genetic-algorithm

December 23, 2023

[423]:
```
import numpy as np
import pandas as pd
import matplotlib.pyplot as plt
import seaborn as sns
from sklearn.model_selection import train_test_split
from sklearn.ensemble import RandomForestClassifier
from sklearn.metrics import accuracy_score, confusion_matrix
from sklearn.model_selection import cross_val_score
from deap import base, creator, tools, algorithms
```

[424]:
```
data = pd.read_csv("/kaggle/input/breast-cancer-wisconsin-data/data.csv")
data.head()
```

[424]:

	id	diagnosis	radius_mean	texture_mean	perimeter_mean	area_mean	\
0	842302	M	17.99	10.38	122.80	1001.0	
1	842517	M	20.57	17.77	132.90	1326.0	
2	84300903	M	19.69	21.25	130.00	1203.0	
3	84348301	M	11.42	20.38	77.58	386.1	
4	84358402	M	20.29	14.34	135.10	1297.0	

	smoothness_mean	compactness_mean	concavity_mean	concave points_mean	\
0	0.11840	0.27760	0.3001	0.14710	
1	0.08474	0.07864	0.0869	0.07017	
2	0.10960	0.15990	0.1974	0.12790	
3	0.14250	0.28390	0.2414	0.10520	
4	0.10030	0.13280	0.1980	0.10430	

	…	texture_worst	perimeter_worst	area_worst	smoothness_worst	\
0	…	17.33	184.60	2019.0	0.1622	
1	…	23.41	158.80	1956.0	0.1238	
2	…	25.53	152.50	1709.0	0.1444	
3	…	26.50	98.87	567.7	0.2098	
4	…	16.67	152.20	1575.0	0.1374	

	compactness_worst	concavity_worst	concave points_worst	symmetry_worst	\
0	0.6656	0.7119	0.2654	0.4601	
1	0.1866	0.2416	0.1860	0.2750	

```
2             0.4245           0.4504                0.2430          0.3613
3             0.8663           0.6869                0.2575          0.6638
4             0.2050           0.4000                0.1625          0.2364

   fractal_dimension_worst  Unnamed: 32
0                  0.11890          NaN
1                  0.08902          NaN
2                  0.08758          NaN
3                  0.17300          NaN
4                  0.07678          NaN

[5 rows x 33 columns]
```

[425]:
```
data.info()
```

```
<class 'pandas.core.frame.DataFrame'>
RangeIndex: 569 entries, 0 to 568
Data columns (total 33 columns):
 #   Column                   Non-Null Count  Dtype
---  ------                   --------------  -----
 0   id                       569 non-null    int64
 1   diagnosis                569 non-null    object
 2   radius_mean              569 non-null    float64
 3   texture_mean             569 non-null    float64
 4   perimeter_mean           569 non-null    float64
 5   area_mean                569 non-null    float64
 6   smoothness_mean          569 non-null    float64
 7   compactness_mean         569 non-null    float64
 8   concavity_mean           569 non-null    float64
 9   concave points_mean      569 non-null    float64
 10  symmetry_mean            569 non-null    float64
 11  fractal_dimension_mean   569 non-null    float64
 12  radius_se                569 non-null    float64
 13  texture_se               569 non-null    float64
 14  perimeter_se             569 non-null    float64
 15  area_se                  569 non-null    float64
 16  smoothness_se            569 non-null    float64
 17  compactness_se           569 non-null    float64
 18  concavity_se             569 non-null    float64
 19  concave points_se        569 non-null    float64
 20  symmetry_se              569 non-null    float64
 21  fractal_dimension_se     569 non-null    float64
 22  radius_worst             569 non-null    float64
 23  texture_worst            569 non-null    float64
 24  perimeter_worst          569 non-null    float64
 25  area_worst               569 non-null    float64
 26  smoothness_worst         569 non-null    float64
```

```
 27  compactness_worst        569 non-null    float64
 28  concavity_worst          569 non-null    float64
 29  concave points_worst     569 non-null    float64
 30  symmetry_worst           569 non-null    float64
 31  fractal_dimension_worst  569 non-null    float64
 32  Unnamed: 32              0 non-null      float64
dtypes: float64(31), int64(1), object(1)
memory usage: 146.8+ KB
```

