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A multi-scale model of cardiac electrophysiology

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1 Works for me dx.doi.org/10.17504/protocols.io.5nkg5cw

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ABSTRACT

Multi-scale computational modeling is a major branch of computational biology as evidenced by the US federal interagency Multi-Scale Modeling Consortium and major international projects. It invariably involves specific and detailed sequences of data analysis and simulation, often with multiple tools and datasets, and the community recognizes improved modularity, reuse, reproducibility, portability and scalability as critical unmet needs in this area. Scientific workflows are a well-recognized strategy for addressing these needs in scientific computing. While there are good examples if the use of scientific workflows in bioinformatics, medical informatics, biomedical imaging and data analysis, there are fewer examples in multi-scale computational modeling in general and cardiac electrophysiology in particular. Cardiac electrophysiology simulation is a mature area of multi-scale computational biology that serves as an excellent use case for developing and testing new scientific workflows. In this dataset, we develop, describe and test a computational workflow that serves as a proof of concept of a platform for the robust integration and implementation of a reusable and reproducible multi-scale cardiac cell and tissue model that is expandable, modular and portable. The workflow described leverages Python and Kepler-Python actor for plotting and pre/post-processing. During all stages of the workflow design, we rely on freely available open-source tools, to make our workflow freely usable by scientists.

EXTERNAL LINK

https://github.com/ClancyLabUCD/Workflow_Kepler

A demonstration of modularity, reuse, reproducibility, portability and scalability for modeling and simulation of cardiac electrophysiology using Kepler Workflows.pdf

UserManual.pdf

1 Creating multi-scale model of cardiac electrophysiology

We developed a workflow containing differential equation models of cardiac physiology that automate the execution of simulations with user defined options of outputs from a single cell, 1 or 2D tissue, and a pseudo-ECG output, which can be compared to experimental or clinical data.

2 Compiling Human_0D1D2DWF program

- **In order to compile 1D2D Human_0D1D2DWF program model,located in Code\Human_0D1D2DWF\1D2D folder in our data set, follow these instructions:**

  To compile the program:

  ————————————————————————————

  (1) Using Intel Compiler:
  icc masterCompute.cpp -openmp -o oneD

  ./oneD initial_WTstates.txt stim_param.txt testOutputFolderTWOd

_____

OR

(2) Using GCC compiler:

g++ masterCompute.cpp -fopenmp -o oneD

./oneD initial_WTstates.txt stim_param.txt testOutputFolderONEd

_____

Input settings in stim_param.txt

1 Set Na blocker drug concentration

2 Set Kr blocker ratio

3 Set basic cycle length (BCL)

4 Set how many beats for 1D (e.g 200).
For 2D, **set beat = 1**

5 Set Ligand concentrations

6 Adjust cAMKII activity levels (expression = 'WT', 'OE', or 'KO')

7. 1D or 2D

8. tissue size = tw * tl. Enter value for tw.

9. tissue size = tw * tl. Enter value for tl.

10. homogeneous or heterogeneous

_____

For 1D simulations: Read initial_WTstates.txt which is the initial variables file corresponding to SS_rabbit_varNames.txt (total variables are 206, although some of them are not used in the model)

(1) outputs generated in ecgs.txt (1D case)

1st column: time
2nd column: ecg

(2) Time course of AP surface (1D)

_____

For 2D simulations: Read in fiber.cell which is generated from 1D simulations

(3) Time snapshots for 2D

- **In order to compile Single_Cell Human_0D1D2DWF program model,located in Code\Human_0D1D2DWF\ Single_Cell folder in our data set, follow these instructions:**

To compile the program:
Using Intel Compiler ICC icc masterCompute.cpp -o singlecell

./singlecell initial_WTstates.txt stim_param.txt testOutputFolder _____

Using GCC

g++ masterCompute.cpp -o singlecell

./singlecell initial_WTstates.txt stim_param.txt testOutputFolder _____

plotall.m collects the results from masterCompute.cpp and plots the time course of voltage or currents

_____

Input settings in stim_param.txt

1. Set Na blocker drug concentration
2. Set Kr blocker ratio
3. Set basic cycle length (BCL)
4. Set how many beats.
5. Set Ligand concentration
6. Adjust cAMKII activity levels (expression = 'WT', 'OE', or 'KO')

_____

initial_WTstates.txt is the initial variables file corresponding to SS_rabbit_varNames.txt (total variables are 206, although some of them are not used in the model)

_____

(1) outputs generated in vm_1Hz.txt 29 Ca bound to Casqn
Ca SR
Na dyad
Na sl 33 Na cytosol
K
Ca dyad
Ca sl
Ca cytosol
Vm

(2) outputs generated in allresult_1Hz.txt
I_Ca_store,
I_to_store[0],
I_Na_store,
I_K1_store,
Jserca,
IKs_store,
IKr_store,
Jleak[0],
Jleak[1],
ICFTR,
pars1.Incx

(3) outputs generated in apds_1Hz.txt

1st column: beat
2nd column: APD90

3 Compiling Mouse_0D1D2DWF program

- **In order to compile 1D2D Mouse_0D1D2DWF program model,located in Code\Mouse_0D1D2DWF\1D2D folder in our data set, follow these instructions:**

To compile the program:

_____

(1) Using Intel Compiler:
icc masterCompute.cpp -openmp -o oneD

./oneD initial_WTstates.txt stim_param.txt testOutputFolderTWOd

---

OR

(2) Using GCC compiler:

g++ masterCompute.cpp -fopenmp -o oneD

./oneD initial_WTstates.txt stim_param.txt testOutputFolderONEd

---

Input settings in stim_param.txt

1 Set Na blocker drug concentration

2 Set Kr blocker ratio

3 Set basic cycle length (BCL)

4 Set how many beats for 1D (e.g 200).
For 2D, **set beat = 1**

5 Set Ligand concentrations

6 Adjust cAMKII activity levels (expression = 'WT', 'OE', or 'KO')

7. 1D or 2D

8. tissue size = tw * tl. Enter value for tw.

