

Pneumonia diagnosis using chest x-ray images

July 26, 2024

1 Data processing

```
[ ]: import cv2
import pandas as pd
import os
import warnings
import numpy as np

warnings.filterwarnings('ignore', message='Intel MKL WARNING')

def process_data(file_path, data_list):
    data = cv2.imread(file_path)
    if data is not None:
        data_resized = cv2.resize(data, (64, 64))
        data_flattened = data_resized.flatten()
        data_normalized = data_flattened / 255.0 # Normalize to [0, 1]
        return data_list.append(data_normalized)
```

```
[ ]: # Convert train normal into data

train_normal_data = []

# Iterate through files in the folder
for filename in os.listdir('../data/train/NORMAL'):
    file_path = os.path.join('../data/train/NORMAL', filename)
    if os.path.isfile(file_path):
        process_data(file_path, train_normal_data)

train_normal_df = pd.DataFrame(train_normal_data)
value_to_set = "disease"
columns = list(train_normal_df.columns)
columns = [value_to_set] + columns[:-1]
train_normal_df = train_normal_df.reindex(columns=columns)
fill_value = 0
train_normal_df.fillna(fill_value, inplace=True)
train_normal_df.head()
```

```
[ ]: disease      0      1      2      3      4      5 \
0      0.0  0.117647  0.117647  0.117647  0.109804  0.109804  0.109804
1      0.0  0.231373  0.231373  0.231373  0.188235  0.188235  0.188235
2      0.0  0.203922  0.203922  0.203922  0.286275  0.286275  0.286275
3      0.0  0.007843  0.007843  0.007843  0.113725  0.113725  0.113725
4      0.0  0.466667  0.466667  0.466667  0.486275  0.486275  0.486275

      6      7      8 ... 12277 12278 12279 12280 \
0  0.105882  0.105882  0.105882 ... 0.000000 0.000000 0.000000 0.000000
1  0.309804  0.309804  0.309804 ... 0.290196 0.290196 0.125490 0.125490
2  0.356863  0.356863  0.356863 ... 0.000000 0.000000 0.000000 0.000000
3  0.168627  0.168627  0.168627 ... 0.000000 0.000000 0.000000 0.000000
4  0.517647  0.517647  0.517647 ... 0.254902 0.254902 0.137255 0.137255

      12281 12282 12283 12284 12285 12286
0  0.000000  0.0  0.0  0.0  0.0  0.0
1  0.125490  0.0  0.0  0.0  0.0  0.0
2  0.000000  0.0  0.0  0.0  0.0  0.0
3  0.000000  0.0  0.0  0.0  0.0  0.0
4  0.137255  0.0  0.0  0.0  0.0  0.0
```

[5 rows x 12288 columns]

```
[ ]: # Convert train pneumonia into data

train_pneumonia_data = []

# Iterate through files in the folder
for filename in os.listdir('../data/train/PNEUMONIA'):
    file_path = os.path.join('../data/train/PNEUMONIA', filename)
    if os.path.isfile(file_path):
        process_data(file_path, train_pneumonia_data)

train_pneumonia_df = pd.DataFrame(train_pneumonia_data)
train_pneumonia_df = pd.DataFrame(train_pneumonia_df)
value_to_set = "disease"
columns = list(train_pneumonia_df.columns)
columns = [value_to_set] + columns[:-1]
train_pneumonia_df = train_pneumonia_df.reindex(columns=columns)
fill_value = 1
train_pneumonia_df.fillna(fill_value, inplace=True)
train_pneumonia_df.head()
```

```
[ ]: disease      0      1      2      3      4      5 \
0      1.0  0.803922  0.803922  0.803922  0.792157  0.792157  0.792157
1      1.0  0.039216  0.039216  0.039216  0.125490  0.125490  0.125490
2      1.0  0.172549  0.172549  0.172549  0.172549  0.172549  0.172549
```

3	1.0	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000
4	1.0	0.752941	0.752941	0.752941	0.521569	0.521569	0.521569

