



Robustness of an Agent-Based Model for Cardiac Action Potentials

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Abstract

Heart arrhythmias, marked by irregular heartbeats, pose serious health risks like stroke and heart failure. Although the cause remains unclear, they are linked to action potential propagation failure, which current models inadequately capture.

Our research develops an agent-based model (ABM) to simulate cardiac action potentials, offering a dynamic representation of cardiac tissue to explore arrhythmia scenarios. This model, which models the diffusion of ions, will deepen the understanding of arrhythmia mechanisms and help identify potential triggers, guiding future analysis and targeted interventions for advancing cardiac research and therapies.

Agent-Based Model

An agent-based model (ABM) is a computational model made up of individual agents, each of which can assume a set of finite states. At each time step, an agent's state is governed by rules that describe interactions with neighboring agents, which may be deterministic or stochastic. These interactions and the evolution of agent states are typically modeled within a grid environment, which can be either two- or three-dimensional.

ABMs are ideal for modeling complex systems with many interacting components. In our model, ions act as agents, and their behavior—such as the propagation of action potentials—can be tracked over time. While ABMs are accessible to construct and mimic real-world systems, they can be computationally intensive and lack comprehensive mathematical analysis tools.

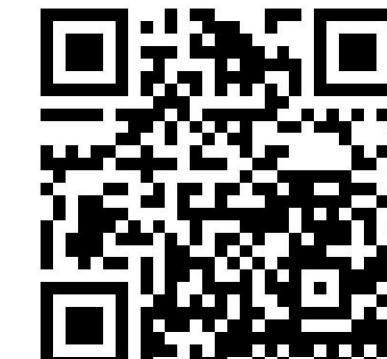
Acknowledgements

This research was generously supported by the William and Linda Frost Fund in the Cal Poly Bailey College of Science and Mathematics.

This research was generously supported by Association for Women in Mathematics.

More Information

See the following QR code for more information about detailed code.



3D Model and Error Graph Code

Discrete Model

In our ABM, we built a discrete model where ions move using a single-neighbor attempt algorithm. [1] The 3D grid is divided into cells, and at each time step, ions move to neighboring cells, simulating diffusion. This discrete approach allows us to track individual ion behavior in three dimensions and compare its accuracy to a continuous model.

Each ion interacts only with its edge-adjacent neighbors, corresponding to the six cells directly connected along the X, Y, and Z axes. At each step, an ion randomly selects one of these neighbors. Stochasticity is introduced using a random number generator, where the ion moves if the movement probability, p_{move} , exceeds the generated random value. This approach captures the randomness inherent in ion diffusion.

Below are snapshots of the diffusion process for the discrete model in 3D.

