

## Combining Multiple Concurrent Physiological Streams to Assessing Patients Condition

Shenda Hong, Zhen Qiu, Jinbo Zhang and Hongyan Li \*

Key Laboratory of Machine Perception, Ministry of Education  
School of EECS, Peking University, Beijing, 100871, China  
{hongshenda, qiuzhen, zhangjinbo, lihy}@cis.pku.edu.cn

### Abstract

Multiple concurrent physiological streams generated by various medical devices play important roles in patient condition assessment. However, these physiological streams need to be analyzed together and output in real-time for precise and timely controlling and management, which poses a non-trivial challenge to existing methods. This paper presents our research on real-time assessing based on this kind of data. To address this problem, we first extract sketches from original data with the help of adaptive sampling and wave splitting algorithm, then define scalable operators on sketches and propose MUNCA (MULTI-dimensional Nearest Center Analysis) to combine these multiple concurrent data together for analysis. Experiments on real data demonstrate the effectiveness and efficiency of the proposed method.

### Introduction

Patient condition assessment is one of the most helpful measure in clinical process. It assesses many aspect of a patient systematically and comprehensively, concludes an over all judgment of patient's condition and gives them proper treatments. It provides clinical staffs a wealth of information for disease controlling and clinical management.

In most cases, clinical staffs assess by their experience. These biomarkers extracted by human-being are very limited for deep-level diagnosis. Recent advances in hospitals, various kinds of devices work together to record physiological streams for one patient. These devices are generating multiple concurrent physiological streams in every moment. It provides clinical staffs a huge amount of data which can be used for patient condition assessment. Assessing from physiological streams is one of the most promising way to promoting assessing accuracy and relieving human power.

However, physiological streams generate continuously in high speed. Even an professional physician can not discover subtle abnormal waves perspectively. Besides, patients in Intensive Care Unit (ICU) require medical attention all the time. It requires a huge demand of specialized clinical staffs which is already in shortage. Thus, assessing patient condition over multiple concurrent physiological streams auto-

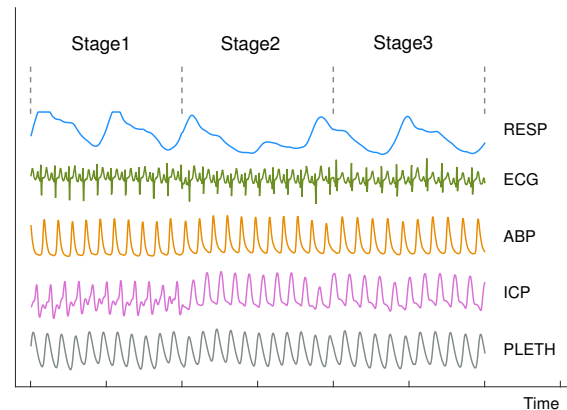


Figure 1: Patient Condition Stages and Related Physiological Streams in ICU

matically and timely has become a significant task (Ghassemi et al. 2015; Hammerla et al. 2015).

However, existing analyzing methods on physiological streams are very limited for above tasks. To combine multiple concurrent physiological streams for assessing while output results in real-time, they faced up with the following three challenges.

1. **High Velocity and Huge Volume** A typical device in ICU is multi-parameter monitor, it generates more than one hundred million points per day per patient (Tang et al. 2007). Effectiveness and efficiency are in dilemma in the situation of high data velocity and huge data volume. Point based methods require huge computation resources which won't output results in real-time. Symbolic based methods summarize a sequence of streaming data which may lose accuracy.
2. **Morphological Analysis** Recent work on analyzing physiological streams has shown the association between morphology and patient condition stages (Chia et al. 2014). It reveals that patients stage is not associated with some exact points, it's determined by the values in a certain period represented as a wave. Small analyzing granularity would be insensitive to overall variation while large analyzing granularity would neglect some critical shifts. Both of them would not consider waves as analyzing

\*Corresponding author

units.

- Concurrency and Correlation** The human body is a complex integration of physiological and pathological processes. Most biological processes are mutually correlated and bound together by physical or physiological control and communication phenomena. Analyzing any single process may only provide partial information and pose difficulties in the comprehension of the process. Physiological streams from various sources including hearts, brains and endocrine require researchers consider every physiological stream concurrently to obtain the complete information. Thus, simply implement methods of single stream in the multiple streams condition repeatedly would get bias results or even contradictory results.

