

Naive Bayes models

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5/1/23

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```
import pandas as pd
import numpy as np
import matplotlib.pyplot as plt
import seaborn as sns
from sklearn.model_selection import cross_val_score
from sklearn.model_selection import GridSearchCV
from sklearn.metrics import (
    roc_curve,
    auc,
    roc_auc_score,
    confusion_matrix,
    classification_report,
    accuracy_score,
    precision_score,
    recall_score,
    f1_score,
    precision_recall_curve,
    average_precision_score,
)
from sklearn.naive_bayes import GaussianNB

# DIRECTORIES
input_path = "../data/processed/"
train_path = "../data/processed/train_data/"
test_path = "../data/processed/test_data/"
results_path = "../models/results/"

# FILES
# MOLECULAR DESCRIPTORS
molecular_descriptors_training_file = "molecular_descriptors_training.csv"
molecular_descriptors_test_file = "molecular_descriptors_test.csv"
# MACCS KEYS
maccs_keys_training_file = "maccs_keys_training.csv"
maccs_keys_test_file = "maccs_keys_test.csv"
# ECFP4 FINGERPRINTS
ecfp4_fingerprints_training_file = "ecfp4_fingerprints_training.csv"
ecfp4_fingerprints_test_file = "ecfp4_fingerprints_test.csv"
# RESULTS FILE
results_file = "results_table.csv"

# LOAD DATA
# MOLECULAR DESCRIPTORS
## TRAINING
molecular_descriptors_training = pd.read_csv(
```

```
        train_path + molecular_descriptors_training_file
    )
    X_training_molecular_descriptors = molecular_descriptors_training.drop(
        columns=["activity"]
    )
    Y_training_molecular_descriptors = molecular_descriptors_training["activity"]
    ## TEST
    molecular_descriptors_test = pd.read_csv(test_path + molecular_descriptors_test_file)
    X_test_molecular_descriptors = molecular_descriptors_test.drop(columns=["activity"])
    Y_test_molecular_descriptors = molecular_descriptors_test["activity"]
    # MACCS KEYS
    ## TRAINING
    macc_keys_training = pd.read_csv(train_path + maccs_keys_training_file)
    X_training_maccs_keys = macc_keys_training.drop(columns=["activity"])
    Y_training_maccs_keys = macc_keys_training["activity"]
    ## TEST
    macc_keys_test = pd.read_csv(test_path + maccs_keys_test_file)
    X_test_maccs_keys = macc_keys_test.drop(columns=["activity"])
    Y_test_maccs_keys = macc_keys_test["activity"]
    # ECFP4 FINGERPRINTS
    ## TRAINING
    ecfp4_fingerprints_training = pd.read_csv(train_path + ecfp4_fingerprints_training_file)
    X_training_ecfp4_fingerprints = ecfp4_fingerprints_training.drop(columns=["activity"])
    Y_training_ecfp4_fingerprints = ecfp4_fingerprints_training["activity"]
    ## TEST
    ecfp4_fingerprints_test = pd.read_csv(test_path + ecfp4_fingerprints_test_file)
    X_test_ecfp4_fingerprints = ecfp4_fingerprints_test.drop(columns=["activity"])
    Y_test_ecfp4_fingerprints = ecfp4_fingerprints_test["activity"]
```

Chapter 1

NAIVE BAYES MODEL FOR MOLECULAR DESCRIPTORS

```
# BUILD A NAIVE BAYES MODEL FOR MOLECULAR DESCRIPTORS DATA. USE GRID SEARCH AND CROSS-VALIDATION
# CREATE A GRID OF POSSIBLE VALUES FOR THE HYPERPARAMETERS
param_grid = {
    "var_smoothing": np.logspace(0, -9, num=100),
}
# CREATE THE GRID SEARCH OBJECT
grid_molecular_descriptors = GridSearchCV(
    estimator=GaussianNB(),
    param_grid=param_grid,
    cv=5,
    n_jobs=-1,
    scoring="roc_auc",
    verbose=1,
)

# FIT THE GRID SEARCH TO THE DATA
grid_molecular_descriptors.fit(
    X_training_molecular_descriptors, Y_training_molecular_descriptors
)
```

Fitting 5 folds for each of 100 candidates, totalling 500 fits