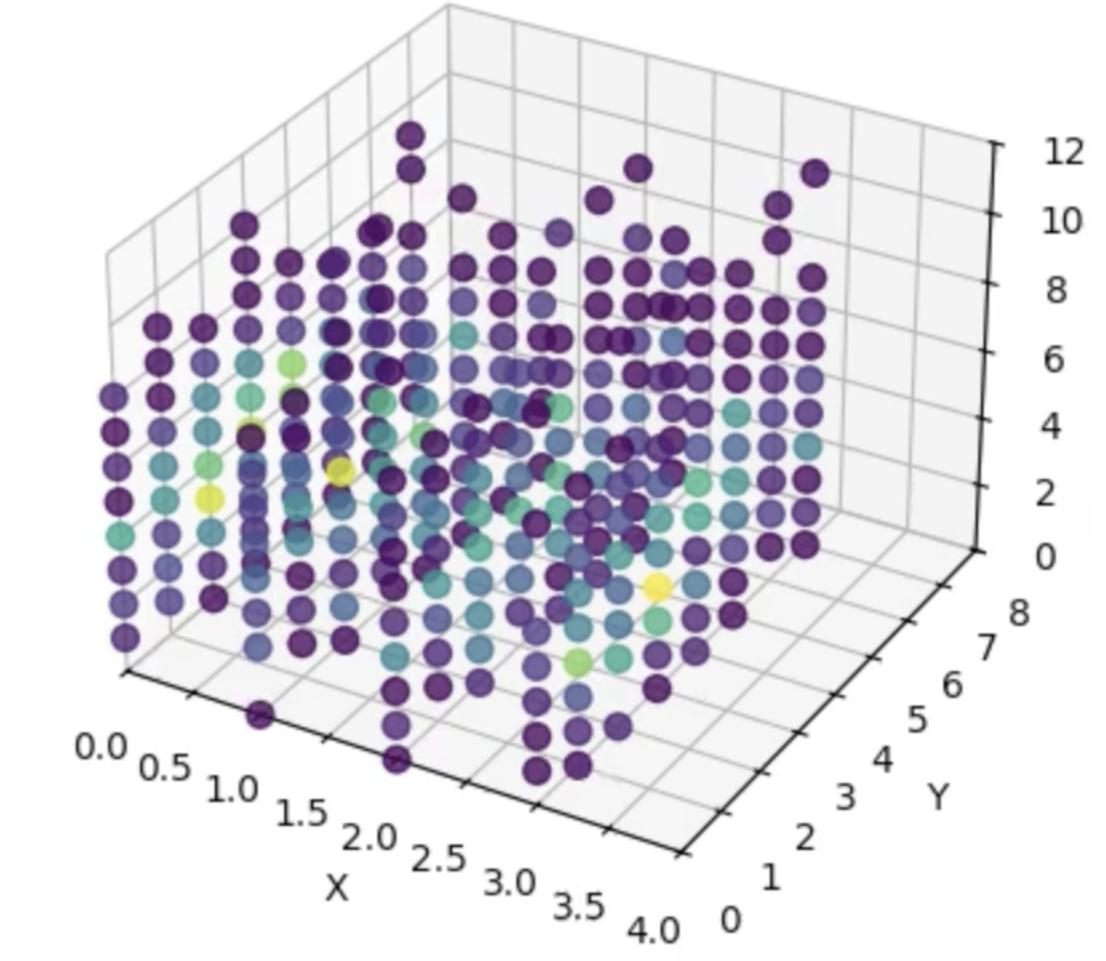


Figure 1: The 3D diffusion of ions based on the discrete model at $t = 0$.