To address these challenges, this paper propose a novel assessing approach for multiple physiological streams. We first introduce an adaptive sampling algorithm to keep a balance between efficiency and effectiveness. Then choose waves as our concerned granularity and use sketches to represent the outline of original data. Finally, we develop MUNCA (MUlti-dimensional Nearest Center Analysis) to combine sketches of various streams together for analysis. Experiments on real data demonstrate the effectiveness and efficiency of the proposed method.

The rest of the paper is organized as follows. First, we describe preliminaries and give an overview of our work. Physiological sketches extraction is introduced afterwards. After we present assessing method based on sketches, we show experiments on our approach. And then we introduce the related work. Lastly, we conclude the research and gives directions for future studies.

## Preliminaries

In this section, we formally define the problem of assessing over multiple physiological streams, and describe the framework of our method.

**Definition 1.** (*Multiple Concurrent Physiological Streams*): Let  $\{S^{(1)}(t), S^{(2)}(t), \dots, S^{(N)}(t)\}$  denote  $N$  source multiple physiological streams that are all associated with one patient.

we use  $\Delta t$  represent sample time interval. Then we can get that  $S^{(d)}(t_0 + \Delta t)$  is the next point of  $S^{(d)}(t_0)$  in  $d$ th stream. For simplicity, we use  $S(t_i)$  or  $S(t)$  to represent one of the physiological streams in this section, other streams are handled similarly.

**Definition 2.** (*Stage*): Let  $Y(t)$  denote the stage function,  $Y(t) \in \{Y_1, Y_2, \dots, Y_L\}$ , the codomain is a finite set of nominal value, which indicate various conditions of a patient.

Some key properties in multiple concurrent physiological streams include (Tang et al. 2007):

- The morphology of waves are similar in a certain stage of all people;
- The morphology of waves are dissimilar in different stages of all people;

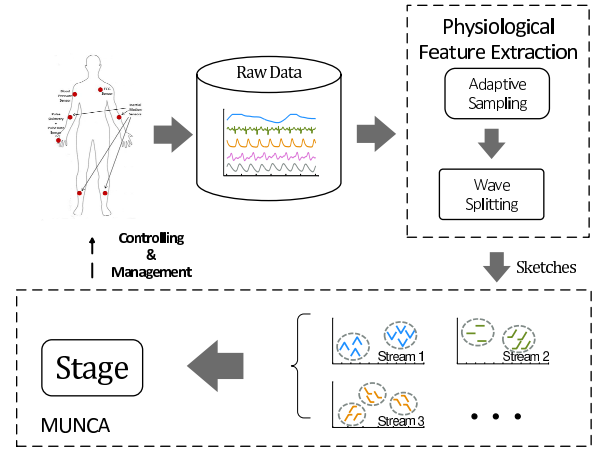


Figure 2: Framework

- Critical shifts appear from one wave to another are considered significant.

Based on that, we propose our approach illustrated in Fig.2. Our goal is to give current stage  $Y(t)$  based on multiple medical streams. We first extract sketches using adaptive sampling and wave splitting algorithm; Then we split each data streams into meaningful waves; Next, we build our assessing method MUNCA and implement online learning. Finally, we can assess current stage over medical streams in real-time.

## Physiological Sketches Extraction

It's critical to extract useful information from such a huge amount of high speed data streams. In this section, we propose a suite of approaches to effectively compress the data while keep the outline of the original data, and split sampled data to get sketches (can be regard as features) for further analysis.

### Adaptive Sampling

To achieve real-time assessing, it's indispensable to extract a fraction of points from original data while keeping the outline. A widely used way is sampling in fixed interval from original data. It's simple and convenient but would lead to concept drifting due to the pseudo periodicity of physiology streams. Advanced methods like PLR (Tang et al. 2007) and SAX (Lin et al. 2003) have the computational complexity of  $O(n^2)$ , which are not satisfied with real-time assessing. Others like PIP (Fu et al. 2008) only capture the local extreme points which is insensitive to overall variation.

