

Comparison of Attractor Reconstruction and HRV Methods for Analysing Blood Pressure Data

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Abstract

Many methods have been proposed for analysing high frequency blood pressure or ECG data. We review a recently proposed new approach for analysing such data based on attractor reconstruction and compare it to heart rate variability that analyses the beat-to-beat intervals. Our new approach uses all the available data and so can detect changes in the shape of the waveform.

1. Introduction

Blood pressure and ECG data can be collected at high sampling frequency over long periods of time and many methods have been proposed for analysing this data in order to diagnose a variety of diseases [1]. Early detection of changes in the data that indicate onset of disease will offer the opportunity for early clinical intervention that is generally much more effective than a late intervention. The key challenge is obtaining a reliable indicator of significant changes in complex data.

We have recently proposed a new method for analysing blood pressure data based on attractor reconstruction. We briefly review this method and then compare it to some methods that come under the banner of heart rate variability (HRV) which analyse beat-to-beat intervals derived from the data.

2. Review of Attractor Reconstruction Method

We have recently proposed a new method of analysing high frequency blood pressure data in order to extract diagnostic information from the data. This method, which is described in [2], consists of four steps.

1. Reconstruct the attractor

We first reconstruct an attractor in a three-dimensional phase space using Takens' delay coordinate method [3].

Thus, if the signal is $x(t)$, we define the two new variables

$$y(t) = x(t - \tau), \quad z(t) = x(t - 2\tau)$$

where $\tau > 0$ is the time delay. The trajectory can then be plotted in the three-dimensional (x, y, z) phase space. A sample of 10 seconds of blood pressure data collected from a healthy conscious mouse using an implanted radiotelemetry device at 1000Hz is shown in Fig. 1. The attractor in the three-dimensional phase space for this data is shown in Fig. 2.

2. Remove baseline variation

One of the problems with analysing blood pressure data is that the average blood pressure (baseline) varies naturally depending on whether the animal is resting, active, sleeping, etc., which results in a non-stationary signal. Many methods have been proposed for eliminating this baseline wander, see for example the review [4]. In [2], we proposed a different method for eliminating this variation from our reconstructed attractor. All of our phase space variables are derived from the single signal $x(t)$ and so if we shift our signal by a constant amount $x(t) \rightarrow x(t) + c$, then we also have a similar shift in the variables y and z . In the phase space, this shift in the signal implies that $(x(t), y(t), z(t)) \rightarrow (x(t) + c, y(t) + c, z(t) + c) = (x(t), y(t), z(t)) + c(1, 1, 1)$. Thus, a constant shift in the signal results in a shift in the phase space in the direction of the vector $(1, 1, 1)$. To eliminate this effect, we project our three-dimensional attractor onto a plane perpendicular to this vector. We do this by defining the new variables

$$u = \frac{1}{3}(x+y+z), \quad v = \frac{1}{\sqrt{6}}(x+y-2z), \quad w = \frac{1}{\sqrt{2}}(x-y)$$

It can be seen from the definition of these variables that a constant shift in the signal implies that $u(t) \rightarrow u(t) + c$ but that there is no change in the variables v and w . The (v, w) plane is orthogonal to the vector $(1, 1, 1)$ and projection of the attractor onto this plane provides a simple method for eliminating baseline variation in the signal. The projection of the attractor in the three-dimensional phase space

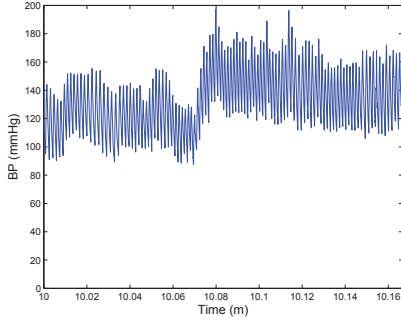


Figure 1. Plot of 10 seconds of blood pressure data.

