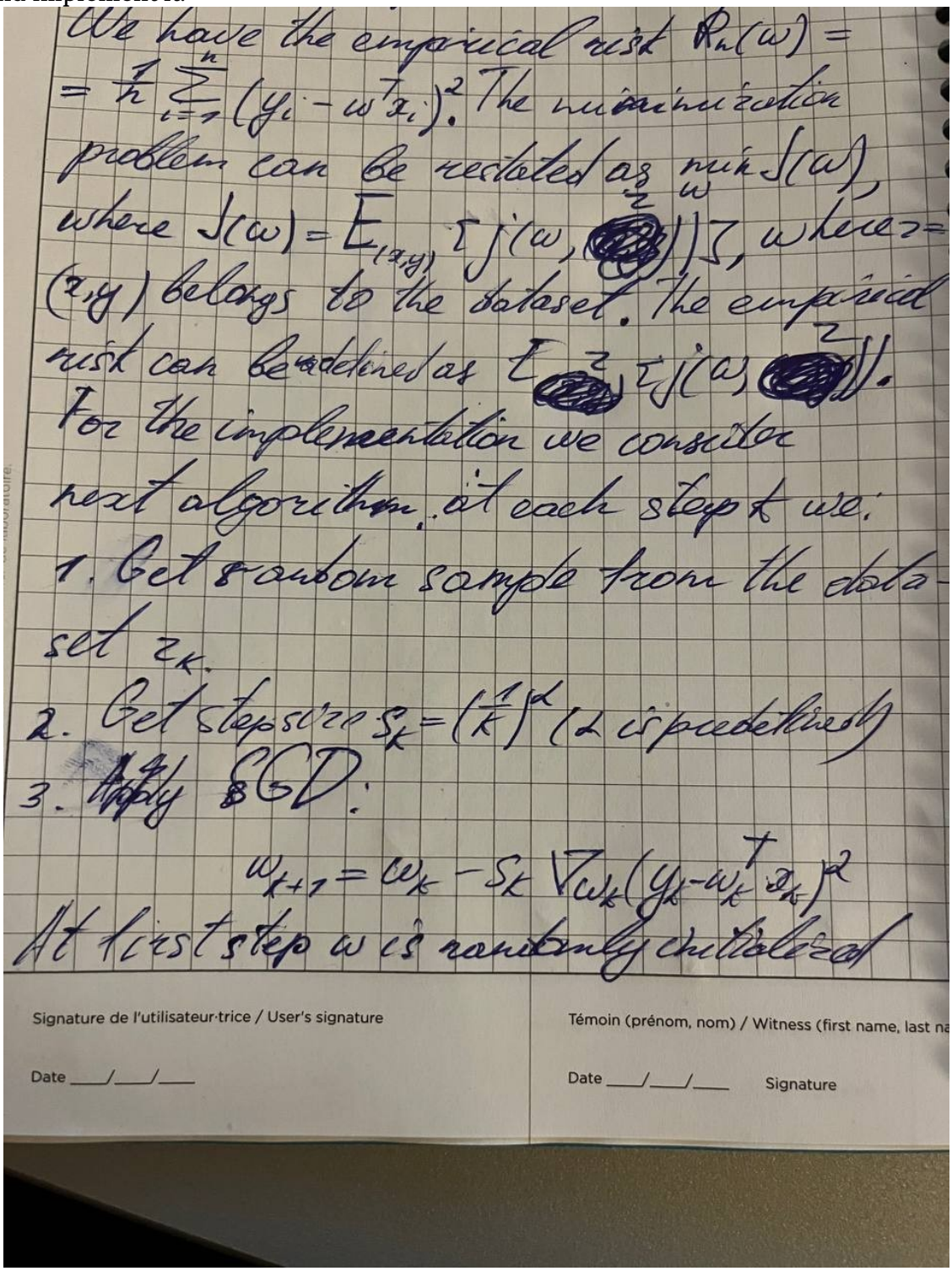
## Exercise 3: Stochastic Gradient Learning in Neural Networks