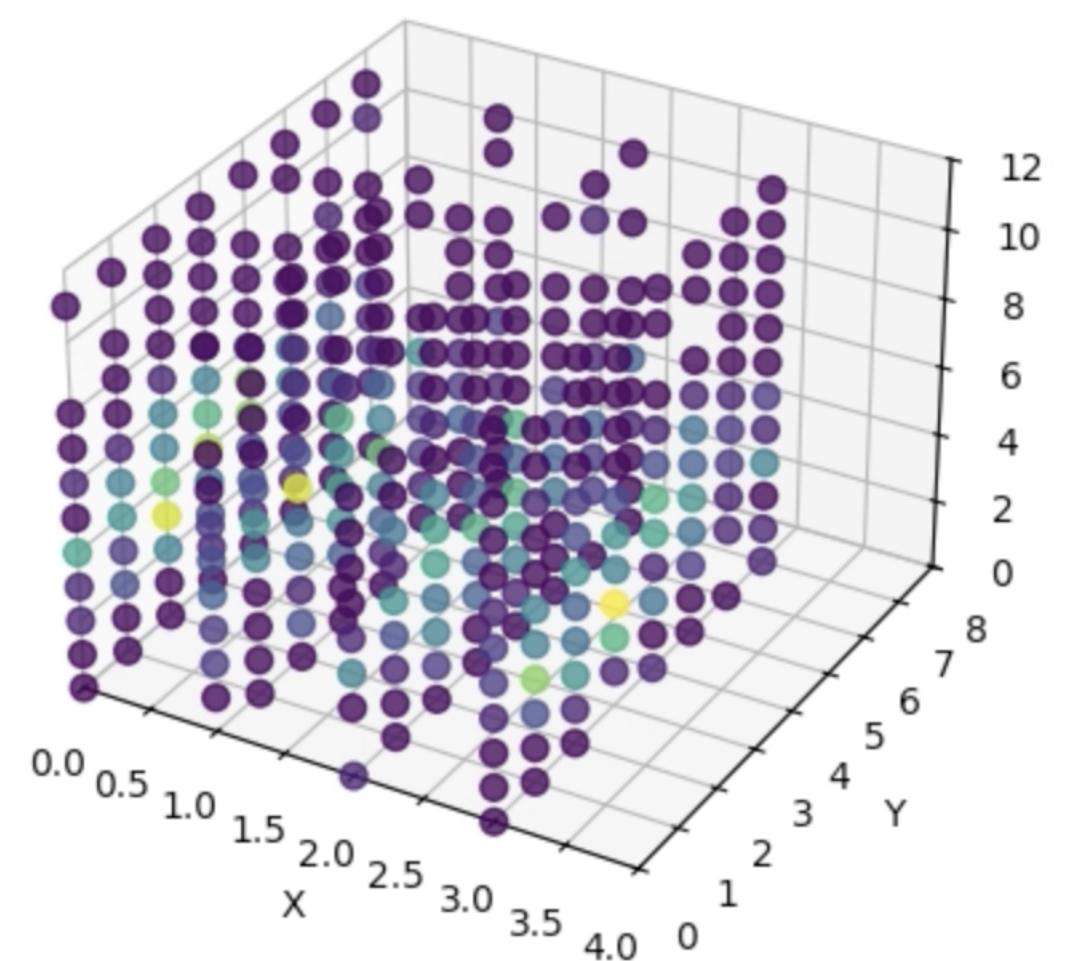


Figure 2: 3D representation of ion diffusion halfway though the diffusion process using the discrete model

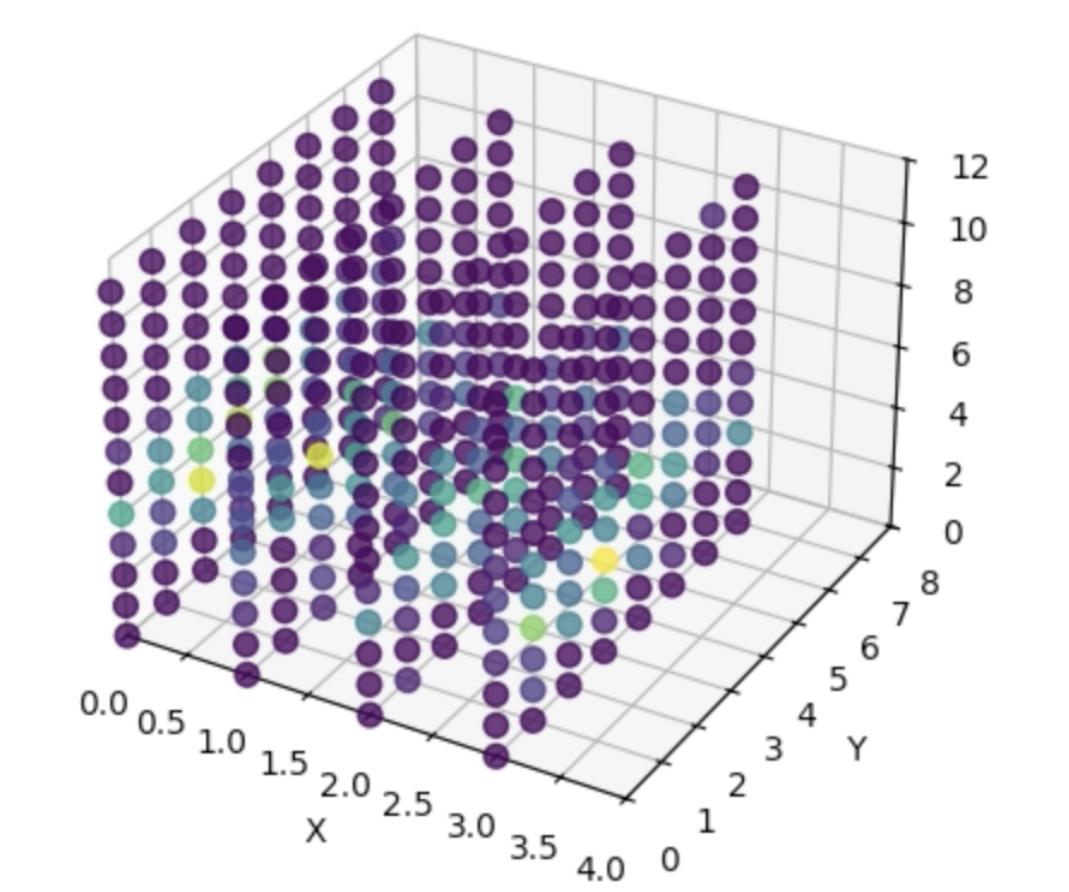


Figure 3: 3D representation of the complete diffusion of ions using the discrete model

Continuous Model

To model the natural diffusion of ions under ideal conditions, we implement a model that employs differential equations and the Crank-Nicolson method to recursively solve the for the next time step, denoted as ϕ^{n+1} . [2]

Now given an initialization of matrices generated by the discrete model, we model the diffusion of ions based on the continuous model. Once given an initialization, the continuous model creates a Laplacian matrix and fills it with values according to our equation. [2] Then at each time step, we solve a linear algebra equation with our solution being a single column vector which represents the potential map of our ions.

