Coupling analysis of epileptic EEG signals based on the multiscale mutual model entropy

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Keywords: multiscale; epileptic; coupling; mutual model entropy

Abstract. The Multiscale Mutual Model Entropy algorithm is presented to quantify the coupling degree between two EEG time series collected at the same time on different scales. We extracted the characteristics of EEG signals from the healthy and epileptics based on the algorithm. The results show that the entropy value of healthy people is higher than that of epileptics. And with the increase of scale, the difference in entropy value between them is more obvious. It indicates that Multiscale Mutual Entropy can distinguish the coupling difference between normal samples and case samples, which is significant for the clinical pathological assessment and brain disease diagnosis.

1. Introduction

Brain electrical signal contains a large number of physiological and pathological information. Researchers have used entropy analysis method for the fields of EEG signals, the human gait information and so on [1]. Entropy analysis method also plays a very important role in the study of nonlinear method of epilepsy early prediction [2]. It has been found that complexity of early brain electric signals will change from high to low. It is very helpful for the nonlinear research of physiological signals with high complexity to measure the complexity of the system using entropy [3, 4].

Early algorithm is Kolmogorov-Sinai entropy (KS) and E-R entropy [5]. In 1991, Pincus put forward the Approximate Entropy [6] (ApEn). Richman et al. [7] improved ApEn and developed the Sample Entropy which can be less dependent on the length of time series. Costa et al. [8] proposed the Multiscale Sample Entropy (MSE) that characterizes the Sample Entropy value of each scale. But it needs a large amount of data for calculation. Mode Entropy [9] (ModEn) is the new algorithm based on the analysis and revisions of ApEn. It is not based on absolute size of data, but with vector shape in time series as similarity criterion. The method has been used on the ECG analysis and obtained good effect.

Considering the multiscale characteristics of complex physiological signals and the advantages of data computation based on ModEn, we put forward the Multiscale Mutual Model Entropy to quantify the coupling degree between two simultaneous acquisitions of time series on different scales. This paper uses the algorithm for EEG signals coupling analysis of healthy people and patients with epilepsy to obtain related conclusion.

2. The basic principle of multiscale Mutual Mode Entropy

For one dimensional discrete time sequence of length N:

$\{x(i): 0 \le i \le N-1\}$

According to the formula (1), construct time series $\{y^{(\tau)}\}$:

$$y_j^{\tau} = 1/\tau \sum_{i=(j-1)\tau+1}^{j\tau} x_i \quad , \quad 1 \le j \le N/\tau \tag{1}$$

Scale factor is τ , and sequence's length is N/τ . When $\tau=1$, $\{y^{(1)}\}$ refers to the original time series.

According to the following algorithm, calculate the different scales of Mutual Model Entropy:

For the two sets of time series of N data points:

$\{u(i):0\le i\le N-1\}$, $\{\mathrm{v}(i):0\le i\le N-1\}$

Randomly select m consecutive points to compose m dimensional vectors:

$$X(i)=[u(i),u(i+1),\cdots,u(i+m-1)],\quad \mathrm{Y}(i)=[\mathrm{v}(i),\mathrm{v}(i+1),\cdots,\mathrm{v}(i+m-1)] \tag{2}$$

Define the mean value of m data points for the baseline values of the vector:

$$B_x(i)=\frac{\sum_{l=0}^{m-1}u(i+l)}{m},$$

$$B_y(i)=\frac{\sum_{l=0}^{m-1}\mathrm{v}(i+l)}{m} \tag{3}$$

According to the baseline, redefine the m dimensional vectors:

$$\begin{aligned}\Psi_x(i)&=\left[u(i)-B_x(i),u(i+1)-B_x(i),\cdots,u(i+m-1)-B_x(i)\right]\\&=\left[\phi_x(i),\phi_x(i+1),\cdots\phi_x(i+m-1)\right]\\\Psi_y(i)&=\left[u(i)-B_y(i),u(i+1)-B_y(i),\cdots,u(i+m-1)-B_y(i)\right]\\&=\left[\phi_y(i),\phi_y(i+1),\cdots\phi_y(i+m-1)\right]\end{aligned} \tag{4}$$

