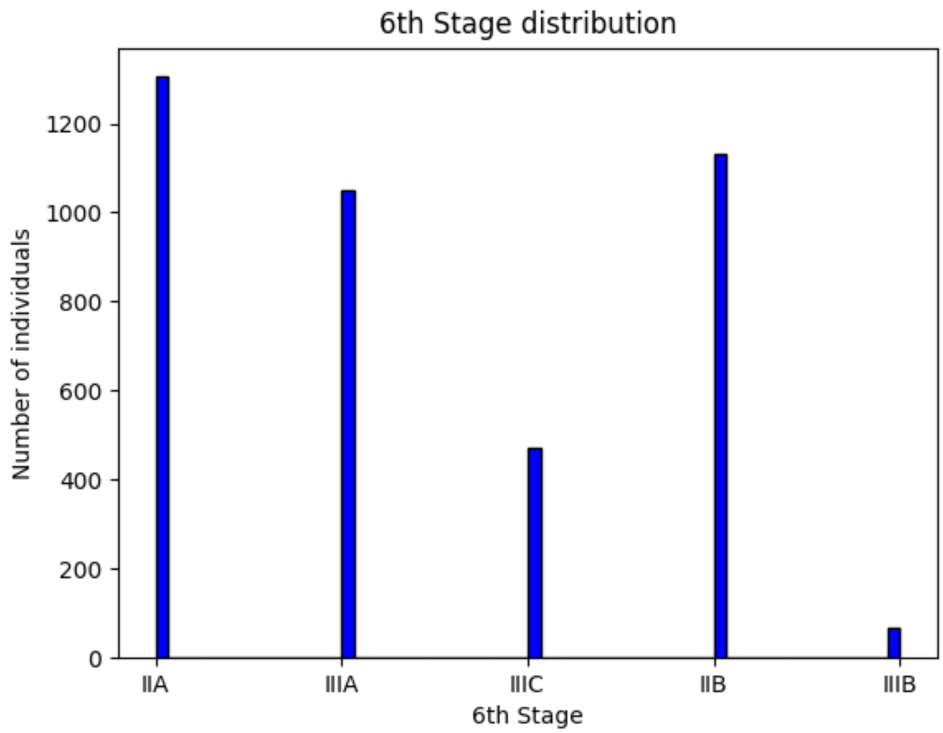
Homework 1

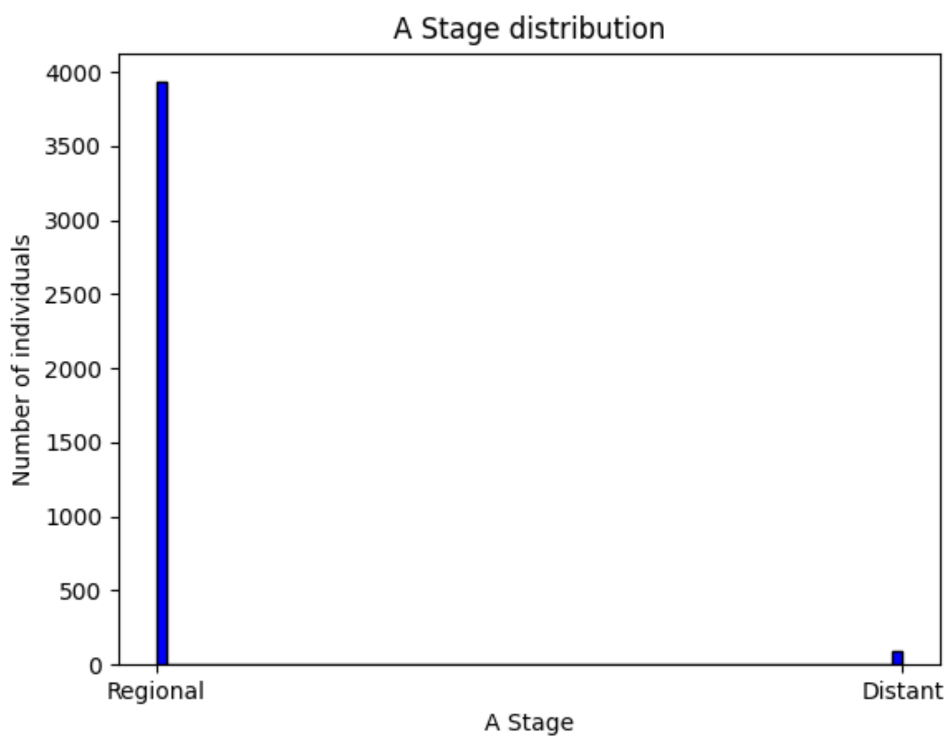
Varun Hoskere

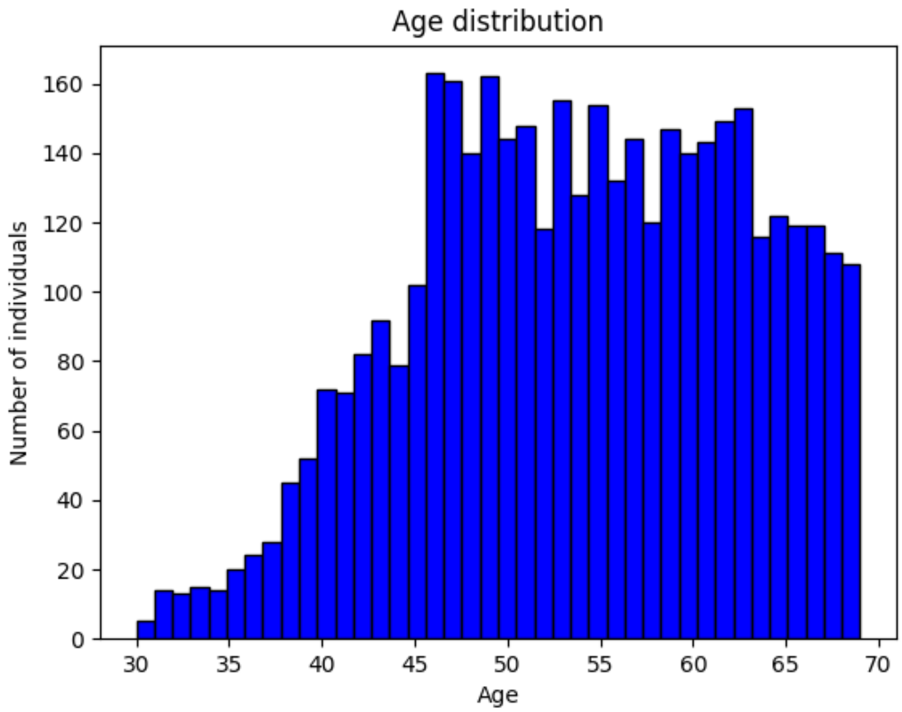
```
import pandas as pd

import matplotlib.pyplot as plt



data = pd.read_csv('Breast_Cancer.csv')

values = []
```

(a)

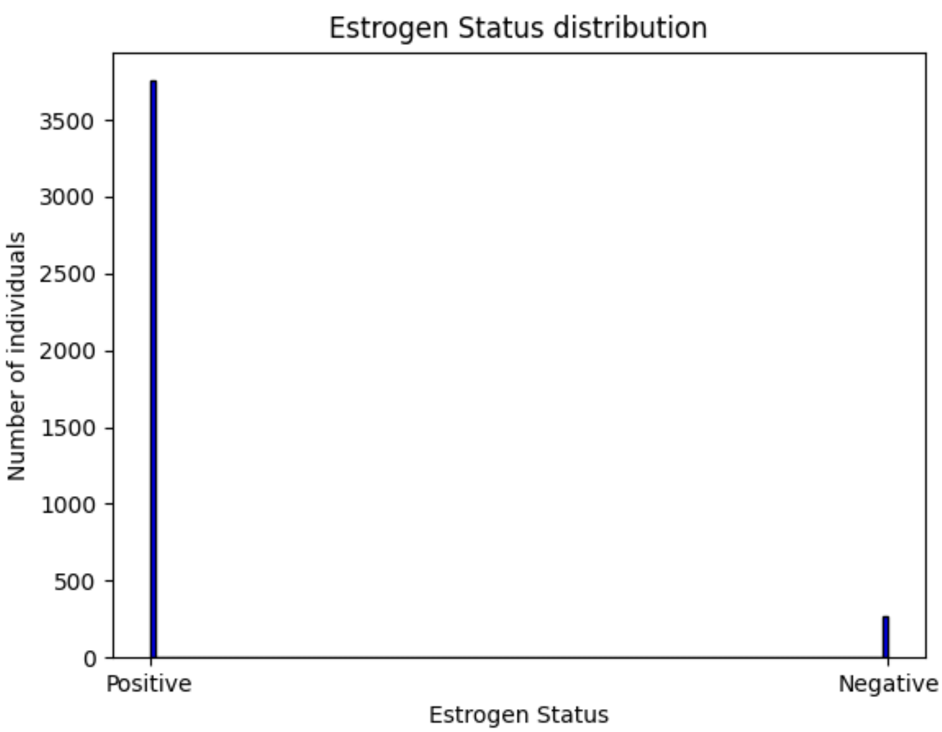
```
def a():
  for variable in list(data.columns):

    for i in data[variable]:
      if i not in values:
        values.append(i)

    plt.hist(data[variable], bins=len(values), color='blue', edgecolor='black')
    plt.title(f'{variable} distribution')
    plt.xlabel(f'{variable}')
    plt.ylabel('Number of individuals')
    plt.savefig(f'{variable} plot.png')
    # plot.show()
  return
```


6th Stage distribution
Number of individuals
0
200
400
600
800
1000
1200
IIA
IIIA
IIIC
IIB
IIIB
6th Stage

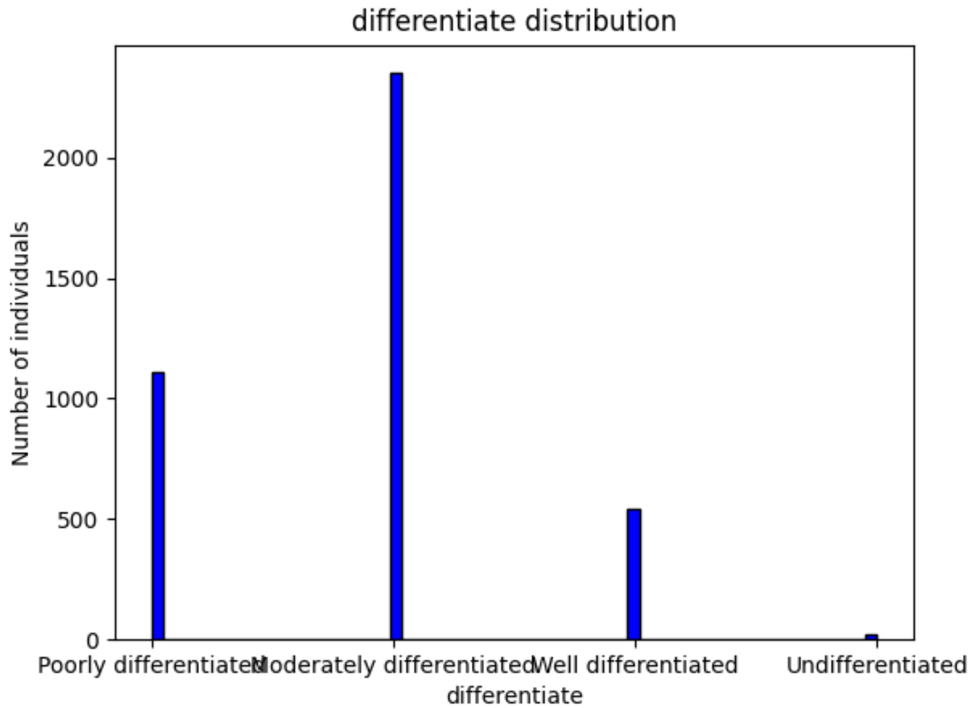

A Stage distribution
Number of individuals
0
500
1000
1500
2000
2500
3000
3500
4000
Regional
Distant
A Stage



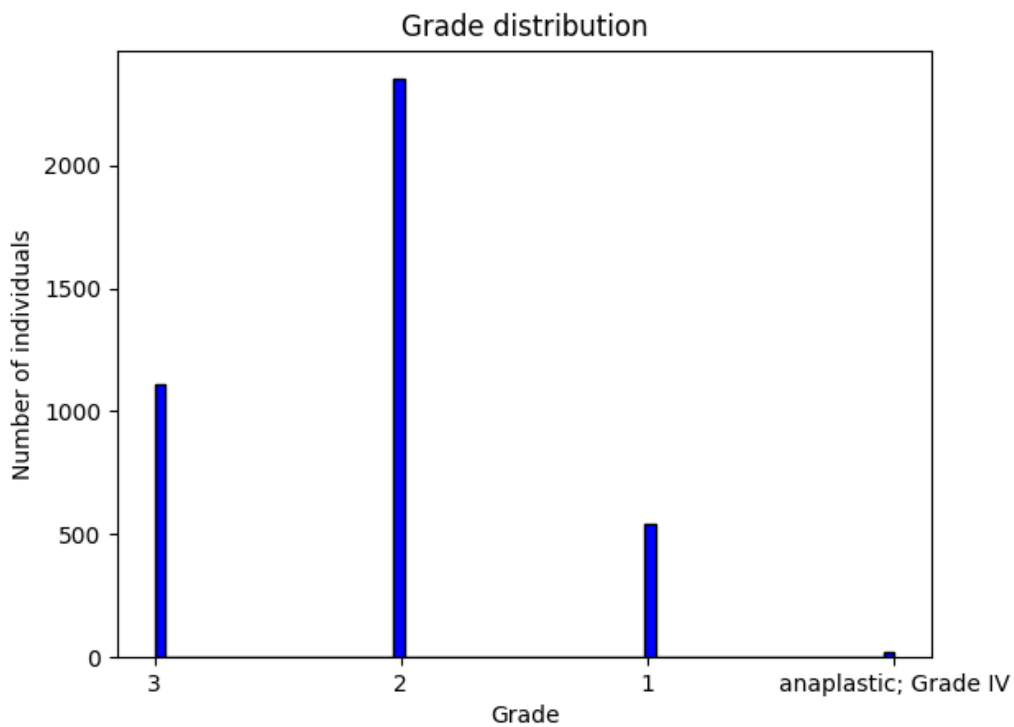
Age distribution
Number of individuals
Age
0
20
40
60
80
100
120
140
160
30
35
40
45
50
55
60
65
70



