Abstract—Recurrence plot analysis is a useful non-linear analysis tool. There are still no well formalised procedures for carrying out this analysis on measured physiological data, and systematising analysis is often difficult. In this paper, the recurrence based embedding is compared to radius based embedding by studying a logistic attractor and measured breathing data collected from sleeping human infants. Recurrence based embedding appears to be a more robust method of carrying out a recurrence analysis when attractor size is likely to be different between datasets. In the infant breathing data, the radius measure calculated at a fixed recurrence, scaled by average respiratory period, allows the accurate discrimination of active sleep from quiet sleep states (AUC = 0.975, Sn = 0.98, Sp = 0.94).

I. INTRODUCTION

Recently it has become apparent that physiological rhythms are governed by non-linear dynamics, and that much of the apparently random fluctuations may actually be chaos rather than noise. Consequently, there have been a number of efforts to investigate the behaviour of physiological systems using non-linear analysis tools. One non-linear tool which is claimed to be particularly suitable for analysing physiological data due to its relative tolerance to short and non-stationary data-sets, is recurrence plot analysis.

Analysis of physiological data using recurrence plots was pioneered by Webber and Zbilut with the recurrence quantification analysis (RQA) framework [1]. The recurrence plot is a qualitative tool for visualising non-linear dynamics in time series data, while RQA was used to quantify structure in the recurrence plots, which in turn quantifies non-linear aspects of the original time series data. There are a number of different RQA measures which quantify different aspects of the system, including phase space structure, complexity, and predictability (sensitivity to initial conditions). Recurrence plot analysis does have disadvantages— in particular it requires a number of set-up parameters, which are specific to application and even individual data-sets. The mathematical interpretations of results for a specific application and embedding conditions are still unclear, despite recent work developing parameters which are embedding condition independent [2]. For an experimentally sound biological investigation it is necessary to apply the same embedding conditions, or method of selecting of embedding parameters, to each data-set analysed. In this paper, the method of appropriately choosing how close phase space points must be to be regarded as recurrent is examined. Two approaches are considered—Applying a common radius to all data sets (herein known as radius based embedding), and applying a common recurrence to all datasets (recurrence based embedding).

The aim of this technical work was to develop robust non-linear analysis tools for investigation of infant respiratory inter-breath interval patterns with the purpose of identifying measures to discriminate active from quiet sleep states. This hypothesis was derived from previous work demonstrating breathing patterns are non-linear [3, 4], and that the non-linear patterns change with sleep state [5]. This could provide the basis of an automated sleep scoring tool. It is proposed that recurrence based embedding is more robust for infant respiratory data, and its advantages are demonstrated on a logistic attractor, and real data collected from 32 healthy sleeping infants.

II. METHOD

A. Experiment 1: Investigating Radius and Recurrence Based Embedding Using the Logistic Attractor

It is possible for an attractor to be scaled in phase space, i.e: expanded or shrunk. The arrangement of the points is still the same, as is the order which the points are visited. It is reasonable to conclude that the non-linear dynamics remain the same, but simply on a different scale. Thus while measures of structure should change, measures of predictability should remain the same.

Let us create a discrete system using the logistic attractor:

\[ x_{n+1} = r \times x_n \times (1 - x_n) \]  

(1)

To generate the time series TS and distance matrix DM:

\[ TS = \{x_1, x_2, \ldots, x_{n-1}, x_n\} \]  

(2)

\[ DM_{ij} = \sqrt{\sum_{n=1}^{n-1} (x_{in} - x_{jn})^2} \]  

(3)
A scaled version of the same system can be generated using:

\[ x_{n+1} = a \times r \times \left( \frac{x_n}{a} \right) \times \left( 1 - \left( \frac{x_n}{a} \right) \right) \]  
(4)

To generate the time series \( TS_{\text{scal}} \) and distance matrix \( DM_{\text{scal}} \):

\[ TS_{\text{scal}} = \{ a_1, a_2, \ldots, a_{n-1}, a_n \} = a \times TS \]  
(5)

\[ DM_{\text{scal}ij} = a \times DM_{ij} \]  
(6)

Using equation (4) with \( r=3.88 \) (chaotic region) and initial \( x_1 = a \times 0.5 \), three series were generated for \( a=1 \) (unscaled), \( a=0.5 \) and \( a=2 \). 1200 series points were generated, with the first 200 discarded as transients. Each time-series was embedded in phase space with a dimension of 1 (the system dimension). The recurrence plot analysis parameters were calculated using radius based embedding (for \( \text{REC}=0.002, 0.0075, 0.15, 0.0225, \) and 0.03) and then recurrence based embedding (for \( \text{REC}=1, 2, 3, 4 \) and 5%).

