```
import itertools
import sys
sys.path.insert(0, os.path.dirname(os.path.realpath('__file__')));
import pandas as pd
from sklearn.metrics import confusion_matrix, classification_report, precision_score, recall_score, log_loss, fl_score, mean_squared_error, roc_auc_score, accu
import time
from services.plotting_service import *
from services.neural network service import
 from services.preprocessing_service import *
from features.get_features import *
from keras.optimizers import SGD, Adam, RMSprop, Adagrad
from hyperopt import hp, Trials, fmin, tpe
#Query and preprecess data
nn_data = NeuralNetworkService().get_nn_data();
categorical_features = Features().get_categorical_features();
numerical_features = Features().get_numerical_features();
imputed_numerical_features = impute_missing_values(numerical_features);
X_train = nn_data['mortality_data']['X_train'];
X_test = nn_data['mortality_data']['X_test'];
Y_train = nn_data['mortality_data']['Y_train'];
Y_test = nn_data['mortality_data']['Y_test'];
def f(params):
    return NeuralNetworkService().train_neural_network(X_train, Y_train, X_test, Y_test, params);
'batch_size': hp.choice('batch_size', [1, 25, 50])
                   };
trials mse = Trials()
best = fmin(fn=f, space=params space, algo=tpe.suggest, max evals=50, trials=trials mse);
# Training neural network with optimal paremeters
params = {'n_layers':6,
            'n_neurons':16,
'optimizer': 'Adam',
            'epochs':50,
            'batch size':50
keras_model = NeuralNetworkService().train_neural_network(X_train, Y_train, X_test, Y_test, params);
'service':'CSURG',
'icd9_group':'diseases of the circulatory system',
                                       'SURGERY_FLAG':'NARROW'
                                      };
'saps_avg':20,
'gcs':9,
                                    'total_mech_vent_time':130
patient lab tests = { 'blood urea nitrogen': [23, 24, 24],
                         'blatelet_count':[230, 240],
'hematocrit':[33, 35],
'potassium': [3.9, 3.8, 4.4],
'sodium':[140, 139],
'creatinine':[1.3,1.2,1.3],
                         'bicarbonate':[25,26],
'white blood_cells':[8.5,9,13],
'blood_glucose':[130, 135,140],
'albumin':[3.5, 3.4]
patient_physio_measures = {'heart_rate':[100,108,105,99],
                               'resp_rate':[22,25,23],
'sys_press':[120, 121, 115],
'dias_press':[70,80,85],
'temp':[98, 98.2, 97.8],
                                'spo2':[97,97.8,98]
         'patient_categorical_features':patient_categorical_features,
'patient_numerical_features':patient_numerical_features,
'patient_lab_tests':patient_lab_tests,
           patient_physio_measures':patient_physio_measures
# Preprocess prediction data
prediction_data = NeuralNetworkService().preprocess_prediction_data(patient_features, imputed_numerical_features, categorical_features);
prediction = keras_model.predict(prediction_data);
n clases = 3
fpr = dict()
tpr = dict()
roc_auc = dict()
for i in range(n_classes):
    Y test = np.array(Y test)
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Y_pred = np.array(Y_pred)
      fpr[i], tpr[i], _ = roc_curve(Y_test[:, i], Y_pred[:, i])
roc_auc[i] = auc(fpr[i], tpr[i])
import seaborn as sns
sns.regplot(x=fpr[0], y = tpr[0])
 import seaborn as sns
def plot_roc_auroc_curves(tpr, fpr, roc_auc, title):
      plt.figure()
      plt.plot(fpr[1], tpr[1], color='green',
     plt.plot(fpr[1], tpr[1], color='green',
    lw=lw, label='ROC Curve (AUC = %0.2f)' % roc_auc[1])
plt.plot([0, 1], [0, 1], color='navy', lw=lw, linestyle='--')
plt.xlim([0.0, 1.0])
plt.ylim([0.0, 1.05])
plt.xlabel('False Positive Rate')
plt.ylabel('True Positive Rate')
plt.title(title)
plt.title(title)
      plt.legend(loc="lower right")
      plt.show()
      plt.savefig('roc_auc.png')
      plt.close()
plot_roc_auroc_curves(tpr[2], fpr[2], roc_auc[2], 'ROC Curve for >12 months mortality')
all_fpr = np.unique(np.concatenate([fpr[i] for i in range(n_classes)]))
mean_tpr = np.zeros_like(all_fpr)
for i in range(n_classes):
    mean_tpr += interp(all_fpr, fpr[i], tpr[i])
mean_tpr /= n_classes
fpr["macro"] = all_fpr
tpr["macro"] = mean_tpr
roc_auc["macro"] = auc(fpr["macro"], tpr["macro"])
plt.figure()
plt.plot([0, 1], [0, 1], 'k--', lw=lw)
plt.xlim([0.0, 1.0])
plt.ylim([0.0, 1.05])
plt.xlabel('Ratio Falsos Positivos')
plt.ylabel('Ratio Veraderos Positivos')
plt.title('Curvas ROC para clasificación multiclase')
plt.legend(loc="lower right")
plt.shew(')
plt.show()
 from mlxtend.evaluate import confusion_matrix
Y_test_ravel = Y_test.argmax(axis = 1)
Y_pred_ravel = Y_pred.argmax(axis = 1)
def plot_confusion_matrix_seaborn(cm):
    cm_norm = cm.astype('float') / cm.sum(axis=1)[:, np.newaxis]
           sns.heatmap(cm_norm, annot=True,
  yticklabels=['<1 mes', '1-12 meses', '>12 meses'],
  xticklabels=['<1 mes', '1-12 meses', '>12 meses'],
      cbar = False)
r.set_title('Matriz de confusión normalizada');
r.set(xlabel='Valor Predicho', ylabel='Valor Real')
plot confusion matrix seaborn(cm)
print(classification_report(Y_test_ravel, Y_pred_ravel))
```