Time Series Analysis for the Navigated iKnife Surgical Tool

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Abstract—The Laboratory for Percutaneous Surgery at Queen's University is developing a cutting edge surgical tool called the iKnife. The goal of the iKnife is to provide real time mass spectrometry feedback to in-vivo surgery environments. A major challenge for the iKnife is synchronizing the location and time of cut data with the feedback from the mass spectrometer. Part of the reason this is challenging is the time between tissue being cut and the smoke arriving at the mass spectrometer is not consistent and depends on numerous environmental variables. In order to solve this problem the state of the iKnife needs to be known in real time. The iKnife can have 4 possible states which are based on its mode of operation: Cut air, cut tissue and coagulate air and coagulate tissue. In order to identify the state of the iKnife, a classifier needs to be trained on the electronic signal of the iKnife when it is in each of its four states. This paper outlines a data analytics process for accurately identifying the state of the iKnife. Link to overleaf:

https://www.overleaf.com/project/5e93df6fdba14b00016100e7

Index Terms—Group 7, Life Sciences, Tissue Detection, Cancer, iKnife, Classification.

1 Introduction and Motivation

Breast cancer is the most common surgically treated cancer in women [10]. The favoured procedure for this condition is breast-conserving surgery, which maximizes remaining healthy breast tissue after surgery [3], [4]). The narrowest possible healthy tissue margin around the tumor is enough to maximize the chance of survival, as outlined in the joint statement of The Society of Surgical Oncology and American Society for Radio Oncology [7]. However, in current clinical practice, 20-30% of patients need revision surgery, because some cancer is left behind after the first surgery due to excision margins containing cancer [5]. A cancer-free margin is difficult to achieve because tumors are not directly visible, and the breast deforms during surgery making spatial tracking difficult [6].

The present method of verifying that surgeons have successfully cut clear margins are by performing ex-vivo analysis by radiologist. While in-vivo surgery refers to a surgery that is taking place on the patient, ex vivo refers to experimentation outside of the patient, with patient samples. This means that breast tissue would be extracted from the tumour and tested for results. However, this produces a significant delay between the procedure and when the radiologist analyses the sample. This can take anywhere between a few days and several weeks. Thus, if cancer is deemed to be left behind, the patient must come back for a follow-up surgery. If a verification method existed real time, this could substantially reduce the medical, economic, and emotional burden of revision surgeries.

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Recently, real-time tissue classification methods have been developed that could warn surgeons when they cut into cancer. One of these technologies is the iKnife. The iKnife analyzes the vapour produced by the cautery, a surgical knife that cuts through tissue by burning it [8]. A surgical system using the iKnife for real-time tissue detection and classification, and real-time position tracking would directly address the problems surrounding breast-conserving surgery. Fusing these two data streams is computationally challenging. The vapour traveling from the cautery to the iKnife passes through a tube causing a temporal delay proportional to the tube's length. Additionally, vapour mixes with air in the tube, blurring the start and end points of the data stream. This further delays vapour processing because more vapour is required to differentiate between tissue types. In contrast, position tracking has high temporal resolution and minimal temporal delay. Thus, by updating the time-accurate position data with the time-delayed tissue data, we will be able to localize the tissue classification stream. Although, to accurately synchronize and fuse these two data streams, we need to first set a ground zero temporally. This means using a system to start time recording in the same frame for both the iKnife and cautery. If this does not occur then we will not be able to determine the temporal delay from the cautery to the iKnife reading.

The biggest challenge with mass spectrometry in an in vivo environment is knowing where a sample was cut from. In order to know where a sample is from you need to know the knife's location, state and the time delay between a sample being cut and its arrival at the mass spectrometer. The state of the iKnife refers to whether it is in cut or coagulate mode and if it is in contact with tissue or not. Since the iKnife is used in vivo the surgeon can only control the mode of the iKnife and needs to know whether they are in

contact with tissue or not. Identifying the state of the iKnife during surgery is a crucial component of tracking the original location of a sample arriving at the mass spectrometer because it will allow the system to accurately detect when the iKnife is in contact with tissue. Solving this problem will lay the foundation of the entire spatial navigation system. Originally we aimed to solve the time delay problem but without an accurate state classifier and the ability to create our own dataset it became unlikely that we would succeed. Therefore, our group focused on creating a model to identify the state of the iKnife based on its electrical signal.

