Overview of the purpose of the provided files:

* “**mRNAlevels.m**”: it contains the mean and standard deviation of the expression levels (mRNA) of different ion channel conductances form males and females, taken from Gaborit et al. (2010) [1]
* “**GeneratePopulation.m**”: this script generates a population of scaling factors of “popsize” (size selected by the user) men and women, using channel mRNA expression levels.
* “**Analize\_population.m**”: it analizes the population created to check the normal distribution of the scaling factors.
* “**Simulate\_population.m**”: this file runs the simulations of the population of models using the endocardial model compiled in ***ORdmD\_sex***.
* “**Double2tex.m**”: this is an auxiliary script that takes a double array and returns a char array with those values.
* “**Analize\_simulations.m**”: it analyzes the simulations of the populations and calculates a set of biomarkers. For the analysis of endocardial simulations, 'analyze\_Tosim\_pop' should be set to one. For the analysis of mid and epicardial simulations, 'analyze\_Tosim\_pop' should be set to 2.
* “**Select\_good\_simulations\_and\_plots.m**”: this script performs the calibration of the populations, accepting models that show biomarkers within the experimental range and rejecting those with any biomarker outside the experimental range. In addition, it plots the action potentials of the populations, showing the accepted and rejected models.
* “**Simulate\_toSim\_population.m**”: this file runs the simulations of the mid and epicardial cells with the parameters of the calibrated populations.

Note that files are distributed in the hope that they will be useful, but WITHOUT ANY WARRANTY; without even the implied warranty of MERCHANTABILITY or FITNESS FOR A PARTICULAR PURPOSE.

# Brief outline of how to build the model population.

1. Run "GeneratePopulation.m" This generates the file for the initial population scaling factors. The number of samples per gender can be determined with the parameter “popsize”. The name of this population will be used as a basis for the following steps.
2. Analyze the generated population with "Analize\_population.m". The distribution of scaling factors for the generated populations of the male and female models can be analyzed.
3. Simulate the endocardial cells of the populations with "Simulate\_population.m".
4. Download simulation results + run “Analize\_simulations.m”. “analize\_ToSim\_pop” has to be set to 0. This calculates the biomarkers of the simulations.
5. Run “Select\_good\_simulations\_and\_plot.m”. This generates a folder with the plots detailing the simulations selected by their scaling factors in 0D endo. 'Analyze\_toSim\_pop' must be 0.
6. Run “Simulate\_toSim\_population.m”. It simulates the population in mid and epicardial.
7. Download simulation results + run “Analize\_simulations.m”. “analize\_ToSim\_pop” has to be different than 0.
8. Run “Select\_good\_simulations\_and\_plot.m”. This time, “Analyze\_toSim\_pop” must be 2. It further calibrates the populations of models, but for the mid and epi population, selecting the simulations by their APD in these cells.

# References

[1] N. Gaborit *et al.*, “Gender-related differences in ion-channel and transporter subunit expression in non-diseased human hearts,” *J Mol Cell Cardiol*, vol. 49, no. 4, pp. 639–646, Oct. 2010, doi: 10.1016/J.YJMCC.2010.06.005.