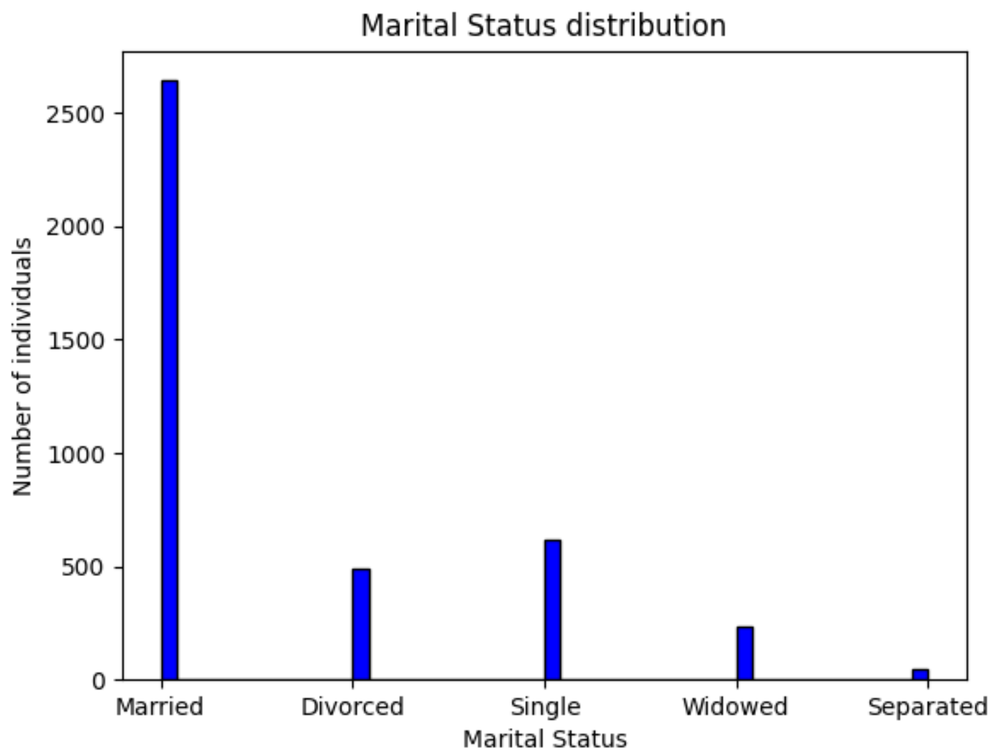
Estrogen Status distribution
Number of individuals
Estrogen Status
0
500
1000
1500
2000
2500
3000
3500
Positive
Negative

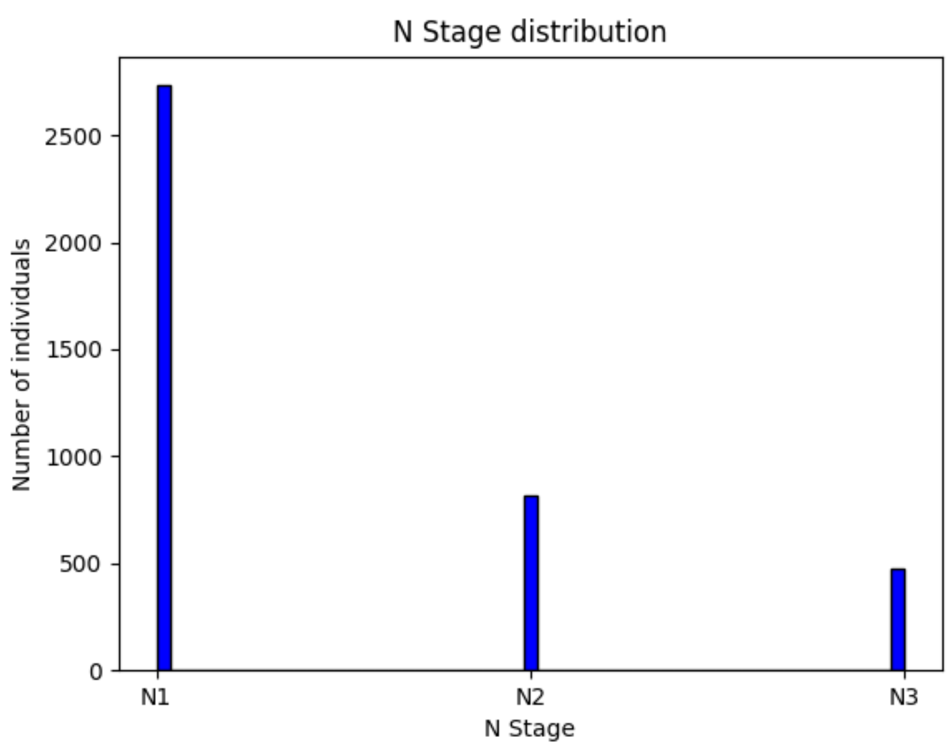


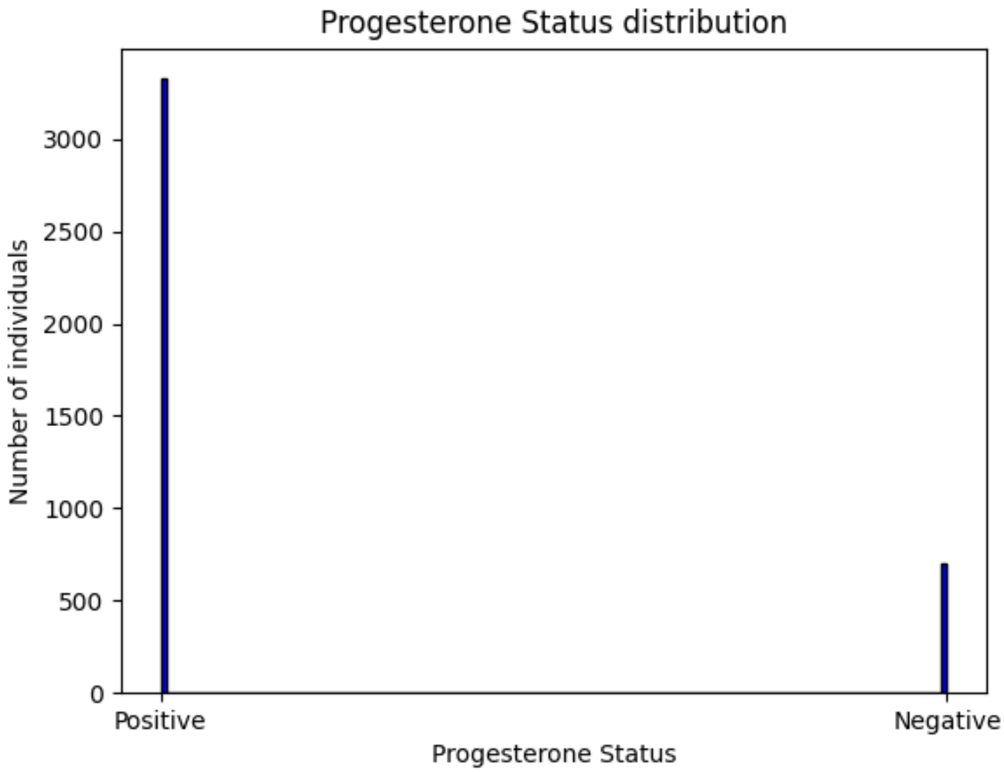
differentiate distribution
Number of individuals
0
500
1000
1500
2000
Poorly differentiated
Moderately differentiated
Well differentiated
Undifferentiated
differentiate

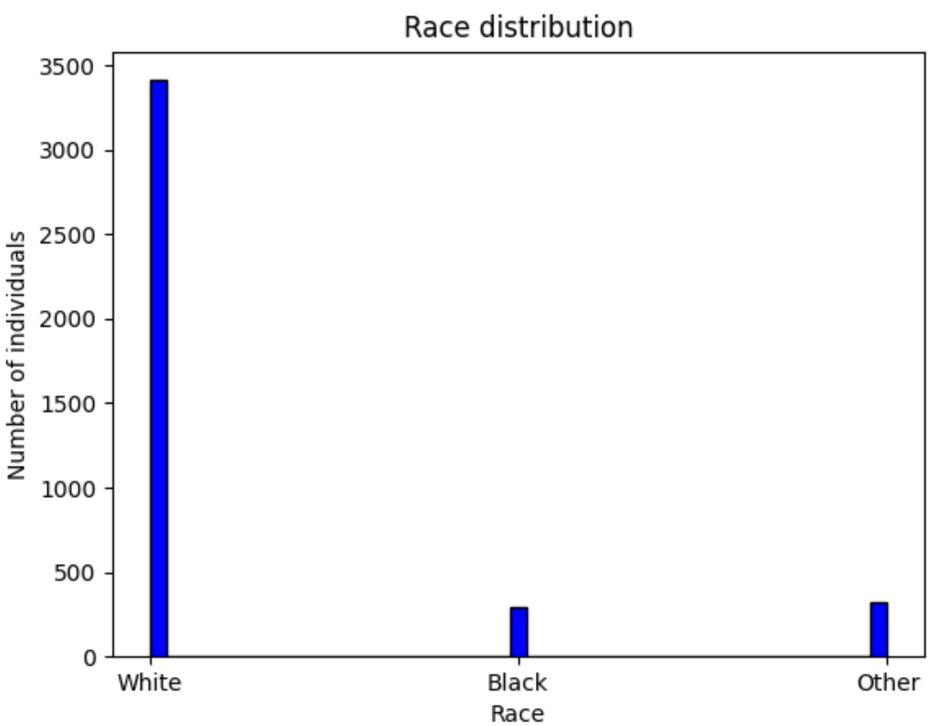


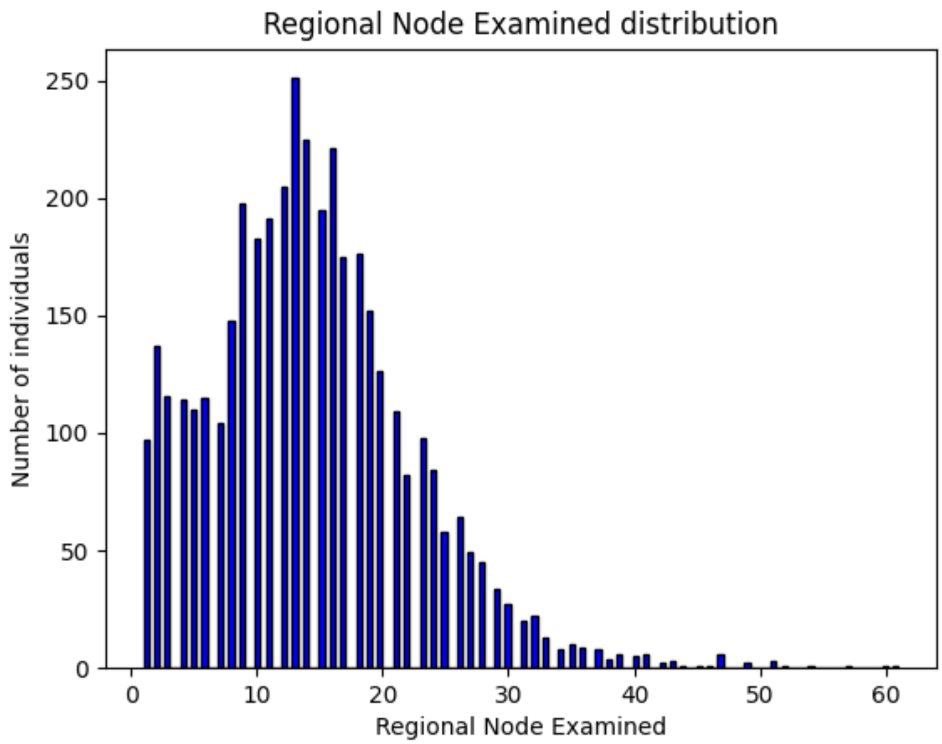
Grade distribution
Number of individuals
0
500
1000
1500
2000
3
2
1
anaplastic; Grade IV
Grade

