Fuzzy clustering of short time series and unevenly distributed sampling points.

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Abstract

This paper proposes a new clustering algorithm in the fuzzy-c-means family, which is designed to cluster time series and is particularly suited for short time series and those with unevenly spaced sampling points. Short time series, which do not allow a conventional statistical model, and unevenly sampled time series appear in many practical situations. The algorithm developed here is motivated by experiments in biology. Conventional clustering algorithms based on the Euclidean distance or the Pearson correlation coefficient, such as hard k-means or hierarchical clustering are not able to include the temporal information in the distance measurement. Uneven sampling commonly occurs in biological experiments. The temporal order of the data is important and the varying length of sampling intervals should be considered in clustering time series. The proposed short time series (STS) distance is able to measure similarity of shapes which are formed by the relative change of amplitude and the corresponding temporal information. We develop a fuzzy time series (FSTS) clustering algorithm by incorporating the STS distance into the standard fuzzy clustering scheme. An example is provided to illustrate the performance of the proposed FSTS clustering algorithm in comparison with fuzzy c-means, k-means and single linkage hierarchical clustering.

Keywords: *Microarray data, unevenly sampled short time series, fuzzy clustering.*

Running Head: *FSTS clustering of time series data.*

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1 Introduction

Microarrays revolutionize the traditional way of one gene per experiment in molecular biology (Brown and Botstein 1999, Duggan et al. 1999, Brazma and Vilo 2000). With microarray experiments it is possible to measure simultaneously the activity levels for thousands of genes. The appropriate clustering of microarray expression data can lead to classification of diseases, identification of co-expressed functionally related genes, functional groupings of genes, and logical descriptions of gene regulation, among others (D'Haeseleer et al. 1999, Tavazoie et al. 1999).

Time course measurements are becoming a common type of experiments in the use of microrarrays, (DeRisi et al. 1997, Chu et al. 1998, Cho et al. 1998, Eisen et al. 1998, Spellman et al. 1998). If a process is subject to variations over time, the conventional measures used for describing similarity (e.g. Euclidean distance) will not provide useful information about the similarity of time series in terms of the cognitive perception of a human (Höppner 2001). An appropriate clustering algorithm for short time series should be able to identify similar shapes which are formed by the relative change of expression and the temporal information, regardless of absolute values. The conventional clustering algorithms based on the Euclidean distance or the Pearson correlation coefficient, such as hard k-means (KM) or hierarchical clustering (HC) are not able to include temporal information in the distance measurement. Figure 1 shows three time series with different shapes. The appropriate distance metric for gene expression clustering would identify that g_2 is more similar to g_3 than to g_1, since the deviation of shape across time of g_3 from the shape of g_2 is less than that of g_1. The Euclidean distance and the Pearson correlation coefficient do not take into account the temporal order and the length of sampling intervals; for these metrics both g_1 and g_3 are equally similar to g_2. In this paper we introduce a new clustering algorithm which is able to use the temporal information of uneven sampling intervals in time series data to evaluate the similarity of the shape in the time domain. This paper is organized as follows: Section 2 defines the objective and basic concepts of the piecewise slope (PS) distance based on the requirements of short time series clustering. In Section 3, the fuzzy short time series (FSTS) algorithm is introduced as a modification of the standard fuzzy c-means algorithm (FCM). Section 4 presents an artificial data set to illustrate and compare the performance of the proposed algorithm with FCM, KM and

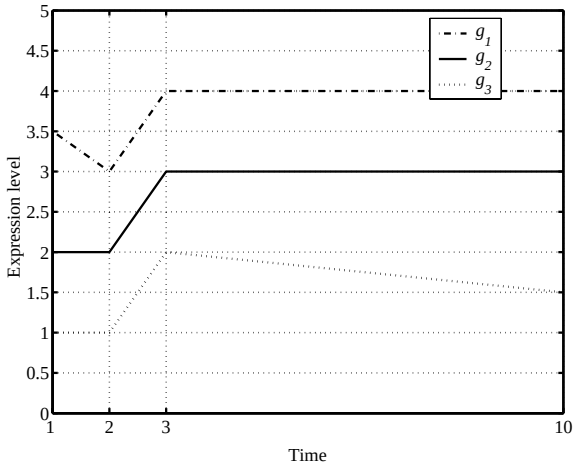


Figure 1: Three unevenly sampled time series with different shapes.

single linkage HC. Finally, conclusions are made in Section 5 summarizing the presented research.

