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Measuring Body Temperature Time Series Regularity Using Approximate Entropy and Sample Entropy

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Abstract— **Approximate Entropy (ApEn) and Sample Entropy (SampEn) have proven to be a valuable analyzing tool for a number of physiological signals. However, the characterization of these metrics is still lacking. We applied ApEn and SampEn to body temperature time series recorded from patients in critical state. This study was aimed at finding the optimal analytical configuration to best distinguish between survivor and non-survivor records, and at gaining additional insight into the characterization of such tools. A statistical analysis of the results was conducted to support the parameter and metric selection criteria for this type of physiological signal.**

I. INTRODUCTION

Approximate Entropy (ApEn) and Sample Entropy (SampEn) are time series regularity measures that have been used in many biomedical fields such as neonatology [1], neurology [2], genetics [3], geriatrics [4], cardiology [5] and endocrinology [6], to name just a few.

ApEn was introduced by Pincus [7] to overcome the entropy computation problems posed by the finite length of real time series or the hypotheses about the generating system. More recently, Richman and Moorman [8] developed an improved regularity metric, SampEn, in order to reduce the inconsistencies and bias of ApEn.

Both ApEn and SampEn require the specification of two parameters, the threshold tolerance r, and the embedding dimension m. Previous experimental studies recommend to select $m = 2$ and r in the range 0.1 to 0.25 times the standard deviation of the time series [8]. However, the regularity measurement may depend on the selection of the parameters in such a way that different results can be obtained for time series of the same regularity, or the same results can be obtained for time series of different regularity.

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In the last few years, it has become increasingly evident that characterization and interpretation of time series regularity measures ([9]–[11]) is of paramount importance to assure results consistency, specially in the context of biomedical signal processing. As a consequence, some guidelines have been published regarding the selection of parameter r [12], [13], the effect of data length [14], [15], the influence of signal characteristics [16], or the influence of a number of parameters [17].

In this regard, the aim of our study was also to characterize ApEn and SampEn. In contrast to previous works, we applied them to a new type of physiological signal in terms of entropy analysis, body temperature records.

Measurement of body temperature along with other vital signals is common practice during hospitalization. Normal body temperature is considered to be 37 °C, although a wide variation may be seen.

For clinical purposes, body temperature has been traditionally used as a marker for fever. A patient is considered febrile if the oral temperature exceeds 37.5 °C. However, this classical use of discrete temperature readings does not exploit the additional clinical information embedded in temperature records, as shown in [18]. Besides, in some patients the clinical state might not be recognized because their temperature does not raise above the set point.

Several recent clinical studies emphasized the importance of continuous body temperature monitoring for other applications, such as stroke prognosis [19], patient survival in critical care units [18] and neurologic outcome after cardiac arrest [20].

We used records from patients at an intensive care unit, whose body temperature was recorded at one sample every 10 minutes during several days. The records were separated in two classes: those belonging to patients that survived and those belonging to those that did not. ApEn and SampEn were computed for each record, for a set of r and m values, and an analysis of variance was carried out to delineate the best parameter and metric setting.

II. METHODS

In this section we will describe the algorithms to compute both ApEn and SampEn. Given a discrete time input data series $x[n]$ of length N (featuring a temperature record), and setting the value for parameters m, and r, the computation is as follows:

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A. ApEn

Draw a data series pattern of length m:

$$x_m(i) = \{x[i], x[i+1], \ldots, x[i+m-1]\},$$

namely, m refers to the number of consecutive temperature measures assumed to form a possible repetitive pattern within $x[n]$, and starting at sample $x[i]$.