```
GridSearchCV(cv=5, estimator=GaussianNB(), n_jobs=-1,
             param_grid={'var_smoothing': array([1.00000000e+00, 8.11130831e-01, 6.57933225e-01,
```

4CHAPTER 1. NAIVE BAYES MODEL FOR MOLECULAR DESCRIPTORS

```
4.32876128e-01, 3.51119173e-01, 2.84803587e-01, 2.31012970e-01,
1.87381742e-01, 1.51991108e-01, 1.23284674e-01, 1.00000000e-01,
8.11130831e-02, 6.57933225e-02, 5.33669923e-02, 4.32876128e-02,
3.51119173e-02, 2.8480358...
1.23284674e-07, 1.00000000e-07, 8.11130831e-08, 6.57933225e-08,
5.33669923e-08, 4.32876128e-08, 3.51119173e-08, 2.84803587e-08,
2.31012970e-08, 1.87381742e-08, 1.51991108e-08, 1.23284674e-08,
1.00000000e-08, 8.11130831e-09, 6.57933225e-09, 5.33669923e-09,
4.32876128e-09, 3.51119173e-09, 2.84803587e-09, 2.31012970e-09,
1.87381742e-09, 1.51991108e-09, 1.23284674e-09, 1.00000000e-09]]},
    scoring='roc_auc', verbose=1)

# WE GET THE BEST KNN MODEL
best_model_molecular_descriptors = grid_molecular_descriptors.best_estimator_
best_model_name = "Naive Bayes Molecular Descriptors"

# PREDICT
Y_pred_molecular_descriptors = best_model_molecular_descriptors.predict(
    X_test_molecular_descriptors
)

# EVALUATE
accuracy = accuracy_score(Y_test_molecular_descriptors, Y_pred_molecular_descriptors)
precision = precision_score(Y_test_molecular_descriptors, Y_pred_molecular_descriptors)
recall = recall_score(Y_test_molecular_descriptors, Y_pred_molecular_descriptors)
auc_molecular_descriptors = roc_auc_score(
    Y_test_molecular_descriptors, Y_pred_molecular_descriptors
)

# AUC TRAINING
Y_pred_train_molecular_descriptors = best_model_molecular_descriptors.predict(
    X_training_molecular_descriptors
)
auc_train_molecular_descriptors = roc_auc_score(
    Y_training_molecular_descriptors, Y_pred_train_molecular_descriptors
)

# CREATE DATAFRAME WITH RESULTS
results_molecular_descriptors = pd.DataFrame(
    {
        "model_name": [best_model_name],
        "accuracy": [round(accuracy, 2)],
        "precision": [round(precision, 2)],
        "recall": [round(recall, 2)],
        "auc": [round(auc_molecular_descriptors, 2)],
        "auc_train": [round(auc_train_molecular_descriptors, 2)],
```



```
    }  
)  
  
# SAVE TABLE_RESULTS.CSV  
table_results = pd.read_csv(results_path + results_file)  
table_results = table_results.append(results_molecular_descriptors)  
table_results.to_csv(results_path + results_file, index=False)
```

/var/folders/3s/vv1d0lmn7g134m4psncn2_q80000gn/T/ipykernel_15279/4156157498.py:3: FutureWarning:

The frame.append method is deprecated and will be removed from pandas in a future version. Use pa

Chapter 2

NAIVE BAYES MODEL FOR MACCS KEYS

```
# BUILD A NAIVE BAYES MODEL FOR MACCS KEYS DATA. USE GRID SEARCH AND CROSS-VALIDATION TO FIND
# CREATE A GRID OF POSSIBLE VALUES FOR THE HYPERPARAMETERS
param_grid = {
    "var_smoothing": np.logspace(0, -9, num=100),
}
# CREATE THE GRID SEARCH OBJECT
grid_maccs_keys = GridSearchCV(
    estimator=GaussianNB(),
    param_grid=param_grid,
    cv=5,
    n_jobs=-1,
    scoring="roc_auc",
    verbose=1,
)

