

Classification of Cardiosynchronous Waveforms by Projection to a Legendre Polynomial Sub-Space

Aaron Jaech, Rebecca Blue, Robert Friedman, Marc O Griofa, Marios Savvides, B.V.K.Vijaya Kumar

Abstract—The use of Radio Frequency Impedance Interrogation (RFII) is being investigated for use as a non-invasive hemodynamic monitoring system and in the capacity of a biometric identifier. Biometric identification of subjects by cardiosynchronous waveform generated through RFII technology could allow the identification of subjects in operational and potentially hostile environments. Here, the filtering methods for extracting a unique biometric signature from the RFII signal are examined, including the use of Cepstral analysis for dynamically estimating the filter parameters. **Methods:** The projection of that signature to a Legendre Polynomial sub-space is proposed for increased class separability in a low dimensional space. Support Vector Machine (SVM) and k-Nearest Neighbor (k=3) classification are performed in the Legendre Polynomial sub-space on a small dataset. **Results:** Both the k-Nearest Neighbor and linear SVM methods demonstrated highly successful classification accuracy, with 93-100% accuracy demonstrated by various classification methods. **Conclusions:** The results are highly encouraging despite the small sample size. Further analysis with a larger dataset will help to refine this process for the eventual application of RFII as a robust biometric identifier.

I. INTRODUCTION

The use of Radio Frequency Impedance Interrogation (RFII) is being investigated for use as a non-invasive hemodynamic monitoring system and in the capacity of a biometric identifier [1-3]. An RFII device is capable of acquiring a cardiosynchronous signal by use of a molecular dipole resonant coupling method. A low power unmodulated radio frequency tone is applied to the thorax near the heart or aorta using a small, close proximity, non-contact near-field RFII probe. When the radio frequency tone matches the cardiac tissue water-bound protein dipole resonant frequency and the probe is matched to body impedance, the RFII system receives an RF signal that is modulated by mechanical activity, generating a cardiosynchronous waveform that features both systolic and diastolic events [1-4].

However, subject identification by RFII signal is complex as it requires robust identification of subjects in multiple physiologic conditions, subject positioning, and in an environment wrought with confounders and interference. In

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this paper, the classification of the RFII signal for subject identification is attempted utilizing a Legendre Polynomial sub-space projection, with both k-Nearest Neighbor and linear Support Vector Machine (SVM) algorithms.

II. METHODS

Data from four subjects were gathered using the RFII device I-channel, Q-channel, and simultaneous ECG while subjects were in a supine position. For each subject, fifteen minutes of signal data as well as the corresponding ECG signals were utilized for subsequent analysis.

Signal Filtration

Before segmenting the RFII signal a low-pass Parks-McClellan filter was applied to the data with a stop band at 27 Hz in order to remove high frequency noise (around 60 Hz) [5]. As the physiologic features of interest generally occur at much lower frequencies, this simple band pass effectively eliminates noise interference from power sources and movement. In addition, the RFII signal is occasionally corrupted by brief periods of high-energy noise. This noise is likely due to excessive movement on behalf of the subject during data recording. The signal noise is easily removed by discarding feature vectors whose Euclidean distance from the mean segmented beat exceed a certain threshold. The number of outliers discarded by this method was less than 4% of the data.

Segmentation and Feature Extraction

Following signal filtration, a Cepstral analysis was applied to estimate subject heart rate [6]. As the RFII signal is cardiosynchronous, the dominant frequency closely corresponds to the heart rate and is therefore readily identified. The Cepstrum is defined as:

$$|F\{\log(|F\{f(t)\}|)\}| \quad (1)$$

where $F(\cdot)$ denotes the 1-D Fourier transform (FT). The Cepstrum for subject 1 is demonstrated in Figure 1, with the bold portion of the plot representing estimated heart rate. After heart rate estimation, a continuous wavelet transform was applied using the Morlet wavelet centered at the heart rate frequency. The zero-crossings of the wavelet-filtered signal are cardiosynchronous with two zero crossings per cardiac cycle (above and below the axis). The RFII signal was segmented by taking a fixed-size window (1.8 seconds of data) around each zero-crossing with a positive derivative.

