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Belief Kullback-Leibler Divergence-based Dynamical Complexity Analysis for Biological Systems

1st Lang Zhang
School of Big Data and Software Engineering
Chongqing University
Chongqing 401331, China
Email: zhanglang_cqu@163.com

2nd Fuyuan Xiao*
School of Big Data and Software Engineering
Chongqing University
Chongqing 401331, China
Email: xiaofuyuan@cqu.edu.cn

***Abstract*—Physical states can be fed back by the physiological signal as it contains the information of healthy systems. Specifically, dynamical time series is valuable data to reflect the pathological states by means of measuring the complexity of time series. Nevertheless, how to measure the complexity of physical signal is still an open issue. In this paper, a novel complexity measurement algorithm based on belief Kullback-Leibler (KL) divergence, called BKLDC, is proposed to calculate the complexity of biological systems time series. BKLDC algorithm firstly truncates biological systems signal into several slices with boundaries. In this case, the interval and border values are taken into account, which can differentiate the time series data. Then, based on the Dempster-Shafer (D-S) evidence theory, the format of time series data is converted to basic probability assignments (BPA). So, the feature of time series is obtained effectively as BKLDC algorithm considers the uncertainty of data signal. Hence, the complexity of physiological signal can be obtained by figuring out the divergence of BPAs. The divergence reflects discrepancy of BPAs, which presents the inherent complexity of data to some extent. In addition, an implementation in cardiac inter-beat interval time series demonstrates the out-performance of BKLDC algorithm for pathological states analysis.**

***Keywords*-D-S evidence theory; Belief KL divergence; Dynamical complexity analysis; Biological systems.**

I. Introduction

Biological systems contains precious information based on physiological signal time series, which benefits pathological researches [1]. Complexity analysis of biological time series plays an important parts in detecting the healthy states of people. In the field of physiology, the more information in time series, the larger complexity should be. In this case, entropy measurement can be used to figure out the uncertainty of time series. At the same time, uncertainty measurement is widely applied in decision making [2]. However, there is still an open issue with conflicting information, which may lead to counter intuitive phenomenon. Hence, scholars have focused on the uncertainty management, and several well-known works have been proposed to make multi-source information more effectively, including random permutation set [3], complex evidence theory [4], weighted network [5], Z-network [6], and so on [7].

Consider that D-S evidence theory can deal with uncertain information in a flexible way [8, 9], because it is a generalization of typical probability, which can be used in weaker conditions. D-S evidence theory is widely used in decision making [10], classification issues [11], and so on [12]. Recently, the complex evidence theory is used in the quantum framework [13], which effectively support quantum decision making [14]. Hence, in this paper, D-S evidence theory is taken into consideration. The feature of biological systems time series can be extracted by converting the format into BPAs. The mass function contains relative information volume [15]. Especially, both singleton sets and multi-element sets can represent characteristics of time series, respectively. Then, the complexity of biological systems can be measured by figuring out the divergence or distance between two BPAs, which is effective criteria to reflect the intrinsic features of time series [16].

Studying recent well-known methods, Xiao et al. [17] considered both subjective weights and objective weights, and proposed a uniform BJS divergence-based method. Zhang and Xiao [18] took the discrepancy and correlationship of both singleton sets and multi-element sets into account by means of $SEB\chi^2$ divergence to measure the difference between belief function. Zhu et al. [19] proposed a generalized Rényi divergence in EEG data analysis. According to methods above, the belief Kullback-Leibler divergence [20] could be used to process the time series data points whether they are on the boundaries of time slices.

In this work, a novel dynamical complexity analysis algorithm for biological systems based on belief KL divergence, called BKLDC, is proposed to figure out the complexity of biological systems time series. Firstly, BKLDC algorithm changes time series into BPAs. It is a step to extract the feature of biological systems. Secondly, the intrinsic feature of time series can be measured by figuring out the divergence between two BPAs. In addition, to show the out-performance of BKLDC algorithm, an application in cardiac inter-beat interval time series is carried out.

The main contribution points of this research are listed as follows:

- Based on D-S evidence theory, BKLDC algorithm

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converts biological time series into mass function.

