SELECTED TOPICS IN BIOMEDICAL SIGNAL PROCESSING: NONLINEAR SIGNAL PROCESSING

1. Deep Learning: EEG-based detection on the atrial fibrillation

In this section we have 4 datasets: a training input data and its corresponding binary output, that indicates whether an atrial fibrillation has been detected or not, and a validating data with its output. The training input is formed by ECG data of 11668 patient, each measurement of 30 seconds. We can observe in the following plot the ECG of a healthy patient and one ECG with AF data.

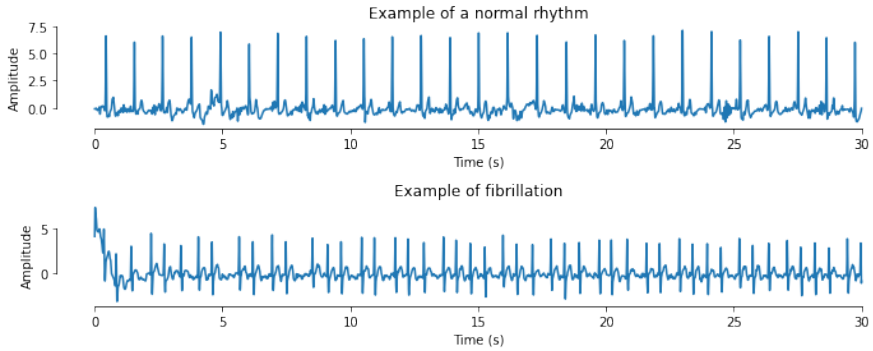


Figure 1: Normal and fibrillated ryhthm

In this graphics we can see the distribution of healthy and AF patients in both datasets.

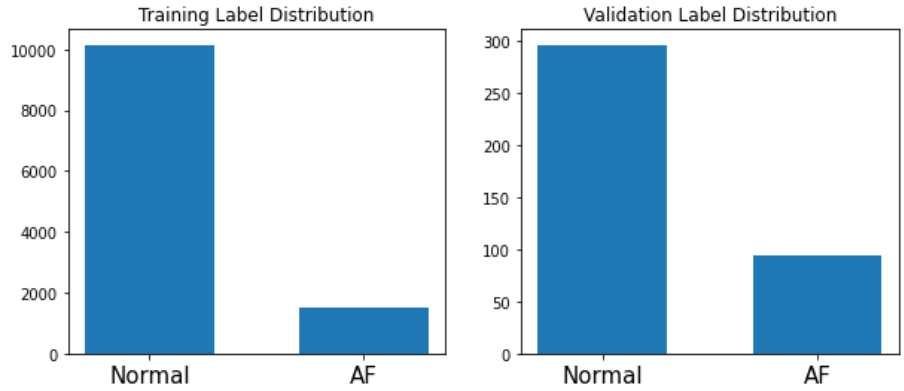


Figure 2: Label distributions

Measurements

In this assignment we will be using the accuracy and the cross-entropy metrics to measure the training process:

- Accuracy: it measures how many results were correctly predicted.

$$Accuracy = \frac{TP + TN}{N}$$

- Cross-entropy: this value increases as the predicted probability diverges from the actual label. The lower this value is, the better model we have reached.

Other metrics can be used with this purpose, considering that our output classification is formed by binary data:

- Precision: it counts the number of TP among all the positive detected (TP+FP).
- Recall: it counts the number of TP over those who should have been marked as positive (TP+FN).
- Specificity: it counts the number of TN over those who should have been marked as negative (TN+FP).

Architecture

After compiling and fitting the model we will observe 4 different parameters:

- Loss: cross-entropy of the training data.
- Accuracy: accuracy of the training data.
- Val_loss: cross-entropy of the validating data.
- Val_accuracy: accuracy of the validating data.