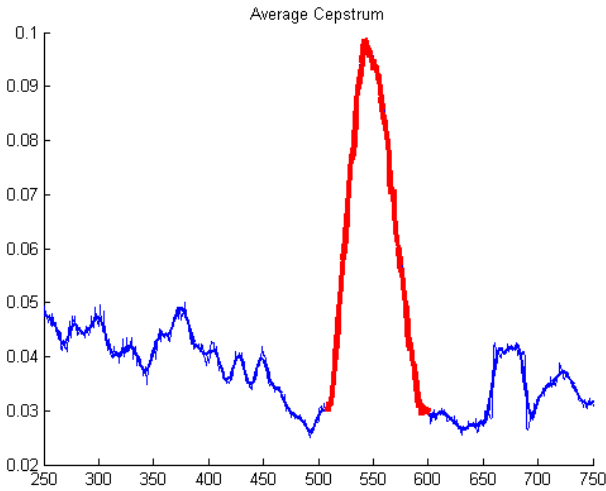


Figure 1: A plot of the Cepstrum for sample data from Subject 1. The Cepstrum estimates the median heart rate at 55.3 bpm while the true median is 54.3 bpm.

As the high frequency portion of the spectrum contains most of the discriminating information, feature vectors are extracted from the RFI signal after it is passed through a high-pass filter. (This filter is also a Parks-McClellan filter with the pass-band set at 1.5 Hz). The signal alignment is highest near the segmentation point and decreases towards both ends of the feature vector. In order to reduce the unwanted variance around the edges of the feature vector the feature vector was multiplied by a tapered cosine window, which effectively restricts the values at the extremes to be near zero. This forces the classifiers to concentrate on the most discriminating portion of the feature vector (Figure 2). All of the feature vectors were normalized to have zero mean and unit energy.

Legendre Polynomials

The n th Legendre Polynomial is defined by the following differential equation:

$$\frac{d}{dx} \left[(1-x^2) \frac{d}{dx} p_n(x) \right] + n(n+1)p_n(x) = 0 \quad (2)$$

However, in practice they are generated by using a recursive equation:

$$(n+1)p_{n+1}(x) = (2n+1)xp_n(x) - np_{n-1}(x) \quad (3)$$

with the following initial conditions:

$$p_0(x) = 1 \quad (4)$$

$$p_1(x) = x \quad (5)$$

The polynomials have the attractive property of orthogonality on the unit interval from -1 to 1. These polynomials have been used as an orthogonal base expansion for biometric recognition of ECG signals; here we apply the same idea to the cardiosynchronous RFI signal to explore its feasibility for biometric recognition in this domain [7].

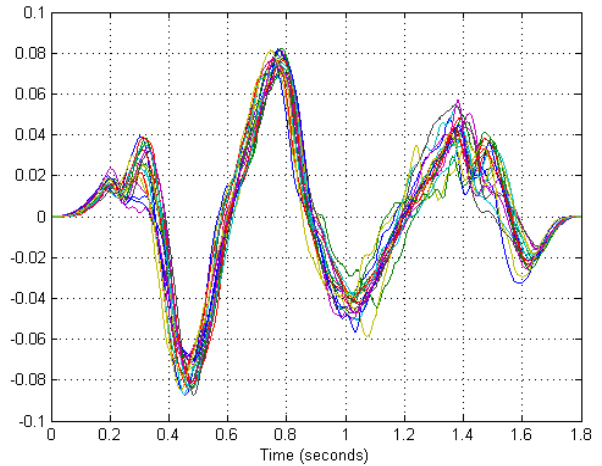


Figure 2: 20 feature vectors from Subject #1

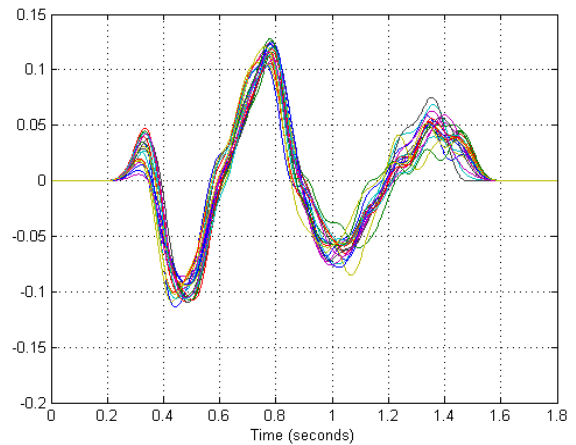


Figure 3: The same 20 feature vectors from Subject #1 after projection to the Legendre sub-space and reconstruction back into the original space.