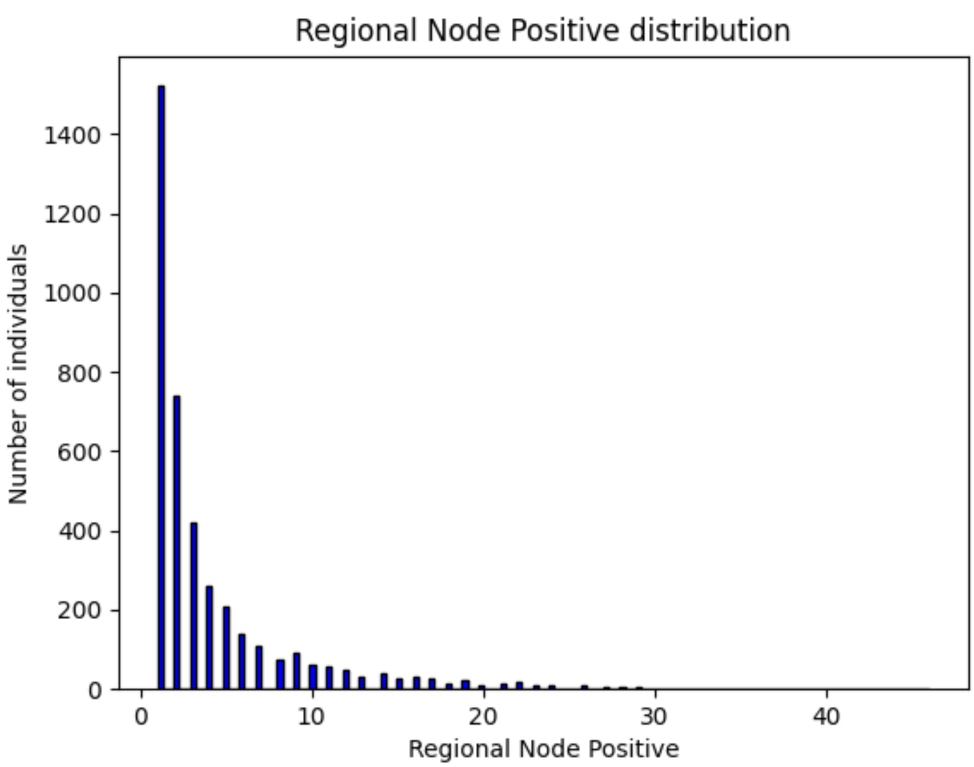

Marital Status distribution
Number of individuals
2500
2000
1500
1000
500
0
Married
Divorced
Single
Widowed
Separated
Marital Status

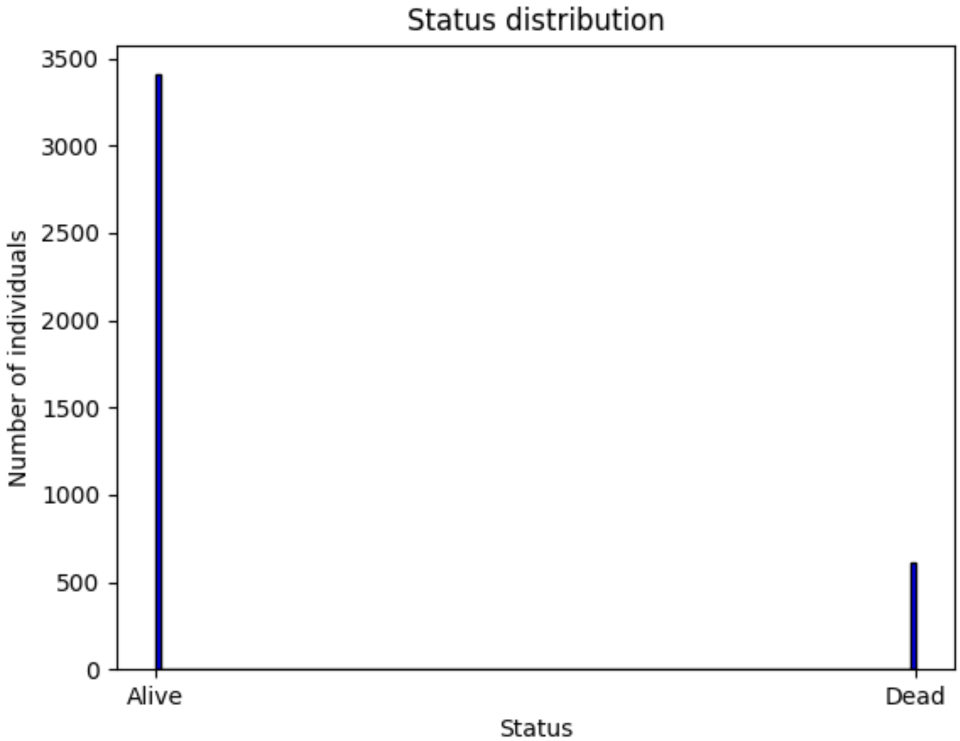

N Stage distribution
Number of individuals
2500
2000
1500
1000
500
0
N1
N2
N3
N Stage


Progesterone Status distribution
Number of individuals
3000
2500
2000
1500
1000
500
0
Positive
Negative
Progesterone Status

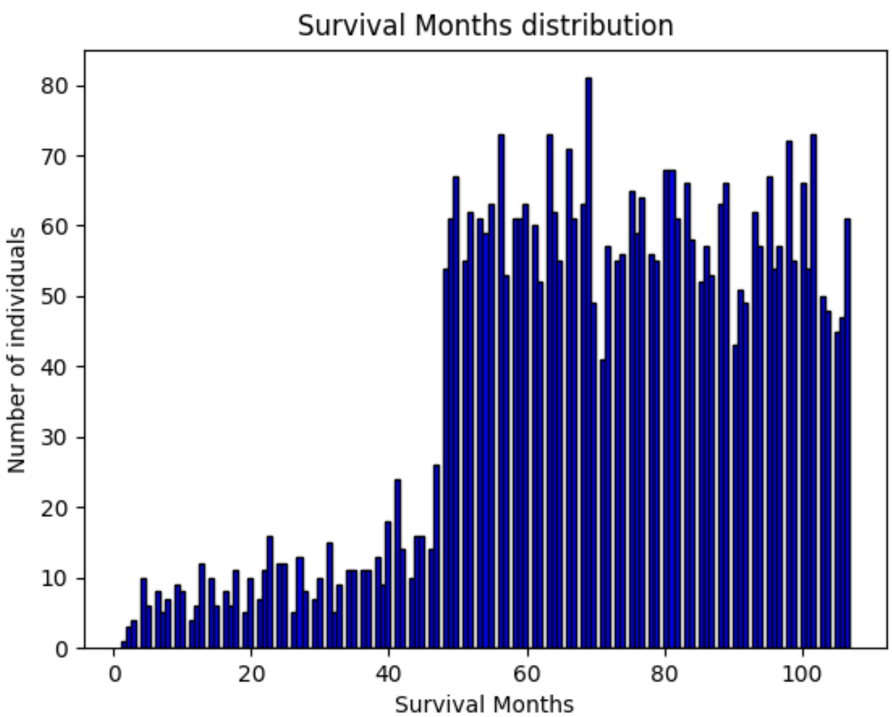

Race distribution
Number of individuals
3500
3000
2500
2000
1500
1000
500
0
White
Black
Other
Race


Regional Node Examined distribution
Number of individuals
Regional Node Examined
0
50
100
150
200
250
0
10
20
30
40
50
60

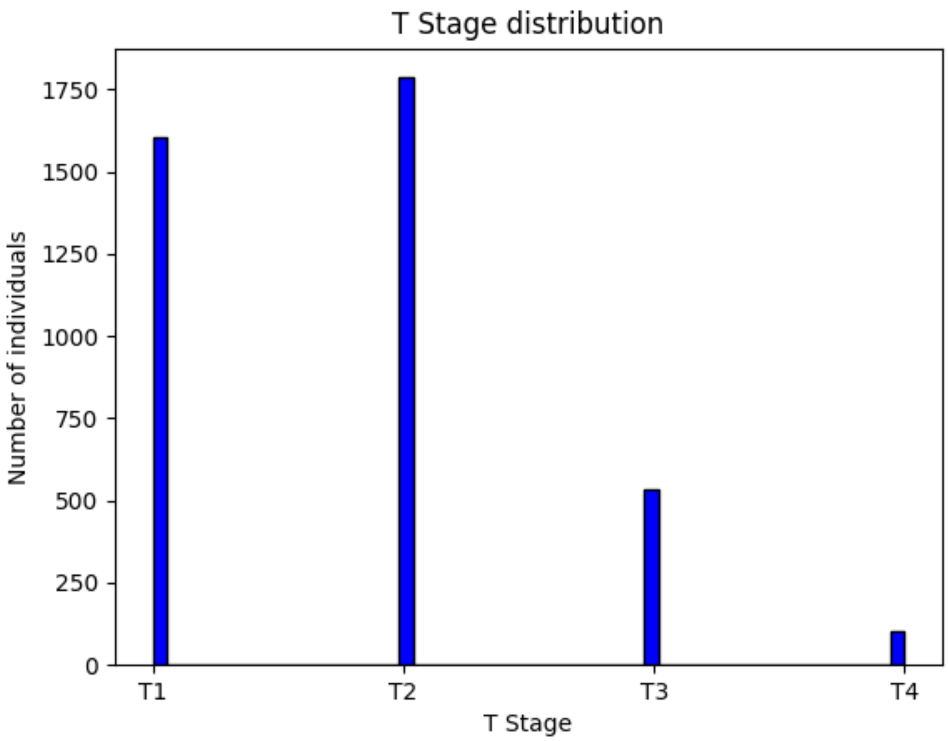

Regional Node Positive distribution
Number of individuals
Regional Node Positive
0
200
400
600
800
1000
1200
1400
0
10
20
30
40

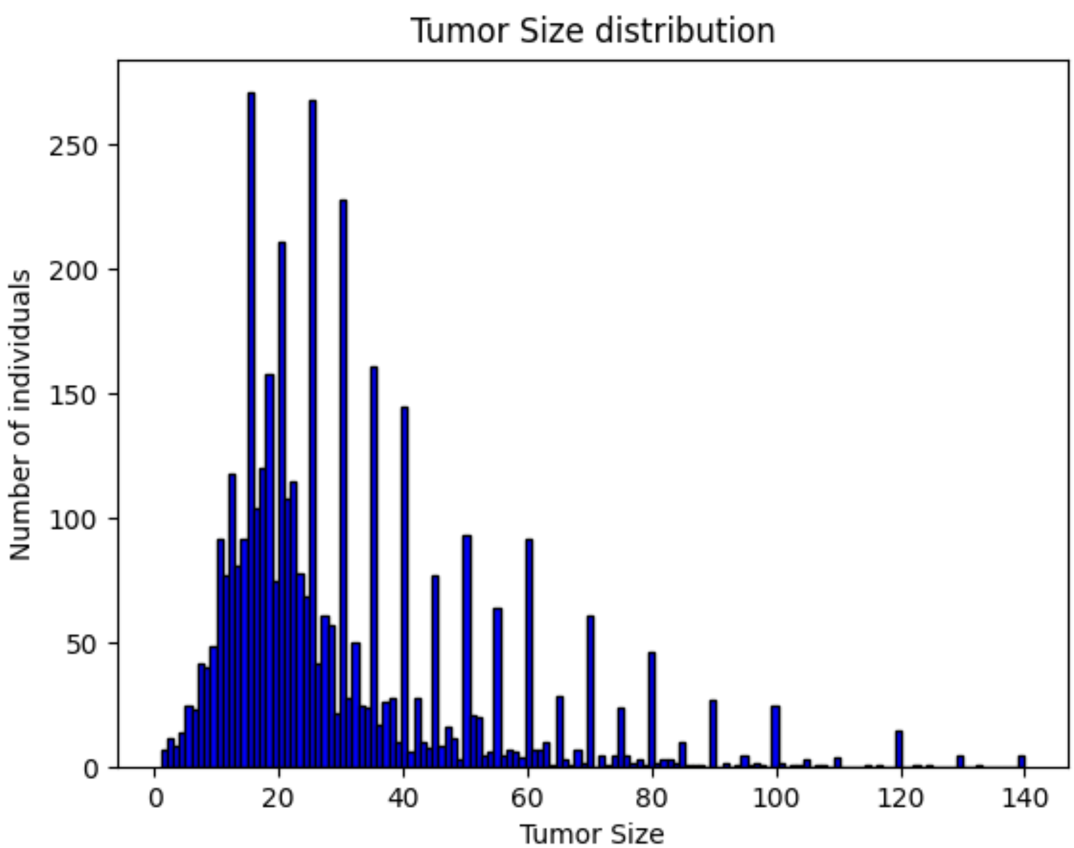


Status distribution
Number of individuals
3500
3000
2500
2000
1500
1000
500
0
Alive
Dead
Status



Survival Months distribution
Number of individuals
80
70
60
50
40
30
20
10
0
0
20
40
60
80
100
Survival Months


T Stage distribution
Number of individuals
0
250
500
750
1000
1250
1500
1750
T1
T2
T3
T4
T Stage

