Beat Discovery from Dimensionality Reduced Perspective Streams of Electrocardiogram Signal Data

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Abstract: Spectral characteristics of ECG traces have identified a stochastic component in the inter-beat interval for triggering a new cardiac cycle. Yet the stream consistently shows impressive reproducibility of the inherent core waveform. Respectively, the presence of close to deterministic structures firmly contends for representing a single cycle ECG wave by a state vector in a low dimensional embedding space. Rather than performing arrhythmia clustering directly on the high dimensional state space, our work first reduces the dimensionality of the extracted raw features. Analysis of heartbeat irregularities becomes then more tractable computationally, and thus claims more relevance to run on emerging wearable and IoT devices that are severely resource and power constraint. In contrast to prior work that searches for a two dimensional embedding space, we project feature vectors onto a three dimensional coordinate frame. This merits an essential depth perception facet to a specialist that qualifies cluster memberships, and furthermore, by removing stream noise, we managed to retain a high percentile level of source energy. We performed extensive analysis and classification experiments on a large arrhythmia dataset, and report robust results to support the intuition of expert neutral similarity.

1 INTRODUCTION

Electrocardiogram (ECG) is a simple and effective tool to assess the electrical and muscular functions of the heart. The shape of the ECG signal (Goldberger and Goldberger, 1977) is commonly considered a faithful representation of cardiac physiology to assist in diagnosing conditions for the heart to beat in irregular or abnormal rhythm, known as Arrhythmia. The interpretation of ECG tracing requires however a considerable amount of cardiology training. One of the major challenges in automating the analysis of cardiac arrhythmias is the lack of coherency in the captured time series of the heartbeat. Poor repeatability of the recorded ECG signal in a succession of tests administered on the same patient, and variability of patient-to-patient morphologies that lend to extensive waveform shape dissimilarities, make it all but difficult for a clustering algorithm (Kaufman and Rousseeuw, 1990) to group complexes consistently, and hence less likely to agree with the more manual process of clinical diagnosis.

In recent years, wearable and Internet-of-Things (IoT) technology for remotely monitoring continuous ECG signals has emerged (Baig et al., 2013). These devices use a non-invasive surface recording that employs from three to twelve electrodes, each connected to a different part of the body. Electrodes measure voltage or current change induced by the heart beat over time and conceptually describe heart activity in separable time series streams. Streams represent a high dimensional state space for extracting raw cardiac features, and often follow arrhythmia clustering directly. However, operating on the large state space is compute intensive and conceived practically infeasible to execute on wearable devices that are highly restricted in compute capacity and power envelope.

A number of attempts have been made to analyze cardiac time series in the context of deterministic dynamical systems. Kantz and Schreiber (Kantz and Schreiber, 1998) argued that heart dynamics contain a stochastic component in the inter-beat time intervals (*RR*-interval) (Goldberger and Goldberger, 1977). On the other hand, they showed that the single cycle ECG wave, a *PQRST* complex (Figure 1), resembles regular structures and can be equally represented by state vectors in a low dimensional embedding space. Inspired by this observation, our work first removes noise from the ECG signal by projecting the original, high dimensional state space onto a lower, three dimensional feature volume, while preserving stream energy to a high percentile. Compared to prior work

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(Li et al., 2012) that resorts to a two dimensional intrinsic space, our 3D projection facilitates a precursory human inspection of arrhythmia formations by means of a vital depth perception. Furthermore, clustering and classification conducted on a dimensionality reduced training set is considerably more computational efficient to better suit portable ECG devices.

As evident from a multitude of research studies that exploit supervised machine learning techniques, an attempt to coerce a cluster to a unique, cardiologist assessed arrhythmia label prove unsuccessful and exhibits under par classification rates (Wenyu et al., 2003). Rather, unsupervised learning from presumed unlabeled heartbeat features and clustering a diverse set of ECG morphologies by endorsing neutral similarity in feature space, is better positioned to discover patient groups that span a membership fusion of several arrhythmia types. In our work, we investigate a discovery (Rajaraman and Ullman, 2011) method that extracts a statistical relation model of arrhythmia bound cases from a large ECG data set, provided by the UCI Machine Learning Repository (UCI, 1987) and constructed of recordings taken from hundreds of patients. The method incorporates both information retrieval (Manning et al., 2008) and unsupervised machine learning (Duda et al., 2001) algorithms. Information retrieval (IR) is rapidly becoming the dominant form of data source access, and our work closely leverages IR practices and follows efficient similarity calculations directly from the well known Vector Space Model (Salton et al., 1975). Furthermore, we are interested in objectively uncovering the underlying cluster nature of abnormal, cardiac rhythm instances presented in the dataset, without resorting to any prior knowledge of a cardiologist review.

