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Факультет «Информатика и системы управления»
Кафедра «Автоматизированные системы обработки информации и управления»

Отчет

Лабораторная работа № 3

По курсу Технологии машинного обучения»

ИСПОЛНИТЕЛЬ:
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Lab3

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1 Lab3

Cancer

[1]:
```
from IPython.display import Image
import numpy as np
import pandas as pd
from sklearn.model_selection import train_test_split
from sklearn.datasets import load_iris, load_boston
from sklearn.metrics import plot_confusion_matrix
from sklearn.neighbors import KNeighborsRegressor, KNeighborsClassifier
from sklearn.model_selection import cross_val_score, cross_validate
from sklearn.model_selection import KFold, RepeatedKFold, LeaveOneOut,␣
↪LeavePOut, ShuffleSplit, StratifiedKFold
from sklearn.metrics import accuracy_score, balanced_accuracy_score
from sklearn.metrics import precision_score, recall_score, f1_score,␣
↪classification_report
from sklearn.metrics import confusion_matrix
from sklearn.metrics import mean_absolute_error, mean_squared_error,␣
↪mean_squared_log_error, median_absolute_error, r2_score
from sklearn.metrics import roc_curve, roc_auc_score
from sklearn.model_selection import GridSearchCV, RandomizedSearchCV
from sklearn.model_selection import learning_curve, validation_curve
import seaborn as sns
import matplotlib.pyplot as plt
%matplotlib inline
sns.set(style="ticks")
```

[2]:
```
from sklearn.datasets import *
cancer = load_breast_cancer()
```

[3]:
```
for x in cancer:
    print(x)
```

```
data
target
frame
target_names
```

```
DESCR
feature_names
filename
```

[4]:
```
cancer['target_names']
```

[4]:
```
array(['malignant', 'benign'], dtype='<U9')
```

[5]:
```
cancer['feature_names']
```

[5]:
```
array(['mean radius', 'mean texture', 'mean perimeter', 'mean area',
       'mean smoothness', 'mean compactness', 'mean concavity',
       'mean concave points', 'mean symmetry', 'mean fractal dimension',
       'radius error', 'texture error', 'perimeter error', 'area error',
       'smoothness error', 'compactness error', 'concavity error',
       'concave points error', 'symmetry error',
       'fractal dimension error', 'worst radius', 'worst texture',
       'worst perimeter', 'worst area', 'worst smoothness',
       'worst compactness', 'worst concavity', 'worst concave points',
       'worst symmetry', 'worst fractal dimension'], dtype='<U23')
```

1.1

[7]:
```
X_train, X_test, Y_train, Y_test = train_test_split(cancer.data, cancer.target,␣
↪test_size=0.2, random_state=1)
```

[8]:
```
X_train.shape, Y_train.shape
```

[8]:
```
((455, 30), (455,))
```

[9]:
```
X_test.shape, Y_test.shape
```

[9]:
```
((114, 30), (114,))
```

1.2

target -

[11]:
```
class_set = KNeighborsClassifier(n_neighbors=3)
class_set.fit(X_train, Y_train)
target_set_0 = class_set.predict(X_train)
target_set_1 = class_set.predict(X_test)
len(target_set_1), target_set_1
```

[11]:
```
(114,
 array([1, 0, 1, 0, 0, 0, 0, 0, 1, 1, 1, 1, 0, 1, 1, 1, 1, 1, 1, 0, 1, 1,
        0, 1, 0, 1, 0, 0, 0, 0, 0, 1, 0, 1, 1, 1, 0, 1, 1, 1, 1, 1, 1, 1,
        1, 0, 1, 1, 1, 0, 0, 0, 1, 1, 1, 1, 1, 0, 1, 1, 1, 0, 1, 0, 1, 1,
        1, 0, 1, 1, 1, 1, 0, 0, 1, 0, 1, 1, 1, 0, 1, 0, 1, 0, 1, 1, 0, 1,
```

```
       0, 1, 1, 0, 1, 1, 0, 0, 1, 1, 1, 1, 1, 1, 1, 1, 0, 1, 1, 1, 0, 0,
       1, 1, 1, 1]))
```

