

Anomaly Detection in ECG Readings Through Evolved Spiking Neural Networks as a Temporal Classification Problem

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Abstract—Ambulatory electrocardiogram (ECG) readings can span anywhere from 30 minutes to 48 hours. A single 30 minute reading can contain up to 650,000 observations. Existing machine learning methods largely depend on computationally expensive algorithms that deduce individual heartbeats from many observations, for classification based on human annotations. The goal of this work is to exploit the intrinsic temporality of spiking neural networks (SNNs) in the context of this problem. The hypothesis is that SNNs can achieve high accuracy in heartbeat classification operating on close to raw ECG data, as it is also inherently temporal. Indirectly, another goal is to evaluate the impact on accuracy from utilizing time as a dimension for tasks on SNNs. In particular, this comparison is compelling due to classification typically being a task best accomplished by deep neural networks (DNNs). In this work, binning SNNs are generated and optimized through the EONS evolutionary algorithm on the MIT-BIH arrhythmia database. A novel interpretation of ECG readings as input to neural networks is proposed and implemented for SNNs. Further, based on this data representation, a SMOTE inspired oversampling technique is implemented and applied to account for data imbalance in training. Results indicate positive trends in performance associated with the application of these methods, in addition to potential implications for arrhythmia data at large.

INTRODUCTION AND MOTIVATION

Heart disease is the leading cause of death in the United States, and one of the leading causes of death worldwide [14]. Detecting anomalous heart rhythms is of great importance in prophylaxis and treatment of heart disease. Ambulatory ECG readings are one such tool in which heart rhythms can be recorded over extended periods of time. These readings consist of two nodes placed in varying positions on the chest that record millivolts per millisecond over the course of anywhere from 30 minutes to 48 hours. Given the granularity of these readings, and their extended duration, an individual reading can contain observations on the order of millions.

Human classification of heart rhythms captured by ECG readings is a time intensive and subjective process. Multiple cardiologists must cross-validate each other's work, analyzing QRS complexes derived across the entirety of readings. QRS complexes are a visualization of a snapshot of a set of observations from an ECG, characterizing a single heartbeat. The volume of heartbeats in a single ambulatory ECG reading makes human classification of heartbeats unsustainable. Thus, machine learning methods have been applied to ambulatory ECG readings many times in the existing literature to address heartbeat classification.

Regions	Age specific death rates from IHD (per 100,000 population)							
	0-4	5-14	15-29	30-44	45-59	60-69	70-79	80+
Low income countries								
East Asia and Pacific	1	1	3	15	79	304	779	1606
Europe and Central Asia	0	0	6	89	517	1591	3571	8598
Latin America and Caribbean	0	0	3	17	126	414	939	1956
Middle East and North Africa	0	0	5	45	304	956	2156	3758
South Asia	2	2	5	35	302	1005	2207	3644
Sub-Saharan Africa	0	0	1	14	139	526	1345	2291
High income countries								
High income countries	0	0	1	13	91	298	805	2253

Figure 1: Heart disease mortality statistics from World Health Organization

One key element of a QRS complex is its R-peak. The R-peak is a point in time around which the QRS complex is centered. It is a metric that in and of itself is sufficient to classify heartbeats, and is therefore the utilized feature for classification in the MIT-BIH arrhythmia database. This database historically has been employed many times towards the generalized end of heartbeat classification. Existing methods in the literature by and large implement complex data preprocessing schemes to derive individual heartbeats for classification, applying computationally expensive algorithms on what is raw temporal data from ECG readings. The hypothesis motivating this work is that SNNs can be applied to raw ECG readings for classification, bypassing the need for data preprocessing approaches with high computational complexity. Further, that SNNs given their ability to run continuously in real-time, could be integrated into ECG devices themselves. This is reinforced by the fact that SNNs tend to have sparse network topologies, lending themselves well to hardware based implementation that could feasibly be applied to devices with minimal processing power. As opposed to algorithmic derivation of heartbeats based on time, SNNs can utilize time itself as a dimension for classification. The temporality of this classification problem makes SNNs a compelling approach as a result.

A secondary goal of this work is to observe SNN performance on classification, framed as anomaly detection in the context of temporal data. DNNs typically exhibit greater performance in the context of classification tasks. However, SNNs are often applicable and performative in real-time control problems such as this one. SNNs have been shown to exhibit positive performance implications for speed, power consumption, and other metrics for problems such as computer vision and robotics. Similar to those tasks, SNNs in this context can produce classifications

based on analyzing trends in ECG readings over time.