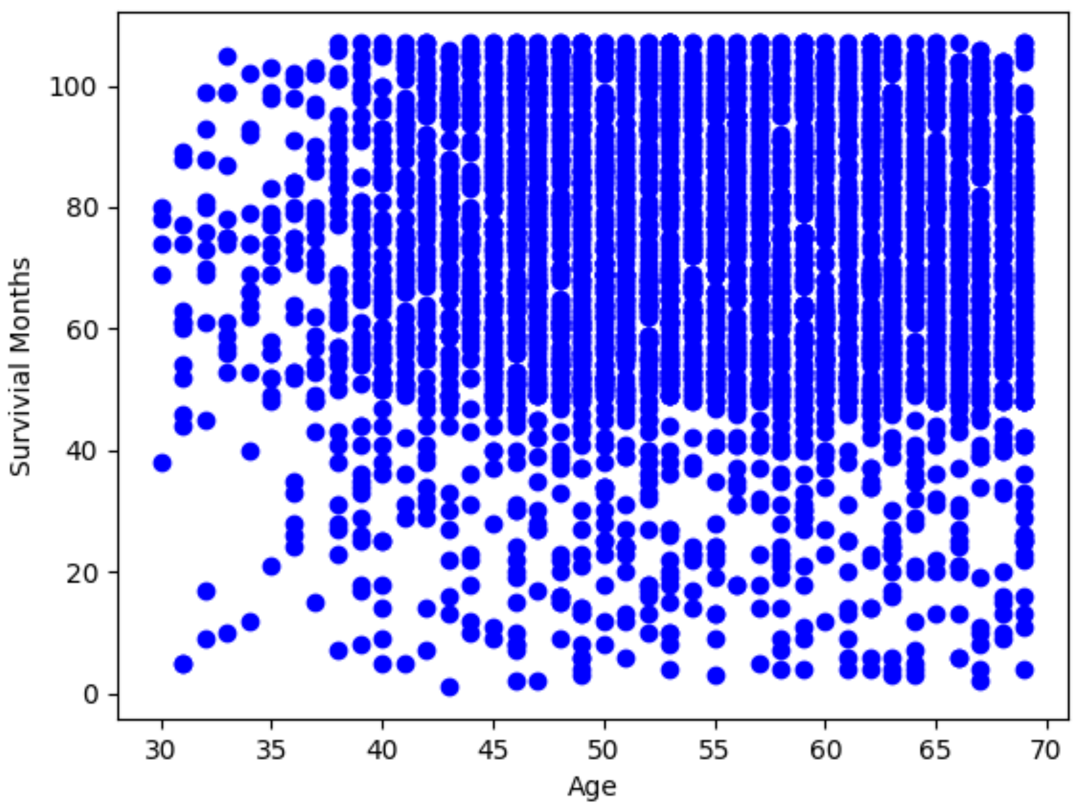

Tumor Size distribution
Number of individuals
0
50
100
150
200
250
0
20
40
60
80
100
120
140
Tumor Size

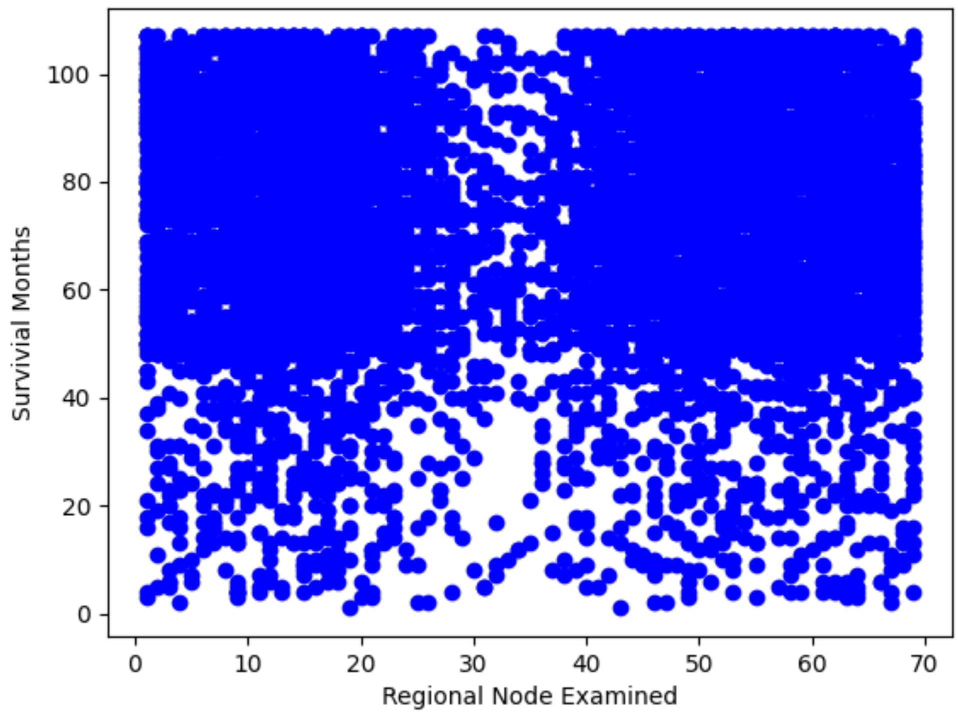
(b)

```
def b():
   # Age, Regional node examined, regional nodde +ve, survival months, tumour size are the continuous variables
   # variables = ['Age', 'Regional Node Examined', 'Regional Node Positive', 'Tumor Size']
   # for var in variables:
   #   plot.scatter(data[var], data['Survival Months'])
   #   plot.savefig(f'{var} vs Surival Months')

   plt.scatter(data['Age'], data['Survival Months'], color='blue')
   plt.xlabel('Age')
   plt.ylabel('Survivial Months')
   # plot.show()
   plt.savefig('Age vs Survival Months')

   plt.scatter(data['Regional Node Examined'], data['Survival Months'], color='blue')
   plt.xlabel('Regional Node Examined')
   plt.ylabel('Survivial Months')
   # plt.show()
   plt.savefig('Regional Node Examined vs Survival Months')

   plt.scatter(data['Tumor Size'], data['Survival Months'], color='blue')
   plt.xlabel('Tumor Size')
   plt.ylabel('Survivial Months')
   # plt.show()
   plt.savefig('Tumor Size vs Survival Months')
```

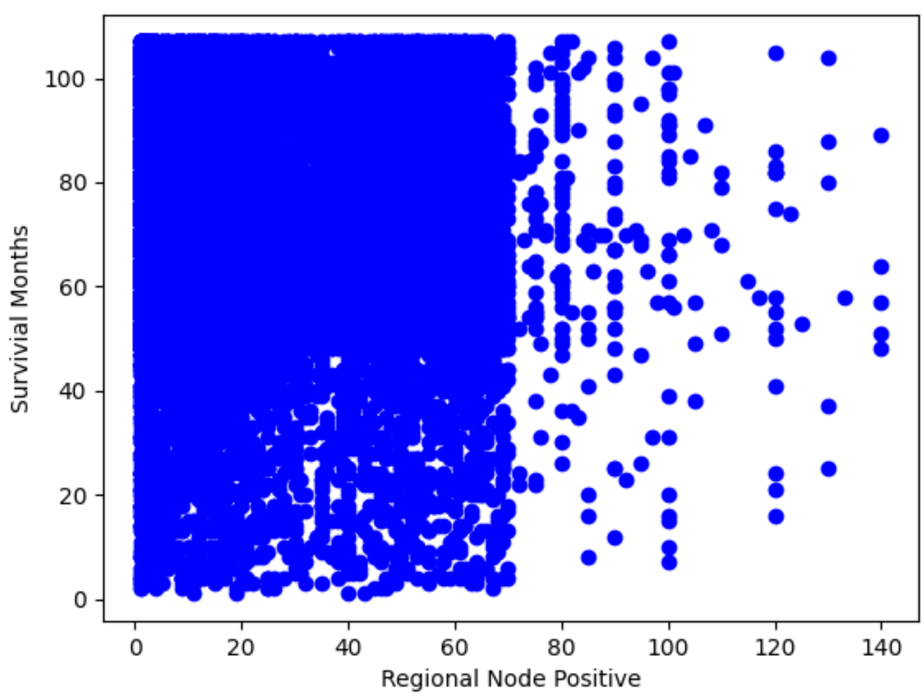
```
    plt.scatter(data['Regional Node Positive'], data['Survival Months'], color='blue')

    plt.xlabel('Regional Node Positive')

    plt.ylabel('Survivial Months')

    plt.savefig('Regional Node Positive vs Survival Months')

    # plt.show()




    return


def bPearsons():

    print("===============")

    print("Pearsons coefficient against Survival Months:")

    print("Age: ", data['Age'].corr(data['Survival Months']))

    print("Regional Node Examined", data['Regional Node Examined'].corr(data['Survival
Months']))

    print("Regional Node Positive", data['Regional Node Positive'].corr(data['Survival
Months']))

    print("Tumor Size", data['Tumor Size'].corr(data['Survival Months']))

    print("===============")

    print()

    return
```

```
varunshankarhoskere@Varuns-MacBook-Pro HW1 % python3 plots.py
================
Pearsons coefficient against Survival Months:
Age:  -0.009389559920833184
Regional Node Examined -0.022054212048869107
Regional Node Positive -0.13521384862427394
Tumor Size -0.08690123938973021
================
```

