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(54) **METHOD AND SYSTEM FOR CHARACTERIZING CARDIOVASCULAR SYSTEMS FROM SINGLE CHANNEL DATA**

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(57) **ABSTRACT**

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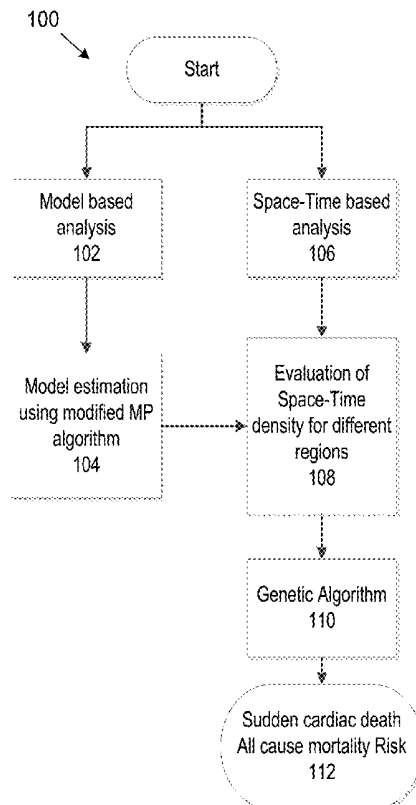
(60) Provisional application No. 61/684,282, filed on Aug. 17, 2012.

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(51) **Int. Cl.**
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Methods to identify and risk stratify disease states, cardiac structural defects, functional cardiac deficiencies induced by teratogens and other toxic agents, pathological substrates, conduction delays and defects, and ejection fraction using single channel biological data obtained from the subject. A modified Matching Pursuit (MP) algorithm may be used to find a noiseless model of the data that is sparse and does not assume periodicity of the signal. After the model is derived, various metrics and subspaces are extracted to characterize the cardiac system. In another method, space-time domain is divided into a number of regions (which is largely determined by the signal length), the density of the signal is computed in each region and input to a learning algorithm to associate them to the desired cardiac dysfunction indicator target.

NON-INVASIVE METHOD AND SYSTEM FOR CHARACTERIZING CARDIOVASCULAR SYSTEMS



**NON-INVASIVE METHOD AND SYSTEM FOR CHARACTERIZING
CARDIOVASCULAR SYSTEMS**

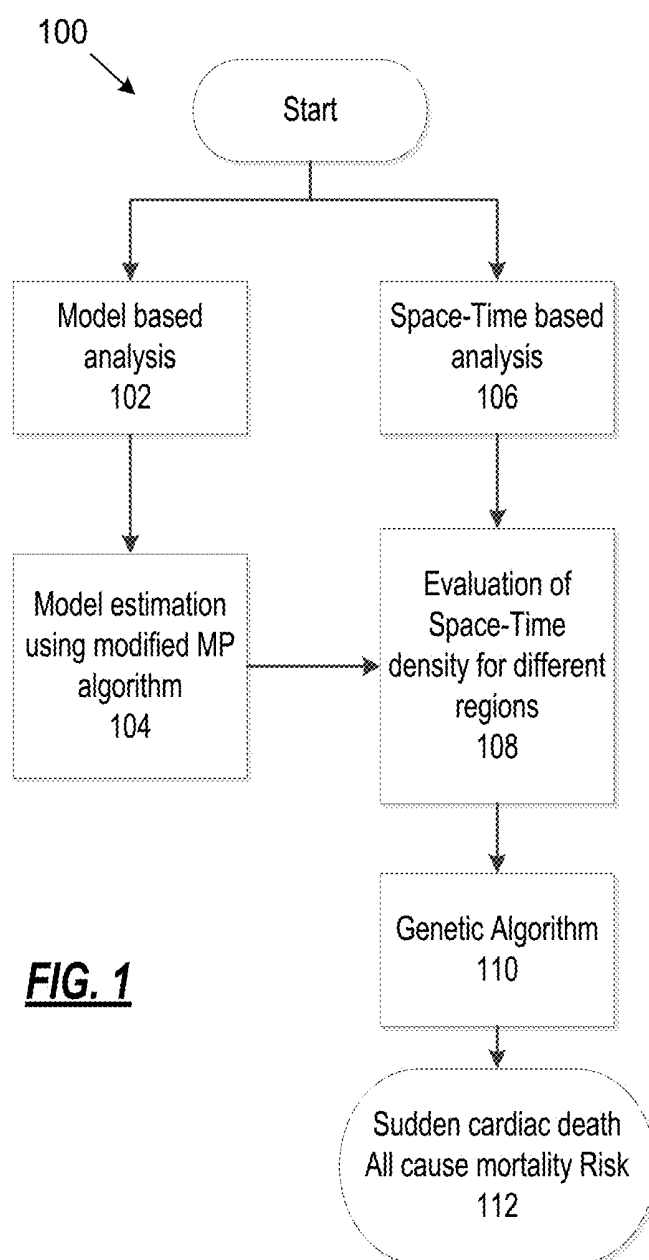


FIG. 1

Model-based Analysis
102

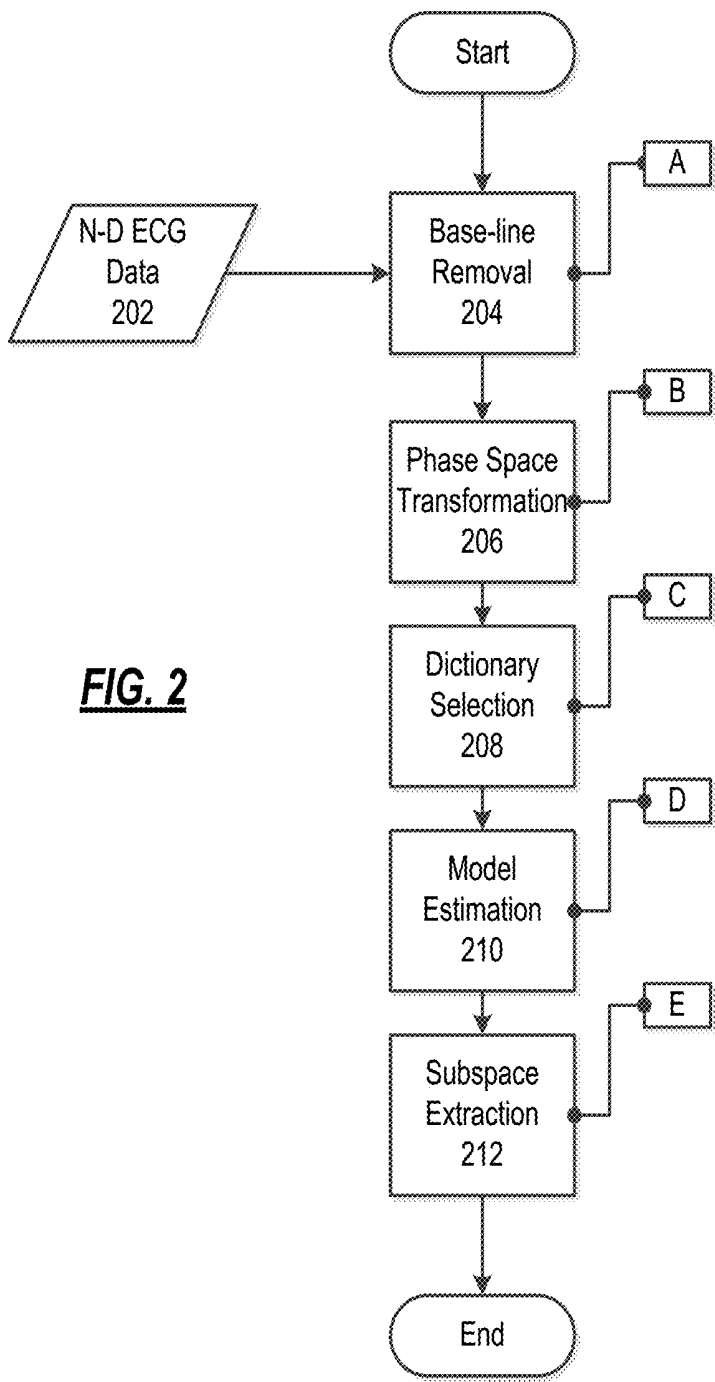


FIG. 2

Phase Space Transformation

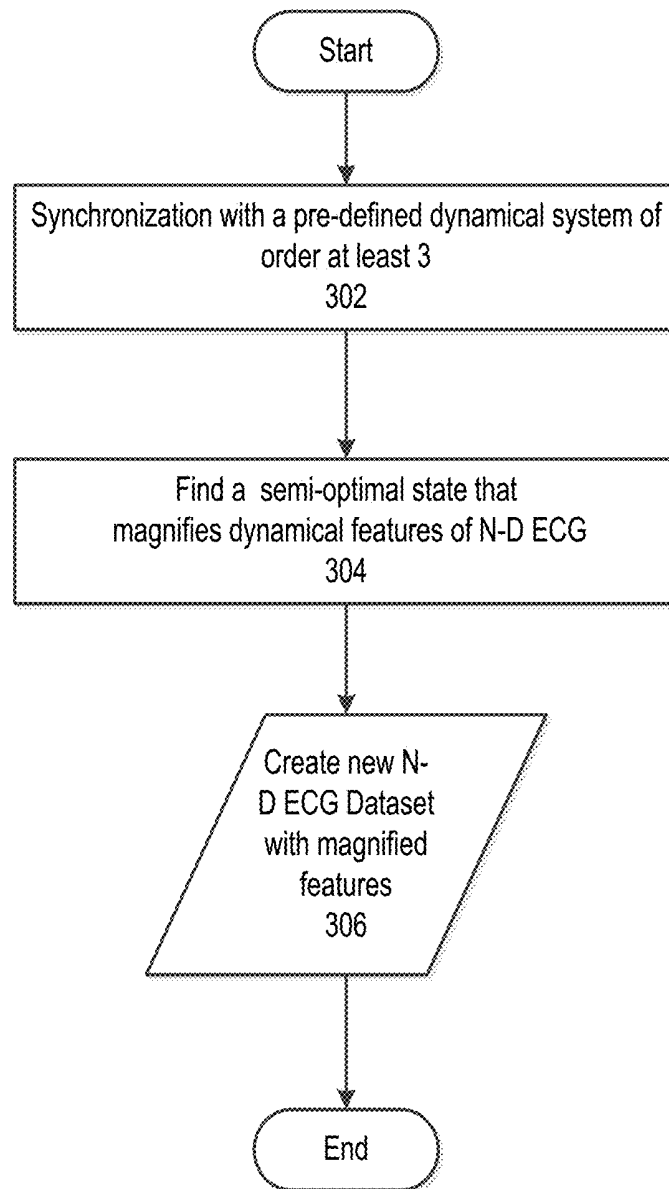


FIG. 3

**Dictionary Selection
208**

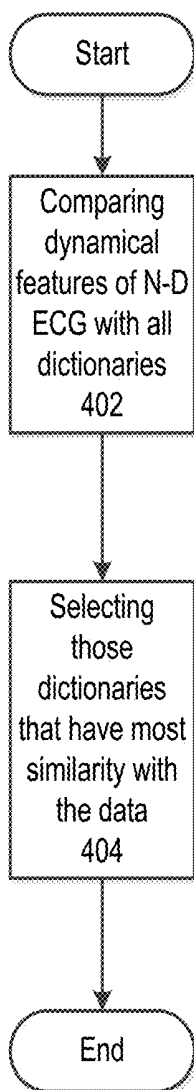


FIG. 4

Model Estimation
210

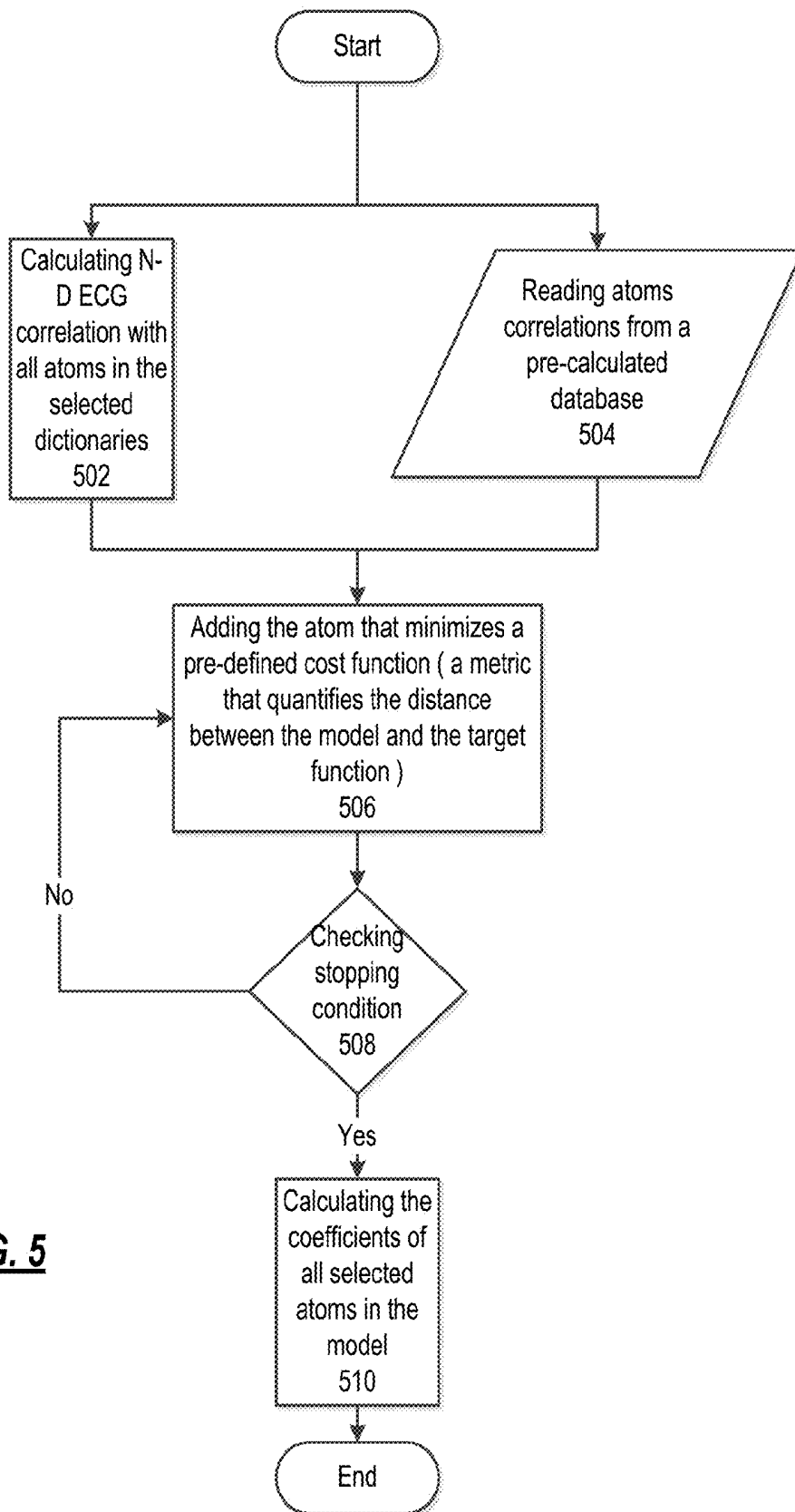


FIG. 5

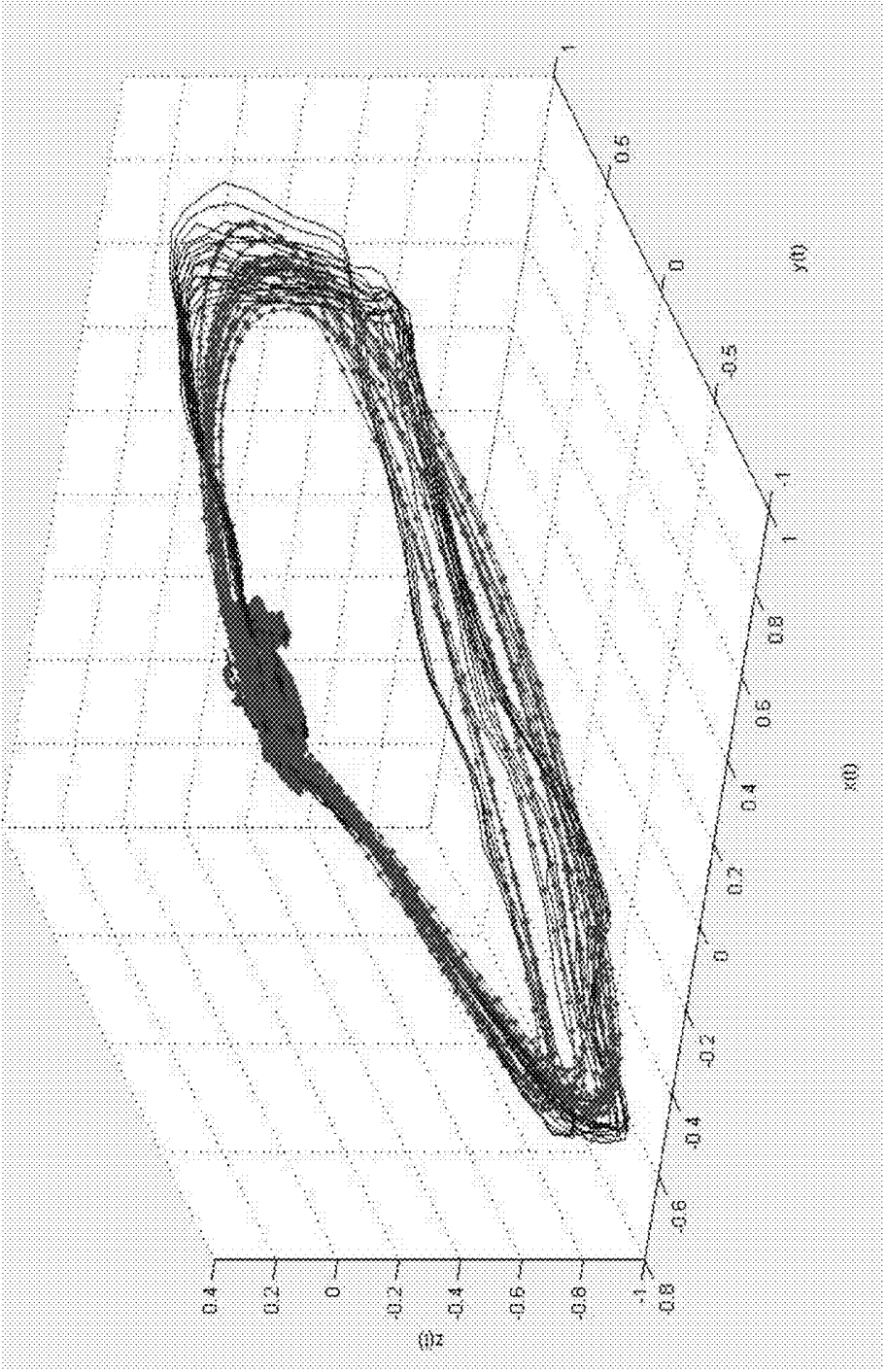


FIG. 6

Period-1 ($c = 4$)

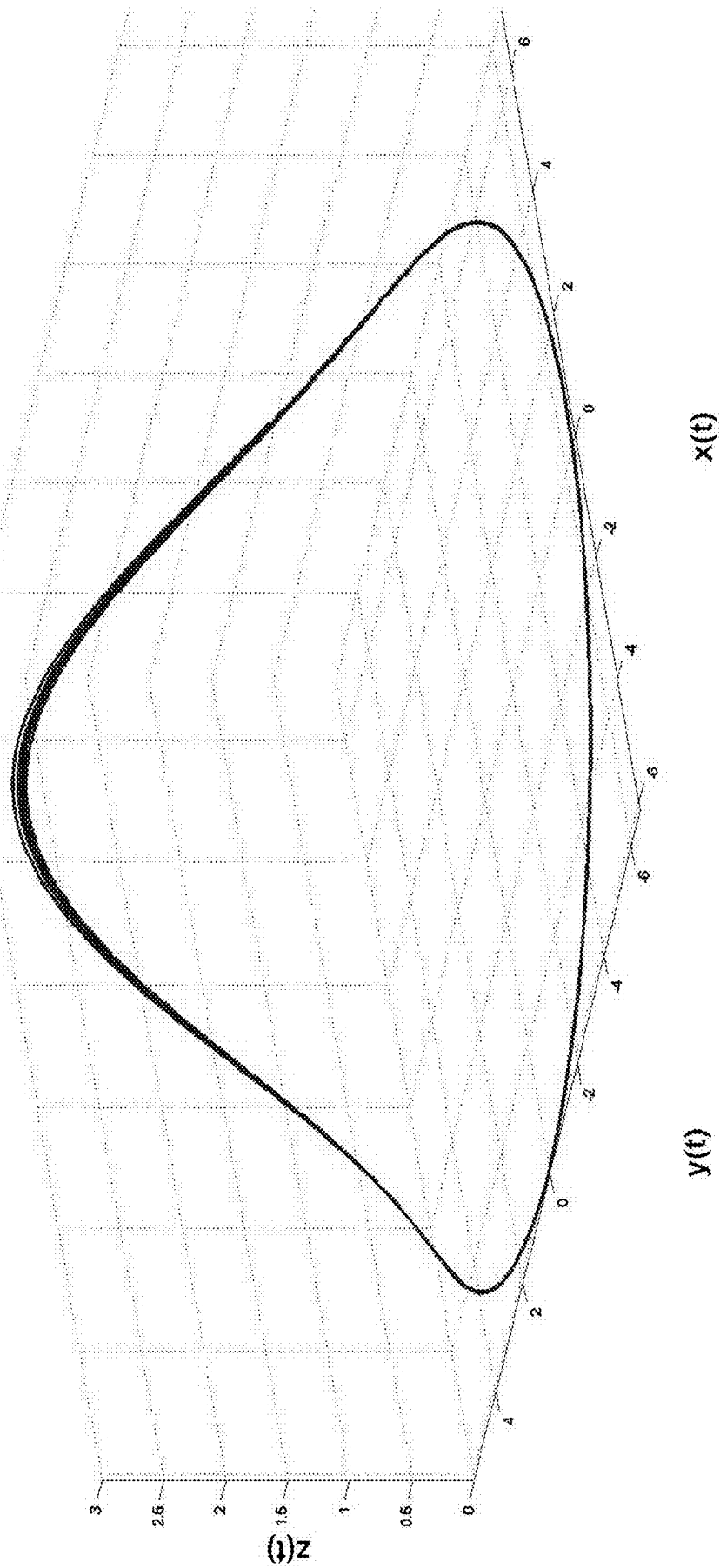


FIG. 7A

Period-2 ($c = 6$)

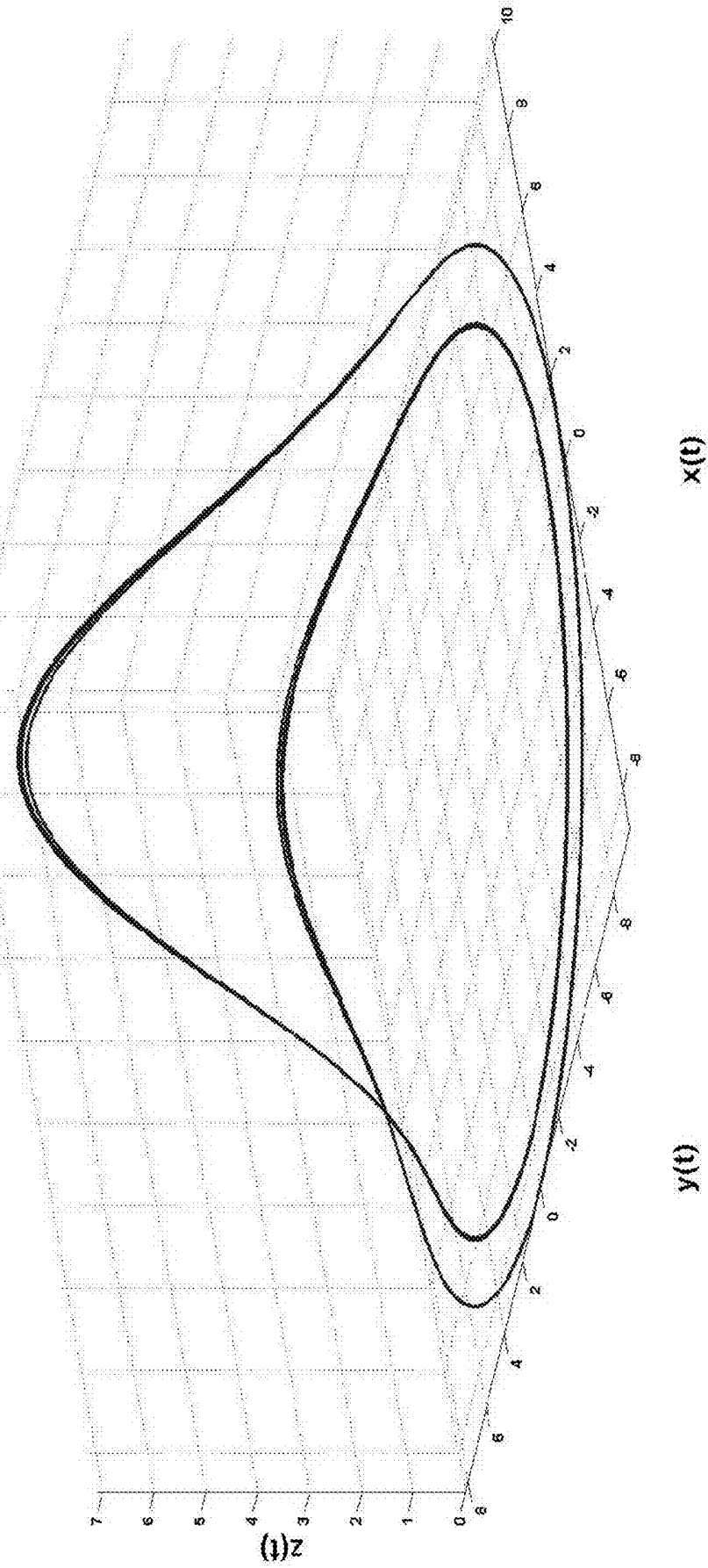


FIG. 7B

Period-4 ($c = 8.5$)

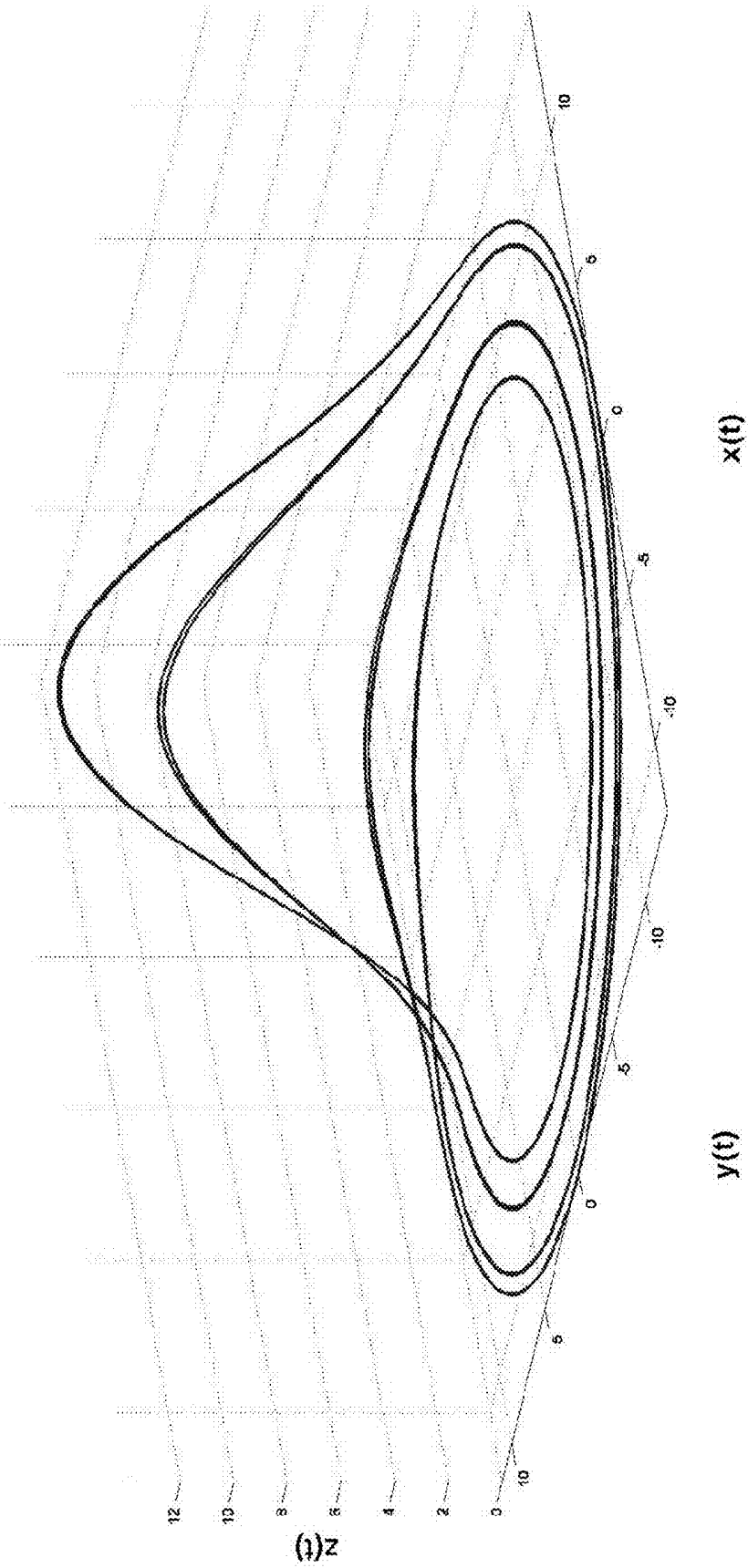


FIG. 7C

Period-8 ($c = 8.7$)

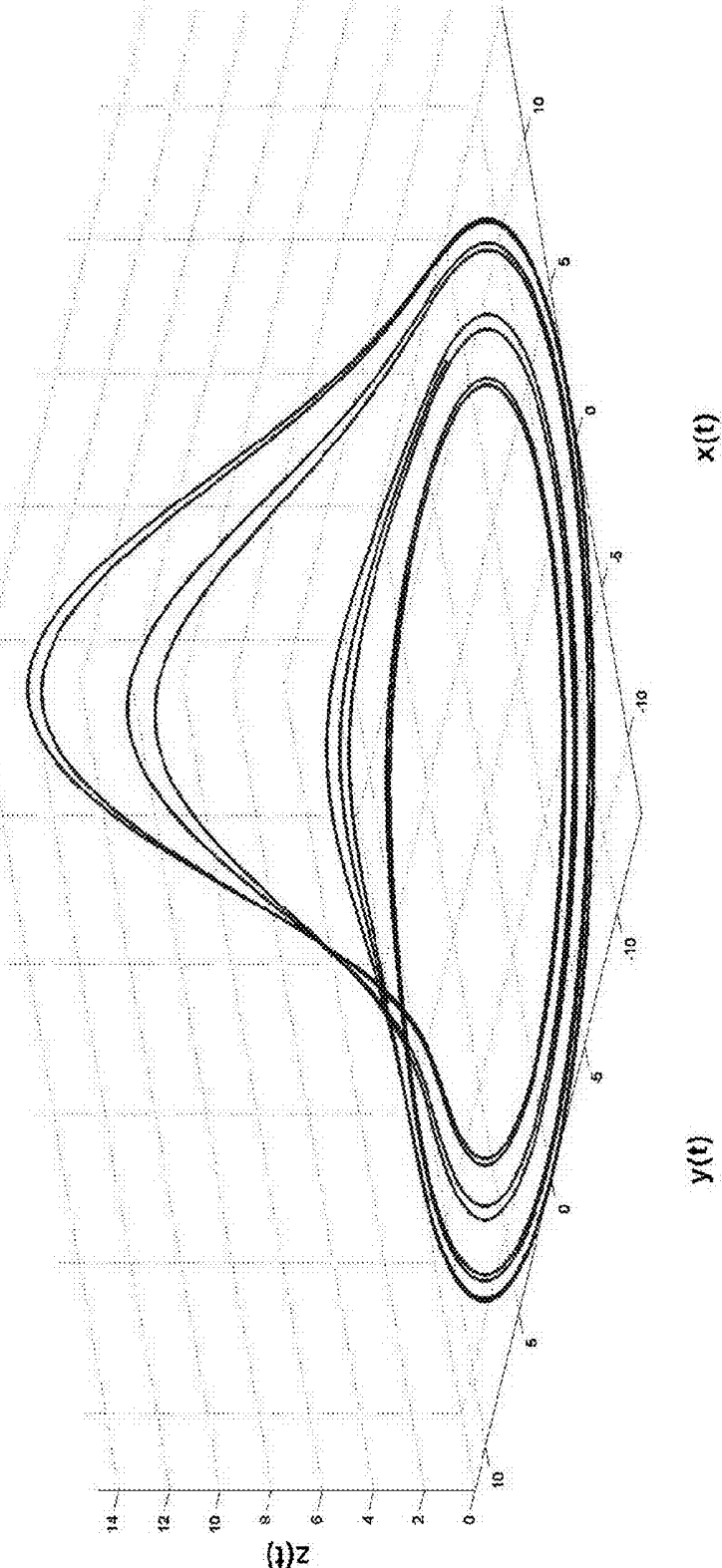


FIG. 7D

Sparse Chaos ($c = 13$)

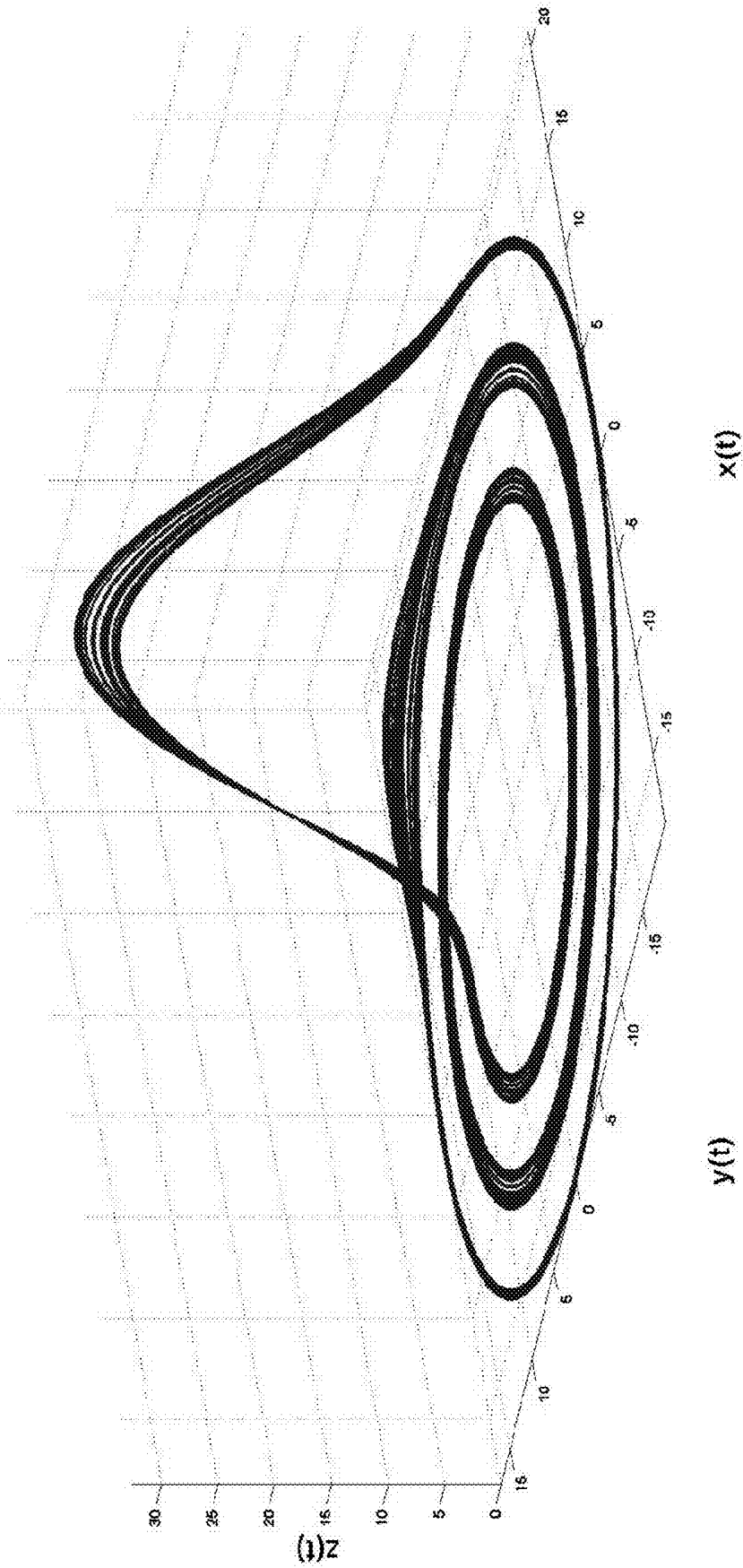


FIG. 7E

Filled-in Chaos ($c = 18$)

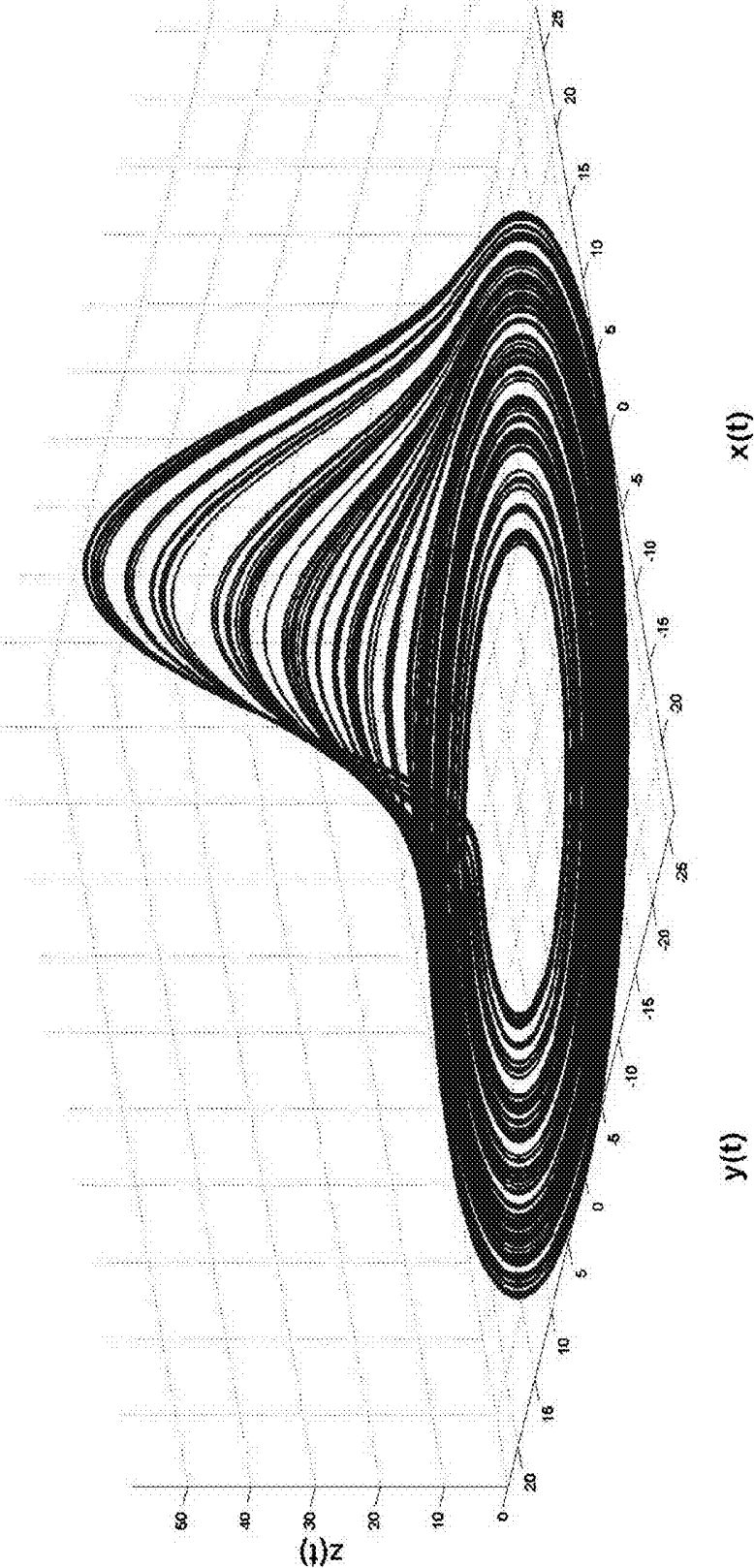


FIG. 7F

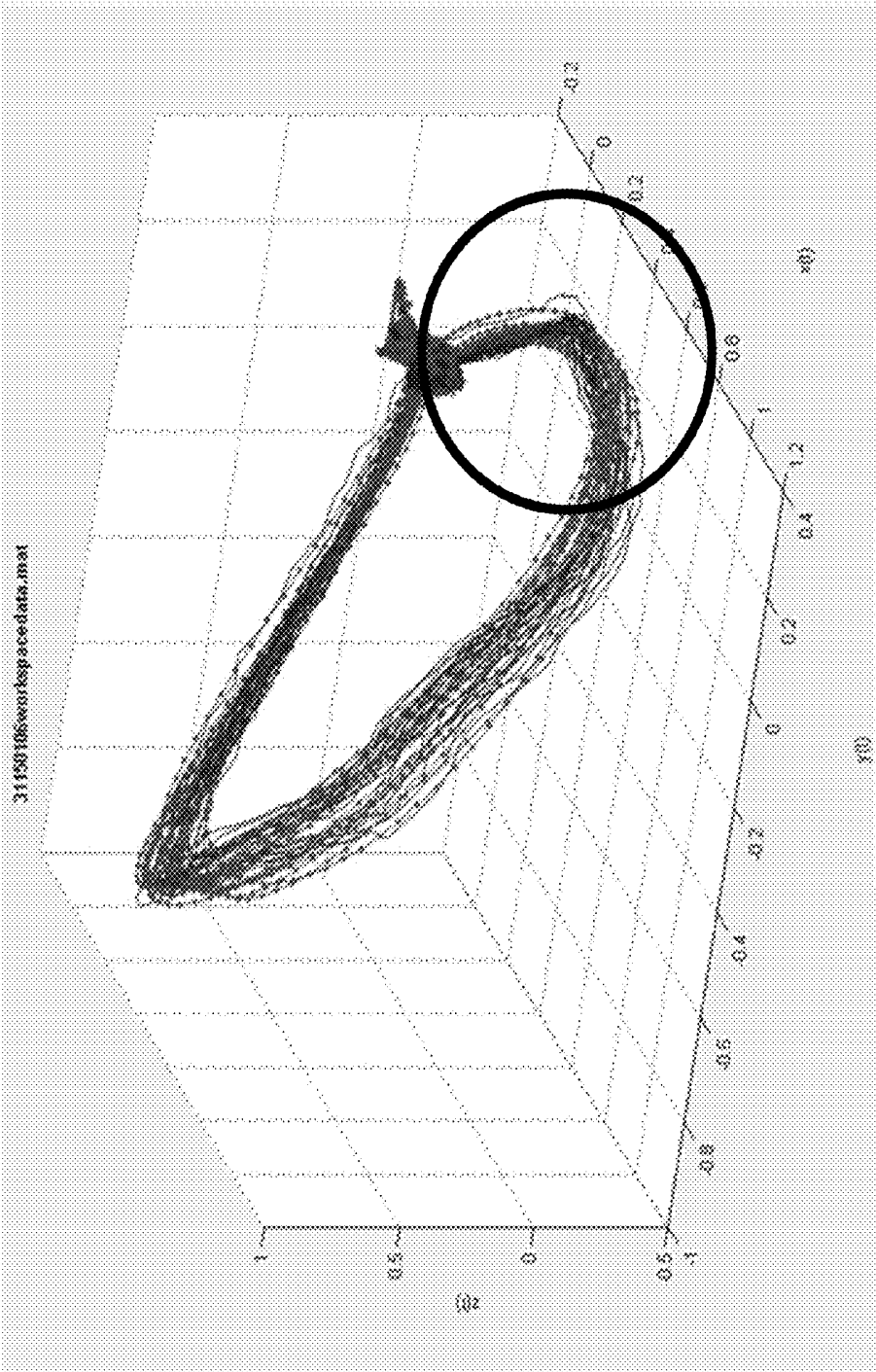


FIG. 8

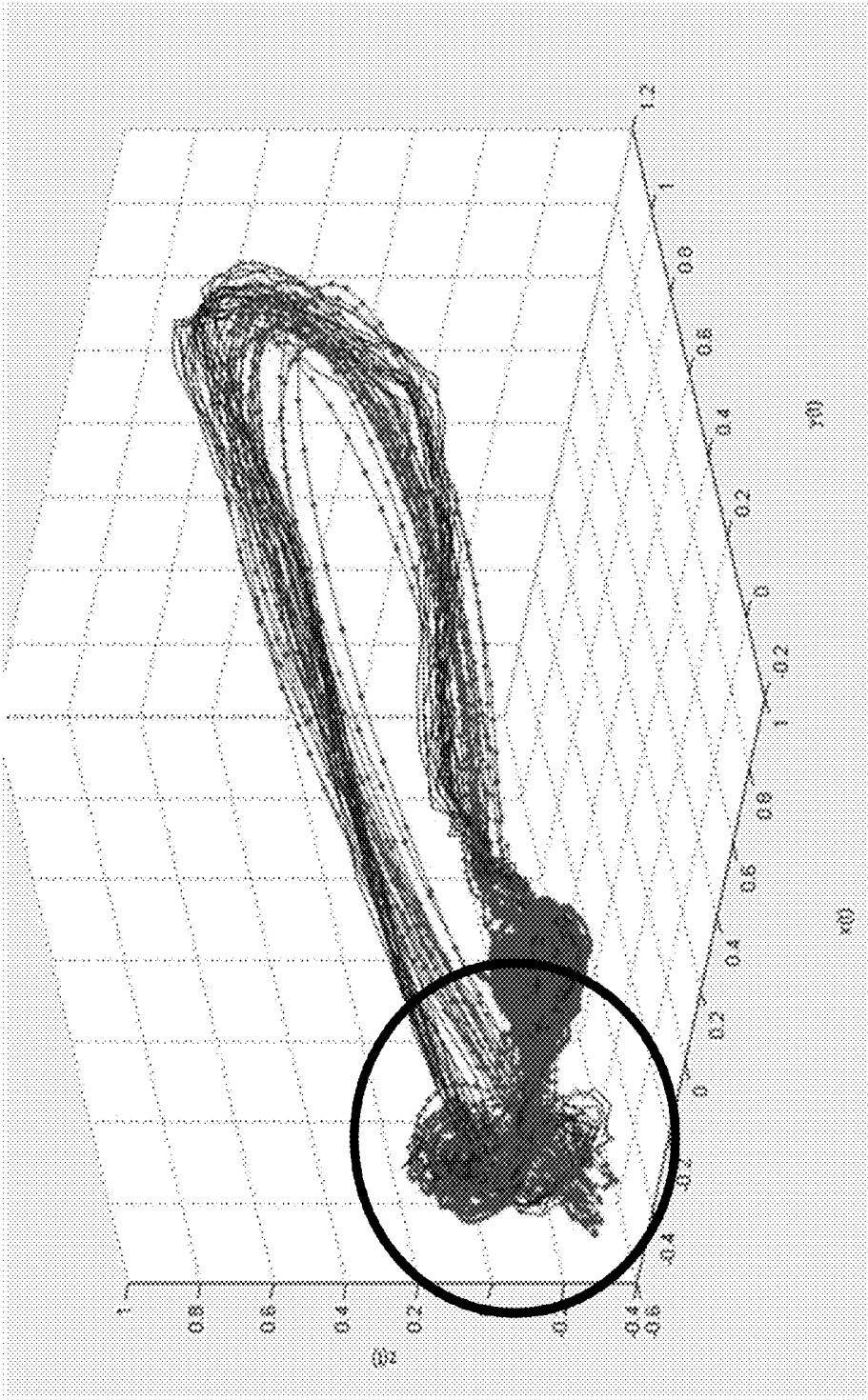
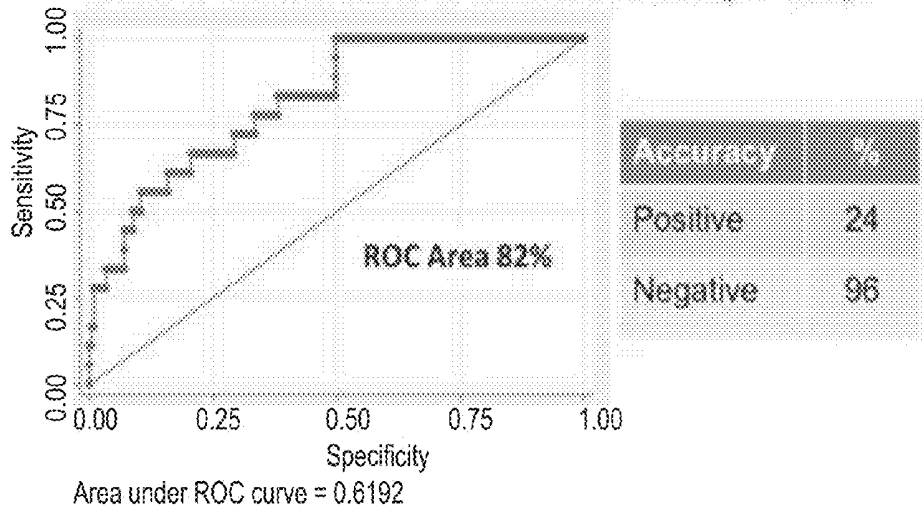


FIG. 9

Blinded analysis of left ventricular ejection fraction, heart rate turbulence slope and T wave alternans voltage combined as continuous measures to predict the risk of cardiac death or resuscitated cardiac arrest (N = 303).



Blinded analysis of the proposed risk assessment approach presented as a ranking of patients to predict the risk of cardiac death or resuscitated cardiac arrest (N = 289).

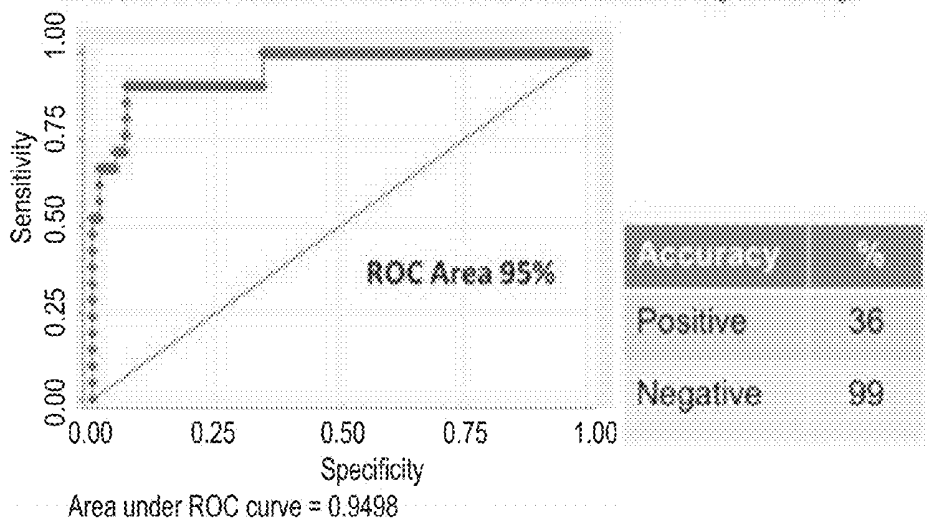


FIG. 10

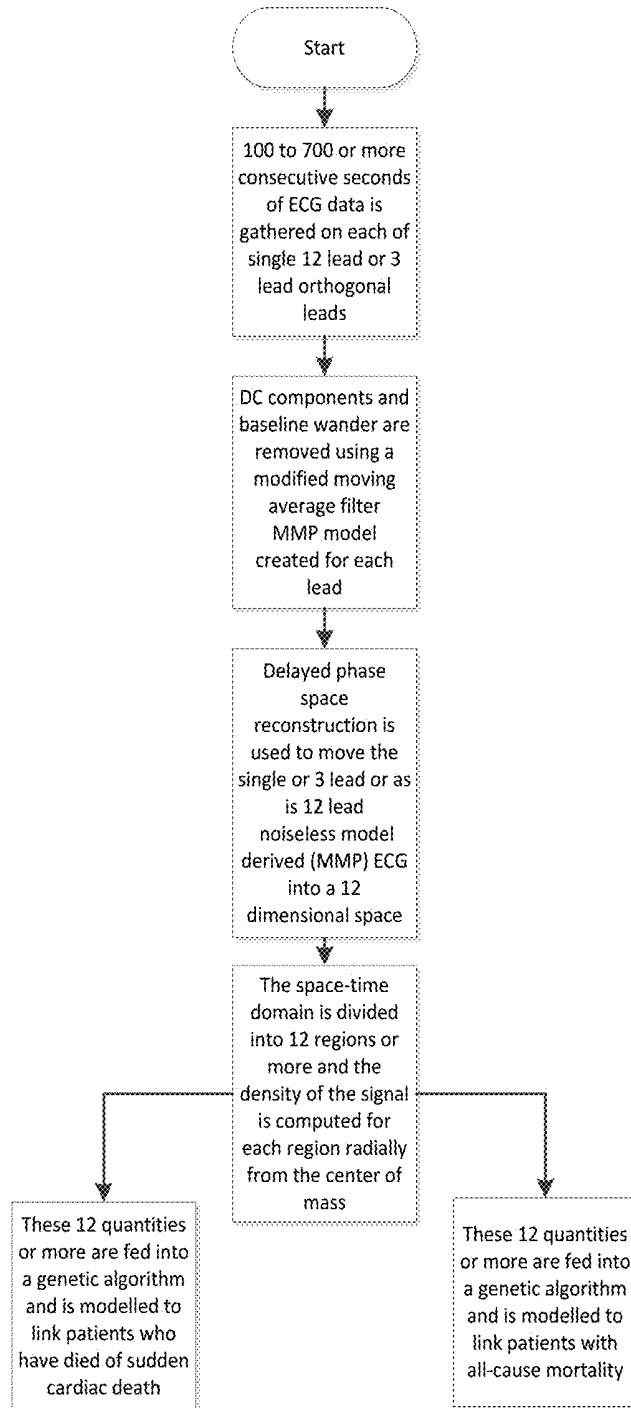


FIG. 11

Alteration in left ventricular morphology score at baseline as compared to 12 months of treatment with placebo (N = 6) versus atorvastatin (N = 6).

		Groups		
		Overall (N = 12)	Placebo (N = 6)	Atorvastatin (N = 6)
Morphology Score	Baseline	3.0 ± 1.4	2.7 ± 1.0	3.2 ± 1.6
	12 months	1.9 ± 1.0	2.5 ± 0.8	1.3 ± 0.6
	Change	- 1.1 ± 1.3	- 0.2 ± 0.7	- 1.9 ± 1.2
	T-test p-value	0.02	0.6	0.009
	Wilcoxon p-value	0.02	0.9	0.03

Data presented as mean ± standard deviation

FIG. 12

Non-Invasive Assessment of patient response to therapy

- 48 year old male presented with symptomatic, new onset Atrial fibrillation. He converted to normal sinus rhythm on Diltiazem and Dronaderone.
- Echocardiography showed left atrial enlargement and abnormal flow near the atrial myocardium.
- A4L CardioAnalysis of ECG shows interesting results in the presence and absence of medications.

Off Medication
Atrial Stability Risk Score =
0.2012

On Medication
Atrial Stability Risk Score =
0.0253

FIG. 13

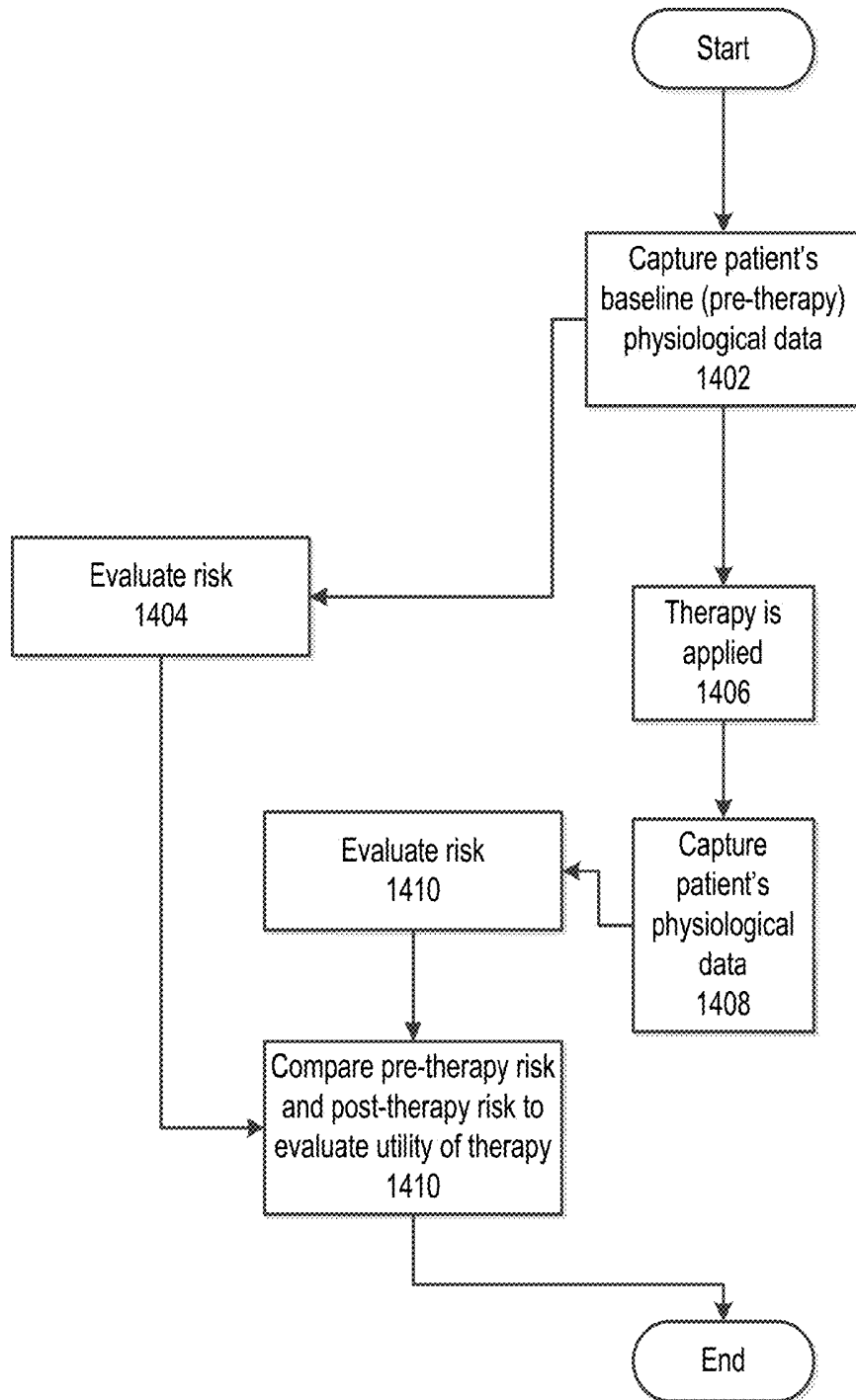


FIG. 14

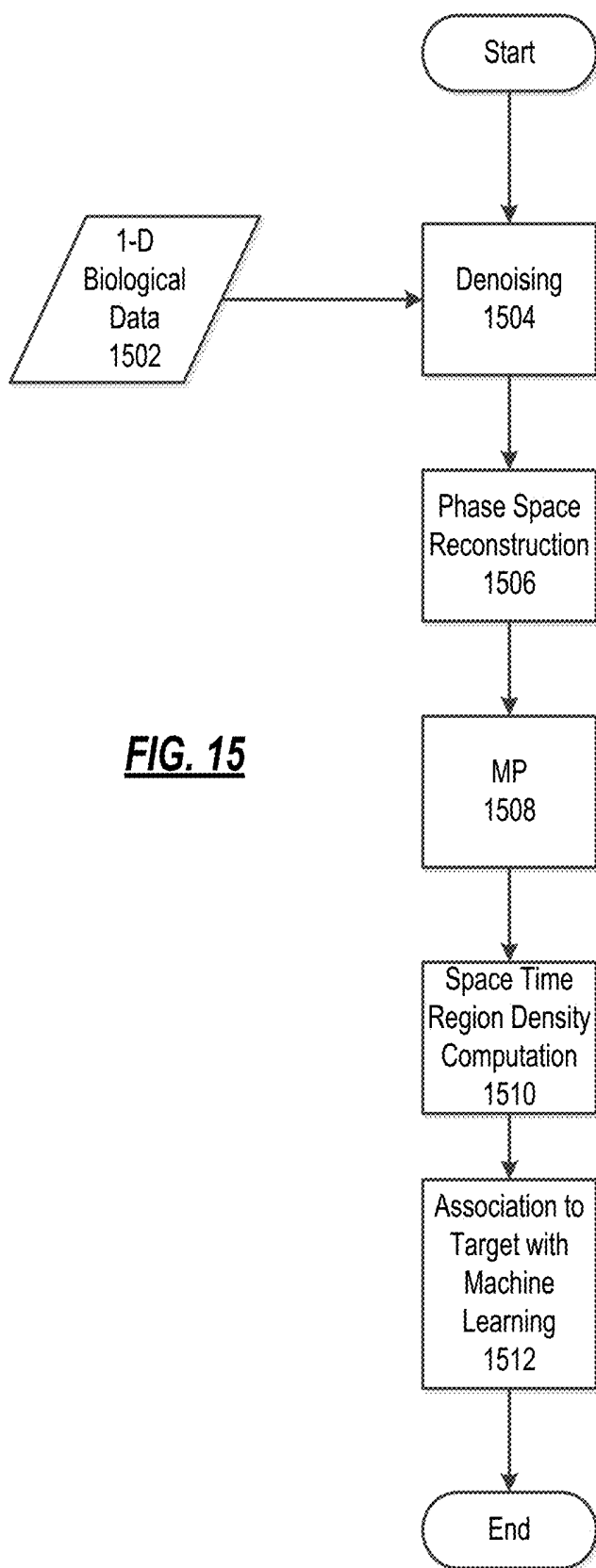
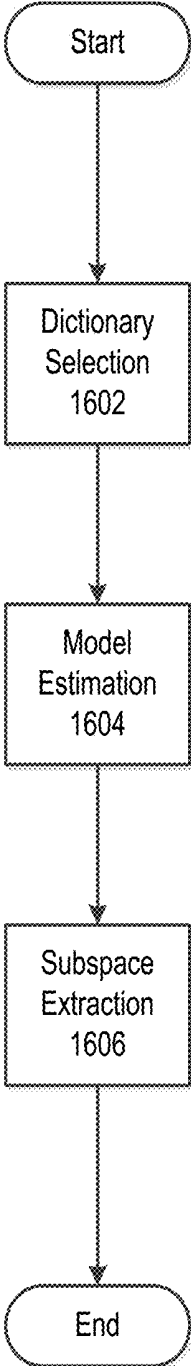


FIG. 15

FIG. 16



METHOD AND SYSTEM FOR CHARACTERIZING CARDIOVASCULAR SYSTEMS FROM SINGLE CHANNEL DATA

CROSS-REFERENCE TO RELATED APPLICATIONS

[0001] This application is continuation-in-part of U.S. patent application Ser. No. 13/970,580, filed Aug. 19, 2013, entitled "NON-INVASIVE METHOD AND SYSTEM FOR CHARACTERIZING CARDIOVASCULAR SYSTEMS FOR ALL-CAUSE MORTALITY AND SUDDEN CARDIAC DEATH RISK," which claims priority to U.S. Provisional Patent Application No. 61/684,282, filed on Aug. 17, 2012, entitled "NON-INVASIVE METHOD AND SYSTEM FOR CHARACTERIZING CARDIOVASCULAR SYSTEMS FOR ALL-CAUSE MORTALITY AND SUDDEN CARDIAC DEATH RISK," each of which is incorporated herein by reference in its entirety.

BACKGROUND

[0002] Present methods employed to assess cardiac and other physiological signals are typically rudimentary. It is claimed that prior methods can be improved upon via techniques that identify novel ECG patterns using advanced mathematical techniques that assess dynamic alterations in cardiac conduction and repolarization along with alterations in vascular and autonomic function. The surface ECG contains information on the electrical properties of the heart and represents the sum of electrical activity of the heart, along with vascular and autonomic nervous system dynamics. Moreover, cardiac electrical activity directly relates to cardiac architecture and alterations in cardiac architecture are detectable on a surface ECG. The challenges are to winnow out information related to abnormalities in cardiac conduction and repolarization, cardiac architecture, along with vascular and autonomic function from noise and other artifacts and to identify novel ECG patterns that reliably predict the development of serious heart rhythm disturbances, sudden cardiac death, other modes of death and all-cause mortality.

[0003] Prior ECG-based methods to identify patients at risk of sudden death and mortality are not sufficiently accurate. Even the best techniques have areas under the receiver operating characteristic curve of 0.80 or less in predicting the development of serious heart rhythm disturbances, sudden cardiac death, and mortality. Hence at least 20% of patients are misclassified. A more accurate method to characterize abnormalities in cardiac conduction and repolarization, cardiac architecture, along with vascular and autonomic function is desirable and necessary. Essential to the clinical utility of this method is the identification of novel ECG patterns that are closely linked to the subsequent development of serious heart rhythm disturbances and fatal cardiac events.

[0004] The current algorithms employed in signal processing of biological signals are rudimentary and can be improved upon using contemporary techniques to evaluate the phase space changes to correlate it to the desired clinical outcome. However, three dimensional phase space is not available from the collected data and hence extra dimensions must be intelligently inferred from the data available. Further, there is a distinct lack of non-invasive tools available to enhance the identification of subjects with cardiac abnormalities to allow the leveraging of that information for diagnosis, prognosis and research.

SUMMARY OF THE DISCLOSURE

[0005] Abnormal cardiac rhythms are associated with the breakdown of spatially coherent activity in heart tissue. Many modeling studies have linked them with the onset of spatiotemporal chaos in the electrophysiological activity of the heart, through the creation and subsequent breakup of spiral or scroll waves. The present disclosure has been designed to evaluate the electrical activity of the heart to assess the presence of heart dysfunction. Quasiperiodic biological data exhibits complex nonlinear variability and morphological characteristics that cannot be efficiently captured by traditional modeling techniques. Two approaches are used to study the dynamical and geometrical properties of the biological data under study. Prior to the application of these techniques, the dimensionality of the data must be increased from one to at least three, using a noiseless fractional derivative based phase space reconstruction. The first method uses a modified Matching Pursuit (MP) algorithm to find a noiseless model of the data that is sparse and does not assume periodicity of the signal. After the model is derived, various metrics are extracted to localize different aberrancies of the heart. In the second method, space-time domain is divided into a number of regions; the density of the signal is computed in each region and input to a machine learning algorithm to associate them to the target under study.

[0006] The present disclosure generally relates to methods and techniques, both non-invasive and invasive, for characterizing cardiovascular systems from single channel biological data such as, but not limited to, electrocardiography (ECG), perfusion, bioimpedance and pressure waves. More specifically, the disclosure relates to methods that utilize data to identify targets with clinical, pharmacological, or basic research utility such as, but not limited to, disease states, cardiac structural defects, functional cardiac deficiencies induced by teratogens and other toxic agents, pathological substrates, conduction delays and defects, and ejection fraction. These targets shall be subsequently collectively referred to as cardiac dysfunction. The single channel data can be obtained from the devices such as a single channel recorder, implantable telemeter, smartphone or other smart handheld consumer devices, smart watch, perfusion sensor, clothing embedded with biometrics sensors, devices that utilize two hands for data collection, and other similar data sources.

[0007] Existing technology endeavors to correlate clinical targets with multidimensional, meaning at least three channels, data using a phase space representation and analysis, whereas the present disclosure is a non-obvious extension that enables the use of one dimensional data, which broadens and facilitates the application of these algorithms. This is contrary to many of the trends in this area of technology, which strive to collect as much data as possible (e.g. using many channels) and in doing so often render the method cumbersome in execution.

[0008] The biological (e.g. ECG) data contains detailed information on the electrophysiology of the myocardium because it represents the summation of the individual action potentials from each and every cardiac cell in syncytium and, in theory, any information that might be determined from measurement of the orchestrated cellular action potential should be available on a global level in the surface ECG. Moreover, information of myocardial tissue architecture and conduction properties is embedded in the ECG. The challenge is the discrimination of the pertinent information from ECG signals while excluding noise contamination.

BRIEF DESCRIPTION OF THE DRAWINGS

[0009] Exemplary embodiments of the present disclosure will hereinafter be described in conjunction with the following drawing figures, wherein like numerals denote like elements, and wherein:

[0010] FIG. 1 shows the steps of the model-based analysis and Space-Time analysis to derive a noiseless model of the ECG data using a modified MP algorithm and linking the dynamical Space density metrics to Sudden Cardiac Death and All-Cause Mortality risk;

[0011] FIG. 2 shows the steps of the model-based analysis to derive a noiseless model from ECG data using a modified MP algorithm;

[0012] FIG. 3 presents process of phase space transformation;

[0013] FIG. 4 illustrates the process of selecting the best dictionaries;

[0014] FIG. 5 sketches model estimation process where sparse linear expansion of selected atoms is used to mimic the ECG signal;

[0015] FIG. 6 illustrates blue trajectories as raw ECG signal plotted in 3-D vectorcardiographic manner, and red trajectories are the noiseless MP model of the blue trajectories with CSF removed;

[0016] FIGS. 7A-7F present different dynamical behaviors of Rossler system for different values of its parameter, c ;

[0017] FIG. 8 presents a mathematical model derived vectorcardiogram as in FIG. 6). The departures between red and blue trajectories represent conduction delays. It is claimed that abrupt changes in impedance responsible for the generation of sub-harmonic frequencies. Scroll wave risk, with a rapid conduction delay. Notice the blue trajectories snake around the red trajectories as shown in the circled region;

[0018] FIG. 9 presents a mathematical model derived vectorcardiogram as in FIG. 6). Vectorcardiogram of a patient after myocardial infarction who later died from sudden cardiac death. The red regions are claimed to represent arrhythmogenic potential (circled region) where a spiral wave rotates around an unexcited core;

[0019] FIG. 10 illustrates receiver-operating characteristic curves of data from the REFINE study;

[0020] FIG. 11 shows the steps of the model-based analysis to derive a noiseless model from ECG data using a modified MP algorithm and linking this to Space-time densities with can be used to create risk metrics for adverse clinical events;

[0021] FIG. 12 is a tabular summary of the results of the Sudden Cardiac Death Morphology parameter in 12 patients, stratified by randomization to atorvastatin and matching placebo;

[0022] FIG. 13 illustrates an assessment of AF severity and therapy action by Atrial Stability Risk Formula(s);

[0023] FIG. 14 is a workflow for assessing the effects (positive and negative) of various interventions that include medications, toxins, chemotherapeutic agents, surgical procedures, and other interventional procedures such as ablation, pacing, shocks and electrical therapies, and genetic therapies;

[0024] FIG. 15 depicts an example dataflow for processing one-dimensional biological data; and

[0025] FIG. 16 illustrates further details of Matching Pursuit (MP) processing in FIG. 15.

DETAILED DESCRIPTION OF THE IMPLEMENTATIONS

[0026] FIG. 1 illustrates a high-level overview of the various processes and algorithms implemented by the present disclosure to determine a sudden cardiac death or mortality risk. At 102, a model based analysis is performed. Additionally or alternatively, at 106, a space-Time based analysis may be performed at 106. At 104, a model estimation using modified MP algorithm is performed. At 108, an evaluation of Space-Time density for different regions is performed. At 110, a genetic algorithm is determined based on the output of 108. At 112, a sudden cardiac death and/or all cause mortality risk is determined. Aspects of FIG. 1 will be described in more detail below.

[0027] FIG. 2 illustrates the steps of the model-based analysis to derive a noiseless model from ECG data using a modified MP algorithm. Step 204 shows the baseline removal step, step 206 represents the phase space transformation step, step 208 presents the dictionary selection step, step 210 illustrates the model estimation step and step 212 demonstrates the subspace extraction step. In FIG. 2, at 202, N-dimensional ECG is input to a modified moving average filter to remove the baseline wander from the data. The output then goes to a phase space transformation process at 206 in which a dynamically rich system (a system that can exhibit many different dynamical behaviors at different values of its parameters) is synchronized with a physiological signal, in this case ECG data, to magnify its dynamical features. For example, Rossler is a good choice as it exhibits various behaviors for different values of its parameters. The defining equations of Rossler system are as follows:

$$\begin{cases} \dot{x} = -y - z \\ \dot{y} = x + ay \\ \dot{z} = b + z(x - c) \end{cases}$$

[0028] where a , b , and c are some constants. For fixed values of $a=b=0.1$, Rossler system exhibits the following behavior for different values of c .

TABLE 1

Value of c	Dynamical Behavior	Phase Space
$c = 4$	Period-1 Orbit	FIG. 7.A
$c = 6$	Period-2 Orbit	FIG. 7.B
$c = 8.5$	Period-4 Orbit	FIG. 7.C
$c = 8.7$	Period-8 Orbit	FIG. 7.D
$c = 13$	Sparse Chaos	FIG. 7.E
$c = 18$	Filled-in Chaos	FIG. 7.F

[0029] The ECG data is synchronized with Rossler system and then a semi-optimal state is identified that magnifies dynamical features of the physiological signal under study, FIG. 3.

[0030] In accordance with FIG. 3, at 302, the ECG is synchronized with a dynamical system. Next, at 304, a semi-optimal state that magnifies the dynamical features of the ECG is found. This creates a new ECG dataset with magnified features at 306. Synchronization refers to phase space based synchronization of the information of the ECG system to the Rossler system. The subspaces that arise from the differences between the synchronization of these two systems are the

magnifications of the dynamical features of the ECG. These subspaces comprise the new ECG dataset.

[0031] Referring again to FIG. 2, at 208, the obtained new dataset is then used to find the best dictionary(ies) that can linearly span the input. Each dictionary, D , is a family of waveforms $D=\{\phi_i|i \in I\}$ that is used to decompose the input. Various dictionaries are now available such as Wavelet Packets, Cosine Packets, Chirplets, and so on. In accordance with some implementations, complex exponential sinusoids and Time-Frequency are used over complete dictionaries synchronized by a dynamically-rich family of post-transient Rossler trajectories.

[0032] FIG. 4 illustrates the process of selecting the best dictionaries. At 402, different dynamical features, such as Lyapunov exponent and correlation dimension, of the ECG or other physiological signal is compared with a family of different dictionaries. At 404, those dictionaries that have most similarity to the dataset is selected to be used for model estimation, i.e. the member atoms of the selected dictionaries form the set of atoms that will be used in MP. The dynamical features of the ECG are compared with all the dictionaries and the dictionaries are selected that have the most similarity with the data

[0033] Referring again to FIG. 2, at 210, the next step is to find a sparse model (extracted from the selected dictionaries) for the physiological signal under study. For example, MP may be used, which is an iterative process that, at each step, chooses the dictionary atom that best correlates with the signal. This process continues until a pre-defined stopping condition occurs, such as if the number of terms exceeds a threshold and/or the distance of the model and the target in the search space is smaller than a threshold. Finally, the coefficients of the selected atoms are computed.

[0034] FIG. 5 sketches the process of model estimation using MP. At 502, the correlation of the ECG dataset with all the atoms in the selected dictionaries is computed. This information, along with the pre-evaluated cross correlation of atoms (504) is used to pick the best atom in each iteration in order to minimize a pre-defined cost function that quantifies a distance in a metric space, such as mean absolute error or mean square error, between the model and the target waveform. After the addition of each atom at 506, a stopping condition is consulted at 508 to determine whether further iterations of the algorithm are necessary. This stopping condition could take into account factors such as the number of atoms already present in the model and the fit of the model against the target waveform. If the stopping condition has been satisfied at 508, the algorithm proceeds to 510 to perform a calculation of the coefficients of the atoms. These coefficients are reclusively calculated using information captured during the iteration of the algorithm in order to optimize the fit of the model against the input waveform. The process begins with reading pre-computed atom correlations and computing the correlations between the input waveform and the atoms. Atoms are iteratively added until the stopping condition is satisfied, at which point the coefficients are calculated

[0035] Returning to FIG. 2, at 212, different subspaces are extracted from the derived model. Various subspaces, namely CSF trajectory, quasi-periodic and chaotic subspaces, low/high-energy subspace, and fractional derivative of the low/high-energy subspace are extracted from the derived model; however, possible subspaces that could be extracted are not

limited to these examples. Each of which represents a dynamical abnormality in the tissue architecture, structure and function.

[0036] The last 20% of the selected atoms are used to form a “low energy subspace” signal corresponding to each of the leads. These low energy signals can be called $x(t)$, $y(t)$, and $z(t)$ assuming 3 leads.

[0037] There are various time domain and frequency domain signal processing techniques which are being used for the analysis of ECG signals to obtain more detailed information. Time domain techniques alone are incapable of quantifying certain fluctuation characteristics of a number of pathologies related to the ECG signal. For example, with regard to the heart, traditional methods for performing frequency-domain analysis of surface ECG signals, such as the Fourier transform, are limited since they do not address the aperiodic random nature of biological and electromagnetic noise or the variation between patients. For example, in case of VT or VF, the heart generates very complex ECG waveforms that have a large variation in morphologies. Dominant frequency analysis on these ECGs can be problematic since non-linear dynamic systems can appear to generate random noise. Discrete fast Fourier transforms and wavelet analysis have been shown experimentally to be incapable of detecting deterministic chaos in the presence of strong periodicity which tends to obscure the underlying non-linear structures. Thus, the detection of complex sub-harmonic frequencies thought to exist in patients at risk for cardiac arrhythmias requires dynamic non-linear analyses. CSF are similarly thought to exist in other types of physiological signals and may be indicative of other pathophysiology not otherwise detectable from the ECG signal using prior methods.

[0038] 3-D Visualization

[0039] The 3-D phase space plot localizes the presence of CSF related to structurally or electrically abnormal heart tissue. The CSF can be measured as a time delay and as a 3-D trajectory in the atrial and ventricular sub-spaces. CSF trajectory is associated with those components of the ECG that could not be captured by the dictionary, i.e. there is no linear combination of the atoms of the selected dictionaries that can represent the CSF trajectory. FIG. 7 shows a CSF removed trajectory (in red) derived from an MP model of ECG.

[0040] The 3-D phase space plot of the present disclosure may be displayed by any type of computing device, including, but not limited to, desktop computers, workstation computers, server computers, cloud computing devices, tablet devices, smart phones, and mobile computing devices.

[0041] Altered atrial and ventricular function is linked to the development of physiological changes that could result in complex sub-harmonics and in high dimensional changes over a series of cardiac cycles. FIG. 7 illustrates one embodiment of a method whereby MP can be used to generate 3-D vectorgram diagrams to describe the complex sub harmonics linked to structural change in the form of anisotropic propagation and localize these electrophysiological changes to correlate this with the development of serious heart rhythm disturbances, sudden cardiac death, other modes of death, and all-cause mortality.

[0042] The last 20% of the selected atoms are used to form a “low energy subspace” signal corresponding to each of the leads. These low energy signals can be called $x(t)$, $y(t)$, and $z(t)$ assuming 3 leads.

[0043] It is likely that many physical phenomena can be modeled more accurately and effectively using fractional

derivatives versus classical integer derivative-based models. Traditional integer order derivatives depend only on the local behavior of a function, while fractional derivatives depend also on the whole history of the function. Fractional derivatives have the unique properties of both a derivative (change) and an Integral (history). Considerable focus on fractional calculus has been simulated by the applications of this concept in different areas of physics and engineering over the last few decades. In this embodiment is a method for detecting complex beat-to-beat sub-harmonic structures in ECG and other physiological signals based on digital differentiation and integration of fractional order. Since these signals are mathematically modeled as a linear combination of the selected atoms, they can be differentiated and integrated of fractional order. Let $x'(t)$, $y'(t)$, and $z'(t)$ be their integer order derivatives respectively, these derivatives and their ratios measure instability only at a local point of the signal and therefore are poor measures of stability for long complex ECG signals with significant beat to beat variability. An alternative to an integer derivative is the use of a fractional calculus to detect abnormal CSF signals in a physiological signal based on its past history.

[0044] Low-energy component subspace (made from the last 20% terms found by MP) can be used to noiselessly find the fractional derivative of this component, since it is a linear combination of selected atoms, and this fractional derivative can be useful to distinguish patients likely versus unlikely to suffer serious heart rhythm disturbances, sudden cardiac death, other modes of death, and all-cause mortality. In addition, there are some useful fractional properties to consider. Thus suppose that $x(t)$, $y(t)$, and $z(t)$ are respectively the X, Y, and Z coordinates of the low-energy component and let $x^\alpha(t)$, $y^\alpha(t)$, and $z^\alpha(t)$ be the irrational fractional derivative of order α that can be any real (or complex) number. Then the magnitude of these irrational fractional derivatives can indicate instability when large and positive. Consider the regions when the irrational fractional derivatives are positive, in such regions, the low energy reentrant wavelets have the potential to generate the arrhythmias responsible for many cases of sudden cardiac death (VT and VF) and other serious clinical events.

[0045] The magnitude of an irrational fractional derivative can be used to help highlight regions of arrhythmogenic potential in the ECG strip.