The main contribution of our work is a novel, statistically driven system that combines IR and unsupervised learning techniques to discover instinctive cluster patterns from presumed unsolicited, ECG signal data. We employ Singular Value Decomposition (SVD) (Cormen et al., 1990) for dimensionality reduction of cardiac streams that is equivalent to spectral decomposition of a matrix, known for finding independent linear correlations of feature vectors to yield the best low rank approximation. For arrhythmia clustering, we use the efficient Clustering Using REpresentatives (CURE) (Guha et al., 1998) method, a hierarchical algorithm that identifies groups of non-spherical shapes and wide variations in size, from perceived inseparable samples. More importantly, CURE is robust to outliers that are prevalent in assembling ECG traces. Owing to a compact cluster representation of a small set of well scattered points, CURE scales to large datasets and the search for cluster similarities is considerably more effective compared to either the centroid or all-points based agglomerative methods. The remainder of this paper is organized as follows. We overview the basics of ECG recording and annotations, and highlight the motivation behind selecting orthogonal features from ECG streams, in section 2. Section 3 briefs on the theory of SVD that leads to our compact, 3D embedding space, whereas in section 4 we review algorithm details of the CURE technique. Following in section 5, we present our evaluation methodology of arrhythmia cluster analysis and classification, and report quantitative results of our experiments. We conclude with a discussion and future prospect remarks, in section 6.

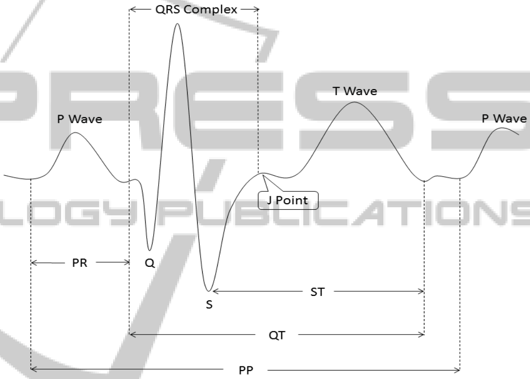


Figure 1: An end-to-end single cycle of normal ECG characteristics, depicting both waves and intervals.

2 ECG STREAMS

An Electrocardiogram (ECG) provides graphical surface recording of electrical cardiac events. Well established electrode configuration tends to result in a specific tracing pattern, and changes in the ECG signal provides the clinician indispensable data about cardiac physiology. The tracing recorded from the electrical activity of the heart forms a series of prominent waves and complexes that are alphabetically labeled as P, Q, R, S, and T. Each deflection occurs in regular intervals for a healthy heart, and represents depolarization or repolarization of myocardial tissue. Figure 1 shows an end-to-end single cycle of a normal ECG signal and identifies conventional notations for waves and basic intervals. A standard 12-lead ECG is performed on a patient by attaching to his or her skin a set of electrodes. The leads are grouped into three frontal plane, bipolar limb leads: I, II, III; three augmented voltage leads: aVR, aVL, aVF; and six transversal plane, chest or precordial leads: $V1-V6$ (Table 1). In essence, the 12-lead test supplies spatial information of electrical events in orthogonal directions, hence each separable recorded stream provides a different view of heart activity, from a unique angle across the body. The interpretation of the 12-lead ECG is multi-faceted and is based on examining rate, rhythm, the *QRS* axis, and the various intervals.

Table 1: A 12-lead ECG and their corresponding axes.

Group	Lead	Orientation
Bipolar Limb	I II III	lateral inferior inferior
Unipolar Limb	aVR aVL aVF	none lateral inferior
Unipolar Chest	$V1-V3$ $V4-V6$	septal or anterior anterior or lateral

The dataset we use is multivariate and coalesces ECG signal features of different categories (Guvenir et al., 1997), each described as a vector, possibly combining real, integer, and boolean element types. A patient class leads off with attributes composed of age, sex, height and weight. As eleven global recording parameters are next and include the heart rate, measured in beats-per-minute, and a selection of average duration figures in milliseconds of the *QRS* complex, *PR* and *QT* intervals, and *P* and *T* waves. Along with frontal plane orientations calculated in angles for each of *QRS*, *P*, *T*, *QRST*, and *J* axes. To describe the dynamics of the multi-faceted signal shape, a pair of 12-view stream sets follows, one set designated for each the period and the amplitude cardiac feature groups. Twelve properties form a period view that comprise average width in milliseconds of each of the *Q*, *R*, *S*, R', and S' waves, with R' and S' signify a small peak right after the *R* and *S* waves, respectively. Succeeded by the number of intrinsic deflections and a collection of six flags to indicate the presence or absence of any of a ragged or a biphasic deflection to each of the *P*, *R*, and *T* waves. Analogously, the per-view amplitude class is made up of ten uniform real attributes. Eight are peak measurements of each of the *P*, *Q*, *R*, *S*, R', S', and *T* waves, together with the *J* depression point, all obtained in increments of 0.1 millivolt steps. In addition, an amplitude perspective contains two area-under-curve elements, respectively defined as $QRSA = 0.1 \cdot \sum_{i=1}^{k} 0.5 \cdot width_{s^{(i)}} \cdot height_{s^{(i)}}$, where k is the count of segments, $s^{(i)}$, presented in the *QRS* complex, and $QRSTA = QRSA + 0.5 \cdot width_T \cdot 0.1 \cdot height_T$ that factors in the *T* wave. For a biphasic *T* wave, the area derivation only considers the bigger segment. A high level overview of our learning framework that operates on the ECG streams is illustrated in Figure 2. Detailed discussion of the pipelined stream transmission from a device to the server is outside the scope of this paper.

