Lungs Auscultation Audios

The auscultation is a technique to explore internal organs of the human body through the stetoscope in order to identify sounds whose are involved in some desease, like crackles and wheezes. These sounds can be identified in a time-frequency analysis, in which several statistic indices can be calculated (Variance, Range, Moving Average, Spectrum average) to build models that help to automatize the diagnosis of Crackles and Wheezes, or even some desease.

This project develops models of **regression and classification** with some of the indices described above using the data set I created in one of my university projects, in which a database of auscultation audios is analyzed, extracting each respiratory cycle from several auscultations performed on 126 patients.

The complete project can be found clicking here (https://github.com/santiagortiiz/Lungs-Auscultation-Signals.git).

And The original audios Database can be found clicking here (https://www.kaggle.com/vbookshelf/respiratory-sound-database)

Let's start by importing principle libraries

In [1]:
```
import random
import numpy as np
import pandas as pd
import seaborn as sns
import matplotlib.pyplot as plt
```

Load the dataset as a DataFrame

The dataset describes each of the 126 patients in two ways, the first of which details their basic information such as age, sex, weight, BMI, and their identification. And the second describes each respiratory cycle including start time, end time, `pathologies detected` , status and `statistical indices` .

Note: The status describes the patient as follows:
State
0 -> Healthy (Respiratory cycle without Crackles or Wheezes)
1 -> Respiratory cycle with Crackles
2 -> Respiratory cycle with Wheezes
3 -> Respiratory cycle with Both (Crackles and Wheezes)

```
In [274]: df = pd.read_excel('auscultation_features.xlsx')
          df
```

Out[274]:

	patient_ID	Diagnosis	age	sex	IMC	weight	height	adq_format	start	end	crackles	wheezes	state	Var	Range	Coars
0	101	URTI	3.0	F	NaN	19.0	99.0	1b1_Al_sc_Meditron	0.036	0.579	0	0	0	0.000048	0.113594	0.00
1	101	URTI	3.0	F	NaN	19.0	99.0	1b1_Al_sc_Meditron	0.579	2.450	0	0	0	0.000066	0.159031	0.01
2	101	URTI	3.0	F	NaN	19.0	99.0	1b1_Al_sc_Meditron	2.450	3.893	0	0	0	0.000044	0.115345	-0.10
3	101	URTI	3.0	F	NaN	19.0	99.0	1b1_Al_sc_Meditron	3.893	5.793	0	0	0	0.000074	0.187316	-0.11
4	101	URTI	3.0	F	NaN	19.0	99.0	1b1_Al_sc_Meditron	5.793	7.521	0	0	0	0.000036	0.117565	-0.01
...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	
6893	226	Pneumonia	4.0	M	NaN	16.7	103.0	1b1_Pl_sc_LittC2SE	11.721	13.693	1	0	1	0.000015	0.056514	-0.00
6894	226	Pneumonia	4.0	M	NaN	16.7	103.0	1b1_Pl_sc_LittC2SE	13.693	15.536	0	0	0	0.000026	0.107412	-0.01
6895	226	Pneumonia	4.0	M	NaN	16.7	103.0	1b1_Pl_sc_LittC2SE	15.536	17.493	0	0	0	0.000017	0.089678	0.00
6896	226	Pneumonia	4.0	M	NaN	16.7	103.0	1b1_Pl_sc_LittC2SE	17.493	19.436	1	0	1	0.000018	0.059962	-0.00
6897	226	Pneumonia	4.0	M	NaN	16.7	103.0	1b1_Pl_sc_LittC2SE	19.436	19.979	0	0	0	0.000042	0.046713	0.00