[0046] Numeric patterns of these irrational fractional derivatives relative to the conduction delays have the potential to distinguish between different arrhythmia mechanisms and modes of death.

[0047] In the second method, space-time domain is divided into a number of regions (12 or more regions) from the center of mass; the density of the baseline-removed ECG signal is computed in each region. These values contain specific information about the non-linear variability of the ECG signal that could be linked to a physiological abnormality such as abnormal calcium channel cycling. Calcium ion (Ca^{++}) is a universal intracellular messenger. In muscle, Ca^{++} is best known for its role in contractile force activation. However, in recent years the critical role of Ca^{++} in other myocyte processes has become increasingly clear. Ca^{++} signaling in cardiac myocytes, as pertaining to electrophysiology (including temporal spatial action potentials and arrhythmia), is linked to excitation-force contraction coupling, modulation of contractile function due to systemic resistance (blood pressure), energy supply-demand balance (including mitochondrial function),

cell death (apoptosis), and transcription regulation. It has been hypothesized that Ca^{++} -dependent ion pump variability occurs aperiodically in pathological cardiac myocytes, this creates significant microvolt variations in the various ECG components (P, Q, R, S, T, U and other) that can be tracked and localized by linking the space-time density structures to 12 or more regions. It should be noted a simple derivative or its ratios are insufficient to characterize space-time density structures over many cardiac cycles. It has been hypothesized that Ca^{++} -dependent ion pump variability occurs aperiodically in pathological cardiac myocytes, this creates microvolt or larger variations in ECG morphology that can be tracked and localized by linking the dynamical space density structures into 12 or more regions.

[0048] Genetic algorithms belong to class of evolutionary algorithms, which generate solutions to optimization problems using techniques inspired by the biological processes of chromosome: separation, crossover, mutation and inheritance occurring in meiosis. Alterations in the genetic code can occur via mutation and/or crossover, and are then propagated in the population via inheritance and selection. The 12 variables from the signal density become terms in an equation and these terms are selected in many different nonlinear combinations (sin, cos, cos h, sin h, Rossler functions, product, division, addition, subtraction, Gaussian, exponential functions) candidates based on the genetic operators inheritance, mutation, selection, and crossover. This generates many offspring function combinations that are evaluated and optimized by freezing all but one variable. The unfrozen variable is optimized to reduce the absolute error of the model. The other variables are optimized and frozen in sequence until all 12 terms have the lowest error. The fitness function seeks to find the solution with the lowest absolute error. This process continues until the highest-ranking solution's fitness has reached a plateau such that successive iterations no longer produce better results. These 12 quantities are input into a genetic algorithm and are modeled to link sudden cardiac death risk and all-cause mortality from the ECG data of patients that died of each cause respectively. The region decision boundaries are agnostic to clinical ECG landmarks commonly referred to as PQRST. The result is two nonlinear nested sinusoidal Gaussian equations for the heart that links the 12 dimensional dynamical space density metrics to outcome ECG data. These same ECG metrics can be used to calculate and predict the risk of serious heart rhythm disturbances, sudden cardiac death, other modes of death, and all-cause mortality.

[0049] Space-time quantities can be mapped to complex phase space differences in 12 dimensional space. Spatial changes in the phase space matrix can be extracted using a non-Fourier or Fourier nD fractional integral summation across all ECG leads on the derived MP model (Typically the order of fractional integral could be -1.5 or -2.5 or any irrational, complex or real number), that creates the 12 dimensional dynamical space density metrics. These metrics for the ventricle are modeled using a genetic algorithm to link nonlinear nested sinusoidal Gaussian equations with 12 independent space-time density metrics variables to associate them with serious heart rhythm disturbances, sudden cardiac death, other modes of death, and all-cause mortality.

[0050] The output of these equations is a risk metric for arrhythmias. Arrhythmogenesis in heart tissue, which is electrically and mechanically coupled excitable media, requires mathematical stability analysis for risk assessment. The

occurrence of critical chaotic instabilities can be anticipated as future events by using stability analysis that reveals the generation and destruction of intermittent chaotic states. These unstable states increase the signal density in high dimensional space resulting in a strengthening of the strange attractor that can be linked to a pathological process intrinsic and extrinsic to the heart. The dynamical signal density in 12 dimensional space or higher is used to create 10 or more non-linear phase space cluster clouds. Computation for phase space dynamical signal densities can be reduced by using 3-D instead of 12 dimensional space in constrained CPU environments like mobile computers. These cluster clouds are agnostic to the traditional ECG landmarks. The moment center is computed for the normalized three or higher dimensional ECG manifold. Dynamical cloud signal densities (SD) are a mixture of Gaussian sinusoidal functions that radiate from the moment center to the outer boundary of the manifold. This allows for mixtures of Integrals of Gaussian sinusoidal and hyperbolic cosine distributions to form complex decision boundaries that can be used to predict the risk for adverse clinical outcomes as shown in the following equations. It is explicitly noted that the formulas below are being provided solely as examples, and should not be construed as limiting the disclosure, as recited in the claims, as variations, modifications, and adaptations of the equations below to achieve the functions of the present disclosure are considered to be within the scope of the appended claims.

[0051] Equation 1 & 2:

$$\begin{aligned} \text{Risk of sudden cardiac death} = & (4+6*\text{gauss}((12100- \\ & 82170*SD1)/(SD2+\sin h(43.48*SD3*\text{gauss}(0. \\ & 1611/(SD4*\text{gauss}(SD5)))+(6.172+9.258*\text{gauss} \\ & (SD6/\cos h(709*\text{gauss}(-2.163*SD7^2/SD8))))/ \\ & \cos h(\text{gauss}(SD9*\text{gauss}(SD10/SD10))))+4. \\ & 054*\text{gauss}(1.954*((6.172+9.258*\text{gauss}(SD6/\cos \\ & h(709*\text{gauss}(-2.163*SD7^2/SD8))))/ \cos h(\text{gauss} \\ & (SD9*\text{gauss}(SD10/SD10))))-11.82))*\text{gauss} \\ & (SD12*SDCSF1^2*SDCSF2/(SD2+ \\ & SDCSF3*SDCSF4)))^2)-4*\text{gauss}(SDCSF2*\sin \\ & h(43.48*SD3*\text{gauss}(0.1611/(SD4*\text{gauss} \\ & (SD5)))+(6.172+9.258*\text{gauss}(SD6/\cos \\ & h(709*\text{gauss}(-2.163*SD7^2/SD8))))/ \cos h(\text{gauss} \\ & (SD9*\text{gauss}(SD10/SD10))))+4.054*\text{gauss}(1.954* \\ & ((6.172+9.258*\text{gauss}(SD6/\cos h(709*\text{gauss}(-2. \\ & 163*SD7^2/SD8))))/ \cos h(\text{gauss}(SD9*\text{gauss} \\ & (SD10/SD10))))-11.82))*\text{gauss} \\ & (SD12*SDCSF1^2*SDCSF2/(SD2+ \\ & SDCSF3*SDCSF4))))*\cos h(SDCSF5)*\sin h(\sin \\ & h(43.48*SD3*\text{gauss}(0.1611/(SD4*\text{gauss} \\ & (SD5)))+(6.172+9.258*\text{gauss}(SD6/\cos \\ & h(709*\text{gauss}(-2.163*SD7^2/SD8))))/ \cos h(\text{gauss} \\ & (SD9*\text{gauss}(SD10/SD10))))+4.054*\text{gauss}(1.954* \\ & ((6.172+9.258*\text{gauss}(SD6/\cos h(709*\text{gauss}(-2. \\ & 163*SD7^2/SD8))))/ \cos h(\text{gauss}(SD9*\text{gauss} \\ & (SD10/SD10))))-11.82))*\text{gauss} \\ & (SD12*SDCSF1^2*SDCSF2/(SD2+ \\ & SDCSF3*SDCSF4))))+SDCSF6*\text{gauss} \\ & (SDCSF7+SDCSF1-4.834)+SDCS7*\text{gauss}(0. \\ & 9287+0.1436*SDCSF7^2+0.1436*SDCSF1^2-0. \\ & 596*SDCSF7-0.596*SDCSF1))*\text{gauss} \\ & ((SDCSF8*SDCSF8*SDCSF9*SDCSF2-0. \\ & 5097*SDCSF8*SDCSF10)/SDCSF11) \end{aligned}$$

$$\begin{aligned} \text{RISK of all cause mortality} = & f\text{gauss}(c1*\cos(SD10+ \\ & SD9+SD8)+\text{gauss}(c2*SD10-c2*\cos h(c4-SD7- \\ & SD2*\text{gauss}(SD1)))) \end{aligned}$$

[0052] SD=cloud space-time signal density

[0053] SDCSF=cloud space-time signal density complex-sub-harmonic-frequency

[0054] c=real number constants

[0055] Ventricular arrhythmia is a metric that gauges the risk of sustained VT and other more serious rhythms that have the potential to produce spontaneous initiation of a serious arrhythmia. Other metrics gauge the risks of various modes of death and all-cause mortality.

[0056] The methods described can also be used to assess therapeutic effectiveness as illustrated by the following data and workflow, as shown in FIG. 14. FIG. 14 illustrates a workflow for assessing the effects (positive and negative) of various interventions that include medications, toxins, chemotherapeutic agents, surgical procedures, and other interventional procedures such as ablation, pacing, shocks and electrical therapies, and genetic therapies. At 1402, a baseline measurement is captured before any therapy is applied and the associated risk is computed at 1404. At 1406, therapy is then applied and the patient's physiological is captured again at 1408. The risk is then computed at 1410 against the second measurement and the two risk scores are compared at 1410 to determine the utility of the therapy.

[0057] Since statins are known to reduce the risk of sudden cardiac death the effect of atorvastatin versus placebo on one of the risk assessment parameters, morphology score, was assessed. As demonstrated in the REFINE cohort analysis (FIG. 10), lower scores indicate a lower risk of sudden cardiac death. The group of patients included in this analysis had hypertrophic cardiomyopathy and were randomized to receive atorvastatin 40 mg daily or matching placebo for 12 months.

[0058] FIG. 10 illustrates receiver-operating characteristic curves of data from the REFINE study (Exner et al., Journal of the American College of Cardiology 2007; 50:2275-84). Upper panel provides the receiver operating characteristic curve (ROC) for the combination of traditional ECG parameters shown to be optimal in that study in predicting the primary outcome of cardiac death or non-fatal cardiac arrest. The lower panel shows the results for the proposed method to identify patients at risk of this same outcome. The area under the ROC curve is significantly larger (p=0.006) for the proposed method (lower panel) as compared to the prior approach (upper panel) when the upper 45 patients characterized at risk using the proposed method is compared to the 45 patients with an ejection fraction under 50% plus impaired heart rate turbulence and abnormal T wave alternans. Moreover, the proposed method results in augmented positive as well as negative predictive accuracy;

[0059] FIG. 11 Shows the steps of the model-based analysis to derive a noiseless model from ECG data using a modified MP algorithm and linking this to Space-time densities which can be used to create risk metrics for adverse clinical events. The ECG data is collected and modeled using MP, followed by a transformation in 12 dimensional space. The space is then divided in 12 or more regions and the signal density is computed in each region. Finally, the 12 or more signal densities are inputted into a genetic algorithm to link the patients who died of sudden death to their corresponding signal densities. This linking is repeated for patients whose death was classified as all-cause.

[0060] As shown, morphology scores significantly improved over time in the atorvastatin-treated patients, but did not change in the patients who were randomly assigned to placebo (FIG. 12). The disclosed methods are applied to generate formulas to assess risk for atrial arrhythmia, such as AF. FIG. 13 shows the atrial risk score of a patient diagnosed with AF, while on the standard of care treatment, and when off

the standard of care treatment. The risk score changes by a factor of 10, indicating this risk score is tracking a) the severity of the AF, and b) the effectiveness of the drug regimen being used to treat the patient. Assessing atrial risk while in sinus rhythm is poorly understood. It is hypothesized that proximal AF is driven by low energy reentrant circuits are insufficient to activate AF continuously. These low energy signals can be detected and quantified using space density metrics described above (see below for exemplar atrial risk formula). These two examples provides evidence that favorable drug effects can be identified using the disclosed methods.

$$\begin{aligned} \text{Atrial Risk Score} = & 4 + 6 * \text{gauss}((12100 - 82170 * \text{SD1}) / \\ & (\text{SD2} + \sin h(43.48 * \text{SD3} * \text{gauss}(0.1611 / \\ & (\text{SD4} * \text{gauss}(\text{SD5})))) + ((6.172 + 9.258 * \text{gauss}(\text{SD6} / \\ & \cos h(709 * \text{gauss}(-2.163 * \text{SD12}^2 / \text{SD1})))) / \cos \\ & h(\text{gauss}(\text{SD2} * \text{gauss}(\text{SD3} / \text{SD4}))) + 4.054 * \text{gauss}(1. \\ & 954 * ((6.172 + 9.258 * \text{gauss}(\text{SD6} / \cos h(709 * \text{gauss} \\ & (-2.163 * \text{SD12}^2 / \text{SD1})))) / \cos h(\text{gauss} \\ & (\text{SD2} * \text{gauss}(\text{SD3} / \text{SD4})))) - 11.82)) * \text{gauss} \\ & (\text{SD5} * \text{SD6}^2 * \text{SD12} / (\text{SD2} + \text{SD1} * \text{SD2}))^2) - \\ & 4 * \text{gauss}(\text{SD12} * \sin h(43.48 * \text{SD3} * \text{gauss}(0.1611 / \\ & (\text{SD4} * \text{gauss}(\text{SD5})))) + ((6.172 + 9.258 * \text{gauss}(\text{SD6} / \\ & \cos h(709 * \text{gauss}(-2.163 * \text{SD12}^2 / \text{SD1})))) / \cos \\ & h(\text{gauss}(\text{SD2} * \text{gauss}(\text{SD3} / \text{SD4}))) + 4.054 * \text{gauss}(1. \\ & 954 * ((6.172 + 9.258 * \text{gauss}(\text{SD6} / \cos h(709 * \text{gauss} \\ & (-2.163 * \text{SD12}^2 / \text{SD1})))) / \cos h(\text{gauss} \\ & (\text{SD2} * \text{gauss}(\text{SD3} / \text{SD4})))) - 11.82)) * \text{gauss} \\ & (\text{SD5} * \text{SD6}^2 * \text{SD12} / (\text{SD2} + \text{SD1} * \text{SD2})) * \cos \\ & h(\text{gauss}1 \text{ Vz}(8)) * \sin h(\sin h(\sin h(43. \\ & 48 * \text{SD3} * \text{gauss}(0.1611 / (\text{SD4} * \text{gauss}(\text{SD5})))) + ((6. \\ & 172 + 9.258 * \text{gauss}(\text{SD6} / \cos h(709 * \text{gauss}(-2. \\ & 163 * \text{SD12}^2 / \text{SD1})))) / \cos h(\text{gauss}(\text{SD2} * \text{gauss} \\ & (\text{SD3} / \text{SD4}))) + 4.054 * \text{gauss}(1.954 * ((6.172 + 9. \\ & 258 * \text{gauss}(\text{SD6} / \cos h(709 * \text{gauss}(-2. \\ & 163 * \text{SD12}^2 / \text{SD1})))) / \cos h(\text{gauss}(\text{SD2} * \text{gauss} \\ & (\text{SD3} / \text{SD4})))) - 11.82)) * \text{gauss} \\ & (\text{SD5} * \text{SD6}^2 * \text{SD12} / (\text{SD2} + \text{SD1} * \text{SD2})))) \end{aligned}$$

