The *in silico* simulation involves solving algebraic calculations and dynamic functions represented as ordinary differential equations (ODEs), which are crucial for modelling the intricate behaviours of biological systems. To efficiently solve these ODEs, the study utilized NVIDIA’s CUDA (Compute Unified Device Architecture)-based parallel processing framework [cuda]. The Rush-Larsen method was selected as the ODE solver due to its ability to balance computational efficiency, numerical stability, and compatibility with the CUDA architecture. In this research, the ODE solver was integrated into the cell model code as a function, enabling seamless execution within the parallelized framework.

Cell model used in this study based on O’Hara et al. 2011 (ORd 2011) [ord]. The model was adapted for GPU compatibility using offsetting, a memory optimization technique that converts multi-dimensional data into contiguous 1D arrays, ensuring efficient alignment with GPU global, shared, and constant memory.

Simulations were conducted in two phases: Phase 1 amplified pharmacological effect of the drug by running 1,000 pacing cycles (simulating 1,000 milliseconds each) to stabilize the system, generating a cache file of final states (e.g., ion channel conductances, membrane potentials). Phase 2 recorded outputs by simulating one additional cycle, producing biomarkers for this study (summarizing APD50/90, calcium transients, and ion current amplitudes) and time-series files (one per sample) with detailed temporal data. Drug testing included control (uses 0 mMol concentration of drug) and (**drugname)** at **(conc)** mMol to assess dose-dependent effects. Validation for this *in silico* method confirmed high accuracy when compared with currently available CPU-based simulation, with a mean absolute error (MAE) of 0.078 mV for action potentials and near-identical biomarker trajectories.

Ref:  
  
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