Homework 2

This jupyter notebook is also accessble as an online colab notebook : https://colab.research.google.com/drive/10KcuDSp9jCx0eFkdQ-UvrS6VPQjmpYPQ#scrollTo=Yj8OAlyA5Tzv (https://colab.research.google.com/drive/10KcuDSp9jCx0eFkdQ-UvrS6VPQjmpYPQ#scrollTo=Yj8OAlyA5Tzv)

Q1

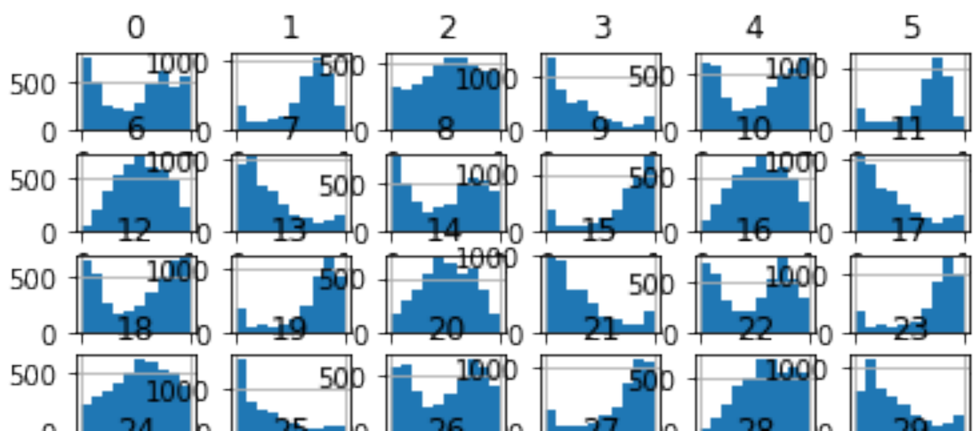
Load & normalize the data

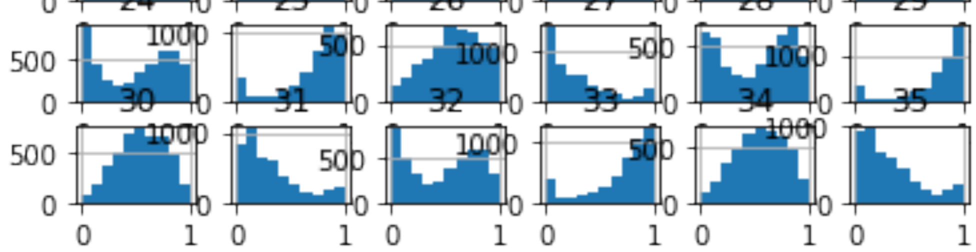
In [2]:

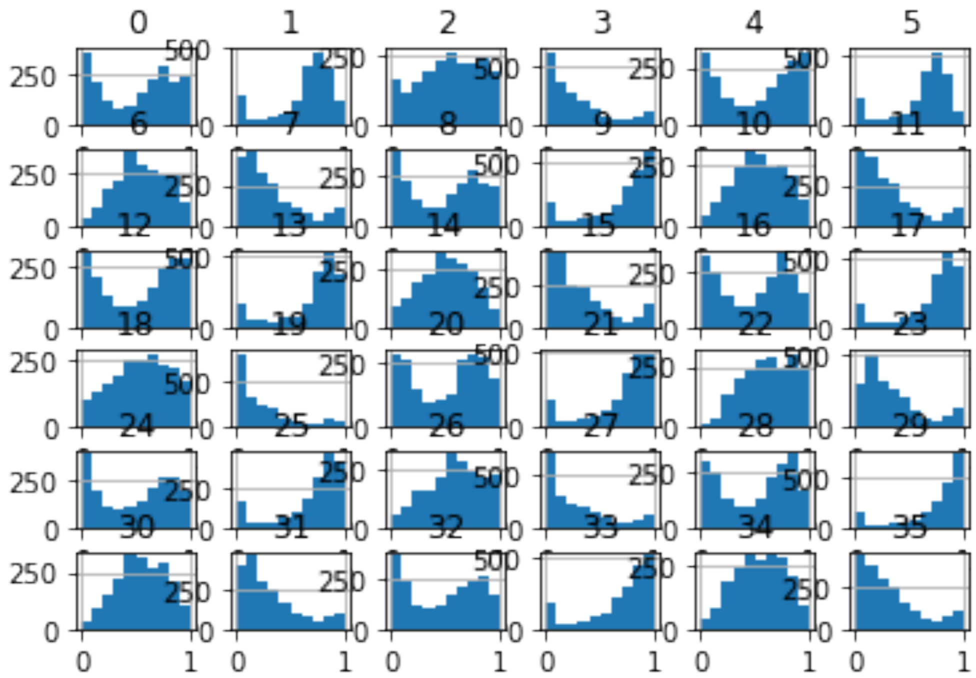
```
import pandas as pd
import numpy as np
from urllib.request import urlopen
import re
from sklearn import preprocessing

data_train = urlopen("https://raw.githubusercontent.com/peterwu19881230/CSCE633_ML_d
data_test = urlopen("https://github.com/peterwu19881230/CSCE633_ML_data/raw/master/s
#Note for the test data: 1. I manually deleted a "NUL" on line 1181 1. I manually de

def parse_data(data):
  rows=[]
  class_=[]
  for line in data: # files are iterable

      string=line.decode("utf-8").rstrip() #rstrip() is to trim EOL
      words=string.split(sep=" ")


      class_.append(words[0])

      words.pop(0) #remove the first element (response variable)

      row=[np.nan]*36 #I have checked that for each row there are at most 36 feature
      for word in words:
        col_result=re.search('([0-9]{1,2}):.*',word) #.* means "0 or more of any cha
        col=int(col_result.group(1))

        value_result=re.search('[0-9]{1,2}:(.*)',word)
```

```
            row[col-1]=float(value_result.group(1))

        rows.append(row)

    df=pd.DataFrame(rows)

    #normalize the data (definition of normalization: https://scikit-learn.org/stable/
    min_max_scaler = preprocessing.MinMaxScaler(feature_range=(0, 1))
    normalized_df=pd.DataFrame(min_max_scaler.fit_transform(df.T), columns=df.index, i
    X=normalized_df

    ##compute response variable
    y=np.where(np.array(class_).astype(int) == 6, 1, 0)

    return(X,y)



X_train, y_train = parse_data(data_train)
X_test, y_test = parse_data(data_test)

#check no. of cols & rows
print(X_train.head())

##verify by printing histograms for all columns
X_train.hist(); #";" is to surpress messages
X_test.hist();
```

```
    0         1         2         3   ...        32        33         3
4        35
0  NaN  1.000000  0.694047  0.427273  ...  0.610156  0.651456  0.23157
9  0.158984
1  NaN  0.890850  0.196389  0.150320  ...  0.796417  0.839826  0.30722
7  0.141549
2  1.0  0.928588  0.771404  0.364708  ...  0.283042  0.448587  0.11340
0  0.002494
3  NaN  0.695489  0.229246  0.113419  ...  0.839346  0.831158  0.67827
0  0.437713
4  NaN  0.567578  0.280369  0.081376  ...  0.553549  0.451600  0.12377
6  0.000000

[5 rows x 36 columns]
```







