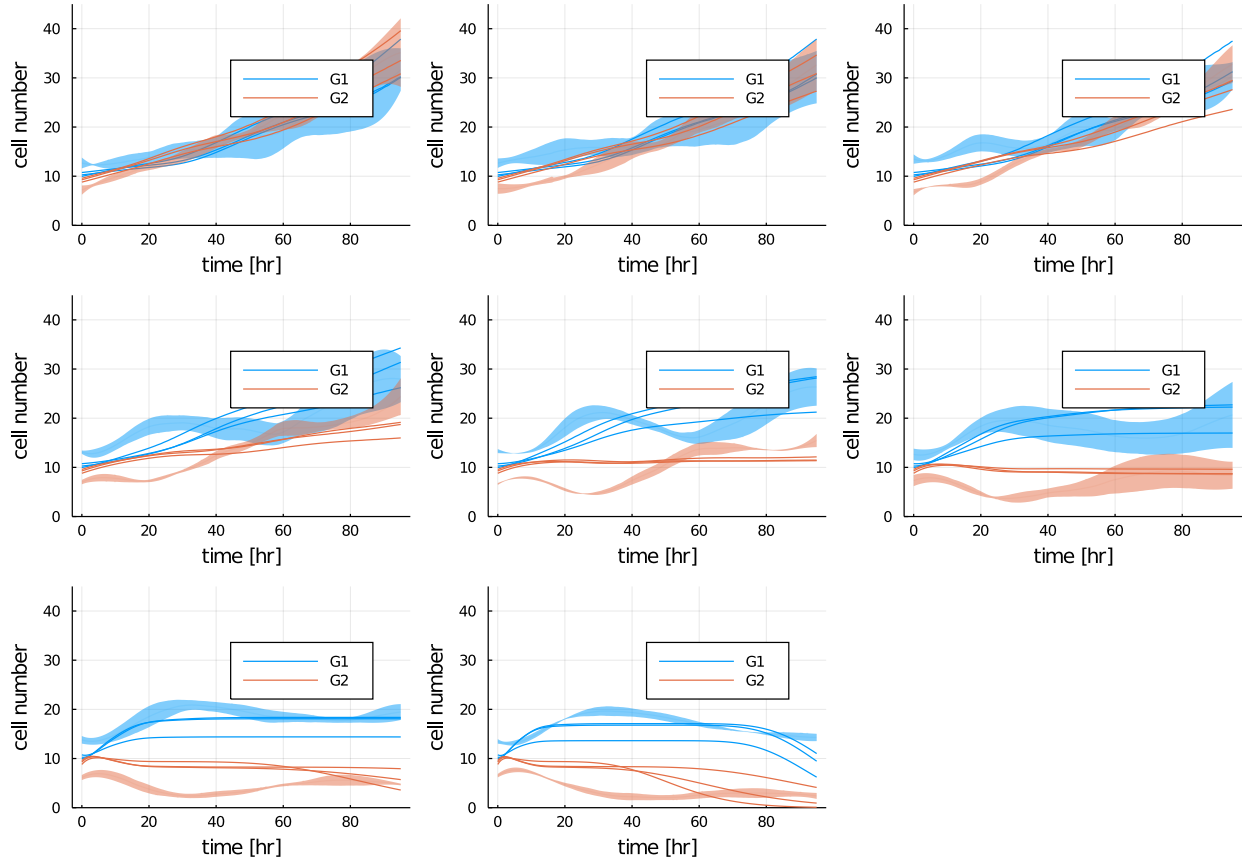
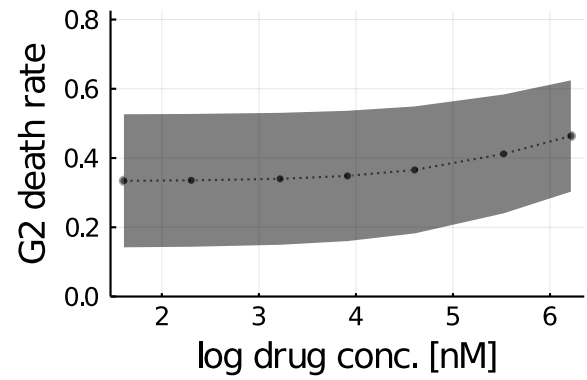
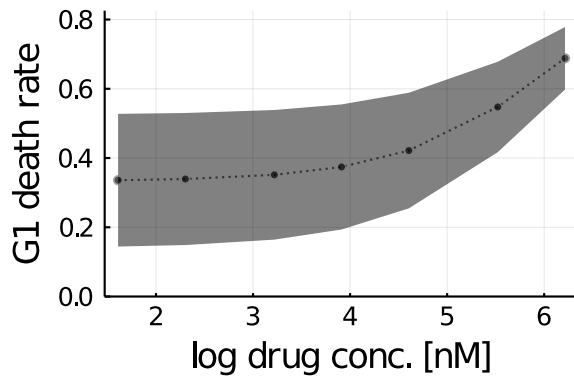
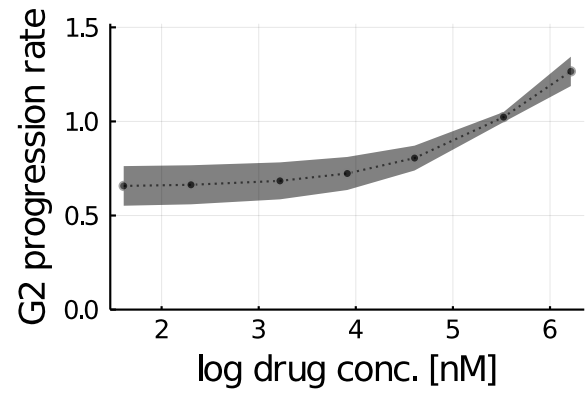
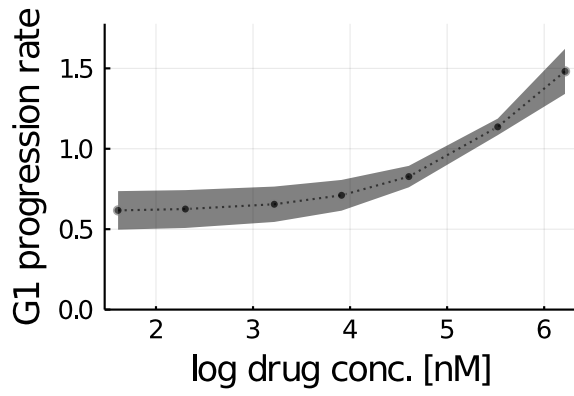


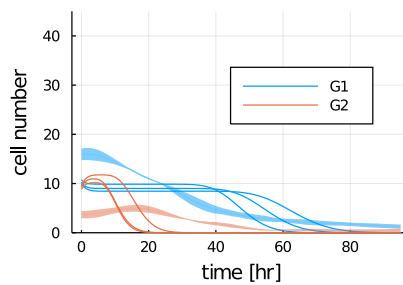
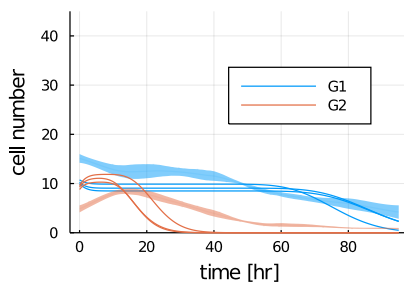