An adaptive way is to associate sampling interval with variation magnitude represented by derivative. However, we can't calculate derivative from streaming data directly since these discrete points can't deduce derivative function. A feasible solution is to use absolute numerical central differentiation to approximate actual derivative as Eq.1 shows. The accuracy can reach to  $O(\Delta t)^4$ .

$$D(t) = \frac{-S(t + 2\Delta t) + 8S(t + \Delta t) - 8S(t - \Delta t) + S(t - 2\Delta t)}{12\Delta t} \quad (1)$$

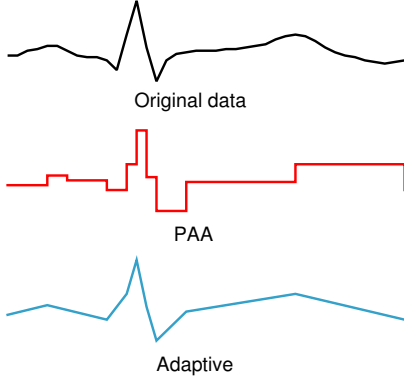


Figure 3: Adaptive Sampling

Intuitively, we want to increase sampling density as  $D(t)$  increasing, and decrease sampling density as  $D(t)$  decreasing. We choose sampling timestamp  $t_i$  using formula:

$$t_i = t_{i-1} + \lfloor \frac{\beta}{|D(t)|} \rfloor \Delta t \quad (2)$$

$$s(i) = S(t_i)$$

Where  $\beta$  is a parameter controlling sampling density,  $s(i)$  is sampled data and  $S(t_i)$  is original data. The computational complexity of sampling is  $O(n)$ .

### Wave Splitting

To get waves for analyzing, we should split each long term stream of multiple concurrent streams into consecutive waves. However, simply dividing data streams in fixed length will accumulate error leading to concept drifting due to the inequality of consecutive waves. Besides, dividing streams into waves at the key points directly will also divide the critical shift into separated parts. To weakening the disturbance of noise and long-term trend while maintaining integrity of waves and critical shifts, while finding split position correctly. It can be achieved by following steps:

1) Differentiation. To obtain information on critical shifts and overcome the concept drift problem.

$$S(t) = \frac{S(t + \Delta t) - S(t - \Delta t)}{2\Delta t} \quad (3)$$

2) Squaring operation. To amplify the magnitude of critical shifts while makes all data points positive.

$$S(t) = S(t)^2 \quad (4)$$

3) Moving average filter. To reduce noise and smooth fluctuation.

$$S(t) = \frac{S(t) + S(t - \Delta t) + \dots + S(t - (M - 1)\Delta t)}{M\Delta t} \quad (5)$$

Where  $M\Delta t$  is the length of moving average.

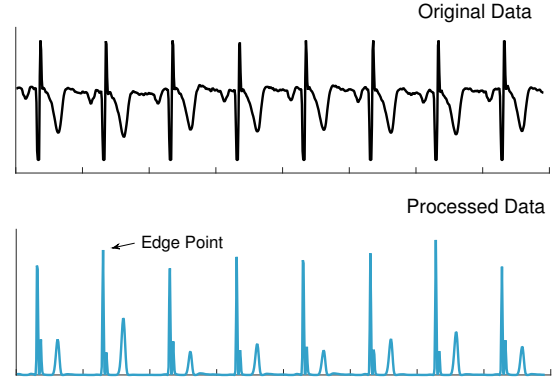


Figure 4: Wave Splitting

4) Divide by edge points. We detect elbow points in processed streams as split position in original streams.

The computational complexity of splitting is  $O(Mn)$ .

### Aligning Sketches

After splitting, we get series of subsequences represents each stream of all multiple concurrent streams. These subsequences are defined as sketches.

**Definition 3.** (Sketch): Some key points sequence that keep the outline of the original waves. The  $i$ th sketch in  $j$ th devices denote as  $sk_j^{(i)}$ .

Besides, aligning sketches in each stream to conduct a batch of input shouldn't be ignored. We choose the first stream as standard timestamp, and align sketches' timestamp in other streams.

### Multi-dimensional Nearest Center Analysis

In this section, we will introduce MUNCA and implement it on these aligned batches of sketches to get assessed stages.

### Scalable Operators on Sketch

After preprocessing, the length of sketches are not the same in most cases. Normal operations can not be applied in Euclid space on different length vectors. A common solution is to truncate the longer sketch to the shorter one, or padding the shorter sketch to the longer one. It may lose importance feature on sketches, or adding nonsense sequence. Another solution is to embed sketches into a lower dimensional space using Multidimensional Scaling (MDS) (Young 2013), but it requires heavy computation.