• Based on belief Kullback-Leibler divergence, BKLDC algorithm can measure the intrinsic feature of time series to reflect the physiological states of subjects.

• An application in cardiac inter-beat interval time series is carried out to distinguish the pathological states, which shows the effectiveness BKLDC algorithm.

The organization of this work is summarized as follows. Section 2 represents the basic concepts. Section 3 shows the detail of BKLDC algorithm. The application and comparison are carried out in Section 4 to demonstrate the performance of the proposed method. Section 5 makes a conclusion of this paper.

II. Preliminaries

In this section, several basic concepts of D-S evidence theory and belief KL divergence are briefly introduced.

A. D-S evidence theory

D-S evidence theory is a generalization of typical probability that can effectively deal with uncertain information fusion [8, 9], because it addresses uncertainty problems in weaker conditions. D-S evidence theory degenerates into classical probability theory when all probability values are known.

Definition 1 (Framework of discernment)**.**

Let the discernment Θ be a finite set which can be defined as:

$$\Theta = \{h_1, h_2, \ldots, h_n\}. \tag{1}$$

Then, its power set 2^Θ can be defined as:

$$2^\Theta = \{\varnothing, \{h_1\}, \ldots, \{h_1, h_2\}, \ldots, \{h_1, h_2, \ldots, h_i\}, \ldots, \Theta\}, \tag{2}$$

where $\varnothing$ indicates the empty set.

Definition 2 (Mass function)**.**

Based on discernment Θ, the mass function m can be defined as:

$$m : 2^\Theta \to [0, 1], \tag{3}$$

with the rule of

$$\sum_{E \in 2^\Theta} m(E) = 1 \quad \text{and} \quad m(\varnothing) = 0. \tag{4}$$

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

Definition 3 (Dempster's rule of combination)**.**

Consider two BPAs m_1 and m_2. The rule of Dempster's combination is describe as:

$$m(B) = \begin{cases} \dfrac{1}{1-k} \displaystyle\sum_{P \cap Q = B} m_1(P) m_2(Q), & B \neq \varnothing, \\ 0, & B = \varnothing, \end{cases} \tag{5}$$

and

$$k = \sum_{P \cap Q = \varnothing} m_1(P) m_2(Q), \tag{6}$$

where P and Q are focal elements and k is regarded as a conflict coefficient.

B. Divergence measure

Kullback-Leibler divergence is usually used to measure the discrepancy between two probabilities. Here, the belief Kullback-Leibler divergence is introduced to measure the divergence degree among evidence.

Definition 4 (Belief Kullback-Leibler divergence)**.**

Let m_1 and m_2 be two BPAs, the belief KL divergence between m_1 and m_2 can be defined as:

$$D_{KL}(m_1, m_2) = \sum_i \frac{1}{2^{|A_i|} - 1} m_1(A_i) \log\left(\frac{m_1(A_i)}{m_2(A_i)}\right), \tag{7}$$

where A_i is the focal elements of mass function and $|\cdot|$ represents the cardinality of focal element. Then, a symmetrical KL divergence based on Eq. (7) can be defined as:

$$\begin{aligned} Div(m_1, m_2) &= Div(m_2, m_1) \\ &= \frac{D_{KL}(m_1, m_2) + D_{KL}(m_2, m_1)}{2}. \end{aligned} \tag{8}$$

In this paper, based on Eq. (8) the symmetrical belief KL divergence is used to measure the discrepancy between two BPAs.

III. Belief KL divergence-based dynamical complexity analysis algorithm for biological systems

To effectively measure dynamical complexity of biological systems, an algorithm based on belief KL divergence, called BKLDC, is proposed in this section. The algorithm can be split into two component. First, a divergence sequence of time series can be obtained based on belief KL divergence. Second, the average value of divergence sequence can be used as complexity value of dynamical biological systems time series. The processing flowchart of BKLDC is shown in Fig. 1.