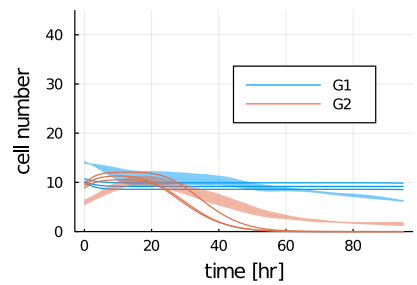
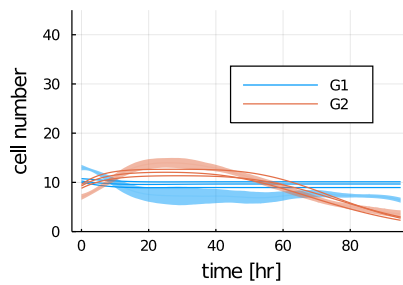
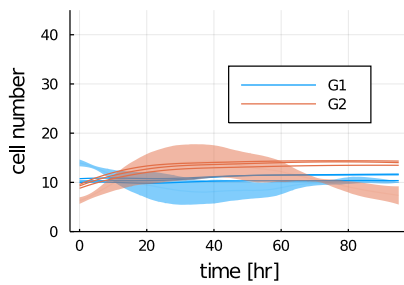
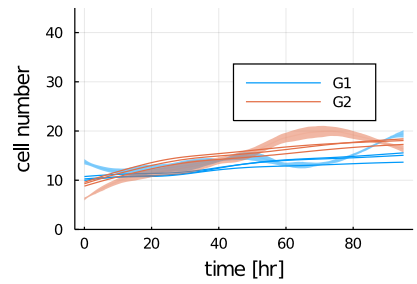
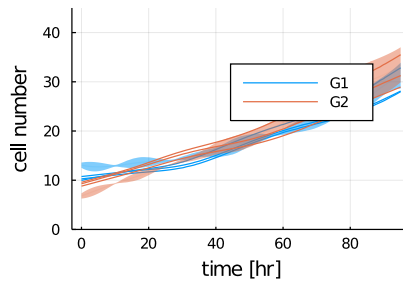
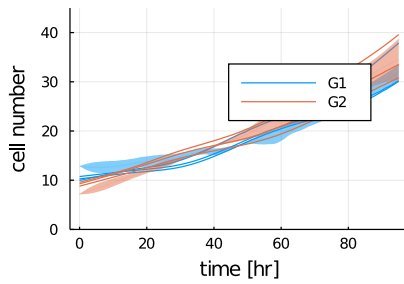
Simulation and representation of the three replicates.

