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COMPARISON OF BLOOD PRESSURE PREDICTION METHODS

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ABSTRACT

In the paper different approaches of predicting blood pressure values are presented. Basically, two methods and theirs modifications are considered. In total, seven algorithms have been examined. Tests have been conducted using both synthetic and clinical data. From our study it follows that none of the examined methods is superior to other.

INTRODUCTION

Monitoring of vital signals for patient, especially when treating her/him in intensive care unit or for disabled or convalescent person, when staying at home, increases her/his safety, since even a transient increase of blood pressure is a high risk factor for the person after an episode of a stroke. The aim of our project is to evaluate few pressure prediction methods which can be utilized in home monitored systems. A reliable prediction algorithm may reduce above mentioned risk since it allows to undertake an appropriate steps to prevent such situations. A long term monitoring of physiological parameters in home care systems differs significantly from the one designed for using at hospital environment, *e.g.* in number of collected signals, number of interventions, *etc*. However, having a lot of reliable data obtained from invasive monitoring at intensive care unit gives a good opportunity for choosing the correct prediction method and calibration model.

There are different approaches to predict signal values knowing its past values *e.g.* based on Taylor series [1], adaptive filtering [2], [3], adaptive weights method, conjugate gradients method (for the solution of positive definite linear systems) [4], time series method [5], Markov chain method [6], neural networks or the model-based approaches. The model-based approaches depend on physiological signal. Following [7]-[8], in our tests we have considered arterial blood pressure. The signal can be sampled evenly or not, which makes certain methods useless. For example, the time series or the adaptive filtering methods require evenly sampled signals. However, if the measurements are made irregularly, then the signal can be re-sampled evenly. It requires an application of the interpolation (or the approximation) procedure, which can affect prediction results as true values of physiological signal are not known (only measured ones). It has to be kept in mind that physiological signals can change very rapidly. There is also another solution for arbitrary sampled signal - an interpolation or, due to measurement noise, an approximation procedure. However, this approach is sensitive to an assumed interpolating function (approximation), *i.e.* linear, quadratic, exponential, *etc*.

Methods discussed in [1]-[5] were tested on synthetic data. The method proposed in [4] is a generalization of the approach presented in [9]-[10]. Our preliminary investigation had shown that the most promising results could be obtained using Taylor and adaptive filtering algorithms. Because of that we have decided to modify our earlier algorithms [11]-[12].

In the following section the considered methods are described. Next, the exemplary results are given. Finally, the discussion and conclusions sections are presented.

MATERIALS AND METHODS

In all cases we assume that there is a given signal $s(t)$. We would like to know the value of $s(t+a)$ assuming that $s(t-b_k)$ is known for some real $a, b_k > 0$ and $b_i \neq b_j$ for $i \neq j$, *i.e.*:

$$s(t+a) = \sum_{k=0}^{n} \alpha_k s(t-b_k), \tag{1}$$

or

$$s(t+a) = \sum_{k=0}^{n} \alpha_k s(t-b_k) + \alpha_{n+1}. \tag{2}$$

where α_k, $k = 0, \ldots, n+1$, are unknown real numbers to be calculated using given prediction method. The prediction model is defined by Eq. (1) or Eq. (2), however α_k coefficients can be calculated in different manners, so the predicted value can be different for each method. We assume that prediction is done only for one sample ahead.

Let us first consider Taylor series approach. In this case we assume that the $s(t)$ can be expanded in Taylor series (or at least it is well approximated by polynomial, which can be expanded in Taylor series). By comparing expansions of the left and the right hand sides of Eq. (1) one obtains a linear system of equations. The solution of this system can be easily calculated using properties of Vandermonde matrix. The advantage of this method is that the coefficients α_k, $k = 0, \ldots, n$ do not depend on t, so they can be calculated only ones for evenly sampled signal. The disadvantage of the method is assumption that the signal (or its approximation) can be expanded into Taylor series. Additionally, using this method the measurement errors are enhanced. It is assumed further that the signal is evenly sampled.

