EasiCS: the objective and fine-grained classification method of cervical spondylosis dysfunction

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Abstract
The precise diagnosis is of great significance in developing precise treatment plans to restore neck function and reduce the burden posed by the cervical spondylosis (CS). However, the current available neck function assessment method are subjective and coarse-grained. In this paper, based on the relationship among CS, cervical structure, cervical vertebra function, and surface electromyography (sEMG), we seek to develop a clustering algorithms on the sEMG data set collected from the clinical environment and implement the division. We proposed and developed the framework EasiCS, which consists of dimension reduction, clustering algorithm EasiSOM, spectral clustering algorithm EasiSC. The EasiCS outperform the commonly used seven algorithms overall.

Introduction
The cervical spondylosis (CS), a common degenerative disease, harms human life and health, affects up to two-thirds of the population, and poses an serious burden on individuals and society (Matz et al. 2009; Kotil and Bilge 2008; Cai et al. 2016; Nana Wang; Wang et al. 2018). Currently, the neck disability index (Howard Vernon) is the most commonly used tool to assess the neck dysfunction (Vernon and Mior 1991). The availability of which are mainly undermined by the coarse-grained and unreasonable classification, despite that the NDI information is subjective and not accurate enough.

The surface electromyography (sEMG) is a non-stationary weak physiological signal collected by the sEMG device, and consists of the Motor Unit Action Potential Trains (MUAPTs) which is generated by motor units and superimposed on the surface of the skin (Nana Wang). The sEMG is the CS-related physiological signals and have the ability to reflect the neck function status closely related to CS (Wang et al. 2018; Falla et al. 2007; Johnston et al. 2008a; Johnston et al. 2008b; Madeleine et al. 2016). What’s more, the signals is non-intrusive and affordable, and the acquisition is convenient. Thus, we seek to use the sEMG data set collected from the clinical environment to provide more objective and fine-grained classification of cervical function.

As a powerful model-based clustering algorithm, the Self-organizing mapping (SOM) has strong ability of the self-learning, self-organizing, adaptive and nonlinear mapping, which is especially suitable for dealing with nonlinear reasoning, recognition, and classification task without the ground truth on the high dimensional and small-sampling data set (Junlin Chen 2017). Thus, we seek to utilize the SOM clustering algorithm to implement the division on the sEMG data set. Despite of the advantages, the stability is critical for clinical application research. And, the stability clusters are defined in our paper as follow: the stable differences between the individuals of different categories. However, it is an challenging task to obtain a stability clustering results as the samples that are assigned to a group by a trained SOM model are assigned to the different group by second trained SOM, compared with the clustering result of the two trained SOM with the different parameter settings.

In order to achieve it, we proposed and developed the classification framework EasiCS to obtain the relative stability clustering results, which consists of dimension reduction, clustering algorithm EasiSOM, spectral clustering algorithm EasiSC as shown in the Figure 1. To the best of our knowledge, the EasiCS is the first effort to utilize the clustering algorithm and sEMG. Compared with the seven commonly used clustering algorithms, the novelty framework EasiCS provide the best overall performance. The cervical spondylosis (CS), a common degenerative disease, harms human life and health, affects up to two-thirds of the population, and poses an serious burden on individuals and society (Matz et al. 2009; Kotil and Bilge 2008; Cai et al. 2016; Nana Wang; Wang et al. 2018). Currently, the neck disability index (Howard Vernon) is the most commonly used tool to assess the neck dysfunction (Vernon and Mior 1991). The availability of which are mainly undermined by the coarse-grained and unreasonable classification, despite that the NDI information is subjective and not accurate enough.

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The CS is a chronic musculoskeletal disorder, which is mainly accompanied by the neck pain and the disability of human-related functions (Hogg-Johnson et al. 2009). The current classification of the CS is based on clinical symptoms and cervical lesion which was in accordance with 2012 ICD-9-CM Diagnosis Code 721(721.0 Cervical spondylosis without myelopathy, 721.1 Cervical spondylosis with myelopathy) and the diagnostic criteria of diagnosis and treatment for CS issued by China Rehabilitation Medicine Association (gui 2010). There are many studies on CS intelligent classification: clinical-symptoms-based method, cervical-vertebra -lesion-based method, neck-muscle-lesion-based method, traditional Chinese medical classification.

