# Assignment-1

## B)

### a) Code:

```
sol1 = DSolve[{y '[t] == β - α * y[t] , y[0] == 0} /. {β → 1, α → 1} , y , {t , 0 , 10}]
sol2 = DSolve[{y '[t] == β - α * y[t] , y[0] == 0} /. {β → 10, α → 1} , y , {t , 0 , 10}]
sol3 = DSolve[{y '[t] == β - α * y[t] , y[0] == 0} /. {β → 100, α → 1} , y , {t , 0 , 10}]

Plot[{y[t] /. sol1 , y[t] /. sol2 , y[t] /. sol3} , {t , 0 , 10} , AxesLabel → {"time" , "Y"} ,
PlotLegends → {"β = 1" , "β = 10" , "β = 100"}]
```
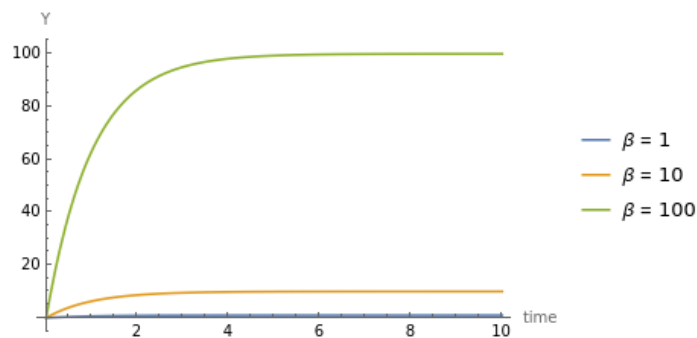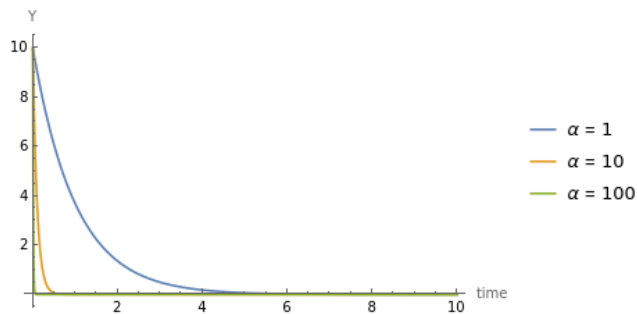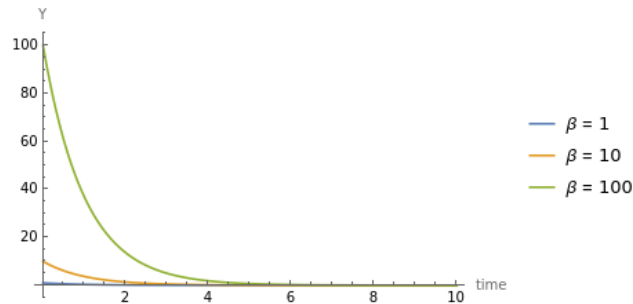


### b) Similarly,
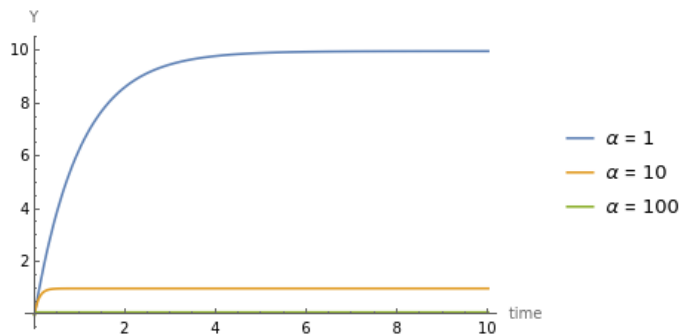


### c) For the off switch, equation governing the dynamics of protein concentration is $y = \beta e^{-\alpha t}$.

Code:

```
sol1 = DSolve[{y '[t] == - α * y[t] , y[0] == β} /. {β → 1, α → 1} , y , {t , 0 , 10}]
sol2 = DSolve[{y '[t] == - α * y[t] , y[0] == β} /. {β → 10, α → 1} , y , {t , 0 , 10}]
sol3 = DSolve[{y '[t] == - α * y[t] , y[0] == β} /. {β → 100, α → 1} , y , {t , 0 , 10}]

Plot[{y[t] /. sol1 , y[t] /. sol2 , y[t] /. sol3} , {t , 0 , 10} , AxesLabel → {"time" , "Y"} , PlotLegends
→ {"β = 1" , "β = 10" , "β = 100"}, PlotRange → All]
```

d) Response times for the above examples are
- Response time for ON switch is $ln2/\alpha$.
- Response time for OFF switch is also $ln2/\alpha$.

# C)

a) When mRNA degradation rate is faster than degradation rate of protein then mRNA reaches its steady state concentration quickly in comparison to the protein levels. The reason is that the typical time for mRNA to reach its steady state concentration is the response time $ln2/\alpha_m$, which is much shorter than the protein response time $ln2/\alpha$, when $\alpha_m \gg \alpha$. Production rate affects only the steady-state concentration of mRNA and protein not their response time.
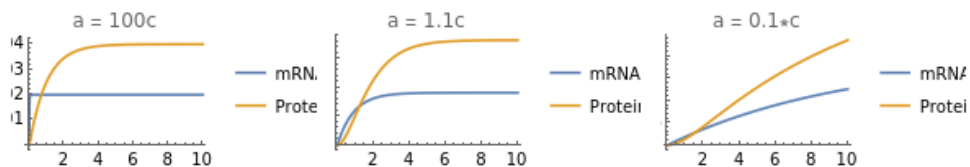


Note in above figure, a = degradation rate of mRNA and c = degradation rate of protein.

b) The scenario in which degradation rate of mRNA is 100 fold faster than the degradation rate of protein is closest to the situation we assumed in the lecture.

c) Degradation rates of mRNA has to be much greater than the degradation rate of protein to safely ignore the mRNA dynamics apply the separation of time scale simplification. As explained in part (a) of the problem, when $\alpha_m \gg \alpha$ then the mRNA reaches its steady state concentration very quickly in comparison to the protein levels. Thus the concentration of mRNA is equal to its steady state concentration for most part of protein dynamics.

$$\frac{dY_m}{dt} = \beta_m - \alpha_m * Y_m \ (mRNA\ dynamics)$$

$$\frac{dY}{dt} = pY_m - \alpha * Y \ (protein\ dynamics)$$

Where $p$ = number of Protein Y copies produced per unit time per mRNA, $Y$ = protein concentation, $Y_m$ = mRNA concentration.

So the steady state concentration of mRNA = $\beta_m/\alpha_m$. And under the assumption $\alpha_m \gg \alpha$ the protein dynamic equation can be approximated as: $\frac{dY}{dt} = p(\beta_m/\alpha_m) - \alpha * Y$. In other words, the effective protein production rate ($\beta$), which is the right-hand side of the above equation, is $p\beta_m/\alpha_m$, which is constant with respect to time.

$$\beta = p\beta_m/\alpha_m$$