approach is different from typical ECG segmentation methods in two ways. First, it avoids any specialized knowledge of the characteristics of the signals to segment them. This allows the extension of the method to other types of signals (ABP and PPG). Second, a multi parameter signal is jointly segmented. Therefore, when one or more signals in the multi parameter signal are corrupted, uncorrupted signals are weighted more, and the joint segmentation is highly influenced by the uncorrupted signals.

The method uses an evolving template (Figure 2), a short multi parameter signal, and matches it with a sliding window of the multi parameter signal. The initial template is derived from an archived signal, and is regularly updated to reflect the time evolution of the signal. The algorithm continuously extracts a non-overlapping window from the signal, and identifies the segment boundary in the window by finding the prefix of the window that most closely matches the template.

The matching is done using weighted time warping (WTW) (Gartheeban and Guttag, 2011), which minimizes the weighted morphological dissimilarity across all the signals. The warped distance between two single parameter signals gives the morphological dissimilarity. Time warping is necessary, because the template and current window can be of different lengths. The weights represent the estimated quality of each signal, which is again computed by the morphological similarity between the signal in the window and its counterpart in the template.

To follow the gradual changes that are common in physiological signals, the template is updated regularly. When the variation of the segment lengths in the neighborhood is small, and the quality estimates of all the channels are above a threshold, the template is updated by averaging the excerpt of the last two segments with the current template time-warped to match the excerpt length.

2.1.1 Weighted Time Warping based Template Matching

Let $S \in \mathbb{R}^{n \times m}$ be a multi parameter time series consisting of $m$ physiological signals, and $Z \in \mathbb{R}^{l \times m}$ be the initial template. The goal is to segment $S$ into a set of quasiperiodic units $Y = \{Y_i\}$ where $Y_i \overset{def}{=} S_{(p_i, p_{i+1})}$, and each unit corresponds to a single heart beat. Here, $S_{(p_i, p_j)}$ denotes the window in the target sequence $S$ from time $t = p_i$ to $t = p_j - 1$.

We require the template (Figure 2) to be comprised of at least two segments. These segments are used to find the quasiperiodic unit $Y_i$ in $Y$. We also assume that we know the locations of the segment boundaries $Z.\ell_1$, $Z.\ell_2$ and $Z.\ell$ in the template. The prototypical template is initially obtained from an archive.

We start the process at some arbitrary point in time $p_{start}$ on the signal that is to be segmented. This need not be an actual segment boundary. We run the algorithm starting at $p_{start}$, continuously segment $S$, and add the segments to $Y$. We also update $Z$ to reflect the evolution of the time series.

An iteration of our method on a single channel ECG signal is illustrated in Figure 3. We start each iteration with the extraction of a window $W = S_{(p_i, p_i+\ell)}$ from $S$ at $p_i$. Here, the window length is given by $v = \ell + e$, where $\ell$ is the length of the template and $e$ is buffer length. In the following discussion, we use $j$ to index individual signals in the multi parameter signal $S$. The window is then detrended and normalized, and the morphological quality estimates $\{q_j\}_m$ (Section 2.2) are computed, where $q_j$ represents the morphological similarity between the channel $W_j$ from $W$ and the corresponding channel $Z_j$ from the template. For each channel $j$, a pairwise Euclidean distance matrix $pD^j$ is calculated between $Z_j$ and $W_j$ (Equations 1-2). The final distance matrix $D$ is obtained by weighting pairwise distance matrix $pD^j$ with $q_j$ (Equation 3).