1. Describe the stochastic gradient descent algorithm for minimizing the empirical risk and implement it.

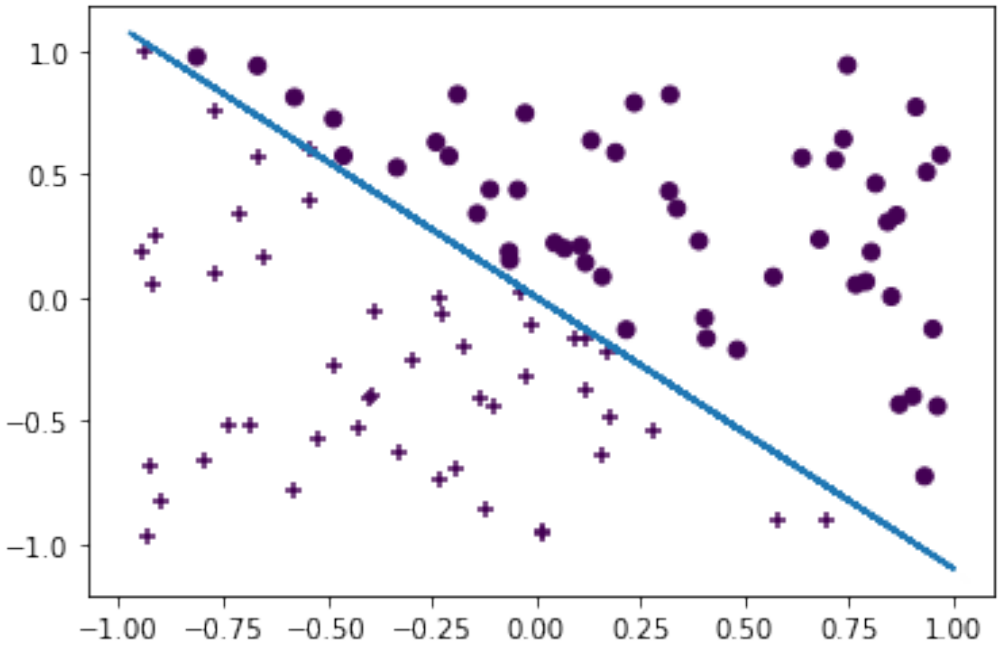



```
import numpy as np
```

```
def sgd(x, y, w, alpha, epochs):
    n = x.shape[0]
    for i in range(epochs):
        k = np.random.randint(1, n)
        e = (1/k)**alpha
        w = w - e*2*(-(y[k-1] - np.dot(w, x[k-1,:])) * x[k-1,:])
        w = w/np.linalg.norm(w)
    return(w)
```

1. Sample a set of observations $\{z_i\}_{i=1}^n$ by generating a collection of random points $x_i$ of $R^2, w \in R^2$ seen as the normal vector of an hyperplane, a straight line here, and assigning the label $y_i$ according to the side of the hyperplane the point $x_i$ is.