Calculate how many nans are there -> Decide to ignore or impute -> Impute

In [3]:

```
print(X_train.isna().sum())

import numpy as np
from sklearn.impute import SimpleImputer

def impute_by_mean(data):
  imp_mean = SimpleImputer(missing_values=np.nan, strategy='mean') #It seems that th
  imp_mean.fit(data)
  return(pd.DataFrame(imp_mean.transform(data)))

X_train_imputed=impute_by_mean(X_train) #print(X_train_imputed.isna().sum())  #this
X_test_imputed=impute_by_mean(X_test)
```

```
0      59
1       0
2      55
3       0
4     231
5       0
6       0
7       0
8      54
9       0
```

```
10      0
11      0
12    259
13    230
14      0
15    172
16     55
17      0
18      0
19      0
20      0
21      0
22      0
23      0
24     63
25    219
26      0
27    156
28      0
29      0
30      0
31      0
32     59
33      0
34      0
35      0
dtype: int64
```

implement SVM

In [4]:

```
from sklearn.svm import SVC
from sklearn.model_selection import GridSearchCV
from sklearn.metrics import classification_report, confusion_matrix
from sklearn.model_selection import cross_val_score

#==============
import warnings
warnings.simplefilter(action='ignore', category=FutureWarning) #avoid the "future wa
#==============



ds = [1,2,3,4]
Cs = [0.001, 0.01, 0.1, 1, 10] #ref: https://medium.com/@aneesha/svm-parameter-tuni
param_grid={'degree':ds,'C':Cs}

grid_search = GridSearchCV(SVC(kernel='poly'), param_grid, cv=10,scoring='accuracy')
grid_search.fit(X_train_imputed, y_train)
```

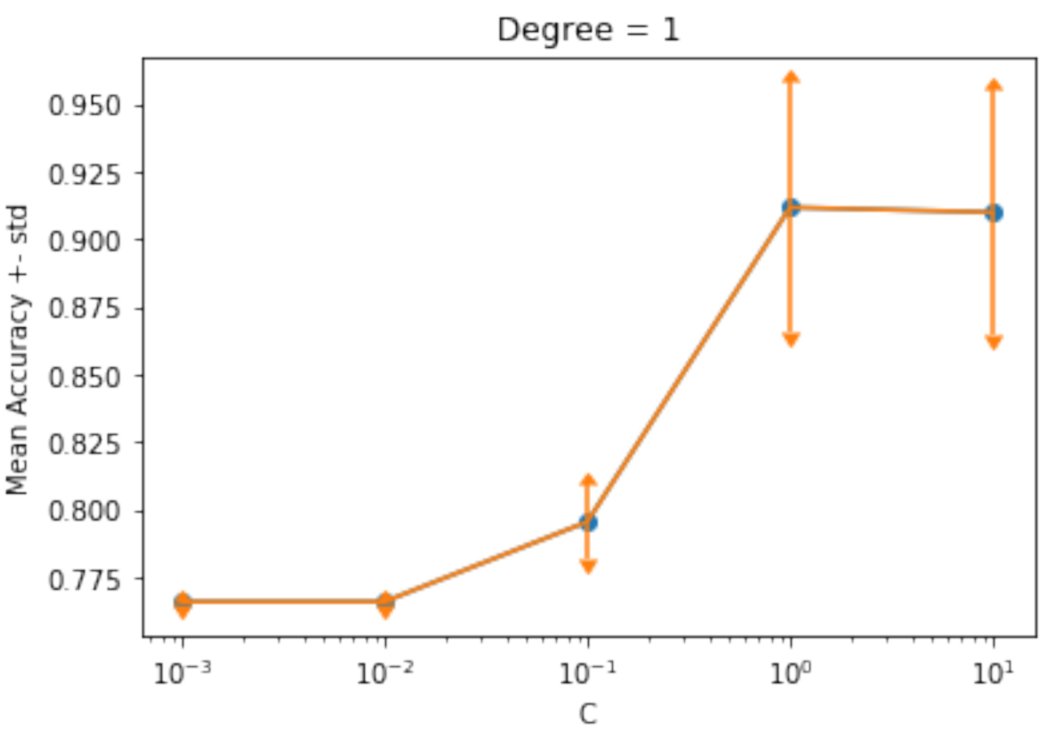
Out[4]:

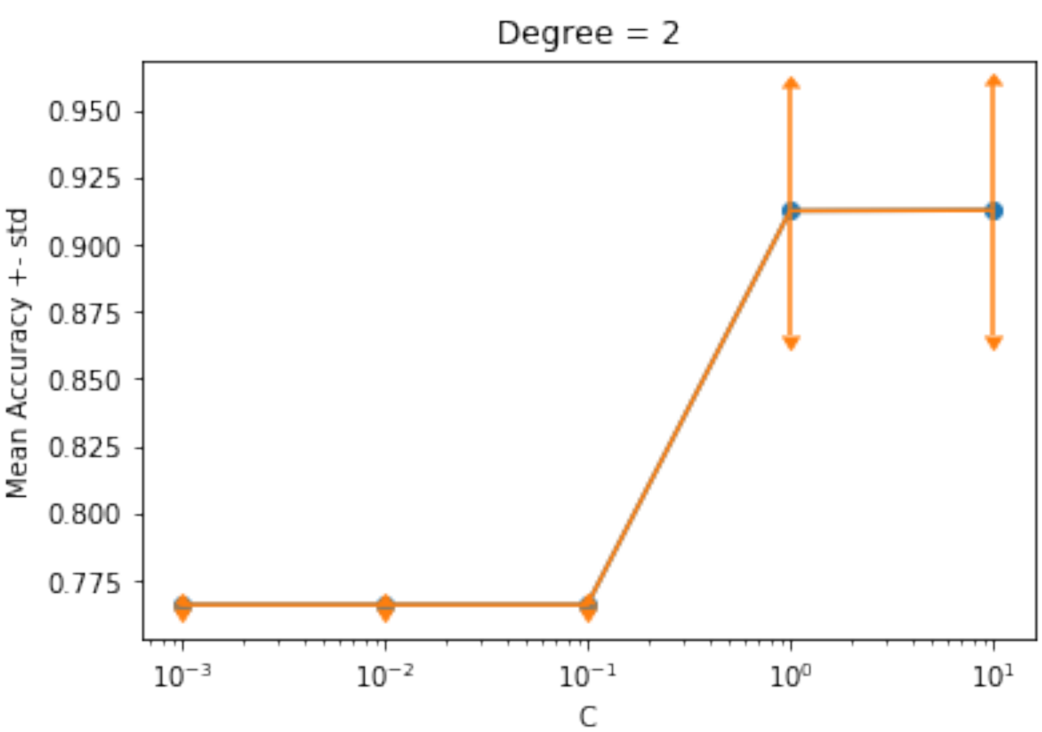
```
GridSearchCV(cv=10, error_score='raise-deprecating',
             estimator=SVC(C=1.0, cache_size=200, class_weight=None, c
oef0=0.0,
                           decision_function_shape='ovr', degree=3,
                           gamma='auto_deprecated', kernel='poly', max
_iter=-1,
                           probability=False, random_state=None, shrin
king=True,
                           tol=0.001, verbose=False),
             iid='warn', n_jobs=None,
             param_grid={'C': [0.001, 0.01, 0.1, 1, 10],
                         'degree': [1, 2, 3, 4]},
             pre_dispatch='2*n_jobs', refit=True, return_train_score=F
alse,
             scoring='accuracy', verbose=0)
```