[426]:
```
data.describe()
```

[426]:

	id	radius_mean	texture_mean	perimeter_mean	area_mean
count	5.690000e+02	569.000000	569.000000	569.000000	569.000000
mean	3.037183e+07	14.127292	19.289649	91.969033	654.889104
std	1.250206e+08	3.524049	4.301036	24.298981	351.914129
min	8.670000e+03	6.981000	9.710000	43.790000	143.500000
25%	8.692180e+05	11.700000	16.170000	75.170000	420.300000
50%	9.060240e+05	13.370000	18.840000	86.240000	551.100000
75%	8.813129e+06	15.780000	21.800000	104.100000	782.700000
max	9.113205e+08	28.110000	39.280000	188.500000	2501.000000

	smoothness_mean	compactness_mean	concavity_mean	concave points_mean
count	569.000000	569.000000	569.000000	569.000000
mean	0.096360	0.104341	0.088799	0.048919
std	0.014064	0.052813	0.079720	0.038803
min	0.052630	0.019380	0.000000	0.000000
25%	0.086370	0.064920	0.029560	0.020310
50%	0.095870	0.092630	0.061540	0.033500
75%	0.105300	0.130400	0.130700	0.074000
max	0.163400	0.345400	0.426800	0.201200

	symmetry_mean	…	texture_worst	perimeter_worst	area_worst
count	569.000000	…	569.000000	569.000000	569.000000
mean	0.181162	…	25.677223	107.261213	880.583128
std	0.027414	…	6.146258	33.602542	569.356993
min	0.106000	…	12.020000	50.410000	185.200000
25%	0.161900	…	21.080000	84.110000	515.300000
50%	0.179200	…	25.410000	97.660000	686.500000
75%	0.195700	…	29.720000	125.400000	1084.000000
max	0.304000	…	49.540000	251.200000	4254.000000

	smoothness_worst	compactness_worst	concavity_worst
count	569.000000	569.000000	569.000000
mean	0.132369	0.254265	0.272188
std	0.022832	0.157336	0.208624
min	0.071170	0.027290	0.000000
25%	0.116600	0.147200	0.114500

```
50%            0.131300           0.211900         0.226700
75%            0.146000           0.339100         0.382900
max            0.222600           1.058000         1.252000

       concave points_worst  symmetry_worst  fractal_dimension_worst  \
count            569.000000      569.000000               569.000000
mean               0.114606        0.290076                 0.083946
std                0.065732        0.061867                 0.018061
min                0.000000        0.156500                 0.055040
25%                0.064930        0.250400                 0.071460
50%                0.099930        0.282200                 0.080040
75%                0.161400        0.317900                 0.092080
max                0.291000        0.663800                 0.207500

       Unnamed: 32
count          0.0
mean           NaN
std            NaN
min            NaN
25%            NaN
50%            NaN
75%            NaN
max            NaN

[8 rows x 32 columns]
```

[427]:
```
# Missing values
data.isna().sum()
```

[427]:
```
id                         0
diagnosis                  0
radius_mean                0
texture_mean               0
perimeter_mean             0
area_mean                  0
smoothness_mean            0
compactness_mean           0
concavity_mean             0
concave points_mean        0
symmetry_mean              0
fractal_dimension_mean     0
radius_se                  0
texture_se                 0
perimeter_se               0
area_se                    0
smoothness_se              0
compactness_se             0
```

```
concavity_se                 0
concave points_se            0
symmetry_se                  0
fractal_dimension_se         0
radius_worst                 0
texture_worst                0
perimeter_worst              0
area_worst                   0
smoothness_worst             0
compactness_worst            0
concavity_worst              0
concave points_worst         0
symmetry_worst               0
fractal_dimension_worst      0
Unnamed: 32                569
dtype: int64
```

