right)^{1/2} .$$

In order to find the optimal $\Delta^{\text{tol}} \in \mathbb{R}^+$ (the allowed state change in between steps):



Relative change of the average timestep Δt (in blue), simulation runtime (in violet) and step acceptance rate (in green) when varying the delta tolerance Δ^{tol} on a log-scale. All three quantities were normalized from their individual extent to $[0, 1]$. The most effective Δ^{tol} is arguably on the order of 10^{-4} .

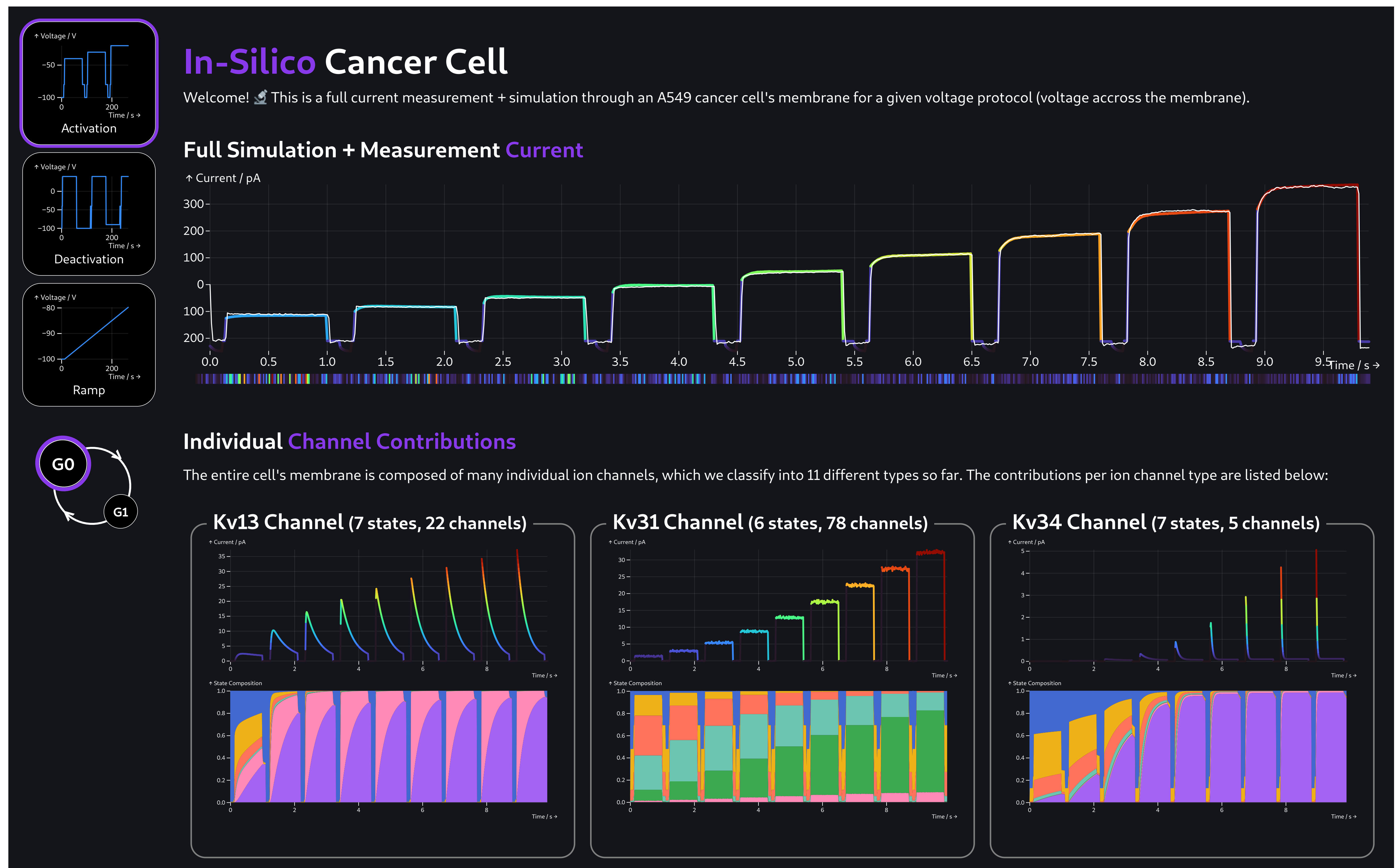
CONCLUSION

Efforts to further enhance and complete the first electrophysiological cancer cell model simulation were fruitful, resulting in a new library implementation, an improved inverse problem solution technique and a live in-browser simulation dashboard. Numerically, the stability of the simulation varies greatly with the time step state change tolerance Δ^{tol} , this could be improved using a higher-order integration scheme. There are also many ideas for further customizations that would improve the live simulation dashboard, opening up future usage perspectives.

