How-To Simulate

Below are the step-by-step instructions for running simulations, which accompany "*https://github.com/drplaugher/PCC_Mutations*". Once the potential controls are identified, use our MATLAB simulator within "comb_pcc_DP.m" to parse the good/bad controls.

1) Under "*Inductions and Control*", use the *Mutation Functions* `F1-F4` to induce the desired mutation.
    a. Node and parameters are already set, all one needs to do is uncomment the desired gene and maintain order when compounding mutations. For example(s)

    KRAS can be induced by using

    ```
    F1 = TruthTable_del_n_temp(F,nv,varF,p, 43,1);
    ```

    KRAS/TP53 can be induced by using

    ```
    F1 = TruthTable_del_n_temp(F,nv,varF,p, 43,1);

    F2 = TruthTable_del_n_temp(F1,nv,varF,p, 64,0);
    ```

    TP53/CDKN2A can be induced by using

    ```
    F2 = TruthTable_del_n_temp(F,nv,varF,p, 64,0);

    F3 = TruthTable_del_n_temp(F2,nv,varF,p, 56,0);
    ```

2) Also under "*Inductions and Control*", use Node/Edge Control Functions `F5-F8` to implement the desired control strategy.
    a. Specific gene numbers are provided in the code for reference
    b. One must continue to compound functions as before in Step 1 if multiple controls are desired
    c. Note that the MATLAB functions for inducing node/edge control are:
    `TruthTable_del_n_temp(F,nv,varF,p, node,v)`

    `TruthTable_del_a_temp(F,nv,varF,p,tail,head,v)`

    (Here `v` indicates the sign of the action where knockout=0, expression =1)

3) Under "*Simulation*", set the desired noise level and choose either the noisy or silent simulation.
    a. Make sure the function being used in the simulation matches the last function being used (aka. `F-F8`, depending on the scenario being simulated)
    b. The variable `Phen` will print the ending phenotype levels, which indicate long term probability of expression.
4) To visually represent the full trajectories of the simulation, use section "*Graphing*". See that the final expression levels are those from Step 3.
    a. Notice that over time, expression levels will appear to converge.

Written by Daniel Plaugher 1/2022

To determine the efficacy of controls, we compare uncontrolled simulations with the appropriate targeted control simulations. Inducing mutations will result in high levels of diseased phenotypes. Thus, a good control will produce low disease levels and high health levels (apoptosis in our case). One can also perform the same steps to run simulations within “thesis_examples.m”, which contains various examples given throughout the thesis.