**Repository of MATLAB Files to reproduce figures from:**

A computational model of induced pluripotent stem-cell derived cardiomyocytes for high throughput risk stratification of KCNQ1 genetic variants

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**Guide to file types:**

**Green Bolded**: main files to generate the corresponding paper figure

**Red bolded**: function files required for main files (differential eqns, analysis, etc.)

Orange: parameter vectors/matrices to parameterize a model/population

*Folder:* **TS1**

* KCNQ1\_mutation\_allVariable\_XXX.mat
  + XXX = mutation name
  + Contains parameter values, initial conditions, and AP outputs for each mutation population
* KCNQ1\_mutation\_allVariable\_WT.mat
  + Contains parameter values, initial conditions, and AP outputs for wild-type population
* **Plot\_IKskinetics.m**: main function to IV and activation curves for mutant and wild-type IKS models, as in Fig. 1
* **Plot\_APs.m**: main function to generate action potentials for mutant and wild-type populations, as in Fig. 2B-D
* **Plot\_CompareMuts.m**: main function to analyze and stratify mutant populations as shown in Fig. 3. Includes outputs for table 1 showing stratification of mutants and percentage of models excluded.

*Folder:* **TS2**

* KCNQ1\_mutation\_allVariable\_XXX.mat
  + XXX = mutation name
  + Contains parameter values, initial conditions, and AP outputs for each mutation population
* KCNQ1\_mutation\_allVariable\_WT.mat
  + Contains parameter values, initial conditions, and AP outputs for wild-type population
* **ipsc\_function.m**: function file containing differential equations for iPSC model
* **Current\_outputs.m**: function file to calculate currents after ode run of ipsc\_function
* **Plot\_IKskinetics.m**: main function to IV and activation curves for mutant and wild-type IKS models, as in Fig. 4A-B
* **Main\_Example\_Cells.m**: main function to generate action potentials and currents during for an exemplar model in any population. Example shown for models in Fig. 5
* **Plot\_CompareMuts.m**: main function to analyze and stratify mutant populations as shown in Fig. 6. Includes outputs for table 2 showing stratification of mutants and percentage of models excluded.