[428]:
```
# Drop the id and 'Unnamed: 32' column as it contains only NaN values
data = data.drop(columns=['id','Unnamed: 32'], axis=1)
data.head()
```

[428]:

	diagnosis	radius_mean	texture_mean	perimeter_mean	area_mean	\
0	M	17.99	10.38	122.80	1001.0	
1	M	20.57	17.77	132.90	1326.0	
2	M	19.69	21.25	130.00	1203.0	
3	M	11.42	20.38	77.58	386.1	
4	M	20.29	14.34	135.10	1297.0	

	smoothness_mean	compactness_mean	concavity_mean	concave points_mean	\
0	0.11840	0.27760	0.3001	0.14710	
1	0.08474	0.07864	0.0869	0.07017	
2	0.10960	0.15990	0.1974	0.12790	
3	0.14250	0.28390	0.2414	0.10520	
4	0.10030	0.13280	0.1980	0.10430	

	symmetry_mean	…	radius_worst	texture_worst	perimeter_worst	\
0	0.2419	…	25.38	17.33	184.60	
1	0.1812	…	24.99	23.41	158.80	
2	0.2069	…	23.57	25.53	152.50	
3	0.2597	…	14.91	26.50	98.87	
4	0.1809	…	22.54	16.67	152.20	

	area_worst	smoothness_worst	compactness_worst	concavity_worst	\
0	2019.0	0.1622	0.6656	0.7119	
1	1956.0	0.1238	0.1866	0.2416	
2	1709.0	0.1444	0.4245	0.4504	
3	567.7	0.2098	0.8663	0.6869	

```
4      1575.0           0.1374            0.2050          0.4000

   concave points_worst  symmetry_worst  fractal_dimension_worst
0                0.2654          0.4601                  0.11890
1                0.1860          0.2750                  0.08902
2                0.2430          0.3613                  0.08758
3                0.2575          0.6638                  0.17300
4                0.1625          0.2364                  0.07678

[5 rows x 31 columns]
```

[429]:
```
data.shape
```

[429]:
```
(569, 31)
```

[430]:
```
# Duplicated observations
data.duplicated().sum()
```

[430]:
```
0
```

[431]:
```
# Map diagnosis to 0 (Benign) and 1 (Malignant)
data['diagnosis'] = data['diagnosis'].map({'M': 1, 'B': 0})
```

[432]:
```
# Separate features and target variable
X = data.drop('diagnosis', axis=1)
y = data['diagnosis']
```

[433]:
```
# Split the data into training, validation, and testing sets
X_train, X_temp, y_train, y_temp = train_test_split(X, y, test_size=0.3,␣
 ↪random_state=42)
X_val, X_test, y_val, y_test = train_test_split(X_temp, y_temp, test_size=0.5,␣
 ↪random_state=42)
```

1 Define the genetic algorithm functions

[434]:
```
def evaluate(individual, X_train, y_train, X_val, y_val):
    # Concatenate the arrays in the individual list
    combined_individual = np.concatenate([np.expand_dims(arr, axis=0) if␣
 ↪len(arr.shape) == 1 else arr for arr in individual])

    # Reshape to match the number of columns in X
    combined_individual = combined_individual.reshape(-1, X_train.shape[1])

    # Create a mask based on the individual's genes
    mask = np.array(combined_individual, dtype=bool)
```

```
    # Select features using the mask
    X_train_selected = X_train.iloc[:, mask]
    X_val_selected = X_val.iloc[:, mask]

    # Train a RandomForestClassifier
    clf = RandomForestClassifier(random_state=42)
    clf.fit(X_train_selected, y_train)

    # Make predictions on the validation set
    y_val_pred = clf.predict(X_val_selected)

    # Calculate accuracy on the validation set
    accuracy_val = accuracy_score(y_val, y_val_pred)

    return accuracy_val,
```