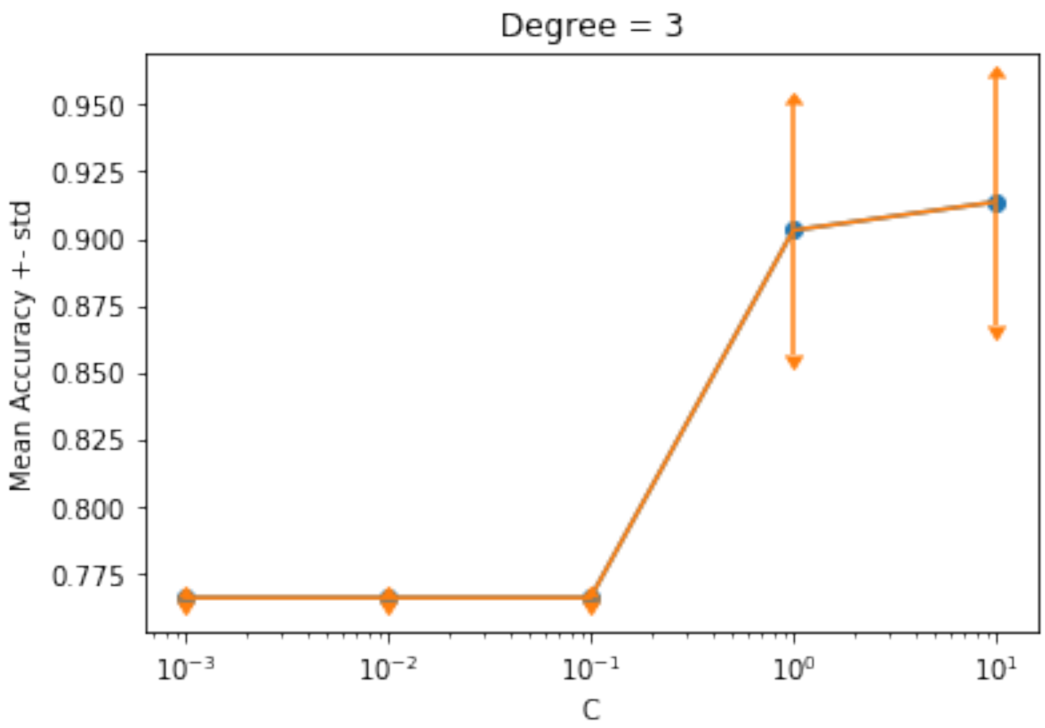
In [5]:

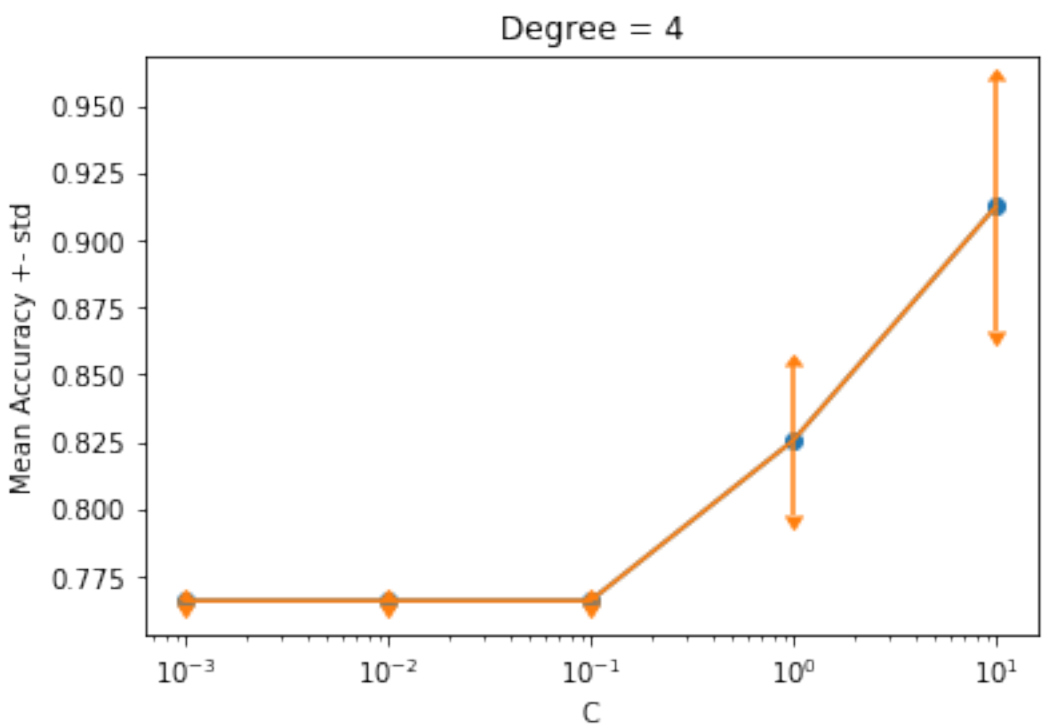
```
#I here use accuracy as the error term

accuracy_list=[]
for i in range(10):
  accuracy_list.append(pd.DataFrame(grid_search.cv_results_['split'+str(i)+'_test_sc

accuracy_df=pd.concat(accuracy_list,axis=0)

## assign column names
params=grid_search.cv_results_['params']
params_string=['C:'+str(param['C'])+'_'+'degree:'+str(param['degree']) for param in
accuracy_df.columns=params_string
```

```
mean_array=np.array([np.mean(accuracy_df[column]) for column in accuracy_df.columns
std_array=np.array([np.std(accuracy_df[column]) for column in accuracy_df.columns])


import matplotlib.pyplot as plt

for d in ds:
  degree_index=list(np.array([0,4,8,12,16])+d-1)
  plt.plot(Cs,mean_array[degree_index])
  plt.errorbar(Cs, mean_array[degree_index], yerr=std_array[degree_index],lolims=Tru
  plt.scatter(Cs,mean_array[degree_index])
  plt.title('Degree = '+str(d))
  plt.xscale('log')
  plt.xlabel('C')
  plt.ylabel('Mean Accuracy +- std')
  plt.show()
```









Best parameters that gives best accuracy:

In [6]:

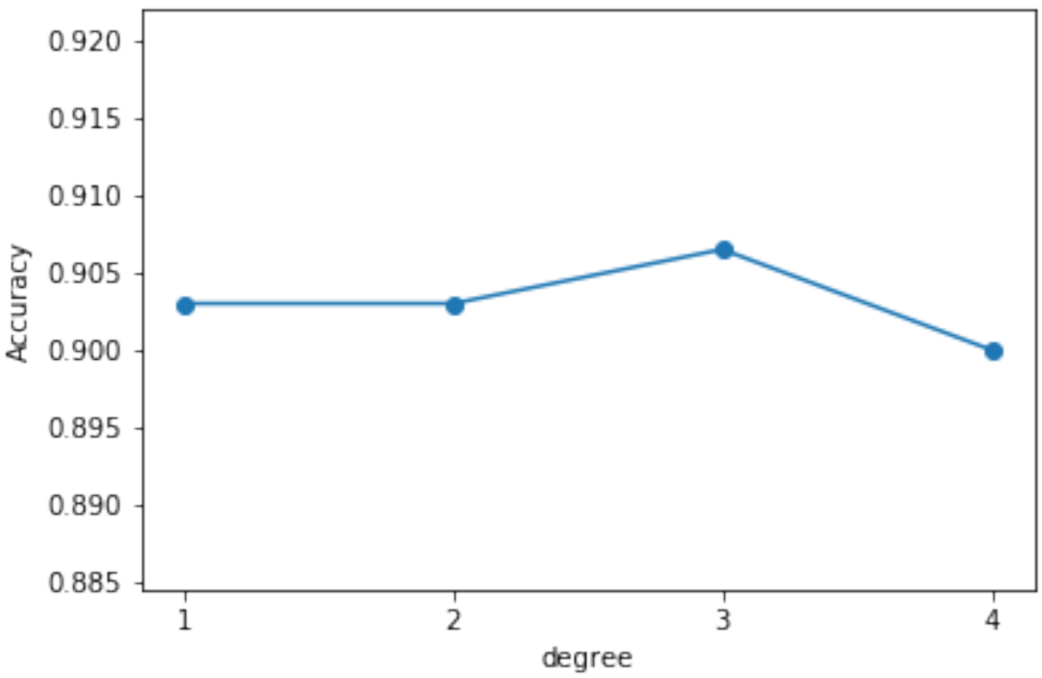
```
grid_search.best_params_
```

Out[6]:

```
{'C': 10, 'degree': 3}
```

In [7]:

```
from sklearn.metrics import accuracy_score

ds = [1,2,3,4]
C=10

accuracy_list=[]
no_support_vectors=[]
for d in ds:
  model=SVC(C=C,kernel='poly',degree=d)
  model.fit(X_train_imputed,y_train)
  no_support_vectors.append(model.n_support_) #no of support vectors for each featu
  accuracy_list.append(accuracy_score(y_test,model.predict(X_test_imputed)))

x=ds
plt.scatter(x,accuracy_list)
plt.plot(x,accuracy_list)
plt.xticks(np.arange(min(x), max(x)+1, 1.0))
plt.xlabel('degree')
plt.ylabel('Accuracy')
plt.show()
```



