Real time Reconstruction of Physiological Signal Morphologies

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Physiological Signals

- **Examples**
  - Electrocardiogram (ECG)
  - Arterial Blood Pressure (ABP)
  - Photoplethysmogram (PPG)
  - Intracranial Pressure (ICP)
  - Respiratory signal

- **Multiparameter Physiological Signal**
  - Multidimensional & Time aligned
  - Obtained from multiple sensor sources

- **Restrictions**
  - Quasiperiodic
  - Correlated
Morphology

- Quasiperiodic physiological signals have similar repeating morphologies.

- Algorithms use signal morphology to detect physiological events:
  - QRS detector: Heart Rate (HR) estimation [1]
  - Premature Ventricular Contraction (PVC) detector: Arrhythmia detection [2]
  - Morphological Variability (MV) estimator: cardiac death prediction [3]

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Signal Corruption

- Sources of Corruption
  - No signal detected
  - Physical Activities
  - Muscle Artifacts (MA)
  - Electromagnetic Interference (EM)
  - Baseline Wander (BW)

- Corruption is often independent among signals
  - Limb movements need not affect all signals
  - Electromagnetic Interference doesn’t affect photoplethysmogram

- But signals are **correlated** and synchronized
  - they share the same source – heart
Motivation

- Example Applications
  - Arrhythmia detection
    - Use of ABP and PPG [1]
    - Suppress false alarms
  - Morphological Variability (MV)

- A uniform method to handle corruption in multi parameter signals

Goal

- **Context**
  - We have a multi parameter signal with corruption
  - m correlated signals
  - Any or all of them might be corrupted at any given time
  - Corruption can be severe – the signal could be completely absent

- **Goal**
  - Identify the corrupted regions
  - If at least one correlated signal is uncorrupted, reconstruct the corrupted regions in **real time**

- Formally posed for first time in Computers in Cardiology (CinC) 2010 Challenge
Overview

Segmentation

- Simultaneous segmentation and signal quality estimation
- Start by matching against pre-supplied template
- Evolve the template over time

Reconstruction

- Uses the output of step 1
- Assuming we have access to uncorrupted signals, build a database of templates from those signals
- On the remaining signal, reconstructs the corrupted regions using these templates
- Evolves the database of templates

Complementary to existing signal processing methods
- Median filter to remove baseline wander [1] & Wavelet denoising [2]

Road Map

- Reconstruction
  - Method
  - Experiments
- Segmentation
  - Method
  - Experiments
- Contributions
Part 1 - Reconstruction
Joint segmentation and signal quality estimation [1]

1. Identify the corrupted segment.
2. For each correlated signal in the corrupted segment:
   1. Construct Feature Vector
   2. Find the closest match from the database.
   3. Align the match to fit the interval.
3. Reconstruct the corrupted segment by fusing the matches.

Data fusion

- For each correlated signal that is free of corruption, we will have a reconstruction.

- Fuse the matches \((y_i; 2 \leq j \leq m)\) from \((m-1)\) correlated signals based on their quality, and build the reconstruction \((Y^\star)\):
  - \(q\) : signal quality
  - \(r\) : correlation between signals
  - \(c\) : cost of match

\[
Y^\star = \frac{\sum_{j=2}^{m} y_j^i \cdot w^j}{\sum_{j=2}^{m} w^j}
\]
\[
w^j = q^j \cdot r^j / c^j
\]
Features

Features serve two purposes [2]

• Speed up the lookups
• Provide a level of abstraction and context that preserves clinically relevant information in matching