In the course of this work, novel data representations and associated methods for the MIT-BIH arrhythmia database are proposed and implemented. These representations and methods are intended to be lightweight in computational cost, and specifically render the data towards the end of SNN application. Binning SNNs [1] are produced through the EONS evolutionary algorithm [2]. An oversampling method specifically for temporal representations of classification data, inspired by SMOTE (synthetic minority oversampling) [12], is implemented. Results indicate positive trends in performance associated with the application of these methods, in addition to potential implications for observations in arrhythmia data at large. Production of SNNs towards this end is ongoing.

RELATED WORK

SNNs historically have been applied to this problem, but predominately in the context of derivation from other neural network approaches. For example, convolutional neural networks, among others, have been converted to SNNs as opposed to the production of SNNs directly. In this work, SNNs are generated natively through evolutionary algorithms. The evolved SNNs in this work are further distinguished by usage of the non-traditional coding schemes in [1], Schuman et al. In large part, DNN approaches are applied to this problem over SNNs due to their generally superior performance on classification tasks. However, these DNN approaches necessitate complex data preprocessing due to their inability to perform classification on individual samples from ECG readings as a consequence of their temporality.

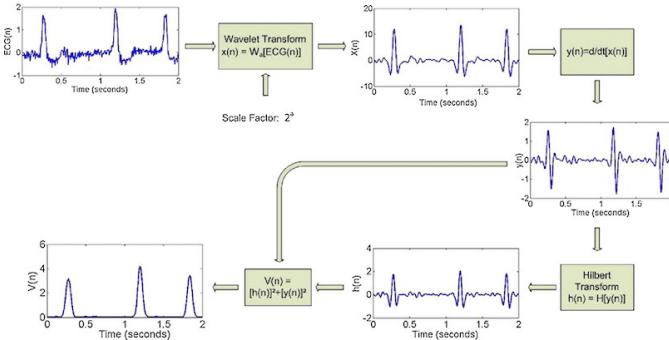


Figure 2: Proposed data transformation method for DNNs

DNN methods applied to this dataset derive heartbeats for classification by applying their preprocessing to a limited set of samples centered around the human annotated R-peaks in the MIT-BIH arrhythmia database. It has been established in the literature that a set of samples surrounding the R-peak, typically 90 on either side, is sufficient for accurate classification. Additionally, of these 2 node readings, one node is often ignored. Similar to the R-peak ranged approach, one node has been shown to be sufficient for accurate classification, and reduces the algorithmic complexity of data preprocessing to a degree. This ultimately produces an R-score, the primary metric by which DNN classification is applied.

The MIT-BIH arrhythmia database consists of dozens of patients. This has resulted in existing publications generally attempting two types of models: patient-specific and class-oriented. However, there are often compromises for one or both of these types of models as a result. Patient-specific models with the R-peak centered method are forced to truncate a significant portion of the data. This is due to the fact that the human annotations classifying beats in the database do not take place at uniform intervals. Many individual samples are lost for both class-oriented and patient-specific models.

This is particularly impactful on patient-specific models where the lesser volume and imbalance of the data already introduces high difficulty in the classification task. Class-oriented models are compromised by the aggregation of patient-specific data into a single set. This is a consequence of the variability in the presentation of anomalous behavior across individuals. Trend analysis is made more difficult by the varying magnitude of individual patient readings, and the necessary loss of data for the application of DNNs.

DNNs necessitate these approaches by their nature. In contrast, SNNs do not have these same limitations. Given the addition of time as a dimension to the problem, a feature intrinsic to SNNs, no individual samples from the ECG readings have to be truncated. SNNs can observe trends in ECG readings over a greater period of time than the existing DNNs to produce classifications. SNNs can also observe data from both ECG nodes, as their raw readings can be processed concurrently. This is beneficial for both patient-specific and class-oriented models. The loss of data is mitigated, benefiting patient-specific models, and there is greater opportunity for the observation of generalized trends for class-oriented models. The SNNs in this work are ran on the software simulated neural processors RISP and RAVENS [15], further lending themselves to direct application in a potential hardware implementation.

METHODS

I. OVERVIEW

Methods for data representation, data manipulation, and permutations of SNNs are proposed and implemented. Lightweight preprocessing methods are applied experimentally and evaluated for performance. Denoising is attempted through normalization, standardization and scaling. Both the traditional R-peak centered representation, and a novel dense representation are tested. On the traditional R-peak representation, SMOTE is applied alongside random majority undersampling. A similar approach is attempted with the proposed dense representation and corresponding SMOTE inspired method. Dimensionality reduction is tested with both representations, evaluating the performance impact of the loss of one ECG node.