In [8]:

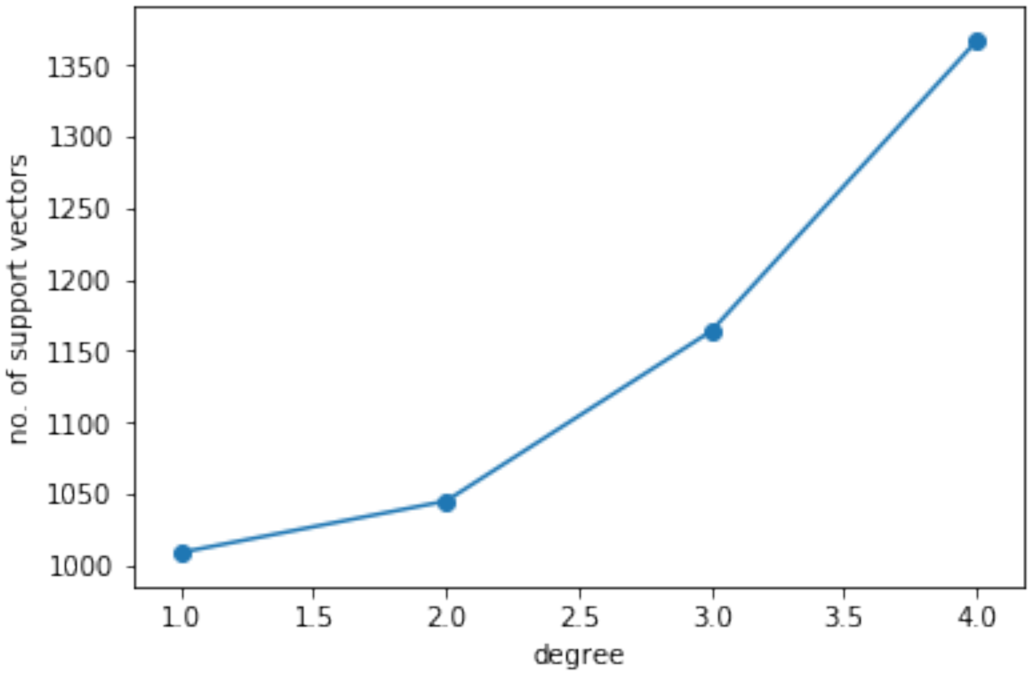
```
no_support_vectors #no. of support vectors for each class (for d=1,2,3,4, respective
```

Out[8]:

```
[array([505, 504], dtype=int32),
 array([525, 520], dtype=int32),
 array([583, 581], dtype=int32),
 array([686, 681], dtype=int32)]
```

In [9]:

```
total_no_support_vectors=[]
for d in ds:
  total_no_support_vectors.append(np.sum(no_support_vectors[d-1]))

plt.plot(ds,total_no_support_vectors)
plt.scatter(ds,total_no_support_vectors)
plt.xlabel('degree')
plt.ylabel('no. of support vectors')
plt.show()
```



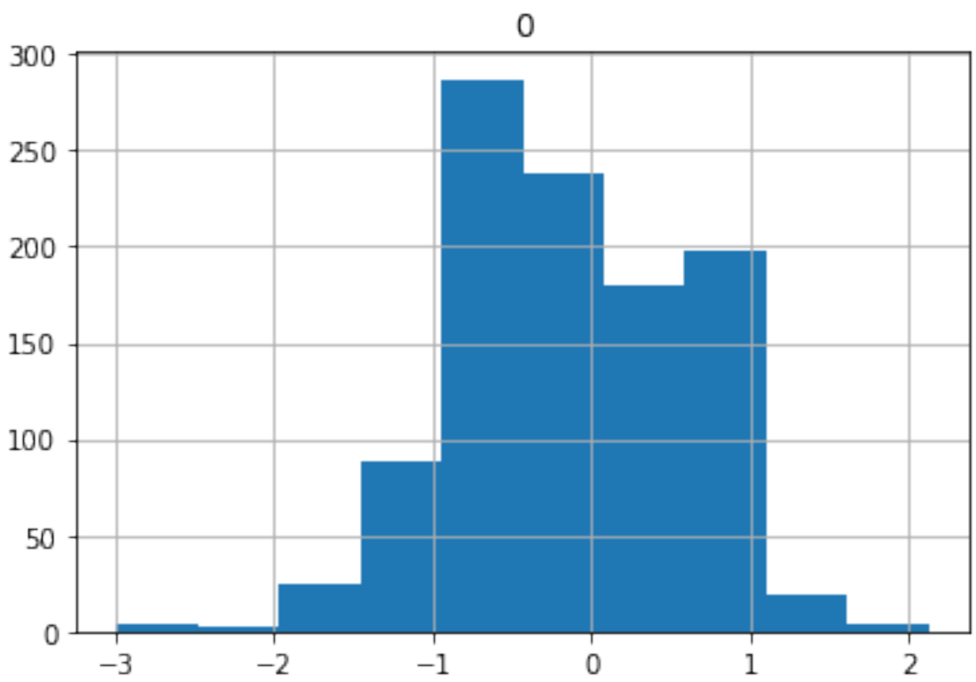
Points that lie on the margin hyperplanes should give the decision function f(x)=0

In [40]:

```
C=10
d=3

model=SVC(C=C,kernel='poly',degree=d)
model.fit(X_train_imputed,y_train)

#ref: https://stackoverflow.com/questions/32074239/sklearn-getting-distance-of-each-
y = model.decision_function(model.support_vectors_)
pd.DataFrame(y).hist()
```

Out[40]:

```
array([[<matplotlib.axes._subplots.AxesSubplot object at 0x7f51203a955
0>]],
      dtype=object)
```



In [42]:

```
np.sum(y==0) #there are many points that are close to the margin (f(x)=0), but there
```

Out[42]:

0

For polynomial kernal: As the parameter d (degree for polynomial kernal) increases, the margin size can be larger (more flexible) and allows more support vectors

For RBF kernal: As the parameter gamma increases, the decision boundary becomes more wiggled (margin size will decrease). In addition, the no. of support vectors will increase

Q2

(a)