<table>
<thead>
<tr>
<th>Feature</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>$f_1 \ldots f_4$</td>
<td>Pre, first-half, second-half, and post segment intervals</td>
</tr>
<tr>
<td>$f_5$</td>
<td>Square root of the total energy</td>
</tr>
<tr>
<td>$f_6 \ldots f_{15}$</td>
<td>The fraction of energy in the $k^{th}$ section (a segment is divided into 10 sections)</td>
</tr>
<tr>
<td>$f_{16}$</td>
<td>Kurtosis of the sample values</td>
</tr>
<tr>
<td>$f_{17}$</td>
<td>DTW distance between the signal in the segment, and the median of the same signal</td>
</tr>
<tr>
<td>$f_{18} \ldots f_{27}$</td>
<td>DTW of $k^{th}$ subsequence (DTW alignment is divided into 10 equal length sections)</td>
</tr>
<tr>
<td>$f_{28}$</td>
<td>Fraction of spectral energy in the QRS complex</td>
</tr>
<tr>
<td>$f_{29}$</td>
<td>Maximum sample value</td>
</tr>
<tr>
<td>$f_{30}$</td>
<td>Minimum sample value</td>
</tr>
</tbody>
</table>

Running Times

- Average segment length: \( l \)
- Signal length: \( n \)
- Number of segments: \( O(n) \)

- Segmentation: \( O(nl^2) \)
- Each reconstruction: \( O(l^2) \)
- Total processing time: \( O(nl^2) \)

- **Real time**

- On a standard PC, method implemented in Matlab, on average, **took 51 seconds** to process a **10 minute long record**
Experiments

On MIT-BIH Arrhythmia Database
On CinC Challenge 2010 Database
Data

- CinC 2010 Challenge Database [1]
  - Contains ECG, ABP, PPG, Respiratory signal, etc
  - 100 records, each 10 minutes long
  - Relatively clean and contain fewer abnormal events

- MIT-BIH Arrhythmia Database [2]
  - Contains 2-channel ECG signals
  - 48 records, each 30 mins long
  - Includes less common but clinically significant arrhythmias.

1 http://physionet.cps.unizar.es/challenge/2010/
2 http://www.physionet.org/physiobank/database/mitdb/
Evaluation Methodology

- Original signal (S)
- Synthetically corrupted signal (S#)
- Reconstructed signal (S*)

- Residual distance (r) : measures the similarity (for example, between S* and S)
  \[ r = \sqrt{\frac{\sum_{k=1}^{n} (S^*[k] - S[k])^2}{n \times \delta_s^2}} \]

- Classification Accuracy (Δ) :
  - Measures the clinical usefulness of the method
  - By comparing the results of a widely used open source heart beat type classifier [1] on each signal (S, S#, and S*)
  \[ \Delta = \frac{n_{\text{disagreement}}}{n_{\text{beats}}} \]

CinC 2010 Challenge

- For the first time posed the problem of reconstructing a corrupted multi parameter physiological signal [1]
  - Multi parameter signal – ECG, ABP and PPG.
  - 10 minutes long, last 30 seconds of one signal is removed, and asked to reconstruct
  - Evaluation: Residual distance & Correlation Coefficient

- Methods used in the challenge
  - Neural network (Highest scoring method) [2]
  - Kalman Filter and Adaptive Filters [3]
  - HMM, PCA, etc.

- Comparison
  - The highest scored method has normalized residual distance 0.17, compared to ours 0.02
  - Not fair, because their results include the tests on 30 additional records requiring reconstruction of respiratory signal and ICP (non-quasiperiodic)

Experiments on MIT-BIH Data

- Learn from first 80% of data.
- Corrupt last 20% of data, and try to reconstruct it.

**E1. Effectiveness of Reconstruction**
- Last 20% is corrupted with AWGN at 0 dB SNR.

**E2. AWGN at Different Noise Levels**
- Last 20% is corrupted with AWGN at different SNR levels

<table>
<thead>
<tr>
<th>SNR Level</th>
<th>R</th>
<th>Δ</th>
</tr>
</thead>
<tbody>
<tr>
<td>-10 dB</td>
<td>0.4</td>
<td>0.022</td>
</tr>
<tr>
<td>0 dB</td>
<td>0.4</td>
<td>0.021</td>
</tr>
<tr>
<td>10 dB</td>
<td>0.41</td>
<td>0.031</td>
</tr>
</tbody>
</table>

Smaller is better
Experiments on MIT-BIH Data

- **E3. Different Noise Types at 10dB SNR**
  - Last 20% is corrupted with different kinds of structured interference at 10 dB SNR
    - Muscle Artifacts (MA)
    - Electromagnetic Interference (EM)
  - Performances of our method are compared.
Experiments of MIT-BIH Data (cont.)