The distance between two generic patterns $x_m(i)$ and $x_m(j)$ is given by:

$$d\left(x_m\left(i\right), x_m(j)\right) = \max\left(\left|x\left[i+k\right] - x\left[j+k\right]\right|\right), 1 \leq k \leq m \quad (1)$$

The distance threshold r determines if $x_m(i)$ and $x_m(j)$ can be considered similar when $d\left(x_m\left(i\right), x_m(j)\right) \leq r$. Given the set of all possible patterns of length $m, (x_m(1), x_m(2), \ldots, x_m(N-m+1))$, it is defined:

$$C_{r,m}(i) = \frac{k_{i,m}(r)}{N-m+1} \quad (2)$$

where $k_{r,m}(i)$ is the number of patterns $x_m(j)$ that are similar to $x_m(i)$ according to the distance threshold r. Hence, $C_{r,m}(i)$ is the fraction of patterns of length m starting at $j, 1 \leq j \leq N-m+1$ whose distance to pattern starting at i, is below the threshold r, that is, they are considered to be similar to pattern $x_m(i)$. This fraction is computed for each pattern, and then another quantity can be defined as:

$$\phi^m(r) = \frac{1}{N-m+1} \sum_{i=1}^{N-m+1} \log C_{r,m}(i).$$

The computation of the ApEn of a temperature epoch $x[n]$, $\text{ApEn}(m, r)$ is then given by:

$$\text{ApEn}(m, r) = \left[\phi^m(r) - \phi^{m+1}(r)\right] \quad (3)$$

B. SampEn

1) Take m vectors $X_m(1), X_m(2), \ldots, X_m(N-m+1)$, defined as $X_m(i) = [x[i], x[i+1], \ldots, x[i+m-1]]$, for $1 \leq i \leq N-m+1$. These vectors are m consecutive values of x, commencing at the ith sample.
2) The distance between vectors $X_m(i)$ and $X_m(j)$, $d[X_m(i), X_m(j)]$ is defined as:

$$d[X_m(i), X_m(j)] = \max(|x[i+k] - x[j+k]|) \quad (4)$$

For a given $X_m(i)$, count the number of $j (1 \leq j \leq N-m, j \neq i)$, such that $d[X_m(i), X_m(j)] \leq r$. This number is denoted as B_i. For $1 \leq i \leq N-m$, two new values are defined and computed, $B_i^m = \frac{1}{N-m-1} B_i$ and $B^m(r) = \frac{1}{N-m} \sum_{i=1}^{N-m} B_i^m(r)$.

3) Length is increased to $m = m+1$, and previous steps are repeated to obtain the counterpart of B with this new value of m, $A_i^m = \frac{1}{N-m-1} A_i$ and $A^m(r) = \frac{1}{N-m} \sum_{i=1}^{N-m} A_i^m(r)$, where B^m is the probability that two sequences coincide for m points, and A^m is the probability that coincide for $m+1$ points.

TABLE I
ANOVA TABLE FOR APEN

Source	SS	DF	MS	F	p
Class	0,382303	1	0,382303	25,41	0,0000
m	1,6831	3	0,561032	37,29	0,0000
r	37,245	8	4,65562	309,42	0,0000
Class–m	0,0119185	3	0,00397283	0,26	0,8513
Class–r	0,194853	8	0,0243566	1,62	0,1148
m–r	4,32099	24	0,180041	11,97	0,0000
Class–m–r	0,0417027	24	0,00173761	0,12	1,0000

TABLE II
ANOVA TABLE FOR SAMPEN

Source	SS	DF	MS	F	p
Class	0,0622215	1	0,0622215	11,93	0,0006
m	0,630268	3	0,210089	40,27	0,0000
r	28,057	8	3,50712	672,17	0,0000
Class–m	0,0110376	3	0,0036792	0,71	0,5490
Class–r	0,0563192	8	0,00703989	1,35	0,2148
m–r	0,781474	24	0,0325614	6,24	0,0000
Class–m–r	0,0172494	24	0,000718724	0,14	1,0000

4) Finally, compute SamEn as $\text{SampEn}(m, r) = \lim\{-\log[\frac{A^m(r)}{B^m(r)}]\}$. Since the time series length is finite, SampEn is estimated as $\text{SampEn}(m, r, N) = -\log[\frac{A^m}{B^m}]$.

III. EXPERIMENTS AND RESULTS

A. Body temperature records

Body temperature series were recorded for 40 subjects with multiple organ failure admitted to the Intensive Care Unit (ICU) of Mostoles Hospital, Madrid(Spain) using a portable temperature data logger. An example of such registers is shown in Fig. 1. The subjects were assigned to one of two classes: survivors S and non-survivors NS. All patients defined as"non-survivors" died in the ICU, before discharge.