# FIT THE GRID SEARCH TO THE DATA
grid_maccs_keys.fit(X_training_maccs_keys, Y_training_maccs_keys)
```

Fitting 5 folds for each of 100 candidates, totalling 500 fits

```
GridSearchCV(cv=5, estimator=GaussianNB(), n_jobs=-1,
             param_grid={'var_smoothing': array([1.00000000e+00, 8.11130831e-01, 6.57933225e-01,
4.32876128e-01, 3.51119173e-01, 2.84803587e-01, 2.31012970e-01,
1.87381742e-01, 1.51991108e-01, 1.23284674e-01, 1.00000000e-01,
8.11130831e-02, 6.57933225e-02, 5.33669923e-02, 4.32876128e-02,
3.51119173e-02, 2.8480358...
```

```

1.23284674e-07, 1.00000000e-07, 8.11130831e-08, 6.57933225e-08,
5.33669923e-08, 4.32876128e-08, 3.51119173e-08, 2.84803587e-08,
2.31012970e-08, 1.87381742e-08, 1.51991108e-08, 1.23284674e-08,
1.00000000e-08, 8.11130831e-09, 6.57933225e-09, 5.33669923e-09,
4.32876128e-09, 3.51119173e-09, 2.84803587e-09, 2.31012970e-09,
1.87381742e-09, 1.51991108e-09, 1.23284674e-09, 1.00000000e-09]]},
        scoring='roc_auc', verbose=1)

# WE GET THE BEST KNN MODEL
best_model_maccs_keys = grid_maccs_keys.best_estimator_
best_model_name = "Naive Bayes MACCS Keys"

# PREDICT
Y_pred_maccs_keys = best_model_maccs_keys.predict(X_test_maccs_keys)
# EVALUATE
accuracy = accuracy_score(Y_test_maccs_keys, Y_pred_maccs_keys)
precision = precision_score(Y_test_maccs_keys, Y_pred_maccs_keys)
recall = recall_score(Y_test_maccs_keys, Y_pred_maccs_keys)
auc_maccs_keys = roc_auc_score(Y_test_maccs_keys, Y_pred_maccs_keys)
# AUC TRAINING
Y_pred_train_maccs_keys = best_model_maccs_keys.predict(X_training_maccs_keys)
auc_train_maccs_keys = roc_auc_score(Y_training_maccs_keys, Y_pred_train_maccs_keys)

# CREATE DATAFRAME WITH RESULTS
results_maccs_keys = pd.DataFrame(
    {
        "model_name": [best_model_name],
        "accuracy": [round(accuracy, 2)],
        "precision": [round(precision, 2)],
        "recall": [round(recall, 2)],
        "auc": [round(auc_maccs_keys, 2)],
        "auc_train": [round(auc_train_maccs_keys, 2)],
    }
)

# SAVE TABLE_RESULTS.CSV
table_results = pd.read_csv(results_path + results_file)
table_results = table_results.append(results_maccs_keys)
table_results.to_csv(results_path + results_file, index=False)

```

/var/folders/3s/vv1d0lmn7g134m4psncn2_q80000gn/T/ipykernel_15279/2186010174.py:3: Futur

The frame.append method is deprecated and will be removed from pandas in a future vers.

Chapter 3

NAIVE BAYES MODEL FOR ECFP4 FINGERPRINTS

```
# BUILD A NAIVE BAYES MODEL FOR ECFP4 FINGERPRINTS DATA. USE GRID SEARCH AND CROSS-VALIDATION
# CREATE A GRID OF POSSIBLE VALUES FOR THE HYPERPARAMETERS
param_grid = {
    "var_smoothing": np.logspace(0, -9, num=100),
}
# CREATE THE GRID SEARCH OBJECT
grid_ecfp4_fingerprints = GridSearchCV(
    estimator=GaussianNB(),
    param_grid=param_grid,
    cv=5,
    n_jobs=-1,
    scoring="roc_auc",
    verbose=1,
)

# FIT THE GRID SEARCH TO THE DATA
grid_ecfp4_fingerprints.fit(
    X_training_ecfp4_fingerprints, Y_training_ecfp4_fingerprints
)
```

Fitting 5 folds for each of 100 candidates, totalling 500 fits