Thus, computation on sketches require special operators that can handle with scalable situation. Inspired by warping path in Dynamic Time Warping (Rakthanmanon et al. 2012), we denote an elastic projection from one sketch to another. For formal definition, a  $m$  length sketch  $s_i = (x_1, x_2, \dots, x_m)$  and a  $n$  length sketch  $s_j = (y_1, y_2, \dots, y_n)$ . then we can get a projection from each point from  $s_i$  to  $s_j$ , vise versa.

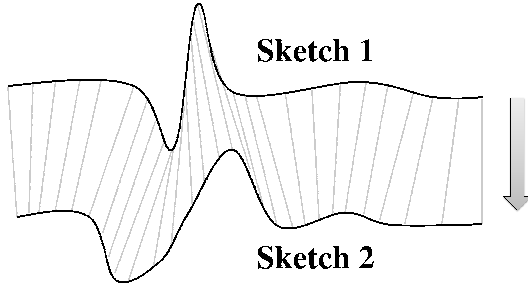


Figure 5: Projection based on DTW

$$P_{s_i}(s_j) = (y'_1, y'_2, \dots, y'_m) \quad (6)$$

$$P_{s_j}(s_i) = (x'_1, x'_2, \dots, x'_n) \quad (7)$$

Note that we project  $n$  length sketch  $s_j$  to  $m$  length in Eq.6.

Then we define plus operation  $\oplus$ , minus operation  $\ominus$  and times operation  $\otimes$  on sketch:

$$s_i \oplus (s_j) = s_i + P_{s_i}(s_j) = (x_1 + y'_1, x_2 + y'_2, \dots, x_m + y'_m) \quad (8)$$

$$s_i \ominus (s_j) = s_i - P_{s_i}(s_j) = (x_1 - y'_1, x_2 - y'_2, \dots, x_m - y'_m) \quad (9)$$

$$s_i \otimes (s_j) = s_i \times P_{s_i}(s_j) = (x_1 \times y'_1, x_2 \times y'_2, \dots, x_m \times y'_m) \quad (10)$$

Note that Commutative Laws is false here because we get different length result if the sketches order are shifted.

The following equations can be easily proofed:

$$c \times s_i = (cx_1, cx_2, \dots, cx_m) \quad (11)$$

$$\|s_i \ominus s_j\|_2 = \sqrt{(x_1 - y'_1)^2 + (x_2 - y'_2)^2 + \dots + (x_m - y'_m)^2} \quad (12)$$

Where  $c$  is a real number,  $\times$  is normal times operator.

### Implementing Online MUNCA

We regard stage function  $Y(t)$  as a random variable. Since stage  $Y$  is a finite nominal value, it's natural that we assume stage  $Y$  is obeying multinomial distribution. Besides, the distribution of sketches should be around a "center" sketch in a particular stage. So we also assume each sketch  $S^{(d)}$  in stream  $S^{(d)}(t)$  obeying gaussian distribution given stage  $Y$ , while these distributions are independent and their covariance matrix are all the same.

$$Y \sim MultiNominal(p_1, p_2, \dots, p_L) \quad (13)$$

$$S^{(d)} | Y = l \sim N(\mu_l, \Sigma)$$

Our goal is to assess stage  $Y$  based on a batch of sketches  $\mathbb{S}$ . We use  $P(\mathbb{S}|Y)$  denote the probability of  $\mathbb{S}$  in stage  $Y$ , and use  $G(\mathbb{S})$  denote the assessing result given  $\mathbb{S}$ . And we

can deduce the following equation:

$$\begin{aligned} G(\mathbb{S}) &= \operatorname{argmax}_Y P(Y | \mathbb{S}) \\ &= \operatorname{argmax}_Y P(\mathbb{S} | Y)P(Y) \\ &= \operatorname{argmax}_Y \prod_{d=1}^N P(S^{(d)} | Y)P(Y) \end{aligned} \quad (14)$$

According to Eq.13,  $P(S^{(d)} | Y)$  obeys the normal distribution:

$$P(S^{(d)} | Y) = \frac{1}{\sqrt{2\pi}^{n/2} |\Sigma|^{1/2}} e^{-(S^{(d)} \ominus \mu_Y)^T \Sigma^{-1} (S^{(d)} \ominus \mu_Y)} \quad (15)$$

Then we can simply deduce Eq.16 based on our assumption.

$$G(\mathbb{S}) = \operatorname{argmax}_Y \prod_{d=1}^N e^{-\|S^{(d)} \ominus \mu_Y\|_2^2} P(Y) \quad (16)$$

Note that each sketch  $S^{(d)}$  obeying gaussian distribution given stage  $Y$  with the same covariance matrix  $\Sigma$ . So we can assign  $\mathbb{S}$  to stage  $Y$  which has the most probability as Eq.16 shows. Intuitively, we actually assign each  $S^{(d)}$  to the nearest center.