	6	7	8	...	12277	12278	12279	12280	\
0	0.811765	0.811765	0.811765	...	0.098039	0.098039	0.133333	0.133333	
1	0.196078	0.196078	0.196078	...	0.000000	0.000000	0.000000	0.000000	
2	0.160784	0.160784	0.160784	...	0.180392	0.180392	0.172549	0.172549	
3	0.000000	0.000000	0.000000	...	0.000000	0.000000	0.000000	0.000000	
4	0.239216	0.239216	0.239216	...	0.215686	0.215686	0.035294	0.035294	

	12281	12282	12283	12284	12285	12286
0	0.133333	0.168627	0.168627	0.168627	0.184314	0.184314
1	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000
2	0.172549	0.192157	0.192157	0.192157	0.211765	0.211765
3	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000
4	0.035294	0.054902	0.054902	0.054902	0.058824	0.058824

[5 rows x 12288 columns]

```
[ ]: # Convert test normal into data

test_normal_data = []

# Iterate through files in the folder
for filename in os.listdir('../data/test/NORMAL'):
    file_path = os.path.join('../data/test/NORMAL', filename)
    if os.path.isfile(file_path):
        process_data(file_path, test_normal_data)

test_normal_df = pd.DataFrame(test_normal_data)
test_normal_df = pd.DataFrame(test_normal_df)
value_to_set = "disease"
columns = list(test_normal_df.columns)
columns = [value_to_set] + columns[:-1]
test_normal_df = test_normal_df.reindex(columns=columns)
fill_value = 0
test_normal_df.fillna(fill_value, inplace=True)
test_normal_df.head()
```

[]:	disease	0	1	2	3	4	5	\
0	0.0	0.082353	0.082353	0.082353	0.086275	0.086275	0.086275	
1	0.0	0.011765	0.011765	0.011765	0.011765	0.011765	0.011765	
2	0.0	0.270588	0.270588	0.270588	0.215686	0.215686	0.215686	
3	0.0	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	
4	0.0	0.074510	0.074510	0.074510	0.290196	0.290196	0.290196	

	6	7	8	...	12277	12278	12279	12280	\
--	---	---	---	-----	-------	-------	-------	-------	---

0	0.074510	0.074510	0.074510	...	0.133333	0.133333	0.145098	0.145098
1	0.015686	0.015686	0.015686	...	0.031373	0.031373	0.023529	0.023529
2	0.200000	0.200000	0.200000	...	0.000000	0.000000	0.000000	0.000000
3	0.047059	0.047059	0.047059	...	0.000000	0.000000	0.000000	0.000000
4	0.372549	0.372549	0.372549	...	0.000000	0.000000	0.007843	0.007843

	12281	12282	12283	12284	12285	12286
0	0.145098	0.094118	0.094118	0.094118	0.160784	0.160784
1	0.023529	0.019608	0.019608	0.019608	0.019608	0.019608
2	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000
3	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000
4	0.007843	0.035294	0.035294	0.035294	0.023529	0.023529

[5 rows x 12288 columns]

```
[ ]: # Convert test pneumonia into data
```

```
test_pneumonia_data = []

# Iterate through files in the folder
for filename in os.listdir('../data/test/PNEUMONIA'):
    file_path = os.path.join('../data/test/PNEUMONIA', filename)
    if os.path.isfile(file_path):
        process_data(file_path, test_pneumonia_data)

test_pneumonia_df = pd.DataFrame(test_pneumonia_data)
test_pneumonia_df = pd.DataFrame(test_pneumonia_df)
value_to_set = "disease"
columns = list(test_pneumonia_df.columns)
columns = [value_to_set] + columns[:-1]
test_pneumonia_df = test_pneumonia_df.reindex(columns=columns)
fill_value = 1
test_pneumonia_df.fillna(fill_value, inplace=True)
test_pneumonia_df.head()
```

```
[ ]:  disease      0      1      2      3      4      5  \
0      1.0  0.105882  0.105882  0.105882  0.486275  0.486275  0.486275
1      1.0  0.513725  0.513725  0.513725  0.294118  0.294118  0.294118
2      1.0  0.847059  0.847059  0.847059  0.815686  0.815686  0.815686
3      1.0  0.462745  0.462745  0.462745  0.372549  0.372549  0.372549
4      1.0  0.090196  0.090196  0.090196  0.223529  0.223529  0.223529

      6      7      8  ...  12277  12278  12279  12280  \
0  0.137255  0.137255  0.137255  ...  0.086275  0.086275  0.090196  0.090196
1  0.015686  0.015686  0.015686  ...  0.058824  0.058824  0.066667  0.066667
2  0.858824  0.858824  0.858824  ...  0.101961  0.101961  0.027451  0.027451
3  0.298039  0.298039  0.298039  ...  0.054902  0.054902  0.074510  0.074510
```