- **E4 : Training Size**
  - The fraction of data used to train the framework is varied from 80% to 20%.
  - The rest is corrupted with AWGN at SNR 0dB.

- **E5 : Online Learning**
  - Only first 20% is used to train the framework.
  - Randomly chosen non-overlapping regions totaling 50% of the record is corrupted with AWGN at SNR 0dB.
  - On the rest (30%), if the framework identifies regions with high signal qualities, it can learn from.
Road Map

- Reconstruction
  - Method
  - Experiments

- Segmentation
  - Method
  - Experiments (optional)

- Contributions
Part 2 - Segmentation

Joint temporal segmentation and signal quality estimation
Joint Segmentation

- Most methods treat the signals separately, and compare the results [1]
  - Segment ECG, ABP and PPG
  - Compare one with another and confirm the correctness

Joint Segmentation

- Why?
  - Signals share the same source – Heart
  - Signals are correlated and synchronized

- How?
  - Simultaneously segment a multi parameter signal
  - Accommodate different kinds of signals

- By jointly segmenting a multi parameter signal we are able to segment the signals over regions when none of the signals can be segmented individually

- We use template matching for joint segmentation

Process ...

- We have a template – two segments long
- We extract a window from the signal
- Match the window with template using dynamic time warping
- Find the prefix of the window that minimizes the cost of matching
- Backtrack, and using the alignment find the point in window that corresponds to the end of the first segment in the template
- Update the template, and continue.
Illustration

Example on a single channel ECG
Illustration – Temporal Segmentation

- **Window**
- **Prefix of the Window**
- **Segment Boundary**
- **Match the end of the first segment**
- **Prefix of the window minimizing the matching distance**

Template

Window
DTW Trick (optional)

\[ A = a_1 a_2 \ldots a_x \ldots a_n \]
\[ B = b_1 b_2 \ldots b_y \ldots b_m \]
\[ c_{x,y} = (a_x - b_y)^2 \]
\[ D = \begin{bmatrix}
  c_{1,1} & c_{1,2} & \ldots & c_{1,m} \\
  c_{2,1} & c_{2,2} & \ldots & c_{2,m} \\
  \vdots & \vdots & \ddots & \vdots \\
  c_{n,1} & \ldots & \ldots & c_{n,m}
\end{bmatrix} \]
\[ aD(A_x, B_y) = D(A_x, B_y) + \min \{ D(A_{x-1}, B_{y-1}), D(A_x, B_{y-1}), D(A_{x-1}, B_y) \} \]
\[ b^* = \arg \min_{k_2} \frac{1}{k_2} aD(k_2, m) \]

Prefix of the window minimizing the matching distance
Illustration – Template Update

after 12 mins

after 12 mins

after 12 mins
Extension to Multi Parameter Signals

Multi Parameter Signal

Multi Parameter Template
Weighted Time Warping

PPG: $pD_{PPG} \times q_1$

ABP: $pD_{ABP} \times q_2$

ECG: $pD_{ECG} \times q_3$
Weighted Time Warping

**DTW**

Single Parameter sequences A, B

\[ A_n = a_1 a_2 ... a_n \]
\[ B_m = b_1 b_2 ... b_m \]
\[ c_{x,y} = |A_x - B_y|^2 \]
\[ pD = \begin{bmatrix} c_{1,1} & c_{1,2} & \ldots & c_{1,m} \\ c_{2,1} & c_{2,2} & \ldots & c_{2,m} \\ \vdots & \vdots & \ddots & \vdots \\ c_{n,1} & \ldots & \ldots & c_{n,m} \end{bmatrix} \]
\[ D = pD \]