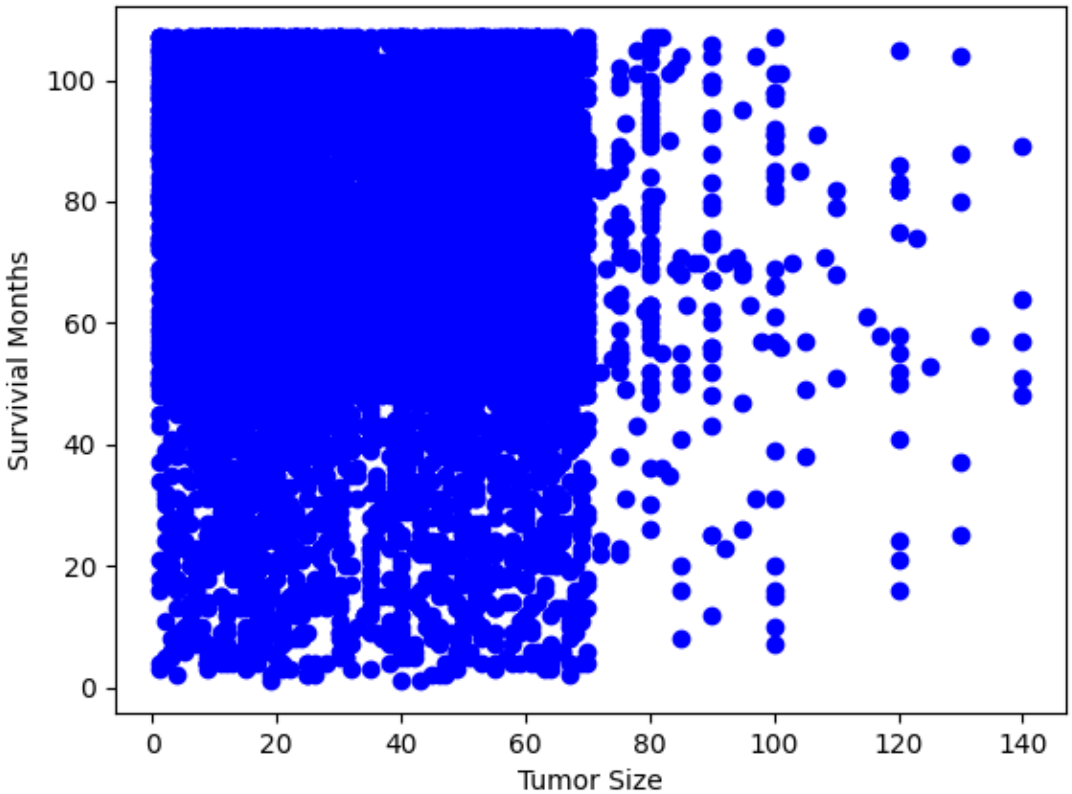




Survivial Months
Regional Node Examined



Survivial Months
Regional Node Positive

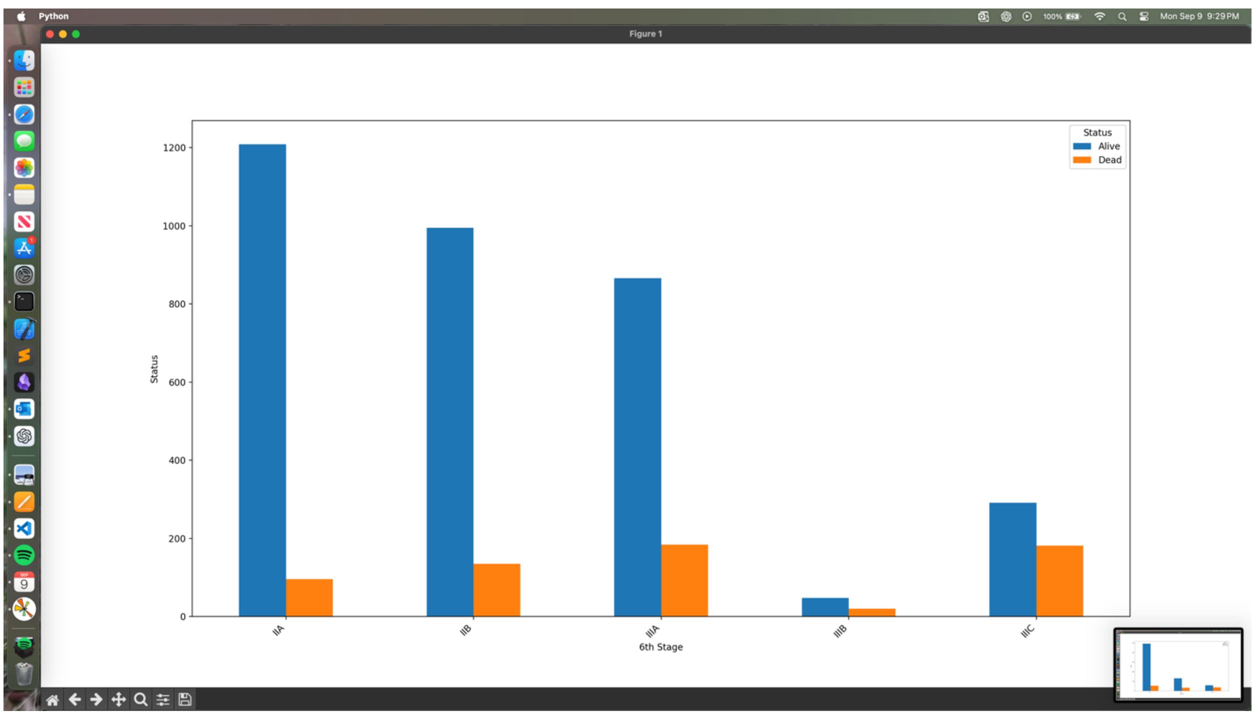


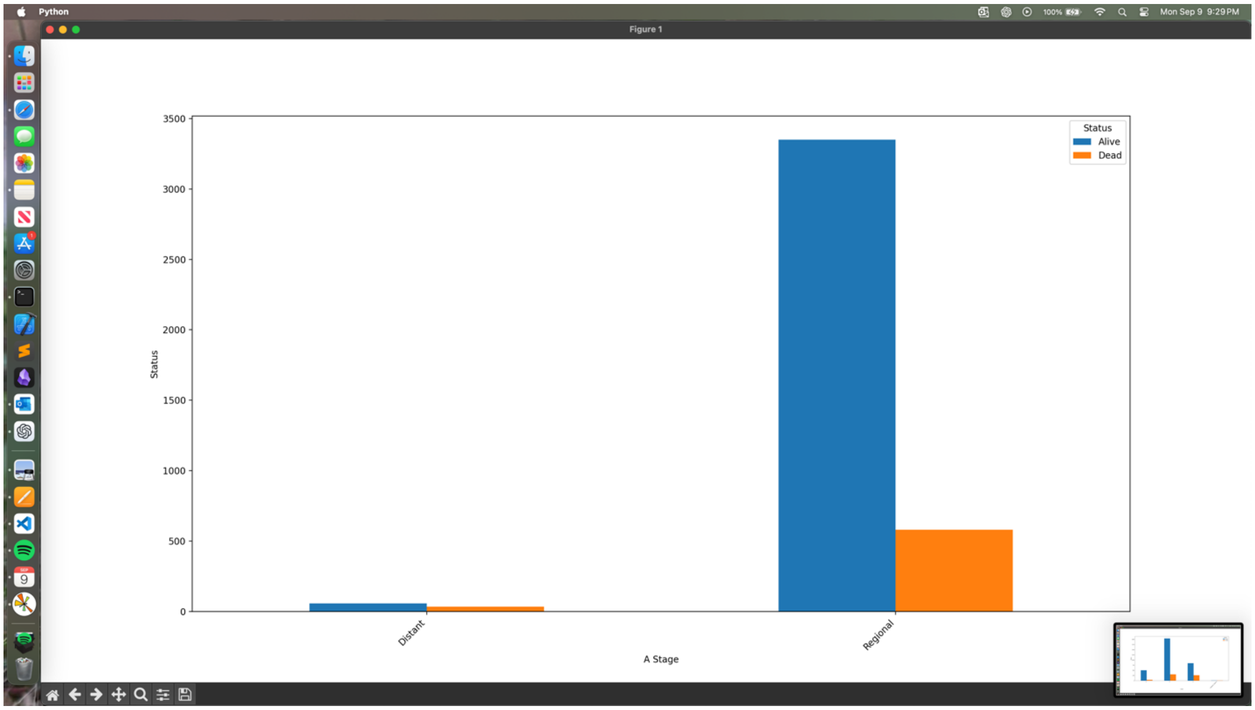
Survivial Months
Tumor Size
0
20
40
60
80
100
120
140

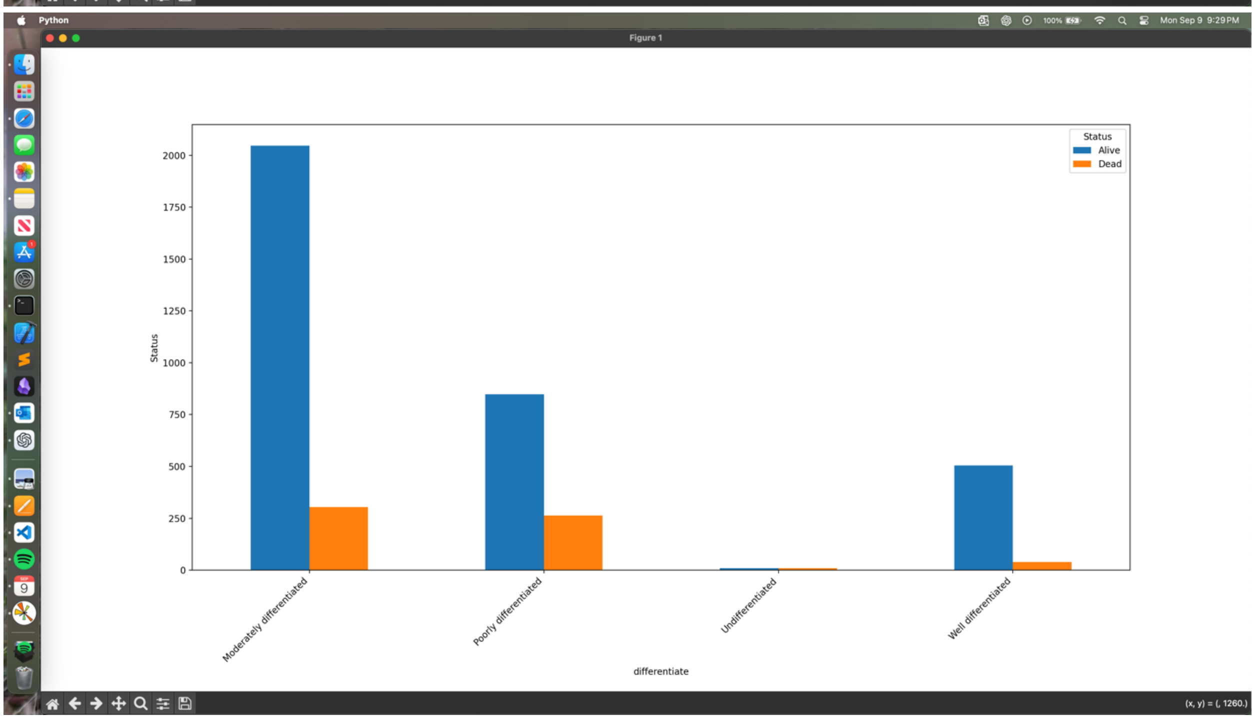
(c)

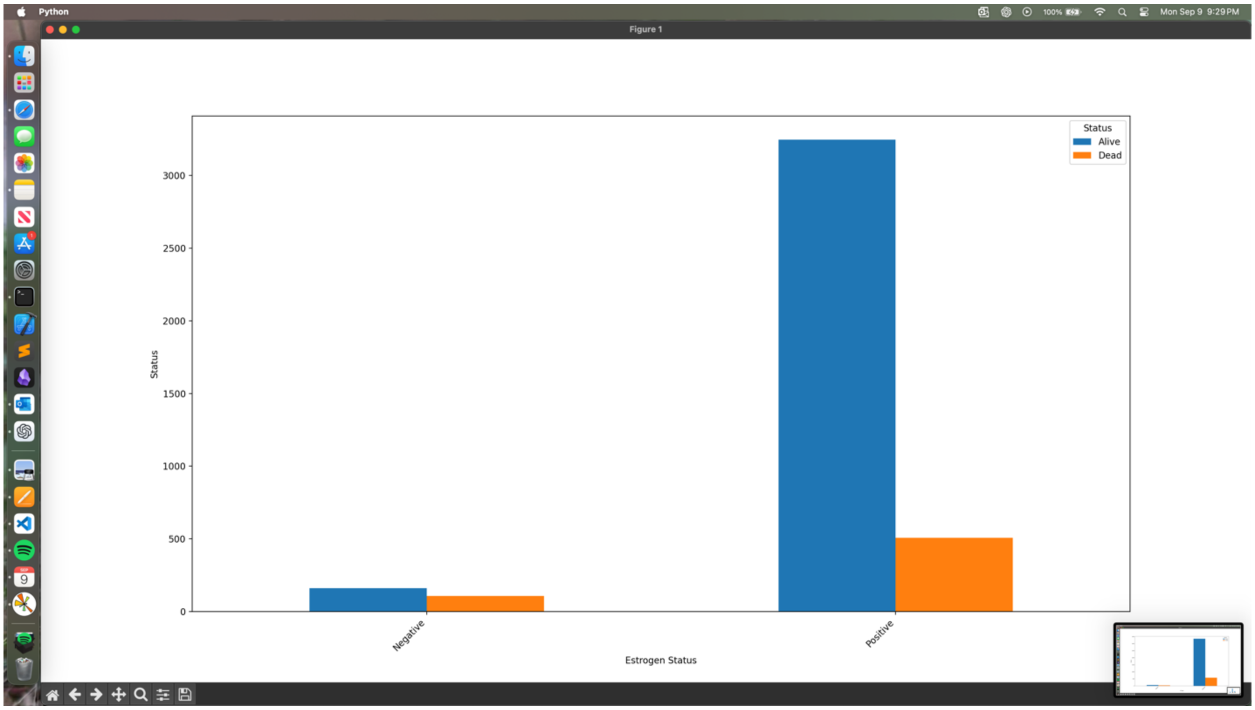
```
def variable_type(data, column_name, threshold=2):
    # print(data[column_name])
    unique_values = []
    for point in data[column_name]:
        if point not in unique_values:
            unique_values.append(point)
    if len(unique_values) > 10:
        return 0
    return 1


def c():
    status = ['Alive', 'Dead']
    vars_x = []
    for variable in list(data.columns):
        if variable_type(data, variable):
            vars_x.append(variable)


    categories = {}
    for var in vars_x:
        categories[var] = []
        for i in data[var]:
            if i not in categories[var]:
                categories[var].append(i)
```

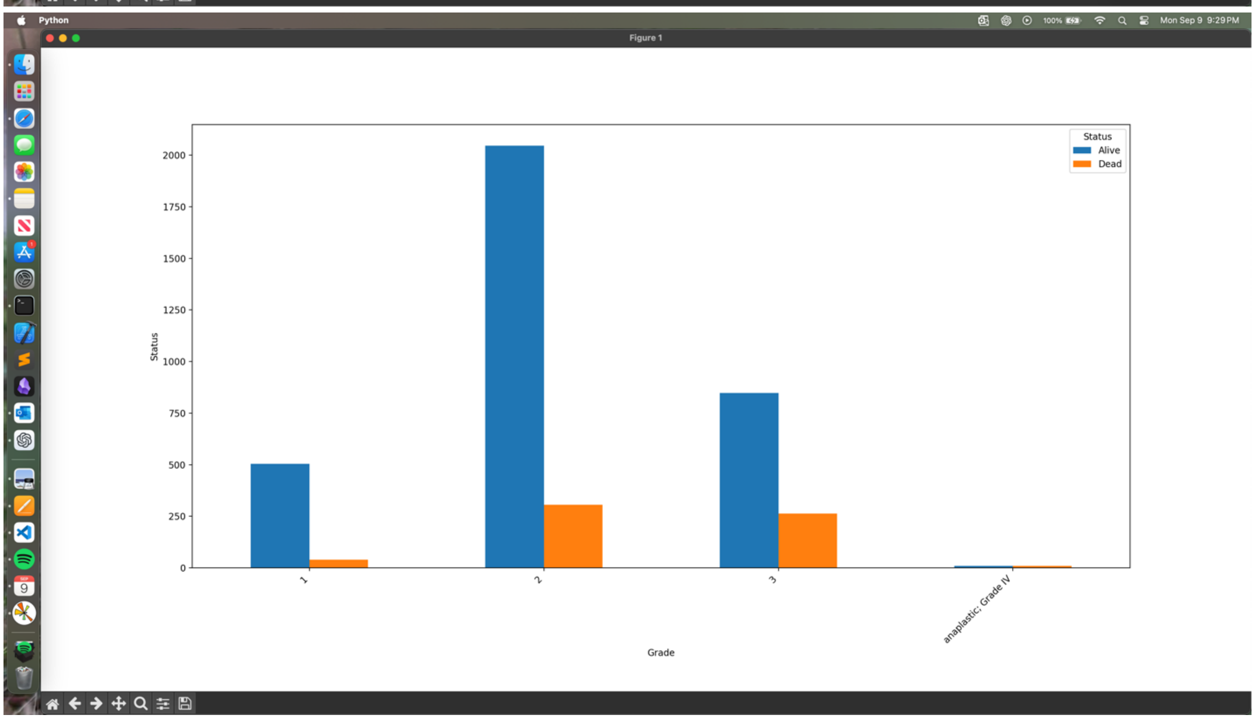
```
for category in categories.keys():
    miniDF = data.groupby([f'{category}', 'Status']).size().reset_index(name='count')
    finalDF = miniDF.pivot(index=f'{category}', columns='Status', values='count')
    finalDF.plot(kind='bar', stacked=False)
    plt.xlabel(f'{category}')
    plt.ylabel('Status')
    plt.xticks(rotation=45, ha='right')
    plt.savefig(f'{category} vs Status.png')
    plt.show()
```