1.3

[12]:
```
accuracy_score(Y_test, target_set_1)
```

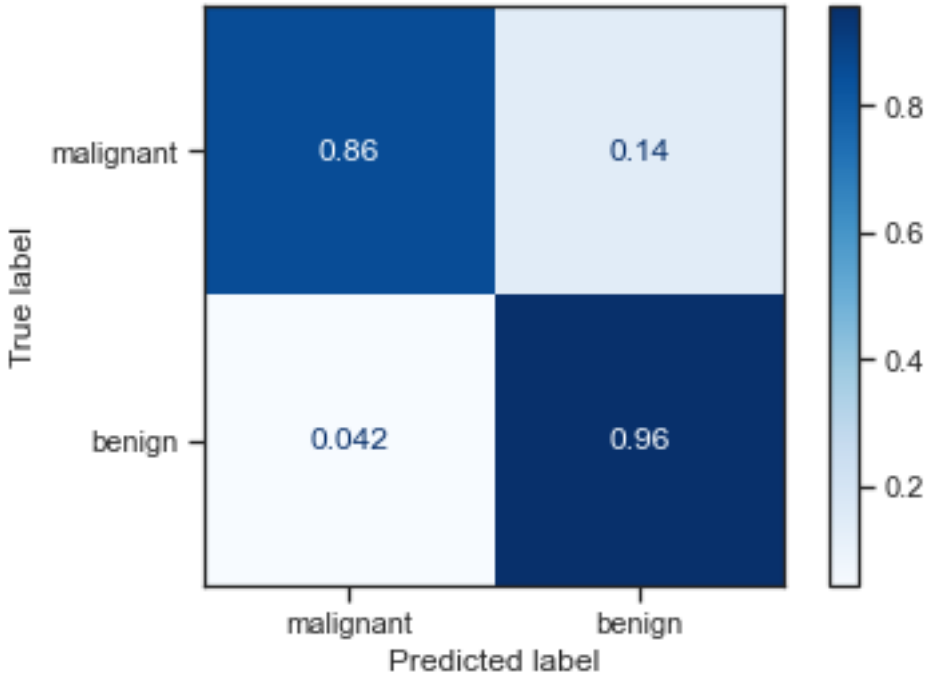
[12]:
```
0.9210526315789473
```

[13]:
```
confusion_matrix(Y_test, target_set_1, labels=[0, 1])
```

[13]:
```
array([[36,  6],
       [ 3, 69]], dtype=int64)
```

[14]:
```
plot_confusion_matrix(class_set, X_test, Y_test,
                      display_labels=cancer.target_names,
                      cmap=plt.cm.Blues, normalize='true')
```

[14]:
```
<sklearn.metrics._plot.confusion_matrix.ConfusionMatrixDisplay at 0x1a592343a90>
```



[15]:
```
f1_score(Y_test,target_set_1)
```

[15]:
```
0.9387755102040817
```

, 0.93 -

1.4

[16]:
```
n_range = np.array(range(2,30,3))
tuned_parameters = [{'n_neighbors': n_range}]
tuned_parameters
```

[16]:
```
[{'n_neighbors': array([ 2,  5,  8, 11, 14, 17, 20, 23, 26, 29])}]
```

[17]:
```
%%time
clf_gs = GridSearchCV(KNeighborsClassifier(), tuned_parameters,␣
↪cv=RepeatedKFold(n_splits=10, n_repeats=5), scoring='accuracy')
clf_gs.fit(cancer.data, cancer.target)
```

```
Wall time: 2.07 s
```