For the clinical-symptoms-based method, with the guidance of the knowledge engineering and expert system construction theory, the work (Jebri et al. 2015) developed the medical diagnostic expert system CSES of cervical spondylosis which use the forward reasoning as the main reasoning mechanism and production rules to represent domain expert knowledge.

For the cervical-spine-lesion-based method, faced with the divergences in the traditional X-ray reading method, the research (Yu et al. 2015) proposed the method based on maximum likelihood theory to solve the type classification of CS, and it is proved to be the effective method. For the degenerative changes of the cervical spine, the research (Jebri et al. 2015) proposed a machine learning approach to detect and localize degenerative changes in lateral X-ray images of the cervical spine, obtaining the 95% accuracy.

For the neck-muscle-lesion-based method, the work (Zhongmin 2011) have demonstrated that there are the stability and reproducibility of myoelectric activity on the surface of normal human cervical muscles, and there are significant differences of surface electromyography index between the cervical spondylosis and the healthy. The work (Nana Wang) proposed a convenient non-harm CS intelligent identify method EasiCNCSII which consists of the sEMG data acquisition and the CS identification, obtaining the 95% accuracy. The research (Wang et al. 2018) proposed an intelligent method EasiDeep based on the deep learning which utilized the surface electromyography (sEMG) signal to identify CS, achieving the state-of-the-art performance. It proves that sEMG contains pathological information of CS which is consistent with the work (Falla et al. 2007; Johnston et al. 2008b; Madeleine et al. 2016). The application of clustering technology has achieved highlighted results in the bioinformatics field as well as the field of image segmentation, object and character recognition. Faced with the problem that the extent to which genomic signatures are shared across tissues is still unclear, the Katherine (Hoadley et al. 2014) developed an integrative analysis to reveal a unified classification into 11 major subtypes. The research (Shen, Olshen, and Ladanyi 2009) developed a joint latent variable model iCluster for integrative

the ability to reflect the neck function status closely related to CS (Wang et al. 2018; Falla et al. 2007; Johnston et al. 2008a; Johnston et al. 2008b; Madeleine et al. 2016). What’s more, the signals is non-intrusive and affordable, and the acquisition is convenient. Thus, we seek to use the sEMG data set collected from the clinical environment to provide more objective and fine-grained classification of cervical function.

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In order to achieve it, we proposed and developed the classification framework EasiCS to obtain the relative stability clustering results, which consists of dimension reduction, clustering algorithm EasiSOM, spectral clustering algorithm EasiSC as shown in the Figure 1. To the best of our knowledge, the EasiCS is the first effort to utilize the clustering algorithm and sEMG. Compared with the seven commonly used clustering algorithms, the novelty framework EasiCS provide the best overall performance.

Figure 1: The EasiCS.
clustering to analyze breast and lung cancer subtype. The research (Shen et al. 2012) utilized the iCluster to present an integrative subtype analysis of the TCGA glioblastoma (GBM) data set, revealing new insights through integrated subtype characterization.

Preliminaries

Participants

The 57 volunteers participated in the study from March 15, 2017 to July 15, 2018 in China, the female number of which is 42 and the male number of which is 15. The subjects have received a clinical diagnosis of the CS, which are in accordance with 2012 ICD-9-CM Diagnosis Code 721 (721.0 Cervical spondylosis without myelopathy, 721.1 Cervical spondylosis with myelopathy) and the criteria of diagnosis and treatment for CS issued by China Rehabilitation Medicine association. The 57 subjects are mainly sedentary people from 27 different occupations and involve 27 types of the CS lesion, the age of which range from 20 to 64.

Dataset

The data set are acquired from 57 volunteers above. The sEMG signal were synchronously recorded from the 6 muscles: the left sternocleidomastoid ($M_0$), the left upper trapezius ($M_1$), the left cervical erector spinae ($M_2$), the right cervical erector spinae ($M_3$), the right upper trapezius ($M_4$) and the right sternocleidomastoid ($M_5$). The volunteers complete the 7 movements $A_{ij}$ ($0 < j < 7$) in sequence, each movement of which is performed 3 times. The sEMG data $S_{i,j}$ is obtained from the muscle $M_i$ activated by the movement $A_j$. The 2949 feature are extracted from the $S_{i,j}$ ($0 < i < 6, 0 < j < 7$), forming a sample $S$. The detail on the $S$ is in the paper (Nana Wang). The 3 samples are from a volunteer, and the 171 ($57 	imes 3$) samples is obtained from the 57 volunteers.

