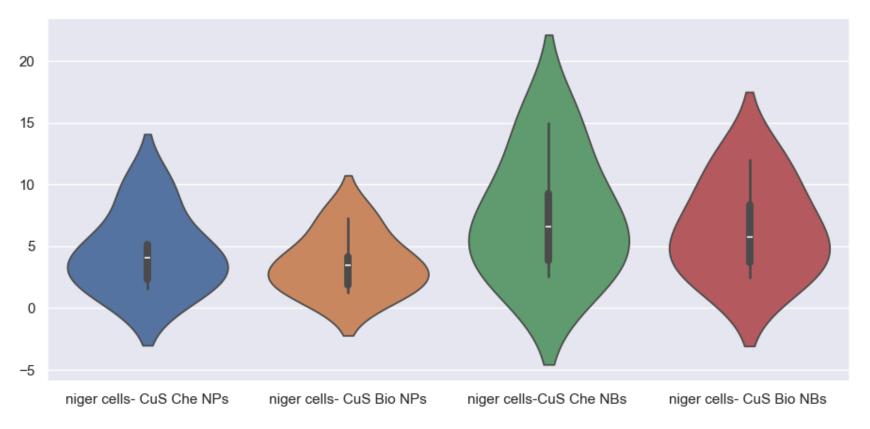
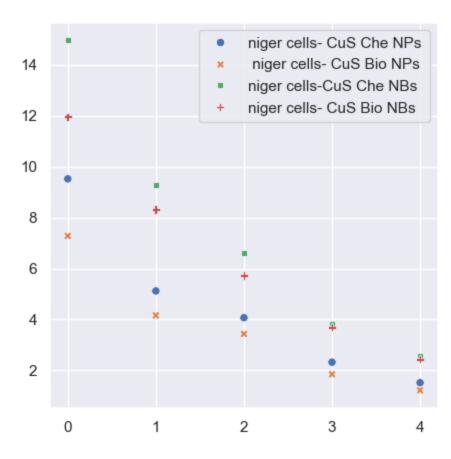
```
# impoting necessary libraries
In [45]:
          import numpy as np
          import pandas as pd
          import matplotlib.pyplot as plt # visualizing data
          %matplotlib inline
          import seaborn as sns
          # importing the csv file
In [46]:
          df = pd.read_csv(r'C:\Users\hp\Desktop\bio Project\1-Amylase.csv',encoding= 'unicode_escape')
In [47]:
          # Description of the Loaded data
          df.describe()
Out[47]:
                 niger cells- CuS Che NPs niger cells- CuS Bio NPs niger cells- CuS Che NBs niger cells- CuS Bio NBs
          count
                                5.00000
                                                       5.000000
                                                                               5.00000
                                                                                                     5.000000
                                4.51040
                                                       3.587800
                                                                               7.44640
                                                                                                     6.426800
          mean
                                                                                                     3.810114
            std
                                3.13833
                                                       2.378137
                                                                               4.93554
            min
                                1.51800
                                                       1.219000
                                                                               2.57400
                                                                                                     2.438000
           25%
                                2.32400
                                                       1.848000
                                                                               3.81800
                                                                                                     3.696000
           50%
                                4.07000
                                                       3.432000
                                                                               6.60000
                                                                                                     5.720000
           75%
                                5.12000
                                                       4.160000
                                                                               9.28000
                                                                                                     8.320000
                                9.52000
                                                       7.280000
                                                                              14.96000
                                                                                                    11.960000
           max
          sns.violinplot(data=df)
In [59]:
          sns.set(rc={'figure.figsize':(11,5)})
```



In [35]: sns.scatterplot(data=df)
sns.set(rc={'figure.figsize':(3,3)})



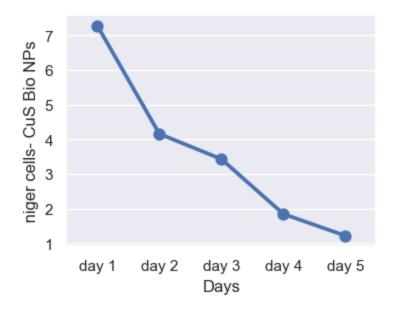
```
In [37]: df = df.groupby(['Days'], as_index=False)['niger cells- CuS Che NPs'].sum().sort_values(by='niger cells- CuS Che NPs
sns.set(rc={'figure.figsize':(4,3)})
sns.pointplot(data = df, x = 'Days',y= 'niger cells- CuS Che NPs')
```

Out[37]: <Axes: xlabel='Days', ylabel='niger cells- CuS Che NPs'>



```
In [66]: df = pd.read_csv(r'C:\Users\hp\Desktop\bio Project\1-Amylase.csv',encoding= 'unicode_escape')
In [68]: df = df.groupby(['Days'], as_index=False)[' niger cells- CuS Bio NPs '].sum().sort_values(by=' niger cells- CuS Bio NPs '].sum().sort_values(by=' niger cells- CuS Bio NPs '].sum().sort_values(by=' niger cells- CuS Bio NPs ')
```

Out[68]: <Axes: xlabel='Days', ylabel=' niger cells- CuS Bio NPs '>



In []: