Image Based Time Series Synchronization for Periodically Moving Targets

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Abstract. Since it is possible to process a huge amount of data using todays computer hardware, the demand for algorithms dealing with this type of data is increasing. A major environment where these algorithms can be applied is obviously found within medical diagnosis and therapy. Nowadays, physicians are able to observe 3D volumes over time. By using such four dimensional datasets, they are able to observe and study movement of certain targets within the patient's body. Usually there are two main sources causing this movement: the patients respiration and the beating heart. Both sources are producing a periodic movement and there is often a demand to know how such a periodic movement affects internal tissue. In this paper, a method is presented to address such periodical moving targets within the body. The paper introduces a method to synchronize a 4D volume data time series with a 2D image time series. In general an assumption is made, that both of the time series are representatives of two corresponding processes with a sufficient amount of overlapping data. Synchronization is defined as the allocation of both time series by using an optimal mapping that relates any frame of one series to a corresponding frame of the other series. In order to consider variations within the time series, the algorithm is based on a probabilistic underlying markov process and is able to detect whether there is any correspondence or not. As the mapping procedure is designed as an optimization process it can be solved by using an optimization technique like simulated annealing or dynamic programming. The effectiveness of the proposed method is shown on an example out of the field of medical therapy. In general the solution can also be used within diagnosis of cardiac motion abnormalities, respiratory motion compensation in image guided interventions, respiratory motion management in radiation therapy and segmentation and registration of 2D+time or 3D+time series.

1 Introduction and Background

The synchronization of two time series in general is well known and has been studied in literature, considerably [1][2]. The main application, that has been looked at in literature deals with indexing very large time series databases [1]. To find a mapping between two time series in general, euclidian distance metrics can be used. Furthermore, dynamic time warping has also to be considered as a technique to accommodate time differences between an input series and a reference series. A classical one dimensional example application for dynamic time warping is the synchronization of two utterances of the same word, known as Levenshtein distance [4]. Furthermore, dynamic time warping can also be used to synchronize two dimensional image time series. As dynamic time warping is based upon dynamic programming [7], it is taken into consideration for solving the stated problem. As dynamic time warping is not suitable to deal with periodicity within the time series, we are using a markov process to incorporate the time dependency and periodicity in the solution [10].

Various image similarity measurement techniques can be used to compare image pairs and have been studied in literature [3]. We focused on mutual information as primary image similarity measurement [5]. Additionally, we are also using singular value decomposition to enforce rank criteria [9].

2 Image Based Synchronization

We consider a 4D image time series, consistent of **i** 3D volumes as reference sequence. This sequence contains one complete cycle of the periodic moving target. Therefore, the movement is divided into **i** different phases and each 3D volume represents one particular phase. In order to be able to compare these phases to the second 2D image time series, including **j** images, the dimension of the volumes has to be reduced by factor one. This is done efficiently by calculating projections of the volume using the same geometry as was used during the acquisition of the 2D image time series [8].

We use a similarity metric to compute the level resemblance among all possible pairs of the two time series [3]. In general it is possible to use any proper metric; by performing tests we identified mutual information as the most suitable metric to use. By using this metric we build up a matrix and apply a normalization technique. Therefore, we are using singular value decomposition to reduce the amount of bias by taking various image pairs into account. Concluding, the result of a rank one forced similarity matrix is subtracted from the original similarity matrix (see figure 1).

Furthermore, we introduce a stochastic process, which represents both of the time series. Since, we are looking for the indices of the second time series with respect to the reference sequence without loosing generality we assume that the elements of the reference time series are in fact the states of the stochastic process. A common way to represent a stochastic process can be performed by using a markov model, which includes the initial probability of each state and a transition matrix that expresses the probability of the next states with

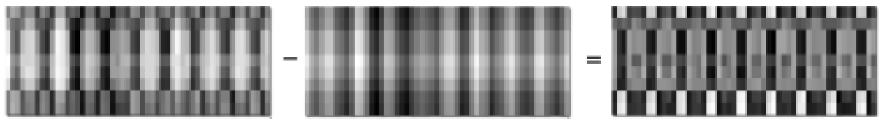

Fig. 1. From left to right: original similarity matrix with gain, computed bias field, similarity matrix without bias field

