465 Homework 6

```
In [15]: import numpy as np
         import matplotlib.pyplot as plt
```

3) You measure the rate of reaction for various concentrations of A. You then add an inhibitor I with a concentration of 0.1 mmol/L and repeat the rate measurements.

```
In [36]: CA= [1,1.29,1.67,2.15,2.78,3.59,4.64,5.99,7.74,10] #(mmol/L)
         rA= [2.85,3.58,4.37,5.33,6.22,7.45,8.8,10.1,11.2,12.8]#(10^-3 mmol / L min ):
          negative rA
         rAI= [1.47,1.77,2.18,2.65,3.19,3.74,4.34,5,5.62,6.26] #(10^-3 mmol / L min ):
          negative rA
         CA1=[1,1/1.29,1/1.67,1/2.15,1/2.78,1/3.59,1/4.64,1/5.99,1/7.74,1/10] #(mmol/L)
         rA1= [1/2.85,1/3.58,1/4.37,1/5.33,1/6.22,1/7.45,1/8.8,1/10.1,1/11.2,1/12.8]
         rAI1= [1/1.47,1/1.77,1/2.18,1/2.65,1/3.19,1/3.74,1/4.34,1/5,1/5.62,1/6.26] #(1
         0^-3 mmol / L min ): negative rA
```

A.) Determine the Michaelis-Menten parameters (KM and Vmax).

```
In [33]: plt.plot(CA1,rA1)
         from scipy.stats import linregress
         linregress(CA1, rA1)
```

```
Out[33]: LinregressResult(slope=0.2996755415586357, intercept=0.04963294030675208, rva
         lue=0.9998112404402427, pvalue=5.55284440468821e-15, stderr=0.002058909562883
         6132)
```
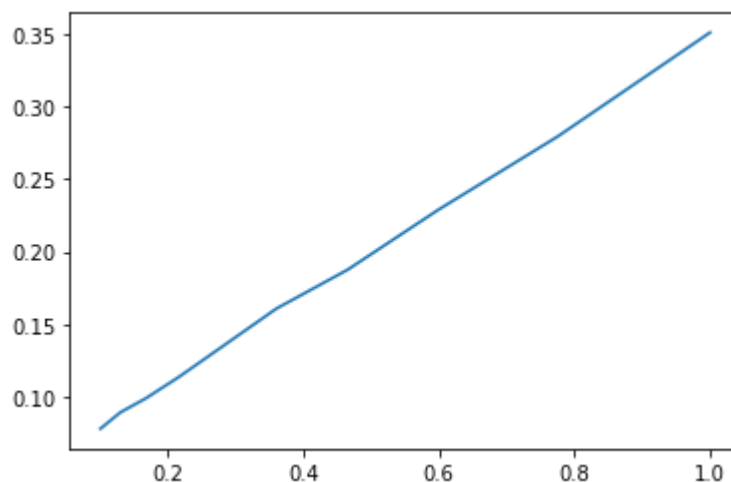
```
In [50]: plt.plot(CA1,rAI1, label = '-r_A,Inhib')
         plt.xlabel("1 / CA")
         plt.ylabel("1 / -rA")
         plt.legend()

         from scipy.stats import linregress
         linregress(CA1, rAI1)
```

Out[50]: LinregressResult(slope=0.5851620712673345, intercept=0.10375227829019698, rva
         lue=0.9996993865611484, pvalue=3.571535324306301e-14, stderr=0.00507397475288
   9391)
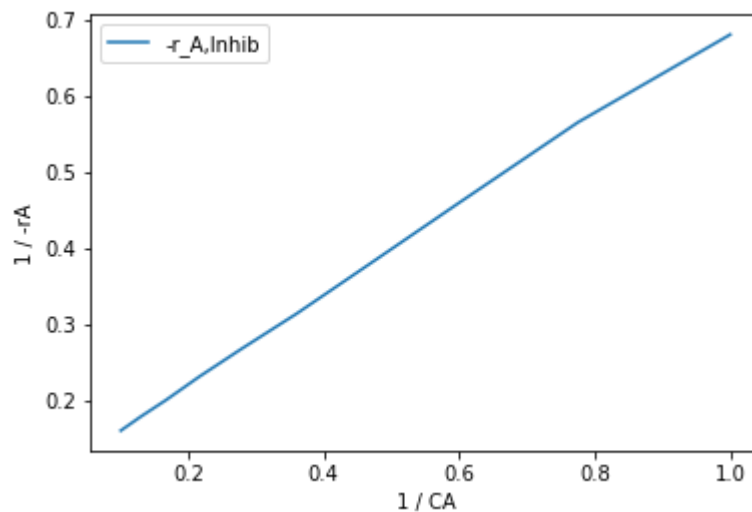

```
In [72]: slope, intercept = np.polyfit(CA1, rA1, 1)
         print(slope, intercept)
         slope, intercept = np.polyfit(CA1, rAI1, 1)
         print(slope, intercept)
```

```
0.29967554155863574 0.04963294030675205
0.5851620712673348 0.10375227829019687
```

For Noncompetitive inhibition KM will be unaffected, while Vmax will be reduced.