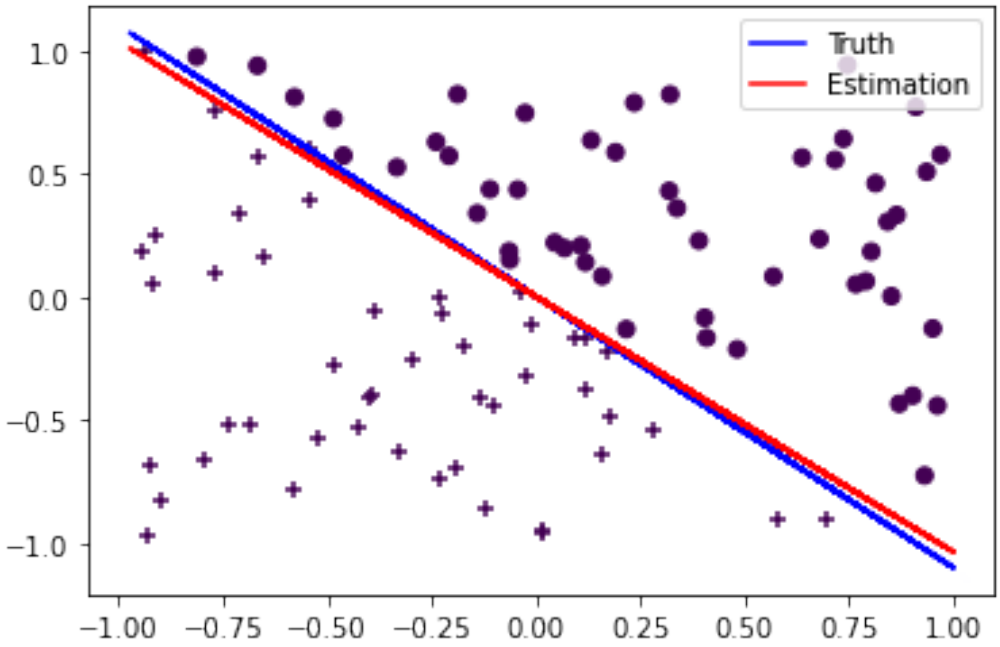
```
import matplotlib.pyplot as plt

n = 100
x = np.random.uniform(-1, 1, (n, 2)) #we can't sample from RxR,
because numpy has restrictions so we will do it in [-1, 1]x[-1, 1]
w = np.random.uniform(-1, 1, (2,))
y = np.sign(np.dot(x, w))
x1 = x[(y.reshape(n,)>0), :]
x2 = x[(y.reshape(n,)<0), :]
t = np.array(np.random.uniform(-1, 1, (n, 1)))
plt.plot(t,-w[0]*t/w[1])
plt.scatter(x1[:, 0], x1[:, 1], c=y[(y.reshape(n,)>0)], marker = '+')
plt.scatter(x2[:, 0], x2[:, 1], c=y[(y.reshape(n,)<0)], marker = 'o');
```




1. Test the algorithm you wrote at the first question over these observations. What is the vector $w^*$ estimated ? Is it far from $w$?

```
w_start = np.random.uniform(-1, 1, (2,))
w_start = w_start/np.linalg.norm(w_start)
w_new = sgd(x, y, w_start, alpha = 0.5, epochs=1000)
plt.scatter(x1[:, 0], x1[:, 1], c=y[(y.reshape(n,)>0)], marker = '+');
plt.scatter(x2[:, 0], x2[:, 1], c=y[(y.reshape(n,)<0)], marker = 'o');
plt.plot(t,-w[0]*t/w[1],color='blue', label = 'Truth')
plt.plot(t,-w_new[0]*t/w_new[1],color='red', label = 'Estimation')
plt.legend();
print("w = ", w)
print("w_new = ", w_new)
print("||w_new - w|| = ", np.linalg.norm(w-w_new))
```

