USE OF RECURRENCE PLOTS IN THE ANALYSIS OF HEART BEAT INTERVALS

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Summary

Cardiac inter-beat intervals have in recent years created much interest with respect to patterns and variability relative to pathologic states and dysrhythmias. The stationarity, time-correlation, and length of this signal, however, cause difficulties relative to its mathematical processing and interpretation. Recurrence plots, which were defined to appreciate the dynamics of a time series, can obviate these constraints. Geometrical properties of our plots provide complexity and local rate of divergence estimates. This method was applied to the heart-rates of subjects with a history of congestive heart failure and heart transplantation as they were administered normal saline.

Introduction

Experimentalists and clinicians dealing with the nonlinear dynamics of biological data have been at once encouraged and disappointed with developments over the past ten years: whereas parameters such as Liapunov exponents, and dimensions have suggested new insights into biological processes, results have also been equivocal due to the assumptions that the data series are autonomous and whose lengths are much longer than the characteristic times of the systems in question. By and large, such assumptions cannot be supported. This has especially been disappointing in the case of cardiac dynamics. Although much presumptive support for such approaches in clinical and experimental cardiology has been forthcoming, practical methods have not. A new graphical tool for the representation of nonlinear dynamics of erratic time series, however, was introduced in 1987 by Eckmann, Kamphorst, and Ruelle, and which we have applied to the analysis of cardiac inter-beat intervals.

Methods

The algorithm begins with a time-ordered sequence of vectors in \( \mathbb{R}^n \), where \( x(t) \) denotes the \( t \)-th point on the orbit. Dots are placed at a point \( (i,j) \) if \( x(j) \) is sufficiently close to \( x(i) \). Here sufficiently close means that \( x(j) \) falls within a ball of radius \( r \) centered at \( x(i) \), where \( r \) is chosen by some suitable method (for example, choose the radius such that \( k \) nearest neighbors lie within the ball.) This array of points is then known as a "recurrence plot." The Eckmann, et al. recurrence plots tend to be nearly symmetric with respect to the diagonal - /because, in general, if \( x(t) \) is close to \( x(j) \) then \( x(j) \) is usually "close" to \( x(t) \). (Notice that the plot is not necessarily symmetric as \( r(t) \) does not have to equal \( r(j) \).) Large-scale diagonal "lines" parallel to \( i = j \) were seen to indicate periodic behavior which was not always visible in the original data. At the same time, the length of small-scale line segments parallel to \( i = j \) were claimed to be proportional to the inverse of the largest positive Liapunov exponent. Additionally, drift was detected by "paler" portions away from the diagonal.

Eckmann et. al. mentioned in their paper, that the vectors \( x(t) \) could be reconstructed from a time-series using the method of time delays. Since we intend to limit ourselves to time-series data, it is useful to recall this method here. We suppose our data consist of a time-ordered sequence of integer values, \( d(i) \). In order to gain insight as to how such a data sequence could arise, we suppose that it has been generated by some dynamic in \( \mathbb{R}^n \).

In other words, we suppose that there are \( n \) variables evolving in time according to some deterministic equation. The time series can be seen as a projection of these variables to a one-dimensional observable. We reconstruct the \( n \)-dimensional dynamics using the time-delay embedding method of Packard, et al. (Note this method requires that we choose an embedding dimension and a time delay, \( \tau \).) In general, \( n \)-dimensional vectors can be reconstructed from a time-series \( d(i) \) for \( i = 1 \) to \( N \), with a delay of \( \tau \), as \( \vec{r} = [d(i), d(i+\tau), d(i+2\tau), \ldots, d(i+n\tau-1)] \) (where \( N \) is the number of data points originally provided.) It is known that a value for \( \tau \) which coincides with the first minimum of the mutual information content provides a good estimate for a reliable reconstruction. For a thorough explanation of the relationship between the delay, \( \tau \) and the amount of new information provided by each subsequent vector, see R. Shaw."
We have modified this algorithm by neglecting the asymmetry and fixing the size of neighborhoods. Note that this produces a symmetric matrix, and it is sufficient to refer to the upper triangle. To make this more graphically intelligible, we calculate the vectors for $t = 1, \ldots, \frac{r_{\max}}{2}$, and create a square matrix.

Once we have our series of vectors, we create our recurrence plot by letting the $t$-th column represent the distance from $\vec{v}_{t-1}$ to the next $t$ successive vectors forward in time, where $h$ is the height of the array. The distances can then be color coded.