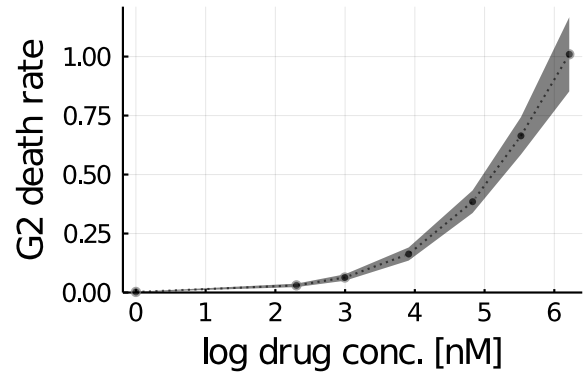
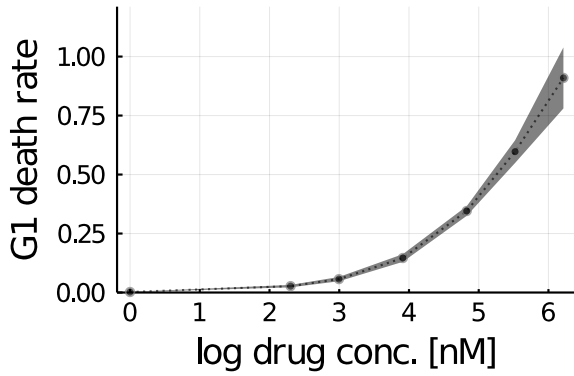
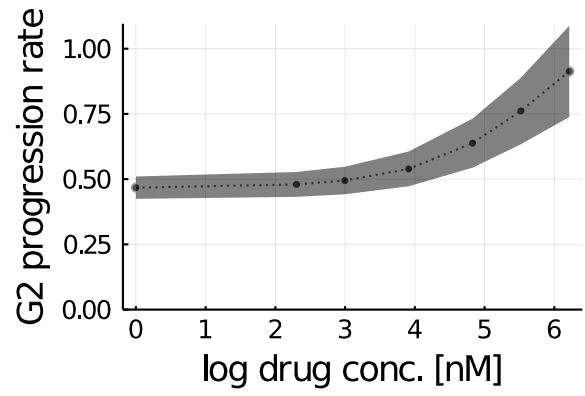
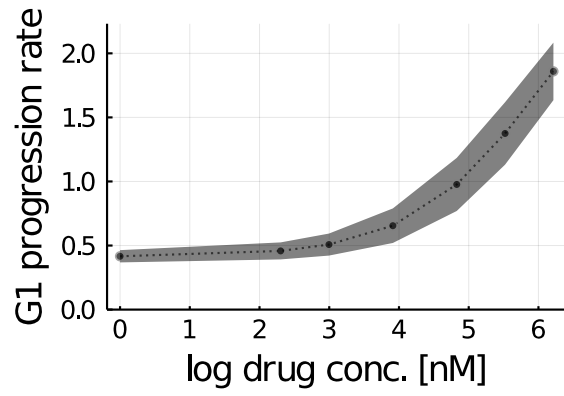
The solid lines show the three simulations, meaning, after obtaining the three sets of the parameters, we calculate the time-series simulation and find the cell number for each time-point, for the three replicates, separately. The