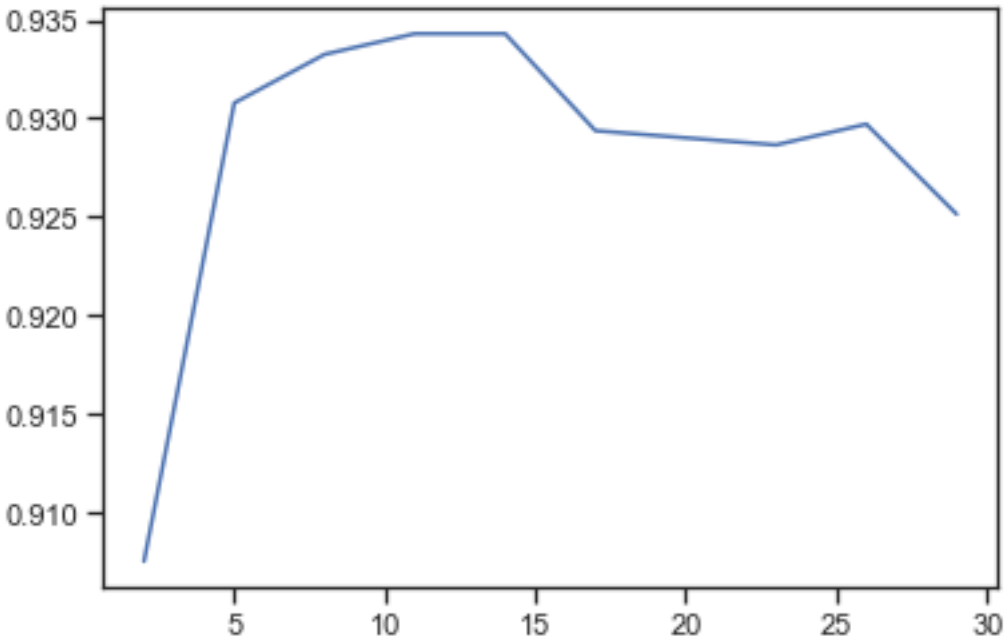
[17]:
```
GridSearchCV(cv=RepeatedKFold(n_repeats=5, n_splits=10, random_state=None),
             estimator=KNeighborsClassifier(),
             param_grid=[{'n_neighbors': array([ 2,  5,  8, 11, 14, 17, 20, 23,
26, 29])}],
             scoring='accuracy')
```

[18]:
```
clf_gs.best_score_, clf_gs.best_params_
```

[18]:
```
(0.9342919799498746, {'n_neighbors': 11})
```

[19]:
```
plt.plot(n_range, clf_gs.cv_results_['mean_test_score'])
```

[19]:
```
[<matplotlib.lines.Line2D at 0x1a592765370>]
```



[20]:
```
%%time
clf_gs = GridSearchCV(KNeighborsClassifier(), tuned_parameters,␣
 ↪cv=ShuffleSplit(n_splits=10), scoring='accuracy')
clf_gs.fit(cancer.data, cancer.target)
```

```
Wall time: 422 ms
```