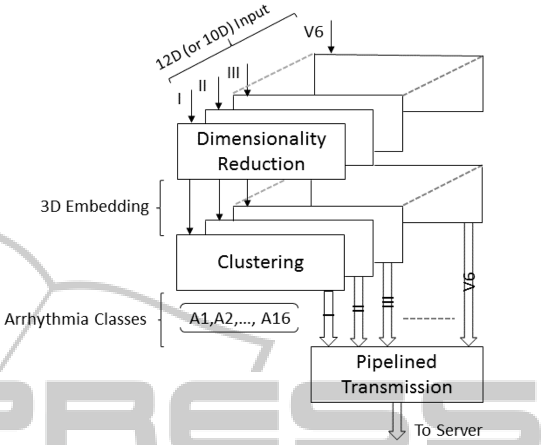


Figure 2: The input to our learning framework is a set of separable ECG streams in either 12-dimensional or 10-dimensional vectors for the period and amplitude groups, respectively. Input streams are each dimensionality reduced to a canonical 3D embedding space, and unlabeled sample points are further clustered into 16 arrhythmia classes. Transmission from any of a wearable or an IoT device to the server is pipelined, one stream at a time.

3 DIMENSIONAL REDUCTION

Directly analyzing an extended time series of the ECG multivariate stream poses a compute efficiency challenge and raises the quest for dimensionality reduction to both explore and perceptually visualize a compact representation of the high dimensional data. In one formulation, Li et al. (Li et al., 2012) exploit Locally Linear Embedding (LLE) (Roweis and Saul, 2000) technique to map the ECG signal onto a single, two dimensional global coordinate system. LLE harnesses neighborhood symmetries of linear reconstructions to learn the global structure of non-linear manifolds. In an alternate prospect, many sources of data are described as a large matrix composition. Amongst many application domains, matrix representation is prominent in recommender systems, social networks, and web page ranking. In our work, we render a collection of ECG feature streams, each as an arrhythmia matrix, *A*, that has patients as its rows, *m*, and the vector elements of cardiac features as columns, *n*. One well established form of matrix analysis is Singular Value Decomposition (SVD) (Cormen et al., 1990) that gracefully leads to data reduction of desired dimensionality at a minimum reconstruction error.

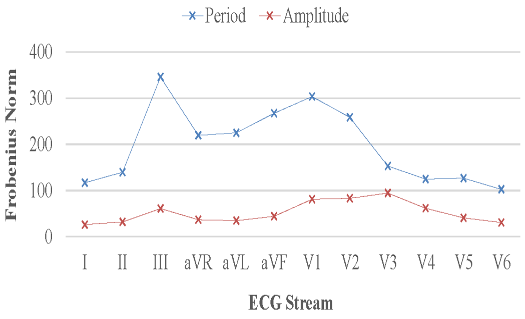


Figure 3: SVD Frobenius norm for similarity between the original arrhythmia data matrix to its reduced form of three dimensions, for each ECG view and parametrized by the period and amplitude feature groups.

Let our input arrhythmia matrix $A \in \mathbb{R}^{mxn}$ be of a rank r, then SVD states that it is always possible to decompose a real matrix into a product of three unique matrices $A = U\Sigma V^T$, where $U \in \mathbb{R}^{mxr}$ and $V \in \mathbb{R}^{nxr}$ are the left and right singular vectors, respectively, and $\Sigma \in \mathbb{R}^{rxr}$ is a diagonal matrix comprised of singular values. The diagonal entries of Σ are all positives and sorted in a descending order ($\sigma_1 \geq \sigma_2 \geq ... \geq 0$). For SVD interpretation, columns r of U, Σ, and V are perceived as concepts (Rajaraman and Ullman, 2011) that are hidden in A, hence U relates patients to concepts, similarly V connects ECG terms to concepts, and Σ attaches a strength or importance to each concept. SVD singles out linear combinations of the data and yields an optimal set of axes to project the data on. Each vector of V constitutes the projection axis of the data, and the corresponding singular value in Σ identifies the variance of data points for the specific dimension. The transformed coordinates in the new projection space are further obtained from the matrix product $U\Sigma$.

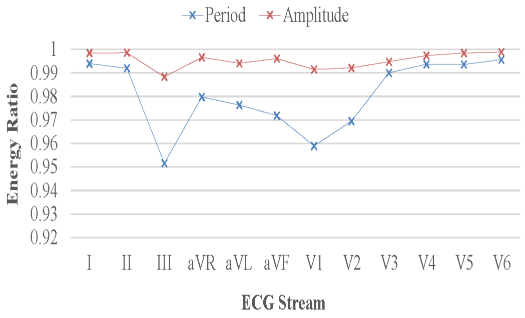


Figure 4: SVD retained energy ratio for arrhythmia data matrix reduction to a three dimensional embedding space, for each ECG view and parametrized by the period and amplitude feature groups.