```
GridSearchCV(cv=5, estimator=GaussianNB(), n_jobs=-1,
             param_grid={'var_smoothing': array([1.00000000e+00, 8.11130831e-01, 6.57933225e-01,
```

```

4.32876128e-01, 3.51119173e-01, 2.84803587e-01, 2.31012970e-01,
1.87381742e-01, 1.51991108e-01, 1.23284674e-01, 1.00000000e-01,
8.11130831e-02, 6.57933225e-02, 5.33669923e-02, 4.32876128e-02,
3.51119173e-02, 2.8480358...
1.23284674e-07, 1.00000000e-07, 8.11130831e-08, 6.57933225e-08,
5.33669923e-08, 4.32876128e-08, 3.51119173e-08, 2.84803587e-08,
2.31012970e-08, 1.87381742e-08, 1.51991108e-08, 1.23284674e-08,
1.00000000e-08, 8.11130831e-09, 6.57933225e-09, 5.33669923e-09,
4.32876128e-09, 3.51119173e-09, 2.84803587e-09, 2.31012970e-09,
1.87381742e-09, 1.51991108e-09, 1.23284674e-09, 1.00000000e-09]]},
    scoring='roc_auc', verbose=1)

# WE GET THE BEST KNN MODEL
best_model_ecfp4_fingerprints = grid_ecfp4_fingerprints.best_estimator_
best_model_name = "Naive Bayes ECFP4 Fingerprints"

# PREDICT
Y_pred_ecfp4_fingerprints = best_model_ecfp4_fingerprints.predict(
    X_test_ecfp4_fingerprints
)

# EVALUATE
accuracy = accuracy_score(Y_test_ecfp4_fingerprints, Y_pred_ecfp4_fingerprints)
precision = precision_score(Y_test_ecfp4_fingerprints, Y_pred_ecfp4_fingerprints)
recall = recall_score(Y_test_ecfp4_fingerprints, Y_pred_ecfp4_fingerprints)
auc_ecfp4_fingerprints = roc_auc_score(
    Y_test_ecfp4_fingerprints, Y_pred_ecfp4_fingerprints
)

# AUC TRAINING
Y_pred_train_ecfp4_fingerprints = best_model_ecfp4_fingerprints.predict(
    X_training_ecfp4_fingerprints
)
auc_train_ecfp4_fingerprints = roc_auc_score(
    Y_training_ecfp4_fingerprints, Y_pred_train_ecfp4_fingerprints
)

# CREATE DATAFRAME WITH RESULTS
results_ecfp4_fingerprints = pd.DataFrame(
    {
        "model_name": [best_model_name],
        "accuracy": [round(accuracy, 2)],
        "precision": [round(precision, 2)],
        "recall": [round(recall, 2)],
        "auc": [round(auc_ecfp4_fingerprints, 2)],
        "auc_train": [round(auc_train_ecfp4_fingerprints, 2)],
    }
)

```

```
    }  
)  
  