4	0.313725	0.313725	0.313725	...	0.003922	0.003922	0.003922	0.003922
---	----------	----------	----------	-----	----------	----------	----------	----------

	12281	12282	12283	12284	12285	12286
0	0.090196	0.098039	0.098039	0.098039	0.098039	0.098039
1	0.066667	0.070588	0.070588	0.070588	0.074510	0.074510
2	0.027451	0.050980	0.050980	0.050980	0.058824	0.058824
3	0.074510	0.086275	0.086275	0.086275	0.090196	0.090196
4	0.003922	0.003922	0.003922	0.003922	0.003922	0.003922

[5 rows x 12288 columns]

```
[ ]: print("Number of rows:", train_normal_df.shape[0])
      print("Number of rows:", train_pneumonia_df.shape[0])
      print("Number of rows:", test_normal_df.shape[0])
      print("Number of rows:", test_pneumonia_df.shape[0])
```

Number of rows: 1349
 Number of rows: 3883
 Number of rows: 234
 Number of rows: 390

```
[ ]: df = pd.concat([train_normal_df, train_pneumonia_df, test_normal_df,
                    ↪test_pneumonia_df], axis=0)
      df.head()
```

[]:	disease	0	1	2	3	4	5	\
0	0.0	0.117647	0.117647	0.117647	0.109804	0.109804	0.109804	
1	0.0	0.231373	0.231373	0.231373	0.188235	0.188235	0.188235	
2	0.0	0.203922	0.203922	0.203922	0.286275	0.286275	0.286275	
3	0.0	0.007843	0.007843	0.007843	0.113725	0.113725	0.113725	
4	0.0	0.466667	0.466667	0.466667	0.486275	0.486275	0.486275	

	6	7	8	...	12277	12278	12279	12280	\
0	0.105882	0.105882	0.105882	...	0.000000	0.000000	0.000000	0.000000	
1	0.309804	0.309804	0.309804	...	0.290196	0.290196	0.125490	0.125490	
2	0.356863	0.356863	0.356863	...	0.000000	0.000000	0.000000	0.000000	
3	0.168627	0.168627	0.168627	...	0.000000	0.000000	0.000000	0.000000	
4	0.517647	0.517647	0.517647	...	0.254902	0.254902	0.137255	0.137255	

	12281	12282	12283	12284	12285	12286
0	0.000000	0.0	0.0	0.0	0.0	0.0
1	0.125490	0.0	0.0	0.0	0.0	0.0
2	0.000000	0.0	0.0	0.0	0.0	0.0
3	0.000000	0.0	0.0	0.0	0.0	0.0
4	0.137255	0.0	0.0	0.0	0.0	0.0

[5 rows x 12288 columns]

2 Dimension reduction: singular value decomposition

```
[ ]: X = df.drop(df.columns[0], axis=1)
     y = df[df.columns[0]]
```

```
[ ]: # Compute SVD
     U, D, V = np.linalg.svd(X, full_matrices=False)
```

Intel MKL WARNING: Support of Intel(R) Streaming SIMD Extensions 4.2 (Intel(R) SSE4.2) enabled only processors has been deprecated. Intel oneAPI Math Kernel Library 2025.0 will require Intel(R) Advanced Vector Extensions (Intel(R) AVX) instructions.