ribbon is the bounds of std of the original data. This shows that even if the model for individual replicates, deviates a little, but on-average it doesn't deviate the standard deviation. So it is reliable. (here again for lapatinib)



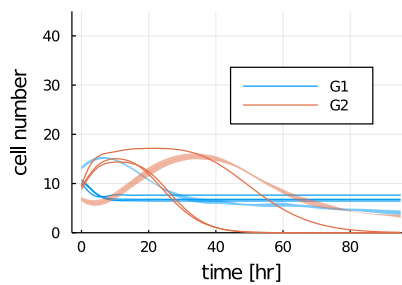
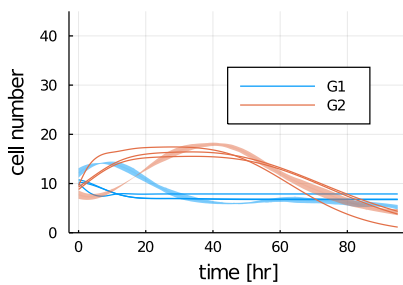
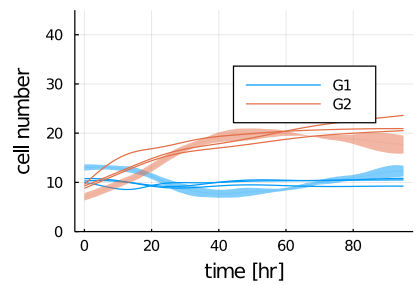
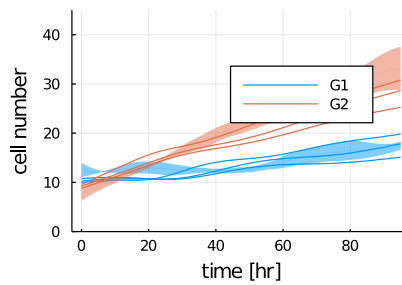
