Human State Classification and Predication for Critical Care Monitoring By Real-time Bio-Signal Analysis

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Abstract

To address the challenges in critical care monitoring, we present a multi-modality bio-signal modeling and analysis modeling framework for real-time human state classification and predication. The novel bioinformatic framework is developed to solve the human state classification and predication issues from two aspects: a) achieve 1:1 mapping between the bio-signal and the human state via discriminant feature analysis and selection by using probabilistic principle component analysis (PPCA); b) avoid time-consuming data analysis and extensive integration resources by using Dynamic Bayesian Network (DBN). In addition, intelligent and automatic selection of the most suitable sensors from the bio-sensor array is also integrated in the proposed DBN.

1. Introduction

In many outdoor (remote/long distance) medical diagnosis and healthcare applications, such as the monitoring of hemorrhagic shock from trauma which is the primary cause of death in battlefield, the medical monitors currently used are unsuitable as they are designed only for collecting and reporting discrete physiologic data. Also, the data collected by the current monitoring systems are mostly confined to standard vital signs which have dubious value in assessing the severity of patient's states. Although some considerable work [1] [2] to date has been made on investigating the feasibility of fusing multi-modality low-level bio-signals and using bioinformatic methods to assess and predict patient's physiological state for medical/health care monitoring and treatment, there are a number of remaining challenges.

To address the above challenges, we propose a wireless, real-time, portable, and wearable critical care monitoring system and a multi-modality bio-signal analysis framework for patient's physiological state assessment and classification. The architecture of the proposed system is shown in Figure 1. In the system, a set of low-level physiological, behavioral, and environmental sensors is selected to collect low-level bio-signals of a patient (e.g. a wounded soldier in battlefield). A central processing unit receives the bio-signals via a wireless module (e.g. ZigBee). These collected bio-signals will be processed and analyzed at the central processing unit for patient's physiological status modeling, classification, and predication. After the bio-signal pre-processing, distinctive features of the bio-signals will be extracted via feature selection and feature discrimination analysis, and then sent to a Dynamic Bayesian Network for real-time physiological state classification and predication. The results will be sent to a doctor wirelessly for diagnosis and treatment. At the same time, these bio-signals and the assessment results will be transmitted to a remote medical center for other doctors' review and data recording. During the monitoring, the central processing unit can also receive data (e.g. personal profile and illness records) from a remote medical center.

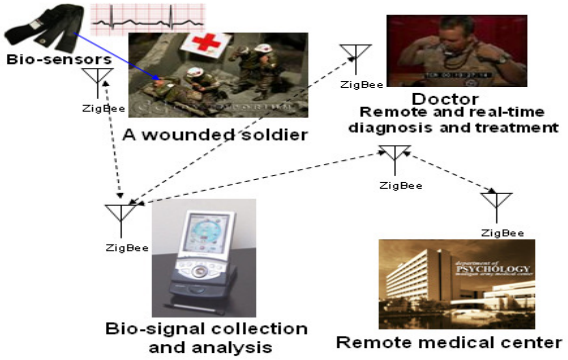

Figure 1 A wireless, portable, wearable critical care monitoring system

2. Bio-signal collection

Since medical and healthcare monitoring environments are very dynamic and the assessment (e.g. hemorrhage inspection of trauma patients in battlefield) is a very challenging and complex task, one

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bio-measurer is obviously not enough to collect suitable physiologic signal for 1:1 mapping between bio-signal and patient's state. Only a set of bio-measures working together can provide the possibility of 1:1 mapping. To do so, we propose to integrate seven different types (electromyogram (EMG), electrocardiograph (ECG) as shown in Figure 2, photoplethysmogram (PPG), galvanic skin response (GSR), perspiration, behavior, and environment) sensors into our proposed wearable sensing device for the collection of patient's low-level bio-signals while recording the environmental changes (e.g. temperature changes). All these non-intrusive sensors can be pasted on an arm belt, or a chest strap, or a glove, which will not affect the action of the inspected patient.