REFERENCES

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- [3] Rasmus Bro and Sijmen De Jong. ‘A fast non-negativity-constrained least squares algorithm’. In: *J. Chemom.* 11.5 (Sept. 1997), pp. 393–401. ISSN: 0886-9383. DOI: [10.1002/\(SICI\)1099-128X\(199709/10\)11:5<393::AID-CEM483>3.0.CO;2-L](https://doi.org/10.1002/(SICI)1099-128X(199709/10)11:5<393::AID-CEM483>3.0.CO;2-L).

LIVE, IN-BROWSER CELL SIMULATION INTERFACE



This interface is available online via in-silico.hce.tugraz.at, try it out!

FORMULATION AS A QUADRATIC PROGRAM

After simulation of the individual channel currents, we want to find

$$\mathbf{N}_{\text{opt}} = \arg \min_{\mathbf{N} \in \mathbb{N}_0^M} \frac{1}{2} \|\mathbf{R}\mathbf{N} - \mathbf{I}_{\text{meas}}\|_2^2 .$$

the number of channels per type, with $\mathbf{I}_{\text{meas}} \in \mathbb{R}^{N_i}$ the experimentally measured current and $\mathbf{R} \in \mathbb{R}^{N_i \times M}$ the matrix of all currents I_k per channel type. Letting $\mathbf{d} := \mathbf{I}_{\text{meas}}$ for brevity,

$$\mathbf{N}_{\text{opt}} \approx \arg \min_{\mathbf{x} \in \mathbb{R}_+^M} f(\mathbf{x}) = \arg \min_{\mathbf{x} \in \mathbb{R}_+^M} \frac{1}{2} \|\mathbf{R}\mathbf{x} - \mathbf{d}\|_2^2 ,$$

with cost function $f : \mathbb{R}^M \rightarrow \mathbb{R}^+$, which we manipulate to

$$\begin{aligned} f(\mathbf{x}) &= \frac{1}{2} (\mathbf{R}\mathbf{x} - \mathbf{d})^T (\mathbf{R}\mathbf{x} - \mathbf{d}) \\ &= \frac{1}{2} (\mathbf{x}^T \mathbf{R}^T \mathbf{R} \mathbf{x} - \mathbf{x}^T \mathbf{R}^T \mathbf{d} - \mathbf{d}^T \mathbf{R} \mathbf{x} + \mathbf{d}^T \mathbf{d}) \\ &= \frac{1}{2} (\mathbf{x}^T \mathbf{P} \mathbf{x} + \mathbf{x}^T \mathbf{q} + \mathbf{q}^T \mathbf{x}) + \mathcal{O}(1) \\ &= \frac{1}{2} \mathbf{x}^T \mathbf{P} \mathbf{x} + \mathbf{q}^T \mathbf{x} + \mathcal{O}(1) \end{aligned}$$

where we let $\mathbf{P} := \mathbf{R}^T \mathbf{R} \in \mathbb{R}^{M \times M}$ and $\mathbf{q} := -\mathbf{R}^T \mathbf{d} \in \mathbb{R}^M$ and leave out the constant $\mathbf{d}^T \mathbf{d}$ as $\mathcal{O}(1)$. We can express the nonnegativity constraint $\mathbf{x} \geq \mathbf{0}$ as an equality constraint using a slack variable $\mathbf{s} \in \mathbb{R}_+^M$,

$$-\mathbf{x} + \mathbf{s} = \mathbf{0} \quad \Leftrightarrow \quad \mathbf{A}\mathbf{x} + \mathbf{s} = \mathbf{b} \quad \text{with} \quad \mathbf{A} = -\mathbf{I} \in \mathbb{R}^{M \times M} \quad \text{and} \quad \mathbf{b} = \mathbf{0} \in \mathbb{R}^M .$$

This leaves us with a constrained *quadratic program*,

$$\begin{aligned} \min_{\mathbf{x} \in \mathbb{R}^M} \quad & \frac{1}{2} \mathbf{x}^T \mathbf{P} \mathbf{x} + \mathbf{q}^T \mathbf{x}, \\ \text{s.t.} \quad & \mathbf{A}\mathbf{x} + \mathbf{s} = \mathbf{b}, \quad \mathbf{s} \in \mathbb{R}_+^M . \end{aligned}$$

The integer solution can then be obtained from rounding,

$$\mathbf{N}_{\text{opt}} = \lfloor \mathbf{x} \rfloor \in \mathbb{N}_0^M .$$

COMPARISON OF OPTIMIZATION METHODS

The different approaches were evaluated on the G0 cell cycle phase with the activation voltage protocol. Runtime estimates were obtained on an Intel™i7-5600U CPU.

Algorithm	Abbreviation	Runtime / ms	RMSE / pA
Particle Swarm Optimization	PSO	22571	27.69
Gradient Descent + More Thuente	GD	18924	32.34
Limited-Memory BFGS + Hager Zhang	LBFGS	4845	32.20
Non-Negative Least Squares [3]	NNLS	318	28.00
Quadratic Program	QP	18	28.13