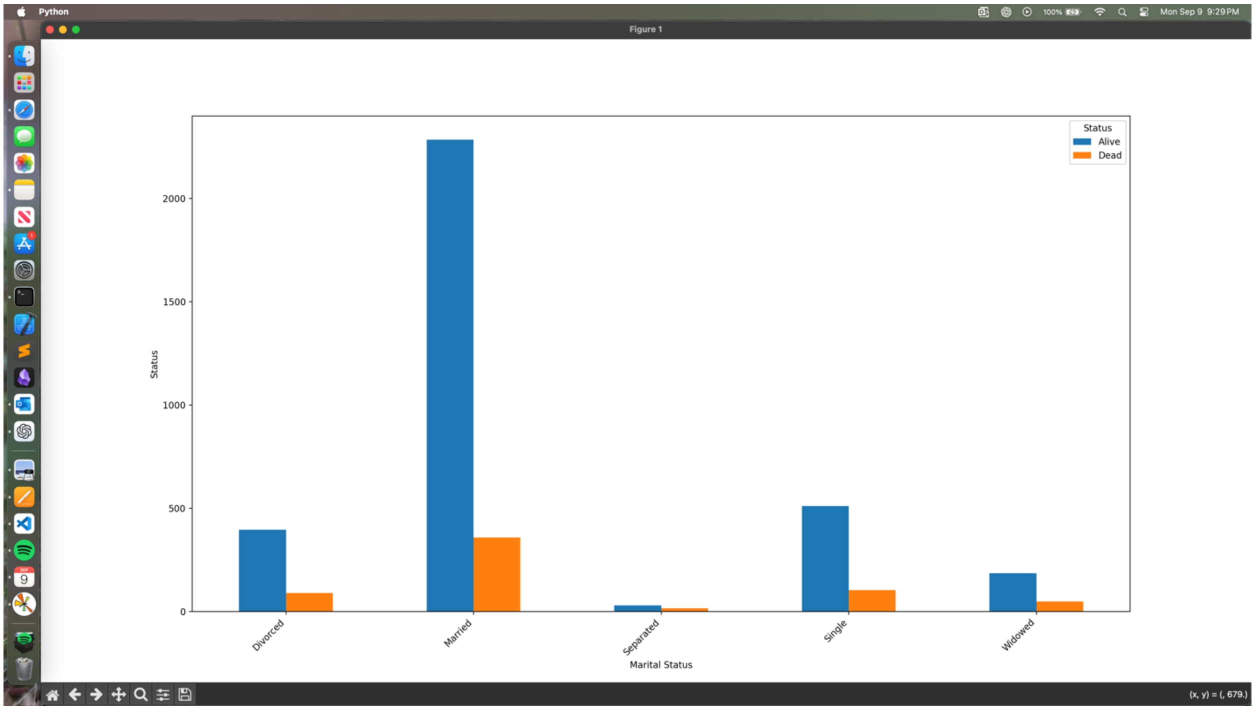


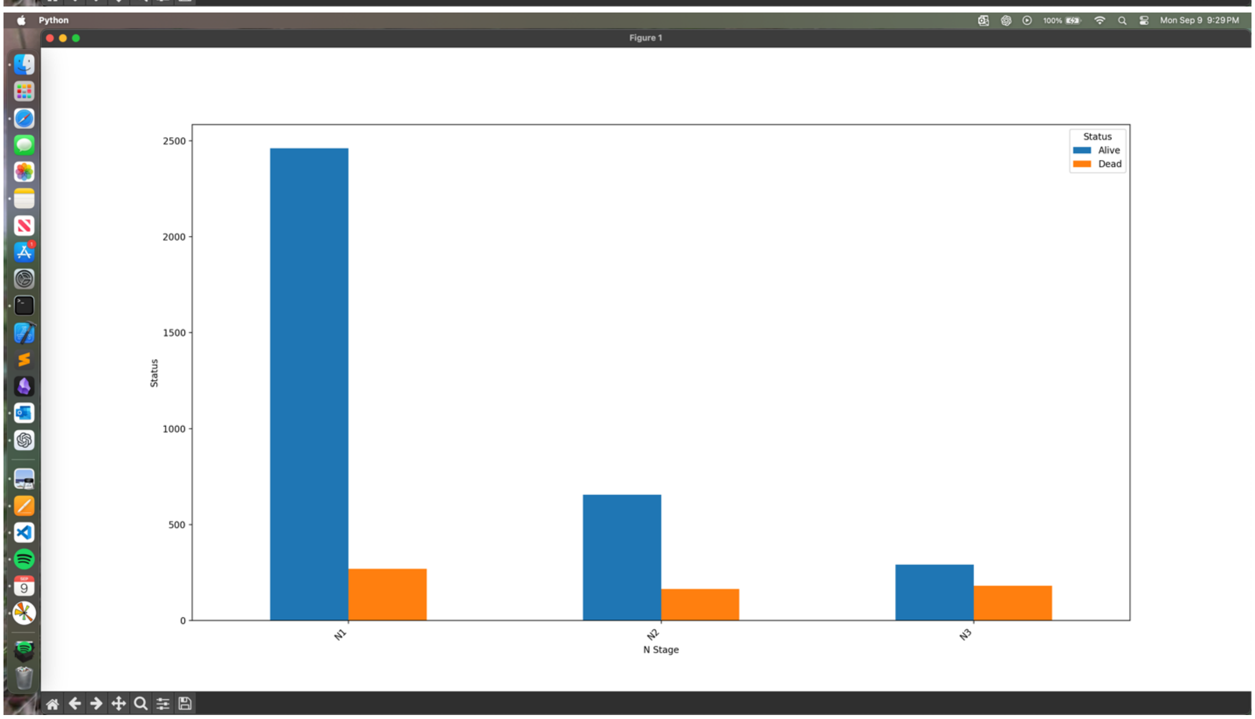

Python
Mon Sep 9 9:29 PM
Figure 1
Status
Alive
Dead
Status
A Stage
Distant
Regional
0
500
1000
1500
2000
2500
3000
3500

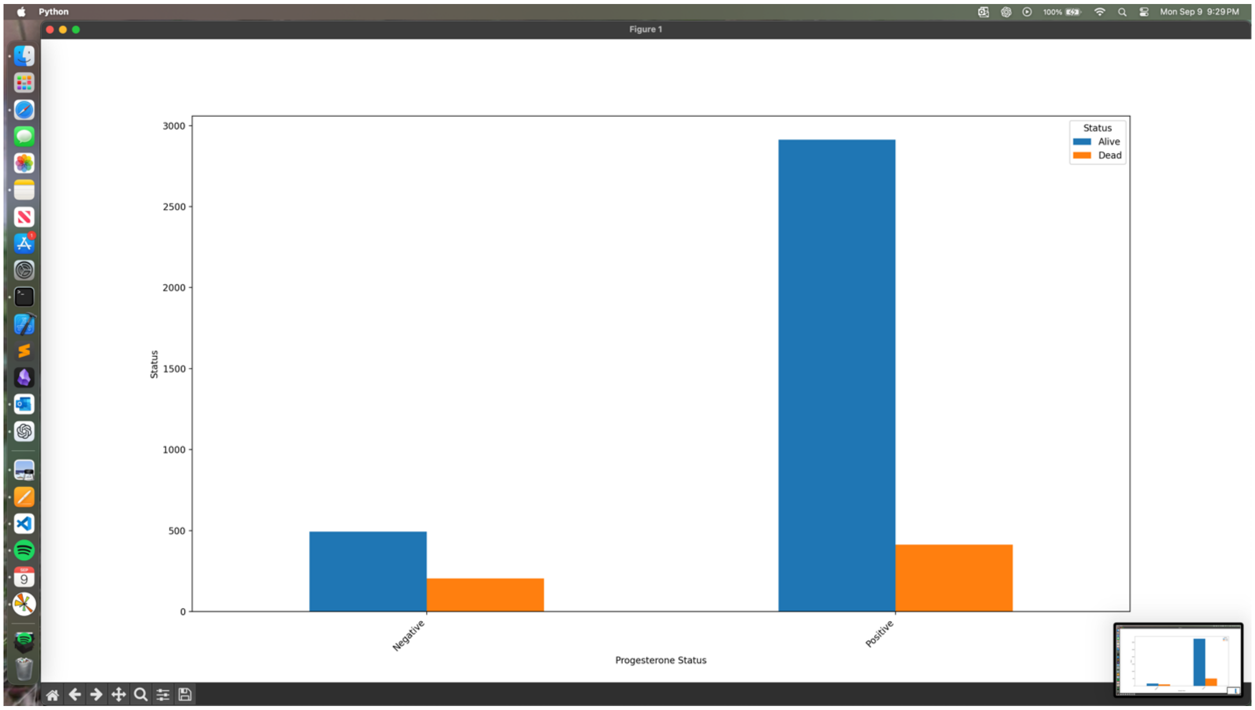

Python
Mon Sep 9 9:29 PM
Figure 1
Status
Alive
Dead
Status
differentiate
Moderately differentiated
Poorly differentiated
Undifferentiated
Well differentiated
0
250
500
750
1000
1250
1500
1750
2000
(x, y) = (, 1260.)


Python
Mon Sep 9 9:29 PM
Figure 1
Status
Alive
Dead
3000
2500
2000
1500
1000
500
0
Status
Negative
Positive
Estrogen Status

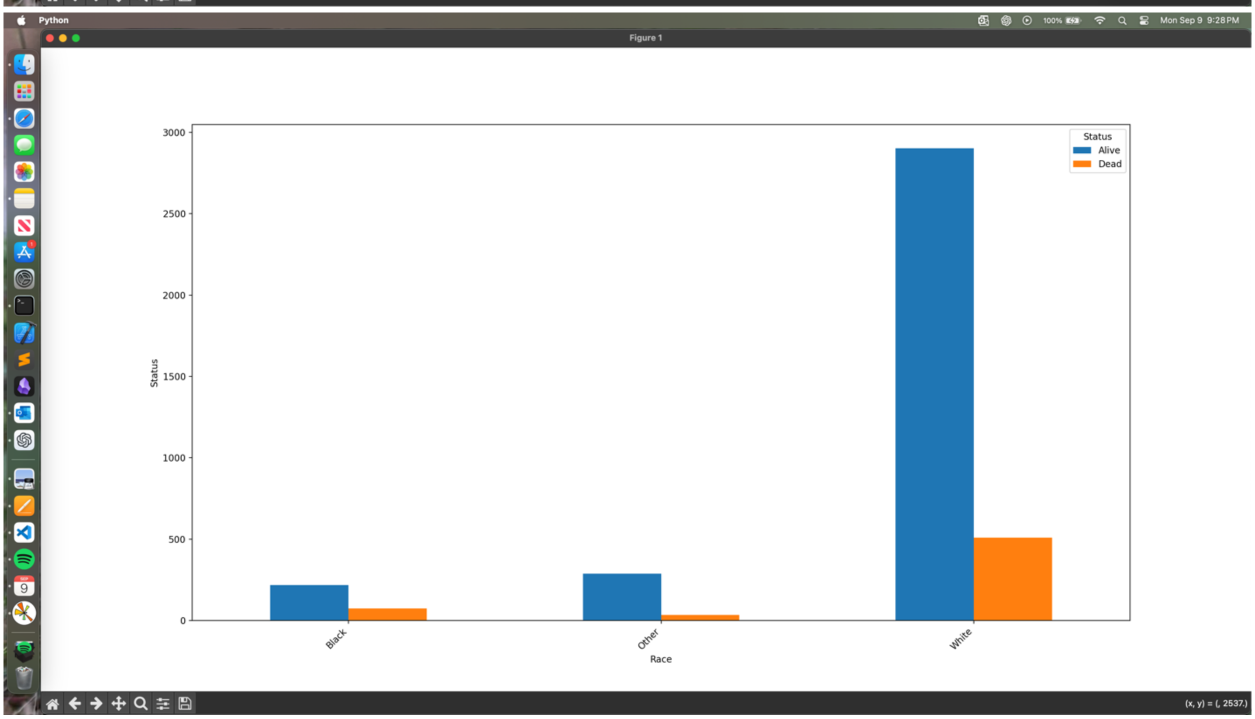

Python
Mon Sep 9 9:29 PM
Figure 1
Status
Alive
Dead
2000
1750
1500
1250
1000
750
500
250
0
Status
1
2
3
anaplastic; Grade IV
Grade


Python
Mon Sep 9 9:29 PM
Figure 1
Status
Alive
Dead
0
500
1000
1500
2000
Status
Divorced
Married
Separated
Single
Widowed
Marital Status
(x, y) = (, 679.)