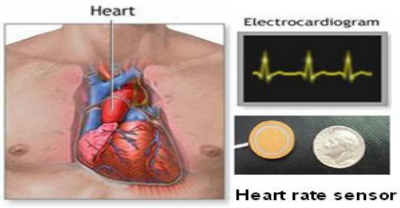

Figure 2 ECG signal

3. Bio-signal analysis and feature selection

One of the most common ways of processing bio-signals is to use feature analysis in time domain. Given a set of bio-signals collected from different sensors, it is very important to find a subset of critical features that can effectively describe patient's state and improve the accuracy of state classification. We believe that the accurate classification of patient's state should be based on the two following conditions: the ability to distinguish between states to each other, and an accurate feature model of each state that should be robust to different people and other types of state during the monitoring. To achieve these goals, we propose to incorporate the multi-sensor information from the context of each state with probabilistic principle component analysis (PPCA). Two types of context (spatial and temporal) are considered.

The distribution of the bio-signal of the stage *k* can be represented by a Gaussian with the mean vector μ_k and covariance matrix C_k:

$$p(z^{(t)} \mid l = k) = N(z^{(t)}; \mu_k, C_k) \tag{1}$$

where *l* is the label of the current state and $z^{(t)}$ is the measurement vector (a window of multi-sensor high-dimensional bio-signals centralized at time *t*). Principle component analysis (PCA) is famous in its strong capability in representing complex data structures for discriminant feature extraction, but it is only one shot of the state in spatial domain without any variation in temporal. The more robust representation is named PPCA model [3] due to its capability of considering the features in both spatial and temporal domains.

$$C_k = \sigma_k^2 I + W_k W_k^T \tag{2}$$

where W_k is a $d_k \times q_k$ matrix, d_k is the dimensionality of z, and $d_k << q_k$. This model provides a good balance between the representation accuracy and the complexity. PPCA for a stage (say *k* stage) is estimated from a set of training data beginning from $z^{(1,k)}$, …, $z^{(t,k)}$. Here $z^{(t,k)}$ is the vector of bio-signals of the stage collected at time *t*.

According to [3], the maximum likelihood estimation of PPCA can be computed as follows:

$$\mu_k = \frac{1}{T}\sum_{i=1}^{T} z^{(i,k)} \tag{3}$$

$$\sigma_k^2 = \frac{1}{d_k - q_k}\sum_{i=q_k+1}^{d_k} \lambda_{i,k} \tag{4}$$

$$W_k = V_{q,k}(\Lambda_{q,k} - \sigma_k^2 I)^{1/2} R \tag{5}$$

where $\lambda_{1,k}$, …, $\lambda_{d,k}$ are the eigenvalues arranged in the descending order of the observation covariance matrix:

$$S_k = \frac{1}{T}\sum_{i=1}^{T}\left[z^{(i,k)} - \mu_k\right]\left[z^{(i,k)} - \mu_k\right]^T \tag{6}$$

Let $v_{1,k}$, …, $v_{d,k}$ be the corresponding eigenvectors. $V_{q,k}$ is the $d_k \times q_k$ matrix whose columns are $v_{1,k}$, …, $v_{q,k}$, $\Lambda_{q,k}$ is the diagonal matrix whose diagonal elements are $\lambda_{1,k}$, …, $\lambda_{d,k}$ and R is an arbitrary $q_k \times q_k$ orthogonal matrix. The covariance matrix can be expressed as:

$$C_k = \sigma_k^2 I + \sum_{i=1}^{q_k}(\lambda_{i,k} - \sigma_k^2) v_{i,k} v_{i,k}^T \tag{7}$$
$$= \sum_{i=1}^{q_k} \lambda_{i,k} v_{i,k} v_{i,k}^T + \sigma_k^2 \sum_{i=q_k+1}^{d_k} v_{i,k} v_{i,k}^T$$

where $\lambda_{1,k}$, …, $\lambda_{q,k}$ are the variances of the first q principal components, σ_k^2 is the average of the variances of the remaining $d_k - q_k$. For these states, their difference between each other is maximized by using PPCA. The features constructed by PPCA are then sent to a Dynamic Bayesian Network (DBN) for modeling (training stage) or state classification (on-line stage).