A comprehensive pipeline for deriving these data representations and manipulations is implemented. Accordingly, for the evaluation of SNNs on the data, automation is implemented to test permutations of SNN parameters on the permutations of the dataset. All of this takes place in the context of TENNLab's

SNN framework, with SNNs generated and optimized via EONS, running on the software simulated RISP and RAVENS neural processors, in the context of their classify application.

II. DATA ANALYSIS

The MIT-BIH arrhythmia database consists of dozens of individual patient readings from ambulatory ECGs. This is raw temporal data consisting of millions of millivolt readings over milliseconds. The ECG node leads utilized between patients is variable, though the majority of readings contain an MLII node and a V node, V 1-5. These nodes indicate location of placement on the chest. The mapping of samples to annotations is not uniform in volume, but the timing in between samples is constant. The extended duration of ambulatory ECGs is the cause of annotations not being uniformly distributed. Periodic instances of arrhythmia are intended to be captured within that extended duration of time. Annotations represent the location of an R-peak. The dataset is temporal, with annotations being differentiated by sets of samples.

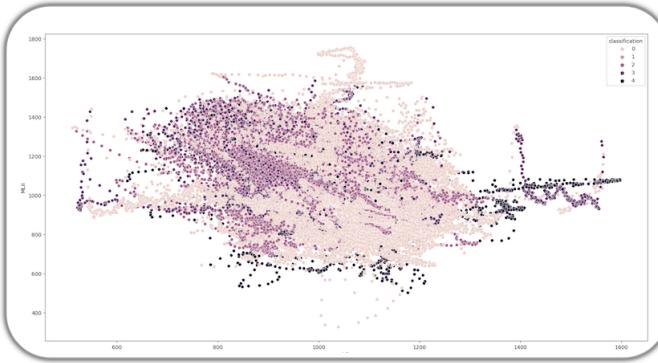


Figure 3: Patient 208 classifications without time

Visibly, the classes are almost entirely impossible to differentiate without the axis of time. The original dataset consists of 15 respective heartbeat classifications. As in existing literature, here, these 15 classes are downsampled to 5 based on the standards set by the Association for the Advancement of Medical Instrumentation. Classes are represented as integers, where 0 indicates a normal beat and 1-4 are varying types of anomalous behavior. The data is heavily biased towards normal beats.

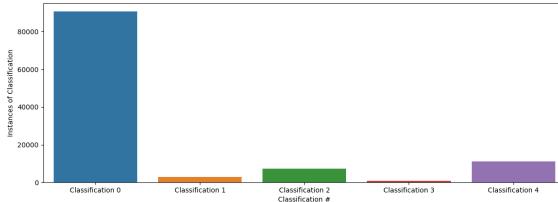


Figure 4: Macroscopic view of class distribution

Further, not all patient datasets contain instances of each class. Many contain only normal beats and one anomalous class.

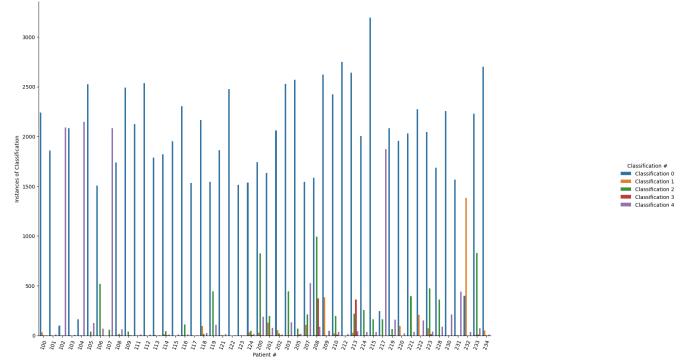


Figure 5: Class distribution from individual patient readings

III. DATA REPRESENTATION

Sequence #	0	1	2	3	4	5	6	7	8	9	...	243	244	245	246
Annotation												N			
...															
Sequence #	405	406	...	496	...	584	585	...	763	764	...	853	...	942	943
Annotation	P											S			

Figure 6: Approach to modeling data after trend leading up to R-peak

The novel representation of data proposed here is referred to as "dense", in accordance with the naming scheme defined in the TENNLab classify application paradigm. The traditional method of defining a range of samples surrounding an R-peak is not employed. Instead, samples are mapped to an annotation leading up to an R-peak, modeling the progression towards it. This approach enables a more holistic view of a patient's heart rhythm over time towards the end of more accurately classifying anomalies, particularly in real-time applications.

The traditional ranged approach is employed as well to benchmark this method. The visualization of both representations, without any manipulations, and time as an axis is modeled below.