6898 rows × 18 columns

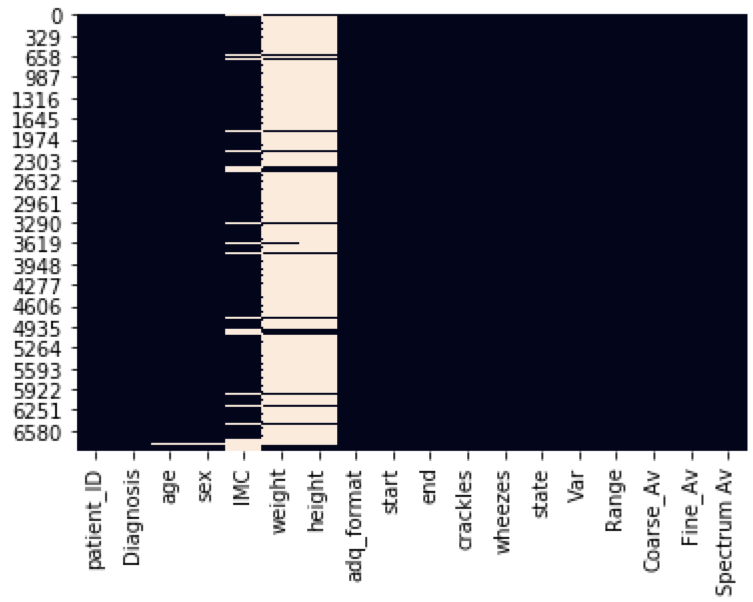
```
In [133]: len(df)
```

```
Out[133]: 6898
```

Preparation required based on missing data

Lets see what proportion of our dataset is `missing` and if it requires some cleaning:

```
In [134]: sns.heatmap(df.isnull(), cbar=False)
          plt.show()
```



```
In [135]: print(np.sum(df.isnull()==True))
```

```
patient_ID        0
Diagnosis         0
age              61
sex              61
IMC             894
weight         6149
height         6172
adq_format        0
start             0
end               0
crackles          0
wheezes           0
state             0
Var               0
Range             0
Coarse_Av         0
Fine_Av           0
Spectrum Av       0
dtype: int64
```

Cleaning dataset

The models in which I am interested, just need the statistical features and the diagnosis, so let's drop IMC, weight, height and the adquisition format columns:

```
In [136]: df.drop(['IMC','weight','height','adq_format'], axis=1, inplace=True)
          features = df.columns
          df
```

Out[136]:

	patient_ID	Diagnosis	age	sex	start	end	crackles	wheezes	state	Var	Range	Coarse_Av	Fine_Av	Spectrum Av
0	101	URTI	3.0	F	0.036	0.579	0	0	0	0.000048	0.113594	0.000446	0.000599	2.537207e-08
1	101	URTI	3.0	F	0.579	2.450	0	0	0	0.000066	0.159031	0.012435	-0.001276	3.532798e-08
2	101	URTI	3.0	F	2.450	3.893	0	0	0	0.000044	0.115345	-0.101963	-0.000701	2.213387e-08
3	101	URTI	3.0	F	3.893	5.793	0	0	0	0.000074	0.187316	-0.113660	-0.000223	3.485673e-08
4	101	URTI	3.0	F	5.793	7.521	0	0	0	0.000036	0.117565	-0.017593	-0.001040	1.806783e-08
...	...	...	...	...	...	...	...	...	...	...	...	...	...	...
6893	226	Pneumonia	4.0	M	11.721	13.693	1	0	1	0.000015	0.056514	-0.005161	-0.005630	7.528343e-09
6894	226	Pneumonia	4.0	M	13.693	15.536	0	0	0	0.000026	0.107412	-0.018191	-0.000332	1.279829e-08
6895	226	Pneumonia	4.0	M	15.536	17.493	0	0	0	0.000017	0.089678	0.002857	0.005618	8.751189e-09
6896	226	Pneumonia	4.0	M	17.493	19.436	1	0	1	0.000018	0.059962	-0.004191	0.002940	8.975479e-09
6897	226	Pneumonia	4.0	M	19.436	19.979	0	0	0	0.000042	0.046713	0.006035	0.000096	2.033625e-08

6898 rows × 14 columns

Then, notice that only 61 values of the age and sex columns are missing, so there are two options:

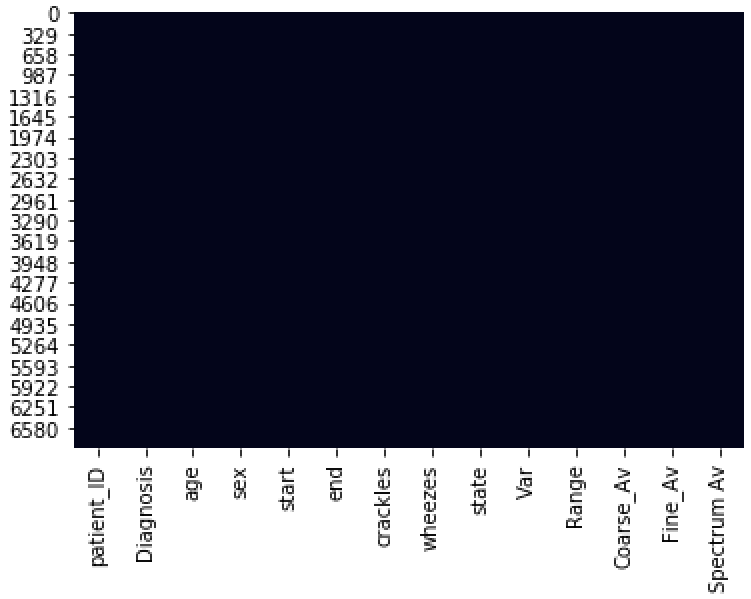
1) Discard the missing data: df = df.dropna()
2) Impute the missing data

Lets go ahead imputing these data with the scikit learn library using the SimpleImputer class

```
In [8]: from sklearn.impute import SimpleImputer
```

In [137]:
```
imp = SimpleImputer(strategy="most_frequent")
df = pd.DataFrame(imp.fit_transform(df), columns = features)
```

In [138]:
```
sns.heatmap(df.isnull(), cbar=False)
plt.show()
print(np.sum(df.isnull()==True))
```



```
patient_ID     0
Diagnosis      0
age            0
sex            0
start          0
end            0
crackles       0
wheezes        0
state          0
Var            0
Range          0
Coarse_Av      0
Fine_Av        0
Spectrum Av    0
dtype: int64
```

Scaling between -1:1 (Normalization with Sckit Learn)

In [11]:
```
from sklearn import preprocessing
```

In [218]:
```
df.loc[:, 'Var':'Spectrum Av'] = preprocessing.scale(df.loc[:, 'Var':'Spectrum Av'])
df['Intercept'] = 1
df
```

Out[218]:

	patient_ID	Diagnosis	age	sex	start	end	crackles	wheezes	state	Var	Range	Coarse_Av	Fine_Av	Spectrum Av	Intercept
3153	158	COPD	63	M	10.276	12.73	0	0	0	-0.333874	-0.252502	-0.00854766	0.342765	-0.335266	1
2195	144	Healthy	3	M	11.836	13.736	0	0	0	-0.408888	-0.877265	0.0520217	0.0109757	-0.406949	1
2130	141	COPD	66	M	18.279	19.307	0	1	2	-0.400046	-0.752192	-0.0269303	-0.025986	-0.397925	1
2502	151	COPD	75	M	12.179	15.701	1	0	1	-0.384935	-0.603046	0.23697	0.0311238	-0.383317	1
2176	143	Healthy	0.25	F	17.25	18.35	0	0	0	-0.409529	-0.853852	-0.00188055	0.0171662	-0.407659	1
...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...
6284	211	COPD	70	F	8.894	10.235	0	0	0	-0.147175	-0.260528	0.1067	-1.51089	-0.1367	1
411	109	COPD	84	F	8.55	10.674	0	0	0	-0.233228	0.437392	0.0418405	0.0393682	-0.2357	1
1511	130	COPD	85	F	18.156	19.194	1	0	1	-0.284592	-0.579716	0.0209268	-0.0706335	-0.283251	1
6118	207	COPD	63	F	1.261	4.583	0	0	0	-0.160055	0.0678598	0.072842	0.630796	-0.160613	1
4025	172	COPD	73	M	14.716	17.571	1	0	1	-0.370377	-0.595794	0.0676996	0.0118841	-0.369563	1

6898 rows × 15 columns

Shuffle the dataset because:

1) Shuffled samples will help us avoid areas of the model that under/overfil the data

2) If we evaluate a movel based on data it has seen before, we may overestimate its performance