First trial

At first, I tried to build the model with 2 cycles of Conv1D(filters=64, kernel_size=3, activation=None) layer and BatchNormalization() and finishing with the GlobalAveragePooling1D.

Layer (type)	**Output Shape**	**Param #**
input_1 (InputLayer)	[(None, 6000)]	0
reshape (Reshape)	(None, 6000, 1)	0
conv1d(Conv1D)	(None, 5998, 64)	256
batch_normalization(BatchNormalization)	(None, 5998, 64)	256
conv1d(Conv1D)	(None, 5996, 64)	12352
batch_normalization(BatchNormalization)	(None, 5996, 64)	256
global_average_pooling1d(GlobalAveragePooling1D)	(None, 64)	0
dense(Dense)	(None, 1)	65
Total params	13,185	
Trainable params	12,929	
Non-trainable params	256	

Results: loss: 0.3864 - accuracy: 0.8701 - val_loss: 0.5950 - val_accuracy: 0.7590.

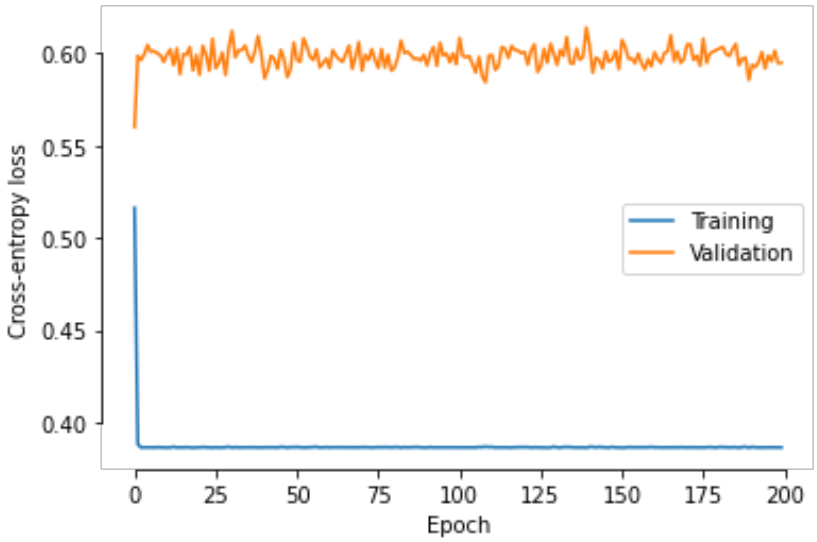


Figure 3: Training and validation entropy

We can observe how the cross-entropy is over 0.6 during all the epochs. As this number should be as lower as possible, we can determine that the model is yet to be improved.

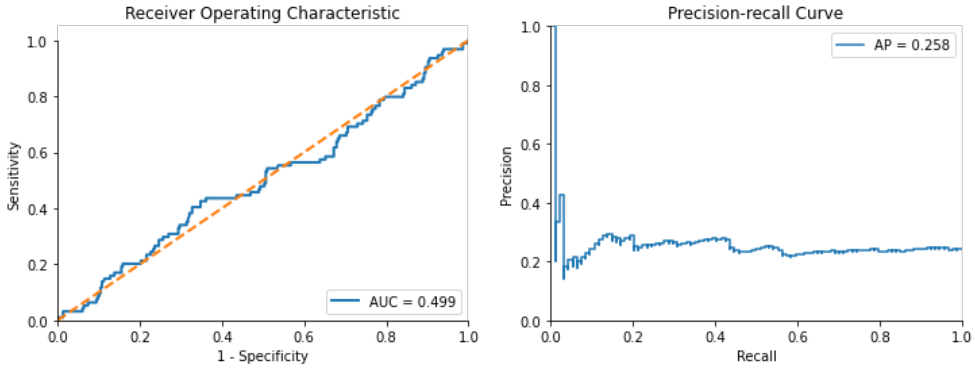


Figure 4: S-S and P-R curve

The AUC parameter can be interpreted as the probability that the model ranks a random positive example more highly than a random negative example. A model whose predictions are completely wrong would have AUC=0, whereas having all the prediction correct leads to AUC=1. We can infer that out model is not a very good one because it has AUC=0.499.