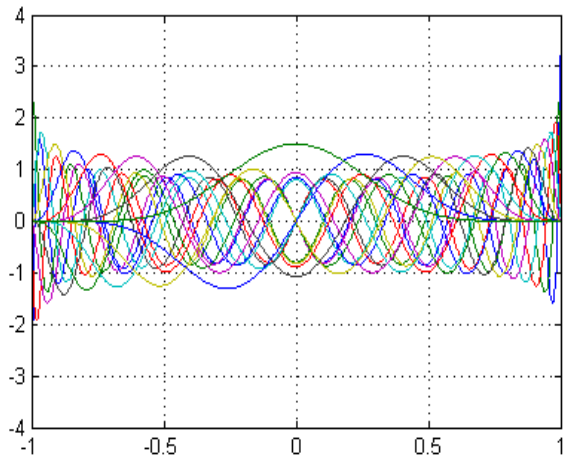


Figure 4: The first 15 Legendre polynomials

The feature vector contains 900 samples, or 1.8 seconds of data sampled 500 times per second. The first 50 Legendre polynomials were used as a subspace. The polynomials are sampled 900 times at equal intervals between -1 and 1. The feature vectors are projected to the Legendre space by multiplying them by the matrix of sampled polynomials.

Classification

Classifiers are trained on 30 samples per subject and tested on 100 samples per subject. The training data represent about a 30 second segment of the recording. There is a gap of two minutes between the end of the training data and the start of the testing data. In order to prevent testing samples from containing overlapping portions of the RFI signal only every third feature in the classification experiments was considered. Classification was performed using the k-Nearest Neighbor algorithm ($k = 3$) and linear Support Vector Machines (SVM). As a baseline, the data were projected to a Discrete Cosine Transform (DCT) sub-space.

III. RESULTS

Both the k-Nearest Neighbor and linear SVM methods demonstrated highly successful classification accuracy. Initial classification results are presented in Tables 1 and 2.

TABLE I. NEAREST NEIGHBOR CLASSIFICATION

Coefficients	Legendre	DCT
3	92.0%	64.0%
5	97.0%	86.5%
7	95.5%	95.0%
9	97.0%	98.0%
15	97.0%	98.5%

TABLE II. SVM CLASSIFICATION

Coefficients	Legendre	DCT
3	93.0%	60.5%
5	94.0%	79.0%
7	95.0%	99.0%
9	96.5%	99.5%
15	96.0%	98.5%

Figures 5-6 summarize accuracy rates for both k-Nearest Neighbor and linear SVM methods.

IV. DISCUSSION

High classification accuracy was achieved utilizing the Legendre Polynomial with both k-Nearest Neighbor and SVM algorithms. In fact, using only a three-dimensional feature vector can achieve a 93% identification rate in comparison to 64% achieved by DCT of similar dimension. The three-dimensional plots in Figures 7 and 8 illustrate the increased linear separability of the samples in the Legendre polynomial sub-space as compared to the DCT sub-space. The advantage of this approach is that there is no data learning used in generating the sub-space, which is the

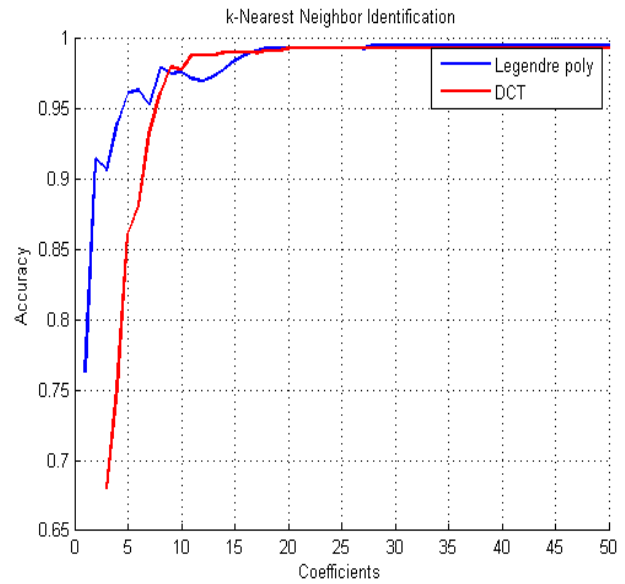


Figure 5: A comparison of classification accuracy for Legendre polynomial sub-space and Discrete Cosine Transform sub-space with varying number of coefficients using the k-Nearest Neighbor classifier.