Then we will implement our method as online learning in Algorithm 1.

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#### Algorithm 1 Updating Center and Probability of $Y$

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1: Input:  $\mathbb{S}$ , center, step,  $P(Y)$ ,  $Y_{true}$ 
2: Output: center, step,  $P(Y)$ 
3: for  $d = 1$  to  $N$  do
4:   cand1 =  $(S^{(d)} \oplus (step - 1)center^{(d)})/step$ 
5:   cand2 =  $((step - 1)center^{(d)} \oplus S^{(d)})/step$ 
6:   dist1 =  $\|cand1 \ominus S^{(d)}\|_2^2 + \|cand1 \ominus center^{(d)}\|_2^2$ 
7:   dist2 =  $\|cand2 \ominus S^{(d)}\|_2^2 + \|cand2 \ominus center^{(d)}\|_2^2$ 
8:   if  $dist1 \leq dist2$  then
9:      $center^{(d)} = cand1$ 
10:  else
11:     $center^{(d)} = cand2$ 
12:  end if
13: end for
14:  $P(Y_{true}) = P(Y_{true}) + 1/step$ 
15:  $step = step + 1$ 
16: return center, step,  $P(Y)$ 

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According to Eq.16, the assessing result is only determined by the center (Expectation)  $\mu_Y$  and probability of stage  $Y$ . So we only have to store  $\mu_Y$  and  $P(Y)$  for assessing, and update them every time when a new batch of sketches is coming. Finally, we can apply Eq.16 using updated  $\mu_Y$  and  $P(Y)$  for assessing.

Note that MUNCA is working on the sketches instead of original data. The computational complexity is  $O(L^2m)$ , where  $L$  is the codomain size of  $Y(t)$ ,  $m$  is the average length of sketch. So the computational complexity of the whole procedure is still  $O(n)$ .

## Experiments

In this section, we conduct a thorough experiments on our method. First we evaluate some issues that affect the performance of proposed method, then we compare it with some existing methods.

### Experimental Settings

We use real datasets instead of synthetic datasets. Two kinds of multiple streams are used in the experiments:

1. MIT-BIH Arrhythmia Database Directory (MITDB) (Goldberger et al. 2000): Two-channel ambulatory ECG recordings contains over 4000 long-term Holter recordings which obtained from inpatients who have premature beats. The stage include Premature ventricular contraction (represent as V) and Normal beat (represent as N)
2. ICU Dataset (ICU) (Tang et al. 2007): Five real physiological streams from multi-parameter monitor including RESP, ECG, ABP, ICP, PLETH are recorded during a six hour period simultaneously from a pediatric patient with traumatic brain injury. The stage include mild (M), severe (S) and emergency (E). The sample rates of the signals are from 125 Hz to 500 Hz, and the whole dataset includes over 25,000,000 data points;

The experiments were conducted on the hardware configuration with 4-core 2.90GHz Intel CPU and 8GB memory running MATLAB R2014a in Windows 7 Professional.

### Method Performance

The first experiment carried out on the ICU Dataset is to test the effectiveness of online learning. As introduced before, we implement MUNCA as online learning style. So it's important to see how fast online learning style achieve a comparable accuracy with training-testing style. Fig.6 shows the learning velocity of MUNCA. We chose sampling density parameter  $\beta$  as 29.05 which will explained later. The straight horizontal line is the accuracy of training testing style (20% training). We can see that online MUNCA achieves rapid accuracy gain from zero to 80% within processing about 10,000 points, which is less than 0.1% of the entire dataset. As more data processed, online learning style is even better than training testing style. The reason is that online learning style can adjust model timely when new data coming. Besides, the big accuracy promotion is because MUNCA only update sketches instead of the original data, which reduce the computational complexity remarkably.