Methodology

In this section, we elaborated our proposed method EasiSC. As shown in Figure 2, the EasiCS consists of three parts: the dimensionality reduction, clustering algorithm EasiSOM, community detection EasiSC.

The dimensionality reduction: locally linear embedding

The high-dimensional sEMG data decreases computational efficiency, increase storage overhead, and cause overfit (Li et al. 2018, Nana Wang), especially for the small sample data sets. Faced with the high-dimensional data, dimensionality reduction is an effective means of data preprocessing. Unlike clustering methods for local dimensionality reduction, the locally linear embedding (LLE), an unsupervised learning algorithm, computes low-dimensional, neighbor-hood-preserving embeddings of high-dimensional inputs and is able to learn the global structure of nonlinear manifolds (Roweis and Saul 2000).

In this paper, we utilized the LLE to deal with the input according to the work (Roweis and Saul 2000). The number of neighbors and the dimension of the data set is set to 30. The $D_o$ is obtained. The general process is shown in the Algorithm 1. The details on calculation are in work (Roweis and Saul 2000).

$$Z_i = (X_i - X_j)^T(X_i - X_j)$$

$$W_i = \frac{Z_i^{-1}1_k}{1_k^T Z_i^{-1}1_k}$$

$$M = (1 - W)(1 - W)^T$$

The EasiSOM

The Self-Organizing Map(SOM) is an excellent tool in exploratory phase of data mining, and projects input space on prototypes of a low-dimensional regular grid that can be effectively utilized to visualize and explore properties of the data (Vesanto, Alhoniemi, and others 2000).

The SOM clustering results are sensitive to initial value settings, leading that there are different clusters result between two trained SOM model with the different parameter settings. And the input $D_o$ of the SOM contains 171 samples from the 57 subjects. A division of the 171 samples reflect the internal relations of the 57 subjects above. Although the divisions are different, we think they contain the common information that reflect the true association of 57 subjects. Thus, according to the ensemble learning, we utilize the multiple SOM algorithm to perform multiple classifications and find a set of partitions to analyze the internal commonality of the division above.

In this paper, as shown in the Algorithm 1 we developed the EasiSOM based on the SOM in our paper, which integrate the 1000 trained SOM to generate the 1000 division results. Finally, a partition set $P_v$ is obtained which includes 625 divisions.

The EasiSC

Next, we seek to find the internal structure of 57 entities behinds the $P_v$. The network is a powerful mechanism, and has the ability to represent the complex relationship between...
Complex systems with interconnected internal entities can be abstracted into networks which have extremely important structure information. The identification of the structure is of crucial importance as they may help to uncover a-prior unknown functional module such as topics in information network or cyber-communities in social networks (Blondel et al. 2008). The spectral clustering algorithm is a classic clustering algorithm based on network topology.

In our work, the EasiSC based on the spectral clustering algorithm are developed to cluster the \( D_o \). As shown in the Algorithm 2, for each sample \( i \) is treated as the network node \( N_i \), and the edge between the node \( N_i \) and \( N_j \) is represented as \( e_{i,j} \). The weight value between nodes is initialized to 0. If the two nodes are divided into the same class in the \( k-th \) division, the weight value is increased by 1. The detail computation on the \( W_{i,j} \) is shown in the Formula 4.

In order to facilitate the subsequent data analysis of 57 subjects, as the clustering results of the three samples of almost all subjects are the same, we mapped the clustering result labels of 171 samples to 57 subject as following rule: the label of a subject is defined as the labels that most samples of a subject have.

\[
W_{i,j} = \sum_{i=1}^{k} X(i,j) \tag{4}
\]

\[
X(i,j) = \begin{cases} 
1 & \text{Sample } i, j \text{ are divided into the same class.} \\
0 & \text{Sample } i, j \text{ are divided into the different class.}
\end{cases}
\]

Where the \( k \) is the number of the divisions from the 625 trained SOM, and the \( i \) and \( j \) is the number of the 171 samples.