2 Piecewise slope distance

This section presents a measurement of similarity for time series DNA microarray data based on the requirements of gene expression time series clustering. The performance of the distance is illustrated by means of simple tests where temporal information is a key aspect.

The objective is to define a distance which is able to capture differences in the shapes, defined by the relative change of expression and the corresponding temporal information, regardless of the difference in absolute values. We approach the problem by considering the time series as piecewise linear functions and measuring the difference of slopes between them. Considering a gene expression profile $x = [x_0, x_1, \ldots, x_{n_t}]$, where n_t is the number of time points, the linear function $x(t)$ between two successive time points t_k and $t_{(k+1)}$ can be defined as $x(t) = m_k t + b_k$, where $t_k \leq t \leq t_{(k+1)}$, and

$$m_k = \frac{x_{(k+1)} - x_k}{t_{(k+1)} - t_k} \quad (1)$$

$$b_k = \frac{t_{(k+1)} x_k - t_k x_{(k+1)}}{t_{(k+1)} - t_k}. \quad (2)$$

The STS distance we propose corresponds to the sum of the squared differences of the slopes obtained by considering time series as linear functions between measurements. The

STS distance between two time series x and v is defined as:

$$d^2_{\mathrm{STS}}(x,v) = \sum_{k=0}^{n_t-1} \left(\frac{v_{(k+1)} - v_k}{t_{(k+1)} - t_k} - \frac{x_{(k+1)} - x_k}{t_{(k+1)} - t_k} \right)^2. \tag{3}$$

To evaluate the performance of this distance in comparison with the Euclidean distance and the Pearson correlation coefficient, two simple tests are performed. The objective of the first test is to evaluate the ability to incorporate temporal information to the comparison of shapes. The objective of the second test is to evaluate the ability to compare shapes regardless of the absolute values.

For the first test, let us consider the time series shown in Figure 1. Table 2 illustrates the corresponding STS distance, Euclidean distance, and the Pearson correlation coefficient between g_2 and g_1, and g_2 and g_1, respectively. The results show that the STS distance is the unique metric which reflects the temporal information in the comparison of shapes.

	Euclidean distance	STS distance	Pearson correlation coefficient
(g_2, g_1)	1.513	0.500	0.904
(g_2, g_3)	1.513	0.071	0.904

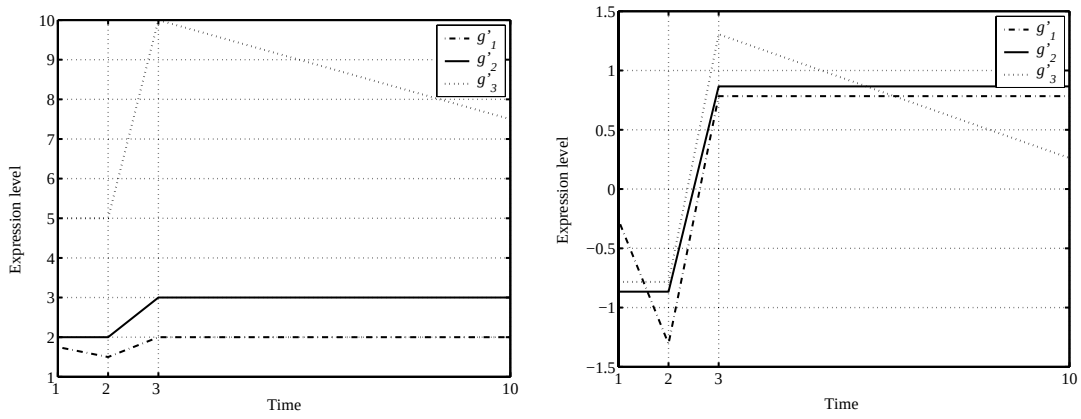
Table 1: STS distance, Euclidean distance, and Pearson correlation coefficient between g_2 and g_1, and g_2 and g_1.