Now we will represent this process as a series of visualizations.

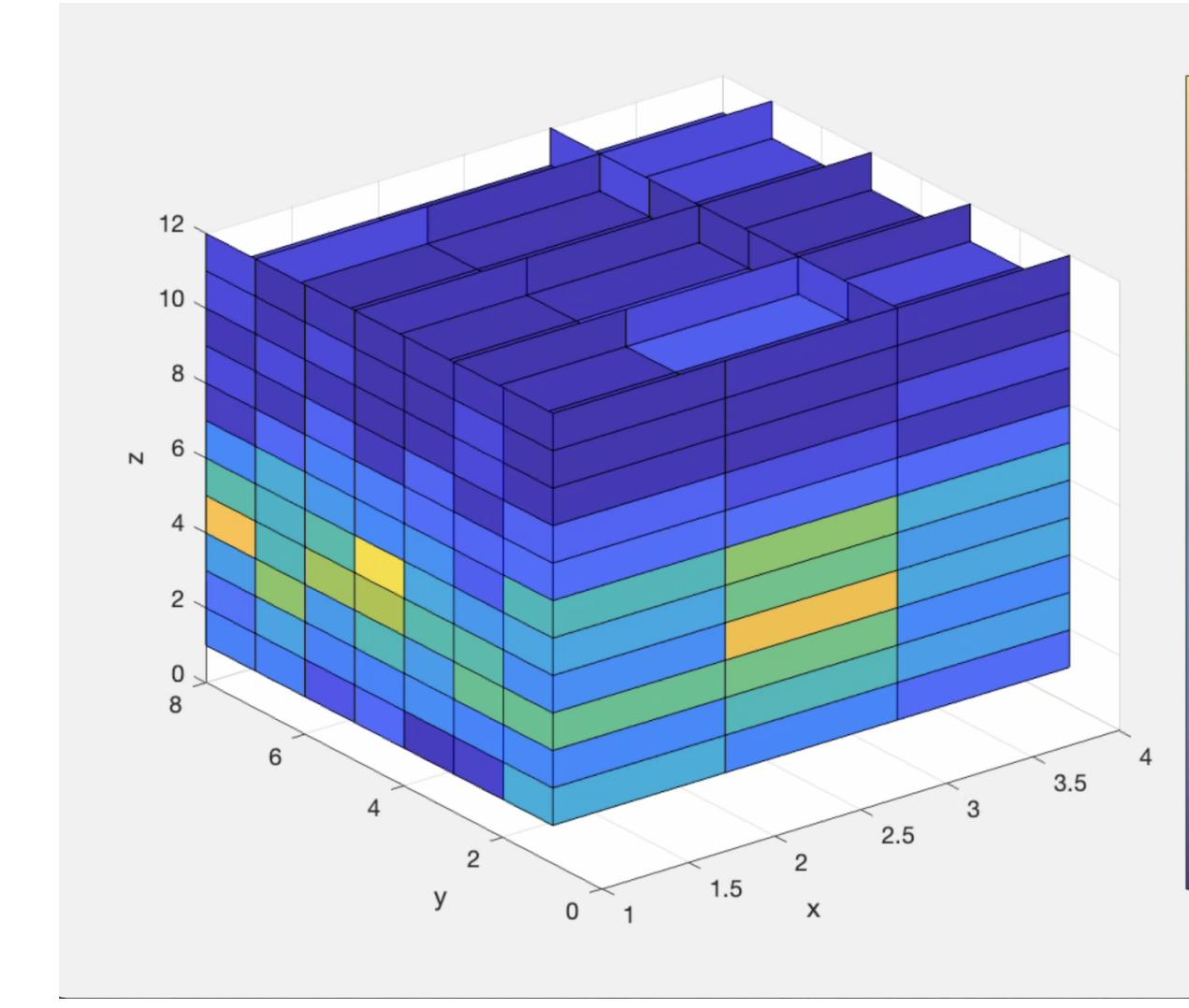


Figure 4: The diffusion of ions based on the continuous model at $t = 0$.