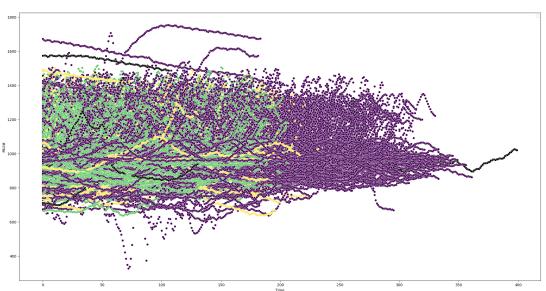


Figure 7: Dense temporal representation without V node

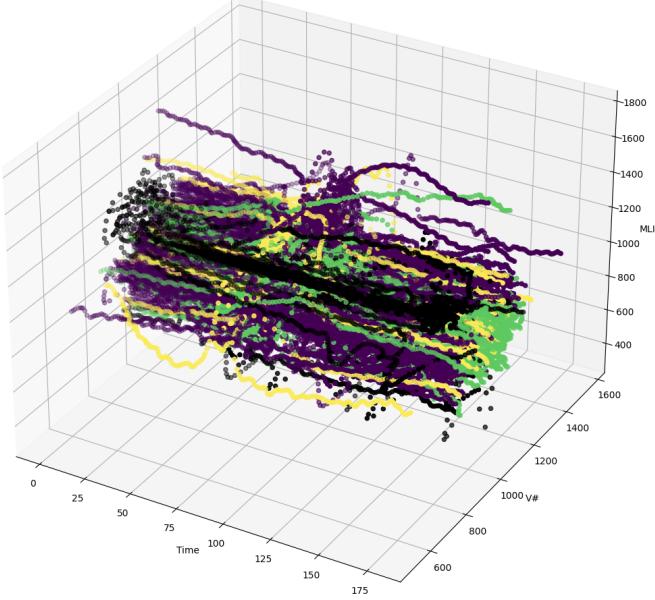


Figure 8: Ranged temporal representation

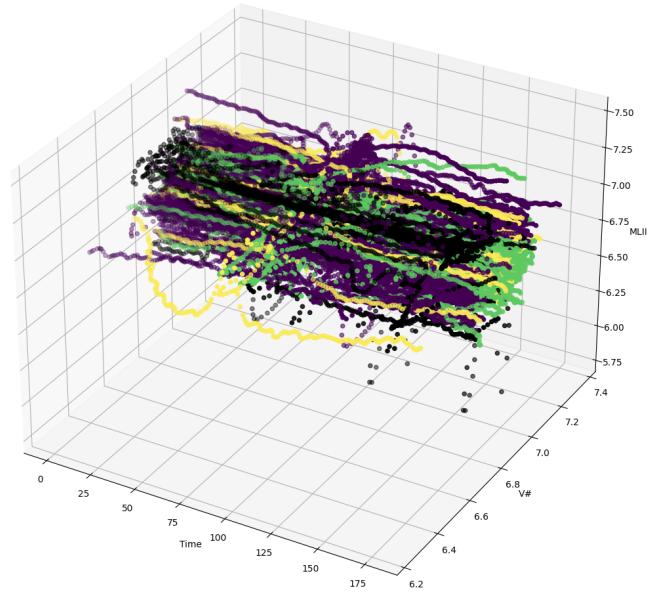


Figure 9: Log scaling on ranged representation

With time as an added dimension to the data, classes start becoming differentiable for both ranged and dense representations. The ranged visualization reflects the emergence of trends in millivolt readings. In contrast, the dense visualization with its overarching usage of time highlights that anomalous behavior tends to emerge across certain intervals of time.

Existing approaches do not account for the fact that V nodes vary between patients. This is another instance of data being lost in model production. This compromises class-oriented, but especially patient-specific, models. Further, the MLII node utilized for classification in the literature is not utilized in all patients. Here, all nodes are able to be utilized for classification, composing the Y and Z axis of these visualizations.

IV. DATA MANIPULATION

Minimal, low-cost methods for denoising were applied to the data dense and ranged representation respectively to account for outliers in the data. These include z-score standardization, logarithmic scaling, and ranged normalization. Ranged normalization in particular was applied due to the scale of the millivolt readings in the data introducing problems for the convergence of certain SNN coding schemes. The effect of these methods are depicted in figures 9 and 10.

Dimensionality reduction in truncating one ECG node was similarly tested to evaluate the loss of data introduced by ignoring half of the sample readings.