For the second test, let us consider a linear transformation of the absolute values of the time series shown in Figure 1. These modified series are shown in Figure 2(a). Since the STS and the Euclidean distance are both sensitive to scaling, a z-score standardization of the series is required for them to neglect absolute values (Everitt 1974). The z-score of the ith time point of a gene x is defined in (4), where $\overline{x}$ is the mean and s_x the standard deviation of all the time points $x_1, \ldots, x_n$ in vector x

$$z_i = \frac{(x_i - \overline{x})}{s_x}. \tag{4}$$

The time series after standardization are shown in Figure 2(b).

Table 2 summarizes the STS distance, the Euclidean distance, and the Pearson correlation coefficient between g'_2 and g'_1, and g'_2 and g'_1. The results show that the STS distance was the unique distance which can properly capture the temporal information.



(a) Before standardization

(b) After standardization

Figure 2: Three unevenly sampled time series data with different shapes, which correspond to linear transformations of the time series in Figure 1.

	Euclidean distance	STS distance	Pearson correlation coefficient
(g_2, g_1)	0.870	1.103	0.904
(g_2, g_3)	0.870	0.386	0.904

Table 2: STS distance, the Euclidean distance, and the Pearson correlation coefficient between g_2' and g_1', and g_2' and g_1'.

3 Fuzzy piecewise slope clustering algorithm

This section introduces the FSTS clustering algorithm as a FCM clustering algorithm (Bezdek 1981). We present the minimization of the standard objective function and the resulting cluster prototypes.

There are a wide variety of clustering algorithms available from diverse disciplines such as pattern recognition, text mining, speech recognition and social sciences amongst others (Everitt 1974, Jain and Dubes 1988). The algorithms are distinguished by the way in which they measure distances between objects and the way they group the objects based upon the measured distances. In the previous section we have already established the way in which we desire the "distance" between objects to be measured; hence, in this section, we focus on the way of grouping the objects based upon the measured distance. For this purpose we select a fuzzy clustering scheme, since fuzzy sets have a more realistic approach to address the concept of similarity than classical sets (Zadeh 1965). A classical set has a crisp or hard boundary where the constituting elements have only two possible values of membership, they either belong or not. In contrast, a fuzzy set is a set with fuzzy boundaries where each element is given a degree of membership to each set.

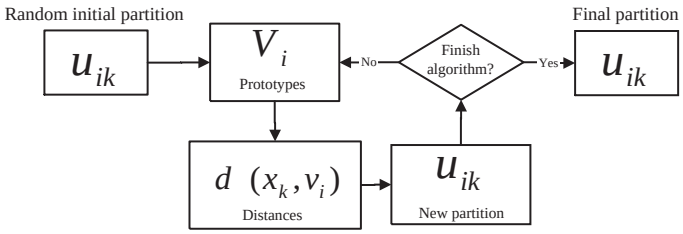


Figure 3: Diagram of the iteration procedure for the FCM clustering algorithms. Considering the partition of a set $X = [x_1, x_2, \ldots, x_g]$, into $2 \leq c < g$ clusters, the fuzzy clustering partition is represented by a matrix $U = [u_{ik}]$, whose elements are the values of the membership degree of the object x_k to the cluster i, $u_i(x_k) = u_{ik}$.