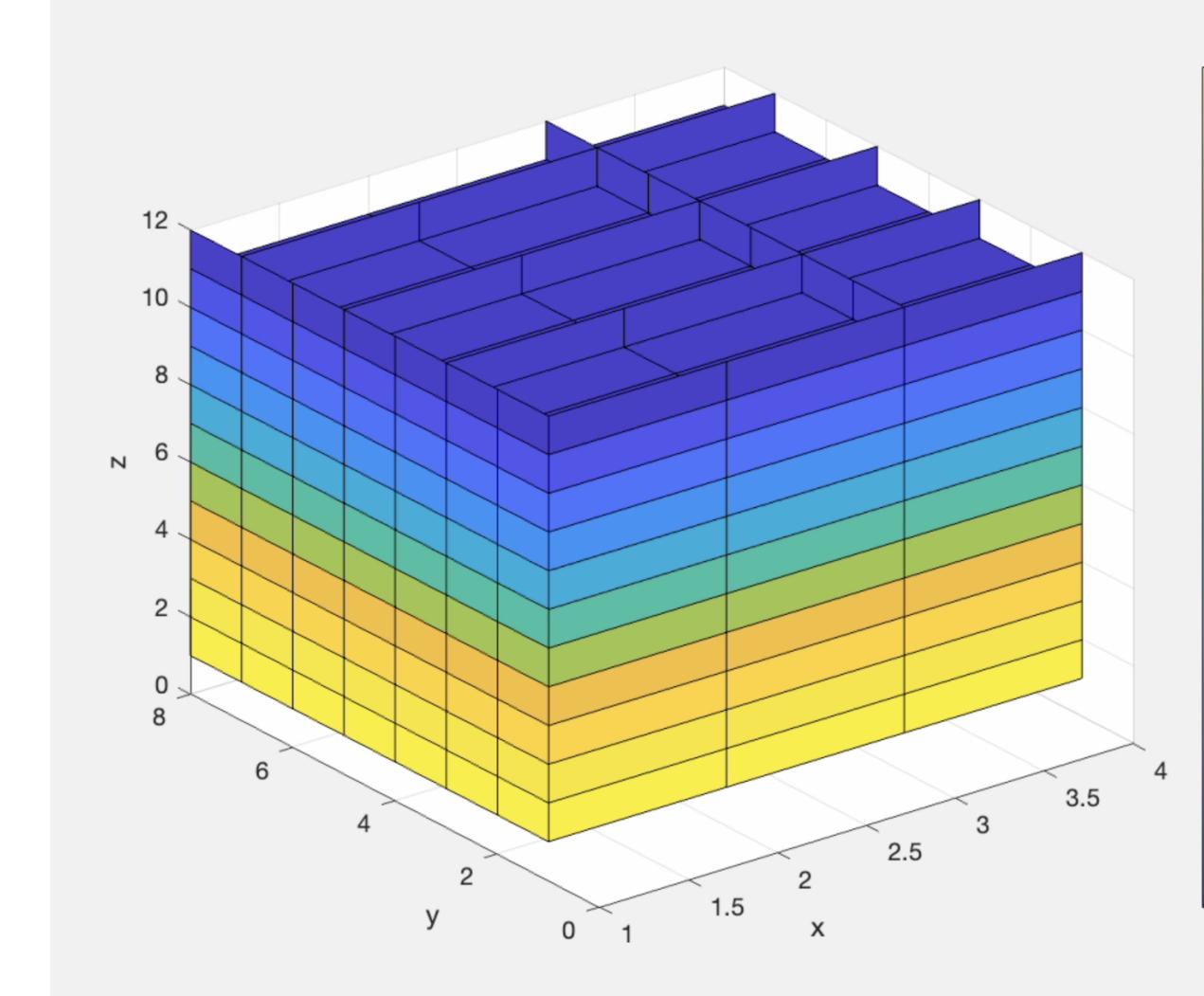


Figure 5: Representing the diffusion of ions halfway though the diffusion process using the continuous model.