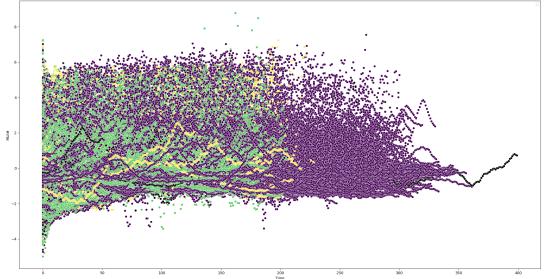


Figure 10: Z-Score standardization on dense representation

The possibility of feature importance bias based on the raw millivolt readings is another motivating factor behind these approaches, particularly with ranged normalization. These approaches are applied based on individual sample to annotation mappings. In other words, the representation of trends leading up to or surrounding an R-peak are manipulated as opposed to manipulating the values along a given timestep. However, this approach is modified subsequently.

The data representation pipeline that produces these permutations is visualized in figure 11. The testing of all aforementioned methods and permutations therein for ranged and dense representations are enabled by this pipeline.

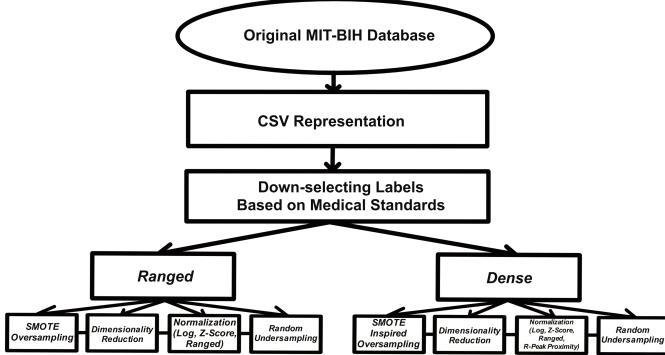


Figure 11: Data representation pipeline

To address the imbalance in the dataset, an additional approach was applied to the data. For the ranged representation, SMOTE was applied followed by random undersampling. However, SMOTE in this context is limited. Due to the representation of time as an axis implicitly for SNNs with the classify application, and the 2 separate ECG nodes being adjacent in each file, only 1 ECG node can be utilized. Therefore, dimensionality reduction is necessary to apply sampling approaches to the ranged representation.

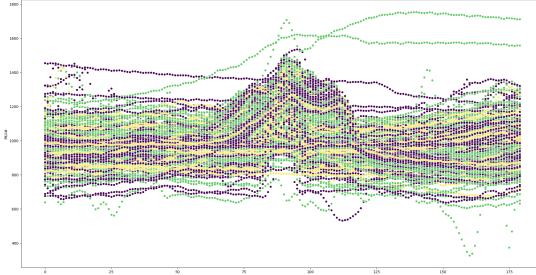


Figure 12: SMOTE on ranged representation

In the same vein, SMOTE cannot be applied to the dense representation of data. This is a consequence of each sample to annotation mapping consisting of a variable number of timesteps. In effect, the number of columns in the dense representation is highly variable. This renders the k-nearest neighbors algorithm employed by SMOTE inapplicable for dense data. This was the motivation behind the development of the following SMOTE inspired sampling methodology.

Algorithm 1: Smote Inspired Synthetic Minority Data Generation

```

Data: PatientCSV, Dimensionality, Proportion, Scalar
Row  $\leftarrow$  Trends leading up to R – peak for patient;
Compute std.dev. for each column of the
respective features;
Compute iterations over minority data to achieve
proportion;
for  $i = 0; i < \text{proportion\_iterations}; i++ \text{ do}$ 
  Randomly select observation pair from
  minority observation set
  /* Iterate over minority data X times to achieve
  proportion, for 2D as pairs */
for  $i < \text{num minority observations} \text{ do}$ 
  Generate perturbation, non – zero float
  from -1 to 1
  /* Iterate over each time step of observation pair
  */ for Each Timestep do
  Apply perturbation to each node value :
   $F(p, s) = \text{timestep\_eading} + ((p * \text{std.dev.of timestep}) * s)$ 
end
  Add perturbed observation pair to each node
  value
end
end
  
```

Figure 13: SMOTE inspired algorithm

The standard deviation at each timestep leading up to an R-peak for a particular patient is computed, separately for each ECG node. A target proportion for the minority classification to make up of the dataset is defined, and utilized to compute the number of iterations to make over the minority set. Subsequently, observation sets, or every timestep for a given sample to annotation mapping for ECG node pairs are selected via a random uniform distribution. Also from a uniformly random distribution, a perturbation is produced between negative 1 and 1. This perturbation is then applied to the standard deviation at each timestep for each node respectively. Perturbations are multiplied by a scalar to increase or decrease their magnitude. The direction of a perturbation, in increasing or decreasing the millivolt readings at a given timestep, is also uniform towards the end of maintaining trends in the data. Ultimately, this algorithm similar to SMOTE produces synthetic minority classification data. However, as opposed to performing perturbation relative to the scale of individual beats for a patient, the trends over time are emphasized by evaluating standard deviation per timestep. This taking place relative to individual patients mitigates the degree to which the synthetic samples introduce noise, as trends for anomalous beats tend to be similar. Two examples of this approach are visualized in figures 14 and 15, as a quinary and binary classification task respectively.