Algorithm 1: The EasiSOM algorithm

**Input:** the data set \( D_o \), the partition number \( n_p \), the number \( I_{n o} \) of input neurons, the number \( O_{n o} \) of output neurons, weight vector \( W \), learning rate \( l \), learning rate threshold \( l_t \), neighborhood size \( r \), and the maximum number \( \text{iter}_m \) of iterations.

**Output:** The \( P_s \) including the \( \text{iter} \) division of the data set \( D_o \).

1. Initialize the iteration number \( \text{iter} = 0 \), \( I_{n o} \), \( O_{n o}, \text{iter}_m = 10000 \) and \( n_p = 1000 \);
2. for \( d_n = 0 \) to \( d_n = n_p \) do
3. while \( \text{iter} < \text{iter}_m \) or \( l < l_t \) do
4. Initialize the \( W, l, l_t, r \);
5. Calculate the winning node for each input sample \( X_i \);
6. Update the weight vector \( W \), learning rate \( l \);
7. \( \text{iter} = \text{iter} + 1 \)
8. end while
9. Compute the division \( p_{\text{iter}} \) of the data set \( D_o \);
10. if \( ICS < 0.099 \) then
11. Add the partition \( p_{\text{iter}} \) to the set \( P_s \).
12. end if
13. end for

Algorithm 2: The EasiSC algorithm

**Input:** \( P_s \)

**Output:** The partition \( C \) of the \( P_s \);

1. Compute the minimum cluster number \( \text{min} \);
2. The maximum cluster number \( \text{max} \);
3. Generate weight matrix \( W \);
4. \( k = \text{min} \)
5. while \( k < \text{max} \) do
6. Construct the similar matrix \( S = W \);
7. Construct the adjacent matrix \( A = S \);
8. Construct a standardized Laplacian matrix \( L_m \);
9. Calculate \( k \) minimum eigenvalues and eigenvectors;
10. Use eigenvectors to transform data set \( P_{s} \) to \( k \) dimension \( P_{s,dk} \);
11. Use the \( k \)-means to cluster the data \( P_{s,dk} \) obtain the \( C \);
12. Compute the \( SC \);
13. Add \( SC \) to \( SC_{\text{list}} \);
14. Add \( i \) to \( i_{\text{list}} \);
15. Add \( C_i \) to \( C_{\text{list}} \);
16. \( k = k + 1 \)
17. end while
18. Calculate the partition \( C_k \) with the largest \( SC \).
19. Map the clustering result \( C_k \) of 171 samples to 57 subject.

Algorithm 3: The EasiCS algorithm

**Input:** sEMG data set \( D \)

**Output:** the partition \( C \)

1. Use LLE to reduce the dimension of \( D \);
2. Use EasiSOM to cluster \( D_o \);
3. Use EasiSC to cluster the \( P_s \).

**Experiments Result and Discussion**

**The metrics**

For the lack of the ground truth (the truth label), it is generally believed that the optimal clustering partition minimizes the intra-cluster distance and maximizes inter-cluster distance. The metric (scikit-learn developers) of the Silhouette Coefficient (\( SC \)), Calinski Harabaz score (\( CH \)), Davies Bouldin score (\( DB \)) are the widely used verification indicator to evaluate the quality of the clusters or the performance of the clustering algorithm. The large Silhouette Coefficient
is, the large Calinski Harabaz score is, the smaller Davies Bouldin score is, the better the quality of the clusters are, the better the clustering algorithm perform. Thus, we utilized the indicators \( SC \), \( CH \) and \( DB \) for overall cluster quality evaluation.

The Model for comparison

We compared the EasiSOM with the seven commonly used clustering models: kmeans, affinity propagation, Meanshift, spectral clustering, agglomerative clustering, gaussian mixtures and Birch on the same data set in the same clustering task as follows:

- Kmeans \((M_0)\): The K-Means is an algorithm for clustering data points by computing the average value. It is one of the best-known, bench marked and simplest clustering algorithms \([\text{MacQueen and others 1967}, \text{Saxena et al. 2017}]\).

- Affinity propagation \((M_1)\): Affinity propagation \([\text{Frey and Dueck 2007}]\) is a clustering algorithm based on ‘information transfer’ between data points, which does not need to specify the number of clusters in advance, and can automatically generate the optimal number of clusters.

- Meanshift \((M_2)\): it is a general nonparametric technique, which is used for the analysis of a complex multimodal feature space and to delineate arbitrarily shaped clusters \([\text{Comaniciu and Meer 2002}]\).