2 Genetic Algorithm Setup

[435]:
```
creator.create("FitnessMax", base.Fitness, weights=(1.0,))
creator.create("Individual", list, fitness=creator.FitnessMax)

toolbox = base.Toolbox()
toolbox.register("attr_bool", np.random.choice, [0, 1], size=X.shape[1])
toolbox.register("individual", tools.initRepeat, creator.Individual, toolbox.
 ↪attr_bool, n=X.shape[1])
toolbox.register("population", tools.initRepeat, list, toolbox.individual)

toolbox.register("evaluate", evaluate, X_train=X_train, y_train=y_train,␣
 ↪X_val=X_val, y_val=y_val)
toolbox.register("mate", tools.cxTwoPoint)
toolbox.register("mutate", tools.mutFlipBit, indpb=0.05)
toolbox.register("select", tools.selTournament, tournsize=3)
```

```
/opt/conda/lib/python3.10/site-packages/deap/creator.py:185: RuntimeWarning: A
class named 'FitnessMax' has already been created and it will be overwritten.
Consider deleting previous creation of that class or rename it.
  warnings.warn("A class named '{0}' has already been created and it "
/opt/conda/lib/python3.10/site-packages/deap/creator.py:185: RuntimeWarning: A
class named 'Individual' has already been created and it will be overwritten.
Consider deleting previous creation of that class or rename it.
  warnings.warn("A class named '{0}' has already been created and it "
```

gen	nevals	avg	min	max
0	10	0.964706	0.964706	0.964706
1	2	0.964706	0.964706	0.964706
2	2	0.964706	0.964706	0.964706
3	2	0.964706	0.964706	0.964706

```
4       2       0.964706        0.964706        0.964706
5       2       0.964706        0.964706        0.964706
```

3 Genetic Algorithm

[ ]:
```
population_size = 10
crossover_prob = 0.8
mutation_prob = 0.2
generations = 5
```

[ ]:
```
population = toolbox.population(n=population_size)
```

[ ]:
```
# Track statistics during the evolution
stats = tools.Statistics(lambda ind: ind.fitness.values)
stats.register("avg", np.mean)
stats.register("min", np.min)
stats.register("max", np.max)
```

4 Execute the genetic algorithm

[ ]:
```
population, logbook = algorithms.eaMuPlusLambda(population, toolbox,␣
 ↪mu=population_size, lambda_=2, cxpb=crossover_prob, mutpb=mutation_prob,␣
 ↪ngen=generations, stats=stats, halloffame=None, verbose=True)
```

[436]:
```
# Extract the best individual
best_individual = tools.selBest(population, k=1)[0]
```

[437]:
```
# Evaluate the best individual on the test set
best_mask = np.array(best_individual, dtype=bool)
X_test_selected = X_test.iloc[:, best_mask]
```

[438]:
```
# Train a RandomForestClassifier with the selected features
best_clf = RandomForestClassifier(random_state=42)
best_clf.fit(X_train.iloc[:, best_mask], y_train)
```

[438]:
```
RandomForestClassifier(random_state=42)
```

[439]:
```
# Make predictions on the test set
y_pred_test = best_clf.predict(X_test_selected)
```

[441]:
```
# Evaluate performance on the test set
from sklearn.metrics import accuracy_score, confusion_matrix,␣
 ↪classification_report

accuracy_test = accuracy_score(y_test, y_pred_test)
```

```
conf_matrix = confusion_matrix(y_test, y_pred_test)
classification_rep = classification_report(y_test, y_pred_test)
```