9. tissue size = tw * tl. Enter value for tl.

10. homogeneous or heterogeneous

For 1D simulations: Read initial_WTstates.txt which is the initial variables file corresponding to SS_rabbit_varNames.txt (total variables are 206, although some of them are not used in the model)

(1) outputs generated in ecgs.txt (1D case)

1st column: time
2nd column: ecg

(2) Time course of AP surface (1D)

For 2D simulations: Read in fiber.cell which is generated from 1D simulations

(3) Time snapshots for 2D

- **In order to compile Single_Cell Mouse_0D1D2DWF program model,located in Code\Mouse_0D1D2DWF\Single_Cell folder in our data set, follow these instructions:**

To compile the program:

Using Intel Compiler ICC icc masterCompute.cpp -o singlecell

./singlecell initial_WTstates.txt stim_param.txt testOutputFolder _____

Using GCC

g++ masterCompute.cpp -o singlecell

./singlecell initial_WTstates.txt stim_param.txt testOutputFolder _____

plotall.m collects the results from masterCompute.cpp and plots the time course of voltage or currents

_____

Input settings in stim_param.txt

1. Set Na blocker drug concentration
2. Set Kr blocker ratio
3. Set basic cycle length (BCL)
4. Set how many beats.
5. Set Ligand concentration
6. Adjust cAMKII activity levels (expression = 'WT', 'OE', or 'KO')

_____

initial_WTstates.txt is the initial variables file corresponding to SS_rabbit_varNames.txt (total variables are 206, although some of them are not used in the model) _____

(1) outputs generated in vm_1Hz.txt
Ca bound to Casqn
Ca SR
Na dyad
Na sl
Na cytosol
K
Ca dyad
Ca sl
Ca cytosol
Vm

(2) outputs generated in allresult_1Hz.txt
I_Ca_store,
I_to_store[0],
I_Na_store,
I_K1_store,
Jserca,
IKs_store,
IKr_store,
Jleak[0],
Jleak[1],
ICFTR, pars1.Incx

(3) outputs generated in apds_1Hz.txt

1st column: beat
2nd column: APD90

4 Compiling Rabbit_0D1D2DWF program

- **In order to compile 1D2D Rabbit_0D1D2DWF program model,located in Code\Rabbit_0D1D2DWF\1D2D folder in our data set, follow these instructions:**

To compile the program:

————————————————————————————

(1) Using Intel Compiler:
icc masterCompute.cpp -openmp -o oneD

./oneD initial_WTstates.txt stim_param.txt testOutputFolderTWOd

_____

OR

(2) Using GCC compiler:

g++ masterCompute.cpp -fopenmp -o oneD

./oneD initial_WTstates.txt stim_param.txt testOutputFolderONEd

_____

Input settings in stim_param.txt

1 Set Na blocker drug concentration

2 Set Kr blocker ratio

3 Set basic cycle length (BCL)

4 Set how many beats for 1D (e.g 200).
For 2D, **set beat = 1**

5 Set Ligand concentrations

6 Adjust cAMKII activity levels (expression = 'WT', 'OE', or 'KO')

7. 1D or 2D

8. tissue size = tw * tl. Enter value for tw.

9. tissue size = tw * tl. Enter value for tl.

10. homogeneous or heterogeneous

_____

For 1D simulations: Read initial_WTstates.txt which is the initial variables file corresponding to SS_rabbit_varNames.txt (total variables are 206, although some of them are not used in the model)

(1) outputs generated in ecgs.txt (1D case)

1st column: time
2nd column: ecg

(2) Time course of ECG (1D)

_____

For 2D simulations: Read in fiber.cell which is generated from 1D simulations

(3) Time snapshots for 2D

- **In order to compile Single_Cell Rabbit_0D1D2DWF program model,located in Code\Rabbit_0D1D2DWF\Single_Cell folder in our data set, follow these instructions:**

To compile the program:

Using Intel Compiler ICC icc masterCompute.cpp -o singlecell

./singlecell initial_WTstates.txt stim_param.txt testOutputFolder _____

Using GCC

g++ masterCompute.cpp -o singlecell

./singlecell initial_WTstates.txt stim_param.txt testOutputFolder _____

plotall.m collects the results from masterCompute.cpp and plots the time course of voltage or currents

_____

Input settings in stim_param.txt

1. Set Na blocker drug concentration
2. Set Kr blocker ratio
3. Set basic cycle length (BCL)
4. Set how many beats.
5. Set Ligand concentration
6. Adjust cAMKII activity levels (expression = 'WT', 'OE', or 'KO')

_____

initial_WTstates.txt is the initial variables file corresponding to SS_rabbit_varNames.txt (total variables are 206, although some of them are not used in the model) _____

(1) outputs generated in vm_1Hz.txt
Ca bound to Casqn
Ca SR
Na dyad
Na sl
Na cytosol
K
Ca dyad
Ca sl
Ca cytosol
Vm

(2) outputs generated in allresult_1Hz.txt

I_Ca_store,
I_to_store[0],
I_Na_store,
I_K1_store,
Jserca,
IKs_store,
IKr_store,
Jleak[0],
Jleak[1],
ICFTR,
pars1.Incx

(3) outputs generated in apds_1Hz.txt

1st column: beat
2nd column: APD90