The parameters considered in this paper are as described by Webber [1] in his recurrence quantification analysis (RQA) platform:

- Radius (RAD): The radius threshold as defined above
- Recurrence (REC): The percentage of points in the RP which are recurrent points
- Line Max (LINEMAX): The length of the longest diagonal line
- Determinism (DET): The percentage of recurrent points which are arranged into diagonal lines of length 2 or greater.

The average diagonal line length, as described by Marwan [6] has also been calculated:

- Line Average (LINEAVE): The average length of the line that recurrent points fall upon.

The RAD REC relationship quantifies structure, while LINEAVE, LINEMAX and DET quantify predictability. In addition, the average IBI (IBIAVE) was also calculated. All recurrence plot analysis in this paper was carried out using programs written by the first author for Matlab environment (© The MathWorks Inc.), but based upon the definitions above.

B. Experiment 2: Investigating radius and recurrence based embedding on infant respiratory data

Overnight sleep-lab polysomnograms ( PSG’s) were obtained from 32 healthy infants aged between 19-153 days (16 Male, 16 Female). A PSG is a clinical tool which monitors many physiological channels of data, normally during an overnight stay in hospital. These channels typically include electroencephalogram (EEG), electrocardiogram (ECG), electromyogram (EMG), and respiratory inductive plethysmography (RIP). This data was "sleep scored" by a respiratory physician using a defined criteria [7]. This is the process of identifying periods, or epochs (normally 30secs), as being active sleep (AS), quiet sleep (QS) or awake (AW). In this section, for illustrative purposes, data from one infant was examined. Typical respiratory data from a period of AS, and a period of QS was extracted. The respiratory data was then converted to inter-breath intervals (IBI’s), and the middle 400 IBI’s extracted. A radius vs. recurrence plot was generated for each of these epochs, and we carried out a recurrence plot analysis, for embedding dimension=8 (selected using the false nearest neighbours technique), using both recurrence, and radius based embedding.

C. Experiment 3: Non-linear respiratory dynamics during different sleep states

From each of the 32 sleep scored healthy infant PSG’s, the 6 longest epochs each of active sleep (AS) and quiet sleep (QS) respiratory inductive plethysmography (RIP) data was extracted for each infant. For each of these epochs RAD, DET, LINEAVE, and LINEMAX was calculated at a REC=2%.

III. RESULTS

A. Experiment 1

Table’s I and II below, respectively, show the RQA results for radius based embedding and recurrence based embedding of the logistic attractor. Results are shown for \( a=0.5, a=1 \) and \( a=2 \). Fig. 1 illustrates how the RAD vs. REC relationship changes as ‘a’ is scaled.

![Fig. 1: RAD vs REC plot for logistic attractor at a=0.5, a=1 and a=2, illustrating the difference in attractor size.](image)

**TABLE I**

<table>
<thead>
<tr>
<th>REC (%)</th>
<th>DET (%)</th>
<th>LINEMAX</th>
<th>LINEAVE</th>
</tr>
</thead>
<tbody>
<tr>
<td>0.002</td>
<td>1.7</td>
<td>0.9</td>
<td>0.5</td>
</tr>
<tr>
<td>0.0008</td>
<td>5.2</td>
<td>3.0</td>
<td>1.6</td>
</tr>
<tr>
<td>0.0125</td>
<td>8.9</td>
<td>5.2</td>
<td>3.0</td>
</tr>
<tr>
<td>0.023</td>
<td>12.4</td>
<td>7.1</td>
<td>4.2</td>
</tr>
</tbody>
</table>

**TABLE II**

<table>
<thead>
<tr>
<th>REC (%)</th>
<th>RAD</th>
<th>DET</th>
<th>LINEAVE</th>
</tr>
</thead>
<tbody>
<tr>
<td>0.0011</td>
<td>1.0</td>
<td>1.0</td>
<td>1.0</td>
</tr>
<tr>
<td>0.0024</td>
<td>1.0</td>
<td>1.0</td>
<td>1.0</td>
</tr>
<tr>
<td>0.0053</td>
<td>1.0</td>
<td>1.0</td>
<td>1.0</td>
</tr>
<tr>
<td>0.0072</td>
<td>1.0</td>
<td>1.0</td>
<td>1.0</td>
</tr>
</tbody>
</table>
B. Experiment 2

Fig. 2 below shows the RAD vs. REC plot for the extracted epochs of AS and QS IBI data, which illustrates the difference in relative attractor sizes between AS and QS. Table III and Table IV summarises the RQA results for the AS and QS epochs using radius and recurrence based embedding respectively.