Temperature was measured all along the admission, until the patient was discharged or considered dead and all monitoring devices were retired. Nevertheless, to avoid the influence of pre-mortem or peri-mortem conditions, the last hour was not included in the analysis. The patients were monitored for a median of 210 hours. Prior to analysis, artifacts were removed from the temperature records. Artifacts can be due to sensor disconnection or border effects. Further details about these records can be found in [18].

B. Results

The regularity of the final discrete time signals obtained from the preprocessing of the body temperature records was estimated using ApEn and SampEn for both classes.

To investigate the association of average ApEn/SampEn with patient class and parameters m and r (including interactions), an analysis of variance (ANOVA) was applied to the means with $m = \{1, 2, 3, 4\}$ and r ranging from 0.1 to 0.9 in 0.1 steps. The results are presented in Tables I and II.

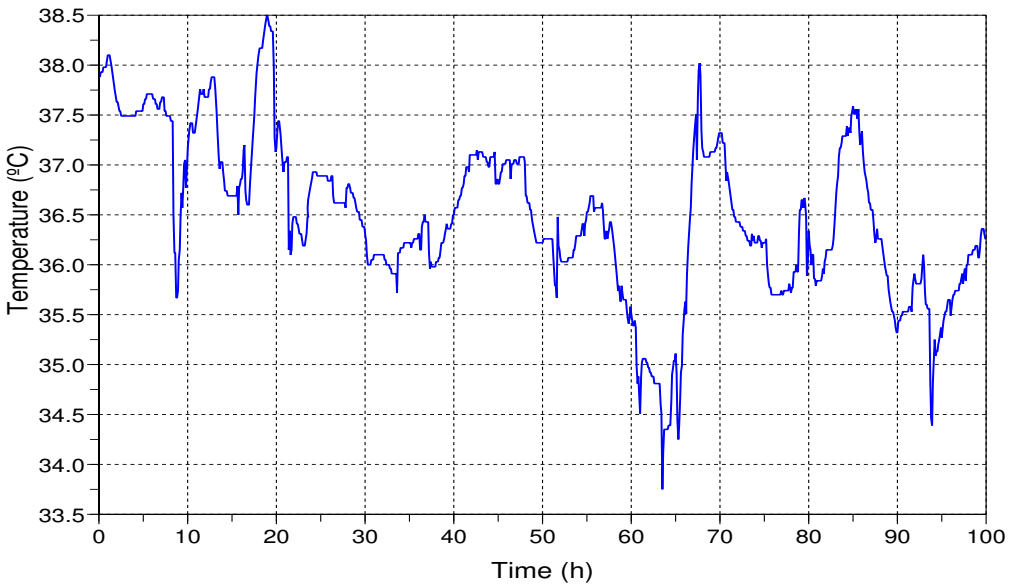

Fig. 1. Example of a body temperature record.

We also studied the interactions of m and r. Fig.2 and Fig.3 depict such interactions for ApEn, and Fig.4 and Fig.5 for SampEn.

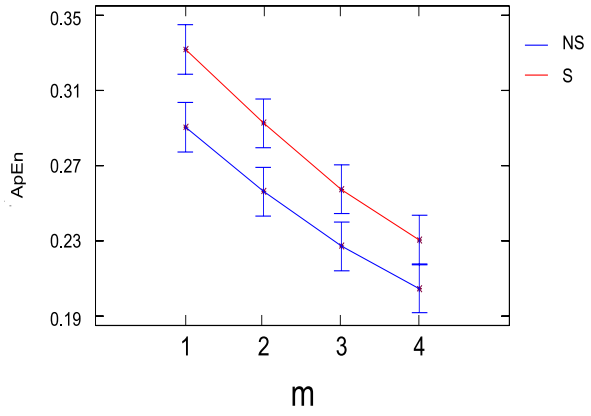

Fig. 2. Influence of m on the separability between the two classes using ApEn. There is only overlapping for $m = 4$, and the maximum separability is achieved with $m = 1$.