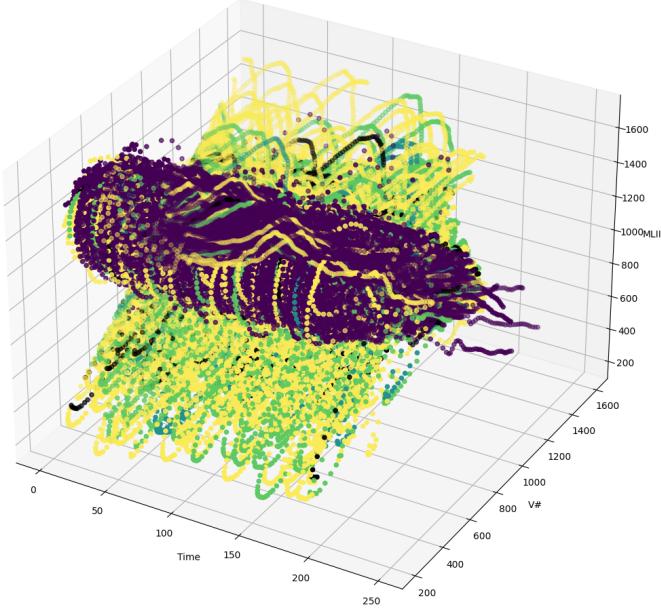


Figure 14: SMOTE inspired oversampling with undersampling on dense

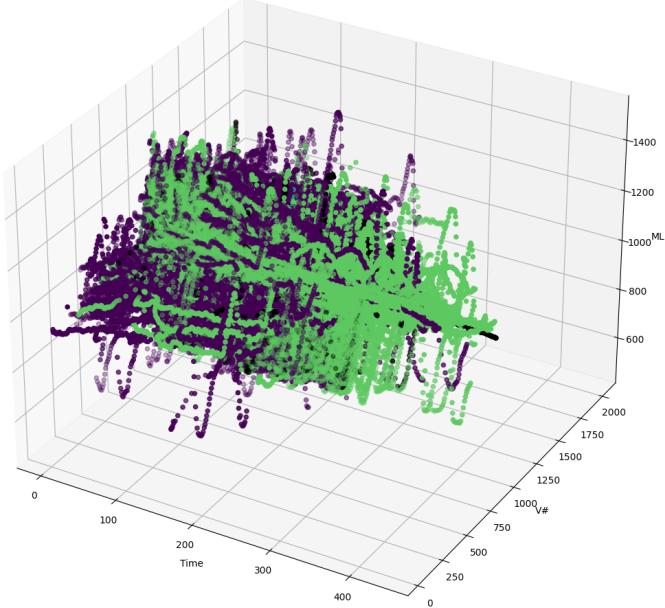


Figure 15: SMOTE inspired oversampling with undersampling on dense

Visibly, SMOTE applied to ranged data tends to conflate classifications due to its inability to utilize a second node. In contrast, normal and anomalous beats become clearly differentiable with the SMOTE inspired approach applied to dense data.

V. TRAVERSING THE SEARCH SPACE

Models are actively being generated based on the aforementioned methods, data representations, and their permutations. The data processing pipeline can incrementally create these rep-

resentations with any number of the aforementioned methods applied. In addition to the many possible data representations proposed here, SNNs themselves have many possible coding schemes and associated parameters. To direct cursory testing, a handful of coding schemes were tested on a subset of patients with varying data representations. Binning spike rate encoding with winner takes all spike decoding was found most effective in these initial tests, and is currently uniformly applied in all models. However, even within this single coding scheme, many parameters exist to be tested. Network and performance analysis automated workflow, shown in figures 15 and 16, was implemented towards the end of expeditiously testing SNN, data representation, neural processor, and classify application configuration permutations.