Reducing the ECG stream data to a k-dimensional space is simplified to zero-ing out the smallest $r-k$ singular values in Σ, and producing the diagonal matrix S. By dropping vectors of small importance, matrix $B = USV$ becomes the best rank-k approximation to A, with maximum similarity quantified by the Frobenius norm

$$|A - B|_F = \sqrt{\Sigma_{ij}(A_{ij} - B_{ij})^2}. \qquad (1)$$

Figure 3 shows similarity between the original arrhythmia data matrix to its reduced form of three dimensions, for each ECG stream and parametrized by the period and amplitude feature groups. For every perspective, matrix columns are markedly reduced from 12 to 3 and from 10 to 3 for the feature groups, respectively. The Frobenius norm distance standard attributes better similarity to the amplitude streams, mostly due to a nonuniform mixture of real and nominal values apparent in a period feature vector. Likewise, Figure 4 depicts qualitative data reduction measures for each cardiac stream in their respective period and amplitude feature groups. The metrics for selecting the number of matrix dimensions to keep is conventionally governed by the energy ratio term $\Sigma_{i=1}^{k} \sigma_i^2 / \Sigma_{i=1}^{r} \sigma_i^2$. A ratio range of 0.8 to 0.9 is deemed acceptable for a reasonable SVD reconstruction error, yet our analysis denotes most energy is retained in the top three matrix columns, with a percentile consistently exceeding 95%, as amplitude views display at least 0.98 proportion.

4 ARRHYTHMIA CLUSTERING

Expert ECG cardiologists largely rely on interpreting visual cues for patient diagnosis, and mainly subscribe to decode recognizable segmentation structures (Hamameh et al., 2011). However, the abundant signal data produced by many small, real-time capture-and-transmit devices necessitate a visual system that is perceptually intuitive and requires effective algorithms to analyze progressively multiple streams of increased dimensionality. In our work, transforming the high dimensional cardiac data to a form both acceptable for human perception and authentic to the original data is facilitated by SVD. Projecting heartbeat data onto a 3D space has the apparent advantage over a 2D planar mapping (Li et al., 2012) in allowing arbitrary rotations around the z axis to render the data model from different vantage points. Multiple viewpoints of ECG streams may reveal otherwise obscured patterns that are essential for a domain expert to make an informed analysis about a patient.

Our framework regards the 12-perspective stream data, emitted from the ECG Holter, as separable and has each of the cardiac views projected onto a perceptually viable 3D space. Figures 5 and 6 further illustrate stream renditions of the period and amplitude feature groups, respectively. Each frame of reference contains 452 patient samples perceived from a prescribed spatial angle, and displayed in a three dimensional space. A closer observation identifies distinct and vital data needed for arrhythmia clustering, but there are also clear indications for instances that overlay each other, although they might belong to a different arrhythmia class, and furthermore, some samples deviate distantly from the formed partitions. Hence, our contention that a clustering method to operate effectively on arrhythmia streams captured from a large number of patients, must grant clusters to form any geometrical shape of variable size, and properly address data point overlaps. In addition, the algorithm is required to be robust in the presence of outliers. We selected the hierarchical Clustering Using REpresentatives (CURE) (Guha et al., 1998) method, explicitly designed to support our set forth prerequisites.

Cluster analysis of ECG recordings is a powerful tool for discovering patients of similar arrhythmia disorders. In contrast to supervised methods, our evaluation proceeds anonymously on presumed unlabeled cardiac data without resorting to prior knowledge of a cardiologist assessment. Several clustering methods have been devised in the domain of data mining, each of its own strengths and shortcomings. For the sake of keeping the description concise, the reader is kindly referred to an excellent survey of clustering methods exclusively applied to time series data (Liao, 2005). CURE stands out as a highly efficient, hierarchical clustering algorithm (Johnson, 1967) that has linear storage requirements $O(n)$ and time complexity of $O(n^2)$ for low dimensional data of n points, each of d dimensionality, and is no worse than the more constrained, centroid-based hierarchical method. CURE is agglomerative and starts by placing each individual data point in a cluster of its own, and successively merges the closest pair of clusters until the number of clusters reduces to k. Each cluster contains a set of representative points, c, chosen to be well scattered in the cluster extent, and are further shrunk towards the cluster centroid by a fractional factor α. Set apart reference points and the contraction operation that follows, serve the objectives for capturing a cluster of arbitrary geometrical profile and mitigating the effects presented by outliers, respectively. The distance between a cluster pair, u and v, is delineated by the closest pair of representative points, p and q, one from each of the clusters

$$dist(u,v) = \min_{p \in u.rep, q \in v.rep} dist(p,q). \qquad (2)$$

As the distance between two points, p and q, often takes a Euclidean form of L_1-norm or L_2-norm metrics, but also a nonmetric similarity function. Our cardiac feature vectors mix real, integer and boolean components and data points may be rather thought of as directions (Baeza-Yates and Ribeiro-Neto, 1999) in the vector space model (Salton et al., 1975). Hence, we chose the adjusted cosine similarity for a distance measure that computes a 0 to 180 degrees angle between two zero-mean point vectors and is defined as