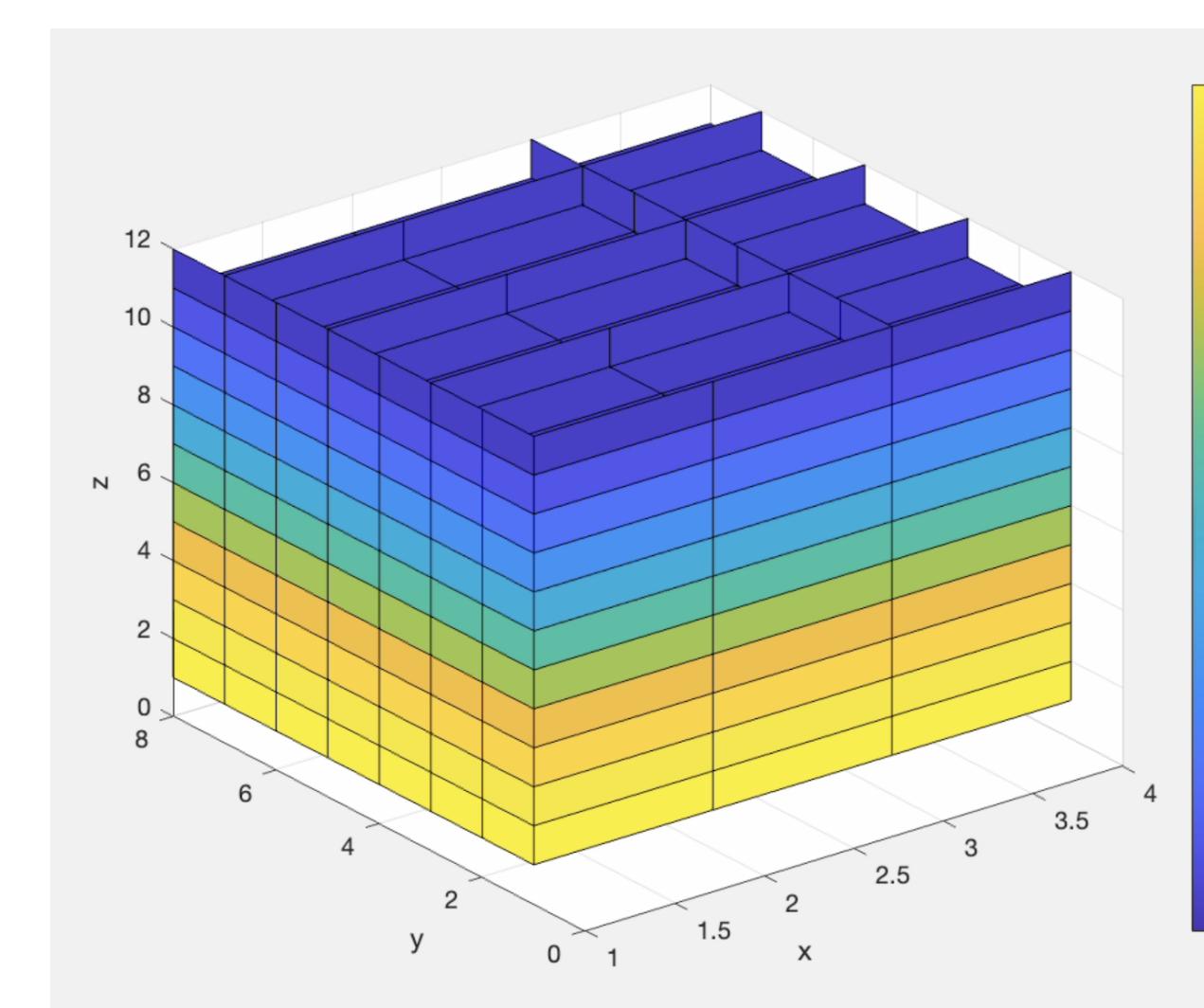


Figure 6: Representing the complete diffusion of ions using the continuous model.

Results

We compare the robustness of the discrete model against our continuous model. The goal of this is to measure the diffusion of the discrete model against the continuous model. We measured the diffusion of ions between the discrete and continuous model by calculating the mean square error at each time step.

We consider our model fully diffused if the number of ions in each space are evenly distributed as $t \rightarrow \infty$.

We calculate the mean square error at each time with varying time steps.

We tested various time steps, with dt range from 5 to 8,000, and noticed the error was minimized between 7,000 and 8,000.