Second trial

I repeated the model adding one more layer of Conv1D and BatchNormalization to see the effect of the number of layers.

Layer (type)	**Output Shape**	**Param #**
input_2 (InputLayer)	[(None, 6000)]	0
Reshape_1 (Reshape)	(None, 6000, 1)	0
conv1d_2(Conv1D)	(None, 5998, 64)	256
batch_normalization_2(BatchNormalization)	(None, 5998, 64)	256
conv1d_3(Conv1D)	(None, 5996, 64)	12352

batch_normalization_3(BatchNormalization)		(None, 5996, 64)	256
conv1d_4(Conv1D)		(None, 5994, 64)	12352
batch_normalization_4(BatchNormalization)		(None, 5994, 64)	256
global_average_pooling1d_1(GlobalAveragePooling1D)		(None, 64)	0
dense(Dense)		(None, 1)	65
Total params	25,793		
Trainable params	25,409		
Non-trainable params	384		

Results: loss: 0.3865 - accuracy: 0.8701 - val_loss: 0.5967 - val_accuracy: 0.7590

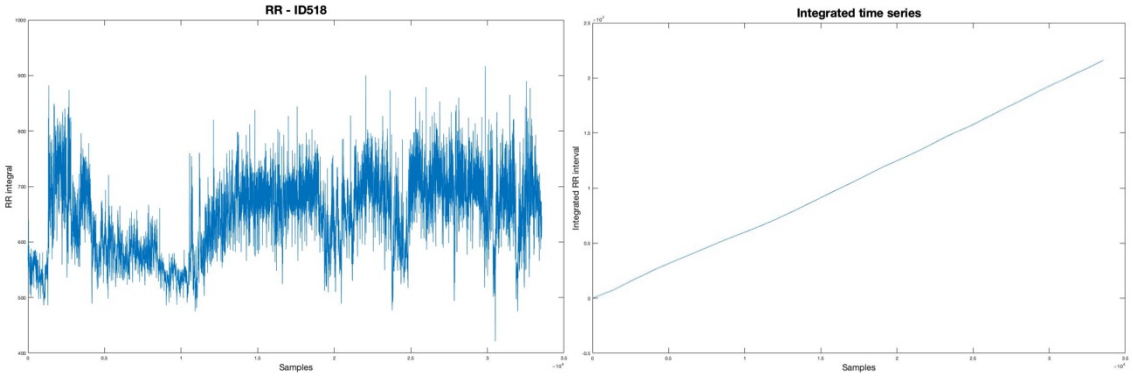
We can observe that these results just as those present in the previous trial, so we can infer that for a low number of layers, adding one more does not make much of a different in the results.