For Noncompetitive inhibition the intersection of these lines will be equal to (-1/KM)

```
In [88]: x = np.linspace(-5,5,100)
         y = 0.29967554155863574*x+0.049632940306752055
         plt.plot(x, y, label='-r_A')
         y1 = 0.5851620712673348*x+0.10375227829019687
         plt.plot(x, y1, label='-r_A,Inhib')
         plt.title('Graph 1/-rA vs 1/CA')
         plt.xlabel("1 / CA")
         plt.ylabel("1 / -rA")
         plt.legend(loc='upper left')
         plt.grid()
         plt.show()
```


Graph 1/-rA vs 1/CA
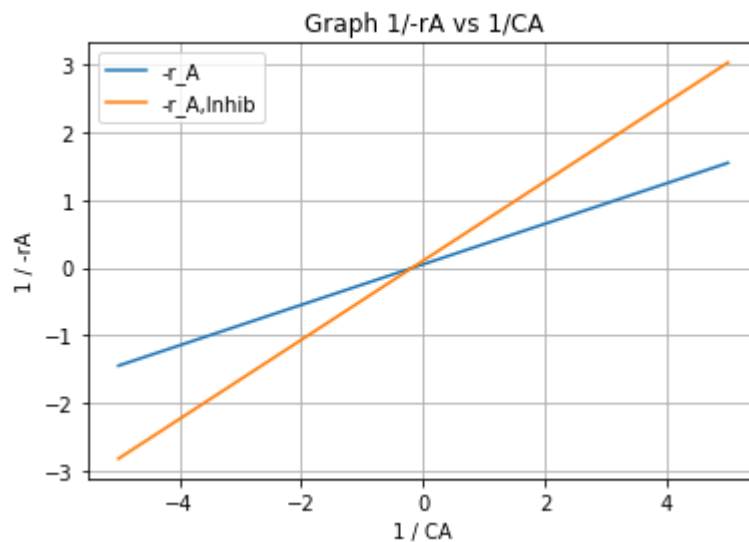
```
In [89]: xi = (0.049632940306752055-0.10375227829019687) / (0.5851620712673348-0.29967
         54155863574)
         yi = 0.29967554155863574 * xi + 0.049632940306752055

         print('(xi,yi), intercept',xi,yi)
```

(xi,yi), intercept -0.18956879695398024 -0.0071761915830510295

(-1/KM) = -0.18956879695398024

KM = 5.2751297474486805

KM = 5.275 **

slope = 0.585 = (KM/Vmax)(1+(I)/KI)

0.585 = (KM/Vmax)(1+(I)/KI)

intercept = 0.103 = (1/Vmax)(1+(I)/KI)

intercept = .04963 = 1/Vmax

intercept = 0.103 = (1/Vmax)(1+(I)/KI)

0.103/.04963 = (1/Vmax)(1+(I)/KI) / [1/Vmax]

(1+(I)/KI) = 2.075 **

slope=0.585 = (KM/Vmax)(1+(I)/KI)

0.585 = (5.275/Vmax)(1+(I)/KI)

0.585 = (5.275/Vmax)2.075

0.2819277 = (5.275/Vmax)

Vmax = 18.71047

Vmax = 18.7 **

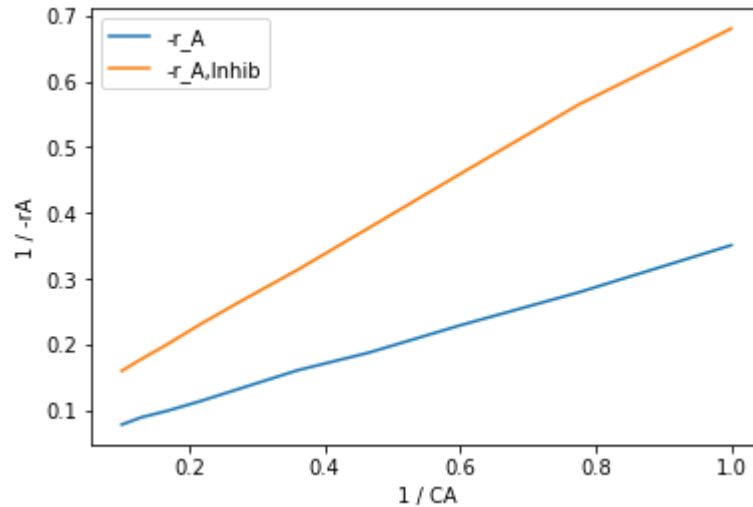# KM = 5.275 **

Vmax = 18.7 **

B.) Using Lineweaver-Burk plots, determine the type of inhibition occurring when the inhibitor I is added to the system.

```
In [81]:  plt.plot(CA1,rA1, label = '-r_A')
          plt.plot(CA1,rAI1, label = '-r_A,Inhib')
          plt.xlabel("1 / CA")
          plt.ylabel("1 / -rA")
          plt.legend()
```

Out[81]: <matplotlib.legend.Legend at 0x2229bb09688>

Because both the intercept has changed and the slope has changed we understand that this is a noncompetitive inhibition

C.) From the slope in your plot in part (b), determine the KI value.

inhibitor I with a concentration of 0.1 mmol/L

0.585 = (KM/Vmax)(1+(I)/KI)

(1+(I)/KI) = 2.075 **

(I)/KI) = 1.075

(0.1 mmol/L)/KI) = 1.075

KI = 1.075/(0.1)

KI = 10.75 mmol/ L