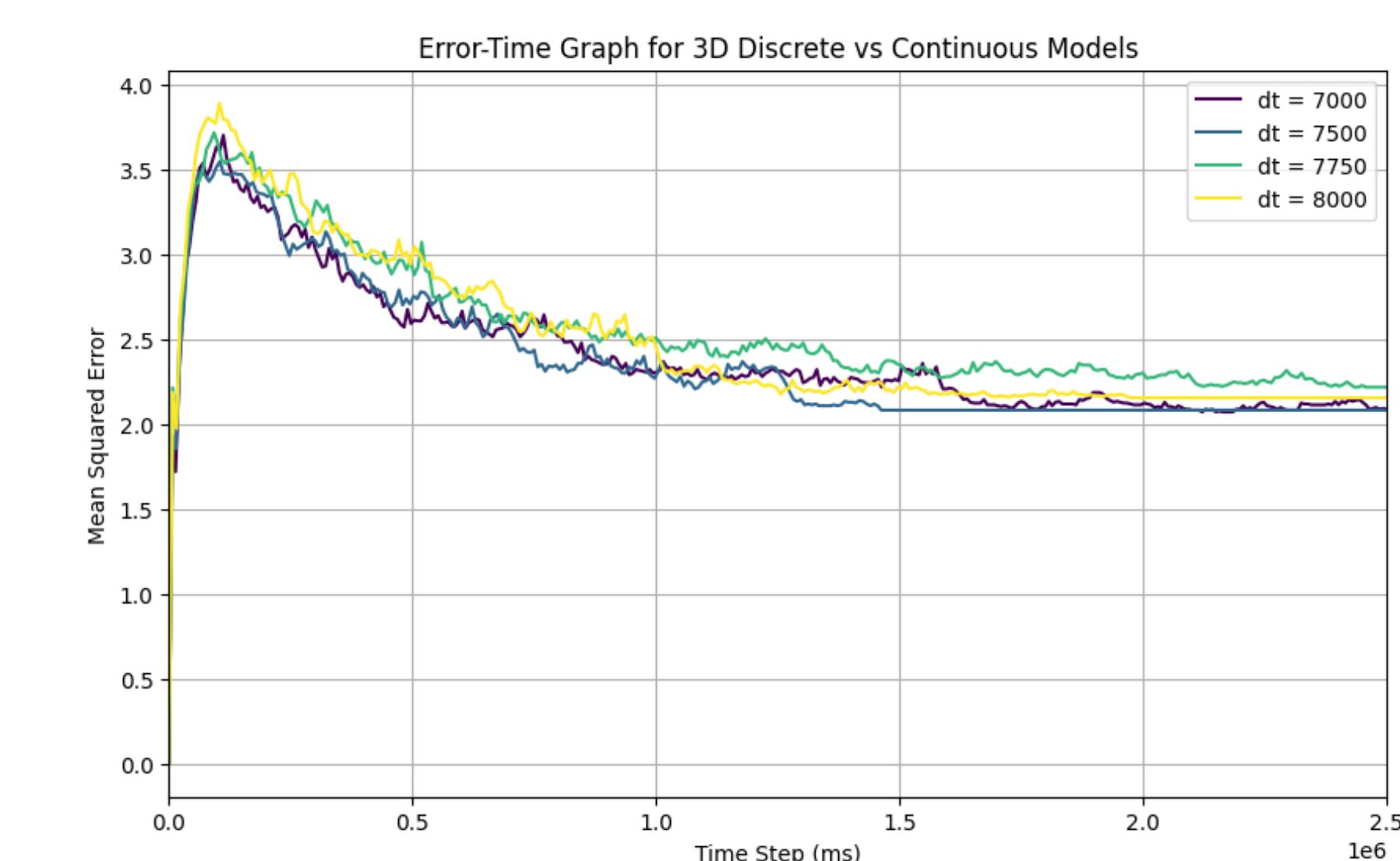


Figure 6: Mean Square Error Time Error graph with time steps $dt = 7000, 7500, 7750, 8000$ with regards to milliseconds.

We wanted to minimize the mean squared error between the continuous and discrete model and to reach that minimum error quickly. We noticed as the time steps got larger the minimum error decreased; however, the mean square error across the different time steps was between 2.1 and 2.6.

A careful investigation determined that the $dt = 7500$ is the best time step that minimizes the mean squared error between the continuous and discrete model, with an mean square error of 2.25.

References

- [1] M. Azimi, Y. Jamali, MRK. Mofrad, *Accounting for Diffusion in Agent Based Models of Reaction-Diffusion Systems with Application to Cytoskeletal Diffusion*, University of Akron, (2011).
- [2] W. Kapner, J. Lin, *Ion Diffusion and Action Potentials in Cardiac Tissue*, California Polytechnic State University- San Luis Obispo, (2023).