Fuzzy clustering is a partitioning-optimization technique which allows objects to belong to several clusters simultaneously with different degrees of membership to each cluster (Bezdek 1981, Höppner et al. 1999). The objective function that measures the desirability of partitions is described in (5), where n_c is the number of clusters, n_g is the number of vectors to cluster, u_{ij} is the value of the membership degree of the vector x_j to the cluster i, and $d^2(x_j, v_i)$ is the squared distance between the vector x_j and the prototype v_i.

$$J(x, v, u) = \sum_{i=1}^{n_c} \sum_{j=1}^{n_g} u_{ij}^w \, d^2(x_j, v_i) \ . \tag{5}$$

Figure 3 illustrates the iteration steps of the FCM algorithm, the representative of the fuzzy clustering algorithms. In order to use the STS distance following the conventional fuzzy clustering scheme, we need to obtain the value of the prototype v_k that minimizes (5), when (3) is used as the distance. Substituting (3) into (5) we obtain

$$J(x, v, u) = \sum_{i=1}^{n_c} \sum_{j=1}^{n_g} u_{ij}^w \sum_{k=0}^{n_t - 1} \left(\frac{v_{i(k+1)} - v_{ik}}{t_{(k+1)} - t_k} - \frac{x_{j(k+1)} - x_{jk}}{t_{(k+1)} - t_k} \right)^2 . \tag{6}$$

The partial derivative of (6) with respect to v_{ik} is:

$$\begin{aligned}
\frac{\partial J(x, v, u)}{\partial v_{ik}} &= \sum_{j=1}^{n_g} u_{ij}^w \, \frac{\partial}{\partial v_{ik}} \left(\left(\frac{v_{(k+1)} - v_k}{t_{(k+1)} - t_k} - \frac{x_{(k+1)} - x_k}{t_{(k+1)} - t_k} \right)^2 + \left(\frac{v_k - v_{(k-1)}}{t_k - t_{(k-1)}} - \frac{x_k - x_{(k-1)}}{t_k - t_{(k-1)}} \right)^2 \right) \\
&= \sum_{j=1}^{n_g} u_{ij}^w \left[\frac{2 \left(v_{ik} - v_{i(k+1)} - x_{jk} + x_{j(k+1)} \right)}{\left(t_k - t_{(k+1)} \right)^2} \right] - \left[\frac{2 \left(v_{i(k-1)} - v_{ik} - x_{j(k-1)} + x_{jk} \right)}{\left(t_k - t_{(k-1)} \right)^2} \right] \\
&= \sum_{j=1}^{g} 2 u_{ij}^w \, \frac{\left(a_k v_{i(k-1)} + b_k v_{ik} + c_k v_{i(k+1)} + d_k x_{j(k-1)} + e_k x_{jk} + f_k x_{j(k+1)} \right)}{\left(t_k - t_{(k+1)} \right)^2 \left(t_k - t_{(k-1)} \right)^2}
\end{aligned} \tag{7}$$

where

$$
\begin{aligned}
a_k &= -(t_{(k+1)} - t_k)^2 \\
b_k &= -(a_k + c_k) \\
c_k &= -(t_k - t_{(k-1)})^2 \\
d_k &= (t_{(k+1)} - t_k)^2 \\
e_k &= -(d_k + f_k) \\
f_k &= (t_k - t_{(k-1)})^2.
\end{aligned}
$$

Setting (7) equal to zero and solving for v_k we have

$$
\begin{aligned}
\sum_{j=1}^{n_g} u_{ij}^w \left(a_k v_{i(k-1)} + b_k v_{ik} + c_k v_{i(k+1)}\right) &= -\sum_{j=1}^{n_g} u_{ij}^w \left(d_k x_{j(k-1)} + e_k x_{jk} + f_k x_{j(k+1)}\right) \\
\left(a_k v_{i(k-1)} + b_k v_{ik} + c_k v_{i(k+1)}\right) \sum_{j=1}^{n_g} u_{ij}^w &= -\sum_{j=1}^{n_g} u_{ij}^w \left(d_k x_{j(k-1)} + e_k x_{jk} + f_k x_{j(k+1)}\right) \\
a_k v_{i(k-1)} + b_k v_{ik} + c_k v_{i(k+1)} &= -\frac{\sum_{j=1}^{n_g} u_{ij}^w \left(d_k x_{j(k-1)} + e_k x_{jk} + f_k x_{j(k+1)}\right)}{\sum_{j=1}^{n_g} u_{ij}^w} \\
a_k v_{i(k-1)} + b_k v_{ik} + c_k v_{i(k+1)} &= m_{ik} \qquad (8)
\end{aligned}
$$