Similarity difference between two vectors:

$$L_{ij}=L[\Psi_x(i),\Psi_y(j)]=\max_{k=0\to m-1}\left[\left|\phi_x(i+k)-\phi_y(j+k)\right|\right] \tag{5}$$

According to threshold value r, calculate the probability of a vector similar with $\Psi(i)$ and define the probability as $C_i^m(r)$:

$$C_i^m(r)=\frac{1}{N-m+1}\sum_{j=0}^{N-m}\theta\left(r-L_{ij}\right) \tag{6}$$

$\theta(z)$ is the unit step function or Heviside function:

$$\theta(z)=\begin{cases}1\ (z>0)\\0\ (z\le 0)\end{cases} \tag{7}$$

Calculating the logarithm, and then averaging as following:

Take logarithm of $C_i^m(r)$ and then ask for the mean of all the variance i:

$$\phi^m=\frac{1}{N-m+1}\sum_{i=0}^{N-m}\ln C_i^m(r) \tag{8}$$

Get Mutual Mode Entropy of this sequence:

$$ModEn(m,r,N)=\phi^m-\phi^{m+1}\qquad m\ge 1 \tag{9}$$

The threshold value r is defined as the mean of the standard deviation of two groups of time series:

$$r=K*(\mathrm{std(u)}+\mathrm{std(v)})/2 \tag{10}$$

std is standard deviation and K is coefficient .The value of K ranges from 0.1 to 0.2. We need obtain the corresponding threshold r as the formula (10) before the entropy calculation.

3. Data processing and analysis

This article uses the EEG data acquired from the General Hospital of Nanjing Military

Command. We randomly selected EEG data from 12 groups of healthy people and 12 groups of epileptics. Each group of data contains EEG samples of two leads called Fp1 and Fp2. Sampling frequency is 512 Hz. We selected 5040 points in each group of data to construct new time series with the scale factor τ (from 1 to 10) and calculated their Mutual Mode Entropy.

White noise often exists in the physiological signals. So it is necessary to explore the Multiscale Mutual Mode Entropy's capability of anti-noise. We add the Gaussian white noise to each group of 5040 points have extracted, and calculate the Entropy. We can get the results after adding white noise.

In order to better analyze the Mutual Mode Entropy of EEG signals in scale changes, we adopted alternative data algorithm IAAFT [10] based on Fourier transform to build a random sequence for entropy calculation. Surrogate data will be as much as possible to retain some properties of original signals, such as time probability distribution and autocorrelation function while the data is also random as far as possible.

4. Results

As Fig.1 shows, the change tendency of the Mutual Mode Entropy of healthy and epileptic group is similar and the entropy value increases as the increase of scale factor. Entropy value of the healthy is higher than that of patients with epilepsy, and with the increase of scale, coupling differences between them is more obvious.

