

**Title:** POMtool: open source tool for creating population of models**Authors:***Ossi Noita, Olli Ylinen, Jari Hyttinen***Keywords:**

Cell and tissue models, biomedical engineering

**Abstract**

In silico model represents single physiological phenomena. Similar way, how trajectory of a rocket can be modelled with physics-model, trajectory of biological organism can be determined with in silico model. For biological organisms, we have an additional challenge: systems we research are not of single phenotype, as we have many different potential samples to take from the population. In addition, biological systems are very robust, and multiple variables affect the same state. This variability in biological systems means that we should not limit ourselves to finding single phenotype answers, instead, we need to create a population of models.

The practice of creating population of models, instead of just parametrizing single instance, is powerful technique to be able to make statements of large population. This can enhance studies, by changing sample size from a single instance to however large a population we are able to generate. The creation of these populations is commonly done very manually. This is because no tool exists to do these easily, and the process is somewhat straightforward. However, as the process is straightforward, it should be automatized.

We introduce POMtool, a publicly available open-source python tool for creating and optimizing model population. It allows the user who has defined a model to optimize their parameters, and then using those to create as large population of models as they desire. It allows use of clusters to utilize distributed nature of the problem but also allows anyone to generate population of models with their chosen platform. The tool is available in <https://github.com/TAU-CBIG/POMtool>.