[442]:
```
# Display results
print(f"Best Individual: {best_individual}")
print("-----------------------------------------------------------")
print(f"Accuracy : {accuracy_test}")
print("-----------------------------------------------------------")
print("Classification Report:")
print(classification_rep)
```

```
Best Individual: [array([1, 1, 1, 0, 0, 1, 0, 0, 1, 0, 1, 1, 0, 0, 0, 0, 1, 0,
1, 1, 1, 1,
       0, 1, 1, 1, 1, 0, 1, 1]), array([1, 0, 1, 1, 1, 0, 0, 0, 1, 1, 1, 1, 1,
1, 1, 0, 0, 0, 1, 1, 1, 0,
       0, 1, 1, 1, 1, 1, 0, 0]), array([1, 0, 0, 0, 0, 0, 1, 1, 1, 1, 0, 1, 1,
0, 1, 0, 1, 0, 0, 1, 1, 0,
       1, 1, 1, 0, 0, 1, 0, 0]), array([1, 1, 1, 1, 0, 0, 1, 1, 1, 1, 1, 0, 0,
0, 0, 0, 1, 1, 1, 0, 0, 1,
       0, 1, 1, 0, 1, 1, 1, 0]), array([0, 1, 0, 0, 1, 0, 1, 1, 1, 1, 1, 1, 1,
0, 1, 0, 0, 0, 0, 0, 1, 1,
       1, 1, 0, 1, 1, 0, 0, 0]), array([0, 1, 0, 1, 1, 1, 1, 1, 0, 1, 1, 0, 1,
1, 0, 0, 1, 1, 1, 1, 0, 1,
       0, 0, 0, 1, 0, 0, 0, 0]), array([0, 0, 1, 1, 0, 1, 0, 1, 0, 1, 1, 1, 1,
0, 1, 1, 0, 1, 1, 0, 1, 0,
       1, 0, 0, 0, 1, 0, 0, 0]), array([1, 0, 1, 0, 1, 1, 0, 0, 0, 1, 0, 0, 0,
1, 0, 0, 1, 1, 0, 1, 1, 1,
       1, 0, 1, 0, 1, 0, 1, 1]), array([1, 1, 0, 1, 1, 0, 0, 1, 1, 0, 1, 0, 0,
0, 0, 0, 0, 1, 1, 1, 0, 1,
       1, 0, 0, 0, 1, 0, 1, 1]), array([0, 1, 1, 0, 0, 1, 0, 1, 0, 1, 0, 1, 0,
1, 0, 0, 0, 0, 1, 0, 0, 1,
       1, 1, 1, 0, 1, 0, 0, 0]), array([0, 1, 0, 1, 0, 0, 1, 1, 1, 0, 0, 1, 1,
0, 0, 1, 1, 0, 1, 0, 1, 0,
       0, 0, 0, 0, 1, 0, 1, 1]), array([1, 0, 0, 1, 1, 1, 1, 0, 1, 0, 0, 1, 1,
0, 1, 0, 1, 1, 1, 0, 1, 0,
       0, 0, 0, 0, 1, 0, 0, 1]), array([0, 1, 0, 0, 0, 0, 0, 1, 0, 1, 1, 0, 0,
0, 1, 1, 1, 0, 0, 1, 0, 0,
       1, 0, 1, 0, 0, 0, 1, 0]), array([0, 0, 1, 0, 0, 0, 1, 0, 0, 0, 1, 1, 0,
0, 0, 0, 0, 1, 1, 1, 0, 1,
       1, 1, 1, 0, 1, 1, 1, 0]), array([0, 1, 0, 0, 0, 1, 0, 0, 0, 0, 0, 0, 0,
1, 0, 1, 0, 0, 1, 1, 0, 0,
       0, 0, 1, 0, 0, 0, 1, 1]), array([1, 0, 0, 1, 0, 1, 0, 1, 1, 1, 0, 0, 1,
0, 0, 0, 1, 1, 1, 0, 1, 1,
       0, 0, 1, 1, 0, 1, 1, 0]), array([1, 1, 0, 1, 1, 0, 0, 1, 1, 0, 0, 0, 1,
0, 0, 1, 0, 0, 0, 1, 0, 1,
       0, 0, 1, 0, 0, 0, 1, 1]), array([1, 0, 0, 0, 1, 1, 0, 0, 0, 0, 0, 1, 0,
0, 1, 0, 0, 1, 1, 1, 1, 0,