Ridge minimizes: $RSS + \lambda \Sigma \beta^2$

error: $\sum_{i=1}^{2} (y_i - \overset{=0}{\cancel{\beta_0}} - \beta_1 x_{i1} - \beta_2 x_{i2})^2 + \lambda (\beta_1^2 + \beta_2^2)$

$$= (y_1 - \beta_1 x_{11} - \beta_2 x_{12})^2 + (y_2 - \beta_1 x_{21} - \beta_2 x_{22})^2 + \lambda (\beta_1^2 + \beta_2^2)$$

$$= (y_1 - x_{11} (\beta_1 + \beta_2))^2 + (y_2 - x_{21} (\beta_1 + \beta_2))^2 + \lambda (\beta_1^2 + \beta_2^2)$$

$$= y_1^2 + y_2^2 - 2 \times (y_1 x_{11} (\beta_1 + \beta_2) + y_2 x_{21} (\beta_1 + \beta_2)) + \lambda (\beta_1 + \beta_2^2)$$

$$= y_1^2 + y_2^2 - 2 \times (\beta_1 + \beta_2) (y_1 x_{11} + y_2 x_{21}) + \lambda (\beta_1^2 + \beta_2^2)$$

$$= y_1^2 + y_2^2 - 2 \times \beta_1 (y_1 x_{11} + y_2 x_{21}) - 2 \times \beta_2 (y_1 x_{11} + y_2 x_{21}) + \lambda (\beta_1^2 + \beta_2^2)$$

(b)

$$\frac{\partial \, error}{\partial \beta_1} = 2 \lambda \beta_1 - 2 \times (y_1 x_{11} + y_2 x_{21}) = 0 \Rightarrow \beta_1 = \frac{y_1 x_{11} + y_2 x_{21}}{\lambda}$$

$$\frac{\partial \, error}{\partial \beta_2} = 2 \lambda \beta_2 - 2 \times (y_1 x_{11} + y_2 x_{21}) = 0 \Rightarrow \beta_2 = \frac{y_1 x_{11} + y_2 x_{21}}{\lambda} = \beta_1$$

(c)

Lasso minimizes: $RSS + \lambda \Sigma|\beta|$

$$error = y_1^2 + y_2^2 - 2\times\beta_1(y_1x_{11} + y_2x_{21}) - 2\times\beta_2(y_1x_{11} + y_2x_{21}) + \lambda(|\beta_1| + |\beta_2|)$$

(d)

$$\frac{d\,error}{d\beta_1} = \lambda \cdot \frac{|\beta_1|}{\beta_1} - 2(y_1x_{11} + y_2x_{21}) = 0$$

$$\frac{d\,error}{d\beta_2} = \lambda \cdot \frac{|\beta_2|}{\beta_2} - 2(y_1x_{11} + y_2x_{21}) = 0$$

β_1 and β_2 both have multiple solutions

Lasso constraint woule have a diamond shape centered at the original of the plane

Q3

In [0]:

```
from sklearn.model_selection import train_test_split

df=pd.read_csv('https://raw.githubusercontent.com/peterwu19881230/CSCE633_ML_data/ma

print('df shape= ')
print(df.shape)

X=df.iloc[:, [0,1,2,3,4,5,6,7,8]]
response=df.iloc[:, [9]]

y=np.where(np.array(response).astype(int) == 4, 1, 0) #1 means malignant

print('no. of malignant= '+ str(np.sum(y)))
print('no. of benign= '+ str(np.sum(y==0)))

X_train, X_test, y_train, y_test = train_test_split(X, y, test_size=0.33, random_sta
```

```
df shape=
(682, 10)
no. of malignant= 239
no. of benign= 443
```

There are only ~35% of the data that are malignant (imbalanced data)

Implement Decision tree

In [56]:

```
from sklearn.tree import DecisionTreeClassifier

max_depth = list(range(1,31))
criterion=['entropy','gini']
param_grid={'criterion':criterion,'max_depth':max_depth}

grid_search = GridSearchCV(DecisionTreeClassifier(), param_grid, cv=10,scoring='accu
grid_search.fit(X_train, y_train)
```

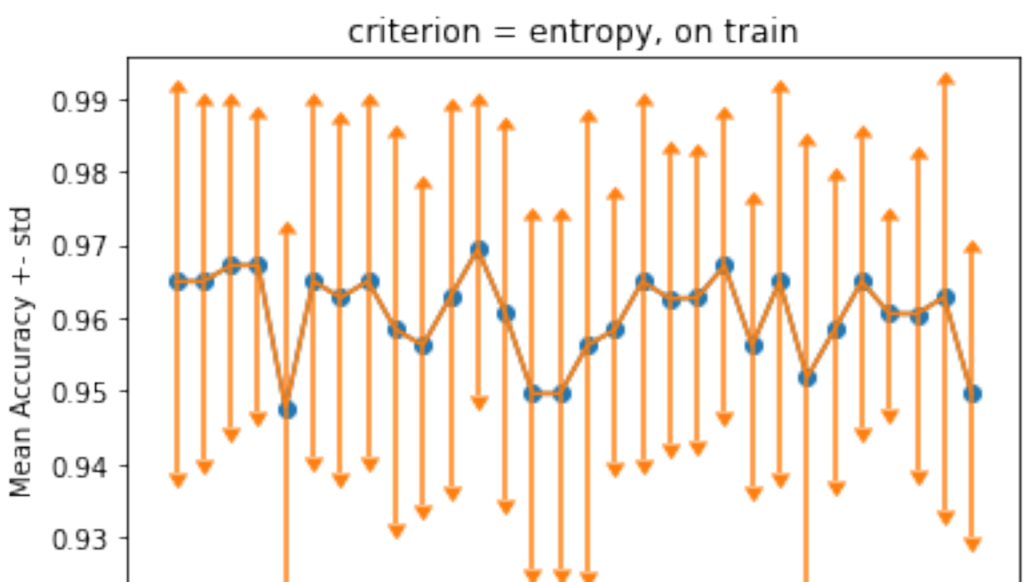
Out[56]:

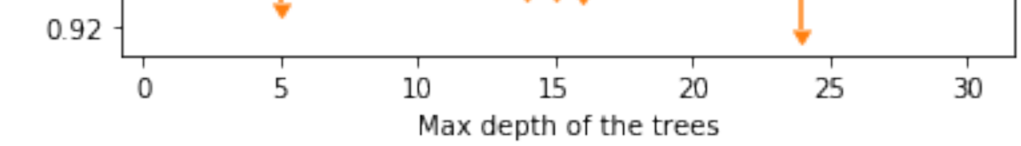
```
GridSearchCV(cv=10, error_score='raise-deprecating',
             estimator=DecisionTreeClassifier(class_weight=None,
                                              criterion='gini', max_de
pth=None,
                                              max_features=None,
                                              max_leaf_nodes=None,

min_impurity_decrease=0.0,
                                              min_impurity_split=None,
                                              min_samples_leaf=1,
                                              min_samples_split=2,

min_weight_fraction_leaf=0.0,
                                              presort=False, random_st
ate=None,
                                              splitter='best'),
             iid='warn', n_jobs=None,
             param_grid={'criterion': ['entropy', 'gini'],
                         'max_depth': [1, 2, 3, 4, 5, 6, 7, 8, 9, 10,
11, 12,
                                       13, 14, 15, 16, 17, 18, 19, 20,
21, 22,
                                       23, 24, 25, 26, 27, 28, 29, 30]
},
             pre_dispatch='2*n_jobs', refit=True, return_train_score=F
alse,
             scoring='accuracy', verbose=0)
```