where

$$
m_{ik} = -\frac{\sum_{j=1}^{n_g} u_{ij}^w \left(d_k x_{j(k-1)} + e_k x_{jk} + f_k x_{j(k+1)}\right)}{\sum_{j=1}^{n_g} u_{ij}^w}.
$$

Equation (8) yields an undetermined system of equations. We know the relations of the prototype values among the time points, but not the absolute value at each time point. That is, we know the shape but not the absolute level. If we add two fixed time points at the beginning of the series with a value of 0, then solving the system for any n_t, the prototypes can be calculated as

$$
\begin{aligned}
v(i,n) &= \sum_{r=2}^{n-3} m_{ir} \prod_{q=1}^{r-1} c_q \left[\prod_{q=r+1}^{n-1} a_q + \prod_{q=r+1}^{n-1} c_q + \sum_{p=r+3}^{n} \prod_{j=p-1}^{n-1} c_j \prod_{j=r+1}^{p-2} a_j \right] \Big/ \prod_{q=2}^{n-1} c_q + \\
& \quad m_{i(n-1)} \prod_{q=1}^{n-2} c_q \Big/ \prod_{q=2}^{n-1} c_q + m_{i(n-2)} \prod_{q=1}^{n-3} c_q (a_{(n-1)} + c_{(n-1)}) \Big/ \prod_{q=2}^{n-1} c_q. \qquad (9)
\end{aligned}
$$

where $m_{i1} = 0$ and $c_1 = 1$.

The same scheme of the iterative process as for the FCM, described in Figure 3 is followed, but the distance and the prototypes are calculated using (3) and (9), respectively. The same three user-defined parameters found in the FCM algorithm; the number of clusters n_c, the threshold of membership to form the clusters α, and the weighting exponent w are also found in the proposed FSTS algorithm. The weighting exponent refers to the fuzziness of the clustering results, a value of one will produce hard clusters and the larger the value of w the fuzzier the clusters become. Figure 4 illustrates the pseudocode of the proposed FSTS clustering algorithm.

STEP 1: Initialization

n_g	:	number of genes
n_t	:	number of time points
X	:	gene expression matrix (GEM) $[n_g \times n_t]$
n_c	:	number of clusters
w	:	fuzzy weighting factor
a	:	threshold for membership
ϵ	:	termination tolerance

STEP 2: Initialization of the partition matrix
Initialize the partition matrix randomly, $U^{(0)}$ $[n_c \times n_g]$.

STEP 3: Repeat for $l = 1, 2, ...$
3.1 Compute the cluster prototypes:
$v(i,1)^{(l)} = 0$,
$v(i,2)^{(l)} = 0$,
For $v(i,n)^{(l)}$ use Equation (9) $1 \leq i \leq n_c, \quad 3 \leq n \leq n_t$.
3.2 Compute the distances:

$$d^2_{\mathrm{STS}}(x_j, v_i) = \sum_{k=0}^{n_t-1} \left(\frac{v^{(l)}_{i(k+1)} - v^{(l)}_{ik}}{t_{(k+1)} - t_k} - \frac{x_{j(k+1)} - x_{jk}}{t_{(k+1)} - t_k} \right)^2$$

$$1 \leq i \leq n_c, \quad 1 \leq j \leq n_g.$$

3.3 Update the partition matrix:
if $d_{\mathrm{STS}ij} > 0$ for $1 \leq i \leq n_c$, $1 \leq j \leq n_g$,

$$u^{(l)}_{ij} = \frac{1}{\sum_{q=1}^{n_c} (d_{\mathrm{STS}ij}/d_{\mathrm{STS}qj})^{1/(w-1)}},$$

otherwise $u^{(l)}_{ij} = 0$ if $d_{\mathrm{STS}ij} > 0$, and $u^{(l)}_{ij} \in [0,1]$ with $\sum_{i=1}^{n_c} u^{(l)}_{ij} = 1$.
until $U^{(l)} - U^{(l-1)} < \epsilon$.

