Details for simulating RACIPE parameter sets outside RACIPE

for any network (GRHL2/EMTRACIPE and so on),

1. ‘network\_parameters.dat’ has all the parameters listed. First column is the parameter index and second column in the number of steady states identified by RACIPE for that parameter set. Parameters are listed from 3rd column onwards.
2. The order of these parameters is listed in the first column of the ‘network.prs’
3. The format of the ODE’s is as follows:

Consider species A, activated by species B and inhibited by species C:

Details of the parameters is as follows:

Prod\_of\_A: Production rate of A

Deg\_of\_A: Degradation rate of A

Hs+ and Hs- : they are modified hill functions called “Hill-shift functions” that represent the fold change in the production rate of target due to the other species.

Act\_of\_BToA: strength of the activation link of B to A. Higher is this value, higher is the corresponding Hs+ and hence higher the production rate of A. At very high values of B, the production rate of A is close to Prod\_of\_A\*Act\_of\_BToA (if no other species effects the production of A).

Inh\_of\_CToA: strength of the inhibition link of C to A. Lower the value, stronger the inhibition

Num\_of\_BToA: hill coefficient. This determines the non-linearity of the hill-shift function. Higher value of this parameter promotes sharp switching dynamics

Trd\_of\_BToA: Threshold value of B at which the hill-shift function becomes (1 + (Act\_of\_BToA -1)/2)/Act\_of\_BToA. This denotes the strength of interaction of B with the promoter of A.