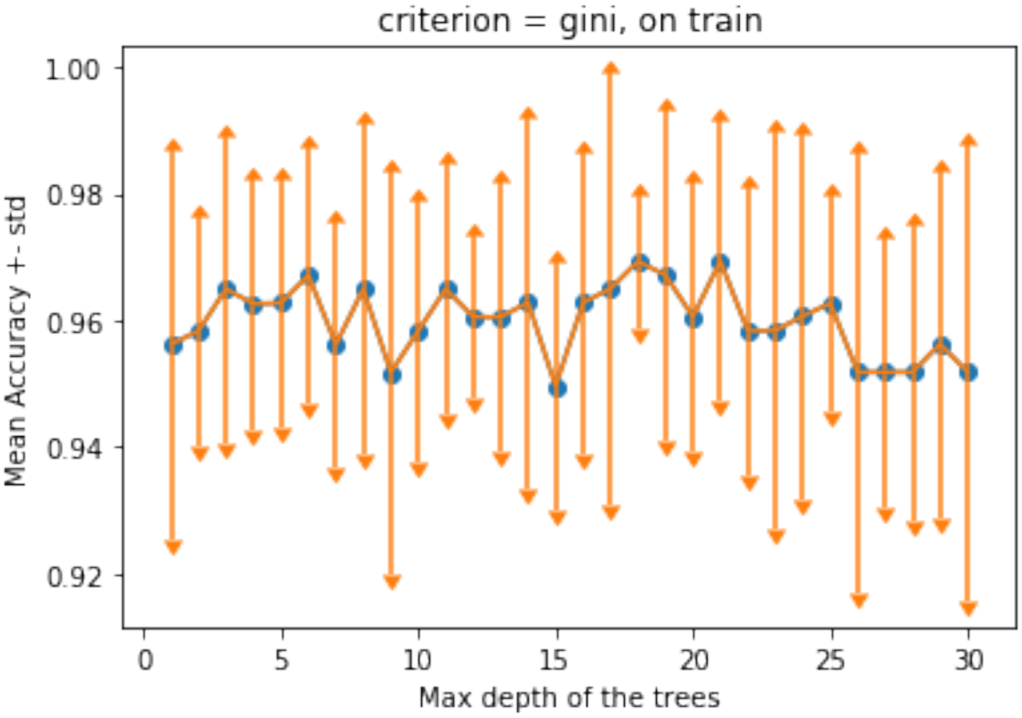
In [60]:

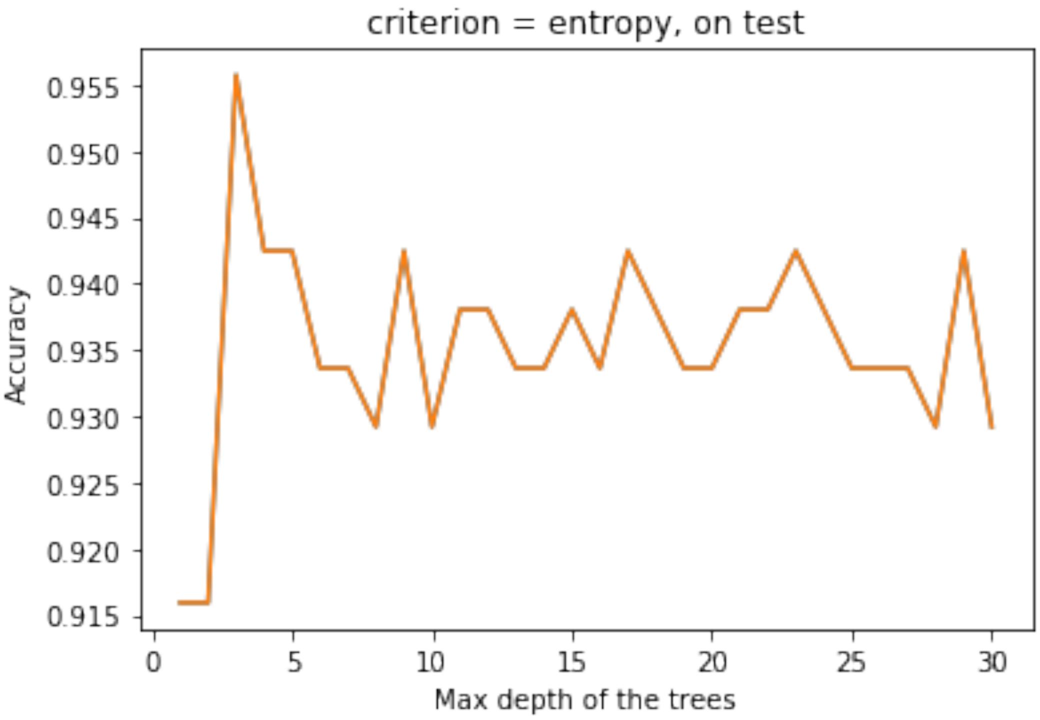
```
accuracy_list=[]
for i in range(10):
  accuracy_list.append(pd.DataFrame(grid_search.cv_results_['split'+str(i)+'_test_sc

accuracy_df=pd.concat(accuracy_list,axis=0)
```

```python
## assign column names
params=grid_search.cv_results_['params']
params_string=['criterion:'+str(param['criterion'])+'_'+'max_depth:'+str(param['max_
accuracy_df.columns=params_string

mean_array=np.array([np.mean(accuracy_df[column]) for column in accuracy_df.columns]
std_array=np.array([np.std(accuracy_df[column]) for column in accuracy_df.columns])


# plot based on training data
for i in [0,1]:
  degree_index=list(np.array(range(1,31))+15*i)
  plt.plot(max_depth,mean_array[degree_index])
  plt.errorbar(max_depth, mean_array[degree_index], yerr=std_array[degree_index],lo
  plt.scatter(max_depth,mean_array[degree_index])
  plt.title('criterion = '+criterion[i]+', '+'on train')
  plt.xlabel('Max depth of the trees')
  plt.ylabel('Mean Accuracy +- std')
  plt.show()


# plot based on test data

for i in [0,1]:

  accuracy_list=[]
  for j in max_depth:
    model=DecisionTreeClassifier(criterion=criterion[i],max_depth=j)
    model.fit(X_train,y_train)
    accuracy_list.append(accuracy_score(y_test,model.predict(X_test)))

  degree_index=list(np.array(range(1,31))+15*i)
  plt.plot(max_depth,np.array(accuracy_list))
  plt.plot(max_depth,np.array(accuracy_list))
  plt.title('criterion = '+criterion[i]+', '+'on test')
  plt.xlabel('Max depth of the trees')
  plt.ylabel('Accuracy')
  plt.show()
```




Max depth of the trees


criterion = gini, on train
Mean Accuracy +- std
Max depth of the trees


criterion = entropy, on test
Accuracy
Max depth of the trees


criterion = gini, on test
Accuracy
Max depth of the trees

Max depth of the trees

Implement Random forest

In [70]:

```
from sklearn.ensemble import RandomForestClassifier

max_depth = list(range(1,31))
criterion=['entropy','gini']
param_grid={'criterion':criterion,'max_depth':max_depth}

grid_search = GridSearchCV(RandomForestClassifier(), param_grid, cv=10,scoring='accu
  #Note: default no. of trees for RandomForestClassifier()= 10

grid_search.fit(X_train, np.array(y_train.ravel())) #I need .ravel() in here for Ra
```

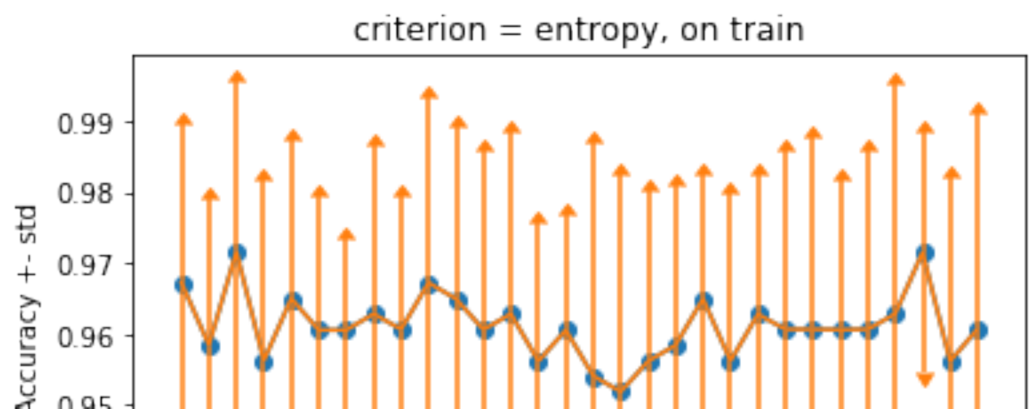
Out[70]:

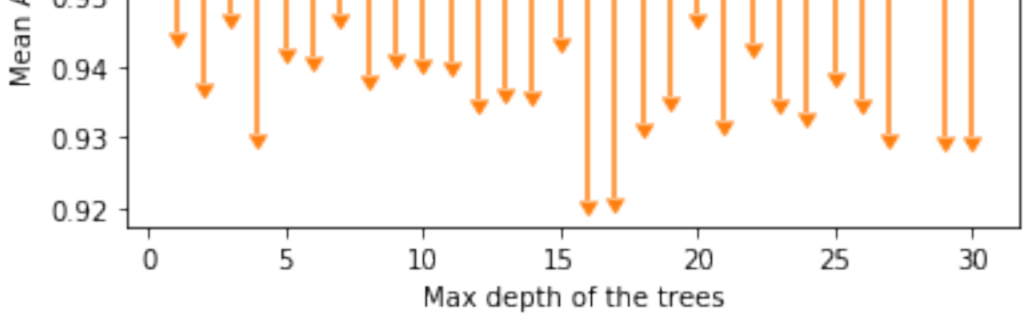
```
GridSearchCV(cv=10, error_score='raise-deprecating',
             estimator=RandomForestClassifier(bootstrap=True, class_we
ight=None,
                                              criterion='gini', max_de
pth=None,
                                              max_features='auto',
                                              max_leaf_nodes=None,

min_impurity_decrease=0.0,
                                              min_impurity_split=None,
                                              min_samples_leaf=1,
                                              min_samples_split=2,

min_weight_fraction_leaf=0.0,
                                              n_estimators='warn', n_j
obs=None,
                                              oob_score=False,
                                              random_state=None, verbo
se=0,
                                              warm_start=False),
             iid='warn', n_jobs=None,
             param_grid={'criterion': ['entropy', 'gini'],
                         'max_depth': [1, 2, 3, 4, 5, 6, 7, 8, 9, 10,
11, 12,
                                       13, 14, 15, 16, 17, 18, 19, 20,
21, 22,
                                       23, 24, 25, 26, 27, 28, 29, 30]
},
             pre_dispatch='2*n_jobs', refit=True, return_train_score=F
alse,
             scoring='accuracy', verbose=0)
```

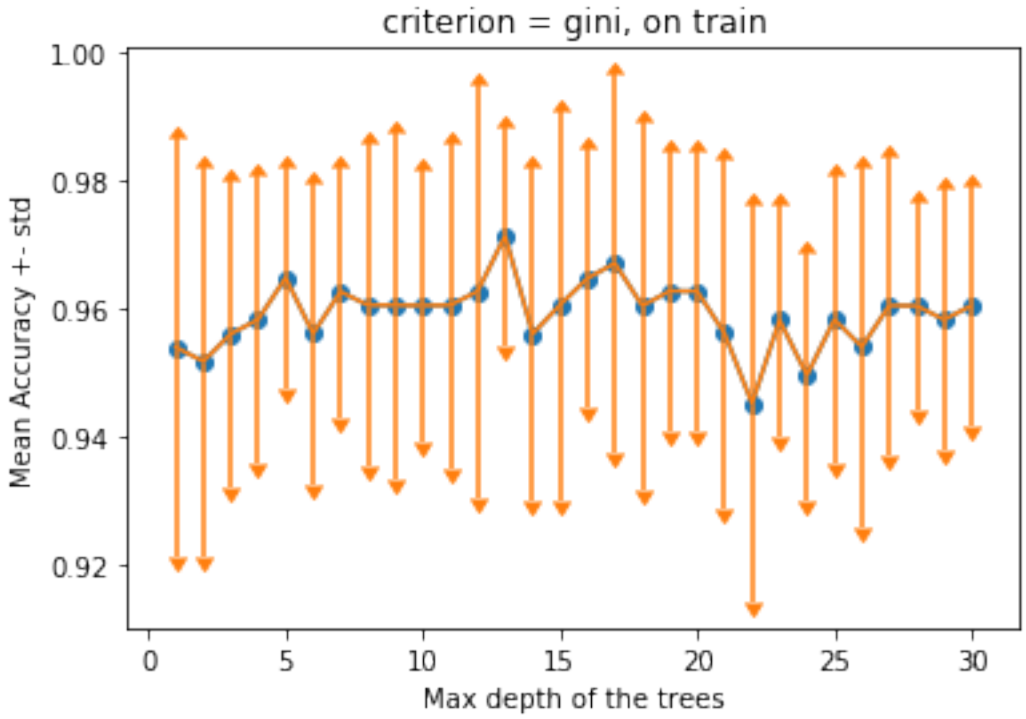
In [97]:

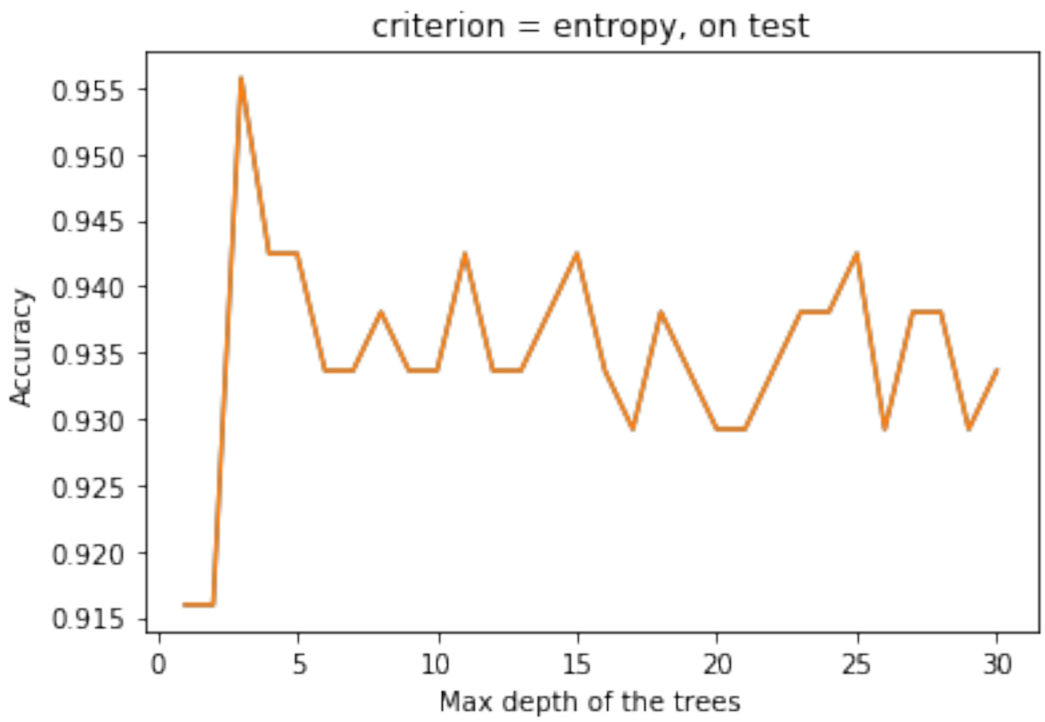
```
accuracy_list=[]
for i in range(10):
```

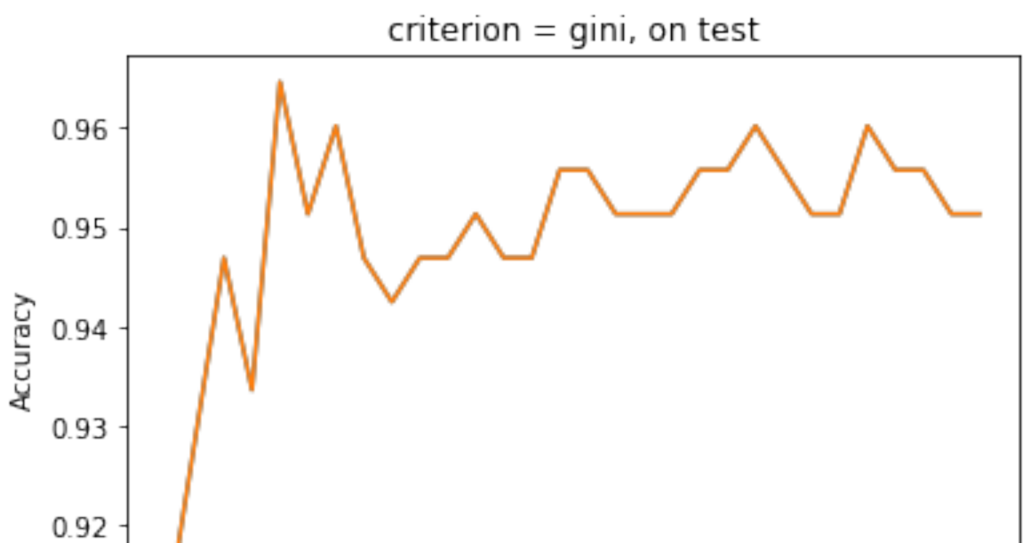
```
  accuracy_list.append(pd.DataFrame(grid_search.cv_results_['split'+str(i)+'_test_sc

accuracy_df=pd.concat(accuracy_list,axis=0)

## assign column names
params=grid_search.cv_results_['params']
params_string=['criterion:'+str(param['criterion'])+'_'+'max_depth:'+str(param['max_
accuracy_df.columns=params_string

mean_array=np.array([np.mean(accuracy_df[column]) for column in accuracy_df.columns]
std_array=np.array([np.std(accuracy_df[column]) for column in accuracy_df.columns])


# plot based on training data
for i in [0,1]:
  degree_index=list(np.array(range(1,31))+15*i)
  plt.plot(max_depth,mean_array[degree_index])
  plt.errorbar(max_depth, mean_array[degree_index], yerr=std_array[degree_index],lo
  plt.scatter(max_depth,mean_array[degree_index])
  plt.title('criterion = '+criterion[i]+', '+'on train')
  plt.xlabel('Max depth of the trees')
  plt.ylabel('Mean Accuracy +- std')
  plt.show()


# plot based on test data

featureImportances=[]
for i in [0,1]:

  accuracy_list=[]
  for j in max_depth:
    model=DecisionTreeClassifier(criterion=criterion[i],max_depth=j)
    model.fit(X_train,y_train)
    featureImportances.append(model.feature_importances_)
    accuracy_list.append(accuracy_score(y_test,model.predict(X_test)))

  degree_index=list(np.array(range(1,31))+15*i)
  plt.plot(max_depth,np.array(accuracy_list))
  plt.plot(max_depth,np.array(accuracy_list))
  plt.title('criterion = '+criterion[i]+', '+'on test')
  plt.xlabel('Max depth of the trees')
  plt.ylabel('Accuracy')
  plt.show()
```

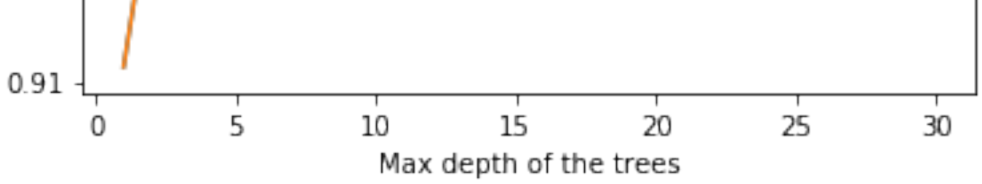



0.94
0.93
0.92
0
5
10
15
20
25
30
Max depth of the trees


criterion = gini, on train
Mean Accuracy +- std
1.00
0.98
0.96
0.94
0.92
0
5
10
15
20
25
30
Max depth of the trees


criterion = entropy, on test
Accuracy
0.955
0.950
0.945
0.940
0.935
0.930
0.925
0.920
0.915
0
5
10
15
20
25
30
Max depth of the trees


criterion = gini, on test
Accuracy
0.96
0.95
0.94
0.93
0.92


0.91
0
5
10
15
20
25
30
Max depth of the trees

In [143]:

```
# show feature importance rankings (using average of all 60 models based on [gini,e

features=['Clump Thickness','Uniformity of Cell Size','Uniformity of Cell Shape','Ma


import scipy.stats as ss
def rank(feature_importance):
  ranking=len(feature_importance) - ss.rankdata(feature_importance,method="max").ast
  return(ranking)

ranking_list=[]
importance_list=[]
for i in range(60):
  importance_list.append(pd.DataFrame(featureImportances[i]).T)
  ranking_list.append(pd.DataFrame(rank(featureImportances[i])).T)


ranking_df=pd.concat(ranking_list,axis=0)
importance_df=pd.concat(importance_list,axis=0)
feature_ranking_list=[pd.DataFrame(features),pd.DataFrame(importance_df.mean(axis=0)

feature_ranking_df=pd.DataFrame(pd.concat(feature_ranking_list,axis=1))
feature_ranking_df.columns=['features','importance mean','ranking mean','ranking std
print(feature_ranking_df)
```

```
                      features  importance mean  ranking mean  ranking 
std
0              Clump Thickness         0.111992      2.033333      0.18
1020
1      Uniformity of Cell Size         0.767551      1.000000      0.00
0000
2     Uniformity of Cell Shape         0.015073      4.766667      1.31
9562
3            Marginal Adhesion         0.004198      7.083333      1.57
6218
4  Single Epithelial Cell Size         0.010265      5.616667      1.15
1148
5                  Bare Nuclei         0.068001      2.933333      0.25
1549
6              Bland Chromatin         0.012347      5.216667      1.48
5428
7              Normal Nucleoli         0.008863      6.116667      1.82
3497
8                      Mitoses         0.001711      7.716667      1.76
6848
```

The rankings were based on the importance of each feature averaged by all the 60 models (by [gini,entropy] X [1~30 max depth of tree]). The accuracy doesn't change significantly across different hyperparameters so averaging all of them should be fine. For the final model I would probabily take out 'Marginal Adhesion' and 'Mitosis' because they are the least important. This can be further confirmed by calculating accuracy after post-pruning the trees

Homework 2

This jupyter notebook is also accessble as an online colab notebook : [https://colab.research.google.com/drive/10KcuDSp9jCx0eFkdQ-UvrS6VPQjmpYPQ#scrollTo=Yj8OAlyA5Tzv (https://colab.research.google.com/drive/10KcuDSp9jCx0eFkdQ-UvrS6VPQjmpYPQ#scrollTo=Yj8OAlyA5Tzv)](https://colab.research.google.com/drive/10KcuDSp9jCx0eFkdQ-UvrS6VPQjmpYPQ#scrollTo=Yj8OAlyA5Tzv)

Q1

Load & normalize the data