**WTW**

Multiparameter Signals \( W \) (window), Template \( Z \)

\[ W_{n \times k} = \{ W^1, W^2, .. W^k \} \]
\[ Z_{m \times k} = \{ Z^1, Z^2, .. Z^k \} \]
\[ c^j_{x,y} = |W^j_x - Z^j_y|^2 \]
\[ pD^j = \begin{bmatrix} c^j_{1,1} & c^j_{1,2} & \ldots & c^j_{1,m} \\ c^j_{2,1} & c^j_{2,2} & \ldots & c^j_{2,m} \\ \vdots & \vdots & \ddots & \vdots \\ c^j_{n,1} & \ldots & \ldots & c^j_{n,m} \end{bmatrix} \]
\[ D = \sqrt{\sum_{j=1}^{k} q_j pD^j} \]

Signal Quality Estimate
Signal Quality Estimation - Existing methods

- **ECG SQI [1]**
  - bSQI – two different algorithms on one channel
  - iSQI – the same algorithm on two different channels
  - kSQI – kurtosis to measure related peakedness
  - sSQI – Power spectral density to verify the QRS energy around 10 Hz

- **ABP SQI [1]**
  - ABP pulse detection to identify abnormalities

- **PPG SQI [2]**
  - By thresholding Hjorth[3] parameters
  - Hjorth parameters measure the activity ($H_0$), mobility ($H_1$), and complexity ($H_2$) of the signal

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SQE - Requirements

- **Spatial Consistency**
  
  (a) Signals are corruption-free
  
  (b) ABP and PPG signals are added with 20dB AWGN
  
  (c) ABP and PPG signals are added with 10dB AWGN

- **Temporal Consistency**
  
  (a) AWGN added signal data
  
  (b) ECGSQI
  
  (c) SQI from morphological dissimilarity
Morphological Dissimilarity

- Warped distance between the template and the corresponding window
- Template update allows us to follow the gradual evolution of the signals
- LCSS [1] instead of DTW
- Advantages
  - Comparable across different signal types
  - Bounded

\[
LCSS(A_x', B_y') = \begin{cases} 
0 & \text{if } A \text{ or } B \text{ is empty} \\
1 + LCSS(A'_{x-1}, B'_{y-1}) & \text{if } |A'_x - B'_y| < \delta_y \text{ and } |x - y| < \delta_x \\
\max\{LCSS(A'_{x-1}, B'_y), LCSS(A'_x, B'_{y-1})\} & \text{otherwise} 
\end{cases}
\]

\[
q = \frac{LCSS(A, B)}{\min\{m, n\}}
\]

Experiments (optional)

On clean signals with transient corruption added
On clean signals altered with Additive White Gaussian Noise (AWGN)
MIMIC data set from Physionet.org [1]
✓ Collected from ICU patients
✓ A multi-parameter physiological signal database with ABP, ECG channels and PPG signals
✓ Sampled at 125 Hz
✓ Human labeled annotations available
✓ 70 records, each longer than an hour

Ex 1 : Baseline

- Compared with widely used QRS detector (uses only one ECG)
  - Pan and Tompkins (P&T) [1] : Shown to be resilient to noise artifacts [2]

- Results
  - Average errors (ms)
    - WTW : < 0.001 ms | P&T : < 0.001 ms
  - The median # errors of 56000 beats (12 hours) across 10 records
    - WTW : 65 (0.1%) | P&T : 330 (0.5%)

- Both methods perform well
  - Data is not hard!
  - Chosen because it was clean

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1 Pan, J. and Tompkins, W. J. Biomedical Engineering, IEEE. 1985.
2 Kohler, B.-U., Hennig, C., and Orglmeister, R. The principles of software QRS detection. 2002.
EX 2: Tolerance to Transient Corruption

- **Data**
  - 1000 excerpts of 5-minute long clean signals from the raw MIMIC data
  - Severe transient corruption is randomly added to five 1-minute long non-overlapping regions
  - Signal interruption, exponential damping, superimposition of high and low frequency signals, overshooting and clipping