In [219]:
```
df = df.sample(frac=1)
df
```

Out[219]:

	patient_ID	Diagnosis	age	sex	start	end	crackles	wheezes	state	Var	Range	Coarse_Av	Fine_Av	Spectrum Av	Intercept
2924	156	COPD	80	M	14.535	17.589	1	1	3	-0.401156	-0.798398	0.200927	0.106203	-0.399382	1
1661	133	COPD	68	M	8.375	10.78	0	0	0	-0.274294	-0.331413	0.121491	-0.266822	-0.270577	1
1605	133	COPD	68	M	7.375	9.946	1	0	1	0.565438	1.09739	0.00611665	1.09806	0.586861	1
343	107	COPD	75	F	16.696	18.887	1	0	1	0.2183	1.93693	0.59383	0.31942	0.21216	1
1331	130	COPD	85	F	5.937	7.83	1	0	1	0.474795	0.825708	3.22218	-0.981882	0.517281	1
...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...
5995	205	COPD	45	M	15.994	19.688	1	0	1	-0.32124	0.704738	-0.0072496	0.164282	-0.323834	1
2361	147	COPD	77	M	8.364	12.794	0	1	2	0.142992	0.875651	-0.0204281	-0.101878	0.139608	1
1020	130	COPD	85	F	0.697	2.423	1	0	1	-0.39095	-0.7327	0.906886	0.378545	-0.389354	1
4174	174	COPD	68	M	0.593	3.331	0	1	2	-0.387805	-0.736466	-0.082893	-0.168168	-0.385898	1
1965	138	COPD	56	F	5.267	9.224	1	0	1	0.468142	1.6861	-0.123771	-0.737297	0.435759	1

6898 rows × 15 columns

Labels to predict:

In [220]:
```
y = df['state'].values.reshape(-1,1)  # -1 means that calculate the dimension of rows, but have 1 column
y = y.tolist()
y[:10]
```

Out[220]:
```
[[3], [0], [1], [1], [1], [0], [1], [0], [0], [2]]
```

Features used to predict:

In [221]:
```python
X = pd.concat([df['Intercept'], df.loc[:, 'Var':'Spectrum Av']], axis=1)
X
```

Out[221]:

	Intercept	Var	Range	Coarse_Av	Fine_Av	Spectrum Av
2924	1	-0.401156	-0.798398	0.200927	0.106203	-0.399382
1661	1	-0.274294	-0.331413	0.121491	-0.266822	-0.270577
1605	1	0.565438	1.09739	0.00611665	1.09806	0.586861
343	1	0.2183	1.93693	0.59383	0.31942	0.21216
1331	1	0.474795	0.825708	3.22218	-0.981882	0.517281
...	...	...	...	...	...	...
5995	1	-0.32124	0.704738	-0.0072496	0.164282	-0.323834
2361	1	0.142992	0.875651	-0.0204281	-0.101878	0.139608
1020	1	-0.39095	-0.7327	0.906886	0.378545	-0.389354
4174	1	-0.387805	-0.736466	-0.082893	-0.168168	-0.385898
1965	1	0.468142	1.6861	-0.123771	-0.737297	0.435759

6898 rows × 6 columns

Data Split

In [222]:
```python
N = len(X)

# 50%, 25%, 25% (non-overlapping) splits

X_train = X[:N//2] # 0%:50%
X_valid = X[N//2:3*N//4] # 50%:75%
X_test = X[3*N//4:] # 75%:100%

y_train = y[:N//2]
y_valid = y[N//2:3*N//4]
y_test = y[3*N//4:]
```

In [223]:
```
# Examine size of data
len(X), len(X_train), len(X_valid), len(X_test)
```

Out[223]:
```
(6898, 3449, 1724, 1725)
```

Rigde model which allows us to implement regression with a regularizer

$$\underbrace{\frac{1}{N}\sum_i (y_i - X_i \cdot \theta)^2}_{\text{MSE}} + \lambda \underbrace{\sum_k \theta_k^2}_{\text{regularizer}}$$

To implement the pipeline, we:

1. Iterate through various values of lambda
2. Fit a ridge regression model for each of these values
3. Evaluate the performance of this model on the validation set
4. Keep track of which model is the best we've seen so far (on the validation set)

In [224]:
```
from sklearn import linear_model
```

In [225]:
```
def MSE(model, X, y):
    predictions = model.predict(X)
    differences = [(a-b)**2 for (a,b) in zip(predictions,y)]
    return sum(differences) / len(differences)
```