- Spectral clustering \((M_3)\): it is a graph-based clustering method. It is simple to implement, can be solved efficiently by standard linear algebra method, and outperforms traditional clustering algorithms \([\text{Von Luxburg 2007}]\).

- Agglomerative clustering \((M_4)\): it is an hierarchical clustering methods and follows the bottom-up approach \([\text{Saxena et al. 2017}]\).

- Gaussian mixtures \((M_5)\): it is a parametric probability density function and commonly used as a parametric model of the probability distribution of continuous measurements or features in a biometric system \([\text{Reynolds 2015}]\).

- Birch \((M_6)\): it is a typical integrated hierarchical clustering algorithm \([\text{Zhang, Ramakrishnan, and Livny 1996}, \text{Ding et al. 2015}]\), which is more suitable for the large amount of data and the large number of clusters.

The comparison of the performance of the model

In order to evaluate the effectiveness of the clustering algorithm, with the metric of \( SC \), \( CH \), \( DB \), and \( ICS \), we compared the performance of the EasiCS with the seven commonly used models as shown in the table 1. And, the EasiCS obtained the largest \( SC \) 0.8220, the second largest value \( CH \) 823.1703, the smallest \( DB \) 0.2408, outperforming the seven algorithms overall.

![Table 1: The performance comparison between different clustering algorithms.](https://example.com/table1.png)

| N  | SC   | CH    | DB    | ICS   |
|----|------|-------|-------|-------|
| \(M_0\) | 56   | 0.4871| 8.7952| 0.9686| 1.75% |
| \(M_1\) | 46   | 0.4547| 7.8716| 1.1452| 2.34% |
| \(M_2\) | 7    | 0.2331| 7.2309| 1.1274| 2.92% |
| \(M_3\) | 48   | 0.4226| 7.5257| 1.2397| 7.60% |
| \(M_4\) | 56   | 0.4535| 8.7116| 0.9800| 5.26% |
| \(M_5\) | 55   | 0.4848| 8.7501| 0.9808| 3.51% |
| \(M_6\) | 56   | 0.4803| 8.9374| 0.9687| 4.68% |
| SOM | 13   | 0.7551| 2740.1569| 0.3399| 4.09% |
| EasiCS | 5    | 0.8220| 823.1703| 0.2408| 1.17% |

![Table 2: The consistency comparison.](https://example.com/table2.png)

| Std_SC   | Std_CH   | Std_DB   |
|----------|----------|----------|
| SOM      | 0.1233   | 5982.5545| 0.1696 |
| EasiCS   | 0.1188   | 606.3688 | 0.0989 |

The model consistency comparison

In order to evaluate the stable of the clustering algorithm, with the metric of \( \text{Std}_\text{num} \), \( \text{Std}_\text{SC} \), \( \text{Std}_\text{CH} \), \( \text{Std}_\text{DB} \) and \( \text{Std}_\text{ICS} \), we compared the performance EasiCS with the SOM in the table 2. And, the EasiCS obtained the smallest \( \text{Std}_\text{num} \) 1.2635, the smallest \( \text{Std}_\text{SC} \) 0.1188, the smallest \( \text{Std}_\text{CH} \) 606.3688, and the smallest \( \text{Std}_\text{DB} \) 0.0989. Compared with the SOM, the EasiCS have the smaller change, which means that the EasiSOM have the more stable cluster result.

Conclusions

In this study, based on the relationship between cervical structure, cervical vertebrae function and CS, we developed the novelty framework based on the clustering algorithms to implement the division of the function, using the high-dimensional and small-sampling of the CS-related sEMG data, which consists of the dimension reduction, clustering algorithm EasiSOM, spectral clustering algorithm EasiSC. With the metric of the Silhouette Coefficient, the Calinski Harabaz score is, the smaller Davies Bouldin score is, the better the quality of the clusters are, the better the clustering algorithm perform. Thus, we utilized the indicators \( SC \), \( CH \) and \( DB \) for overall cluster quality evaluation.
Harabaz score and the Davies Bouldin score, the EasiCS achieved the best overall performance compared with the seven commonly used clustering algorithms.

Thus, we will collect and utilize more diverse and comprehensive data to classify CS more precisely and explore the law behind the pathogenesis of CS and classification, providing more knowledge about CS prevention and treatment.

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