$$sim(p,q) = \frac{(p-p_m)(q-q_m)}{\|(p-p_m)\|_2 \|(q-q_m)\|_2}, \qquad (3)$$

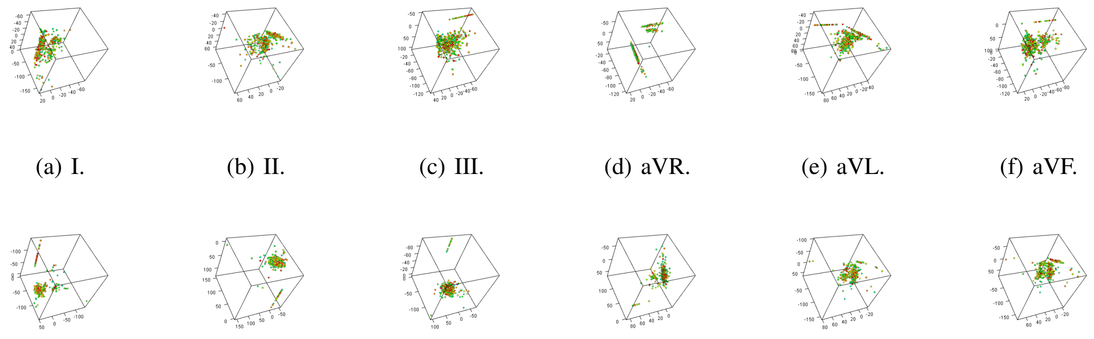
where p_m and q_m are the mean of p and q, respectively. Adjusted cosine similarity is widely used in the domain of item-based collaborative filtering.

5 EMPIRICAL EVALUATION

To validate our system in practice, we have implemented a software library that realizes the cluster analysis of ECG streams in several stages. After collecting and cleaning the archived cardiac data, our library commences with extracting patient, global, period and amplitude based feature vectors. Our features are regarded as unlabeled, and follow an explicit clustering process. In addition to detecting the presence or absence of arrhythmia individually, each of the constructed groups represent an objective arrhythmia class and our goal is to further explore and quantify the relations between automatically machine generated clusters to cardiologist diagnoses.

5.1 Experimental Setup

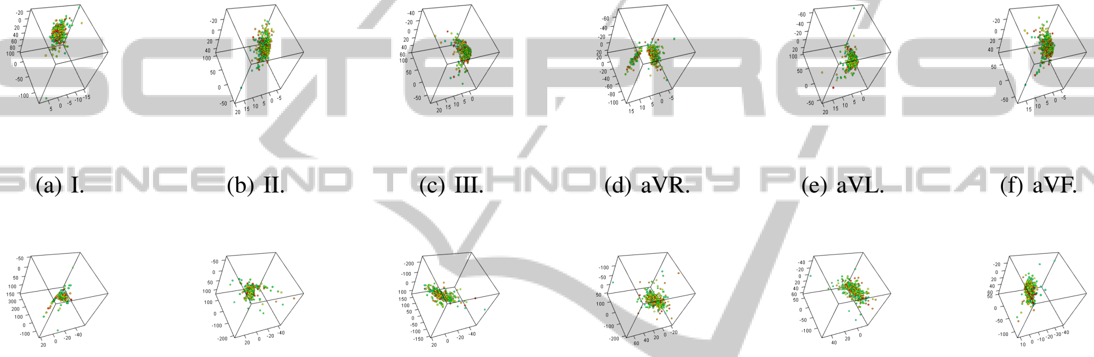
Our work exploits the R programming language (R, 1997) to acquire the raw arrhythmia data and fosters cleanup to serve useful in our software environment. We use the extensive and well maintained arrhythmia dataset from the UCI Machine Learning Repository (UCI, 1987), comprised of 452 patient instances with each ECG trace represented as a 279 feature vector elements, and chose to impute missing values, manifested primarily in the axis orientation columns, with the mean of the present feature items. For our study, we selected the time series attributes held in the 12-perspective, period and amplitude cardiac groups that total a majority of 264 features, intentionally leaving patient and global properties outside the scope of this work. The measured figures of the dynamic signal were obtained using the ECG system jointly developed by IBM and Mount Sinai University Hospital. As a point of reference, expert cardiologist evaluation



(a) I. (b) II. (c) III. (d) aVR. (e) aVL. (f) aVF.

(g) V1. (h) V2. (i) V3. (j) V4. (k) V5. (l) V6.

Figure 5: Cardiac period feature group: visually depicted, separable 12-perspective ECG streams, each contains 452 patient instances viewed from a user set vantage point and displayed in a three dimensional space.



(a) I. (b) II. (c) III. (d) aVR. (e) aVL. (f) aVF.

(g) V1. (h) V2. (i) V3. (j) V4. (k) V5. (l) V6.

Figure 6: Cardiac amplitude feature group: visually depicted, separable 12-perspective ECG streams, each contains 452 patient instances viewed from a user set vantage point and displayed in a three dimensional space.

is attached to each patient record and lists 16 types of commonly observed cardiac arrhythmia (Table 2).