IV. DISCUSSION

The results indicated that both ApEn and SampEn can distinguish between the two classes ($p_{ApEn} = 0.0000, p_{SampEn} = 0.0006$), with ApEn providing a slightly higher separability ($F_{ApEn} = 25.41, F_{SampEn} = 11.93$). The interaction between classes and parameters r and m are not significant, whereas there is a significant interaction between r and m, in both cases.

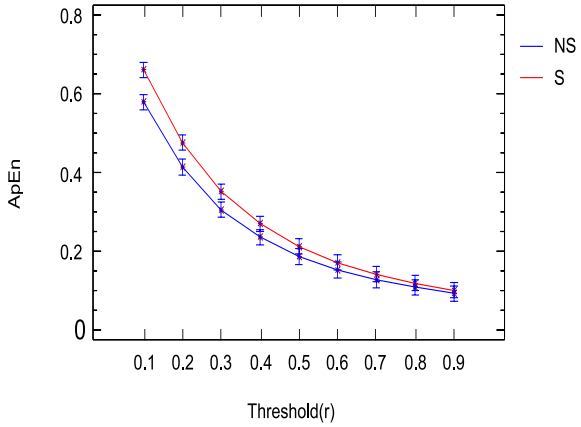

Fig. 3. Influence of r on the separability between the two classes using ApEn. To avoid overlapping, r should fall in the interval between 0.1 and 0.2.

There is no overlapping for ApEn when m ranges from 1 to 3, and r is 0.1 or 0.2. Regarding SampEn, there is overlapping for m greater than 1, and for all r values. Additionaly, there is a trend inversion at r between 0.1 and 0.2 for SampEn.

V. CONCLUSION

In contrast to other previous similar studies, ApEn appears to provide better results than SampEn in this specific case. For all the r and m values tested, ApEn exhibits higher separability, with no parameter interaction. Conversely, the

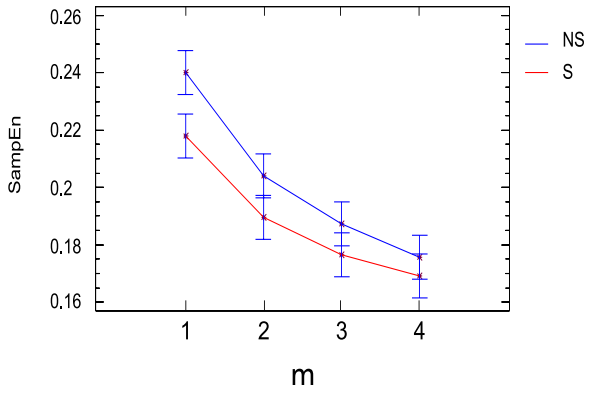

Fig. 4. Influence of m on the separability between the two classes using SampEn. There is only overlapping for all m values except $m = 1$.

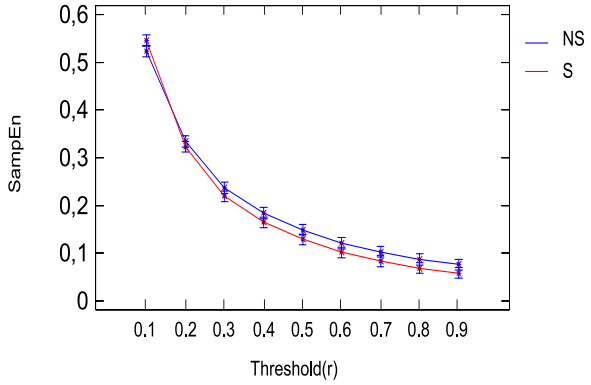

Fig. 5. Influence of r on the separability between the two classes using SampEn. To minimize overlapping, r should be 0.5. Additionally, there is interaction for r smaller than 0.2, and therefore these range should be avoided.

separability provided by SampEn is lower, and there is interaction for parameter r, yielding opposed results if r is below or above 0.2. Therefore, we recommend to use ApEn for body temperature records, with the parameters $m = 1$ and $r = 0.1$.

This study does not question the superior performance of SampEn over ApEn previously reported in a number of publications in terms of bias, consistency, and parameter dependence. However, our results indicate that ApEn can not be discarded as a regularity metric since in a few cases it might outperform SampEn.

VI. ACKNOWLEDGMENTS

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