In [226]:
```
# Variables to keep track of the current best model and MSE
bestModel = None
bestMSE = None
```

In [227]:
```
for lamb in [0.01, 0.1, 1, 10, 100]:
    # Fit a model for each lambda value
    model = linear_model.Ridge(lamb, fit_intercept=False)
    model.fit(X_train, y_train)

    mseTrain = MSE(model, X_train, y_train)
    mseValid = MSE(model, X_valid, y_valid)

    print("lambda = " + str(lamb) + ", training/validation error" + str(mseTrain) + '/' + str(mseValid))

    if not bestModel or mseValid < bestMSE:
        bestModel = model
        bestMSE = mseValid
```

```
lambda = 0.01, training/validation error[0.86022051]/[0.87735039]
lambda = 0.1, training/validation error[0.86022127]/[0.8773391]
lambda = 1, training/validation error[0.86025821]/[0.87728537]
lambda = 10, training/validation error[0.86046107]/[0.87739919]
lambda = 100, training/validation error[0.86099701]/[0.8794343]
```

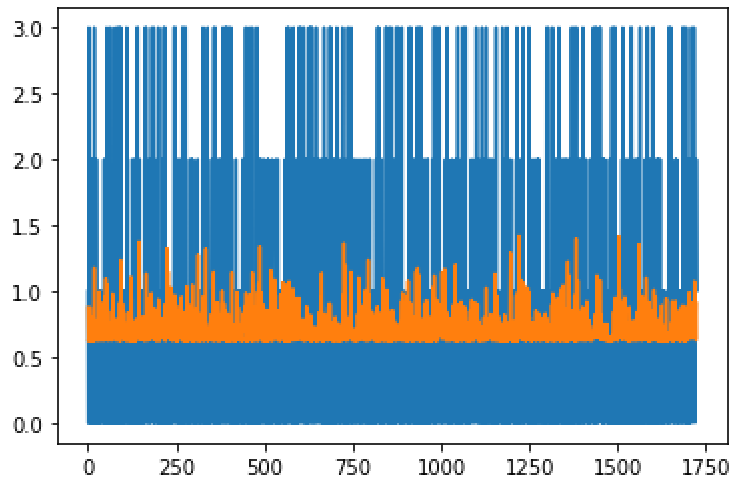
In [228]:
```
mseTest = MSE(bestModel, X_test, y_test)
print("test error = " + str(mseTest))
```

```
test error = [0.85992539]
```

In [229]:
```
FVU = mseTest / np.var(y_test)
R2 = 1 - FVU
print("R2 = " + str(R2))
```

```
R2 = [0.02974691]
```

In [230]:
```
plt.figure()
plt.plot(y_test)
plt.plot(model.predict(X_test))
plt.show()
```



Conclusion: As we see, this problem can't be solve by a linear regression model because the features have an extreamly small value, so lets try to perform a classification in healthy and sick respiratory cycles

Classification

In [275]:
```
df.loc[df['state'] != 0, 'state'] = True
df.loc[df['state'] == 0, 'state'] = False
df
```

Out[275]:

atient_ID	Diagnosis	age	sex	IMC	weight	height	adq_format	start	end	crackles	wheezes	state	Var	Range	Coarse_Av	F
101	URTI	3.0	F	NaN	19.0	99.0	1b1_Al_sc_Meditron	0.036	0.579	0	0	False	0.000048	0.113594	0.000446	0.(
101	URTI	3.0	F	NaN	19.0	99.0	1b1_Al_sc_Meditron	0.579	2.450	0	0	False	0.000066	0.159031	0.012435	-0.(
101	URTI	3.0	F	NaN	19.0	99.0	1b1_Al_sc_Meditron	2.450	3.893	0	0	False	0.000044	0.115345	-0.101963	-0.(
101	URTI	3.0	F	NaN	19.0	99.0	1b1_Al_sc_Meditron	3.893	5.793	0	0	False	0.000074	0.187316	-0.113660	-0.(
101	URTI	3.0	F	NaN	19.0	99.0	1b1_Al_sc_Meditron	5.793	7.521	0	0	False	0.000036	0.117565	-0.017593	-0.(
...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	
226	Pneumonia	4.0	M	NaN	16.7	103.0	1b1_Pl_sc_LittC2SE	11.721	13.693	1	0	True	0.000015	0.056514	-0.005161	-0.(
226	Pneumonia	4.0	M	NaN	16.7	103.0	1b1_Pl_sc_LittC2SE	13.693	15.536	0	0	False	0.000026	0.107412	-0.018191	-0.(
226	Pneumonia	4.0	M	NaN	16.7	103.0	1b1_Pl_sc_LittC2SE	15.536	17.493	0	0	False	0.000017	0.089678	0.002857	0.(
226	Pneumonia	4.0	M	NaN	16.7	103.0	1b1_Pl_sc_LittC2SE	17.493	19.436	1	0	True	0.000018	0.059962	-0.004191	0.(
226	Pneumonia	4.0	M	NaN	16.7	103.0	1b1_Pl_sc_LittC2SE	19.436	19.979	0	0	False	0.000042	0.046713	0.006035	0.(