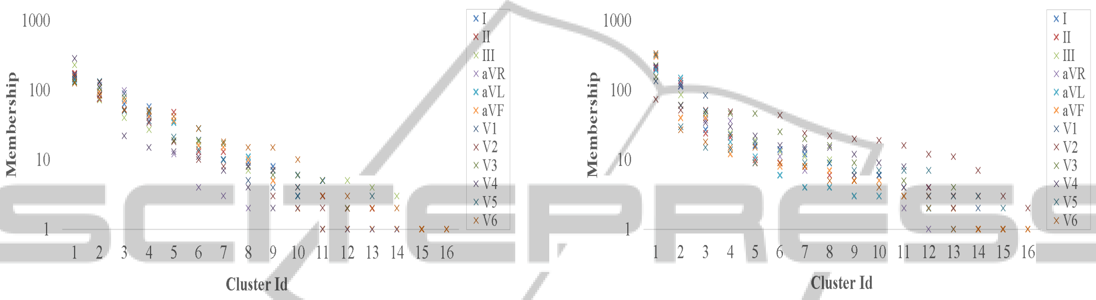
Our arrhythmia clustering is entirely autonomous and avoids consulting a specialist diagnosis apriori. Rather than found on a basis of fixed and unique assignment of a single arrhythmia type to a patient (Guvenir et al., 1997), our unsupervised methodology clusters objectively by similarity in cardiac feature space, and is therefore impartial to manual process constraints. Hence, our generated arrhythmia groups are each exposed to potentially contain a fusion of a subset of the arrhythmia types specified in Table 2. CURE is handed the input parameter k to follow the generation of 16 logical groups for each of the separable, 12-perspective ECG streams, leading thereof to a 192 multi-class classification paradigm. For our reported experiments, we consistently use in a cluster four representative points, c, that is the minimum set required to provide concavity for the cluster geometrical shape, and chose a shrinking factor, α, of 0.2 to resonate with the all-points model and distant from a more limiting, single centroid based algorithm.

5.2 Experimental Results

Our clustering process solely relies on automatic feature extraction from natively recorded ECG data and incorporates statistical methods to facilitate the search of unsolicited arrhythmia patterns and discover global relations of cardiac irregularities that are not necessarily bound to an individual patient evaluation. Pertinently, our analysis experiments exploit 452 patient records that are SVD dimensionality reduced to a 3D projection space, and are further partitioned across 16 relational arrays. First, we studied the inherent allocation nature of the patient records. Respectively, Figure 7 shows in a log scale cluster membership distribution of arrhythmia for both the cardiac period and amplitude feature groups, each parametrized by the twelve ECG perspectives. Plotted curves are spread fairly consistently across views, yet the amplitude chart exhibits a higher dynamic range, most likely ow-

Table 2: Arrhythmia types and distribution assessed by an expert cardiologist.

Class	Arrhythmia	Dist	Class	Arrhythmia	Dist
1	Normal	245	9	Left Bundle Branch Block	9
2	Coronary Artery	44	10	Right Bundle Branch Block	50
3	Anterior Myocardial Infraction	15	11	One Degree Atrioventricular Block	0
4	Inferior Myocardial Infraction	15	12	Second Degree Atrioventricular Block	0
5	Sinus Tachycardia	13	13	Third Degree Atrioventricular Block	0
6	Sinus Bradycardia	25	14	Left Ventricular Hypertrophy	4
7	Ventricular Premature Contraction	3	15	Atrial Fibrillation or Flutter	5
8	Supraventricular Premature Contraction	2	16	Other	22



(a) Period feature group.

(b) Amplitude feature group.

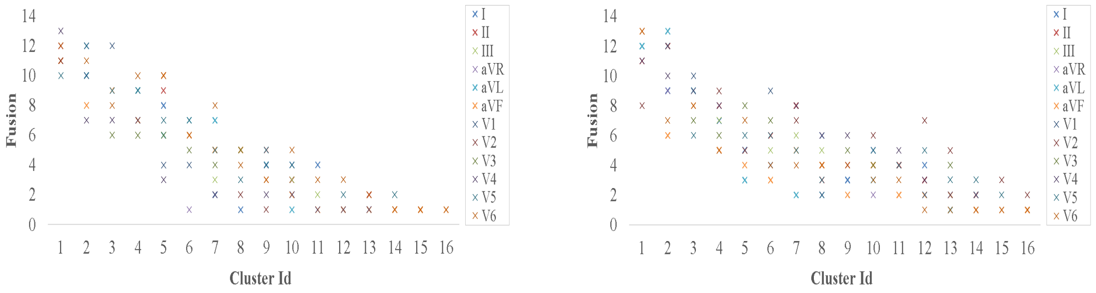
Figure 7: Cluster membership distribution of 452 patient instances for both the cardiac period and amplitude feature groups, each parametrized by an ECG perspective. Patient membership count in each of our unlabeled and statistically learned clusters is shown in a log scale.

ing to a uniform vector type of real feature elements.

