Belief χ^2 Divergence-based Dynamical Complexity Analysis for Biological Systems

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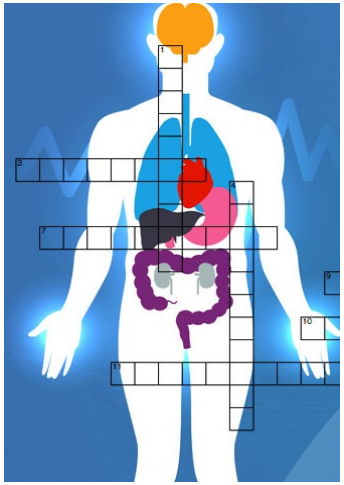
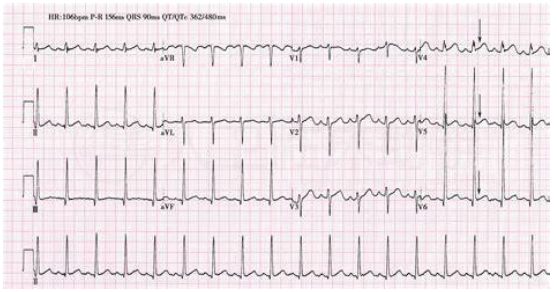
Outline

Background



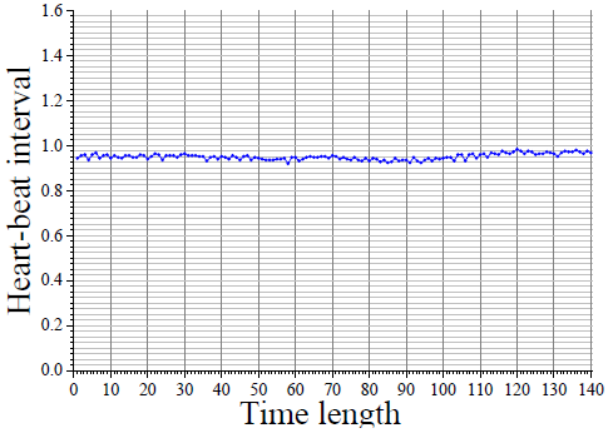
Biological systems

EEG signals



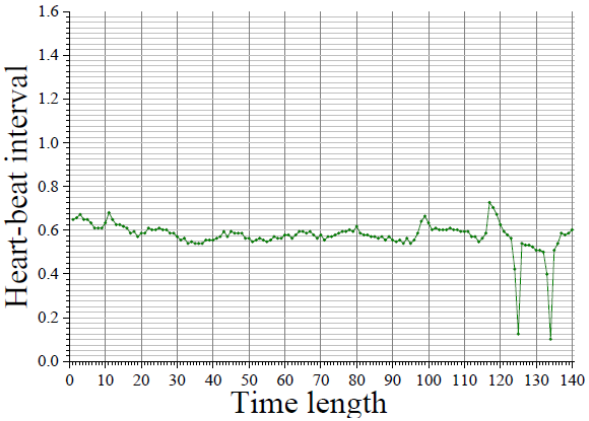
Cardiac inter-beat signals

Background



Pathological subjects

More information



Healthy subjects

- **Recent works for uncertain information management:**

Deng entropy

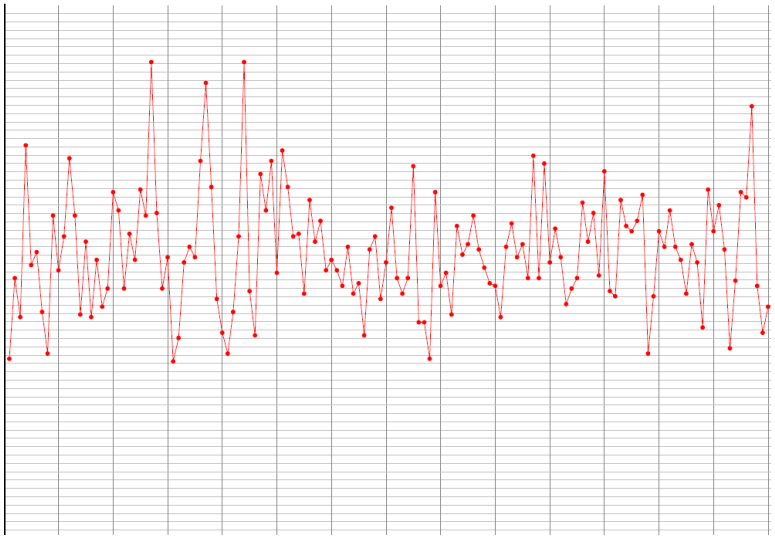
Z-network

Information quality

Belief entropy

TDBF

Motivation



Sophisticated structure

↓

Feature extraction based on Dempster-Shafer evidence theory — BPAs

↓

Process the time series data points whether they are on the boundaries of time slice

Preliminaries

- **Dempster-Shafer evidence theory**

Definition 1 (Framework of discernment).

Let Θ be a set that consists of r mutually exclusive and collectively exhaustive events,

$$\Theta = \{e_1, e_2, \dots, e_i, \dots, e_r\}$$

which indicates the framework of discernment. The power set 2^Θ is used to describe uncertainty which can be defined as follows:

$$2^\Theta = \{\emptyset, \{e_1\}, \dots, \{e_r\}, \{e_1, e_2\}, \dots, \{e_1, e_2, \dots, e_h\}, \dots, \Theta\},$$

where $\emptyset$ indicates the empty set.

Definition 2 (Mass function).

Based on the frame of discernment Θ, m as a mass function, also known as BPA, is a mapping from 2^Θ to [0,1] which is defined as:

$$m: 2^\Theta \to [0,1].$$

Because events must arise from propositions in the framework of discernment and empty set is not the cause of the events, it abides the rule of

$$\sum_{E \in 2^\Theta} m(E) = 1 \text{ and } m(\emptyset) = 0.$$

If $m(E) > 0$ E is a focal element.

Preliminaries

- ***SEB*χ^2 divergence measure**

Let m_1 and m_2 be two BPAs. The $SEB\chi^2$ divergence measure [30] can be defined as:

$$D_{SEB\chi^2}(m_1, m_2) = \frac{1}{2}\left[D_{EB\chi^2}\left(m_1, \frac{m_1 + m_2}{2}\right) + D_{EB\chi^2}\left(m_2, \frac{m_1 + m_2}{2}\right)\right]. \tag{5}$$

Symmetry

where

$$D_{EB\chi^2}(m_1, m_2) = \sqrt{\left(\frac{m_1(\theta)}{\sqrt{m_2(\theta)}} - \sqrt{m_2(\theta)}\right)' \Psi \left(\frac{m_1(\theta)}{\sqrt{m_2(\theta)}} - \sqrt{m_2(\theta)}\right)}, \tag{6}$$

with $\theta \in \Theta$, and

$$\Psi(F_i, F_j) = \frac{2^{|F_i \cap F_j|} - 1}{2^{|F_i|} - 1} \cdot \frac{2^{|F_i \cap F_j|} - 1}{2^{|F_j|} - 1}. \tag{7}$$

Consider the number of element

F_i and F_j represent m_1 and m_2 $(i, j = 1, 2, \ldots, 2^{n-1})$. $|\cdot|$ indicates the cardinality of a BPA. Ψ can be regarded as correlation coefficient [34].

The Proposed Method (DCA)