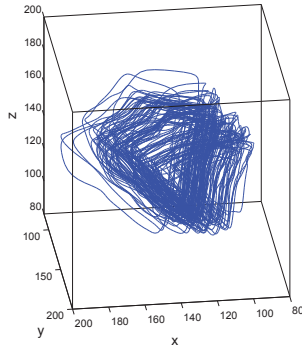


Figure 2. Plot of the data in the three-dimensional reconstructed phase space using $\tau = 31$ ms.

in Fig. 2 onto the (v, w) plane is shown in Fig. 3. We note that the attractor in Fig. 2 is quite messy and has a lot of movement in the direction of the $x = y = z$ axis, which is due to the large amount of baseline variation in the data. However, once this has been eliminated, we obtain a much more uniform attractor in the (v, w) plane.

3. Construct a density

The next step in our approach is to construct a density on a uniform grid in the (v, w) plane, since this will be a more useful representation of the attractor than a blur of lines in the phase space. The density function derived from the projected attractor in Fig. 3 is shown in Fig. 4.

We have not yet considered how to choose the time delay τ . Many methods have been proposed for the optimal choice of τ , with minimisation of mutual information being a popular method [5]. Again, we take a different approach. We note that the blood pressure data is approximately (but certainly not exactly) periodic. We have proved in [2] that if $x(t)$ is periodic with period T then the trajectory in the (v, w) plane has a threefold rotational symmetry about the origin if $\tau = T/3$ or $\tau = 2T/3$. Thus, for our non-periodic data, we choose τ to make the attractor in the (v, w) plane “as symmetric as possible”. To be more precise, if the density function is given by $D(\tau)$, then

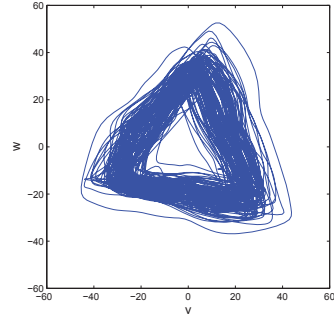


Figure 3. Plot of the attractor shown in Fig. 2 projected onto the (v, w) plane using $\tau = 31$ ms.

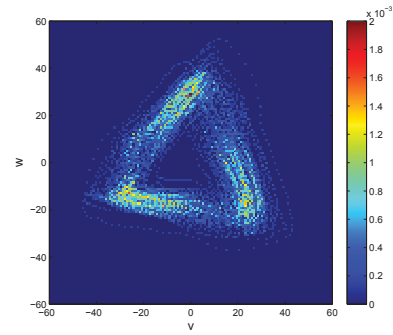


Figure 4. The density generated from the attractor shown in Fig. 3.

we define $D_1(\tau) = D(\tau)$ and generate two more density functions $D_2(\tau)$ and $D_3(\tau)$ from the attractor in the (v, w) plane rotated by $2\pi/3$ and $4\pi/3$ respectively. We then define

$$D_s(\tau) = \frac{1}{3}(D_1(\tau) + D_2(\tau) + D_3(\tau))$$

We note that $D_s(\tau)$ has threefold rotational symmetry by construction. Moreover, if the original density $D(\tau)$ also has threefold symmetry, then $D_s(\tau) = D(\tau)$. We choose τ by minimising the “distance” between $D_s(\tau)$ and $D(\tau)$ which we define by

$$S(D(\tau)) = \|D(\tau) - D_s(\tau)\|_2$$

A plot of the symmetry measure $S(D(\tau))$ for the attractor shown in Fig. 3 is given in Fig. 5. From this, it can be seen that there are two local minima which occur at $\tau = 31$ ms and $\tau = 62$ ms and these correspond to approximately one third and two thirds of the average period of the data respectively. Thus, we clearly have an average period of 93ms. We define τ_{opt} to be the value of τ at the first minimum of $S(D(\tau))$. Note that we have used $\tau = \tau_{\text{opt}}$ for the plots in Figs 2,3,4. This approach results in τ_{opt} being approximately one third of the average period of the data, and so we can determine the average period as $3\tau_{\text{opt}}$.