2. Nonlinear Signal Analysis

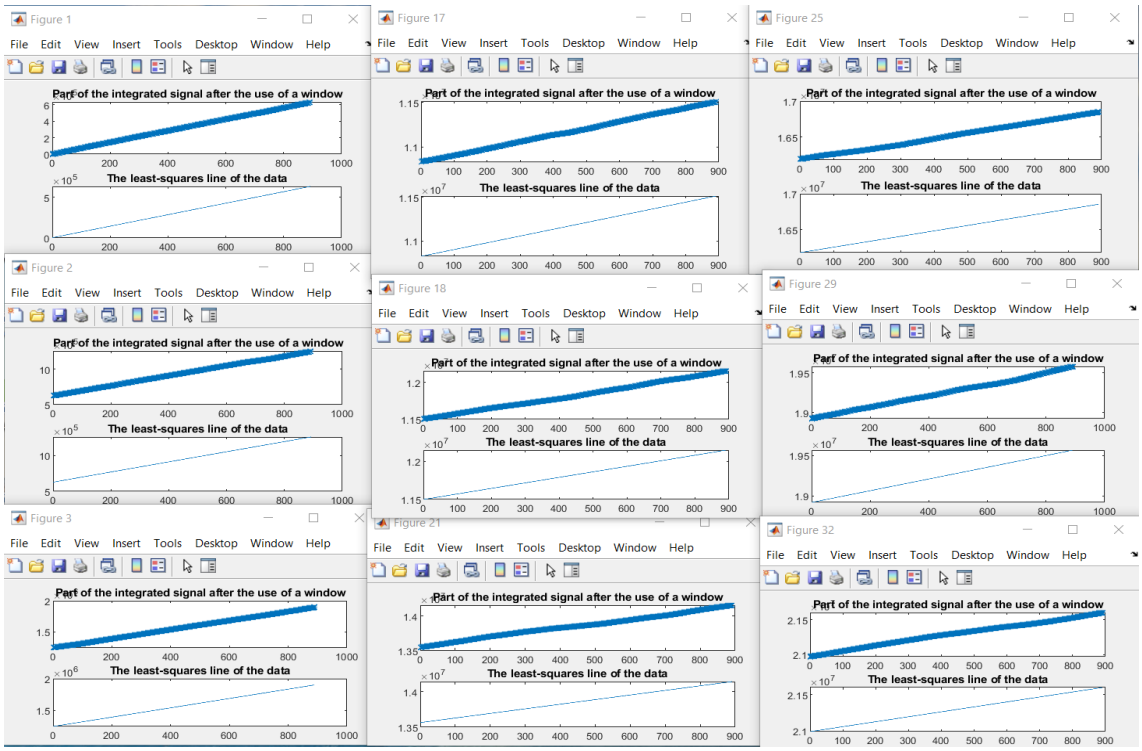
At this exercise we need to handle two populations of two women with different levels of anxiety. More specifically, we are asked to take the RR intervals of their HRV and to and compute their nonlinear characteristics.

2.1. Detrended Fluctuation Analysis

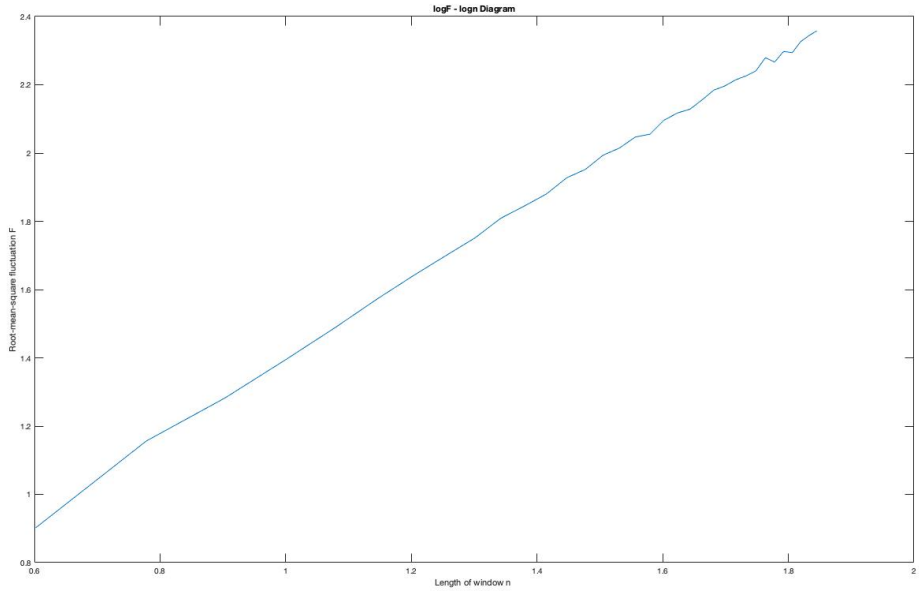
At first, we plotted one of the RR interval series and its integrated time series.