- **Mean errors in ms (mean segment length 521 ms)**
  - WTW (ours) : 2.89 ms | P&T (theirs) : 387.32 ms
Transient Corruption

PPG

ABP

ECG III
Ex 3 : Tolerance to AWGN

- **Data**
  - 1000 excerpts of 5-minute long clean signals from the raw MIMC data
  - Additive White Gaussian Noise (AWGN) is added to all \( m \) channels, or all but one randomly picked channel \((m-1)\)

- **Mean errors in ms (mean segment length 521 ms)**

<table>
<thead>
<tr>
<th>Signal to Noise Ratio (SNR Level)</th>
<th>P&amp;T</th>
<th>WTW</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td></td>
<td>All (m) channels</td>
</tr>
<tr>
<td>20 dB</td>
<td>12 ms</td>
<td>0.87 ms</td>
</tr>
<tr>
<td>10 dB</td>
<td>188 ms</td>
<td>3.27 ms</td>
</tr>
<tr>
<td>0 dB</td>
<td>303 ms</td>
<td>5.81 ms</td>
</tr>
</tbody>
</table>
AWGN at SNR 10dB

PPG

ABP

ECG III
Contributions

- Morphological Reconstruction
  - On non-overlapping corrupted quasiperiodic units
  - Formulate as a learning problem
  - Using template matching
  - Develop tools and optimizations to make template matching viable

- Segmentation
  - Joint Segmentation of multi parameter quasiperiodic signals
  - Weighted Time Warping (WTW)
    -Extension of DTW to multi parameter signals
  - Morphological Dissimilarity
    - Novel method for physiological signal quality estimate
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Backup Slides A

Dynamic Time Warping (DTW), characteristics, and Longest Common Subsequence (LCSS)
Dynamic Time Warping (DTW)

- Measure of similarity between two sequences varying in length
- The sequences are warped in time to find an optimal alignment [1]
- Achieved by minimizing the global distance between the sequences

Dynamic Programming Computation

$$A_n = a_1a_2...a_n$$
$$B_m = b_1b_2...b_m$$

$$aD(A_x, B_y) = D(A_x, B_y) + \min\{D(A_{x-1}, B_{y-1}), D(A_x, B_{y-1}), D(A_{x-1}, B_y)\}$$
Path Constraints

- DTW, in its basic form, is very flexible – can result in extreme matching

- Can be controlled by local and global path constraints [1]

\[
\begin{align*}
    d(x,y) &= c(x,y) + \min\{d(x-1,y-1), d(x,y-1), d(x-1,y)\} \\
    d(x,y) &= c(x,y) + \min\{d(x-1,y-1), d(x-1,y-2) + c(x,y-1), d(x-2,y-1) + c(x-1,y), d(x-1,y-3) + c(x,y-1) + c(x,y-2)\}
\end{align*}
\]

- Results is better – physiologically plausible matching

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Longest Common Subsequence (LCSS)

- LCSS allows two sequences to be stretched for matching without rearranging the order of the elements by allowing some elements to be unmatched.

- LCSS is highly resilient to noise [1]
  - Lets us control the extent of warping by $\delta_x$
  - It also allows us to decide the pair wise similarity between two elements in the sequences by $\delta_y$

- LCSS measures similarity – not distance.

### LCSS Vs. DTW

$$LCSS(A_x, B_y) = \begin{cases} 
0 & \text{if A or B is empty} \\
1 + LCSS(A_{x-1}, B_{y-1}) & \text{if } |a_x - b_y| < \delta_y \text{ and} \\
\max\{LCSS(A_{x-1}, B_y), |x - y| < \delta_x \} & \text{otherwise}
\end{cases}$$

$$aD(A_x, B_y) = D(A_x, B_y) + \min\{D(A_{x-1}, B_{y-1}), D(A_x, B_{y-1}), D(A_{x-1}, B_y)\}$$