vs × 18 columns

In [294]:
```
y_class = np.ravel(df['state'].values.reshape(-1,1).tolist())
y_class[:10]
```

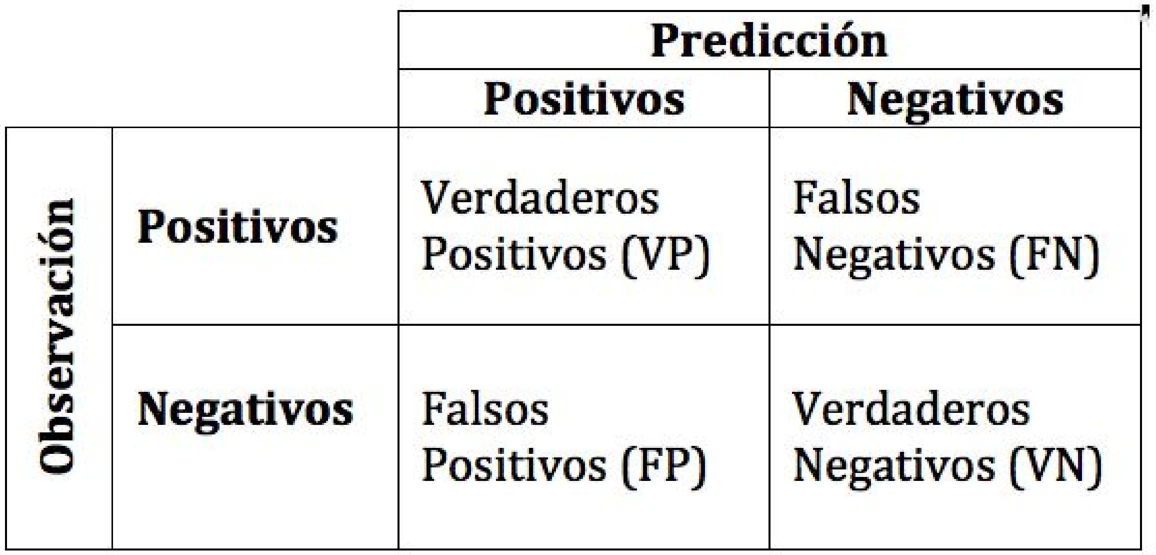
Out[294]:
```
array([False, False, False, False, False, False, False, False, False,
       False])
```

In [295]:
```
modelLin = linear_model.LogisticRegression(max_iter=100, multi_class='ovr',n_jobs=1,solver='liblinear') #Basic Linear Mode
modelLin.fit(X, y_class)
```

Out[295]:
```
LogisticRegression(C=1.0, class_weight=None, dual=False, fit_intercept=True,
                   intercept_scaling=1, l1_ratio=None, max_iter=100,
                   multi_class='ovr', n_jobs=1, penalty='l2', random_state=None,
                   solver='liblinear', tol=0.0001, verbose=0, warm_start=False)
```

In [296]:
```
predictions = modelLin.predict(X)
correct = predictions == y_class
correct
```

Out[296]:
```
array([ True,  True,  True, ...,  True, False,  True])
```



		Predicción	
		Positivos	Negativos
Observación	Positivos	Verdaderos Positivos (VP)	Falsos Negativos (FN)
	Negativos	Falsos Positivos (FP)	Verdaderos Negativos (VN)