4. Human state modeling and classification

We propose a probabilistic framework based on Dynamic Bayesian Network (DBN) for modeling and

predicting patient's state. A DBN is a probabilistic paradigm that explicitly models random variables and their spatial and temporal dependences. In addition, it allows patient's state classification from different modalities to be systematically represented and their impacts on patient's state to be propagated and integrated. A DBN is a directed acyclic graph consisting of nodes and directed links among the nodes. While nodes represent random events, the links characterize probabilistic dependencies among the nodes. Specifically, a link to a node indicates the probabilistic dependence of the node on its parents.

4.1 Human state modeling

The first step for DBN modeling is to identify those hypothesis events and group them into a set of mutually exclusive patient's situations to form the target hypothesis variables. The second step is to identify the observable data that may reveal something about the hypothesis variables and then group them into information variables. Typical factors that affect the patient's state may include the environmental context, the patient's profile, and the patient's physical condition. Since patient's state develops over time, it is important to model the temporal evolution of patient's state. In general, a Dynamic Bayesian Network is made up of interconnected time slices of static Bayesian Networks, and the relations between two consecutive time slices are modeled by a Hidden Markov model.

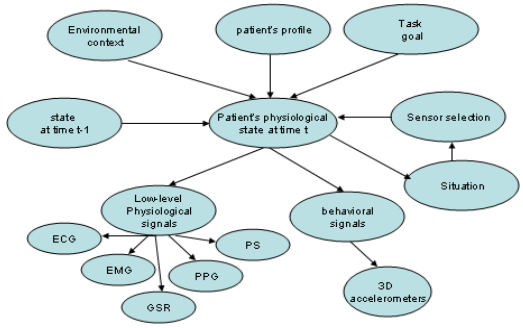

Figure 3 A probabilistic model based on DBN for human physiological state classification

Putting all of these factors together, the DBN for modeling the patient's state is constructed as shown in Figure 3. The target node in this model is patient's state and the nodes above the target node represent various factors that could affect patient's state. The nodes below the target node represent sensor measurements reflecting patient's state. These nodes are collectively referred to as measurement variables.

More formally, we assume a prior distribution over models structures as $P(M)$ and a prior distribution over parameters for each model structure $P(\theta \mid M)$, a data set D is used to form a posterior distribution over models using Bayes rule:

$$P(M \mid D) = \frac{\int P(D \mid \theta, M) P(\theta \mid M) d\theta P(M)}{P(D)} \quad (8)$$

where the uncertainty in the parameters is considered. For a given model structure, the posterior distribution over the parameters can be computed:

$$P(\theta \mid M, D) = \frac{P(D \mid \theta, M) P(\theta \mid M)}{P(D \mid M)} \quad (9)$$

4.2 Model parameterization

Once the topology of the model has been created, the next task is to parameterize the model. Quantitatively, a DBN uses conditional probability distributions (CPD) to depict the relations among various nodes. The CPDs of a DBN can be either learned from training data or specified subjectively by domain experts. In case of multiple causes for a single event, certain casual-independence assumptions [5] may be used to simplify the parameterization. The subjectively specified network can later be refined by the available training data using one of the existing learning methods such as the maximum likelihood method. The parameters can be learned by computing:

$$\theta^* = \arg\max_{\theta} P(D \mid \theta) P(\theta) \quad (10)$$

where $P(\theta)$ is a prior. When all nodes are observed, this computation can be done in a closed-form [4].

4.3 Active sensor selection

Although a lot of sensors are available in the system, the usage of more sensors incurs more cost for acquiring information. For making a timely and efficient predication on patient's state, it is important to avoid unnecessary or unproductive sensory actions. This is accomplished with active sensing. We use value-of-information (VOI) to guide the selection of sensors. The VOI of a sensor set is defined as the difference in the maximum expected utilities with and without the information collected from this set. It evaluates how valuable a sensor set is by considering both the benefit on accurate modeling and the cost of using the sensors.