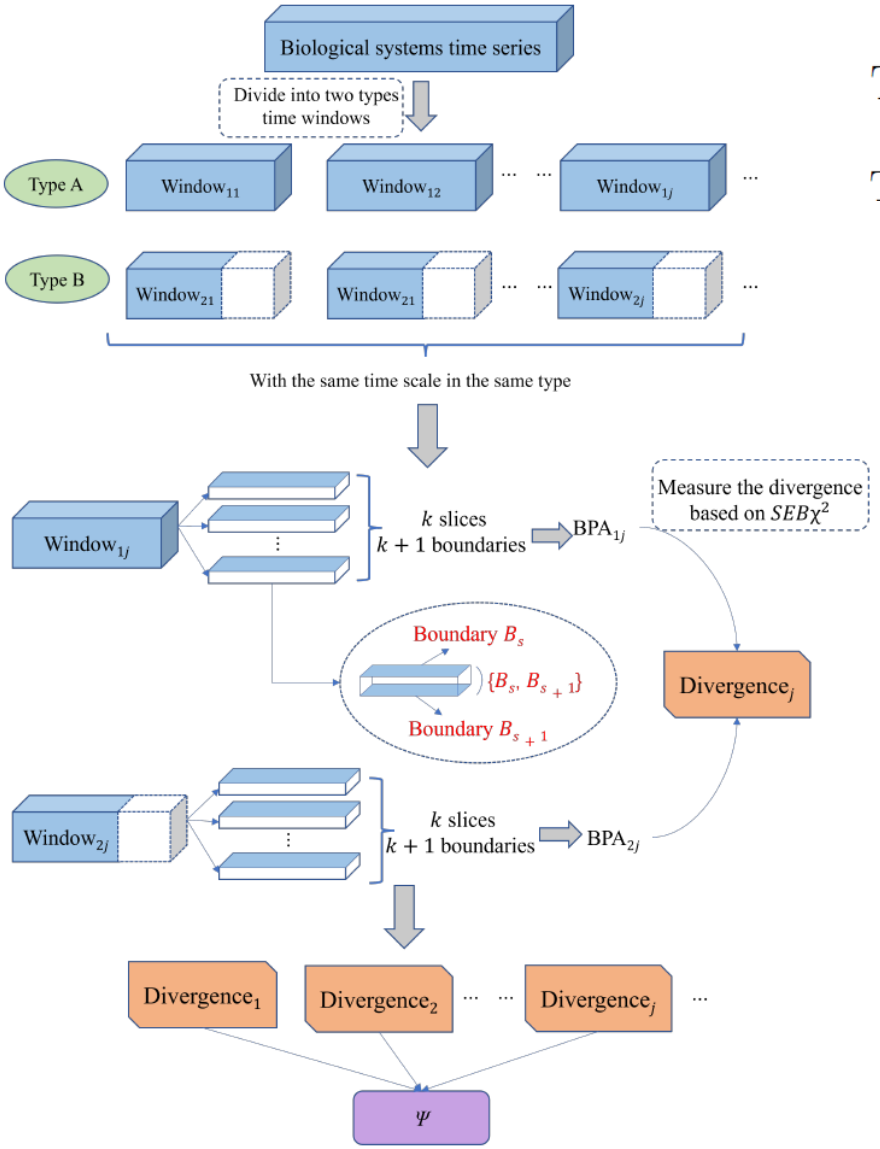


Fig. 1: Flowchart of the DCA algorithm for biological systems.

- **Two lists of consecutive non-overlapping time windows**

$$\text{Type A } w_{Aj}^{(\tau)} = \{x_{(j-1)\tau+1}, \cdots, x_{(j-1)\tau+\tau}\}$$

$$\text{Type B } w_{Bj}^{(\tau)} = \{x_{(j-1)\tau+1}, \cdots, x_{(j-1)\tau+\upsilon}\}$$

- **Focal element of BPA**

$$m_{ij}(\{B_s, B_{s+1}\}) = \frac{p}{|w_{ij}|}, \qquad i \in \{A, B\},$$

$$m_{ij}(\{B_s\}) = \frac{q}{|w_{ij}|} \qquad i \in \{A, B\}.$$

- ***Div$_j$* in each corresponding window**

$$Div_j = D_{SEB\chi^2}(m_{Aj}, m_{Bj}).$$

- **The average divergence represents the complexity of a biological system time series Ψ**

$$\Psi = \frac{\sum_{i=1}^{N/\tau} Div_i}{N/\tau}.$$

The Proposed Method

The pseudocode of dynamical complexity analysis algorithm for biological systems based on $SEB\chi^2$ divergence is shown in Algorithm 1.

Algorithm 1: Complexity analysis algorithm for biological systems based on $SEB\chi^2$ divergence

Input: Biological systems time series $\{x_i\} = \{x_1, \ldots, x_N\}$;
Output: Complexity result Ψ

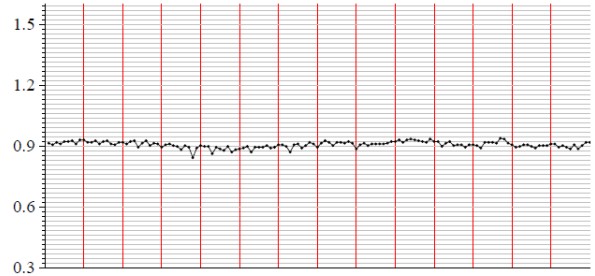
Split the time series $\{x_i\}$ into two types of windows $\left\{w_{Aj}^{(\tau)}\right\}$ and $\left\{w_{Bj}^{(\tau)}\right\}$;
Determine the lower and upper sides of time interval $\{x_{min}, x_{max}\}$;
Divided each time window into k slices;
Count the number of data points on or between boundaries;
for $i=1; i \leq N/\tau$ **do**
    Figure out the BPAs m_{1i} and m_{2i} of each time window by using the Eq. (8) and Eq. (9);
end
for $i=1; i \leq N/\tau$ **do**
    Calculate the divergence Div_i in each corresponding window by using Eq. (10);
end
Calculate the complexity of biological systems time series Ψ by using Eq. (11);
return Ψ.