To create a state classifier a sample data set was generated in an ex-vivo surgical environment by cutting tissue samples with the iKnife and recording the electronic signal measured at the end of the iKnife. Due to COVID-19 the group was not allowed into the lab and we needed to use data that we had previously recorded. The raw data was then converted into a time series. We performed extensive feature engineering on the dataset to find distinguishable aspects of the four states. In the end, the mean and the fourier frequency of the time series was the most effective. We used these two features to train our SVM and achieved 100% accuracy on an 80-20 training testing split.

2 Related Work

In this section we will outline three related studies that were used to develop a better understanding of the problem and different efforts being developed.

2.1 Navigated real-time molecular analysis in the operating theatre, demonstration of concept [1]

Published Venue: SPIE Medical Imaging: Image-Guided Procedures, Robotic Interventions, and Modeling , March 2019 **Authors:** Asselin, Mark, Kaufmann, Martin, Wiercigroch, Julia, Ungi, Tamas, Lasso, Andras, et al.

The iKnife project has a number of papers written on the difficulties of real time in-vivo mass spectrometry. This paper proposes the concept of a spatially navigated iKnife for realtime mass spectrometry using a REIMS system. Asselin explains the importance of a spatially navigated knife and the subsystems required to enable it. The system he outlines involves a REIMS subsystem, a spatially navigated image capture subsystem and a time synchronization subsystem. These three subsystems in conjunction enable a spatially navigated knife. The paper reported a 99.3% accuracy detecting tissue with the REIMS process. The strong results showed promise for the iKnife if the spatial navigation problem is solved.

2.2 Identification of electrocautery state to enable spatially navigated intra operative mass spectrometry tissue analysis [2]

Published Venue: Hamlyn Symposium on Medical Robotics 2019 **Authors:** M. Asselin, A. Jamzad, A. Lasso, T. Ungi, J. Rudan, G. Fichtinger

In this paper Asselin focuses on the challenges of identifying the state of the electrocautery (iKnife) based on the electronic signal it produces. This paper was very helpful because it is exactly the problem that we are trying to solve. The authors proposed an unsupervised clustering model because it would allow the knife to be re-callibrated in-vivo if need be. The idea behind an unsupervised model sounded clever but in practice it is unreasonable for the surgeon to need an understanding of clustering to make the iKnife work.

2.3 Rapid evaporative ionisation mass spectrometry of electrosurgical vapours for the identification of breast pathology: towards an intelligent knife for breast cancer surgery [9]

Published Venue: Breast Cancer Research Open Access **Authors:** Edward R. St John, Julia Balog, James S. McKenzie, Merja Rossi, April Covington, Laura Muirhead, Zsolt Bodai, Francesca Rosini, Abigail V. M. Speller, Sami Shousha, Rathi Ramakrishnan, Ara Darzi, Zoltan Takats and Daniel R. Leff

This paper addresses the fundamental aspect of our project, rapid evaporative ionisation mass spectrometry (REIMS). REIMS is the key system that collects and analyzes tissue samples. The importance of this paper is that it points to the combination of an electrocautery (knife) and REIMS into an intelligent knife (iKnife) that classifies tissue in real time. This paper is one of the first papers to do this properly. The paper is written in the context of positive margin in breast cancer surgeries. Positive margin refers to tumors being left behind during surgery and often results in a revision surgery. This paper shed light on a very powerful application of the iKnife and stressed the importance and requirements for an accurate spatially navigated system.

3 Methodology

This section will outline the stepwise approach to solving our problem statement. By outlining our data pipeline in a clear manner, we hope to provide a reproducible manual for future researchers to work.

3.1 Data collection:

While we did not extract our data directly from the cautery in this experiment, it would be important to mention how we would gather our data under non-COVID-19 settings.

Prior to the experiment, fresh meat (any type will be suitable) or tofu samples must be collected. Once acquired and secured to the iKnife table, we will attach the oscilloscope to the ground end of the cautery tool. This will provide us with a voltage data stream from the cautery. At this point, we will need to ensure our data stream is being synchronized and saved. To accomplish this, we will utilize a software called Slicer, a surgical system software that was developed in conjunction with Harvard. It is used around the world for various types of research including brain surgery, navigational tracking, and oncology. For our purposes, it will provide saving and exportation to NumPy of the data stream.