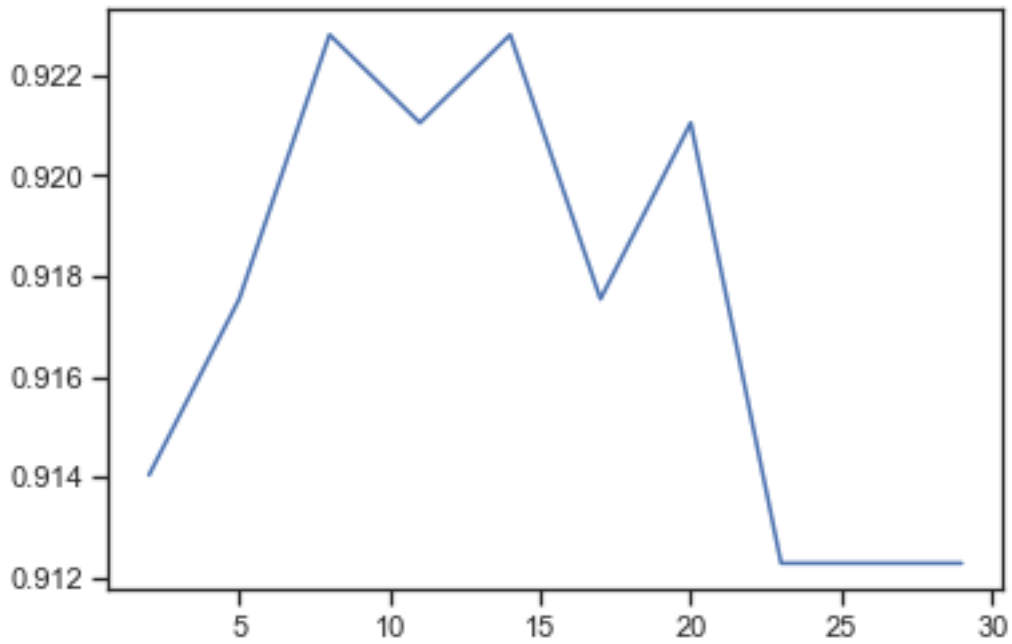
[20]:
```
GridSearchCV(cv=ShuffleSplit(n_splits=10, random_state=None, test_size=None,
train_size=None),
             estimator=KNeighborsClassifier(),
             param_grid=[{'n_neighbors': array([ 2,  5,  8, 11, 14, 17, 20, 23,
26, 29])}],
             scoring='accuracy')
```

[21]:
```
clf_gs.best_score_, clf_gs.best_params_
```

[21]:
```
(0.9228070175438597, {'n_neighbors': 8})
```

[22]:
```
plt.plot(n_range, clf_gs.cv_results_['mean_test_score'])
```

[22]:
```
[<matplotlib.lines.Line2D at 0x1a5927a5eb0>]
```



[23]:
```
%%time
clf_gs = GridSearchCV(KNeighborsClassifier(), tuned_parameters,␣
 ↪cv=LeaveOneOut(), scoring='accuracy')
clf_gs.fit(cancer.data, cancer.target)
```

```
Wall time: 15.6 s
```

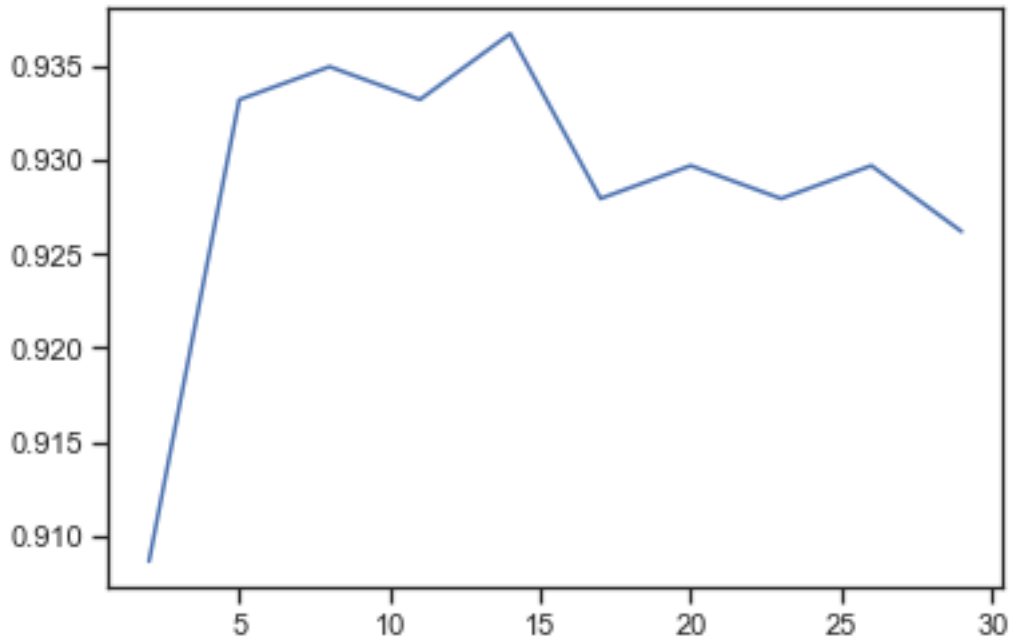
[23]:
```
GridSearchCV(cv=LeaveOneOut(), estimator=KNeighborsClassifier(),
             param_grid=[{'n_neighbors': array([ 2,  5,  8, 11, 14, 17, 20, 23,
 26, 29])}],
             scoring='accuracy')
```

[24]:
```
clf_gs.best_score_, clf_gs.best_params_
```

[24]:
```
(0.9367311072056239, {'n_neighbors': 14})
```

[25]:
```
plt.plot(n_range, clf_gs.cv_results_['mean_test_score'])
```

[25]:
```
[<matplotlib.lines.Line2D at 0x1a592a53a00>]
```



Loo 14, ShuffleSplit 11, Kfold 8.

[26]:
```
%%time
n_range = np.array(range(1,15,1))
tuned_parameters = [{'n_neighbors': n_range}]
clf_gs = GridSearchCV(KNeighborsClassifier(), tuned_parameters,␣
 ↪cv=LeaveOneOut(), scoring='accuracy')
```

```
clf_gs.fit(cancer.data, cancer.target)
```

```
Wall time: 21.6 s
```

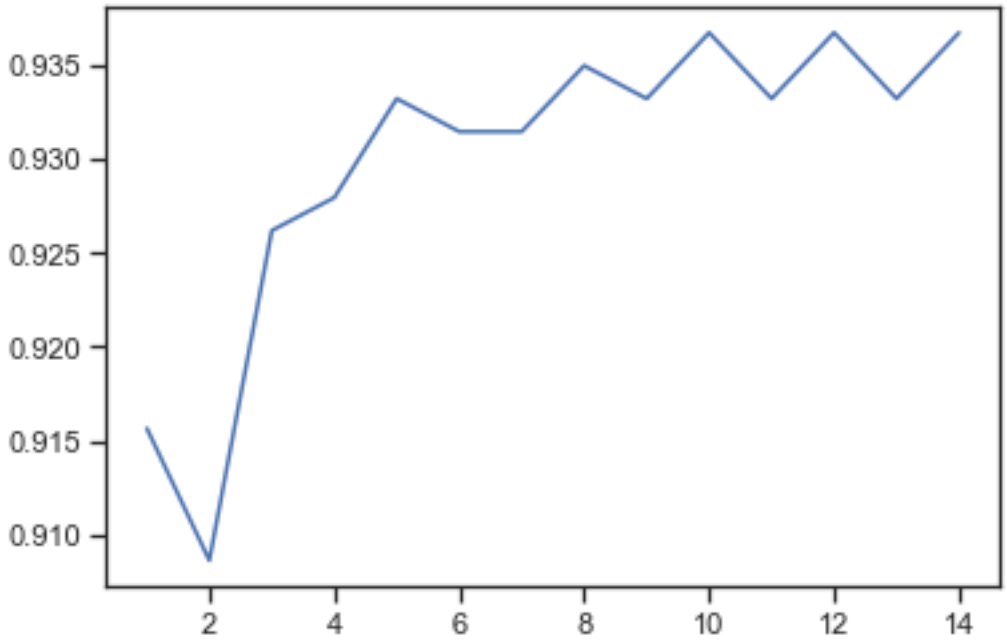
[26]:
```
GridSearchCV(cv=LeaveOneOut(), estimator=KNeighborsClassifier(),
             param_grid=[{'n_neighbors': array([ 1,  2,  3,  4,  5,  6,  7,  8,
 9, 10, 11, 12, 13, 14])}],
             scoring='accuracy')
```

[27]:
```
clf_gs.best_score_, clf_gs.best_params_
```

[27]:
```
(0.9367311072056239, {'n_neighbors': 10})
```

[28]:
```
plt.plot(n_range, clf_gs.cv_results_['mean_test_score'])
```

[28]:
```
[<matplotlib.lines.Line2D at 0x1a592c8ac10>]
```



: 10, 0,936. , 0.921 2

[29]:
```
clf_gs.best_estimator_.fit(X_train, Y_train)
target2_0 = clf_gs.best_estimator_.predict(X_train)
target2_1 = clf_gs.best_estimator_.predict(X_test)
```

[30]:
```
accuracy_score(Y_train, target2_0), accuracy_score(Y_test, target2_1)
```

[30]:
```
(0.9362637362637363, 0.9298245614035088)
```

[31]:
```
accuracy_score(Y_train, target_set_0), accuracy_score(Y_test, target_set_1)
```

[31]:
```
(0.9516483516483516, 0.9210526315789473)
```

[32]:
```
def plot_validation_curve(estimator, title, X, y,
                          param_name, param_range, cv,
                          scoring="accuracy"):

    train_scores, test_scores = validation_curve(
        estimator, X, y, param_name=param_name, param_range=param_range,
        cv=cv, scoring=scoring, n_jobs=1)
    train_scores_mean = np.mean(train_scores, axis=1)
    train_scores_std = np.std(train_scores, axis=1)
    test_scores_mean = np.mean(test_scores, axis=1)
    test_scores_std = np.std(test_scores, axis=1)

    plt.title(title)
    plt.xlabel(param_name)
    plt.ylabel(str(scoring))
    plt.ylim(0.0, 1.1)
    lw = 2
    plt.plot(param_range, train_scores_mean, label="Training score",
                 color="darkorange", lw=lw)
    plt.fill_between(param_range, train_scores_mean - train_scores_std,
                     train_scores_mean + train_scores_std, alpha=0.4,
                     color="darkorange", lw=lw)
    plt.plot(param_range, test_scores_mean, label="Cross-validation score",
                 color="navy", lw=lw)
    plt.fill_between(param_range, test_scores_mean - test_scores_std,
                     test_scores_mean + test_scores_std, alpha=0.2,
                     color="navy", lw=lw)
    plt.legend(loc="best")
    return plt

def plot_learning_curve(estimator, title, X, y, ylim=None, cv=None,
                        n_jobs=None, train_sizes=np.linspace(.1, 1.0, 5)):
    plt.figure()
    plt.title(title)
    if ylim is not None:
        plt.ylim(*ylim)
    plt.xlabel("Training examples")
    plt.ylabel("Score")
    train_sizes, train_scores, test_scores = learning_curve(
        estimator, X, y, cv=cv, n_jobs=n_jobs, train_sizes=train_sizes)
    train_scores_mean = np.mean(train_scores, axis=1)
    train_scores_std = np.std(train_scores, axis=1)
    test_scores_mean = np.mean(test_scores, axis=1)
```

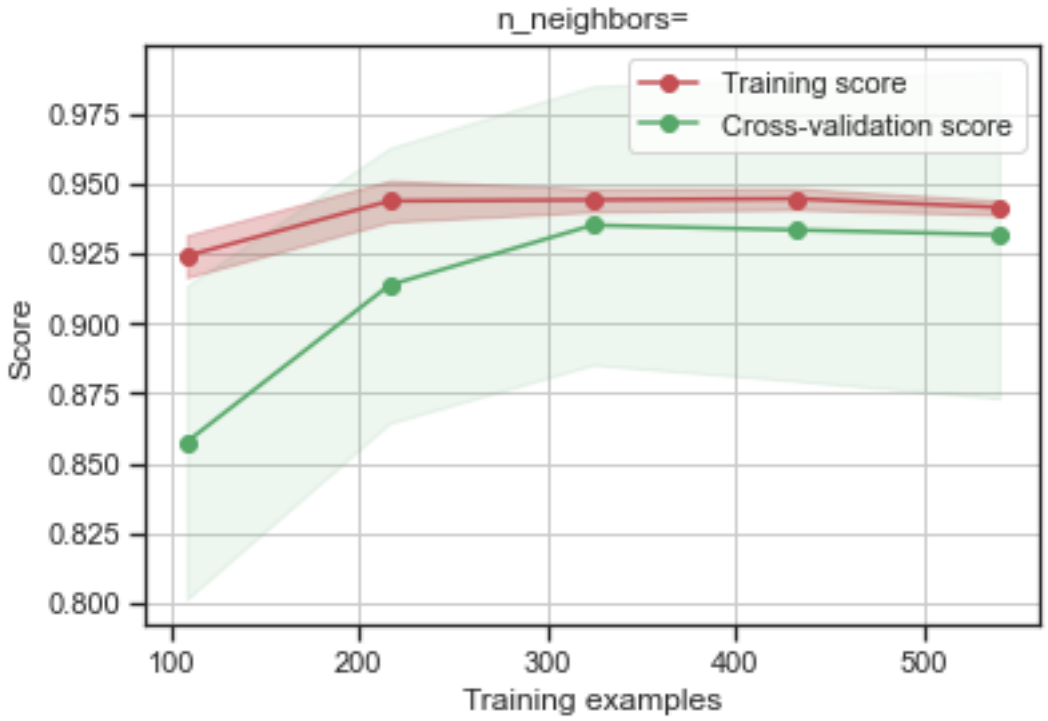
```
    test_scores_std = np.std(test_scores, axis=1)
    plt.grid()

    plt.fill_between(train_sizes, train_scores_mean - train_scores_std,
                     train_scores_mean + train_scores_std, alpha=0.3,
                     color="r")
    plt.fill_between(train_sizes, test_scores_mean - test_scores_std,
                     test_scores_mean + test_scores_std, alpha=0.1, color="g")
    plt.plot(train_sizes, train_scores_mean, 'o-', color="r",
             label="Training score")
    plt.plot(train_sizes, test_scores_mean, 'o-', color="g",
             label="Cross-validation score")

    plt.legend(loc="best")
    return plt
```

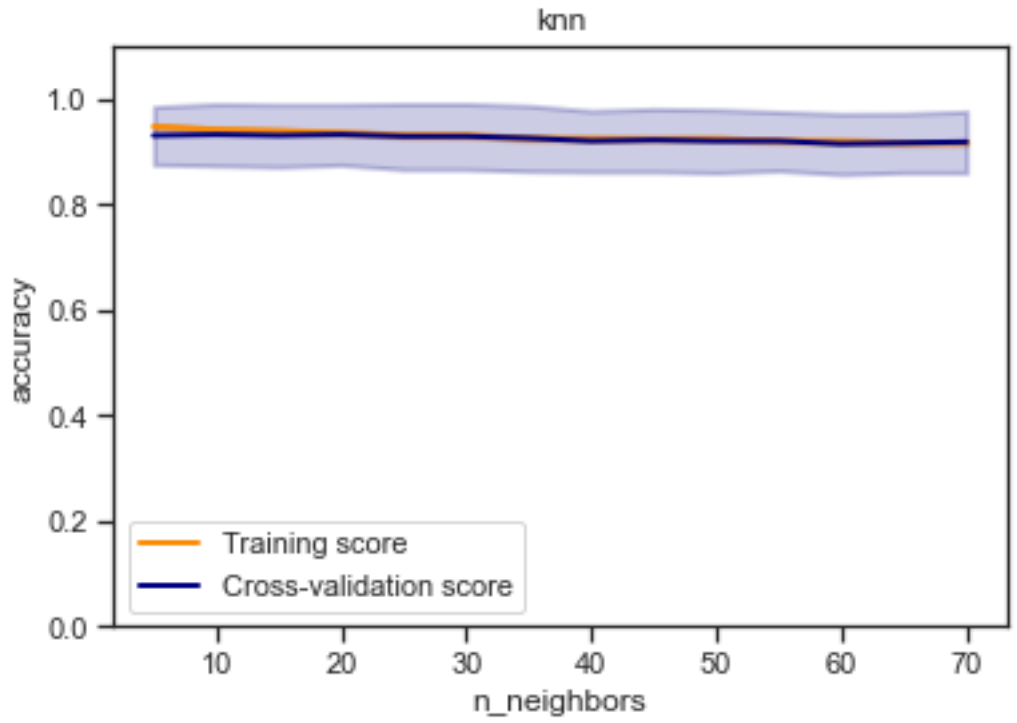
[33]:
```
plot_learning_curve(clf_gs.best_estimator_, 'n_neighbors=',
                    cancer.data, cancer.target, cv=20, train_sizes=np.linspace(.
↪2, 1.0, 5))
```

