Overview of the purpose of the provided files:

* “**ORdmD.cellml**” is a CellML file containing the ORdmD model.
* “**ORdmD scaling factors.xlsx**” is an Excel file with the scaling factors for the 860 models in the accepted population of models. Rows correspond to models and columns to conductances. Each column contains a header indicating the conductance to which it corresponds. Each conductance is given as a scaling factor of the value of that conductance in the ORdmD model in the default endocardial configuration.
* “**TorORd scaling factors.xlsx**” is an Excel file with the scaling factors for the 810 models in the accepted population of models. Rows correspond to models and columns to conductances. Each column contains a header indicating the conductance to which it corresponds. Each conductance is given as a scaling factor of the value of that conductance in the TorORd model in the default endocardial configuration.
* “**ORdmD.m**” is the MATLAB function with the ORdmD model. “**runORdmD.m**” is the simulation core of the ORdmD model, primarily computing the derivative of state variables over time. It uses as inputs the scaling factors for a given model and the number of beats that will be saved. To compute the simulation it uses “**X0.mat**”, which is a matrix that contains the initial conditions.
* “**model\_Torord\_dynCl.m**” is the MATLAB function with the TorORd model. This code was published by Tomek et al. (2019). The script for running a simulation is “**modelRunner.m**”. “**getStartingState.m**” is also a script associated with this model. It generates the initial conditions for the simulations.
* “**Population\_TorORd.m**” and “**Population\_ORdmD.m**” are the scripts for generating and simulating the populations of ToORd an ORdmD models, respectively. The variable trials defines the number of initial models (before the calibration).
* “**calculateBiomarkers\_calibration.m**” is a MATALB functions that calculates the 15 biomarkers used for the calibration of the populations. It uses as inputs 4 structures, corresponding to the simulations of the initials population under control conditions, under IKs\*0.1, under IKr\*0.7 and under IK1\*0.5.
* “**calculate10biomark.m**” is the function for calculating the arrhythmogenic biomarkers of a given simulation.
* “**optimizeSVM.m**”: script for optimizing and training a SVM classifier.

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.