In the first component, the time series of biological systems is described as $\mathcal{H} = \{t_1, \ldots, t_i, \ldots, t_N\}$ with length N. To measure the intrinsic discrepancy, two types of consecutive and non-overlapping time windows are taken into account to divided time series as type X $\left\{w_{Xi}^{(\eta)}\right\}$ and type Y $\left\{w_{Yj}^{(\eta)}\right\}$. Here, $w_{Xj}^{(\eta)} = \left\{t_{(j-1)\eta+1}, \ldots, t_{(j-1)\eta+\eta}\right\}$ is of length η, where j is the window index which ranges from 1 to N/η. Type Y is the truncation of type X in each corresponding window as $w_{Yj}^{(\eta)} = \left\{t_{(j-1)\eta+1}, \ldots, t_{(j-1)\eta+\delta}\right\}$, where $\delta < \eta$.

Then, the lower and the upper boundaries of time series $\mathcal{H}$ are regarded as r_{min} and r_{max}, respectively. Next, the time interval is equally split into k slices. Each slice contains an upper boundary and a lower boundary, such as M_s and M_{s+1} of the sth slice. Hence, a slice can represents the

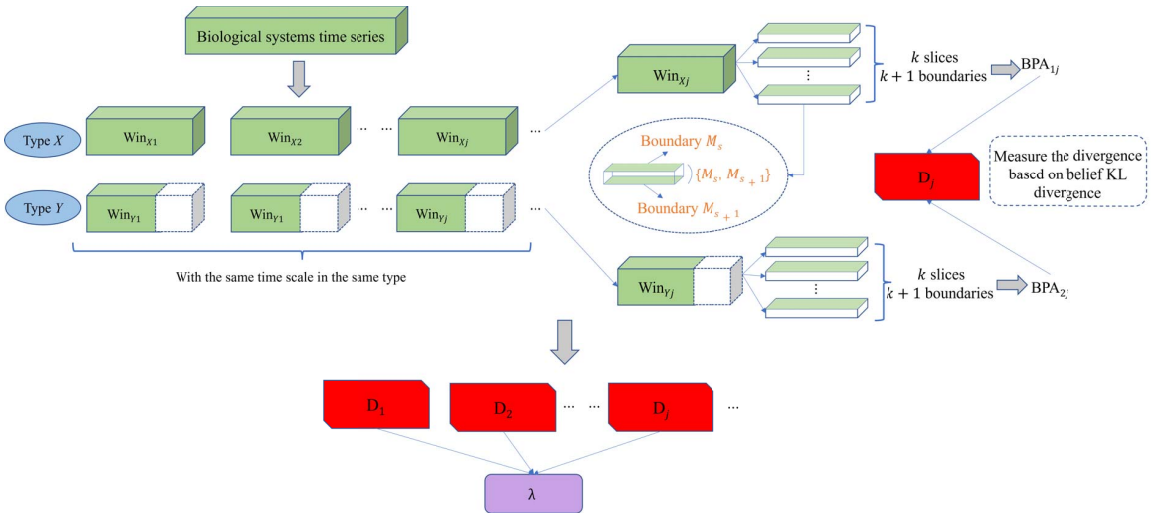

Figure 1. Flowchart of the BKLDC algorithm for biological systems.

specific state. If data points are in the same slice, then it can be consider that they are in the same state. Specifically, a data point is consider to have concrete state when it falls on the boarder. On the contrary, it has an uncertain state when falls in the interval.

Let the total number of data points over w_{ij} between M_s and M_{s+1} be p_{ij}. Specifically, let data points γ of length q_{ij} fall on the border M_s coincidentally. The BPAs based on each time window can be defined as:

$$m_{ij}: \begin{cases} m_{ij}^{(\eta)}(\{M_s\}) = \dfrac{q_{ij}}{|w_{ij}|}, & \text{if } \gamma \text{ falls on the boundary } s, \\ m_{ij}^{(\eta)}(\{M_s, M_{s+1}\}) = \dfrac{p_{ij}}{|w_{ij}|}, & \text{otherwise,} \end{cases} \tag{9}$$

where $i \in \{X, Y\}$. Next, considering that points are all in the interval, the divergence $D_j^{(\eta)}$ in each corresponding window is figured out based on symmetrical belief KL divergence measure:

$$\begin{aligned} D_j^{(\eta)} &= Div(m_{Xj}, m_{Yj}) \\ &= \frac{1}{2} \cdot \sum_{s=1}^{k} \frac{m_{Xj}(\{M_s, M_{s+1}\})}{2^{|\{M_s, M_{s+1}\}|} - 1} \log \left(\frac{m_{Xj}(\{M_s, M_{s+1}\})}{m_{Yj}(\{M_s, M_{s+1}\})} \right) \\ &+ \frac{1}{2} \cdot \sum_{s=1}^{k} \frac{m_{Yj}(\{M_s, M_{s+1}\})}{2^{|\{M_s, M_{s+1}\}|} - 1} \log \left(\frac{m_{Yj}(\{M_s, M_{s+1}\})}{m_{Xj}(\{M_s, M_{s+1}\})} \right) \\ &= \frac{1}{2} \cdot \sum_{s=1}^{k} \left(\frac{p_{Xj}}{3 \cdot |w_{Xj}|} - \frac{p_{Yj}}{3 \cdot |w_{Yj}|} \right) \log \frac{p_{Xj} \cdot |w_{Yj}|}{p_{Yj} \cdot |w_{Xj}|}. \end{aligned} \tag{10}$$

Hence, a belief KL divergence sequence $\left\{ D_j^{(\eta)} \right\}$ of original time series is constructed.

Property 1. When all the data fall on the boundaries of time window, the $D_j^{(\eta)}$ degenerates to:

$$\begin{aligned} D_j^{(\eta)} &= Div(m_{Xj}, m_{Yj}) \\ &= \frac{1}{2} \cdot \sum_{s=1}^{k} \frac{m_{Xj}(\{M_s\})}{2^{|\{M_s\}|} - 1} \log \left(\frac{m_{Xj}(\{M_s\})}{m_{Yj}(\{M_s\})} \right) \\ &+ \frac{1}{2} \cdot \sum_{s=1}^{k} \frac{m_{Yj}(\{M_s\})}{2^{|\{M_s\}|} - 1} \log \left(\frac{m_{Yj}(\{M_s\})}{m_{Xj}(\{M_s\})} \right) \\ &= \frac{1}{2} \cdot \sum_{s=1}^{k} \left(\frac{q_{Xj}}{|w_{Xj}|} - \frac{q_{Yj}}{|w_{Yj}|} \right) \log \frac{q_{Xj} \cdot |w_{Yj}|}{q_{Yj} \cdot |w_{Xj}|}. \end{aligned} \tag{11}$$

Property 2. $D_j^{(\eta)}$ is symmetric as:

$$D_j^{(\eta)} = Div(m_{Xj}, m_{Yj}) = Div(m_{Yj}, m_{Xj}) \tag{12}$$

Property 3. When $m_{Xj} = m_{Yj}$, the $D_j^{(\eta)}$ is regarded as:

$$D_j^{(\eta)} = 0. \tag{13}$$

Then, in the second component of BKLDC algorithm, the average value of divergence sequence $D_j^{(\eta)}$ is obtained as the complexity value Φ of a biological systems time series:

$$\lambda = \frac{\sum_{i=1}^{N/\eta} D_j^{(\eta)}}{N/\eta}. \tag{14}$$

The pseudocode of dynamical complexity analysis algorithm for biological systems based on belief KL divergence is shown in Algorithm 1.

IV. Application in Cardiac Inter-beat Interval Time Series Classification

In this section, the biological systems time series data is taken into account, which shows the way of selecting

Algorithm 1: Complexity analysis algorithm for biological systems based on belief KL divergence

Input: Biological systems time series $\mathcal{H} = \{t_1, \ldots, t_N\}$;
Output: Complexity result λ

Split the time series $\{x_i\}$ into two types of windows $\left\{w_{Xj}^{(\eta)}\right\}$ and $\left\{w_{Yj}^{(\eta)}\right\}$;
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*$\leq N/\eta$ **do**
    Figure out the BPAs m_{1i} and m_{2i} of each time window by using Eq. (9);
end
for *i=1;i*$\leq N/\eta$ **do**
    Calculate the divergence $D_j^{(\eta)}$ in each corresponding window by using Eq. (10);
end
Calculate the complexity of biological systems time series λ by using Eq. (14);
return λ.

valid data points. Next, an implement of BKLDC algorithm for biological systems is carried out to show the effective performance in specific time series. Here lists the software that used: Origin® (The MicroCal, Inc., Northampton, MA, USA) with version of 2021 (64-bit) 9.8.0.200.

A. Data Description

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

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

The above databases are long-term ECG (Electrocardiography) databases with 20-24 hours record. The numbers of subject are 15, 18 and 84, respectively. Before the experiment, data sets need be processed by extract the feature fragments. Each subject in CHF and Healthy databases is truncated into 5 sets inter-beat interval time series by utilizing the first 500 data points from 10,000 data points. Then, 75 records in AF data sets are adopted according to the annotation in PhysioNet. finally, there are 240 sets inter-beat interval time series. Specifically, 75, 90 and 75 records are from CHF Healthy and AF, respectively.

Next, the time series is processed. First, to release the influence of noise and detection error, data points $\{t_i\}$ are ranked and split into 1000 segments. Then, the 1_{st} and 999_{th} 1000-quantiles of the ranked segments are regarded as $r_{min} = 0.3$ and $r_{max} = 1.6$.

B. Implementation of the BKLDC algorithm

Three representative instances from CHF, Healthy and AF are carried out to demonstrate the process of BKLDC algorithm for biological systems. To simplify the experiment, each time series is analyzed with 140 data points, whose parameters are at $\eta = 10$, $\delta = 5$ and $k = 55$. In this case, each time series will be split into 14 time windows.

Fig. 2 shows three representative time series, respectively. Note that CHF subject has the highest heart-beat interval, and the interval between heartbeats tends to flatten out. Compared with Healthy subject, the heartbeat of AF subject fluctuate more obviously.

According to Eqs. (9)-(13), Table I and Fig. 3 demonstrate the process of first component of BKLDC algorithm. The divergence sequence of each subject can be obtained, which shows the inner feature of time series. After observing three divergence sequences, note that CHF subject has the lowest divergence values in time windows, while that of Healthy subjects rise and down at higher values. Correspondingly, the divergence sequence of AF is at a moderate level. In this case, it can be regarded that the first component of BKLDC can effectively extract the feature of time series.

Then, based on Eq. (14), the complexity of biological time series can be obtained as 0.0143 of CHF, 0.0468 of CHF and 0.0331 of AF. Hence, Healthy subject reaches the highest complexity while CHF subject has lowest complexity value. It is in line with the reality, because healthy people have the most complex biological systems to control the operation in heart system. On the contrary, the complexity of biological systems in pathological groups is relatively low, because they have partial loss of heart function. In addition, AF subjects have larger change range than CHF subjects with sharp increase and decrease trend. Hence, the complexity rule should be followed as: Healthy subjects $<$ AF subjects $<$ CHF subjects.

Next, figure out the complexity value of 240 sets inter-beat interval time series. Fig. 4 shows a scatter diagram to illustrate the performance of BKLDC algorithm in three different kinds of subjects. Based on the distribution of all the scatter points, it can be found that Healthy people reaches highest complexity value most of the time. Relatively, CHF subjects are at the bottom, while complexity value of AF subjects are higher than CHF and lower than Healthy. In this case, BKLDC shows out-performance to extract the characteristic of biological systems time series.