[33]:
```
<module 'matplotlib.pyplot' from 'C:\\Users\\ksarb\\anaconda3\\lib\\site-
packages\\matplotlib\\pyplot.py'>
```



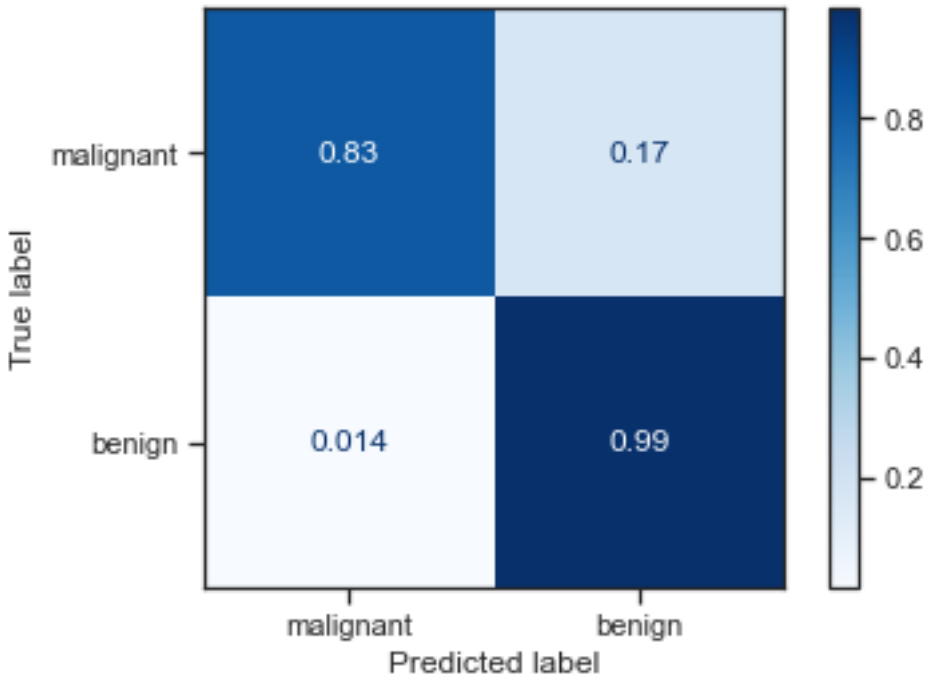
[34]:
```
n_range2 = np.array(range(5,75,5))
plot_validation_curve(clf_gs.best_estimator_, 'knn',
                      cancer.data, cancer.target,
                      param_name='n_neighbors', param_range=n_range2,
                      cv=20, scoring="accuracy")
```

[34]:
```
<module 'matplotlib.pyplot' from 'C:\\Users\\ksarb\\anaconda3\\lib\\site-
packages\\matplotlib\\pyplot.py'>
```



[35]:
```
plot_confusion_matrix(clf_gs.best_estimator_, X_test, Y_test,
                      display_labels=cancer.target_names,
                      cmap=plt.cm.Blues, normalize='true')
```

[35]:
```
<sklearn.metrics._plot.confusion_matrix.ConfusionMatrixDisplay at 0x1a58cb8bc10>
```


malignant
benign
True label
0.83
0.17
0.014
0.99
malignant
benign
Predicted label
0.8
0.6
0.4
0.2

1.5

10. 93.8%.

, .

, 17% - .