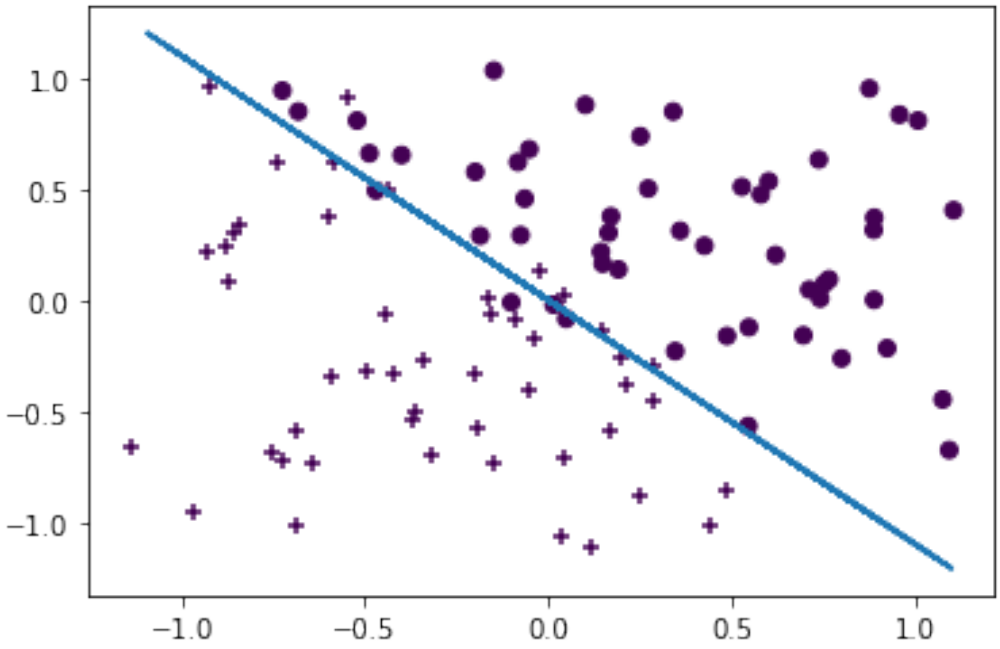
```
w =  [-0.78800457 -0.71518575]
w_new =  [-0.7200128  -0.69396078]
||w_new - w|| =  0.07122766170443
```




As we can see SGD worked pretty well, w almost the same, error is pretty small.

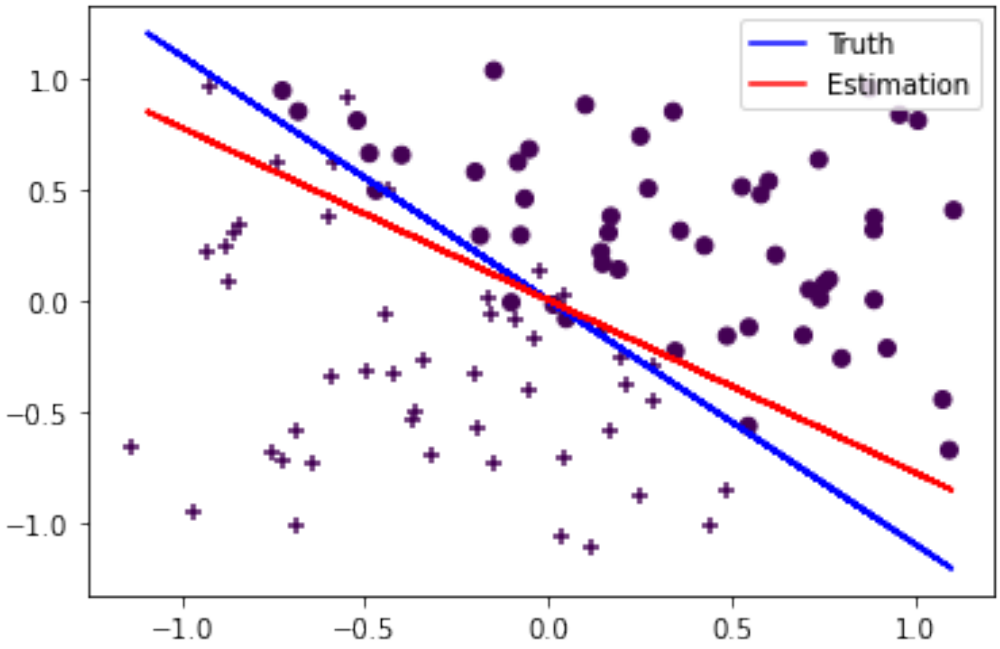
1. Noise your observations $\left(z_i\right)_{i=1}^n$ with an additive Gaussian noise and perform the optimization again. Compare with the result of question three.

```
s = 0.1
x_n = x + np.random.normal(0, s, (n, 2))
x1 = x_n[(y.reshape(n,)>0), :]
x2 = x_n[(y.reshape(n,)<0), :]
t = np.array(np.random.uniform(-1-s, 1+s, (n, 1)))
plt.plot(t,-w[0]*t/w[1])
plt.scatter(x1[:, 0], x1[:, 1], c=y[(y.reshape(n,)>0)], marker = '+')
plt.scatter(x2[:, 0], x2[:, 1], c=y[(y.reshape(n,)<0)], marker = 'o');
```