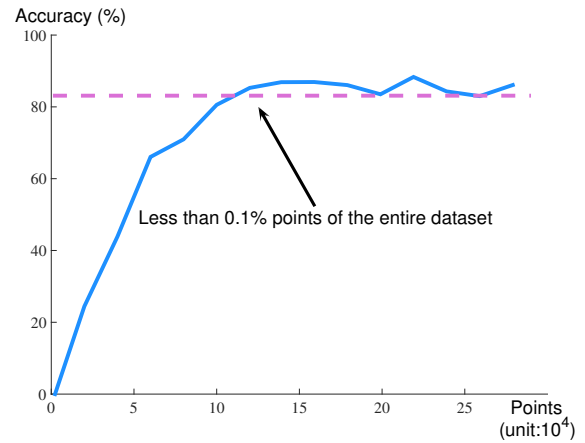


Figure 6: Learning Velocity

To further see how the size of sketches affect the assessing accuracy, we also carried out experiments on our adaptive sampling algorithm. As shown in Fig.7, with sketches size increasing, the similarity of sketches and original waves is also increasing, leading to the promotion of assessing accuracy. When the size of sketches is about 10% of the original waves in average, the assessing accuracy is steady which means that sketches are very close to original waves. The elbow point is 7.9% of the original waves in average, which is the best sketch size choice for achieving good efficiency while keep rational accuracy. And the parameter  $\beta$  is set to 29.05, So we choose it for all of our experiments in ICU dataset.

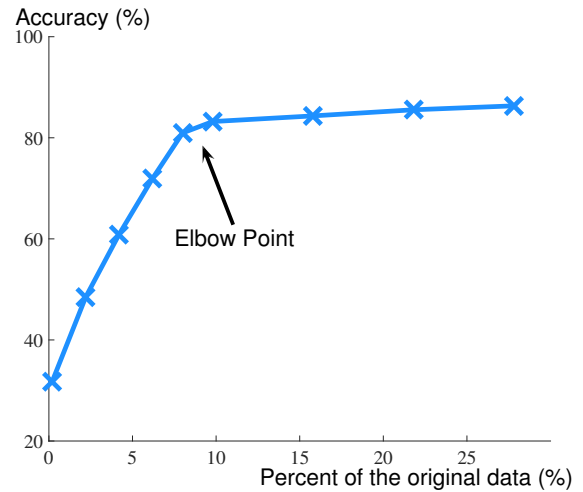


Figure 7: Sketch Size vs Assessing Accuracy

### Comparison with Other Methods

As we illustrated in Related Work, these assessing method can be loosely divided into three categories. To get a comprehensive result, we compared our method with three most relevant methods from three categories: Regression(Chen et al. 2002) (point based), FastShapelet(Keogh and Rakthan-

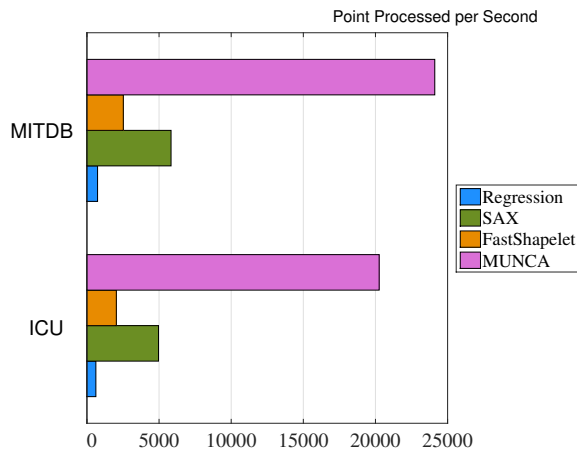


Figure 8: Processing Efficiency

manon 2013) (wave based) and SAX(Lin et al. 2003) (symbolic based).

The first experiment is about processing efficiency. We implemented these four methods both on MITDB dataset and ICU dataset. The average numbers of data points processed per second are illustrated in Fig.8. The result shows that the Regression has the slowest procession speed because it takes every point as concerned granularity. SAX and FastShapelet perform better than Regression, because they take waves (FastShapelet) or a sequence of points (SAX) as concerned granularity. Similarly, MUNCA takes waves into analysis but it still performs much better than FastShapelet. The main reason is that MUNCA also use sketches to represent waves, which remarkably reduce computational complexity for the assessing procedure.

