For a given network that is seen in Figure 1, initial kinesis control the activity of three other kinases with concentrations [Y1], [Y2] and Y[3] through weights  $w_1$ ,  $w_2$ ,  $w_3$ ,  $w_4$ ,  $w_5$ ,  $w_6$ . And, [Y1], [Y2] and Y[3] control the activity of Z through weights  $w_7$ ,  $w_8$ ,  $w_9$ .

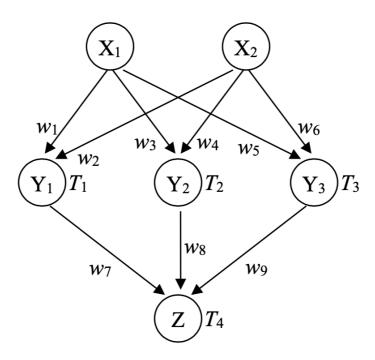


Figure 1: The given network

Firstly, the randomized network parameters, weights and tresholds, are initialized. In addition, the multi-layer perceptron network is defined.

```
from matplotlib import colors
import matplotlib.pyplot as plt
import matplotlib
import numpy as np
from random import random
# generates 101-element array from 0 to 1.01 in 0.01 increments
x = np.arange(0, 1.01, 0.01)
# creates 2-D coordinate arrays, given one-dimensional coordinate arrays x1, x2
X1, X2 = np.meshgrid(x, x)
# random weights and tresholds
w = np.random.normal(loc=0.0, scale=1.0, size=9)
T = np.random.normal(loc=0.0, scale=1.0, size=4)
# multi-layer perceptron network
Y1= (w[0] * X1 + w[1] * X2 >= T[0])
Y2 = (w[2] * X1 + w[3] * X2 >= T[1])
Y3 = (w[4] * X1 + w[5] * X2 >= T[2])
```

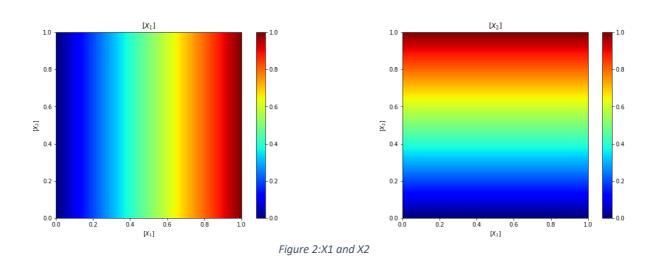
```
And X1 and X2 can be seen in Figure 2.

fig=plt.figure(figsize=(20,6))
ax=fig.add_subplot(1,2,1)
h=ax.imshow(X1,origin='lower',extent=[0,1,0,1],cmap=matplotlib.cm.jet)
ax.set_xlabel('$[X_1]$')
ax.set_ylabel('$[X_2]$')
ax.set_title('$[X_1]$')
fig.colorbar(h)

ax=fig.add_subplot(1,2,2)
h=ax.imshow(X2,origin='lower',extent=[0,1,0,1],cmap=matplotlib.cm.jet)
ax.set_xlabel('$[X_1]$')
ax.set_xlabel('$[X_2]$')
ax.set_title('$[X_2]$')
```

Z = (w[6] \* Y1 + w[7] \* Y2 + w[8] \* Y3 >= T[3])

fig.colorbar(h)



## Besides, the desired response of this network is as shown in Figure 2.

```
# desired response
border =
np.logical_or(np.logical_and(X1>=0.3,X1<=0.6),np.logical_and(X2>=0.2,X2
<=0.7))

fig, ax = plt.subplots()
plt.imshow(border,cmap='OrRd',interpolation='None',extent=[0,1,0,1])
plt.xlabel('x1')
plt.ylabel('x2')
plt.grid(linestyle='--')
plt.show()</pre>
```