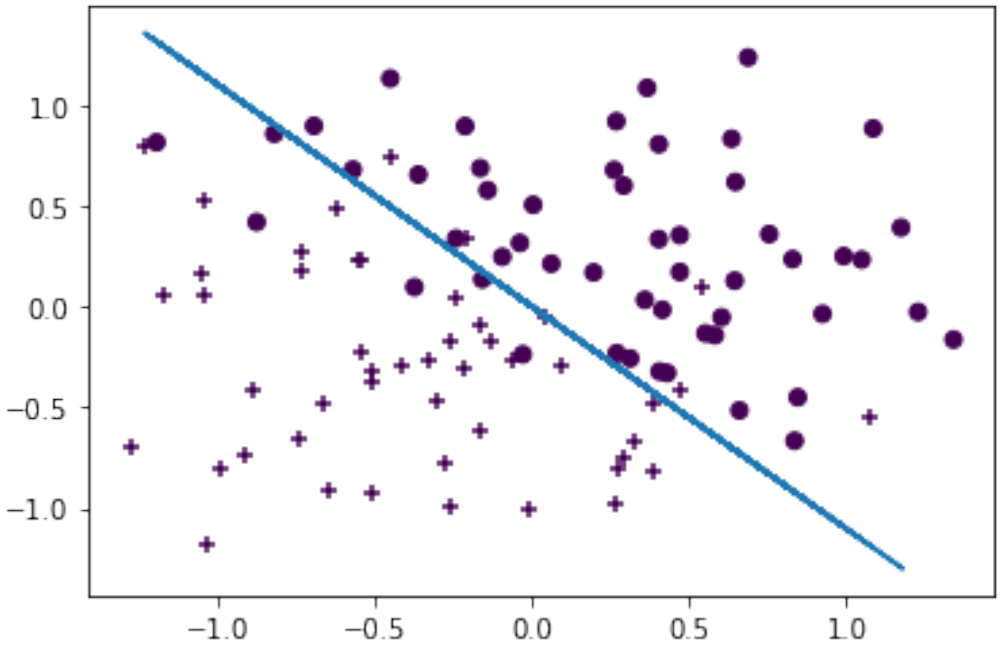

```
w_start = np.random.uniform(-1, 1, (2,))
w_start = w_start/np.linalg.norm(w_start)
w_new = sgd(x_n, y, w_start, alpha = 0.5, epochs=1000)
plt.scatter(x1[:, 0], x1[:, 1], c=y[(y.reshape(n,)>0)], marker = '+');
plt.scatter(x2[:, 0], x2[:, 1], c=y[(y.reshape(n,)<0)], marker = 'o');
plt.plot(t,-w[0]*t/w[1],color='blue', label = 'Truth')
plt.plot(t,-w_new[0]*t/w_new[1],color='red', label = 'Estimation')
plt.legend();
print("w = ", w)
print("w_new = ", w_new)
print("||w_new - w|| = ", np.linalg.norm(w-w_new))
```

```
w =  [-0.78800457 -0.71518575]
w_new =  [-0.61429923 -0.78907316]
||w_new - w|| =  0.18876677487892818
```