4.4 Human state classification

Given the parameterized patient's state model, patient's state inference can start as soon as the nodes representing contextual variables and the nodes for state measurements are instantiated. The model systematically propagates the impacts of the instantiated nodes and estimates their impacts on the

patient's state node by updating its probability. Specifically, three streams of information, one travels bottom-up from the state measurements, one travels top-down from the contextual variables, and one travels from left to right, converge in the state node and then update the probability of the patient's state using a probabilistic inference method such as the junction tree method. Given an estimate of patient's state, we can then use the variations of patient's state to predict/classify the current state of the patient. Assume a set of observations $D = \{Y_1, ..., Y_{t-1}\}$, we can predict the next observation, Y_t, based on the data and DBN models with Bayesian predication:

$$P(Y_t \mid D) = \int P(Y_t \mid \theta, M, D) P(\theta \mid M, D) P(M \mid D) d\theta dM \quad (11)$$

5. Preliminary results

We designed bio-experiments to verify the effectiveness and efficiency of our proposed human physiological state classification and predication scheme. First, laboratory experiments (trials) of various hemorrhage situations (four levels/classes from mitigative to heavy were defined in our tests) have been performed to 20 human subjects with a chest strap and an arm-belt to attach all bio-sensors on human body. During the tests, the physiological signals and the associated behaviors of the human subjects, and the environment parameters were recorded. 300 data sets for a three-day period of observations were recorded and chosen for our study. Totally 927 states (all belong to Level 1 to 4) were manually labeled for these data sets as ground truth. 100 data sets including 323 states were chosen randomly for training. The other data (200 data sets with 604 states) were used for testing. For performance comparison, we also implemented Linear discriminant analysis (LDA) and PCA to compare with PPCA. The ROC curves of using LDA, PCA, and PPCA features together with two classifiers (DBN and support vector machine) for Situation Level 4 (the most severity) classification are shown in Figure 4 and Figure 5 respectively. From these figures, we can see that PPCA-based classifiers have the best performance for human state classification. Similar results for Situation Level 1, 2, and 3 classification were observed.

Table 1 Experimental results

Severity level	State No.	Error rate (SVM)	Error rate (BN)	Error rate (DBN)
Level 1	203	0.27	0.28	0.21
Level 2	142	0.22	0.21	0.15
Level 3	134	0.28	0.26	0.18
Level 4	125	0.31	0.27	0.19

For performance comparison, we also implemented a static Bayesian Network (BN) and used it to compare with support vector machine (SVM) and DBN. The comparison results of using SVM, BN, and DBN with PPCA features for human state classification are briefly summarized in Table 1. From the table, we can see that compared with SVM and BN, there has near 30% improvement on accuracy by using DBN.

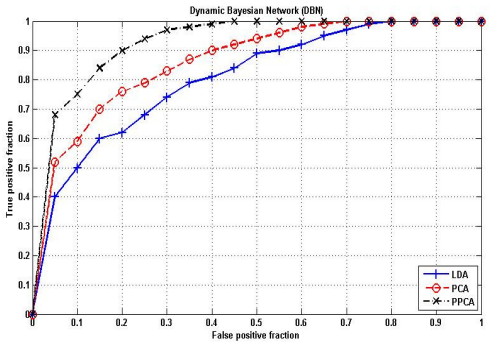

Figure 4 ROC curves by using DBN

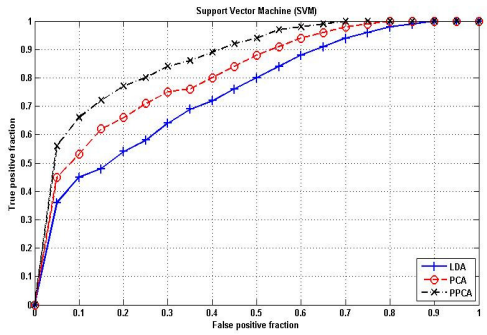

Figure 5 ROC curves by using SVM

6. Conclusion

We have presented an innovative scheme for real-time human physiological state classification and predication via low-level bio-signal analysis and modeling. The feasibility and effectiveness of the proposed scheme have been validated by our preliminary test results.

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