Next, we examined the relations of our arrhythmia grouping to a human expert analysis, in both the contextual level and proportionality of irregular cardiac type assignment. Learning from ECG recordings of a plurality of patients by applying neutral similarity practices is predicted to reveal multiple arrhythmia types attached to a single patient. Hence, grouping cardiac irregularities is equally bound to observe a fusion effect with memberships that span several arrhythmia categories. In our experiments, we inquire the cardiologist evaluation for each person post clustering, and assess the blend of cardiac abnormalities in a cluster. Figure 8 shows arrhythmia type fusion in clustering our dataset for both the cardiac period and amplitude feature groups, each parametrized by the set of ECG perspectives. Some clusters noticeably abide by owning a single and distinct arrhythmia class, however most groups do contain several cardiac anomalies with a count that ranges from two to thirteen. Correspondingly, Figure 9 shows in relative error terms, membership distribution comparison of machine generated clusters to a manual cardiologist assessment (Table 2). For the former, we take the average across the 12-view ECG streams for each the cardiac period and amplitude feature groups. Evidently, our distributions track well and are for most part inline with the partitions concluded from diagnoses conducted by a professional. Noticeable however are fairly large errors for both the largest arrhythmia classes and for clusters identified by an expert as containing no patients and are therefore statistically unreasoned. For computational stability, we set empty, manually assessed clusters to own one patient.

We have extended our discovery study to data that is outside the scope of our acquired, ECG training set by artificially generating synthetic cardiac streams. In a sense, this set of query feature vectors is best regarded as means to distort the original ECG signal in a controlled manner. To this extent, a query vector element is randomly selected in the range prescribed by statistically summarizing every feature attribute in the original dataset. For each the period and amplitude feature groups and for each ECG perspective, we produced 50 test vectors to total 600 records per cardiac collection, with an aggregate of 1200 query vectors. In its entirety, query data is fully excluded from A, our SVD matrix representation of the raw arrhythmia dataset. Each query vector, q, first undergoes transformation onto the concept space by utilizing the SVD V matrix and performing qV, and further dimensionality reduced to our working, 3D projection space.

To feature match the query data, we ultimately attempt to correlate a query perspective to a training set cardiac view. We accomplish this by employing a k-nearest neighbor (KNN) (Cormen et al., 1990)



(a) Period feature group.

(b) Amplitude feature group.

Figure 8: Arrhythmia type fusion in clustering 452 patient instances for both the cardiac period and amplitude feature groups, each parametrized by an ECG perspective. Shown are the number of unique, expertly analyzed arrhythmia classes in each of the unlabeled and statistically learned clusters.

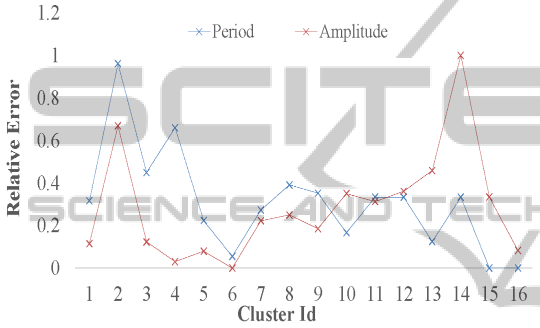


Figure 9: Comparing membership distribution of machine generated clusters to a manual cardiologist assessment for 452 patient instances. For the former, we take the average across the 12-view ECG streams for each the period and amplitude feature groups. Shown in relative error terms.

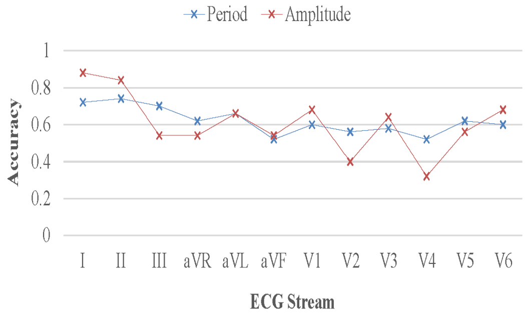
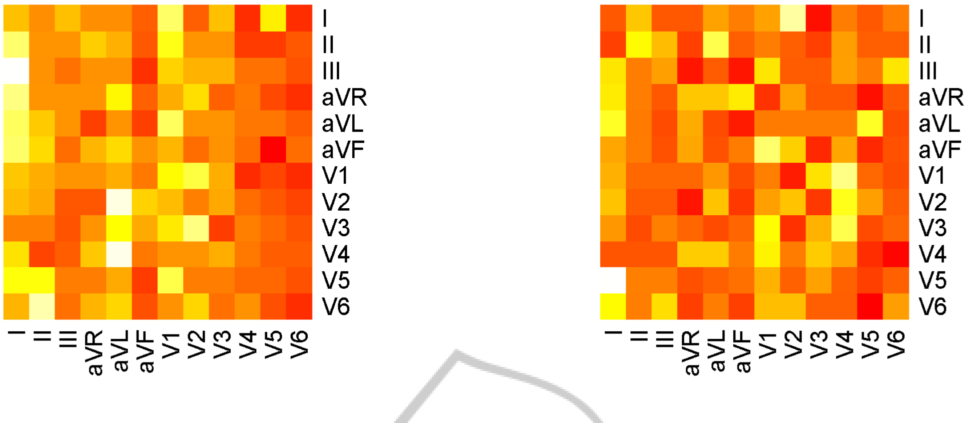