Once we synchronize our oscilloscope with slicer, we can begin our testing protocol. The cautery tool has two (2) different modes: cut and coagulate. Cut mode is a method to burn tissue and perform the function of a scalpel, while coagulate mode acts to stop bleeding if a surgeon cuts a blood

vessel. There are two possible states each cautery mode can be in: on while burning air (cautery is not touching the patient) or on while burning tissue. Thus, there are four total states that we will be collecting data in: cautery cut mode to air, cautery cut mode to tissue, cautery coagulate mode to air, and cautery coagulate mode to tissue.

3.2 Step 1: Hypothesizing learning model

Prior to data visualization, we knew that our goal was going to be classification. We had an assumption that we would not require high dimensionality and may in fact require very simple classification consisting of only one or two objects. Thus, we decided to use a support vector machine (SVM) as our learning model.

An SVM is a machine learning algorithm that is capable of performing both regression and classification. It is easy to use, reliable, and fast. One of the greatest benefits of an SVM is its ability to operate as a semi-black box model. This means that it provides a partial understanding of its analysis technique. While there is hidden complexity in an SVM, you can perform initial visualization on your clustering and get a valid sense of how the model will operate.

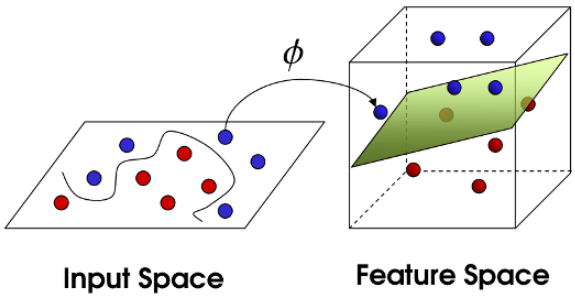

Fig. 1. Example of mapping SVM functionality

Our learning will be supervised which is supported in SVM applications. An SVM works by taking data points in the input space and mapping them with a function to a higher spatial dimension called the feature space. In the feature space, it is possible to build a linear hyperplane to separate classes and complete classification. After this hyperplane separates classes it will then project future data points into the feature space and depending on where it falls in relation to the hyperplane(s), it will classify the point respectively.

Therefore, with low dimensional data and simple classification, an SVM is a perfect choice for our project.

3.3 Data Pipeline Step 2: Data Analysis and Visualization

Our next step was to attempt to gain an intuition of what our data looked like. This was done through the visualization of the sine waves which corresponded to our pseudo-voltage readings from the cautery (Figure 2-5). For each different state of our cautery we plotted their respective voltages. This allowed for the intuition on the differences between each wave function. While performing a visual inspection, we focused on looking for differences in amplitude, frequency, and phase shifts. This was fundamental to our feature engineering phase. We kept in mind that our goal was to extract features from each voltage reading that would give us unique information about each state. This would be done in the way of a mathematical function so as to provide objects for our learning model.