After the calculation of the integrated time series (step 1), we divided it into windows of equal length n. In each window of length n, we fitted a least-squares line to the data. In the following figures we have plotted some parts of the integrated series of a signal RR cut by a window of specific length (the samples are represented as 'x' and not '.') and the least-squares line which corresponds to this data.



After the calculation of the root-mean-square fluctuation F in every window with length n, we plotted the diagram logF – logn. As we expected the value of F increases with the window size as you can detect in the next diagram.



We estimated separately the scaling components α1 and α2 for the different signals of every population and we incorporated these values in two arrays.

a1_high = 2.8297 3.2291 2.8737 2.6137 3.1694 → **mean(a1_high)** = 2.9431

a1_low = 3.1665 2.8806 2.9605 2.6509 2.4380 → **mean(a1_low)** = 2.8193

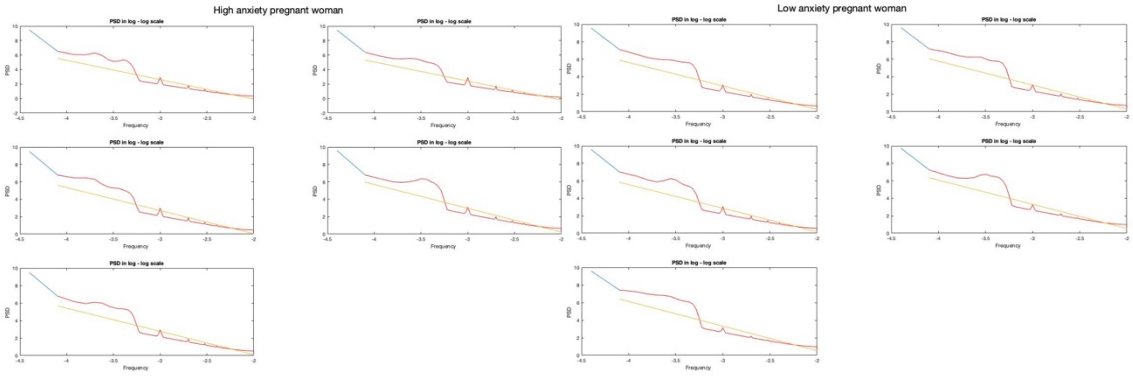
a2_high = 2.4944 2.5568 2.2625 2.6287 2.3549 → **mean(a2_high)** = 2.4515

a2_low = 2.1902 2.0858 2.1565 2.3355 1.9841 → **mean(a2_low)** = 2.1504

As we can observe, the long-term scaling exponent α2 is more helpful for the separation of the signals given that its value differs more when it corresponds to signals which come from pregnant women with high or low anxiety. More specifically, its value has the tendency of being smaller when it is about low anxious pregnant women.

2.2. Frequency drop-off

Firstly, we resampled the data (via the function resample) because the initial ones were indexed by heartbeat and so we needed more samples. Then we created a function which plots the log(power) versus log(f), and by keeping only the samples which correspond to the frequency range [10^ (-4): 10^ -(2)] it calculates the regression line of these data for every resampled signal and returns its slope. The pictures below represent the plots for the two different populations.