Figure 10: Classification accuracy in cross validating a combined arrhythmia collection of query and training feature vectors, for each ECG view and parametrized by the period and amplitude feature groups.

baseline classification model that performs a majority voting. Every query vector, q, is sought after the most similar ECG training record by linearly iterating the arrhythmia dataset and computing for each pair the adjusted cosine similarity. The time complexity of this process is $O(nm)$, with n the number of exclusive training instances and m the number of queries. Throughout, the number of ECG view occurrences for each query perspective collection is accumulated and the highest view score is elected. First, we cross validated each query vector, q, against an inclusive, $m+n$ combined training dataset, using the holdout method with a 90/10 two-way data split. Figure 10 depicts our accuracy rates for each ECG perspective and parametrized by the period and amplitude cardiac group. The period group traces a more smoother curve and tops at a rate of 0.72, in contrast to an 0.88 peak for the amplitude group. Secondly, we provisioned an additional step to evaluate the query test set, m, on the exclusive training set, n. A confusion matrix that enumerates predicted against actual ECG perspectives, for each of the period and amplitude feature groups is further depicted in Figure 11. Results emerge rather underfitting and strongly imply that the arrhythmia collection we use for training is insufficient to properly represent the highly variant hypothesis space of the query data.

We compared our unsupervised learning results to the ones obtained by the originators of the ECG training dataset (Guvenir et al., 1997). Barring our cross validation methodology that exploits exclusive query data, our overall average accuracy of 0.61 is right on par with their supervised VF15 algorithm that uses however the raw dataset of fully populated attributes and successively processes each into an interval data structure. Unlike our setup that operates on the source cardiac features verbatim, and reduces their dimensionality by a factor of 4 and 3.33 for the period and amplitude group, respectively. The work by Li et al. (Li et al., 2012) that exploits two-dimensional manifolds uses for evaluation a relatively small and pre-annotated dataset of eight patients, each described by six statistically driven features, and recorded from three perspective ECG streams. A striking disparity from our 452 patient instances, each represented as a pair of 12 cardiac views, to make a fair and sustain-



(a) Period feature group.

(b) Amplitude feature group.

Figure 11: Confusion matrices of query data classification for each the period and amplitude feature groups. Showing predicted against expected behavior of each of the 12-perspective ECG streams.

able system level comparison on performance. On the other hand, we contend that our 3D visuals of Figure 5 and 6 reveal authentically both cluster formations and outliers to better assist a specialist in cardiac anomaly analysis, whereas a two-dimensional projection is less informative and more limited to exception detection.

6 CONCLUSIONS

We have demonstrated the apparent potential in deploying information retrieval and unsupervised machine learning methods to accomplish the discovery of cardiac arrhythmia categories. By disregarding any prior cardiologist knowledge from presumed unlabeled ECG recordings, our proposed system is generic and scalable, and relies entirely on objective closeness metrics in feature space. To accommodate continuous streaming and the immediate response required for detecting abnormal cardiac behavior, our framework separates ECG perspective channels for effective transmission and progressive analysis, and reduces the dimensionality of each to fit the low power and communication constraint, wearables and IoT devices. Raw data projection onto a three dimensional embedding space integrates a vital stage for a specialist to administer preparatory inspection of arrhythmia clusters, and is of considerable advantage compared to a 2D planar mapping in facilitating spatial data visualization to minimize obstruction.

Our contribution to regard an ECG recording as disjoint and compact perspective entities is substantiated by the efficacy of our cluster analysis, data visualization for human depth perception, and classification. Unlike most systems that tend to aggregate all cardiac view channels into a single discipline. With the intuition of a scheduling scheme that prioritizes the submission of a single ECG perspective at a time, rather than issuing all view channels as a composite, a better overlap of stream transmission latency from an ECG device with either machine or human expert analysis on the receiving end, is attained. Our system classification rate commensurates with a corresponding supervised model that incurs a higher computational cost by employing the unpacked dimensionality of features. However, to ameliorate a fairly impaired performance of cross validating a trained ECG with exclusively generated, random cardiac test streams, requires an expanded dataset of patient instances.

A direct progression of our work is to extract cardiac features directly from a live ECG signal, and to assess the efficiency of our devised pipelined scheduler for communicating distinct ECG perspectives in a real world, many-devices-to-a-hub network formation. We look forward to advance our study and incorporate an augmented and a more statistically reasoned, ECG training dataset that makes the evaluation of an exclusive test query collection of large variance more robust. Lastly, the flexibility of our software allows us to pursue a higher level correlation of ECG perspective pairs for both clustering and improved recognition of visualization cues, and better understand second order set of arrhythmia relations.

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