Intel MKL WARNING: Support of Intel(R) Streaming SIMD Extensions 4.2 (Intel(R) SSE4.2) enabled only processors has been deprecated. Intel oneAPI Math Kernel Library 2025.0 will require Intel(R) Advanced Vector Extensions (Intel(R) AVX) instructions.

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Intel MKL WARNING: Support of Intel(R) Streaming SIMD Extensions 4.2 (Intel(R) SSE4.2) enabled only processors has been deprecated. Intel oneAPI Math Kernel Library 2025.0 will require Intel(R) Advanced Vector Extensions (Intel(R) AVX) instructions.

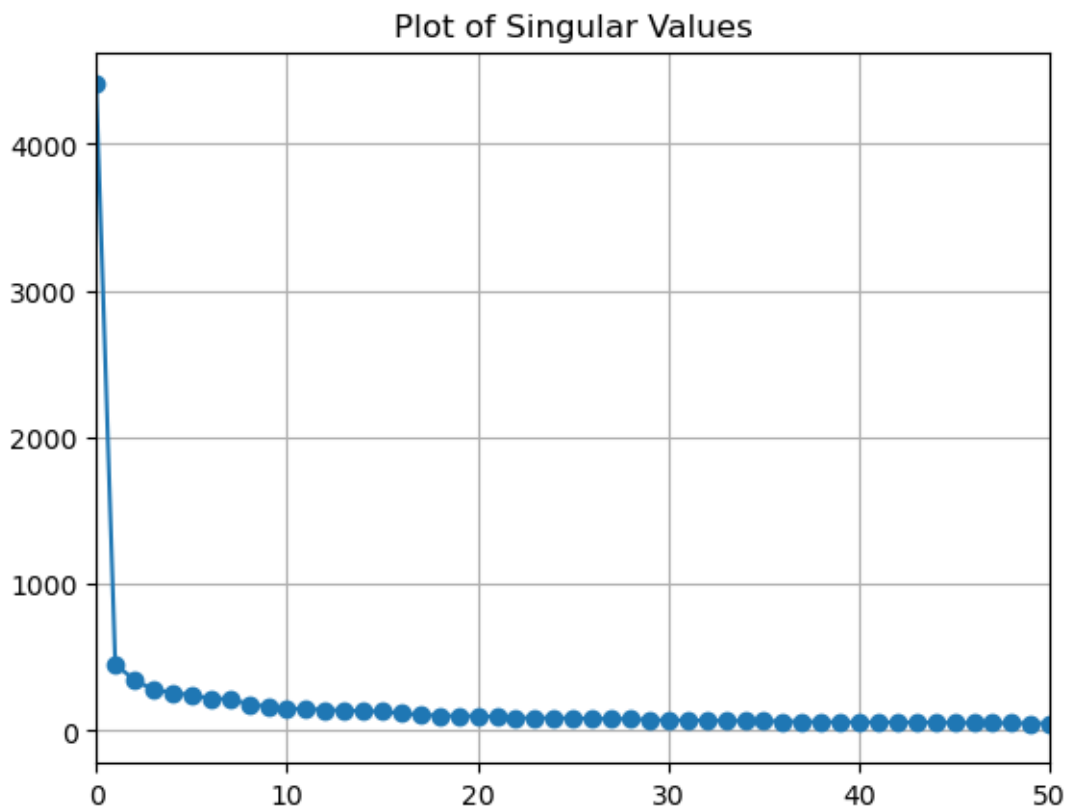
Intel MKL WARNING: Support of Intel(R) Streaming SIMD Extensions 4.2 (Intel(R) SSE4.2) enabled only processors has been deprecated. Intel oneAPI Math Kernel Library 2025.0 will require Intel(R) Advanced Vector Extensions (Intel(R) AVX) instructions.