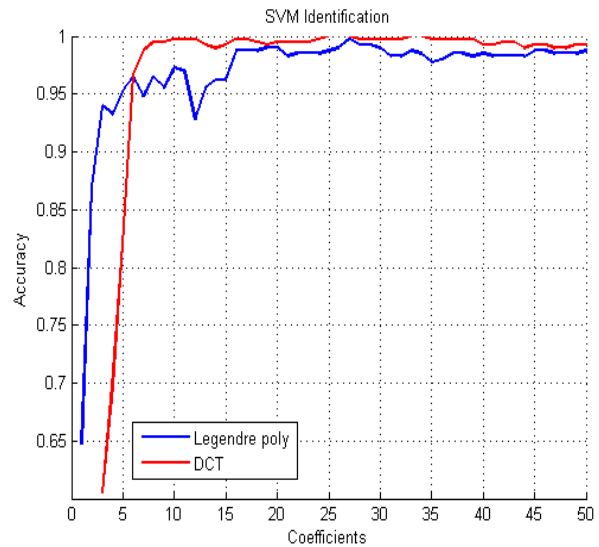


Figure 6: A comparison of classification accuracy for Legendre polynomial sub-space and Discrete Cosine Transform sub-space with varying number of coefficients using the SVM classifier.

advantage of using a data-independent expansion based on Orthogonal Legendre Polynomial Basis expansion and Discrete Cosine Transform.

These results are highly encouraging despite the small sample size. Further analysis with a larger dataset will help to refine this process for the development of an integrated hardware platform and eventual application of RFI as a robust biometric identifier.

ACKNOWLEDGMENTS

The authors would like to thank Innovative Health Applications and the Biomedical Research Laboratory at Kennedy Space Center, and the Engineering Department at Noninvasive Medical Technologies for their invaluable assistance and guidance throughout this project.

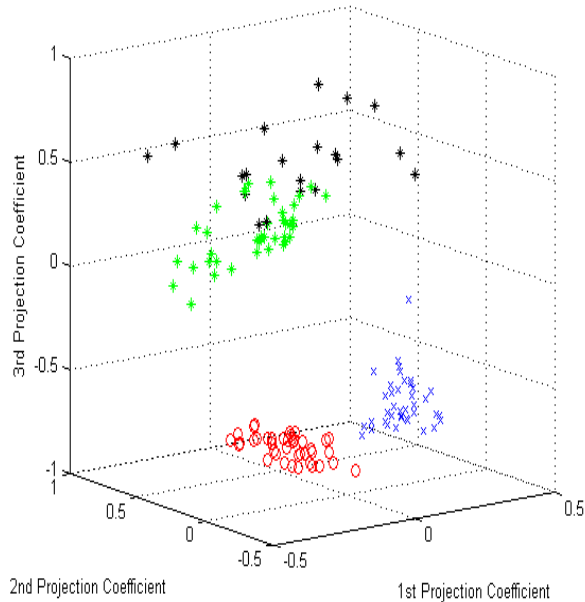


Figure7: 40 samples from each of the 4 subjects plotted in the 3-dimensional Legendre polynomial sub-space.

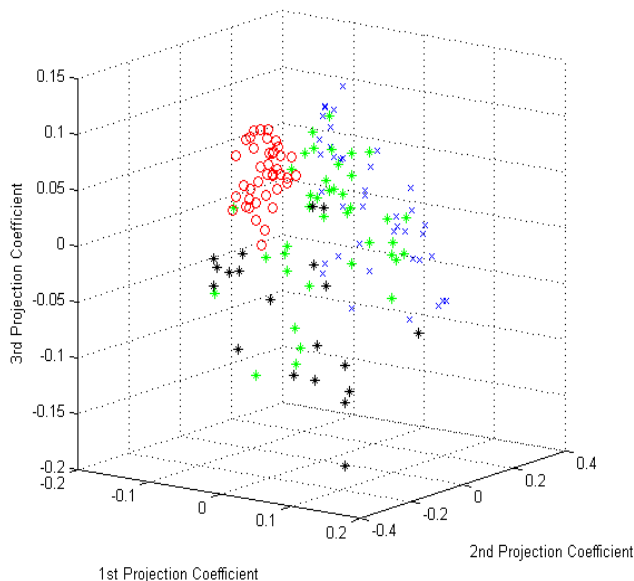


Figure8: 40 samples from each of the 4 subjects plotted in the 3-dimensional DCT sub-space.

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