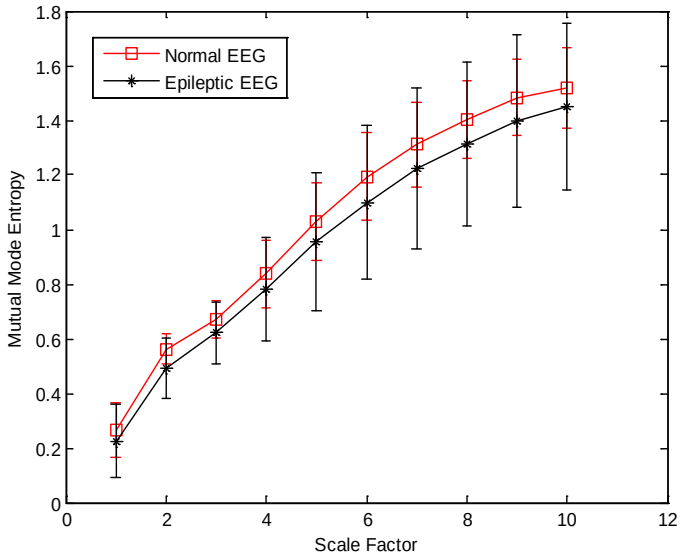

Fig.1 the mean and standard deviation of the healthy and epileptic's entropy

From Fig.2, we can find that after adding white Gaussian noise, the calculation results have high similarity with the original data on each scale. It shows that Mutual Mode Entropy has good anti-noise and anti-interference ability. It is also very suitable for coupling analysis of physiological signals.

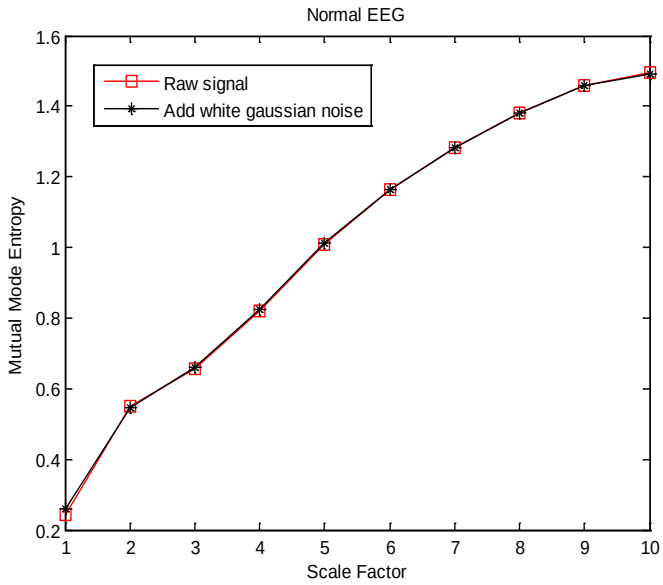

Fig.2 the result of the healthy group after adding noise

Fig.3 and Fig.4 show the calculation results of the original data and its surrogate data. In the 1st scale, the difference between them is small. But with the increase of scale, the increasing trend of entropy value of surrogate data is gradually gentle, which leads to the bigger and bigger difference with the original data. Entropy value of the healthy sample and the epileptic sample is much higher than that of their surrogate data. To some extent, it also illustrates the algorithm can be used to analyze physiological signal with high complexity on the scale transform.