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```
[ ]: import matplotlib.pyplot as plt

x_values = np.arange(len(D))
plt.plot(x_values, D, marker='o', linestyle='--')
plt.xlim(0, 50)
plt.title('Plot of Singular Values')
plt.grid(True)
plt.show()
```



Based on this elbow plot, additional components beyond 20 would not contribute much additional information to the model.

```
[ ]: # Dimension-reduced X
V20 = np.transpose(V)[: , :20]
DR_X = X.values @ V20
```

```
[ ]: arr = y.values
y = arr.reshape(-1, 1)
df = pd.concat([pd.DataFrame(y).rename(columns={0: 'disease'}), pd.
↳ DataFrame(DR_X)], axis=1)
df.head()
```

```
[ ]:      disease      0      1      2      3      4      5  \
0      0.0 -55.337547  11.189257  0.969288 -8.103200  2.430869 -1.146683
1      0.0 -54.702970 -4.086767 -4.363943  3.081711 -0.664137  1.970735
2      0.0 -63.044600  1.002935 -7.537691 -6.473655  1.696616  2.288390
3      0.0 -54.321275 -5.898212 -2.937312 -8.790238  0.726498 -0.568197
4      0.0 -67.651331  6.718537 -7.945233 -0.536995  1.810724  3.996124

      6      7      8  ...      10      11      12      13  \
```



```

0  2.988481 -4.039937  6.199420 ...  0.981185 -0.509654  4.006090 -0.193792
1  0.320779 -1.787443  2.583499 ... -0.473178 -1.701906 -0.431524  1.228657
2  1.674289 -0.141939 -1.281375 ... -2.079441 -0.387920 -1.936197 -0.314772
3  2.704220  4.149871 -0.841565 ...  2.641541  1.463082 -0.473949 -0.956462
4 -2.179091  0.839701 -2.102178 ... -2.362217  1.960484  2.895017  0.562866

```

```

          14          15          16          17          18          19
0  0.568191 -1.433567  0.050123 -0.263677  1.224021 -1.287958
1 -1.162580  1.818841  1.238074  1.130522 -1.587421  1.303172
2 -0.884854 -2.530839 -0.716002  0.965882 -1.142154 -0.603895
3 -2.194333 -1.976931 -1.922920 -0.338298 -0.184530  0.363268
4  2.162667  1.745250  0.131177  0.026476 -0.984771  1.237131

```

[5 rows x 21 columns]

3 Testing classifiers, including further investigation of SVM kernels

```

[ ]: from sklearn.linear_model import LogisticRegression
from sklearn.tree import DecisionTreeClassifier
from sklearn.ensemble import RandomForestClassifier
from sklearn.neighbors import KNeighborsClassifier
from sklearn.svm import SVC
from sklearn.model_selection import StratifiedKFold
from sklearn.metrics import roc_auc_score
from sklearn.metrics import accuracy_score

classifiers = {
    'Logistic Regression': LogisticRegression(),
    'Random Forest': RandomForestClassifier(),
    'K Nearest Neighbors': KNeighborsClassifier(),
    'Support Vector Machine (RBF)': SVC(probability=True),
    'Support Vector Machine (Linear)': SVC(kernel = "linear", probability=True),
    'Support Vector Machine (Polynomial)': SVC(kernel = "poly",
    ↪probability=True),
    'Support Vector Machine (Sigmoid)': SVC(kernel = "sigmoid",
    ↪probability=True),
}

skf = StratifiedKFold(n_splits=10, shuffle=True, random_state=42)

scores = {name: {'Accuracy': [], 'AUC': []} for name in classifiers.keys()}

for train_index, test_index in skf.split(df.drop(columns='disease'),
    ↪df['disease']):

```

```

X_train, X_test = df.drop(columns='disease').iloc[train_index], df.
↳drop(columns='disease').iloc[test_index]
y_train, y_test = df['disease'].iloc[train_index], df['disease'].
↳iloc[test_index]

for clf_name, clf in classifiers.items():
    # Train classifier
    clf.fit(X_train, y_train)

