ABSTRACT

Complexity measures are a set of statistical methods that enable the estimation of system regularity. This methods are based on nonlinear signal processing techniques that allow signal characterization without any underlying assumption on stationarity or ergodicity.

These nonlinear processing techniques are being widely used over biological signals due to their nature. Biological signals are characterized by an irregular, nonlinear and time–varying behavior. This chaotic behavior makes traditional linear methods fail as they can not fully characterize it.

Regularity measures work well in practice, as they can unveil information from the signals which otherways in not possible. They can discern between healthy and pathologic estates, predict the ocurrence of an epileptic seizure or classify between sleep stages, among others. Even though there application is useful, it presents some controversy, as there is no previous characterization on how to apply them or even how the results should be interpreted.

This thesis proposes a deep characterization of some of the most common complexity measures. A characterization of Approximate Entropy (ApEn), Sample Entropy (SampEn), MultiScale Entropy (MSE), Detrended Fluctuation Analysis (DFA), Rényi Square Entropy (QSE) and the Coefficient of Sample Entropy (CosEn) is driven against situation where biological signals suffered sample loss or present a limited length.

Sample loss is actually quite common where most of the signal transduction and recording is made somehow in an ambulatory manner and the storage capabilities is limited (data compression) or signals are wirelessly transmitted over channels that can present unstable conditions or interference that can cause sample loss. The limited length of the recordings can be due to a manual annotation or cumbersome and uncomfortable recording techniques.

A parametric characterization of short length entropy measures is performed and two unsupervised optimization techniques for the analysis of short record length by means of QSE and CosEn is proposed.

This thesis shows a similar behavior of the considered complexity measures against a similar scenario while preserving the segmentation capabilities between classes with independence to the biological recording on analysis, as long as their application is done in the correct manner.

SampEn has proven to be the most stable measure and with wider applicability in medium length records ($300 < N < 5000$) against both, random and uniform, sample loss. Cross correlation coefficient for SampEn relay over 0.8 up tu a 70 % sample loss. Wether biological records show high variability MSE is recommended as the coarse grained series introduce signal soften and template decorrelation.

In short length signals ($100 < N < 300$) DFA is recommended. DFA allows complexity characterization in a robust and reliable way. It has a high computational cost and a visual inspection for scaling region delimitiation should be performed.

Finally in very short length records ($N < 100$) Cosen is recommended. Human hipertensive records with less than 55 samples have been segmented with good statistical validity and better results than QSE.