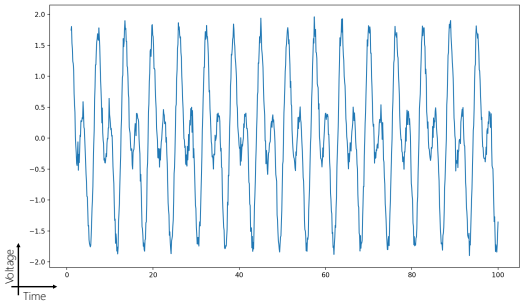

Fig. 2. Voltage reading for state cut-air

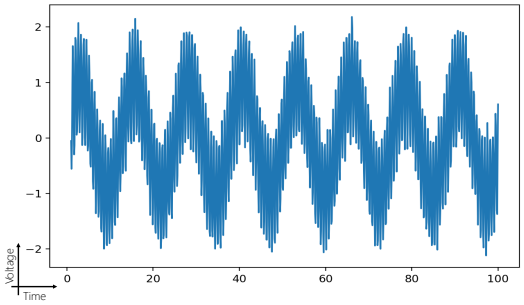

Fig. 3. Voltage reading for state cut-tissue

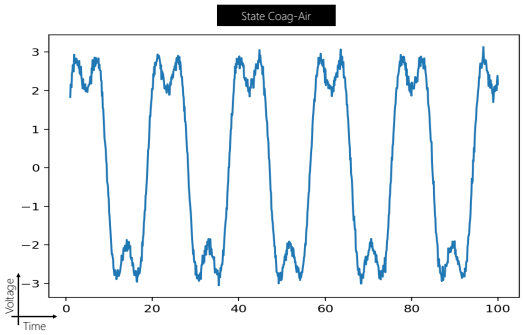

Fig. 4. Voltage reading for state coagulate-air

An important reminder is that our data was stored in a series of NumPy arrays. This meant that our data was not wave functions, but rather a series of points in an array that matplotlib was plotting as a wave. Therefore, we decided to plot an individual voltage state as a scatter plot to further our intuition (Figure 6).

Once we got a good sense of what our data looked like, we performed a training-testing split. We followed the standard procedure with our training set consisting of 80% of the input data and the testing set the remaining 20%.

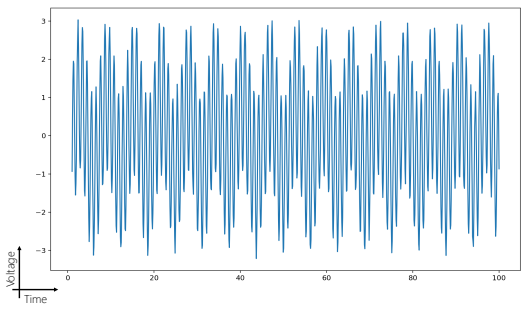

Fig. 5. Voltage reading for state coagulate-tissue

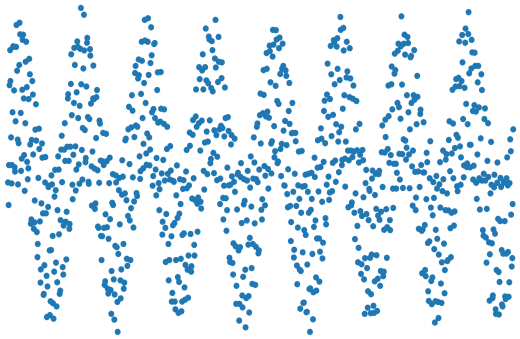

Fig. 6. Voltage reading for state: Coagulate-Tissue

Prior to determining which functions would be of value, we needed to hypothesize what these functions may be. We created a list of potential functions and then ran preliminary diagnostic testing by doing visualization. Some of our functions for feature engineering included: mean, median, mode, point differences, standard deviation, differentiation, integration, and Fourier frequency. Since our data is stored within a NumPy array we were able to perform simplistic functions on the entire array. This is why mean, median, and mode were some of the first functions tested, it was a simple function application. Additionally, point differences was an approximation method to perform a pseudo differentiation of each voltage graph. By subtracting each point from the previous points value, we could get a sense of the rate of change in the voltage across the time sample. However, this proved to be ineffective and a poor classifier. This was also the case with standard deviation, differentiation, and integration of our voltage signals. After these trials, we decided to import a Fourier transform module into python and perform more advanced feature extraction and engineering. Since we do not have the exact sine functions of the voltages and could not calculate frequency through the sine formula, we required external applications to infer the voltage frequency. Thus, we performed a Fourier frequency calculation through the module to determine the average frequency across each sample. This proved extremely effective.

Our next step was to select our two top performing functions to put into our leaning model and apply classification. However, while we had several well performing functions (mean, median, mode, Fourier frequency), each function had at least one overlapping cluster (a cluster containing two cautery states). In order to combat this, we needed to select two functions that did have the same state in the overlapping clusters. By doing this, we would ensure that each respective function would pull away the data points in the opposing functions overlapping cluster. To do this, we plotted each function against the cautery states. Then, matched the two functions who did not cluster the same two states. This was done through visual inspection of each function vs. cautery graph. Since we knew that some groups would cluster together for one particular function, we ensured that our selection would not cluster the same two states. We found that mean and Fourier frequency were effective functions to show adequate differentiation in clustering.