To minimize the influence of noise the algorithm is modified to obtain overdetermined system of linear equations, *i.e.*:

$$\begin{bmatrix} 1 & 1 & \cdots & 1 & 1 \\ -b_0 & -b_1 & \cdots & -b_{n-1} & -b_n \\ \cdots & \cdots & \cdots & \cdots & \cdots \\ -b_0^{m-1} & -b_1^{m-1} & \cdots & -b_{n-1}^{m-1} & -b_n^{m-1} \\ -b_0^{m} & -b_1^{m} & \cdots & -b_{n-1}^{m} & -b_n^{m} \end{bmatrix} \begin{bmatrix} \alpha_0 \\ \alpha_1 \\ \cdots \\ \alpha_{n-1} \\ \alpha_n \end{bmatrix} \approx \begin{bmatrix} 1 \\ a \\ \cdots \\ a^{m-1} \\ a^m \end{bmatrix}, \tag{3}$$

where $m \geq n$, which means that we are looking for inexact matching of $s(t+a)$, *i.e.* only its approximation. Such approach gives lower noise enhancement. As a comparison we have considered minimization problem of the form:

$$\|s(t+\Delta t) - \sum_{k=0}^{n} \alpha_k s(t-k\Delta t)\|_2^2 = \sum_{i=0}^{m} (s(t_i+\Delta t) - \sum_{k=0}^{n} \alpha_k s(t_i - k\Delta t))^2 \tag{4}$$

and

$$\|s(t+\Delta t) - \sum_{k=0}^{n} \alpha_k s(t-k\Delta t) - \alpha_{n+1}\|_2^2 = \sum_{i=0}^{m} (s(t_i+\Delta t) - \sum_{k=0}^{n} \alpha_k s(t_i - k\Delta t) - \alpha_{n+1})^2, \tag{5}$$

where Δt is time interval between successive samples. In practice, the value of Δt is defined by the measurement interval, which should be chosen in accordance to the fastest signal change that we want to observe (it depends on type of physiological signal and requirements following from

other conditions). This approach is close to the prediction based on adaptive filtering with biased estimators. The approach described by Eq. (4) is considered as similar to that presented by Eq. (1), while approach based on Eq. (5) follows from Eq. (2) and autoregressive model approach.

Since physiological signal can be approximated by autoregressive model of low order (typically equal to 2) we consider $n = 1, 2, 3, 4$ (*i.e.* prediction using 2, 3, 4 and 5 last samples) and $m = n$ (only for Eq. (1)) , $2(n+1)-1, 3(n+1)-1, 4(n+1)-1$ and $5(n+1)-1$. Basing on these two approaches next two prediction methods were proposed.

The first one is based on switching between prediction obtained from solving problem Eq. (3) and Eq. (4) or Eq. (5) basing on the quality of last prediction. The predictor with smaller prediction error for last sample was chosen:

$$\hat{s}(t) = \begin{cases} \hat{s}_1(t) & \text{if} \quad |\hat{s}_1(t-\Delta t) - s(t-\Delta t)| \leq |\hat{s}_2(t-\Delta t) - s(t-\Delta t)|, \\ \hat{s}_2(t) & \text{if} \quad |\hat{s}_2(t-\Delta t) - s(t-\Delta t)| < |\hat{s}_1(t-\Delta t) - s(t-\Delta t)|, \end{cases} \tag{6}$$

where $\hat{s}_1(t)$ and $\hat{s}_2(t)$ are predicted values obtained from Taylor series expansion combined with least squares - Eq. (3) (T+LS), and autoregression approach - Eq. (5) (AR) or autoregression without a constant - Eq. (4) (mAR).

The second approach is based on linear combination of predictors [13]-[14], which can be used even if few different sources of signals are given. In our case number of sources is restricted to one, but different prediction methods are considered, *i.e.*:

$$\hat{s}(t) = w_1(t)\hat{s}_1(t) + w_2(t)\hat{s}_2(t), \tag{7}$$

where $\hat{s}_1(t)$ and $\hat{s}_2(t)$ have the same meaning as in Eq. (6). The coefficients $w_1(t)$ and $w_2(t)$ were calculated using approximation of variance of relative prediction error for both methods, *i.e.*:

$$w_1(t) = \frac{Var((\hat{s}_2(t) - s(t))/s(t))}{Var((\hat{s}_1(t) - s(t))/s(t)) + Var((\hat{s}_2(t) - s(t))/s(t))}, \tag{8}$$

$$w_2(t) = \frac{Var((\hat{s}_1(t) - s(t))/s(t))}{Var((\hat{s}_1(t) - s(t))/s(t)) + Var((\hat{s}_2(t) - s(t))/s(t))} = 1 - w_1(t). \tag{9}$$