    # Make predictions
    y_pred = clf.predict(X_test)

    # Make predictions for AUC if possible, check if the classifier
↳supports predict_proba
    if hasattr(clf, "predict_proba"):
        y_prob = clf.predict_proba(X_test)[:, 1]
        auc = roc_auc_score(y_test, y_prob)
        scores[clf_name]['AUC'].append(auc)
    else:
        y_prob = clf.decision_function(X_test) # For models like SVC with
↳'probability=False'
        auc = roc_auc_score(y_test, y_prob)
        scores[clf_name]['AUC'].append(auc)

    accuracy = accuracy_score(y_test, y_pred)
    scores[clf_name]['Accuracy'].append(accuracy)

print()
print()

for clf_name in classifiers:
    mean_accuracy = np.mean(scores[clf_name]['Accuracy'])
    mean_auc = np.mean(scores[clf_name]['AUC'])
    print(f"{clf_name}: Mean Accuracy = {mean_accuracy * 100:.2f}%, Mean AUC =
↳{mean_auc:.4f}")

```

/Users/brookestevens/opt/anaconda3/envs/myenv/lib/python3.9/site-packages/sklearn/linear_model/_logistic.py:469: ConvergenceWarning: lbfgs failed to converge (status=1):
STOP: TOTAL NO. of ITERATIONS REACHED LIMIT.

Increase the number of iterations (max_iter) or scale the data as shown in:

<https://scikit-learn.org/stable/modules/preprocessing.html>

Please also refer to the documentation for alternative solver options:

https://scikit-learn.org/stable/modules/linear_model.html#logistic-regression

```
n_iter_i = _check_optimize_result(
```

```
/Users/brookestevens/opt/anaconda3/envs/myenv/lib/python3.9/site-  
packages/sklearn/linear_model/_logistic.py:469: ConvergenceWarning: lbfgs failed  
to converge (status=1):  
STOP: TOTAL NO. of ITERATIONS REACHED LIMIT.
```

Increase the number of iterations (max_iter) or scale the data as shown in:

<https://scikit-learn.org/stable/modules/preprocessing.html>

Please also refer to the documentation for alternative solver options:

[https://scikit-learn.org/stable/modules/linear_model.html#logistic-
regression](https://scikit-learn.org/stable/modules/linear_model.html#logistic-regression)

```
n_iter_i = _check_optimize_result(  
/Users/brookestevens/opt/anaconda3/envs/myenv/lib/python3.9/site-  
packages/sklearn/linear_model/_logistic.py:469: ConvergenceWarning: lbfgs failed  
to converge (status=1):  
STOP: TOTAL NO. of ITERATIONS REACHED LIMIT.
```

Increase the number of iterations (max_iter) or scale the data as shown in:

<https://scikit-learn.org/stable/modules/preprocessing.html>

Please also refer to the documentation for alternative solver options:

[https://scikit-learn.org/stable/modules/linear_model.html#logistic-
regression](https://scikit-learn.org/stable/modules/linear_model.html#logistic-regression)

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n_iter_i = _check_optimize_result(  
/Users/brookestevens/opt/anaconda3/envs/myenv/lib/python3.9/site-  
packages/sklearn/linear_model/_logistic.py:469: ConvergenceWarning: lbfgs failed  
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https://scikit-learn.org/stable/modules/linear_model.html#logistic-regression

```
n_iter_i = _check_optimize_result(
```

Logistic Regression: Mean Accuracy = 92.64%, Mean AUC = 0.9718

Random Forest: Mean Accuracy = 93.02%, Mean AUC = 0.9731

K Nearest Neighbors: Mean Accuracy = 92.40%, Mean AUC = 0.9555

Support Vector Machine (RBF): Mean Accuracy = 93.07%, Mean AUC = 0.9756

Support Vector Machine (Linear): Mean Accuracy = 92.74%, Mean AUC = 0.9717

Support Vector Machine (Polynomial): Mean Accuracy = 92.57%, Mean AUC = 0.9704

Support Vector Machine (Sigmoid): Mean Accuracy = 78.69%, Mean AUC = 0.7981