sl_high = -2.6749 -2.6298 -2.6508 -2.7386 -2.6875 → **mean(sl_high)** = -2,6763

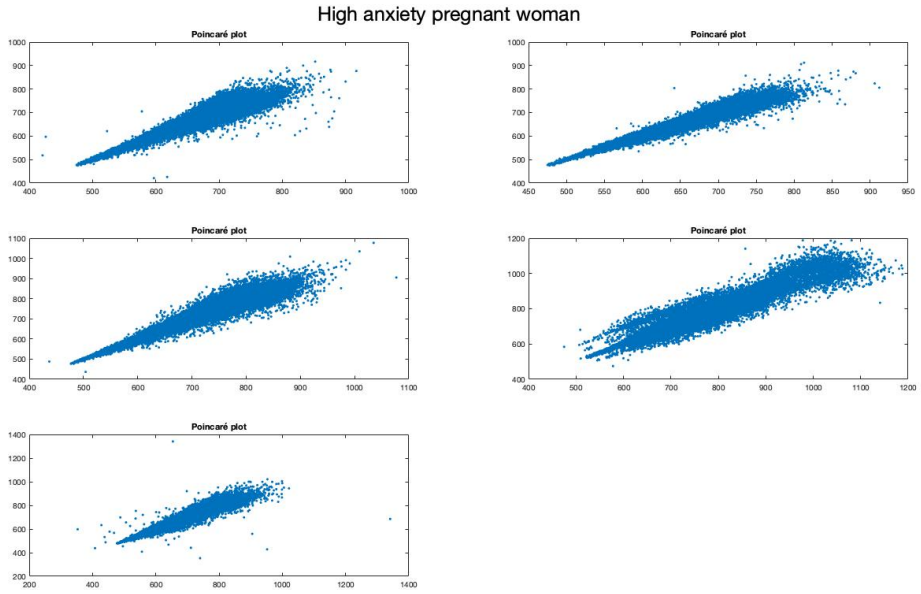
sl_low = -2.6875 -2.7474 -2.7112 -2.7598 -2.8028 → **mean(sl_low)** = -2,7418

We can observe that the value of the slope is usually smaller for the women with low level of anxiety, but we cannot be sure for the kind of the signal only based on the value of the slope as the differences are extremely small.

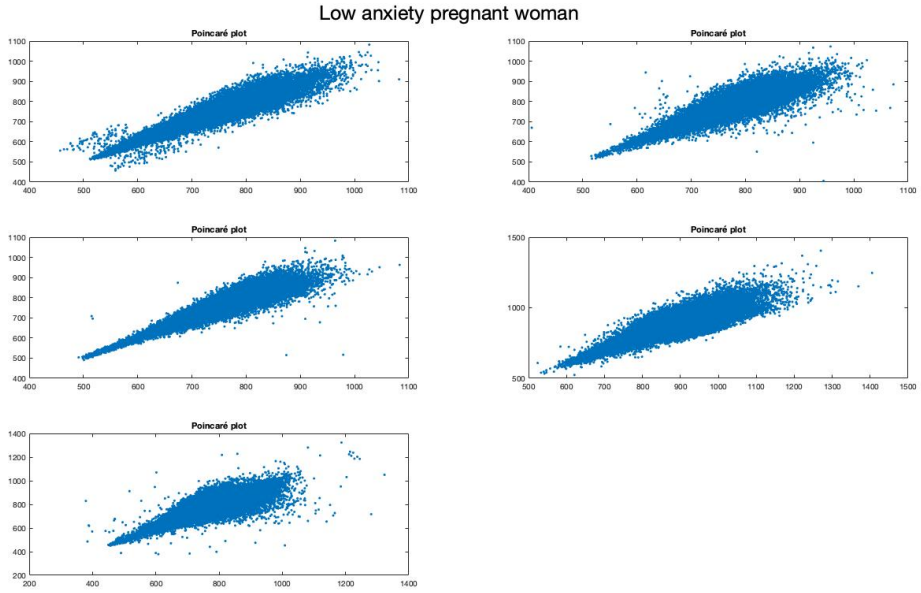
2.3. Poincaré plot

We created a function (named poincare_plot) which evaluates the Poincaré plot of a signal and calculates the SD1 and SD2. By applying it to every signal of the two populations we gathered the values of SD1 and SD2 to two different matrices corresponding to high anxiety pregnant women and low anxiety pregnant women. Then, we calculated the average of these matrices and we realized that the mean value of SD1 and SD2 is higher for the women with low anxiety.