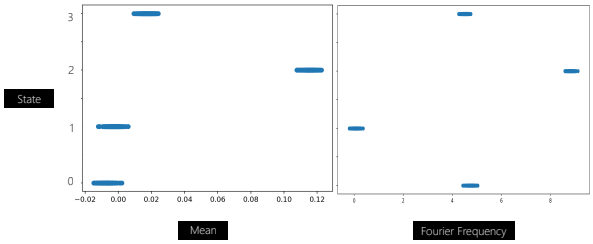

Fig. 7. Group clustering with mean and Fourier frequency

3.4 Step 3: Split, engineer data features, and visualize clusters

After we selected mean and Fourier frequency as our objects, we wanted to double check our clustering to ensure it was adequate based on visual inspection. As seen in SHOW FIG, the clustering was extremely effective.

After this confirmation, we were ready to apply the same pre-processing to our testing data. While it was most likely safe to complete training/testing split afterwards, we wanted to limit biases in our analysis. Since we were performing feature engineering and visualization, in addition to clustering techniques prior to running our model, it was important that we did not bias our data set.

3.5 Step 4: Train model

Once we completed our feature analysis, it was time to train the model. We placed our training data set into our SVM and ran the module.

4 Dataset

The ideal dataset for this project is numerous time series representing the iKnife's electronic signal while in each given state and with multiple tissue samples. The data set used in our experiment to represent the elecro-cautery signal consisted of a four dimensional NumPy array. Each of the four arrays represents a different feature including: cautery state (0 = cut-air, 1 = cut-tissue, 2 = coag-air, 3 = coag tissue), samples (1000 samples), time (10s for each sample), voltage.

The voltage and time dimensions are sub-dimensions within each sample. In other words, for each sample, there exists a voltage vs. time collection, and this collection existed in a specific cautery state. Figure 8 represents this visually. While this image may seem like it is only 3 dimensional, NumPy uses a grouping factor to classify the time and voltage readings.

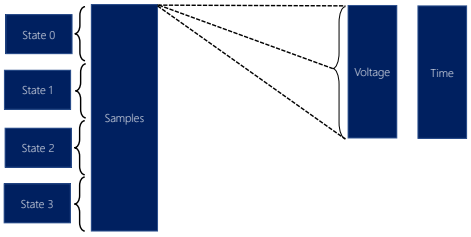

Fig. 8. Four dimensional NumPy Array

As explained in the data collection section within methodology, we extracted the voltage data from an oscilloscope attached to the ground end of the cautery. Each sample was collected over 10 seconds while the cautery was in a specific state. The data was offloaded from the oscilloscope to a surgical navigation system called Slicer. This allowed us to easily export our data into a NumPy array.

However, due to COVID-19, Kingston General Hospital (KGH) was closed to all non-essential research. Thus, we were unable to use the iKnife making it impossible to collect data and generate our dataset. Instead, we generated a dataset a representative of the original. This was done by an MSc. Candidate who is familiar with the research and has seen the output from the oscilloscope. This ensured that our data would be highly similar and transferable once KGH opens up to research and we get to perform a collection. This was done by generating multiple sine waves and combined them for complexity within each state. Following this, the data was exported as points with equal time interval sampling to the oscilloscope. This export resulted in a serious of data points for our dataset.

The drawback to this is that we cannot guarantee that our data, and thus model, are perfect representations of the voltage readings. While we can be certain there exists similarities, it is impossible to know that the datasets will have the exact same distinguishing features that allowed for differentiation in this model. Thus, we understand that slight modifications may occur, however the overall generalization of the model will apply.

5 Experiments and Results

In this section, we will focus on the tangible values and numerical figures of our experiment. After that, will we review what our results mean in the context of our research study. Finally, we will look back on our analysis and discuss some limitations.

5.1 Step 5 of Data Pipeline: Show test results + tune parameters

It was found that our model was able to classify 100% of our testing data. We did not perform any hyper parameter tuning because it was not necessary with such a high accuracy. In addition to these results, we visualized our SVM model's classification and performed a Receiver Operating Characteristic (ROC) Curve. A ROC curve plots the false positive rates against the false negative rates. This is an extremely important metric because it explains where your model is making incorrect predictions and as a result, provides a lot of value to the researcher. However, because of the success of our model, the ROC curve did not provide any interesting insights as both false positive and false negative rates were 0%.

