Singularities of the Heart Beat as Demonstrated by Recurrence Quantification Analysis

Joseph P. Zbilut\(^1\), Zhihong Hu\(^2\), Alessandro Giuliani\(^3\), Charles L. Webber, Jr.\(^4\)

Abstract – Deterministic, chaotic, nonlinear dynamics have enjoyed considerable popularity in the analysis of physiological systems. Many models, however, fail to incorporate some basic features of the involved physiology. Our research using experimental data from ECGs analyzed by recurrence quantification analysis (RQA) suggest that some of these dynamics can be better modeled by singularities of differential equations, alternating with oscillations which result in multi choice responses to excitations. ECGs of 34 healthy volunteers were recorded for 512 consecutive beats. Recurrence plots suggested discontinuities at the T-P interval, and the durations of the T-P and P-T intervals were manually calculated. Although the distributions of these two intervals were found to be similar (KS two sample test, \( p = \text{NS} \)), RQA demonstrated that the T-P interval approached the embedding limit of pseudo random numbers \( [\text{pseudo random} = 4; \ T-P = 4 \ (95\% \ CI = 3.6-4.3)] \). This suggests the primary stochastic process of ECGs is located in the T-P interval and represents a singularity of the dynamics alternating with the determinism of the P-T interval. The dynamics are thus discontinuous and poorly represented by FFT and other, nonlinear transform techniques.

Key words - Recurrence quantification, terminal dynamics, Lipschitz conditions, heart beats, nonlinear dynamics, chaos, singularity

I. INTRODUCTION

The intent of this paper is 1) to outline a theory of nonlinear dynamics which occurs when Lipschitz conditions of differential equations are relaxed; 2) to demonstrate how such dynamics may better model certain physiological processes more closely than deterministic chaos or other traditional means; and 3) demonstrate how recurrence quantification analysis (RQA) is the most suitable method for detecting such dynamics. An example from evaluation of heart beats is presented. Emphasis is placed on the fact that traditional chaos (and other signal processing methods) fully determine the time evolution of a system, whereas physiological systems must constantly readjust, and often display features of stochasticity.

II. SINGULARITIES

Considerable efforts have been expended to determine if physiological systems can be modeled as nonlinear chaotic dynamics. A motivation has been the recognition that often the time series of physiologically derived observables appear chaotic, although they are clearly generated by some form of determinism. Unfortunately, these attempts have not been distinguished by unequivocal results (Zbilut, 1991). Whereas the physical sciences can generate reasonably long stationary data, the biological sciences have great difficulty (Eckmann and Ruelle, 1992). Additionally, greater amounts of noise often attend the biological data. Some of the difficulties have been attributed to the algorithms used to quantify chaotic invariants, such as dimensions, entropies, and Liapunov exponents. Other, more traditional methods, such as FFTs have also exhibited well known difficulties. As a result much energy has been devoted to analyzing various methods of calculation and conditioning to real life data and conditioning to real life data.

In the case of biological data, a fundamental problem has not been addressed; namely, the correspondence of biological data to the fundamental assumptions of chaos and other fully determined models. Specifically, it is noted that chaotic dynamics are continuous, deterministic systems. Although the time series of such systems are random looking, processes which generate them are not: their behavior is, by definition, rigid. Biological systems, on the other hand, require stability, yet at the same time adaptability in the face of changing environmental needs. Although these facts are obvious, the consequences are seldom appreciated. To suggest that physiologic data is chaotic, would assume that such systems are ultimately very unstable. This comes as a result from the recognition that the way to change a chaotic system is to change its control variable or by creating specific perturbations, but, as is known, very small changes can produce significantly different behavior. As a result much energy has been devoted to analyzing various methods of calculation. Insofar as noise is ubiquitous in biological systems, it would seem that instability might be a significant problem for such systems. Furthermore, it would seem that considerable energy might be required for an organism to maintain such control variables. Even if the noise is controlled, the performance of the system is fully prescribed by the initial conditions. To change the system would require external input to overcome the inertia of the past. Yet,
experimental evidence clearly demonstrates that most organisms can easily adapt within a range of parameters, and exhibit considerable variances within stationary bounds. Also, it is noted that performance in neural control systems is often parallel and/or asynchronous—processes which do not have adequate models in deterministic nonlinear dynamics (Huberman and Glance, 1993). Finally, there is a subtle problem dealing with time scales: chaotic systems are by and large insulated from the microscopic world by a large difference in scale, whereas biologic systems are integrated from molecular to macroscopic.

A fundamental problem in the application of nonlinear dynamics to physiological systems is that fact that they are still classical: they require Lipschitz conditions to guarantee the uniqueness of solutions subject to prescribed initial conditions. For a dynamical system all the derivatives are bounded. This condition allows for the description of classical Newtonian dynamics within the traditional theory of differential equations, such that reversibility and predictability are guaranteed (recall the chaotic dynamics can be predicted if it were possible to know the initial conditions with infinite precision and devoid of noise). This results in an infinite time of approaching an attractor. Clearly, however, such observations are not typical in real systems—especially biological. One way to overcome these problems is to violate the requirement of Lipschitz conditions (Zak, Zbilut and Meyers, 1997). By doing so, at singularities of the phase space, the dynamics forgets its past as soon as it approaches these singularities (Fig.1). Additionally, the architecture of such systems is able to be activated not only by external inputs and infinitesimal noise of any kind, but also by internal biological rhythms. Such critical points can be placed in a network with others which are weakly coupled, and can perform parallel tasks.