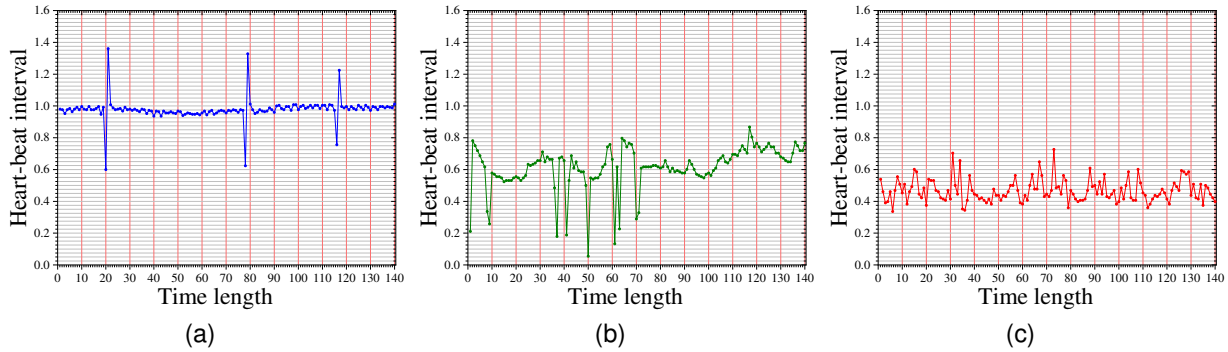

Figure 2. The original time series with 140 data points of specific instances. (a) Original time series of CHF subject. (b) Original time series of Healthy subject. (c) Original time series of AF subject.

Table I
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	Win_8	Win_9	Win_{10}	Win_{11}	Win_{12}	Win_{13}	Win_{14}
CHF	0.0138	0.0303	0.0299	0.0074	0.0377	0.0135	0.0000	0.0211	0.0048	0.0000	0.0000	0.0231	0.0068	0.0116
Healthy	0.0693	0.0377	0.0530	0.0231	0.0462	0.0578	0.0578	0.0135	0.0693	0.0693	0.0395	0.0578	0.0213	0.0530
AF	0.0279	0.0231	0.0462	0.0462	0.0048	0.0462	0.0231	0.0395	0.0351	0.0279	0.0414	0.0279	0.0578	0.0163

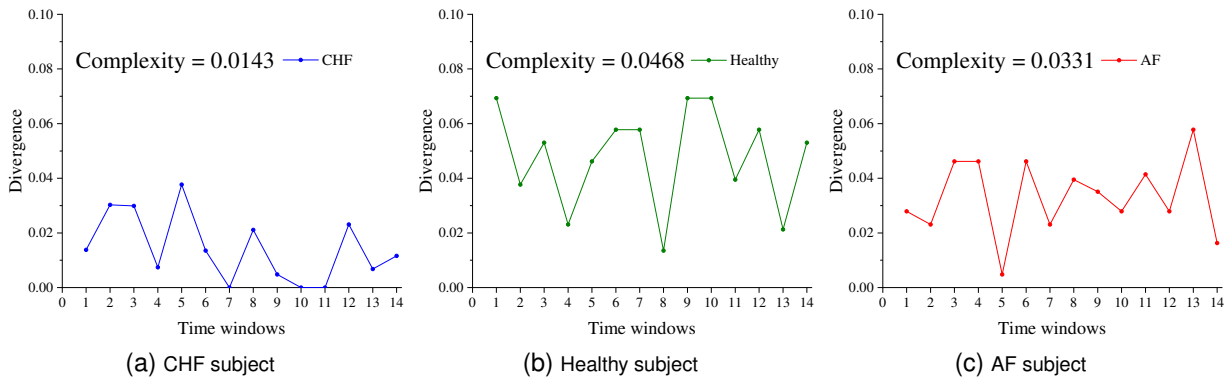

Figure 3. Demonstration of BKLDC algorithm for biological systems on representative subjects.

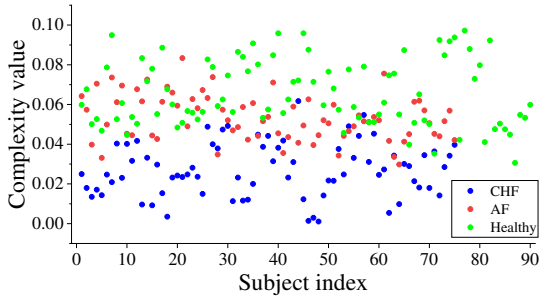

Figure 4. The complexity value in 240 sets cardiac inter-beat interval time series.

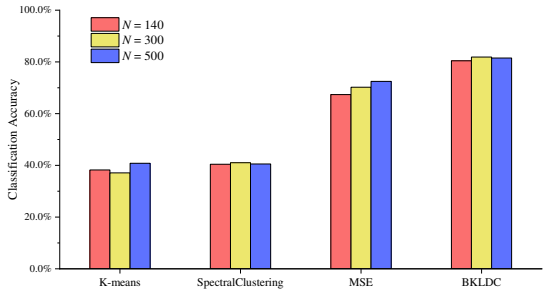

Figure 5. The pattern classification accuracy in cardiac inter-beat interval time series.