![REC vs. RAD plot of IBI data for an AS and QS epoch](image)

**Fig. 2: REC vs. RAD plot of IBI data for an AS and QS epoch**

<table>
<thead>
<tr>
<th>RAD (SD)</th>
<th>DET (%)</th>
<th>LINEAVE</th>
<th>LINEAV</th>
<th>INEMAX</th>
<th>IBI (SD)</th>
</tr>
</thead>
<tbody>
<tr>
<td>AS Mean</td>
<td>0.77</td>
<td>83.0</td>
<td>15.7</td>
<td>4.48</td>
<td>1.88</td>
</tr>
<tr>
<td>(SD)</td>
<td>(0.29)</td>
<td>(3.6)</td>
<td>(4.8)</td>
<td>(0.95)</td>
<td>(0.43)</td>
</tr>
<tr>
<td>QS Mean</td>
<td>0.33</td>
<td>81.0</td>
<td>14.5</td>
<td>4.03</td>
<td>1.97</td>
</tr>
<tr>
<td>(SD)</td>
<td>(0.11)</td>
<td>(3.4)</td>
<td>(4.0)</td>
<td>(0.77)</td>
<td>(0.47)</td>
</tr>
</tbody>
</table>

**Table III**

<table>
<thead>
<tr>
<th>RAD DET (%)</th>
<th>LINEAV</th>
<th>LINEAV</th>
</tr>
</thead>
<tbody>
<tr>
<td>0.2</td>
<td>0.01</td>
<td>100</td>
</tr>
<tr>
<td>0.3</td>
<td>0.01</td>
<td>85.7</td>
</tr>
<tr>
<td>0.4</td>
<td>0.04</td>
<td>55.6</td>
</tr>
<tr>
<td>0.5</td>
<td>0.17</td>
<td>67.7</td>
</tr>
<tr>
<td>0.6</td>
<td>0.46</td>
<td>72.8</td>
</tr>
<tr>
<td>0.7</td>
<td>1.06</td>
<td>79.9</td>
</tr>
<tr>
<td>0.8</td>
<td>2.11</td>
<td>82.2</td>
</tr>
</tbody>
</table>

**Table IV**

C. Experiment 3

Table V below summarises the results of experiment 3, with the average and standard deviations of RQA parameters across all AS and QS epochs calculated. The Student’s t test was used to determine whether differences in values between AS and QS were statistically significant. There was a statistically significant difference in all parameters between AS and QS, with p<0.05.

**IV. Discussion**

In experiment 1, three chaotic attractors were engineered. The three attractors were identical except for their scaling, i.e: the structure in phase space has been scaled, but the dynamics of the systems remain the same. Thus it is expected that recurrence plot structure measurements will have changed, but predictability measures should remain the same. In the results for radius based embedding (table I), it can be seen than the REC measure changes with attractor scaling, reflecting the real system change. However predictability measures (DET, LINEAVE, LINEMAX) also vary. This is illustrated in Fig. 3. When recurrence based embedding is used, RAD changes with a (and in fact scales by a) reflecting the change in attractor size. Predictability measures remain the same, accurately reflecting that system chaos has not changed. In the mathematically engineered system, recurrence based embedding appears more robust where system scaling may be different across datasets; in particular, it appears to measure predictability independent of the structure scale.

**Table V**

In experiment 2, infant IBI data during AS and QS was considered. The relative attractor sizes of AS and QS data are illustrated in the REC vs. RAD plot in fig. 2, where it is seen that AS RAD is higher than QS RAD at all values of REC, indicating AS attractor size is larger. In choosing an embedding threshold for a recurrence plot analysis it is considered. The relative attractor sizes of AS and QS data are illustrated in the REC vs. RAD plot in fig. 2, where it is seen that AS RAD is higher than QS RAD at all values of REC, indicating AS attractor size is larger. In choosing an embedding threshold for a recurrence plot analysis it is suggested that RAD be selected such that the recurrence plot is not too sparse, nor should it be saturated [8]. This “accepted” range of corresponding REC is 0.1% to 5%. Inspecting fig. 2, there is no common RAD which would satisfy this for requirement for both AS and QS. In table III, QS is in this range for RAD=0.2 and 0.3, however AS is too...
sparse. AS is in this range at RAD=0.7 and 0.8, whereas QS is saturated.