```

```
       0, 1, 0, 0, 0, 0, 0, 1]), array([0, 1, 0, 1, 0, 0, 1, 0, 0, 0, 0, 0, 0,
1, 0, 1, 0, 1, 0, 1, 1, 1,
       1, 1, 0, 1, 1, 1, 1, 0]), array([1, 0, 1, 1, 0, 1, 0, 0, 1, 1, 1, 0, 0,
0, 1, 0, 1, 0, 1, 0, 0, 1,
       1, 1, 1, 1, 1, 0, 0, 1]), array([1, 1, 1, 0, 0, 0, 1, 1, 0, 1, 1, 0, 1,
1, 0, 0, 1, 1, 0, 1, 0, 0,
       1, 1, 0, 1, 1, 0, 1, 1]), array([1, 0, 1, 0, 1, 0, 1, 0, 1, 1, 0, 1, 1,
1, 1, 0, 0, 0, 0, 0, 1, 1,
       1, 1, 1, 1, 0, 1, 0, 1]), array([1, 1, 1, 1, 1, 1, 0, 0, 1, 1, 0, 0, 0,
1, 1, 1, 0, 0, 1, 0, 0, 1,
       0, 0, 1, 0, 1, 0, 1, 0]), array([1, 1, 0, 0, 0, 0, 0, 0, 0, 1, 0, 0, 0,
1, 0, 0, 1, 1, 0, 1, 1, 1,
       1, 1, 1, 0, 0, 0, 1, 0]), array([0, 1, 1, 1, 0, 0, 0, 0, 0, 1, 0, 0, 0,
1, 1, 1, 1, 0, 0, 0, 1, 1,
       0, 0, 1, 1, 0, 0, 0, 0]), array([0, 1, 1, 1, 0, 0, 1, 0, 0, 0, 1, 1, 0,
0, 1, 1, 0, 1, 1, 0, 1, 0,
       0, 1, 0, 1, 1, 0, 0, 1]), array([1, 1, 0, 1, 0, 1, 1, 0, 0, 1, 0, 1, 1,
1, 1, 0, 0, 0, 1, 1, 0, 1,
       1, 1, 1, 0, 1, 1, 0, 1]), array([0, 0, 1, 0, 0, 1, 0, 1, 1, 0, 1, 1, 0,
0, 1, 0, 0, 1, 1, 1, 0, 1,
       1, 1, 0, 1, 0, 0, 0, 1]), array([1, 0, 0, 1, 0, 0, 1, 1, 0, 1, 0, 0, 1,
1, 0, 1, 0, 1, 0, 0, 1, 0,
       0, 0, 1, 0, 1, 0, 0, 0]), array([0, 0, 0, 1, 1, 1, 1, 0, 1, 1, 1, 1, 1,
1, 1, 1, 0, 1, 1, 0, 1, 0,
       0, 0, 1, 1, 1, 1, 0, 1])]
------------------------------------------------------------
Accuracy : 0.9534883720930233
------------------------------------------------------------
Classification Report:
              precision    recall  f1-score   support

           0       0.97      0.97      0.97        60
           1       0.92      0.92      0.92        26

    accuracy                           0.95        86
   macro avg       0.94      0.94      0.94        86
weighted avg       0.95      0.95      0.95        86
```

[443]:
```
print("Confusion Matrix:")
print(conf_matrix)
```

```
Confusion Matrix:
[[58  2]
 [ 2 24]]
```

[445]:
```
# Plot confusion matrix as a heatmap
plt.figure(figsize=(8, 6))
sns.heatmap(conf_matrix, annot=True, fmt='d', cmap='coolwarm', cbar=True,␣
 ↪annot_kws={"size": 14})
plt.title('Confusion Matrix')
plt.xlabel('Predicted Labels')
plt.ylabel('True Labels')
plt.show()
```