C. Classification in Cardiac Inter-beat Interval Time Series Based on BKLDC

In this section, an application in cardiac inter-beat interval time series classification is carried out to demonstrate the effectiveness of BKLDC algorithm. The evaluation index, sensitivity of pathological subjects and specificity of healthy subjects are defined as follows:

$$\begin{aligned} &\text{Specificity:} V_{sp} = \frac{T_H}{T_H + F_H}, \\ &\text{Sensitivity:} V_{se} = \frac{T_P}{T_P + F_P}, \\ &\text{Accuracy:} V_{ac} = \frac{T_H + T_P}{T_H + F_H + T_P + F_P}, \end{aligned} \tag{15}$$

where T_H and F_H represent the amount of healthy subjects that classified correctly and falsely, respectively. Besides, T_P and F_P represent the amount of pathology subjects that classified correctly and falsely.

At $\eta = 10$, $\delta = 5$ and $k = 55$, three different lengths of time series are taken into consideration as: $N = 140$, $N = 300$ and $N = 500$. Based on Eq. (15), Table II shows the evaluation criteria value. It can be found that BKLDC algorithm has outstanding results even with smaller data size. Hence, the proposed method is able to select the healthy subjects from pathological subjects at one time when there is a few data points. In other words, BKLDC algorithm is not sensitive to the length of time series, which shows the robustness that can be applied in other applications.

Table II
THE EVALUATION INDEX VALUE IN APPLICATION BASED ON BKLDC.

	$N = 140$	$N = 300$	$N = 500$
V_{se} in CHF	0.7013	0.7267	0.7133
V_{se} in AF	0.8333	0.7933	0.8215
V_{sp} in Healthy	0.8230	0.8124	0.8248
Accuracy	0.8044	0.8189	0.8150

D. Comparison

In this part, several classical machine learning methods and a well-known method [21], MSE, are used to make comparison with BKLDC algorithm. The cardiac inter-beat interval time series pattern classification accuracy is shown in Table III, and Fig. 5 is a bar chart to show the accuracy criteria based on different data lengths.

It can be found that the proposed method, BKLDC, reaches the highest classification accuracy of 0.8189 at $N = 300$. Compared with classical machine learning methods, including K-means and Spectral Clustering, BKLDC far outperforms them. The BKLDC is twice as accurate as the classical machine learning methods. Considering MSE, it has higher accuracy values than classical machine learning method, and as the length of data points increases, so does the accuracy. Nevertheless, MSE still can not catch up with the BKLDC.

Therefore, according to the information above, BKLDC algorithm shows superiority to measure the complexity of biological systems, and can make high classification accuracy to distinguish healthy subjects and pathological subjects.

Table III
THE PATTER CLASSIFICATION ACCURACY BASED ON DIFFERENT METHODS.

	$N = 140$	$N = 300$	$N = 500$
K-means	0.3822	0.3711	0.4078
Spectral clustering	0.4044	0.4100	0.4056
MSE	0.6738	0.7024	0.7248
BKLDC	0.8044	0.8189	0.8150

V. CONCLUSION

Biological systems contained various information to reflect the states of people. Especially, the complexity analysis for physiological time series was important. This research proposed a novel complexity analysis method, called BKLDC, which could be applied in biological systems detection. BKLDC converted time series into BPAs based on Dempster-Shafer evidence theory. Specifically, the boundary and interval values were represented differently to illustrate feature effectively. Then, belief Kullback-Leibler divergence was taken into account to measure the inner discrepancy of time series. In addition, an application in cardiac inter-beat interval time series was carried out. BKLDC shew good performance in complexity analysis for biological systems. Besides, BKLDC could distinguish healthy subjects and pathological subjects effectively. In the future study, time series should be processed to better extract features, and the algorithm should be optimized to adapt more biological systems data.