Feature extraction

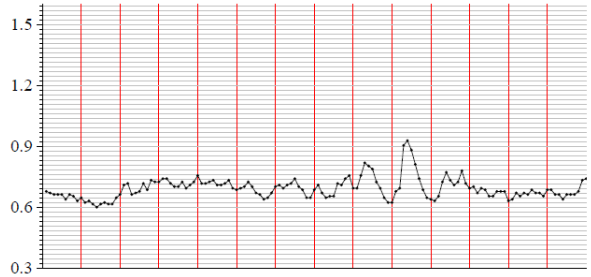
Complexity measurement

Simulation Experiments

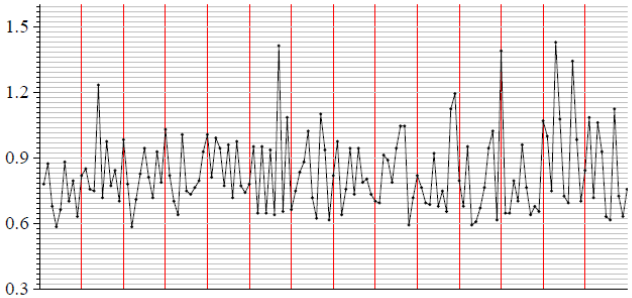
Cardiac inter-beat time series



Original time series of CHF



Original time series of Healthy



Original time series of AF

In this study, cardiac inter-beat interval time series is applied to demonstrate the feasibility of DCA algorithm for biological systems complexity analysis. The data is selected from the databases on PhysioNet as follows:

- BIDMC Congestive Heart Failure Database (CHF);
- MIT-BIH Normal Sinus Rhythm Database (Healthy);
- Long Term AF Database (AF).

Simulation Experiments

Data processing

- Each subject is truncated into 5 sets interbeat interval time series by utilizing the first 500 data points from 10,000 data points.
- Hence, there are 240 sets inter-beat interval time series. Specifically, 75, 90 and 75 records are from CHF Healthy and AF, respectively.
- The data points $\{x_i\}$ are ranked and split into 1000 segments. To release the influence of noise and detection error, the $1st$ and $999th$ 1000-quantiles of the ranked segments are regarded as x_{min}= 0.3 and x_{max} = 1.6

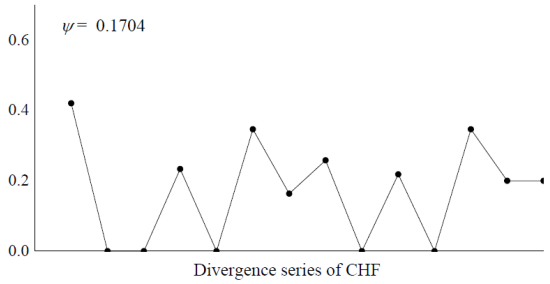
Simulation Experiments

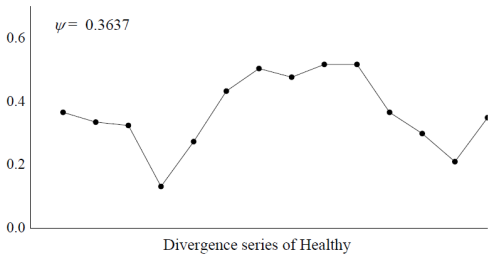
- Table 1 shows the 14 divergence values for each time window of data sets, respectively.

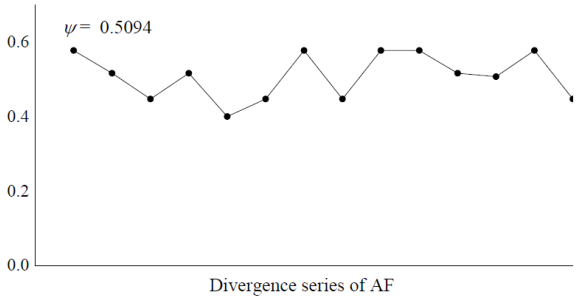
Table 1: The divergence value of CHF, Healthy and AF in each time window.

Subject	Win_1	Win_2	Win_3	Win_4	Win_5	Win_6	Win_7
CHF	0.4201	0.0000	0.0000	0.2335	0.0000	0.3464	0.1633
Healthy	0.3651	0.3342	0.3237	0.1309	0.2725	0.4320	0.5033
AF	0.5773	0.5164	0.4472	0.5164	0.4000	0.4472	0.5773
Subject	Win_8	Win_9	Win_{10}	Win_{11}	Win_{12}	Win_{13}	Win_{14}
CHF	0.2582	0.0000	0.2182	0.0000	0.3464	0.2000	0.2000
Healthy	0.4761	0.5164	0.5164	0.3651	0.2981	0.2093	0.4381
AF	0.4472	0.5773	0.5773	0.5164	0.5071	0.5773	0.4472

- Fig. 2 shows the three original time series and divergence series, respectively.







Conclusion

Contribution:

- Biological systems time series data is converted into mass function by using the D-S evidence theory, where feature of data can be extracted.
- The proposed DCA algorithm proposes an effective way to figure out the complexity of time series data in biological systems by generating BPAs and measure the average divergence of them.
- An application for pathological states analysis in cardiac inter-beat interval time series is carried out to illustrate the effectiveness of DCA algorithm.

Future work:

- The time complexity of the DCA algorithm for biological systems should be addressed to adapt to real-time data flexibly.

THANK YOU VERY MUCH!

Any questions and comments are welcome!

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