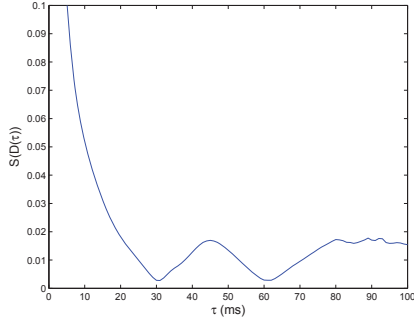


Figure 5. Plot of the symmetry measure $S(D(\tau))$.

4. Generate time traces

The final step of our approach consists of performing the analysis described above on a time window which is then moved through the data. The average period ($3\tau_{\text{opt}}$) and the minimum value of the symmetry measure ($S(D(\tau_{\text{opt}}))$) for each window can then be plotted as a time trace, as shown in Fig. 6, where we have used a window length of 10s. Many other measures can be derived from the density for each window, each of which generate their own time trace, as described in [2].

3. Heart Rate Variability

A common method for analysing blood pressure and ECG data is to consider heart rate variability (HRV) in which variation in the length of the beat-to-beat (or RR) intervals is analysed. The effect of many physiological conditions can be detected using HRV, such as myocardial infarction, cardiac arrhythmia and renal failure [1]. We note that by considering only these intervals, any variation in the baseline is effectively ignored. However, any variation in the cycle between the peaks, which relates to both cardiac and vascular changes, is also ignored.

In order to compare HRV methods with our approach, we have again used a time window and calculated the length of the beat-to-beat intervals in that window. The average interval length was found and the window again moved through the data to give a time trace. For the data shown in Fig. 1, the average interval length is 91.08ms, which is very close to the value of 93ms obtained using our method. Indeed, it can be seen in Fig. 6 that this average interval length gives very good agreement with the average period obtained using our approach described above as the time window moves through 10 minutes of data.

There are many measures that can be computed from the beat-to-beat intervals [1]. We have chosen to consider the Poincaré plot in which the points (RR_n, RR_{n+1}) are plotted. The perpendicular distances of the points from the lines $y = x$ and $y = -x + 2R_m$, where R_m is the mean of the RR intervals, are determined and the standard de-

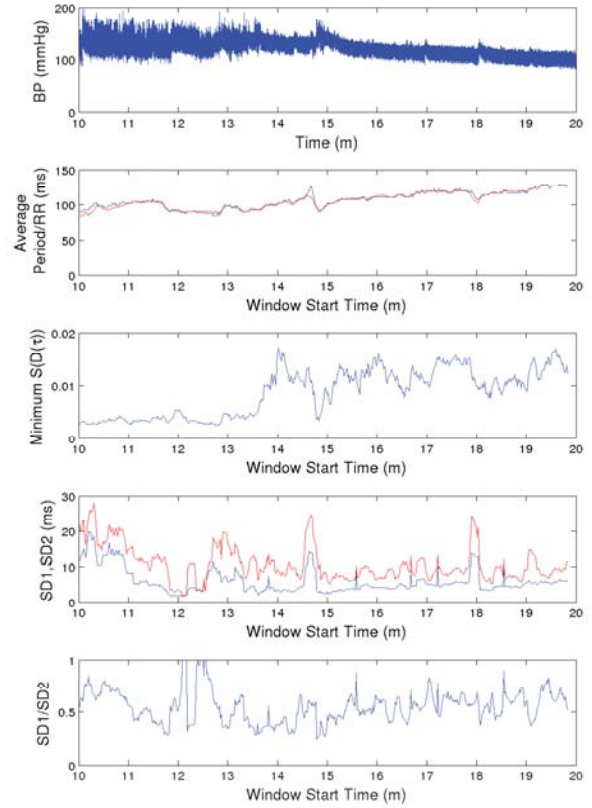


Figure 6. Time traces derived from a moving window of length 10s. Top: Blood pressure data; Second: Average period ($3\tau_{\text{opt}}$) (blue), average RR interval length (red); Third: First minimum of the symmetry measure $S(D(\tau_{\text{opt}}))$; Fourth: SD1 (blue), SD2 (red); Fifth: SD1/SD2 ratio.

viations of these distances SD1 and SD2 respectively can then be found. These are used as the semi-minor and semi-major axes of an ellipse centred on the point (R_m, R_m) and aligned with the line $y = x$. The quantities SD1, SD2 and the ratio SD1/SD2 are used diagnostically [1]. We have computed SD1 and SD2 for each window of data. The time trace of these measures together with the ratio SD1/SD2 is also shown in Fig. 6.