Figure 4: Pseudo code of the FSTS clustering algorithm.

4 Illustrative example

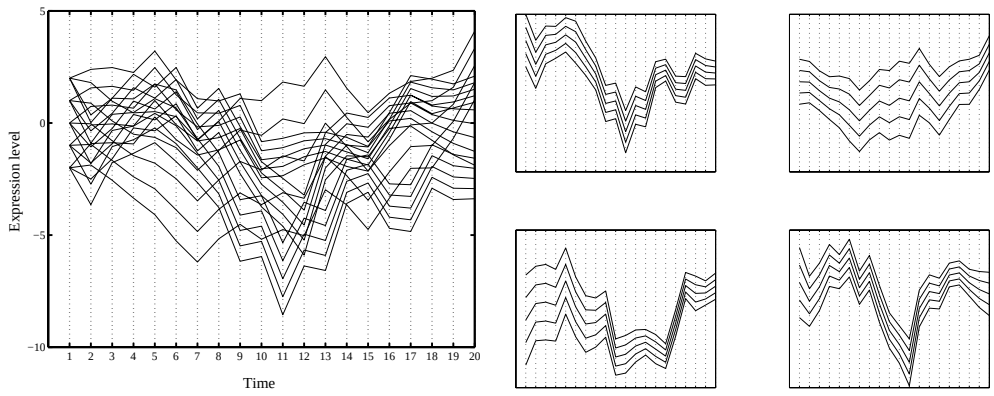
This section presents a simple artificial data set to illustrate and compare the performance of the proposed FSTS clustering algorithm in terms of the cognitive perception of a human.

Four groups of five vectors were created where each group has the same parameters of linear transformation between time points, as shown in Table 4. That is, for the group i, $1 \leq i < 4$, $x_{j(k+1)} = m_{ik}x_{jk} + b_{ik}$, with $0 \leq k < (n_t - 1)$ and $1 \leq j < 5$. The values of m and b were obtained randomly for each group.

Time points	Value
x_0	initial value
x_1	$m_1x_0 + b_1$
x_2	$m_2x_1 + b_2$
$\vdots$	$\vdots$
x_{n_t}	$m_{(n_t-1)}x_{(n_t-1)} + b_{(n_t-1)}$

Table 3: Artificial profile $x = [x_0, x_1, \ldots, x_{n_t}]$. A group of vectors with similar shape can be obtained by changing the initial value.

The resulting artificial data set, shown in Figure 5(a), was clustered using FCM, FSTS, KM and HC algorithms, respectively. All the algorithms were able to identify the four clusters shown in Figure 5(b) successfully. The clustering parameters were $w = 1.6$ and $\alpha = 0.4$ for the two fuzzy algorithms.