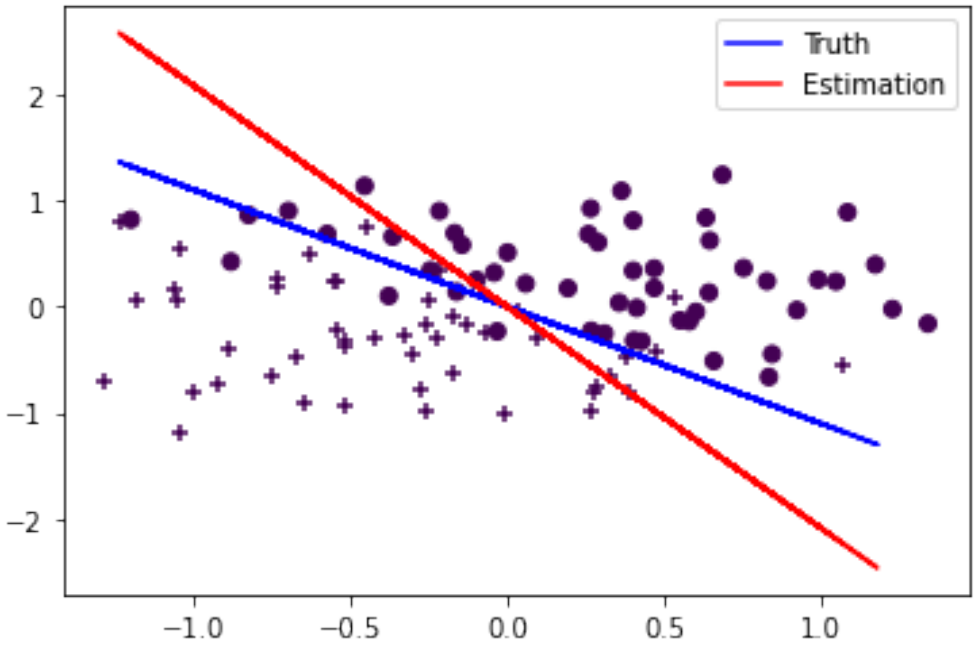

With noisy data we have worse situation. Let's test with larger sigma.

```
s = 0.25
x_n = x + np.random.normal(0, s, (n, 2))
x1 = x_n[(y.reshape(n,)>0), :]
x2 = x_n[(y.reshape(n,)<0), :]
t = np.array(np.random.uniform(-1-s, 1+s, (n, 1)))
plt.plot(t,-w[0]*t/w[1])
plt.scatter(x1[:, 0], x1[:, 1], c=y[(y.reshape(n,)>0)], marker = '+')
plt.scatter(x2[:, 0], x2[:, 1], c=y[(y.reshape(n,)<0)], marker = 'o');
```



```
w_start = np.random.uniform(-1, 1, (2,))
w_start = w_start/np.linalg.norm(w_start)
w_new = sgd(x_n, y, w_start, alpha = 0.5, epochs=1000)
w_new = w_new/np.linalg.norm(w_new)
plt.scatter(x1[:, 0], x1[:, 1], c=y[(y.reshape(n,)>0)], marker = '+');
plt.scatter(x2[:, 0], x2[:, 1], c=y[(y.reshape(n,)<0)], marker = 'o');
plt.plot(t,-w[0]*t/w[1],color='blue', label = 'Truth')
plt.plot(t,-w_new[0]*t/w_new[1],color='red', label = 'Estimation')
plt.legend();
print("w = ", w)
print("w_new = ", w_new)
print("||w_new - w|| = ", np.linalg.norm(w-w_new))
```

```
w =  [-0.78800457 -0.71518575]
w_new =  [-0.90173174 -0.43229605]
||w_new - w|| =  0.3048941662124477
```




The larger the noise, the larger the error. The SGD doesn't really stably perform with noisy data. However, even without noisy data model can produce big errors in some runs.