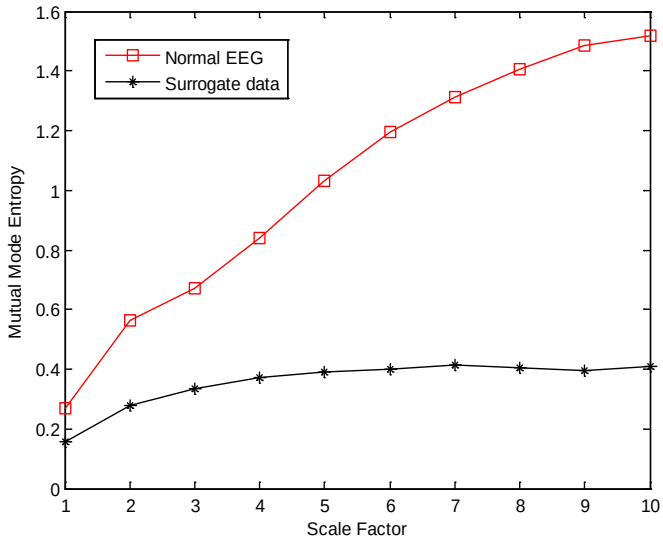

Fig.3 (healthy group) the results of raw data and surrogate data

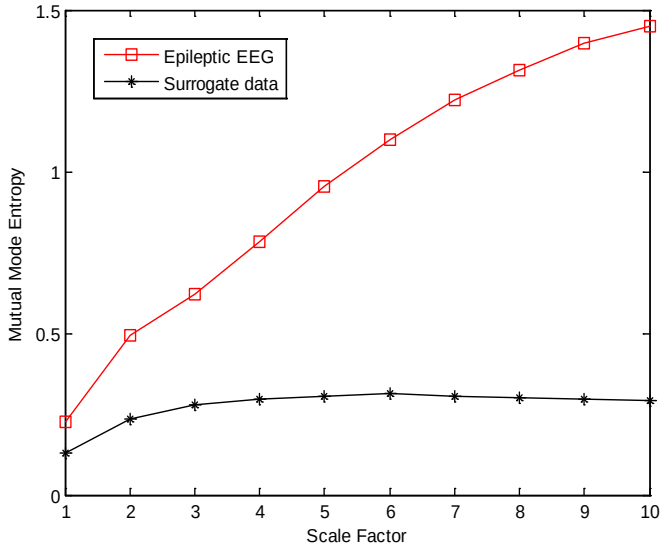

Fig.4 (epileptic group) the results of raw data and surrogate data

5. Conclusions

Multiscale Mutual Mode Entropy algorithm is proposed in this paper. After verification, it can well analyze coupling information of the healthy and epileptics' EEG time series. The Results show that there exists a bigger difference in large scale between the two groups, and calculations are not affected by noise in the process of scale change. It is indicated that Multiscale Mutual Entropy is suitable for the early prediction of epilepsy to distinguish the coupling difference between normal samples and case samples. The algorithm is also significant for the clinical pathological assessment and brain disease diagnosis.

Acknowledgements

Project supported by the National Natural Science Foundation of China (Grant Nos. 61271082, 61401518), Jiangsu Provincial Key R & D Program (Social Development) (Grant No. BE2015700), the Natural Science Foundation of Jiangsu Province (Grant No. BK20141432), the Foundation of Nanjing General Hospital of Nanjing Military Command (Grant No. 2014019), Nanjing Medical Science and Technology Project (Grant No. 201503009) and the Fundamental Research Funds for the Central Universities (Grant No. FY2014LX0039).

References

[1] Bandt C & Pompe B. Permutation entropy: A natural complexity measure for time series [J]. Physical Review Letters, 2002, 88(17).

[2] Dojnow P. Multifractal analysis of correlation properties of electroencephalograms (EEG) [J]. C. R. Acad. Bulg. Sci., 2007, 60(6): 607-612.

[3] Li J, Ning X B, Wu W & Ma X F. Detecting dynamical complexity changes in time series using the base-scale entropy [J]. Chin. Phys., 2005, 14(12): 2428-2432.

[4] Acharya U R, Molinari F, Sree S V, Chattopadhyay S, Ng K H & Suri J S. Automated diagnosis of epileptic EEG using entropies[J]. Biomed. Signal Process. Control,2012, 7(4): 401-408.

[5] Eckmann J P & Ruelle D. Ergodic theory of chaos and strange attractors [J]. Rev. Mod. Phys., 1985, 57(3): 617-656.

[6] Pincus S M. Approximate entropy as a measure of system complexity [J]. Proc. Natl. Acad. Sci.

U. S. A., 1991, 88(6): 2297-2301.

[7] Richman J S & Moorman J R. Physiological time-series analysis using approximate entropy and sample entropy [J]. Am. J. Physiol.-Heart Circul. Physiol., 2000, 278(6): H2039-H2049.

[8] Costa M, Goldberger A L & Peng C K. Multiscale entropy analysis of complex physiologic time series [J]. Physical Review Letters, 2002, 89(6): 068102.

[9] Ning X B, Xu Y L, Wang J & Ma X F. Approximate entropy analysis of short-term HFECG based on wave mode [J]. Physica A, 2005, 346(3-4): 475-483.

[10] Schreiber T & Schmitz A. Improved surrogate data for nonlinearity tests [J]. Physical Review Letters, 1996, 77(4): 635-638.