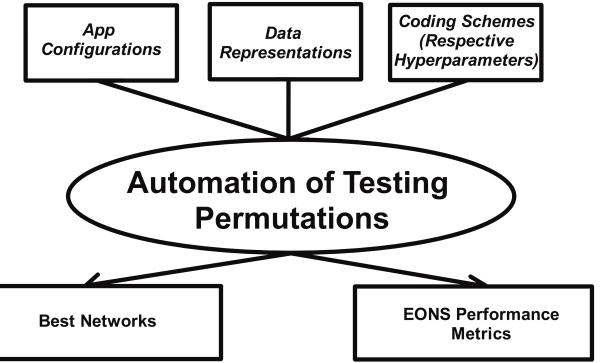


Figure 16: Automation pipeline

```

{
  "app": ["classify"],
  "proc": ["risp", "ravens"],
  "encoder": {
    "temporal": {
      "ov_interval": [1, 50, 100],
      "higher_earlier": ["false", "true"]
    },
    "decoder": {
      "spikes": {
        "binning_style": ["WTA"]
      }
    }
  },
  "extra_eons_params": {
    "population_size": [50]
  },
  "extra_params_static": {
    "threads": [16],
    "episodes": [10],
    "epochs": [50],
    "max_fitness": [0.96],
    "sim_time": [1800]
  },
  "data_rep_folders": ["ranged_mitbih", "ranged_normalized_mitbih", "dense_binary_mitbih"],
  "app_config": ["classify_ranged.json", "classify_ranged_normalized.json",
    "classify_dense_binary.json"]
}
  
```

Figure 17: Example testing run for automation pipeline

This automation interfaces with the TENNLab framework to perform generalized testing. Generated networks and their associated performance metrics are autonomously stored. This is currently a brute force grid search, as in the largely discrete search space of these data representations and coding schemes, methods such as bayesian optimization are not applicable.

RESULTS

The fitness function utilized up to this point is f1 score. Thousands of networks have been generated, the majority of which are patient-specific due to the cost of creating class-oriented models. The aggregation of patient data into one set results in gigabytes of data to process. Without sampling methods, the SNNs produced so far tend to perform well initially and stagnate in early epochs. This is reflective of their overwhelming bias towards identifying the majority class, which is to be expected given the dataset. This is problematic, as these models perform badly by the metric of specificity. SMOTE applied to ranged data curbs accuracy. This is desirable in a sense, except that those models similarly stagnate. This is to be expected, given the extent to which the heartbeat classifications were visually distinguishable in the prior visualization.

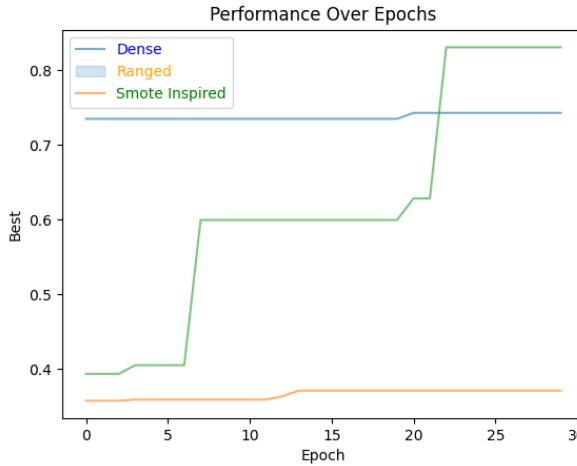


Figure 18: Performance over epochs of evolution for data representations

However, the dense representation of data with the novel SMOTE inspired algorithm previously described achieves both ends. Models perform poorly initially, and improve to high accuracy over epochs of evolution. These models achieve a high f1 score and good specificity, actually detecting anomalous behavior in heart rhythms. The performance of the proposed data representations, with binary classification is shown below. Patient 207 notably has above average balance compared to most of the readings in the dataset, but the performance gains of the sampling methods are apparent regardless. Denoising approaches have tended to have little performance impact, at times even negatively affecting f1 score. However, further testing is required on the sampled approaches.

F1	Dense	Ranged	Dense Sampled	Ranged sampled
Raw	.436706	.513198	.830734	.428252
Min-Max	.371479	.513084	Untested	Untested
Log	.506502	.507985	Untested	Untested
Z-Score	.536205	.509258	Untested	Untested
No V#	.647582	.513084	Untested	.790472

Figure 19: Performance of data representations on patient 207

A handful of class-oriented specifiers have been generated. The associated statistics based on the confusion matrix of one such binary model are charted in figure 20.