1. Test the algorithm on the Breast Cancer Wisconsin (Diagnostic) Data Set

```
import pandas as pd
names = ['Sample code number', 'Clump Thickness', 'Uniformity of Cell
Size',
         'Uniformity of Cell Shape', 'Marginal Adhesion', 'Single
Epithelial Cell Size',
         'Bare Nuclei', 'Bland Chromatin', 'Normal Nucleoli',
         'Mitoses', 'Class']
df = pd.read_csv('breast-cancer-wisconsin.data', header=None,
```

```
names=names)
df.head()
```

```
   Sample code number  Clump Thickness  Uniformity of Cell Size  \
0             1000025                5                        1
1             1002945                5                        4
2             1015425                3                        1
3             1016277                6                        8
4             1017023                4                        1

   Uniformity of Cell Shape  Marginal Adhesion  Single Epithelial Cell
Size  \
0                         1                  1
2
1                         4                  5
7
2                         1                  1
2
3                         8                  1
3
4                         1                  3
2

  Bare Nuclei  Bland Chromatin  Normal Nucleoli  Mitoses  Class
0           1                3                1        1      2
1          10                3                2        1      2
2           2                3                1        1      2
3           4                3                7        1      2
4           1                3                1        1      2
```

```
for name in df.columns[1:]:
  print(df[name].unique())
```

```
[ 5  3  6  4  8  1  2  7 10  9]
[ 1  4  8 10  2  3  7  5  6  9]
[ 1  4  8 10  2  3  5  6  7  9]
[ 1  5  3  8 10  4  6  2  9  7]
[ 2  7  3  1  6  4  5  8 10  9]
['1' '10' '2' '4' '3' '9' '7' '?' '5' '8' '6']
[ 3  9  1  2  4  5  7  8  6 10]
[ 1  2  7  4  5  3 10  6  9  8]
[ 1  5  4  2  3  7 10  8  6]
[2 4]
```

```
df['Bare Nuclei'].unique()
```

```
array(['1', '10', '2', '4', '3', '9', '7', '?', '5', '8', '6'],
      dtype=object)
```

There are ? in Bare Nuclei, so we will replace it with np.Nan, then with median.

```
df['Bare Nuclei'] = df['Bare Nuclei'].replace('?', np.nan)
df['Bare Nuclei'].unique()
```

```
array(['1', '10', '2', '4', '3', '9', '7', nan, '5', '8', '6'],
      dtype=object)
```

```
df['Bare Nuclei'] = pd.to_numeric(df['Bare Nuclei'])
df['Bare Nuclei'] = df['Bare Nuclei'].replace(np.nan, df['Bare
Nuclei'].median())
df['Bare Nuclei'].unique()
```

```
array([ 1., 10.,  2.,  4.,  3.,  9.,  7.,  5.,  8.,  6.])
```

```
for name in df.columns[1:]:
  print(df[name].unique())
```

```
[ 5  3  6  4  8  1  2  7 10  9]
[ 1  4  8 10  2  3  7  5  6  9]
[ 1  4  8 10  2  3  5  6  7  9]
[ 1  5  3  8 10  4  6  2  9  7]
[ 2  7  3  1  6  4  5  8 10  9]
[ 1. 10.  2.  4.  3.  9.  7.  5.  8.  6.]
[ 3  9  1  2  4  5  7  8  6 10]
[ 1  2  7  4  5  3 10  6  9  8]
[ 1  5  4  2  3  7 10  8  6]
[2 4]
```

The class column has Benign (2) and Malignant (4). Let's replace 2 with -1 and 4 with 1 and delete code column.

```
df['Class'] = df['Class'] - 3
del df['Sample code number']
df.head()
```

```
   Clump Thickness  Uniformity of Cell Size  Uniformity of Cell Shape
\
0                5                        1                         1

1                5                        4                         4

2                3                        1                         1

3                6                        8                         8

4                4                        1                         1


   Marginal Adhesion  Single Epithelial Cell Size  Bare Nuclei  \
0                  1                            2          1.0
1                  5                            7         10.0
2                  1                            2          2.0
```

```
3                   1                            3          4.0
4                   3                            2          1.0

   Bland Chromatin  Normal Nucleoli  Mitoses  Class
0                3                1        1     -1
1                3                2        1     -1
2                3                1        1     -1
3                3                7        1     -1
4                3                1        1     -1
```