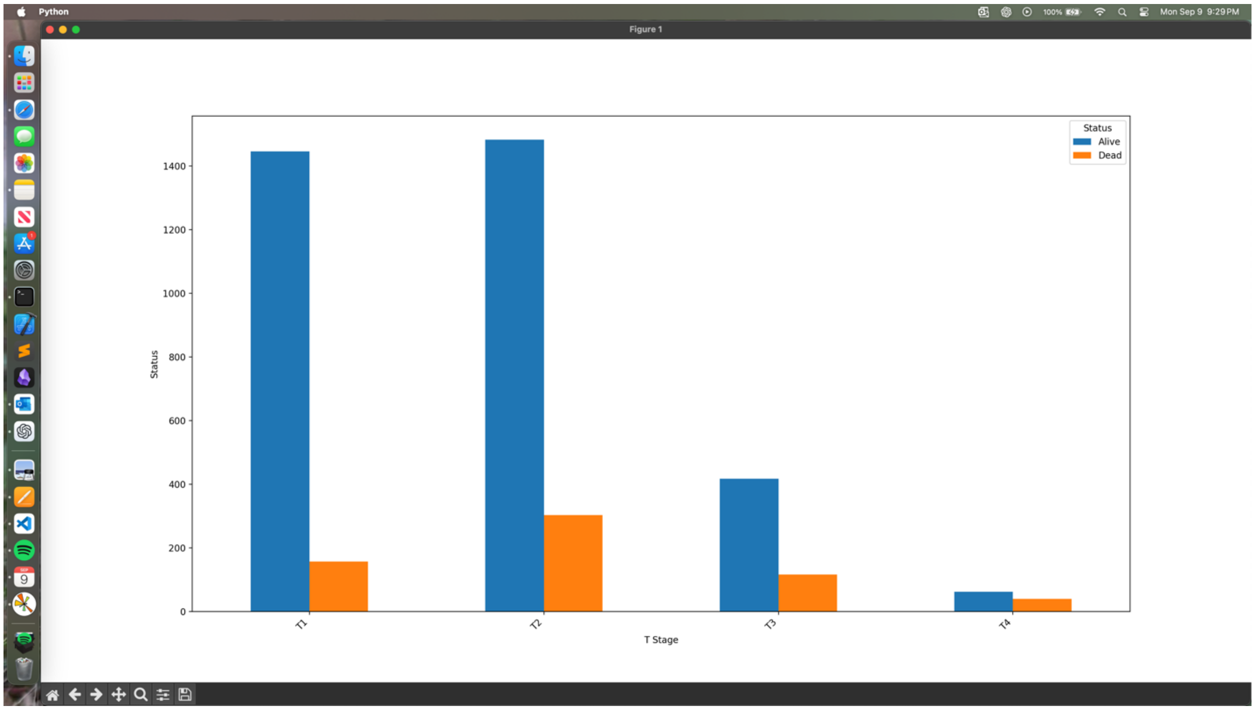

Python
Mon Sep 9 9:29 PM
Figure 1
Status
Alive
Dead
0
500
1000
1500
2000
2500
Status
N1
N2
N3
N Stage



Python
Mon Sep 9 9:29 PM
Figure 1
Status
Alive
Dead
Status
0
500
1000
1500
2000
2500
3000
Negative
Positive
Progesterone Status



Python
Mon Sep 9 9:28 PM
Figure 1
Status
Alive
Dead
Status
0
500
1000
1500
2000
2500
3000
Black
Other
White
Race
(x, y) = (, 2537.)


Python
Mon Sep 9 9:29 PM
Figure 1
Status
Alive
Dead
1400
1200
1000
800
600
400
200
0
Status
T1
T2
T3
T4
T Stage

(d) K N N Algorithm

```
import pandas as pd
import math
from collections import Counter
# import time as t
from tqdm import tqdm
import random
data = pd.read_csv('Breast_Cancer.csv')
def compute_distances(point1, point2):
  """
    Age, survival months, regional node positive, regional node examined and Tumor size
    are the continuous variables. Euclidean distance is used for measuring similarity
    between these variables.

    Race, Marital Status, T Stage, N Stage, 6th Stage, Defferentiated, Grade, A Stage,
    Estrogen Status, Progesterone Status are the categorical values. Hamming distance
    is used for measuring the similarity across these variables.
  """
  euclidean_distance = math.sqrt(
    (point1['Age'] - point2['Age'] ) **2+
    (point1['Tumor Size'] - point2['Tumor Size'] ) **2+
    (point1['Regional Node Examined'] - point2['Regional Node Examined']) **2+
    (point1['Regional Node Positive'] - point2['Regional Node Positive'] ) **2+
    (point1['Survival Months'] - point2['Survival Months'])**2
  )
```

```
    # print("ed: ", euclidean_distance)



    hamming_distance = (
      (0 if point1['Race']==point2['Race'] else 1) +
      (0 if point1['Marital Status']==point2['Marital Status'] else 1) +
      (0 if point1['T Stage']==point2['T Stage'] else 1) +
      (0 if point1['N Stage']==point2['N Stage'] else 1) +
      (0 if point1['6th Stage']==point2['6th Stage'] else 1) +
      (0 if point1['differentiate']==point2['differentiate'] else 1) +
      (0 if point1['Grade']==point2['Grade'] else 1) +
      (0 if point1['A Stage']==point2['A Stage'] else 1) +
      (0 if point1['Estrogen Status']==point2['Estrogen Status'] else 1) +
      (0 if point1['Progesterone Status']==point2['Progesterone Status'] else 1)
    )


    # print("hd: ", hamming_distance)
    return euclidean_distance + hamming_distance


def split_dataset(data):
    totalRows = data.shape[0] - 1

    """
```

```
    split data into train, validation and testing sets : 75-15-15% each
    find the total size of the dataset and *0.75, .15, .15
  """
  train_boundary = math.floor(0.70*totalRows)
  val_boundary = train_boundary + math.ceil(0.15*totalRows)
  test_boundary = val_boundary + math.ceil(0.15*totalRows)

  train_data = data.iloc[:train_boundary]
  val_data = data.iloc[train_boundary:val_boundary]
  test_data = data.iloc[val_boundary:test_boundary]

  train_Y = train_data['Status']
  train_X = train_data.drop(['Status'], axis=1)

  val_Y = val_data['Status']
  val_X = val_data.drop(['Status'], axis=1)

  test_Y = test_data['Status']
  test_X = test_data.drop(['Status'], axis=1)

  # print(train_X.shape[0])
  # print(val_X.shape[0])

  return train_X, train_Y, val_X, val_Y, test_X, test_Y

data['ID'] = data.index
```

```
train_X, train_Y, val_X, val_Y, test_X, test_Y = split_dataset(data.sample(frac=1))
point_distance_map = {}
val_point_to_sorted_distances = {}
for val_index in tqdm(range(val_X.shape[0])):
  for train_index in range(train_X.shape[0]):
    distance = compute_distances(val_X.iloc[val_index], train_X.iloc[train_index])
    point_distance_map[train_index] = distance
  sorted_distances = dict(sorted(point_distance_map.items(), key=lambda item: item[1]))
  val_point_to_sorted_distances[val_index] = sorted_distances
def get_k_neighbours(k):
  kNeighbours = {}
  for val_point in val_point_to_sorted_distances:
    neighbours = val_point_to_sorted_distances[val_point]
    kNeighbours[val_point] = list(neighbours.keys())[:k]
  return kNeighbours


def predict_for_val(kNeighbours):
  validation_predictions = {}
  for val_point in kNeighbours.keys():
    output = []
    for neigh in kNeighbours[val_point]:
      # print(train_X.loc[train_X['ID'] == neigh])
      output.append(train_Y.iloc[neigh])
      pred_status, trash = Counter(output).most_common()[0]
      validation_predictions[val_point] = pred_status
```

```
    return validation_predictions


tp = {}
fp = {}
tn = {}
fn = {}


def confusion_matrix(predictions, k, actual_Y):
    global tp
    global tn
    global fn
    global fp
    tp.setdefault(k,0)
    tn.setdefault(k,0)
    fn.setdefault(k,0)
    fp.setdefault(k,0)
    for point in predictions:
        if predictions[point] == actual_Y.iloc[point]:
            if actual_Y.iloc[point] == 'Alive':

                tp[k]+=1
            else:
                tn[k]+=1
        else:
            if actual_Y.iloc[point] == 'Alive':
                fn[k]+=1
```

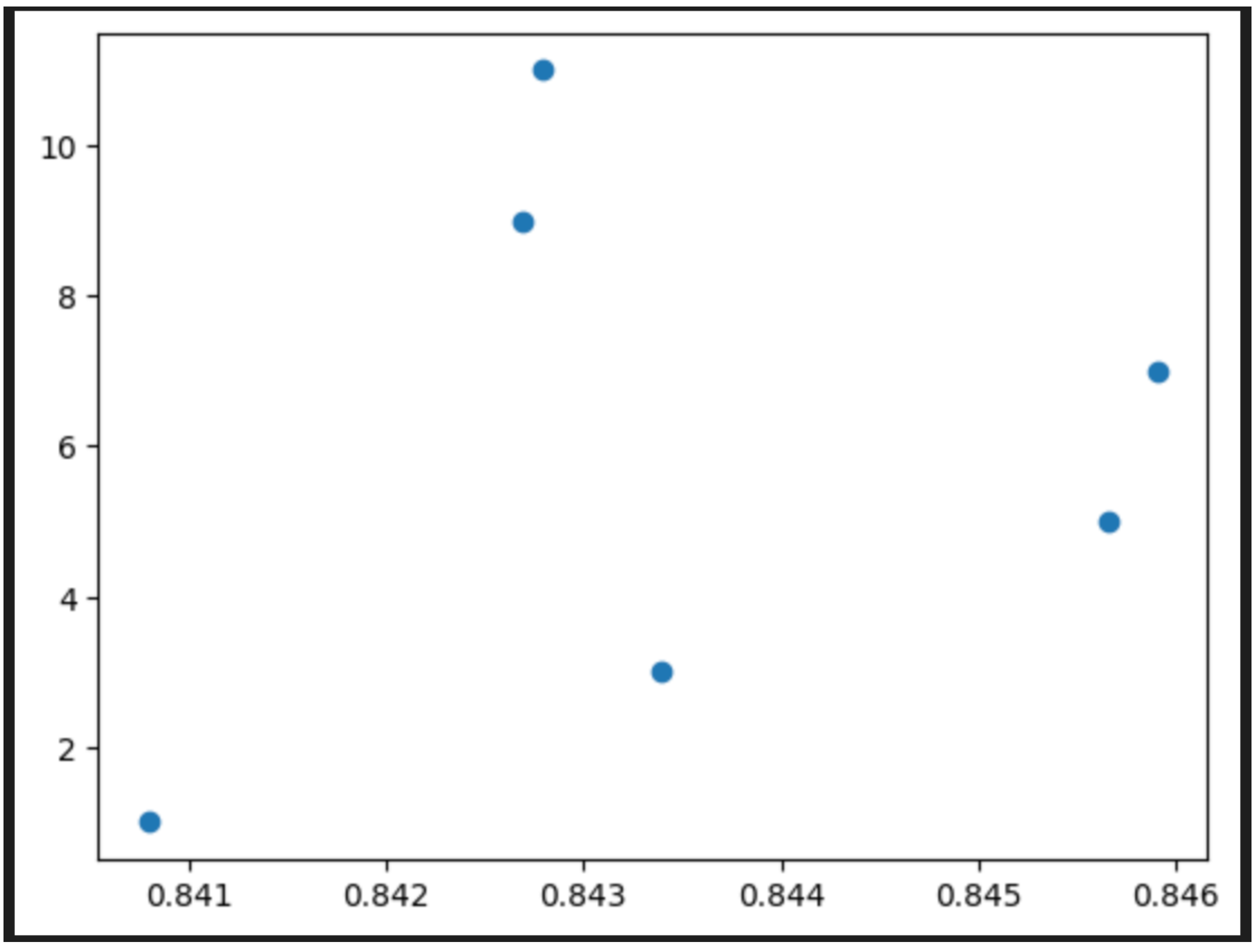
```
          else:
            fp[k]+=1


def compute_accuracies(tp, fp, tn, fn, k):
  recall_1 = tp[k]/(tp[k]+fn[k])
  recall_2 = tn[k]/(tn[k]+fp[k])
  return ((tp[k]+tn[k])/(tp[k]+tn[k]+fp[k]+tn[k])) , (0.5*(recall_1 + recall_2)) , (2*tp[k] / (2*tp[k] + fp[k] + fn[k]))


accuracies = []
bAccuracies = []
f1_scores = []
for k in [1,3,5,7,9,11]:
  kNeighbours = get_k_neighbours(k)
  validation_predictions = predict_for_val(kNeighbours=kNeighbours)
  confusion_matrix(validation_predictions, k, val_Y)
  acc , bAcc , f1 = compute_accuracies(tp, fp, tn, fn, k)
  accuracies.append(acc)
  bAccuracies.append(bAcc)
  f1_scores.append(f1)
  print(f"For k = {k} :  Accuracy = {acc}------Balanced Accuracy = {bAcc}------F1 score = {f1}")

print("==========================================================================================================================")
```

```
For k = 1 :  Accuracy = 0.8407960199004975------Balanced Accuracy = 0.6553067585301837------F1 score = 0.9064609450337512
==============================================================================================================
For k = 3 :  Accuracy = 0.8433931484502447------Balanced Accuracy = 0.6567011154855643------F1 score = 0.917221693625119
==============================================================================================================
For k = 5 :  Accuracy = 0.8456591639871383------Balanced Accuracy = 0.6655593832020997------F1 score = 0.9264150943396227
==============================================================================================================
For k = 7 :  Accuracy = 0.8459069020866774------Balanced Accuracy = 0.6623195538057743------F1 score = 0.9275634995296331
==============================================================================================================
For k = 9 :  Accuracy = 0.8426892950391645------Balanced Accuracy = 0.6279963639811791------F1 score = 0.9176382098533283
==============================================================================================================
For k = 11 :  Accuracy = 0.8427919112850619------Balanced Accuracy = 0.6250290194847448------F1 score = 0.9181681681681682
==============================================================================================================
```