The variance was estimated taking into account prediction results for all samples before moment t. The quality of such prediction can be evaluated using one of the criterion described in [15], [16]. For our purposes the most important is prediction error *i.e.* $\hat{s}(t) - s(t)$, so we use as a prediction quality a following measure q:

$$q = \sqrt{\frac{\sum_{i=1}^{N}(\hat{s}(t_i) - s(t_i))^2}{N}}, \tag{10}$$

where $\hat{s}(t_i)$ is calculated estimator of $s(t_i)$ and N is the total number of samples for which prediction has been done.

Seven (*i.e.* Taylor series expansion combined with least squares - Eq. (3) (T+LS), autoregression approach - Eq. (5) (AR) and autoregression without a constant - Eq. (4) (mAR), linear combination of T+LS and AR (l(T+LS+AR)) - Eq. (7), linear combination of T+LS and mAR (l(T+LS-mAR)) - Eq. (7), competitive T+LS and AR (c(T+LS-AR)) - Eq. (6) and competitive T+LS and mAR (c(T+LS-mAR)) - Eq. (6)) described above methods were tested on data obtained from four persons: three female at age of 47, 52 and 70 and one male at age 86. The measurements included diastolic and systolic values of arterial blood pressure (measured with the invasive method in the distal artery of the upper limb). Physiological data recordings were performed using the S5 DATEX/OHMEDA system for monitoring critically ill patients. Digital data were transferred by the serial port to the Computer Information System developed and used in the Intensive Care Unit of the Department of Hyperbaric Medicine and Sea Rescue, Medical University of Gdańsk. The arterial blood pressure was measured, on average, each 30 seconds (*i.e.* $\Delta t = 30$ seconds). We decide to choose two largest continuous monitoring periods for both systolic and diastolic pressure for each patient. It gives 16 cases in total (four persons times two types of blood

pressure - systolic and diastolic ones - times two different time periods). The number of samples for each case was varying from 257 to 1177.

RESULTS

For each case the best results were chosen, *i.e.* the value of n and m parameters which minimized the q error. The following figures present comparison of prediction results for examined methods. Fig. 1 shows example of signal and its predictions for the worse and the best case, where quality of the case was measured by value of q. The original signal is drawn with bold line, while its prediction with solid and doted lines. Only the best and the worst predictions are shown. The prediction errors for the same data are presented in Fig. 2. Again the prediction errors only for the best and the worst method are shown. Fig. 3 shows prediction error q for the cases presented in previous figures for all considered methods. Consecutive numbers on the x-axis (Fig. 3) correspond to the methods T+LS, AR, c(T+LS-AR), l(T+LS-AR), mAR, c(T+LS-mAR), l(T+LS-mAR).

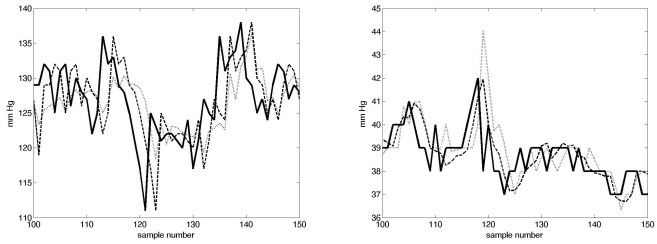

Figure 1. Signal (bold line) and examples of its predictions for the worse (left - $n = 2$, $m = 3$ dotted (l(T+LS-mAR method)) and dashed (T+LS method) lines) and the best (right - $n = 4$, $m = 4$ dotted (AR method) and dashed (c(T+LS-mAR) method) lines) case.

