Systems Biology

Assignment 3

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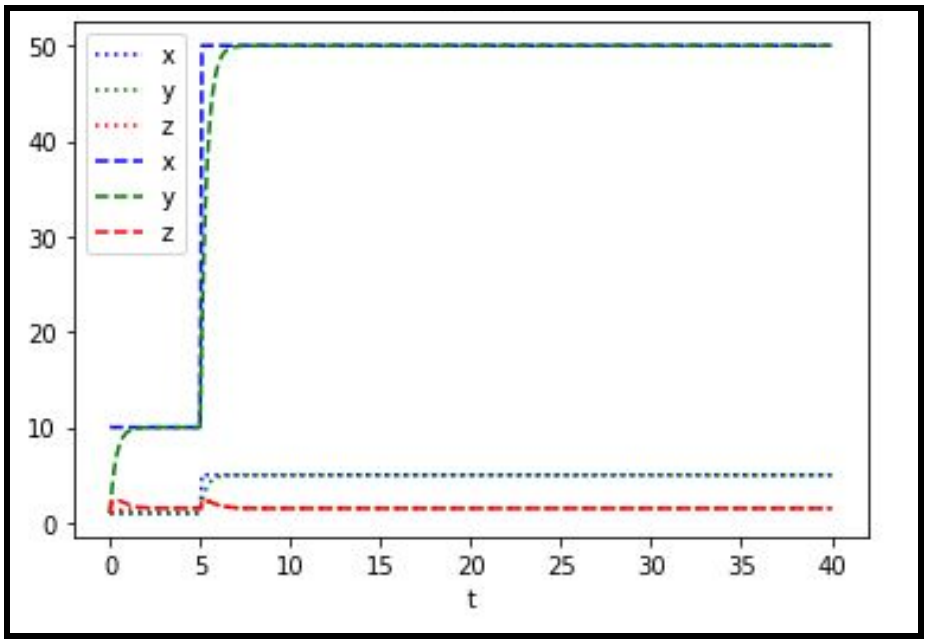
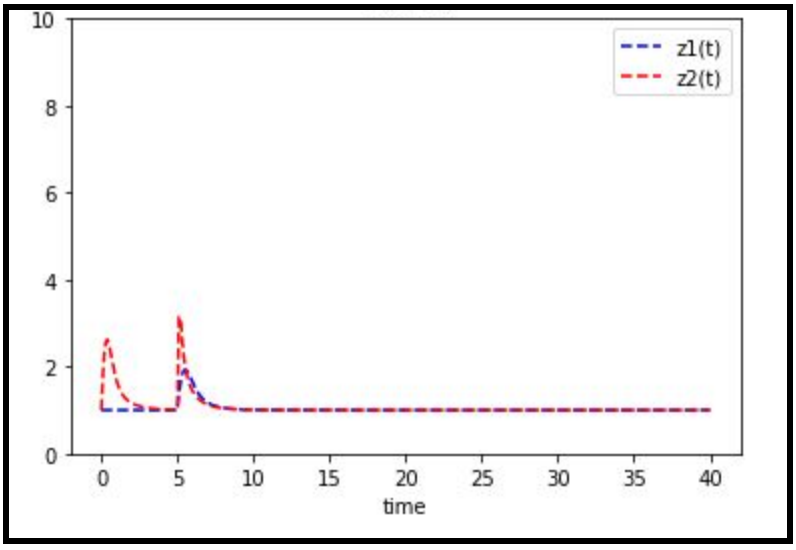
1. dz/dt = ksz* x/y - kdz * z



In the plot above, we can see that the red dotted and red hyphenated lines overlap, signifying fold change detection in the FFL.

- Signal 1 to 5: Dotted lines
- Signal 10 to 50: Hyphenated lines
- X in each case - Blue
- Y in each case - Green
- Z in each case - Red

2. dz/dt =ksz*x - kdz *y*z



In the plot above, we can see that the red dotted and red hyphenated lines do not overlap, signifying NO fold change detection in the FFL

- Red - Z when signal is 10 to 50
- Blue - Z when signal is 1 to 5

Parameter values that can give fold change detection

- The degradation and production rates (b1, a1, b2 and a2) were varied but no change in the plots was detected (This was done on XPP).
- Y/K > ~ 10 (fold-change detection also requires that X be in the linear regime in regulating the Y promoter)
- X should be linear (fold-change detection also requires that X be in the linear regime in regulating the Y promoter)

For the three cases:

1. Mutually exclusive:
   Parameter range for fold-change detection is greatest and requires only that Y saturates the Z promoter (Y0/K2 >> 1)

2. Independent binding:
   Also requires X activation of the Z promoter is linear (X0/K1 << 1)
3. Cooperative binding:
   Further requires that binding of both activators be relatively rare as compared to bonding of Y alone (X0Y0/K3 << 1)

Basic Code

1.

```
init z=1,y=1
param b1=1,a1=1,b2=1,a2=1

z'=b1*x/y-a1*z
y'=b2*x-a2*y

x=1+4*heav(t-30)

aux signal=x

@ total=90,dt=0.1,method=stiff
@ bounds=1000000
@ NPLOT=3,yp1=z,yp2=y,yp3=signal
@ total=90
done
```

2.

```
init z=1,y=1
param b1=2,a1=1,b2=2,a2=2

z'=b1*x-a1*z*y
y'=b2*x-a2*y

x=1+4*heav(t-30)

aux signal=x

@ total=90,dt=0.1,method=stiff
@ bounds=1000000
@ NPLOT=3,yp1=z,yp2=y,yp3=signal
@ total=90
done
```