Measure	Value	Derivation
Sensitivity	0.9327	$TPR = TP / (TP + FN)$
Specificity	0.1566	$SPC = TN / (FP + TN)$
Precision	0.8199	$PPV = TP / (TP + FP)$
Negative Predictive Value	0.3609	$NPV = TN / (TN + FN)$
False Positive Rate	0.8434	$FPR = FP / (FP + TN)$
False Discovery Rate	0.1801	$FDR = FP / (FP + TP)$
False Negative Rate	0.0673	$FNR = FN / (FN + TP)$
Accuracy	0.7809	$ACC = (TP + TN) / (P + N)$
F1 Score	0.8726	$F1 = 2TP / (2TP + FP + FN)$

Figure 20: Class-oriented model statistics from confusion matrix

One example of the network topology resultant from EONS is shown below. The network has in this case notably evolved to disconnect one of the ECG nodes as input. Simultaneously, it evolved to completely disconnect one of the possible classifications for patient 205 due to the scarcity of its representation in the data.

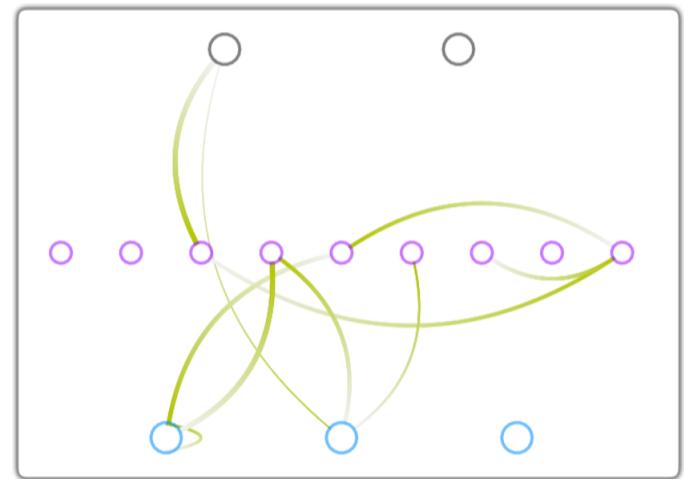


Figure 21: Patient Specific Model 205, 90% F1 Score

CONCLUSIONS

In general, the dense representation of data outperformed the traditional ranged approach for SNNs. This may indicate that the proposed SNNs are evolving to find previously undetected trends

in heart rhythms leading up to anomalous beats. Aspects of data representation have significant performance impacts. Most notably among them, the holistic approach of analyzing trends leading up to an R-peak, utilizing both ECG nodes, under the paradigm of the SMOTE inspired method. Denoising having performed poorly up to this point may indicate that "noise" in the data is actually meaningful for heart rhythms at large. This is a preliminary hypothesis however, as the normalization, scaling, and standardization approaches applied require further testing in the context of sampling. Additionally, they are key in generating class-oriented models.

SNNs were found that can achieve high performance with raw ECG data. However, for the purpose of training, extreme data imbalance has to be addressed given the currently tested coding schemes. Irrespective of this, it has been shown that utilizing time as a dimension as opposed to complex data preprocessing schemes is sufficient for class differentiation in ECG readings. Further, that SNNs accomplish this task with far less structural complexity. Although temporal classification tasks are rare, in the context of temporal data, SNNs become competitive with DNNs. Existing DNNs do still outperform the SNNs produced as a product of the work accomplished up to this point.

However, this comparison is not fully mature. The search space documented here is wide and not fully traversed due to the computational complexity involved. Spiking neural networks themselves offer great benefits in compute cost and power, as indicated by the shown network topology. But, for this application, evolutionary optimization of them is computationally heavy. It is possible that other coding schemes need to be evaluated. Training methods alternative to evolution such as spike-timing-dependent plasticity may be beneficial. Performance on the simulated RISP and RAVENS processors implies that deployment on ECG devices may be possible, particularly given the simplicity of these networks.

FUTURE WORK

Further testing of coding schemes and associated parameters is ongoing. Should another high performing scheme be found, bayesian optimization for its parameters that exist in a continuous space can be implemented. Particularly for datasets that contain greater imbalance, a custom fitness function can be implemented. The current thought is to utilize f1 score as a foundation, but penalize based on poor specificity. This could also serve to mitigate the degree of sampling necessary on more balanced datasets. Other biologically-inspired methods for SNNs are an area of interest. Especially given the continuous dense approach proposed, characteristics such as activation potential leak may yield greater performance. Further testing of the currently implemented SNNs that have been trained on sampled data must take place in the context of their original dataset. Deploying the proposed SNNs on ambulatory ECGs or wearable devices with similar function is an area of interest, to evaluate power consumption and performance on actual hardware.

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