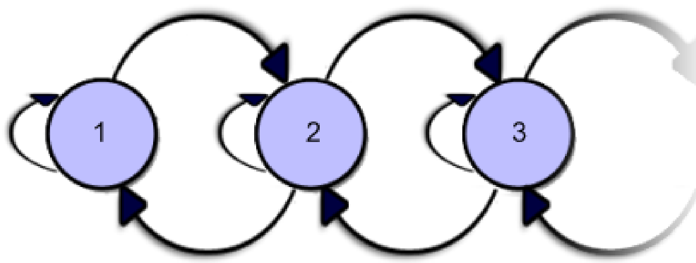

Fig. 2. An example for a markov chain, the blue circles indicate the states including the transition probability directions

respect to the previous state (see figure 2). The state transition probabilites can be estimated by using the Baum-Welch algorithm [6]. In order to account for possible deviations from the reference states, we add an additional unknown state to the reference set. This unknown state accounts for any possible new conditions that can happen on the second series and has not been present in the reference sequence. The image similarity level for this additional state quantifies a non-matching (poorly matching) case. For this purpose, since the number of none matching pairs supersedes the number of matching pairs, we use the median of the maximums of various columns. By subtracting the range of the similarity values of the corresponding column from this value we have determined the similarity level for the additional state.

In order to compute the mapping function, we set up a cost function, in which the parameters are the labels for any image in the second time series relating them back to the reference states including the unknown state. The cost function consists of two terms, where the first one represents the image similarity matrix (data) and the second one the markov process (model). According to this, we set up a function where we can maximize the a posteriori probability by using Bayes' theorem. In respect of the Bayes theorem the first term represents the likelihood and the second term the a priori knowledge as shown in equation 1.

$$\widetilde{\mathcal{L}} = \arg\max_{\mathcal{L}} \underbrace{\left(\prod_{j=0}^{j<K} M(\mathcal{L}(j), j)\right)}_{likelihood} \times \underbrace{\left(P_0(\mathcal{L}(0)) \prod_{j=1}^{j<K-1} \mathbf{S}(\mathcal{L}(j), \mathcal{L}(j+1))\right)}_{prior} \quad (1)$$

We are optimizing this cost function by using a dynamic programming approach which incorporates the a priori knowledge.

$$\mathbf{Q}(i,j) = \begin{cases} \infty & j < 0 \\ \mathbf{M}(i,j) \times P_0(i) & j = 0 \\ \mathbf{M}(i,j) + \max_i \left(\mathbf{Q}(i,j-1) \times \mathbf{S}(i,j)\right) & otherwise \end{cases} \tag{2}$$

Once we have computed the matrix $\mathbf{Q}$ in equation 2 recursively, we can solve the above stated optimization problem as follows:

$$\widetilde{\mathcal{L}}(j) = \tilde{i} = \arg\max_i \mathbf{Q}(i,j) \qquad for \quad j \in [0, K]. \tag{3}$$

3 Experimental Results

In order to evaluate the performance and usability of the proposed method, it was applied and tested on a medical therapy problem. Gated radiation therapy is one application where a periodical motion is occurring and needs to be determined. We took several 4D-CT scans from patients with a corresponding fluoroscopic sequence and used the algorithm to synchronize both sequences. The goal was to determine the position of a tumor related to the actual breathing phase based on the reference sequence. We tested the algorithm using both, synthetic generated fluoroscopic sequences and real acquisitions. As the 4D dataset was acquired prior to the fluoroscopic sequence, all these sequences had slightly different patterns than the reference sequence. To judge the quality of the algorithm we define two error measures, where the first error metric indicates wrong labeled no-match situations and the second wrong labeled frames. Correct correspondences for each frame out of the reference sequence were determined by using split-screen and a blending display method. All tests were performed on an Intel Centrino Duo CPU with 2.0 GHz and 2 GB of RAM using a NVIDIA Quadro FX 2500 display adapter. The average error of wrong labeled no-match situations was 11 percent and 9 percent for wrong labeled frames. Therefore in average 91 percent of all frames are correctly labeled.

4 Summary and Conclusion

We proposed a model based image synchronization technique based on Dynamic Programming. The procedure is able to find a mapping between a 4D data set used as a reference and a 2D image sequence. By building up an image similarity table first, we establish and solve a cost function afterwards. This function incorporates both the image similarity values and the temporal aspect by using a stochastically model based on a markov model as the underlying process. The method was tested on synthetic and patient data and shows in average a correct labeling of the frames in 91 percent.

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