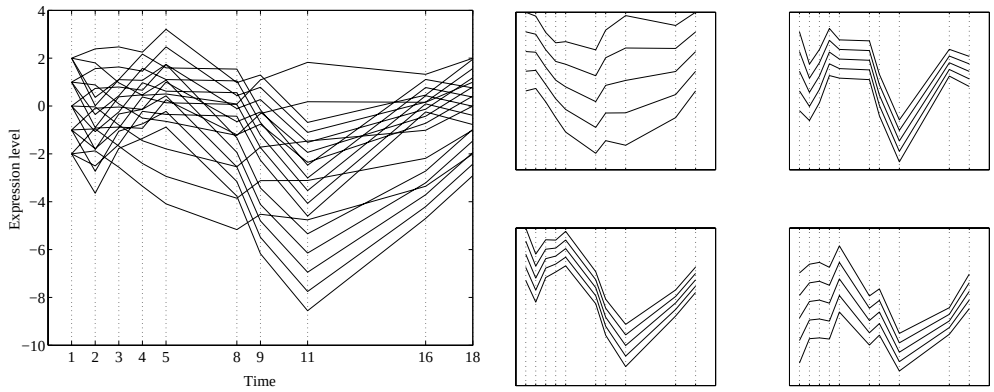


(a) Artificial Data (b) Clustering results

Figure 5: Artificial data set and clustering results for FCM, FSTS, HK and HC algorithms.

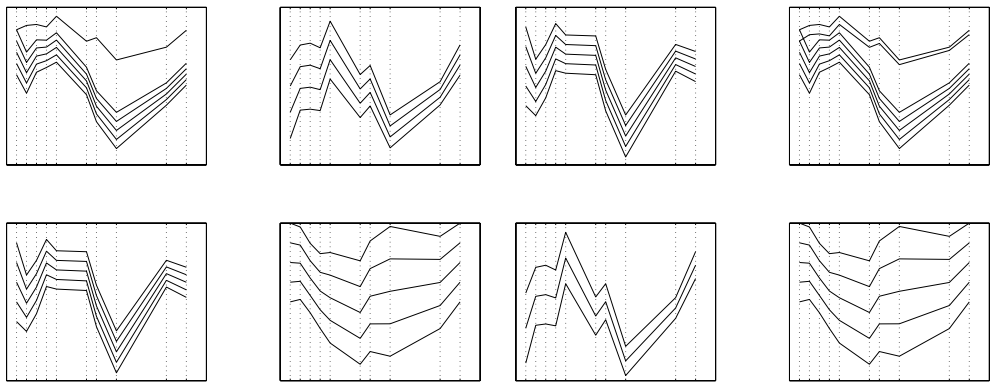
The second test used a subset of the artificial data set shown in Figure 5(a). The original data set was "resampled" selecting 10 time points randomly out of the 20 original time points. The resulting data set is shown in Figure 6(a). In this case, only the FSTS algorithm is able to identify the four clusters successfully, while FCM and HC identify two clusters and the other two mixed, as shown in Figure 7 and HC does not produce consistent results. The clustering parameters for the FSTS algorithm were $w = 1.2$ and $\alpha = 0.6$. Different parameters were tested for the FCM, $1.2 < w < 2.5$ and $0.3 < \alpha < 0.6$

giving unsuccessful results. Finally the algorithms were evaluated using the three time series data presented in Section 2. The objective is to cluster g_1, g_2 and g_3 in two clusters. The FSTS algorithm is the unique method capable of grouping g_2 with g_3 separated from g_1 consistently. FCM, HK, and HC do not have consistent results since they find g_2 as similar to g_1 as to g_3 as described in Section 2.



(a) Unevenly resampled artificial data (b) Consituting clusters

Figure 6: Unevenly resampled artificial data set and the constituting clusters.



(a) FCM clustering results (b) HC clustering results

Figure 7: Clustering results for FCM and HC algorithms.

5 Conclusions

The FSTS clustering algorithm was presented as a new approach to cluster short time-series. The algorithm is particularly well suited for varying intervals between time points, a situation that occurs in many practical situations, in particular in biology. The FSTS algorithm is able to identify similar shapes formed by the relative change and the temporal information, regardless of the absolute levels. Conventional clustering algorithms, includ-

ing FCM, KM, or HC, are not able to properly include the temporal information in the distance metric. We tackled the problem by considering the time series as piecewise linear functions and measuring the difference of slopes between the functions. We illustrated the algorithm with an artificial data set. The FSTS algorithm showed better performance than the conventional algorithms in clustering unevenly sampled short time series data.

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