To compile the program:

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(1) Using Intel Compiler:

icc masterCompute.cpp -openmp -o oneD

./oneD initial\_WTstates.txt stim\_param.txt testOutputFolderTWOd

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OR

(2) Using GCC compiler:

g++ masterCompute.cpp -fopenmp -o oneD

./oneD initial\_WTstates.txt stim\_param.txt testOutputFolderONEd

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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

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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)

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

(3) Time snapshots for 2D