**Fig. 4: Plot of RAD vs. LINEMAX for a AS and QS epoch. Illustrates how QS LINEMAX increases with the saturation of the RP, while AS RP is still too sparse.**

For a given RAD, LINEMAX values are an order of magnitude higher for QS, and simply not comparable, as illustrated in Fig. 4. In Fig. 5, it can be seen that even attempting a compromise in optimum RAD for AS and QS (RAD=0.55), yields RP’s which are obviously too sparse in AS, and saturated in QS.

**Fig. 5: Recurrence plots for AS and QS at RAD=0.55.**

In light of experiment 1 results, recurrence based embedding appears ideal for this situation. In table IV, RAD values for given REC are higher in AS reflecting the larger attractor size, while LINEAVE and LINEMAX are in the same order of magnitude, presumably indicating predictability results are more comparable. In Fig. 6 AS and QS RP’s are given for a common REC=2%. By definition, RP’s are equally filled. The arrangement of recurrent points is different, and this presumably represents the difference in AS and QS breathing dynamics.

**Fig. 6: Recurrence plots for AS and QS at REC=2%.**

One of the aims of this study was to identify non-linear methods of discriminating between AS and QS. By inspecting the frequency histograms of AS and QS for the RAD, LINEAVE, LINEMAX, DET and IBIAVE measures it was observed that RAD was the best discriminator. It was also observed that high values of RAD were associated with high IBIAVE values. To investigate further, RAD was plotted against IBIAVE for each epoch of AS and QS (Fig. 7). It can be observed that there is an apparently linear scaling relationship between IBIAVE and RAD, possibly due to attractor scaling with changing respiratory rate. Quite strikingly, AS and QS epochs cluster separately on this linear structure, indicating that a linear line, with threshold gradient of RAD/IBIAVE is an accurate discriminator of AS from QS.

**Fig. 7: Plot of IBIAVE vs. RAD for AS and QS**

To test the effectiveness of this discriminator, the RAD/IBIAVE measure was calculated for each epoch of IBI data. In Fig. 8 (b) the frequency histogram of RAD/IBIAVE is plotted, illustrating graphically the discrimination ability. To quantify discrimination ability, a receiver operator characteristic (ROC) curve was constructed (Fig. 8 (a)). The ROC curve yielded an area under curve of 0.98. At a RAD/IBIAVE threshold of 0.24, active sleep was able to be identified with Sn=0.98 and Sp=0.94.
There are two main aims a non-linear investigation of a physiological system may wish to achieve. Firstly, it may aim to develop discrimination tools which may be used to distinguish between states of health, disease and developmental stages, as has been demonstrated with the AS QS discrimination. The second aim is to use non-linear investigations to better understand the function of underlying systems. In the first case, we are looking for distinguishing characteristics, and are not concerned with the interpretation of what that discrimination means. Here embedding is somewhat arbitrary and the investigator would be looking to modify embedding conditions to best discriminate. In the second case however, it is likely that conclusions about function/operation of the studied system are being made on the basis of results. For example that pathology is associated with decreased chaos [11],[12]. It is necessary in this case, that results are accurately interpreted in terms of embedding conditions, and that measures of predictability are independent of the scale of the system structure.

Respiratory patterns are dynamic, both in a short time-scale, as the body responds to the environment and changing physiological state (such as sleep states) [9], and in the longer timescale with age related development [10]. In a wider clinical study of respiratory patterns, it is necessary to be able to determine whether breathing patterns have changed in structure (i.e: the attractor has simply scaled with a changing respiratory rate), or whether there is also a change in dynamic behaviour. Based upon the results presented in this paper, recurrence based embedding appears to more robustly allow the independent, accurate measurement of structure and predictability when compared to radius based embedding.

V. CONCLUSION

In a clinical investigation of non-linear infant respiratory IBI patterns, it is likely that a range of different phase space attractor sizes will be encountered and thus recurrence based embedding is the most appropriate method of threshold selection. Our analysis of clinical results indicates non-linear behaviour is different between IBI patterns during infant active and quiet sleep. The measure RAD/IBI, provides a method of accurately discriminating active from quiet sleep based on only respiratory data, and could potentially provide the mathematical basis of an automated sleep scoring tool. With increased understanding of the correct interpretation of recurrence plot analysis results for given embedding conditions, recurrence plot analysis may also further the understanding of the respiratory control system, and how it changes and develops through different physiological states, with disease and with increasing age.

ACKNOWLEDGMENT

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REFERENCES