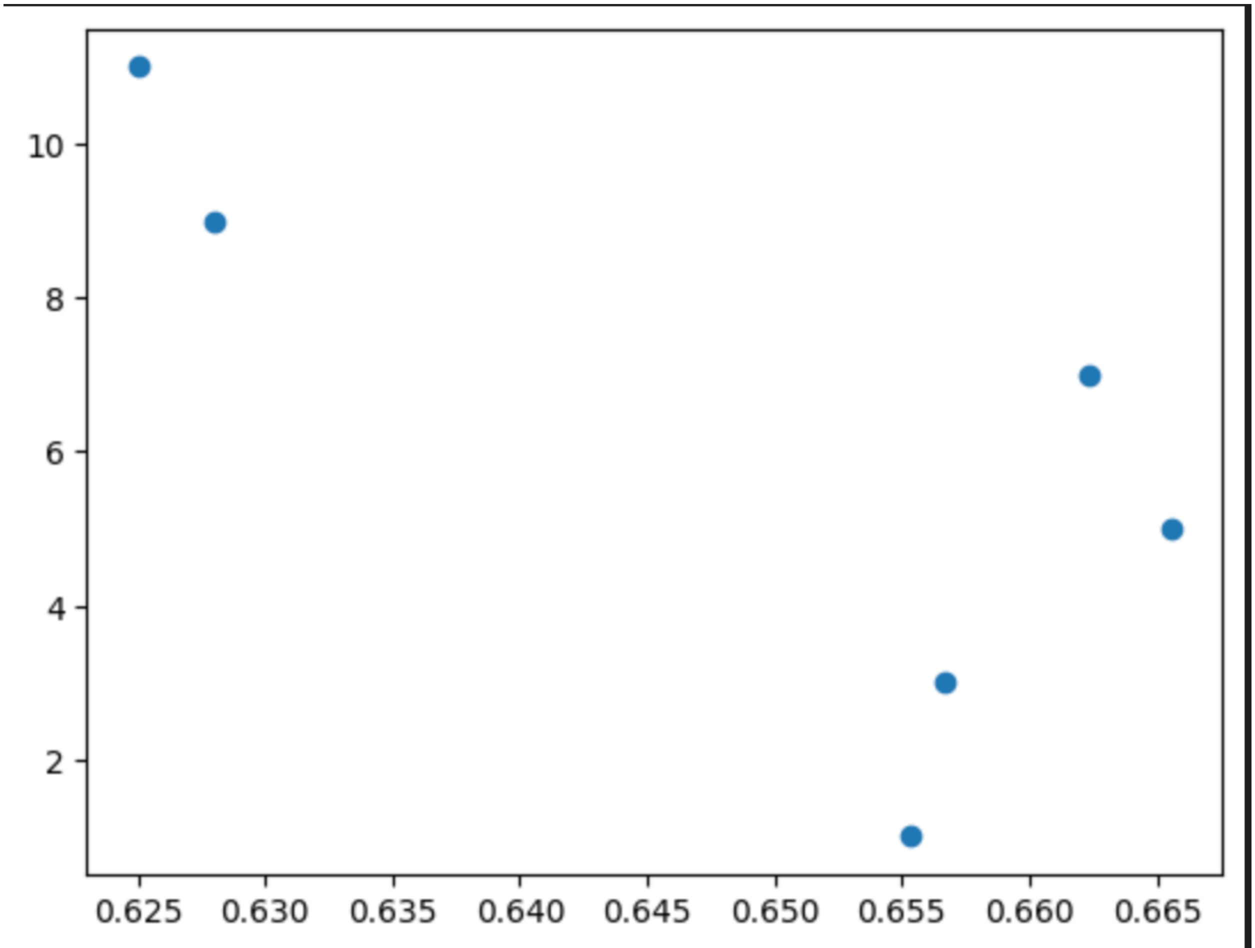
```
Best value for K based on :
    1. Accuracy : K*=9
    2. Balanced accuracy : K**=9
    3. F1 score : K+=11
```

import matplotlib.pyplot as plt

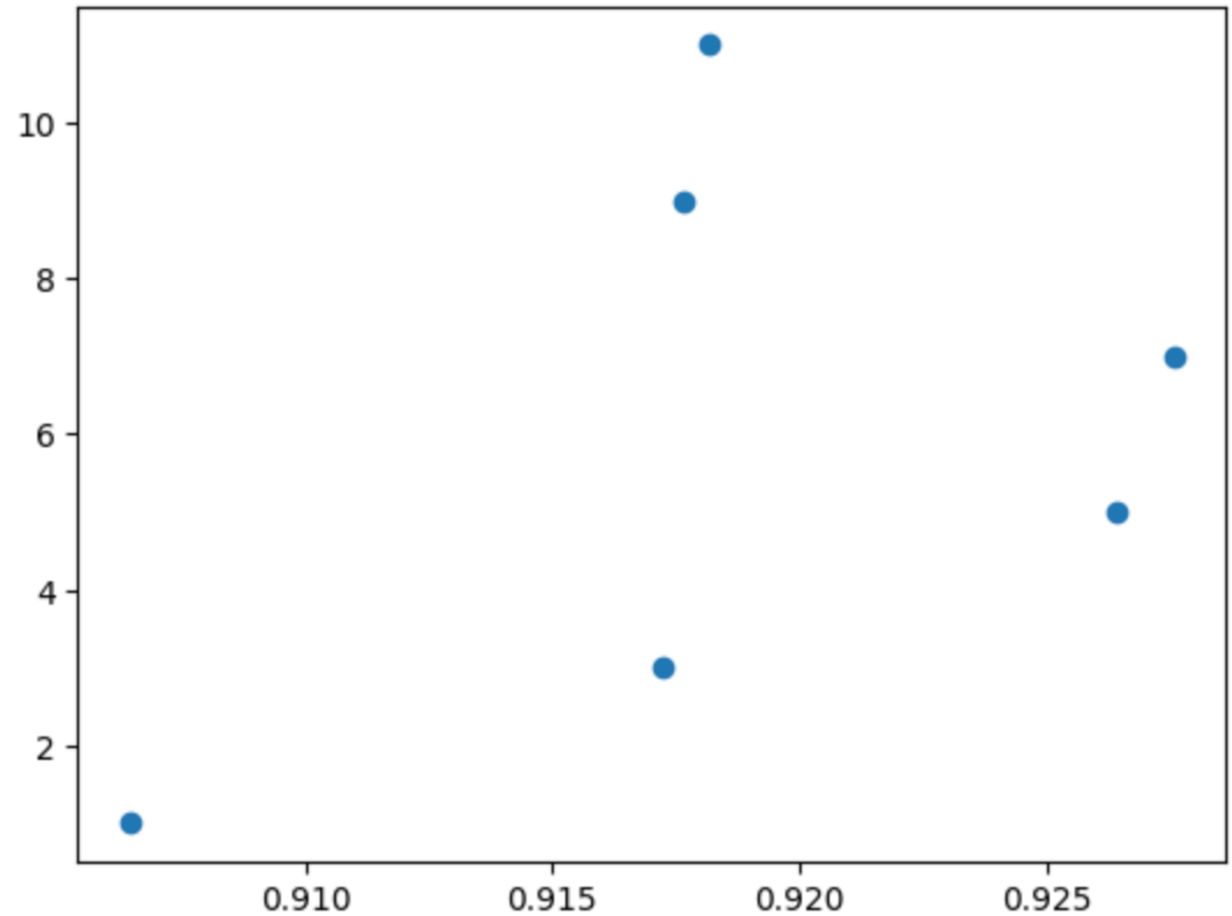
plt.scatter(accuracies, [1,3,5,7,9,11])



```
plt.scatter(bAccuracies, [1,3,5,7,9,11])
```




```
plt.scatter(f1_scores, [1,3,5,7,9,11])
```




```
point_distance_map = {}
test_point_to_sorted_distances = {}
for test_index in tqdm(range(test_X.shape[0])):
   for train_index in range(train_X.shape[0]):
      distance = compute_distances(test_X.iloc[test_index], train_X.iloc[train_index])
      point_distance_map[train_index] = distance
   sorted_distances = dict(sorted(point_distance_map.items(), key=lambda item: item[1]))
   test_point_to_sorted_distances[test_index] = sorted_distances
def get_k_neighbours(k):
   kNeighbours = {}
```

```
    for test_point in test_point_to_sorted_distances:
        neighbours = test_point_to_sorted_distances[test_point]
        kNeighbours[test_point] = list(neighbours.keys())[:k]
    return kNeighbours
def predict_for_test(kNeighbours):
    test_predictions = {}
    for test_point in kNeighbours.keys():
        output = []
        for neigh in kNeighbours[test_point]:
            # print(train_X.loc[train_X['ID'] == neigh])
            output.append(train_Y.iloc[neigh])
            pred_status, trash = Counter(output).most_common()[0]
            test_predictions[test_point] = pred_status
    return test_predictions
for k in [9,11]:
    kNeighbours = get_k_neighbours(k)
    test_predictions = predict_for_test(kNeighbours=kNeighbours)
    confusion_matrix(test_predictions, k, test_Y)
    acc , bAcc , f1 = compute_accuracies(tp, fp, tn, fn, k)
    print(f"For k = {k} :  Accuracy = {acc}------Balanced Accuracy = {bAcc}------F1 score = {f1}")

print("======================================================================================================================")
```

```
For k = 9 :  Accuracy = 0.825------Balanced Accuracy = 0.4647495361781076------F1 score = 0.8662900188323918
======================================================================================================================
For k = 11 :  Accuracy = 0.8256227758007118------Balanced Accuracy = 0.46672582076308783------F1 score = 0.868421052631579
======================================================================================================================
```

K* = 9, K**9 = , K⁺ = 11

(e) I do not think that would be a good idea because the data on which the model is trained is dominated by people belonging to the race 'White'. Any predictions made based on the given dataset will inevitably be biased towards the status of individuals belonging to the 'White' race.

(d)

```
tp_W = 0

tn_W = 0

fn_W = 0

fp_W = 0


tp_B = 0

tn_B = 0

fn_B = 0

fp_B = 0


tp_O = 0

tn_O = 0

fn_O = 0

fp_O = 0


def confusion_matrix_optimal(predictions, k, actual_Y):

  for point in predictions:

    if test_X.iloc[point]['Race'] == "White" :

      if predictions[point] == actual_Y.iloc[point]:

        if actual_Y.iloc[point] == 'Alive':
```

```
            global tp_W
            tp_W+=1
        else:
            global tn_W
            tn_W+=1
    else:
        if actual_Y.iloc[point] == 'Alive':
            global fn_W
            fn_W+=1
        else:
            global fp_W
            fp_W+=1
elif test_X.iloc[point]['Race'] == "Black":
    if predictions[point] == actual_Y.iloc[point]:
        if actual_Y.iloc[point] == 'Alive':
            global tp_B
            tp_B+=1
        else:
            global tn_B
            tn_B+=1
    else:
        if actual_Y.iloc[point] == 'Alive':
            global fn_B
            fn_B+=1
        else:
            global fp_B
```

```
                fp_B+=1
        elif test_X.iloc[point]['Race'] == "Other":
            if predictions[point] == actual_Y.iloc[point]:
                if actual_Y.iloc[point] == 'Alive':
                    global tp_O
                    tp_O+=1
                else:
                    global tn_O
                    tn_O+=1
            else:
                if actual_Y.iloc[point] == 'Alive':
                    global fn_O
                    fn_O+=1
                else:
                    global fp_O
                    fp_O+=1

kNeighbours = get_k_neighbours(11)
test_predictions = predict_for_test(kNeighbours)
confusion_matrix_optimal(test_predictions, 11, test_Y)
def compute_accuracies_optimal(tp, fp, tn, fn, k):
    recall_1 = tp/(tp+fn)
    recall_2 = tn/(tn+fp)
    return ((tp+tn)/(tp+tn+fp+tn)) , (0.5*(recall_1 + recall_2)) , (2*tp / (2*tp + fp + fn))

f1_W = compute_accuracies_optimal(tp=tp_W, tn=tn_W, fp=fp_W, fn=fn_W, k=11)
```

f1_B = compute_accuracies_optimal(tp=tp_B, tn=tn_B, fp=fp_B, fn=fn_B, k=11)

f1_O = compute_accuracies_optimal(tp=tp_O, tn=tn_O, fp=fp_O, fn=fn_O, k=11)

f1_W[2], f1_B[2], f1_O[2]

```
(0.8706009745533297, 0.8387096774193549, 0.8641975308641975)
```

F1 Scored for

1. White: 0.8706
2. Black: 0.8387
3. Other: 0.8641

Comments:

The above code only implements a basic version of the KNN algorithm. There are multiple scopes for optimization, which I have not implemented due to lack of time. For example, the functions for computing distances between two validation and train can be generalized, and then would not be needed to be duplicated and modified for computing the same distance set between train and test sets. The distance computation has scope for performance optimization by using numpy arrays. However, for simplicity's sake I stuck with straightforward simple approach.