Consider, for example, a simple equation without uniqueness, \( \frac{dx}{dt} = x^{\frac{3}{2}} \cos \alpha \). At the singular solution, \( x = 0 \) (which is unstable, for instance at \( r = 0 \)), a small noise drives the motion to the regular solutions, \( x = \pm (2/3 \alpha \sin \alpha)^{\frac{1}{2}} \) with equal probabilities. Indeed, any prescribed distribution can be implemented by using non-Lipschitz dynamics. It is important to emphasize, however, the fundamental difference between the probabilistic properties of these non-Lipschitz dynamics (n.b., we term these dynamics also "terminal dynamics", and "nondeterministic" dynamics) and those of traditional stochastic or differential equations: the randomness of stochastic differential equations is caused by random initial conditions, random force or random coefficients; in chaotic equations small (but finite) random changes of initial conditions are amplified by a mechanism of instability. But in both cases the differential operator itself remains deterministic (Table 1).

<table>
<thead>
<tr>
<th>Chaotic (deterministic) dynamics</th>
<th>Non-Lipschitz (Terminal dynamics)</th>
</tr>
</thead>
<tbody>
<tr>
<td>Dependent on initial conditions</td>
<td>Dependent on singularity</td>
</tr>
<tr>
<td>Attractor present</td>
<td>No attractor in the usual sense</td>
</tr>
<tr>
<td>Spreads uncertainty over entire attractor; i.e., global instability</td>
<td>Uncertainty at singular points</td>
</tr>
<tr>
<td>Smooth stretching and folding of attractor</td>
<td>Random spread of points in region of phase space (stochastic attractor)</td>
</tr>
<tr>
<td>Cantor set</td>
<td>Countable combinatorial set</td>
</tr>
<tr>
<td>Behavior varies</td>
<td>Dynamics well behaved away from singular points</td>
</tr>
<tr>
<td>Information decreases with time</td>
<td>Information infinite at singularity (knowledge of past is zero)</td>
</tr>
<tr>
<td>Short term predictability</td>
<td>Predictability based on probability evolution</td>
</tr>
<tr>
<td>Controlled by external forces</td>
<td>Easily controlled at singularity</td>
</tr>
<tr>
<td>Time is a continuum</td>
<td>Near singularity, future time evolution is decoupled from past</td>
</tr>
</tbody>
</table>

In contradistinction to this, in non-Lipschitz dynamics, randomness results from the violation of the uniqueness of the solution at equilibrium points, and therefore, the differential operator itself generates random solutions. Furthermore, the singular point can be part of a larger chain of oscillators which become self-organizing. Interestingly enough, when such dynamics are analyzed numerically for Liapunov exponents, positive values are obtained, which is not
surprising since the solutions are characterized by an infinite divergence.

There is an inherent difficulty in identifying such singular dynamics in real life data, since typical methods assume smooth dynamics. A method which obviates this problem is recurrence quantification analysis (RQA). The method is basically a distance matrix modified to accommodate embedding and scaling for nearest neighbors, and has been extensively described elsewhere (see, e.g., Zbilut, Giuliani and Webber, 1998; Zbilut, Giuliani, Webber and Colosimo, 1998; Manetti, Ceruso, Giuliani, Webber, and Zbilut, 1999.). We used it to explore the dynamics of the heart beat by means of the relation between REC (number of recurrent points in the dynamics) and DET (recurrent points constituting line segments) at different embedding choices, in order to differentiate pure statistical vs deterministic recurrences.

III. HEART BEAT INTERVALS

We analyzed 512 beat consecutive heart beat intervals of 34 young, health volunteers. Recurrence plots demonstrated discontinuities between the beats located at the T-P interval (Fig. 2). Consequently, the ECG time series were manually calculated to separate the T-P vs. P-T durations (Fig. 3). The Kolmogorov-Smirnoff test demonstrated that the distributions were similar. However, when subjected to analysis for the embedding limit by RQA, the T-P intervals were found to be significantly different from the P-T intervals (p < 0.0001; based on equal segment lengths). (By embedding limit we mean the embedding at which the calculated value for DET drops to zero, while %REC continues to have positive values. We have found this strategy to be a good index for the degree of "randomness" of a process.) In fact the RQA analysis suggested that the T-P intervals were similar to random numbers, whereas the P-T durations were more typical of deterministic processes. Thus it can be seen the major portion of "randomness resides in the singularity of the T-P interval, which is often treated as smooth dynamics by most signal processing methods.

IV. CONCLUSIONS

The above findings are consistent with the theory of terminal, "non-Lipschitz" processes, and suggests that FFT based and other nonlinear algorithms have a fundamental difficulty in characterizing such dynamics.

Non-Lipschitz dynamics appear to be a natural consequence of physiological complexity. With several levels of control, it appears that multiple branching solutions to basic equations of motion are necessary to give an organism the ability to "fine tune" a given system according to second-by-second changing physiological requirements. By contrast, transformation of the system on some levels toward complete determinism or toward complete randomness may be a marker of pathology.

What is of more interest is that traditional signal processing methods (both linear and nonlinear) which do not allow for the possibility of such punctuated dynamics may be ill-equipped to analyze them. RQA, on the other hand, which does not imply transforms or functionals, may be better suited for their analysis.

V. RQA PROGRAMS

RQA programs used for the analysis may be obtained through links on the webpage located at http://www.rushu.rush.edu/molbio/physiozbi.html.

BIBLIOGRAPHY


1Department of Molecular Biophysics and Physiology
Rush University
1653 W. Congress
Chicago, IL 60612 USA
zbilut@rush.edu

2Physiology Department
Stritch School of Medicine
Loyola University
2160 S. First Street
Maywood, IL 60150 USA
zhu1@luc.edu

3TCE Laboratory
Istituto Superiore di Sanita
Viale Regina Elena 299
00161 Rome, Italy
alessandro.giuliani@iss.it

4Physiology Department
Stritch School of Medicine
Loyola University
2160 S. First Street
Maywood, IL 60150 USA
Cwebber@luc.edu