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REFERENCES

[1] H. Cui, L. Zhou, Y. Li, B. Kang, Belief entropy-of-entropy and its application in the cardiac interbeat interval time series analysis, Chaos, Solitons & Fractals 155 (2022) 111736. doi:10.1016/j.chaos.2021.111736.

[2] H. Garg, S.-M. Chen, Multiattribute group decision making based on neutrality aggregation operators of

q-rung orthopair fuzzy sets, Information Sciences 517 (2020) 427–447.

[3] Y. Deng, Random permutation set, International Journal of Computers Communications & Control 17 (1) (2022) 4542. doi:https://doi.org/10.15837/ijccc.2022.1.4542.

[4] F. Xiao, Z. Cao, C.-T. Lin, A complex weighted discounting multisource information fusion with its application in pattern classification, IEEE Transactions on Knowledge and Data Engineering (2022) DOI: 10.1109/TKDE.2022.3206871.

[5] L. Chen, Y. Deng, K. H. Cheong, Probability transformation of mass function: A weighted network method based on the ordered visibility graph, Engineering Applications of Artificial Intelligence 105 (2021) 104438.

[6] W. Jiang, Y. Cao, X. Deng, A novel Z-network model based on Bayesian network and Z-number, IEEE Transactions on Fuzzy Systems 28 (8) (2020) 1585–1599.

[7] L. Xiong, X. Su, H. Qian, Conflicting evidence combination from the perspective of networks, Information Sciences 580 (2021) 408–418.

[8] A. P. Dempster, Upper and lower probabilities induced by a multivalued mapping, in: Classic works of the Dempster-Shafer theory of belief functions, Springer, 2008, pp. 57–72.

[9] G. Shafer, A mathematical theory of evidence, in: A mathematical theory of evidence, Princeton university press, 1976.

[10] L. Fei, Y. Feng, A dynamic framework of multi-attribute decision making under Pythagorean fuzzy environment by using Dempster–Shafer theory, Engineering Applications of Artificial Intelligence 101 (2021) 104213.

[11] Z. Liu, Y. Liu, J. Dezert, F. Cuzzolin, Evidence combination based on credal belief redistribution for pattern classification, IEEE Transactions on Fuzzy Systems 28 (4) (2020) 618–631.

[12] X. Xu, D. Zhang, Y. Bai, L. Chang, J. Li, Evidence reasoning rule-based classifier with uncertainty quantification, Information Sciences 516 (2020) 192–204.

[13] F. Xiao, Generalized quantum evidence theory, Applied Intelligence (2022) DOI: 10.1007/s10489–022–04181–0.

[14] F. Xiao, W. Pedrycz, Negation of the quantum mass function for multisource quantum information fusion with its application to pattern classification, IEEE Transactions on Pattern Analysis and Machine Intelligence (2022) DOI: 10.1109/TPAMI.2022.3167045.

[15] Y. Deng, Information volume of mass function, International Journal of Computers Communications & Control 15 (6) (2020) 3983.

[16] D. Han, J. Dezert, Y. Yang, Belief interval-based distance measures in the theory of belief functions, IEEE Transactions on Systems, Man, and Cybernetics: Systems 48 (6) (2018) 833–850.

[17] F. Xiao, J. Wen, W. Pedrycz, Generalized divergence-based decision making method with an application to pattern classification, IEEE Transactions on Knowledge and Data Engineering (2022) DOI: 10.1109/TKDE.2022.3177896.

[18] L. Zhang, F. Xiao, A novel belief $\chi 2$ divergence for multisource information fusion and its application in pattern classification, International Journal of Intelligent Systems (2022) DOI: 10.1002/int.22912.

[19] C. Zhu, F. Xiao, Z. Cao, A generalized Rényi divergence for multi-source information fusion with its application in EEG data analysis, Information Sciences (2022) DOI: 10.1016/j.ins.2022.05.012.

[20] Y. Song, Y. Deng, Divergence measure of belief function and its application in data fusion, IEEE Access 7 (2019) 107465–107472.

[21] M. Costa, A. L. Goldberger, C.-K. Peng, Multiscale entropy analysis of complex physiologic time series, Physical review letters 89 (6) (2002) 068102.