We have written a C language program allowing us to choose an embedding dimension, a delay, a particular norm, and the number of vectors displayed. Once the plot has been drawn, we can select a particular pixel within an interesting area. (Fig. 1)

![Image](image_url)

**Fig. 1:** Two dimensional disk demonstrating properties of norms.

Thus, the $l_1$ norm is most likely to determine that a vector in the reconstruction is within a $b$-neighborhood of another vector. This norm serves to emphasize the outline of the reconstruction; i.e., the largest vector component dominates. Alternatively, for a fixed $b$, the $l_\infty$ norm should find the fewest number of recurrences in a given reconstruction. Hence, using this norm reveals more information about the local behavior of the reconstruction. The $l_\infty$ norm has intermediate effects. If the time series is routinely embedded in $\mathbb{R}^n$ for $n > 5$, using the $l_1$ norm, where recurrences are rare, an increase in recurrences becomes more robust in its significance.

We have primarily used the $l_1$ norm to determine the distance between vectors, so we let $l_{t_{(i,j)}}$ denote the distance from $\vec{v}_{t_{(i,j)}}$ to $\vec{v}_t$. We assume that $(x,y) = (0,0)$ is the lower left-hand corner. Notice that if the point $(x,y)$ on our plot corresponds to the distance $l_{t_{(i,j)}}$, then $(x+1,y)$ corresponds to $l_{t_{(i+1,j)}}$ by definition. In general, we compute the range of distances achieved within a particular data set, and color code those distances which are less than or equal to a percentage of this range.

One of the more obvious features in our plots is horizontal line segments. Such line segments correspond to sequences of points $(x,y), (x+1,y), \ldots, (x+k,y)$ which, in turn, correspond to sequences of distances $l_{t_{(i,j)}}, l_{t_{(i+1,j)}}, \ldots, l_{t_{(i+k,j)}}$. If we suppose that, at least locally, the system is described by a hyperbolic dynamic, then we know that these vectors are diverging at the rate of $\lambda$, where $\lambda$ is the largest positive Liapunov exponent. Thus, if the distance data is suitably re-normalized, then the length of this line segment, $k$, defines an upper bound on this exponent for the local dynamics. Important to note also, is that this feature is seen even with relatively few data points ($<500$) of experimental time series.

In addition to local rate of divergence information provided by the lengths of horizontal line segments, a recurrence plot also provides an estimate of the pointwise mass function $^\ast$

\[
\frac{1}{T_{x_0}} \cdot B_{x_0}(r)
\]

Furthermore, this dimensional complexity estimate is readily-discernible, at least qualitatively, as a more cluttered plot corresponds to a higher-dimensional signal.

**Patients and Procedures**

Five cardiac transplant patients and 3 cardiomyopathy patients underwent volume loading with 2 L of normal saline over 1 hr. ECG's were...
recorded on a digital instrumentation recorder at baseline, and after 1 and 2 L. Blood samples were also taken for analysis of norepinephrine (NE), and renin (R). The ECG's were analyzed off-line for measurement of RR intervals with an R wave detector (CWE, Inc).

Results

Recurrence plots manifested qualitative changes with the loading events as compared to baseline, and supported other calculations (power law scaling, NE, and R levels) suggesting significant physiological changes. The recurrence plots appeared to mirror these changes by increased numbers of recurrences, with a concomitant decrease in "clutter" between the first and second liters. After the second liter, the plots tended to appear more like the baseline. (Fig. 1 and Fig. 3)

Fig. 2: Example of recurrence plot for subject at baseline for 10% of the range. Note few recurrences. (This and subsequent plots modified for black and white printing; the basic algorithm is as described in text.)

Fig. 3: Recurrence plot immediately prior to a subject who experienced a brief run of ventricular tachycardia (after 1 liter).

One subject experienced a brief run of ventricular tachycardia after 1 L., which was noteworthy for increased areas of recurrence as well as periodicities immediately prior to the tachycardia. (Fig. 3)

Discussion

In general the results from the plots tend to parallel changes in NE and R levels, namely, that there tended to be increased recurrences after one liter. After the second liter there were fewer changes and the appearance was somewhat similar to the baseline. This may be related to time lags associated with compensatory mechanisms: after one liter these compensatory changes are not yet fully operational, but are so after two liters. This is understandable in transplant patients whose hearts are denervated. In the CHF patients research suggests that they are functionally denervated due to their pathology.

The increased recurrences suggest a decrease in dimensionality and entropy. This is to say that under such circumstances the heart becomes more informationally isolated from its controls. This confirms our previous findings that with significant cardiac events such as myocardial infarctions, the entropy of the beats decreases.

The implications from this are that there appear to be important changes in the dimensionality of inter-beat intervals which accompany pathology. One interesting finding is the appearance of periodic-like structures preceding tachycardia. This finding was not typically found with other subjects. Thus there may be subtle changes in recurrence plots for patients at risk for dysrhythmia, as opposed to global functional changes.

Conclusions

Constructing a recurrence plot in the fashion we have described is an efficient means of recovering dynamical information not easily obtained by other means about heart beats. This method does not require as much data as more traditional methods, and is computationally quick, as well. Qualitative information about local divergence rates and relative dimensionality of the original signal are visually obvious. Furthermore, this information emphasizes that adiabatic systems may be usefully analyzed without requiring the reconstruction of an entire attractor.
References