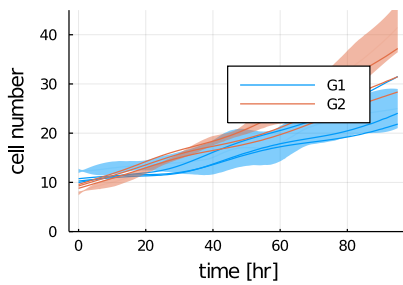
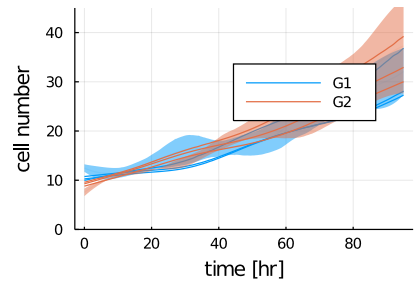
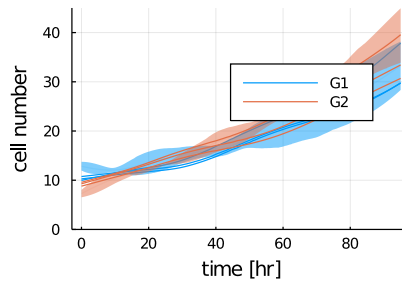
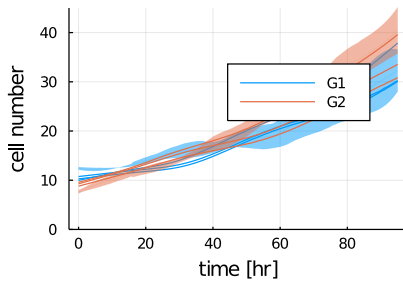


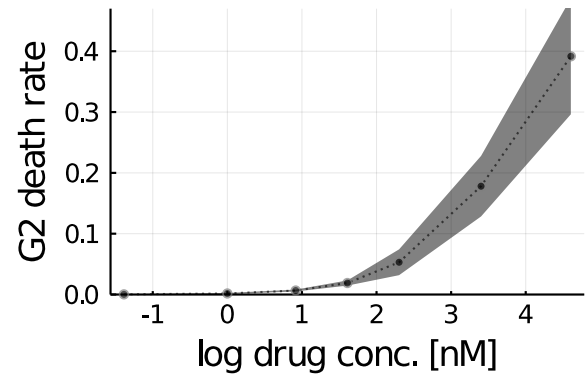
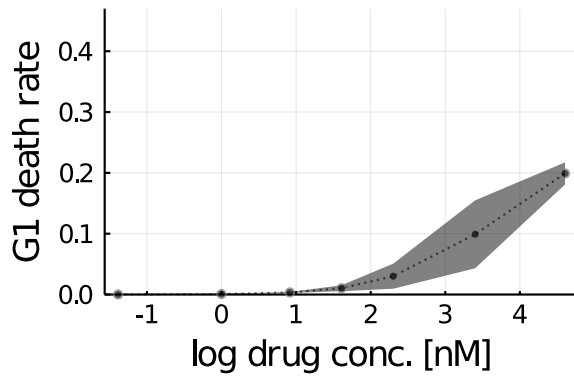
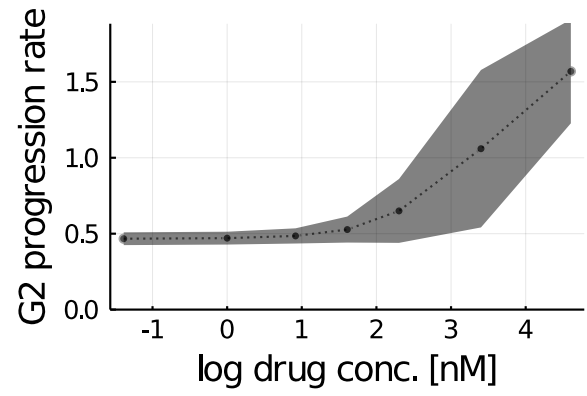
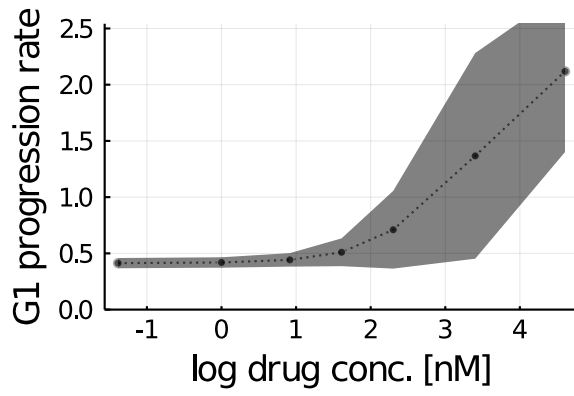
0.1 Doxorubicin



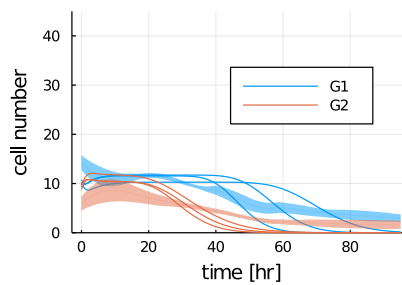