Accuracy = 100%
ROC curve = 1.00

TABLE 1
Statistical Results

Kernel = Linear
c = 1.0

TABLE 2
Hyper-parameters

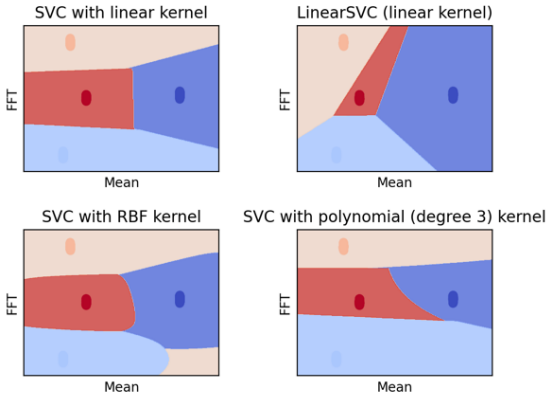

Fig. 9. Clustering separation from SVM

5.2 What do our results mean?

In the context of our research assignment, our results indicate a successful application of a previously used machine learning algorithm to solve a novel problem. In other words, we have successfully developed an algorithm that will be able to classify the cautery state in real time. This means that one of our pivotal steps in developing a real-time cancerous classification tool is in much closer grasp.

5.3 Limitations

There were however, many different things we tried that failed during our research investigation. One of the biggest

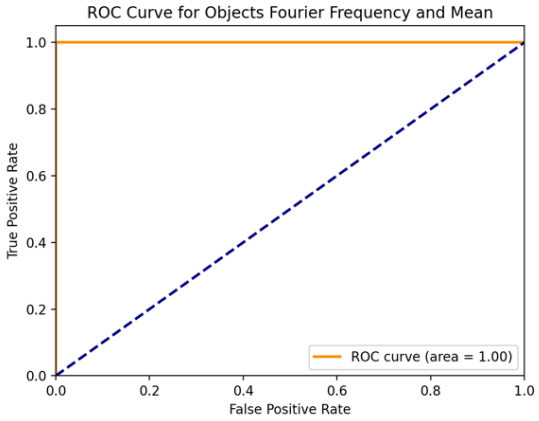

Fig. 10. ROC Curve

challenges was building a function for classification. A common theme was inadequate clustering from the function. This occurred with the calculation of mode, median, integration and differentiation. What was interesting however, was when we attempted to calculate point differences and peak frequency. When calculating point differences, we performed a normalization which ended up making our functions very similar to each other and thus a poor classifier. Therefore, this did not provide any beneficial results.

Another challenge we faced was calculating frequency. Prior to using Fourier frequency, we developed a ”peak finding” algorithm to approximate the frequency of the sine function. This algorithm worked by traversing through the indexes of the array one by one. At each point i, we would determine if i was greater than i+1 and i-1. If so, we would assume that point represents a peak and mark it down. At the end of the traversal, we would have points at a standardized point in time. If we then accounted for the period of sampling time in the graph, we could determine the frequency of our wave. However, there were many issues with this algorithm. The first issue pertained to noise in our data set. This meant that we got random points where i was greater that i+1 and i-1, which showed up as false-peaks at varying locations. This threw off our calculations and resulted in inaccurate calculations of frequency. Second, was that our peaks were not standard. There were multiple different sine waves making up our voltages. This meant that frequency was not uniform and thus once again, inaccurate. Therefore, we switched our frequency metric to Fourier transforms and has much greater success.

As with usual coding developments, there were numerous inefficiencies initially. One of the most notable was the lack of efficient and clear functions along with poor use of object-oriented techniques. Once we transitioned our code away from numerous iterations (as seen in our GitHub repository) our software became much more efficient, easier to read, and resulted in a cleaner analysis.

5.4 Issues with validity: data may be off because of development

The final notable potential issue with the validity of our analysis is the use of generated data. While we have a good understanding of what the data coming out of the oscilloscope will look like, our understandings are never perfect. Thus, it is important to note that even though this development has been highly successful, further alterations and modifications may be required depending on the outcome of cautery voltage data.