4. Comparison of the Two Approaches

High frequency blood pressure data generates large amounts of data and it is important to extract useful information from the data. This often involves reducing the large dataset to a much smaller one for analysis. All the HRV methods reduce the available data by considering only the length of the beat-to-beat intervals and then extracting a variety of measures from this reduced dataset which can be related to various diseases. The disadvantage

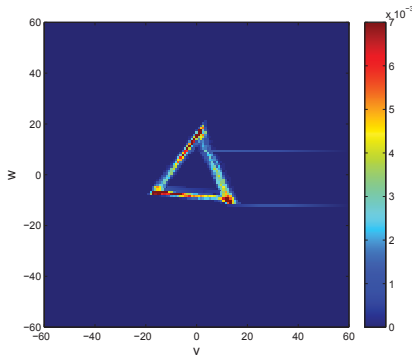


Figure 7. The density generated from the attractor at time $t = 20$ m.

of this approach is that all the data regarding the shape of the waveform is discarded, and it is reasonable to suppose that there is useful information contained in the waveform shape that could also be used diagnostically.

Our approach uses all of the available data and extracts various measures from a time window, which then generate time traces as the window is moved through the data. This method will be sensitive both to changes in the beat-to-beat intervals and to changes in the shape of the waveform and so may be able to detect significant changes in the data that HRV cannot.

For our example data shown in Fig. 6 (top), there is a clear transition in the symmetry measure $S(D(\tau_{\text{opt}}))$ between 13 and 14 minutes. This is due to a significant change in the structure of the attractor in the (v, w) plane. The attractor in Fig. 4 is typical when the symmetry measure is low, and this changes to an attractor similar to that shown in Fig. 7 when the symmetry measure is high. However, in the plots of average period/RR intervals, SD1 and SD2 and the SD1/SD2 ratio, there is no obvious transition at this point and so the transition that we observe in the symmetry measure must be due to a change in the shape of the waveform.

We note that there are sharp transitions in SD1 and SD2 at various points. However, these measures are generally quite noisy and do not clearly indicate a transition in the data. Using a longer time window would reduce the noise in these measures, but may also smooth out any transitions in the measures.

5. Conclusions

We have described our new approach using attractor reconstruction for analysing blood pressure data and have compared this with some HRV measures. Our approach uses all of the data but factors out the baseline variation by projecting the three-dimensional attractor onto a plane.

One of the strengths of this approach is its simplicity.

With HRV, it can be difficult to correctly identify the peaks in the data as there are sometimes smaller peaks that occur, particularly as the blood pressure decreases during diastole. Many of the algorithms for eliminating baseline wander are also quite complex [4].

Our method is also very robust. Occasional artifacts in the data will have little influence on the density from which measures are derived, and so do not have to be removed. In contrast, many HRV methods require careful removal of artifacts and ectopic beats from the data before analysis [1]. Also, by analysing all the available data, we are able to detect both cardiac and vascular changes.

While we have analysed blood pressure data, clearly this approach could also be used to analyse any approximately periodic signal such as ECG, PPG, respiratory waveform, etc.

In this work, we have concentrated on just two measures derived from our projected attractor, namely the average period and the minimum of the symmetry measure. Our average period shows excellent agreement with the average of the RR intervals. A clear transition in the data can be observed from the symmetry measure and from Figs 4 and 7 we can see that this transition is associated with a significant change in the variability in the data.

There are many more measures that can be extracted from our reconstructed attractor and preliminary results indicate that these can be useful for the early detection of sepsis in mice. The next stage of development for this new approach is to determine the physiological significance of the different derivable measures and quantify the early onset of various diseases from our collection of time traces of measures derived from the attractor.

References

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