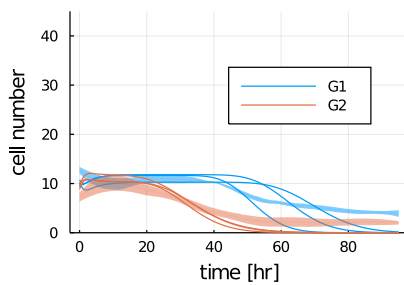
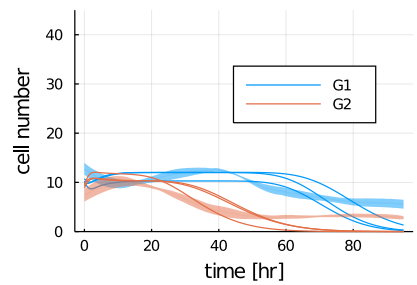
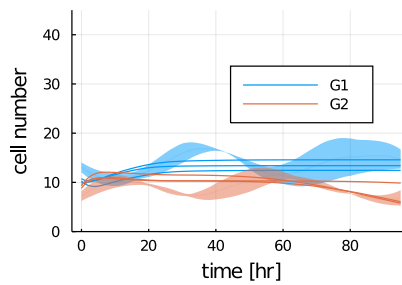
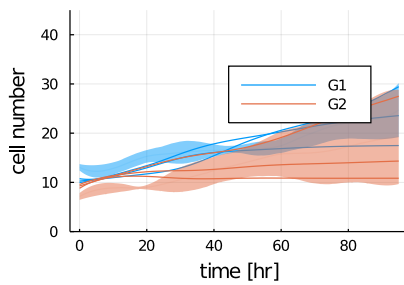
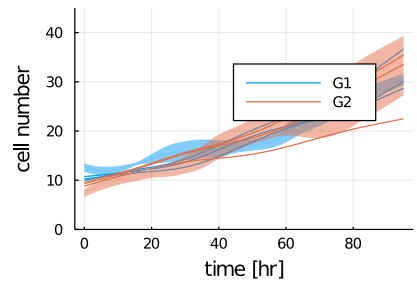
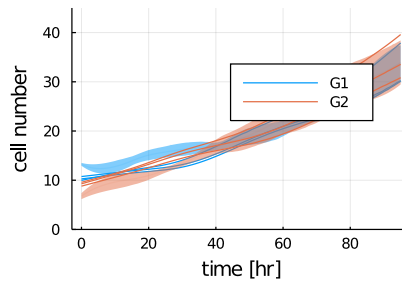
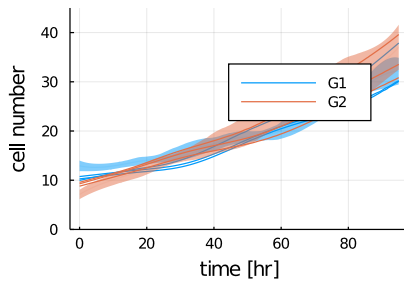


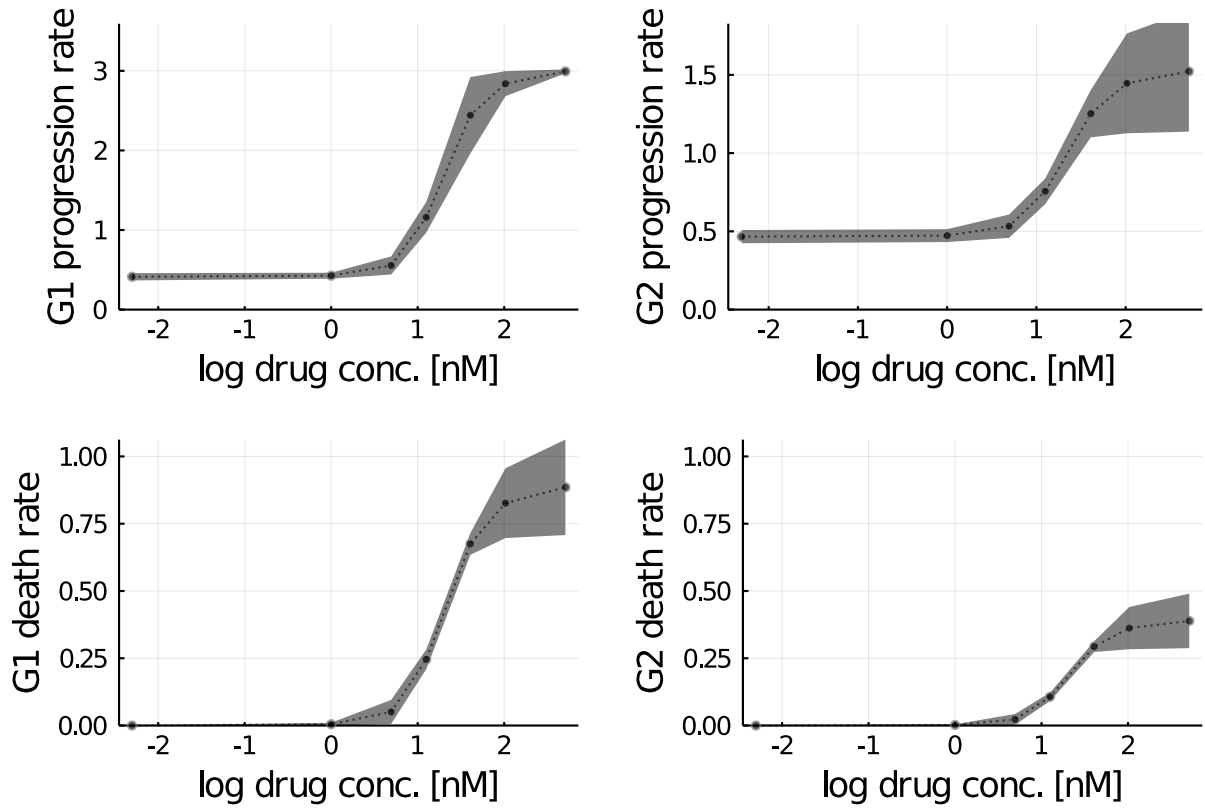
0.2 Gemcitabine





0.3 Paclitaxel





0.4 Palbociclib