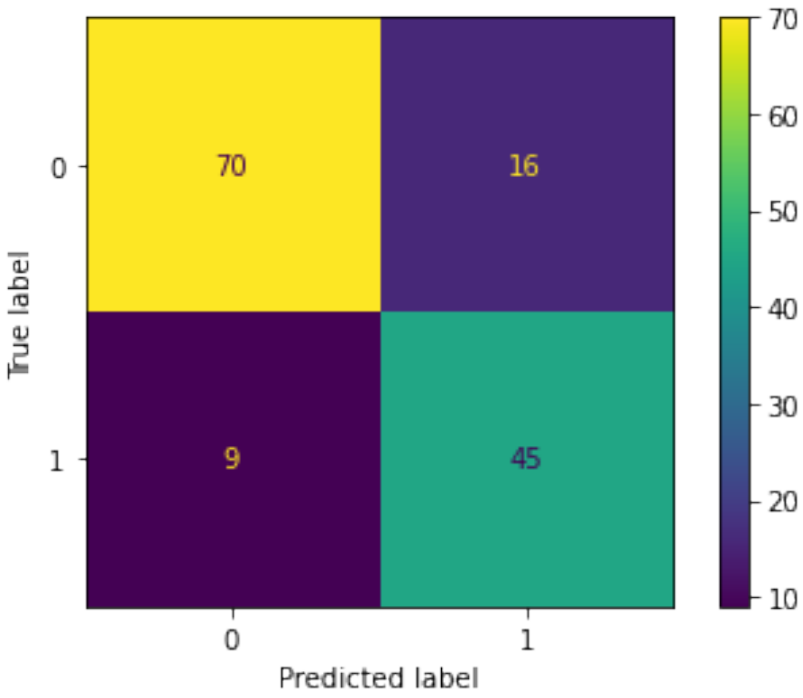
Next we will retrieve x and, normalize train data and split it for testing and training.

```
from sklearn.model_selection import train_test_split
from sklearn.preprocessing import Normalizer

X = df.iloc[:,:-1].values
y = df.iloc[:,-1].values
X_train, X_test, y_train, y_test = train_test_split(X, y, test_size =
0.2, random_state=171)
scaler = Normalizer().fit(X_train)
x_train = scaler.transform(X_train)
scaler = Normalizer().fit(X_test)
x_test = scaler.transform(X_test)
```

Next, we will perfrom the SGD and check it performance with Confusion

```
from sklearn.metrics import accuracy_score, confusion_matrix,
ConfusionMatrixDisplay, f1_score, precision_score, recall_score

w_start = np.random.uniform(-1, 1, (X_train.shape[1],))
w_start = w_start/np.linalg.norm(w_start)
w_new = sgd(X_train, y_train, w_start, alpha=0.6, epochs=10000)
y_new = [np.sign(i) for i in list(X_test.dot(w_new))]
print('Accuracy = ', accuracy_score(y_test, y_new))
print('Presicion = ', precision_score(y_test, y_new))
print('Recall = ', recall_score(y_test, y_new))
print('F1-score = ', f1_score(y_test, y_new))
ConfusionMatrixDisplay(confusion_matrix(y_test, y_new)).plot();
```

```
Accuracy =  0.8214285714285714
Presicion =  0.7377049180327869
Recall =  0.8333333333333334
F1-score =  0.782608695652174
```




As we can see all scores look descent, accuracy is 82%. Presicion, recall and f1-score on almost the same level 0.8.