High anxiety pregnant women (ID 518, 542, 547, 562, 576)



Low anxiety pregnant women (ID 507, 514, 571, 619, 621)



Comment: For a healthy heart, the cloud of points presents a comet shape.

	High anxiety women	Low anxiety women
SD1 mean	16.3886	29.9356
SD2 mean	115.8825	122.6678
SDRR mean	82.7674	89.4170

Comment: In general, the SD1 width reflects the parasympathetic activity and the SD2 length reflects the sympathetic modulation.

2.4. Nonlinear HRV measures

Explanations: **FD** = fractal dimension, **SE** = Shannon Entropy, **LE** = Lyapunov Exponent, **CD** = Correlation Dimension.

Via the use of the file *nonlin_measures.m* we tried to calculate the mean of the nonlinear measures of every population and to compare them.

Comment: We used a delay of 1 and an embedding dimension of 8 to compute the correlation dimension.

FD_high = 1.7875 1.7964 1.7672 1.7848 1.6773

SE_high = 0.6562 0.5844 0.4857 0.6723 0.5658

LE_high = 0.3012 0.1633 0.3635 0.4212 0.3700

CD_high = 3.5492 3.7723 3.3176 3.7171 3.7627

FD_low = 1.8160 1.8251 1.8108 1.8100 1.7925

SE_low = 0.7947 1.2307 1.0104 1.3818 1.4054

LE_low = 0.3144 0.5271 0.4801 0.8816 0.9535

CD_low = 3.8726 3.8712 3.7733 3.8310 4.101

	High anxiety pregnant women	Low anxiety pregnant women
mean(FD)	1.7626	1.8109
mean(SE)	0.5929	1.1666
mean(LE)	0.3238	0.6313
mean(CD)	3.6238	3.8899

As we can detect the values of the nonlinear HRV measures are always larger for the population of low anxious pregnant women. We believe that we shouldn't classify only based only on one given feature, but we should use all of them because in this way we will end up to more accurate conclusions about the kind of population where our initial signal belongs.

Some of the features provide additional information. For example, if SD1/SD2 is highly correlated with the short-term scaling component α1(DFA) according to the slides of our course. Furthermore, the correlation dimension (CD) is one of the most widely used measures of fractal dimension and it can be considered as a measure for the number of independent variables needed to define the total system in phase space.

Usefulness of methods:

The Poincaré plot allows assessing the heartbeat dynamics based on a simplified phase-space embedding. The shape of the plot provides summary information on the behavior of the heart. For a healthy heart, the cloud of points presents a comet shape.

As for the fractal dimension (FD), it is a statistical index of how details in a pattern change with the scale at which it is measured. The higher the FD, the more irregular the signal is, i.e., the more self-similar the signal will be.

Additionally, the value of the scaling factors α in DFA can be considered as an indicator of the "roughness" of the time series: the larger the value of α, the smoother the time series.

As for the Lyapunov exponent, it is a measure of the system dependency on the initial conditions but also quantifies the predictability of the system. The value of LE increases (so we have lower predictability) when the degree of chaos becomes higher. A positive LE is a strong indicator of chaos, but it doesn't happen in the signals with which we are occupied with.

As far as the sample entropy is concerned, a smaller value indicates more self-similarity or less noise.

The values of FD, LE and SE is higher for the second population (low anxiety pregnant women) and so these signals present less self-similarity (their behavior is more difficult to be predicted).

Conclusion: By using these nonlinear methods we can study the heart rate variability in pregnant women with high and low anxiety. They help us to end up to different interpretations of the same conclusion, that the signals of low anxiety pregnant women present less self-similarity.

3. References:

- https://www.mathworks.com/matlabcentral/answers/24958-poincare-plot-for-hrv
- https://www.mdpi.com/1099-4300/22/3/309/htm
- https://en.wikipedia.org/wiki/Sample_entropy