# SAVE TABLE_RESULTS.CSV  
table_results = pd.read_csv(results_path + results_file)  
table_results = table_results.append(results_ecfp4_fingerprints)  
table_results.to_csv(results_path + results_file, index=False)
```

/var/folders/3s/vv1d0lmn7g134m4psncn2_q80000gn/T/ipykernel_15279/3124268929.py:3: FutureWarning:

The frame.append method is deprecated and will be removed from pandas in a future version. Use pa

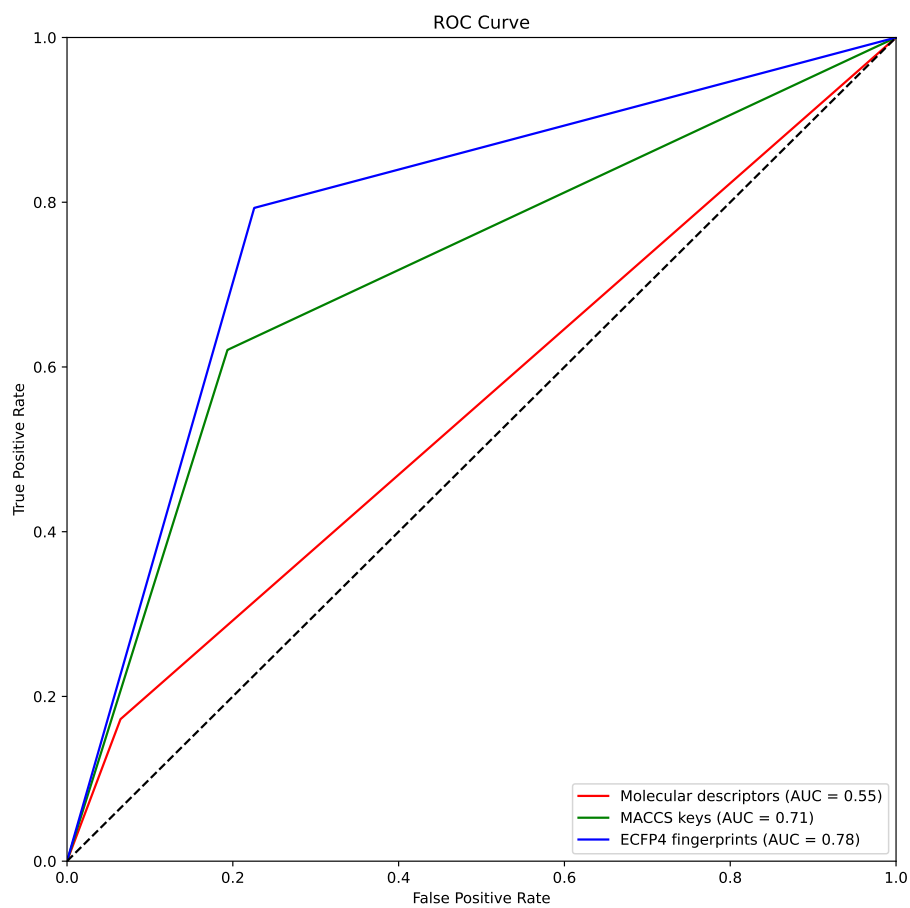
Chapter 4

RESULTS FOR NAIVE BAYES MODELS

```
# GET FPR AND TPR FOR ALL MODELS
# MOLECULAR DESCRIPTORS
fpr_molecular_descriptors, tpr_molecular_descriptors, _ = roc_curve(
    Y_test_molecular_descriptors, Y_pred_molecular_descriptors
)
# MACCS KEYS
fpr_maccs_keys, tpr_maccs_keys, _ = roc_curve(Y_test_maccs_keys, Y_pred_maccs_keys)
# ECFP4 FINGERPRINTS
fpr_ecfp4_fingerprints, tpr_ecfp4_fingerprints, _ = roc_curve(
    Y_test_ecfp4_fingerprints, Y_pred_ecfp4_fingerprints
)

# PLOT ALL THE ROC CURVES IN THE SAME PLOT
plt.figure(figsize=(10, 10))
plt.plot(
    fpr_molecular_descriptors,
    tpr_molecular_descriptors,
    color="red",
    label="Molecular descriptors (AUC = %0.2f)" % auc_molecular_descriptors,
)
plt.plot(
    fpr_maccs_keys,
    tpr_maccs_keys,
    color="green",
    label="MACCS keys (AUC = %0.2f)" % auc_maccs_keys,
```

```
)
plt.plot(
    fpr_ecfp4_fingerprints,
    tpr_ecfp4_fingerprints,
    color="blue",
    label="ECFP4 fingerprints (AUC = %0.2f)" % auc_ecfp4_fingerprints,
)
plt.plot([0, 1], [0, 1], color="black", linestyle="--")
plt.xlim([0.0, 1.0])
plt.ylim([0.0, 1.0])
plt.xlabel("False Positive Rate")
plt.ylabel("True Positive Rate")
plt.title("ROC Curve")
plt.legend(loc="lower right")
plt.savefig(results_path + "knn_roc_curve.png")
plt.show()
```



```
# DROP DUPLICATES FROM TABLE_RESULTS.CSV ACCORDING TO MODEL_NAME
table_results = pd.read_csv(results_path + results_file)
table_results = table_results.drop_duplicates(subset=["model_name"])
table_results.to_csv(results_path + results_file, index=False)
```