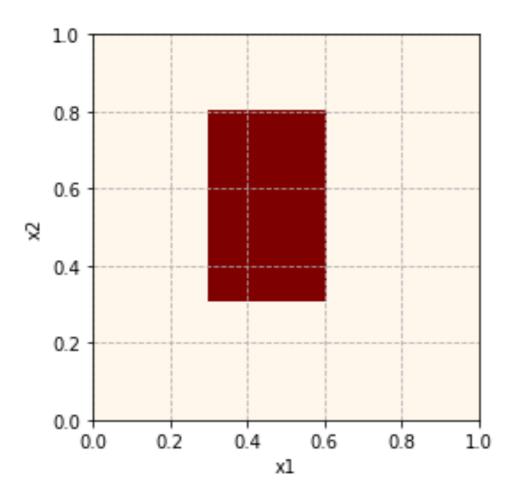


Figure 3: Desired response of the network

And the initial response characteristic of the system can be obtained by getting the difference between current response and desired respones.

```
# initial response characteristic of the system
err=np.sum(border != Z)
print(100*err/(len(border)**2))
```

The error rate is approximately 23.3% for a sample given in Figure 3.

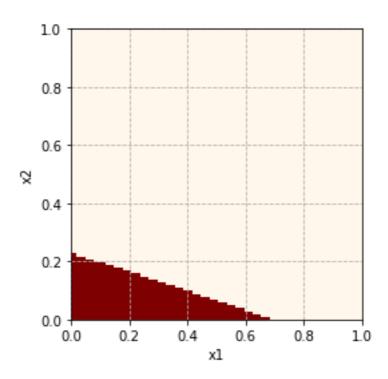


Figure 4:Initial response of the network

## As requested, iteration is applied for the best response.

```
#initialization for the good variables
w_new=w
T new=T
Z_new=Z
i =0
#iterate for the best scenario
while i<100000:
    w =np.random.normal(loc=w new,scale=1.0,size=9)
    T =np.random.normal(loc=T_new,scale=1.0,size=4)
    \mathtt{Y1=\left(w\left[0\right]\ \star\ X1\ +\ w\left[1\right]\ \star\ X2\ >=\ T\left[0\right]\right)}
    Y2 = (w[2] * X1 + w[3] * X2 >= T[1])
    Y3=(w[4] * X1 + w[5] * X2 >= T[2])
    Z=(w[6] * Y1 + w[7] * Y2 + w[8] * Y3 >= T[3])
    #find the difference
    err_best=np.sum(border != Z)
    #change the condition
    if err_best < err:</pre>
         w_new=w
```

```
T_new=T
    Z_new=Z
    err=err_best

i=i+1

fig, ax = plt.subplots()
plt.imshow(border != Z_new, extent=[0,1,0,1], cmap='OrRd')
plt.title('', fontsize=8)
plt.xlabel('x1')
plt.ylabel('x2')
plt.grid(linestyle='--')
plt.show()

print(100*err/(len(border)**2))
```

The difference between desired and the best response for a sample is given in Figure 4.

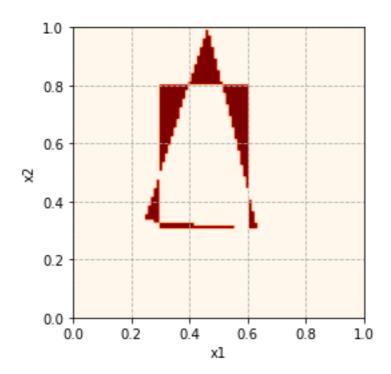


Figure 5: The difference between desired and the best response

The improved rate is approximately 5.38% for the parameters below.

-3.06793
4.27503
-2.7551
2.05969
0.340394
-4.71902
9.20858
-2.26693
-5.98004
-1.94117
2.41218
-5.64457
-4.45549

The whole code can be accessed in Colab Notebook<sup>1</sup>.

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 $<sup>^{1}\,\</sup>underline{\text{https://colab.research.google.com/drive/1k4pYShZHtdzolLPCoG1Gf\_EFIC06KcsE\#scrollTo=b98JLk0merAQ}$