- **VP** es la cantidad de *positivos* que fueron *clasificados correctamente* como positivos por el modelo.
- **VN** es la cantidad de *negativos* que fueron *clasificados correctamente* como negativos por el modelo.
- **FN** es la cantidad de *positivos* que fueron *clasificados incorrectamente* como negativos. **Error tipo 2** (Falsos Negativos)
- **FP** es la cantidad de *negativos* que fueron *clasificados incorrectamente* como positivos. **Error tipo 1** (Falsos positivos)

In [298]:
```python
# p: Prediction
# l: Label
TP = sum([(p and l) for (p,l) in zip(predictions, y_class)])
FP = sum([(p and not l) for (p,l) in zip(predictions, y_class)])
TN = sum([(not p and not l) for (p,l) in zip(predictions, y_class)])
FN = sum([(not p and l) for (p,l) in zip(predictions, y_class)])
```

In [299]:
```python
print("TP = " + str(TP))
print("FP = " + str(FP))
print("TN = " + str(TN))
print("FN = " + str(FN))
```

```
TP = 218
FP = 180
TN = 3462
FN = 3038
```

```
In [300]: TF_Accuracy = (TP + TN) / (TP + TN + FP + FN)
          TF_Accuracy

Out[300]: 0.5334879675268194
```

```
In [301]: TPR = TP / (TP + FN) # Number of data that were positive, and that were labeled
          TNR = TN / (TN + FP) # Number of data that were negative, and that were labeled
          print(TPR, '\n',TNR)

          0.06695331695331695
           0.9505766062602965
```

```
In [302]: BER = 1 - 1/2 * (TPR + TNR)
          print("Balanced error rate = " + str(BER))

          Balanced error rate = 0.49123503839319327
```

```
In [303]: precision = TP / (TP + FP)
          recall = TP / (TP + FN)

          precision, recall

Out[303]: (0.5477386934673367, 0.06695331695331695)
```

```
In [304]: F1 = 2 * (precision*recall) / (precision + recall)
          F1

Out[304]: 0.11932129173508484
```

And in case of the True labels (sick respiratory cycles) are more important:

Next we want to sort our predictions by confidence.
First we obtain the **confidences** from the model:

```
In [305]: confidences = model.decision_function(X)
          confidences
```

```
Out[305]: array([ 0.10262646,  0.07467153,  0.0549044 , ...,  0.17507139,
                  0.06829087, -0.0267003 ])
```

Then we sort them along de with the labels

```
In [316]: confidencesAndLabels = list(zip(confidences, y_class))
          confidencesAndLabels[:5]
```

```
Out[316]: [(0.10262646118669831, False),
           (0.07467152887165264, False),
           (0.05490440262215493, False),
           (0.042249699355202536, False),
           (0.37435466720459515, False)]
```

```
In [307]: confidencesAndLabels.sort()
          confidencesAndLabels.reverse()
```

At this point we can discard the confidences

```
In [308]: labelsRankedByConfidence = [z[1] for z in confidencesAndLabels]
          labelsRankedByConfidence[:5]
```

```
Out[308]: [True, True, False, True, True]
```

```
In [309]: def precisionAtK(K, y_sorted):
              return sum(y_sorted[:K]) / K

          def recallAtK(K, y_sorted):
              return sum(y_sorted[:K]) / sum(y_sorted)
```

```
In [310]: precisionAtK(50, labelsRankedByConfidence)
```

```
Out[310]: 0.6
```

```
In [311]: precisionAtK(1000, labelsRankedByConfidence)

Out[311]: 0.504

In [312]: precisionAtK(10000, labelsRankedByConfidence)

Out[312]: 0.3256

In [313]: recallAtK(50, labelsRankedByConfidence)

Out[313]: 0.009213759213759214

In [314]: recallAtK(1000, labelsRankedByConfidence)

Out[314]: 0.1547911547911548

In [315]: recallAtK(10000, labelsRankedByConfidence)

Out[315]: 1.0
```

Conclusion: The performed model it more or less good, in the aproximately 50% of cases, it can predict the state of the respiratory cycle

```
In [ ]:
```