[0061] Characterizing Cardiovascular Systems from One-Dimensional Channel Data

[0062] FIG. 15 illustrates example operations performed in a model-based analysis to derive a noiseless model from biological data using a modified MP algorithm and one-dimensional biological data 1502. At 1504, the one-dimensional biological data 1502 may be prepared using an operation such as threshold wavelet denoising. For example, biorthogonal 3.3 wavelet may be used as it is effective at denoising the one-dimensional biological data 1502; however, other options are possible to denoise the data 1502. At 5016, a baseline is removed and additional dimensions (at least two) are constructed by taking fractional derivatives to define a phase space system, which in a general sense is known as a phase space reconstruction (PSR).

[0063] At 1508, a MP process is performed on the data. The MP process is shown in greater detail with reference to FIG. 16.

[0064] An alternative to an integer derivative is the use of a fractional calculus to detect abnormal components in a signal based on its past history. Traditional integer order derivatives depend on the local behavior of a function, while fractional derivatives depend on the whole history of the function. In the last few decades, considerable focus on fractional calculus has been stimulated by the applications of this concept in different areas of physics and engineering. Integer derivatives and their ratios measure instability only at a local point of the signal and therefore are poor measures of stability for complex biological signals. For this reason, the use of fractional derivatives in the PSR are attractive in the scope of this

disclosure. Regarding the computation of the fractional derivatives, the signal's frequency components can be phase shifted by an amount determined by the order of the derivative. FFT can be used to convert to the frequency domain.

[0065] At 1602, the data transformed by PSR is then used to find the best dictionary(ies) that can linearly span the input. Each dictionary, D, is a family of waveforms $D = \{\phi_i | i \in I\}$ that is used to decompose the input. Various dictionaries are now available such as Wavelet Packets, Cosine Packets, Chirplets, and so on. In this disclosure, complex exponential sinusoids and time-frequency over complete dictionaries are used. Different dynamical features, such as Lyapunov exponent and correlation dimension, of the dataset of signals are compared with a family of different dictionaries for the purpose of dictionary selection. Those dictionaries that have most similarity to the dataset are selected to be used for model estimation.

[0066] Next, at 1604, a sparse model is determined (as extracted from the selected dictionaries) for the signal under study. MP is an iterative process that, at each step, chooses the dictionary atom that best correlates with the signal, taking into account the pre-evaluated cross correlations between the atoms. This atom selection continues until a pre-defined stopping condition occurs, such as if the number of terms exceeds a threshold and/or the distance of the model and the target in the search space is smaller than a threshold. Finally, the coefficients of the selected atoms are computed.

[0067] At 1606, different subspaces are extracted from the derived model. Various subspaces, namely complex-sub-harmonic-frequencies (CSF) trajectory, quasi-periodic and chaotic subspaces, low/high-energy subspace, and fractional derivative of the low/high-energy subspace are extracted from the derived model; however, possible subspaces that could be extracted are not limited to these examples, each of which represents a dynamical abnormality in the activity of the heart.

[0068] There are various time domain and frequency domain signal processing techniques which are being used for the analysis of biological signals to obtain more detailed information. Unfortunately, the time domain techniques are incapable of quantifying certain fluctuation characteristics of a number of pathologies related to the biological signal. For example, with regard to the heart, traditional methods for performing frequency-domain analysis of ECG signals, such as the Fourier transform, are limited since they do not address the aperiodic random nature of biological and electromagnetic noise or the variation between patients. Discrete fast Fourier transforms and wavelet analysis have been shown experimentally to be incapable of detecting deterministic chaos in the presence of strong periodicity which tends to obscure the underlying non-linear structures. Thus, the detection of complex sub-harmonic frequencies which are thought to exist in abnormalities such as arrhythmia requires dynamic non-linear analyses such as the techniques described in this disclosure.

[0069] Approximately the last 20% of the terms selected by MP compose the low-energy component subspace, which has some useful properties. First, the fractional derivative of this component can be noiselessly determined, since it is a linear combination of selected atoms, and this fractional derivative can be useful to distinguish different disease states. In addition, there are some useful fractional properties to consider. Thus suppose that $x(t)$, $y(t)$, and $z(t)$ are respectively the X, Y, and Z coordinates of the low-energy component and let $x^\alpha(t)$,

$y^\alpha(t)$, and $z^\alpha(t)$ be their irrational fractional derivative of order that can be any real (or complex) number. Then the magnitude of these irrational fractional derivatives can indicate instability when large and positive. These instabilities can be quantified and used as system identification features to associate the signal to the target outcome in a machine learning algorithm.

[0070] Returning to FIG. 15, at 1510, the space-time domain is divided into a number of regions (which is largely determined by the signal length) and the density of the various time series (including the noiseless signal and the MP model) is computed in each region. These values contain specific information about the non-linear variability of the biological signal that could be linked to electrophysiological abnormality and calcium channel cycling. Calcium (Ca) ion is a universal intracellular messenger. In muscle, Ca ion is best known for its role in contractile force activation. However, in recent years the critical role of Ca ion in other myocyte processes has become increasingly clear. Calcium ion signaling in cardiac myocytes, as pertaining to electrophysiology (including temporal spatial action potentials and arrhythmia), is linked to excitation-force contraction coupling, modulation of contractile function due to systemic resistance (blood pressure), energy supply-demand balance (including mitochondrial function), cell death (apoptosis), and transcription regulation. It has been hypothesized that Ca-dependent ion pump variability occurs aperiodically in pathological cardiac myocytes, this creates significant microvolt beat to beat variations in the P wave, the QRS and T wave morphology of the ECG signal that can be tracked and localized as an electrophysiological abnormality by linking the space time density structures to a specified number of regions.

[0071] The output of the components of the disclosure described up to this point can be thought of as a vector of features unique to each signal. In the training phase where the signal is associated to a known value of the target, which can include, but is not limited to, disease states, cardiac structural defects, functional cardiac deficiencies induced by teratogens and other toxic agents, pathological substrates, conduction delays and defects, and ejection fraction, the map between the features and the target is estimated using machine learning algorithms.

[0072] At 1512, machine learning algorithms are used to associate the feature vectors to the target to create a predictor, such that when the feature vector of a previously unseen signal is presented to the predictor during the prediction phase it will output an inference regarding the value of the target of that signal. There are several suitable algorithms that can be used to perform this learning computation, including, but not limited to, genetic algorithm mediated map generation and artificial neural networks, both of which are inspired by biology.

[0073] Genetic algorithms belong to class of evolutionary algorithms, which generate solutions to optimization problems using techniques inspired by natural evolution in genetics of meiosis cell divisions with DNA. Alterations in the genetic code can occur in a genetic pool of progeny with genetic operators such as inheritance, mutation, selection, and crossover. The specified number of variables from the signal density become terms in an equation and these terms are selected in many different nonlinear combinations (basic arithmetic operations, trigonometric and inverse trigonometric functions, Rossler functions, Gaussian, exponential functions, squashing function) candidates based on the genetics

operators such as inheritance, mutation, selection, and crossover. This generates many offspring function combinations which are evaluated and optimized by freezing all but one variable. The unfrozen variable is optimized to reduce an error metric of the model. The other variables are optimized and frozen in sequence until all terms have the lowest error. The fitness function seeks to find the solution with the lowest absolute error. This process continues until the highest ranking solution's fitness has reached a plateau such that successive iterations no longer produce better results. The results of the application of the genetic algorithm is an estimation of the mapping between the features and the target attribute. The genetic learning algorithm is employed as described by the general framework above.

[0074] The artificial neural network (ANN) is another machine learning algorithm which is suitable in the context of the general learning framework described for this disclosure. ANN is also biologically inspired as it is meant to emulate the spatial summation of action potentials to propagate information in biological neural networks of the central nervous system. The ANN is computationally represented as a graph, where the nodes in the graph are neurons containing activation functions (typically sigmoidal) and they are connected by weighted edges. Typically ANNs has an input layer of neurons which receives the feature vector, at least one hidden layer, followed by an output layer which represents the predicted value of the target. ANNs, when properly configured, have the powerful property of a universal function approximator, meaning it can approximate to arbitrary precision any function with compact range and domain using a finite number of neurons. The ANN is trained to predict the target attribute as a non-linear combination of the features using the backpropagation algorithm, in which the features are passed through the network, the outputs observed, and the errors propagated backwards through the graph in order to update the weights such that the prediction error is lower. All of the features are passed through the ANN a number of iterations, which is described as the number of training epochs. There are other parameters embedded in the implementation of the ANN which allow the predictor to generalize better to new data. The ANN algorithm is employed as described by the general framework above.

[0075] Having thus described several embodiments of the claimed invention, it will be rather apparent to those skilled in the art that the foregoing detailed disclosure is intended to be presented by way of example only, and is not limiting. Many advantages for non-invasive method and system for location of an abnormality in a heart have been discussed herein. Various alterations, improvements, and modifications will occur and are intended to those skilled in the art, though not expressly stated herein. Any alterations, improvements, and modifications are intended to be suggested hereby, and are within the spirit and the scope of the claimed invention. Additionally, the recited order of the processing elements or sequences, or the use of numbers, letters, or other designations therefore, is not intended to limit the claimed processes to any order except as may be specified in the claims. Accordingly, the claimed invention is limited only by the following claims and equivalents thereto.

What is claimed is:

1. A method for identifying cardiac dysfunction, comprising:

obtaining single channel biological data for the heart; and processing solely the single channel biological data to detect cardiac dysfunction.

2. The method of claim 1, wherein the step of processing the data includes the creation of a phase space diagram from the data using a phase space reconstruction with fractional derivatives.

3. The method of claim 1, wherein the single channel biological data comprises at least one heart beat cycle and wherein the abnormality in the heart is detected within a predetermined time interval within the heart beat cycle.

4. The method of claim 3, wherein the predetermined time interval is 10 seconds, and wherein the predetermined time interval is used in detecting cardiac dysfunction.

5. The method of claim 3, wherein the heart beat cycle corresponds to a vector sum of electrical activation of the heart, and a pathway is used with N dimensional space density time information in determining presence of cardiac dysfunction.

6. The method of claim 5, wherein variables from signal density become feature vectors which are associated to cardiac dysfunction indicator target attributes using machine learning algorithms.

7. The method of claim 6, wherein the machine learning algorithms include a genetic algorithm mediated map generation or artificial neural network.

8. The method of claim 6, further comprising associating an effectiveness of patient therapies including an effectiveness of cardioactive medications.

9. The method of claim 6, further comprising evaluating cardiotoxicity and teratogenic nature of medications.

10. The method of claim 1, wherein the method identifies at least one of disease states, cardiac structural defects, functional cardiac deficiencies induced by teratogens and other toxic agents, pathological substrates, conduction delays and defects, and ejection fraction in a mammalian heart.

11. The method of claim 1, further comprising obtaining the single channel biological data from one of a single channel recorder, an implantable telemeter, a smartphone or other smart handheld consumer devices, a smart watch, a perfusion sensor, or clothing embedded with biometrics sensors.

* * * * *

专利名称(译)	用于从单通道数据表征心血管系统的方法和系统		
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[标]申请(专利权)人(译)	ANALYTICS FOR LIFE		
申请(专利权)人(译)	ANALYTICS FOR LIFE		
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发明人	BURTON, TIMOTHY RAMCHANDANI, SHYAMLAL HOWE-PATTERSON, MATTHEW YAZDI, MOHSEN GUPTA, SUNNY		
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摘要(译)

使用从受试者获得的单通道生物学数据鉴定和风险分层疾病状态，心脏结构缺陷，由致畸剂和其他毒性剂引起的功能性心脏缺陷，病理基质，传导延迟和缺陷以及射血分数的方法。可以使用修改的匹配追踪 (MP) 算法来找到稀疏的数据的无噪声模型，并且不假设信号的周期性。在导出模型之后，提取各种度量和子空间以表征心脏系统。在另一种方法中，时空域被划分为多个区域 (其主要由信号长度确定) ，在每个区域中计算信号的密度并输入到学习算法以将它们与期望的心脏功能障碍相关联。指标目标。

NON-INVASIVE METHOD AND SYSTEM FOR CHARACTERIZING CARDIOVASCULAR SYSTEMS