At last, we compared assessing accuracy between these four methods. We compared the assessing result with the true stage  $Y(t)$  to evaluate the accuracy. As SAX and FastShapelet can't handle with assessing on multiple data streams concurrently. We implemented them on each stream of these multiple streams, and chose the best accuracy as the result. The assessing accuracy is shown in Fig.9. The result indicates that the Regression performs worse than three other methods. The reason is that it takes every point into analysis while the value of stage is actually related to the morphology of a wave, not the exact value of the points. SAX is better than regression but still much worse than FastShapelet and MUNCA. The accuracy of MUNCA is better than FastShapelet in MITDB dataset while the accuracy of FastShapelet is better than MUNCA in ICU dataset. The reason is that ICU dataset has more concurrent streams than MITDB dataset, and we chose the best accuracy within them for FastShapelet, so we actually got a bias result. In real world implementation, it's very unrealistic to evaluate every streams on multiple data streams.

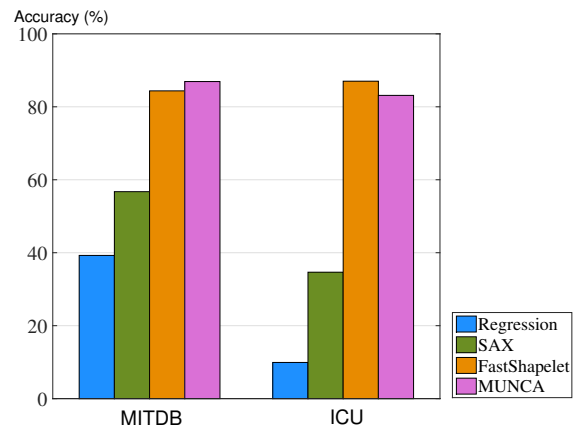


Figure 9: Assessing Accuracy

## Related Work

Most of the existing assessing methods are based on single physiological stream. Some can handle with multiple physiological streams. These techniques can be loosely divided into three categories:

A number of assessing method are point based analysis. In (Chen et al. 2002), they investigated regression method to analyze streaming data. (Huang et al. 2014) used critical points to assess from multiple medical sensor data streams. (Torres and Aguilar-Ruiz 2014) and (Chen, Zou, and Tu 2012) built similarity-based approaches to estimate the distance for assessing. (Rutkowski et al. 2014) applied decision trees for assessing the class of data streams. These methods assess stage over exact value of points directly, so they are slow on large volume data streams, and they don't take the morphology of waves into consideration.

Another category of work is wave based analysis, they split to get the waves and assess stage based on the morphology of waves. (Ye and Keogh 2011) used prototypical snippets called Shapelet to classify unlabeled streams within some previously learned distance threshold. It achieves superior accuracy on many datasets but its computational complexity is cubic and intractable on large datasets. So in (Keogh and Rakthanmanon 2013), they sped up Shapelet to quadratic running time while keeping accuracy. But both of them still focus on single stream, they can't handle with multiple data streams concurrently. (McGovern et al. 2011) introduced motif to multiple data streams. But concurrent motifs are very rare in multiple data streams so it can't give results in most cases.

Besides, some methods use symbol to represent a sequence of points, then assess stage based on symbols' semantics. (Yeh, Dai, and Chen 2007) and (Tang et al. 2007) used piecewise linear regression to fit a sequence of points and get the symbol. SAX (Lin et al. 2003) is a widely used representation method, and has implemented in financial markets (Canelas, Neves, and Horta 2013), computer vision (Junejo and Aghbari 2012), etc. These symbolic methods would neglect some critical shifts and they still not consider

multiple streams.

## Conclusion

In this paper, we addressed the problem of real-time assessing patients' condition over multiple concurrent physiological streams. Our major innovative work include:

1. We introduce an adaptive sampling algorithm to keep a balance between efficiency and performance. Our method achieve real-time output while keep good precision.
2. We choose waves as our concerned granularity and use sketches to represent the outline of original data. Sketches can capture both the short term fluctuation and the long term variation.
3. We develop MUNCA to combine various data streams together for analysis. Experiments on real data demonstrate the effectiveness and efficiency of the proposed method.

In the future, we will further consider these multiple concurrent physiological streams that have highly multicollinearity, and extend our work to assessing Parkinson's Disease.

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