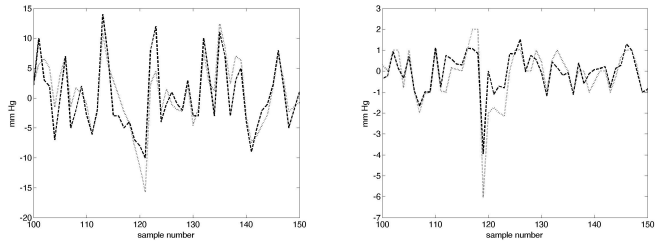

Figure 2. Prediction error for the worse (left - $n = 2$, $m = 3$ dotted (l(T+LS-mAR method) and dashed (T+LS method) lines)) and the best (right - $n = 4$, $m = 4$ dotted (AR method) and dashed (c(T+LS-mAR) method) lines) case.

DISCUSSION

The modeling of vital signals is a complicated task since there are many factors affecting such signals. Moreover, these factors may change according to a physiological/pathological state of the patient. This is the reason, why it is so hard to choose appropriate model describing the signal. Because of that we have considered only two simple models, which can be applied to any of physiological signals, since only theirs past values are used to predict its future values. The accuracy of prediction value, inter alia, depends on the number of past samples taken into account and how the predicted moment is distant from the present according to measurement interval. This is the problem of all prediction models. This problem is related to physiological state of the

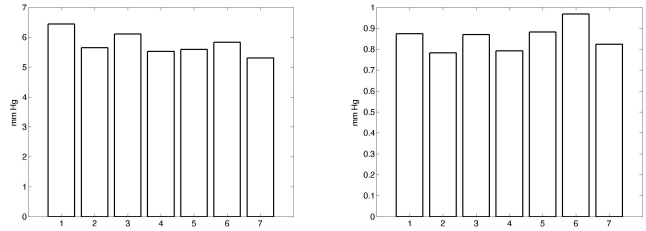

Figure 3. Prediction error q for worse (left) and the best (right) case for different considered methods for the worse (left) and the best (right) case.

patient. If patient is stable then longer historical data can be taken into account and prediction can be calculated for longer time interval ahead. In general, we do not know if the patient condition will change rapidly, so we want to use not too many historical data to obtain good prediction. For this reason we consider not only auto-correlation approach for calculation α_k coefficients but also others like Taylor series approach. More sophisticated models will include some knowledge of physiological processes. However, the problem is that not all parameters, required for proper construction of such models, are possible to be monitored.

In general the measurement data are corrupted by the noise. The noise can be introduced by patient movements or measurement system (for example round off of measurement data). Because of that the prediction method can not assume that past signal values are known exactly. This is the reason, why overdetermined systems of equations were considered. Solution of such systems is obtained in the sense of 2-norm minimization.

Clearly, non of predictors gave the best results in all cases. There is also no optimal value of n, nor optimal value of m. Even for the same patient for different time moments the lowest prediction error q is obtained for different values of n and m. The lowest prediction error for the same patient but different time series can be obtained for different predictors as well. Hence, the results for systole and diastole pressure are also different. The best results were obtained for the prediction based on Eq. (7), where estimates were done by Eq. (3) and Eq. (5). The lowest prediction error has been obtained mainly for $n = 1$ and $m = 5(n+1)-1$. This means that only two last samples are enough for good approximation, but more approximation (Eq. (3)) or the longer history (Eq. (5)) is taken into account, the better results are obtained (smaller value of q).

Maximal prediction error q for the best method was lower than 6 mm Hg. Typically was about 1-3 mm Hg, while for one series was less than 0.8 mmHg. Thus, we do not observe large differences between used methods (see Fig. 3). The relative prediction error:

$$qr = \sqrt{\frac{1}{N}\sum_{i=1}^{N}\left(\frac{\hat{s}(t_i) - s(t_i)}{s(t_i)}\right)^2} \tag{11}$$

was lower than 5.65% for the worst case and lower than 1.46% for the best case.

It should be remember that measurement data are subject to error introduced by measurement system itself (accuracy of the measurements). Part of measurement error is generated by round off pressure values to integer ones. This mean, the prediction error about 0.5 mm Hg can be devoted to measurements round off.

CONCLUSIONS

There is no optimal method to predict exact value of the physiological signals. Depending on the data and certain approach the results are different. However, the obtained results show that any of analyzed methods can be applied for practical purposes. It follows from the fact that measurement error for noninvasive blood pressure method is typically no bigger than +/- 3mm Hg.

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