We do not believe to have any issues with over fitting, lack of data, or any bias beyond that mentioned above.

6 Discussion

Due to the outbreak of COVID-19 the project has required several alterations in order to proceed within the original time frame. Most notably a new data set and target was required.

The first action item upon the outbreak was to re-evaluate the goals and targets, this meant cutting the initial project and changing gears into a more feasible analysis given the constraints. Secondly, with the closure of the Laboratory of Percutaneous Surgery there was no opportunity to gather more data. As a remedy, Mark Asselin, a supervisor in the lab was able to fabricate data for the use of the project. As the realm of appropriate values and outputs were known this provided a strong alternate to the missing data. The attained data corresponded to a different target than the one originally set out to predict. Initially the goal of the project was to predict classification time delays based on parameters around the iKnife, and a regression analysis was to be run using a support vector machine regression algorithm.

The new project target became one of classification: to determine the cauterization state from oscilloscope outputs. From here all further progressions were made to ensure modularity and continuity was maintained, so that once real data was collected it could be analyzed without any code alterations. Despite the aforementioned changes the project remains applicable and the software and machine learning algorithm developed will be implemented directly once our data set becomes available.

Throughout the project several trials and errors were encountered. One of the challenges faced was in developing functions to separate variables. The team wanted to ensure that the variables were separated in the most optimal way for the SVM. Some options explored include point differences, standard deviation, convolutions, derivatives and integrals. All these were put through the pipeline with little success. Another area the team experienced challenges was in the structure of the code. Classes and objects were not used initially, which meant that the design of the code was highly repetitive and inefficient. Additionally, multiple loops were used to perform a single function where pre-developed functions could be implemented. An example of this was the initial “peak finding” algorithm that was built to determine frequency. This necessary as the sin function of our waves was unknown, therefore the frequency had to be approximated. However, it was realized, after consulting with stakeholders, that a fourier transform in the FFT module could be utilized to find the frequency.

Upon reflection it was realized that the team did not initially spend enough time visualizing and analyzing the

clusters due to time constraints. This resulted in us working blind a lot of the time. The team learnt that it is incredibly valuable to have an intuitive understanding of datasets before performing any sort of analysis. Once clustering was revisited and the understanding was ameliorated, the separation of variables was able to be improved and as a direct result the prediction accuracy increased.

When building the SVM algorithm the team dove in before truly understanding its functionality and how the harvested data fit into it. This was found to be rather limiting as fine tuning the model became quite difficult. After realizing this a more transparent algorithm development was opted for to develop a better understanding of machine learning concepts and their functions. There was a noticeable improvement in accuracy after altering the model.

One of the reasons for selecting this project was due to its benevolence and positive impact on the world of surgery. By improving the classification of cauterized tissues a reduction in the rates of revision surgeries will be seen as surgeons will be able to improve resections. Additionally, there will be better minimal margins, that means doctors will be able to reduce the amount of healthy tissue resected during surgeries. Both of these points lead to improved patient satisfaction as multiple operations can be stressful both physically and psychologically. Another positive outcome of the project is the decreased economic burden, currently 35% of breast surgeries have to be re-performed as is the case with many other cancer removal surgeries. This places a strain on resources and becomes quite expensive. This project has the ability to drastically reduce these costs and limitations thus improving hospital workflow.

7 Group Member Contributios

The table below summarizes the work contributions of each team member.

Member	Contributions
J. Ehrlich	Managing data collection, and communication with the Perk Lab. Contributing to the development of the preprocessing code and the regression code
M. Buchan	Contributing to the development of the preprocessing code and the regression code.
A. Glover	Managing GitHub repository, and contributing to the developing of the regression

8 Replication Package

A replication package for the project can be found on Github by following the link listed below.
Link:https://github.com/JoshEhrlich/Caut-Signal?fbclid=IwAR2vcGgRdq3s$_3$3$HHypiK$ – $fnZubJUHPaKTNnE{-}xZPS6mZSLgwxn0RwtyOmQ$

9 Conclusion and Future Work

The goal of the Navigated iKnife project is to utilize mass spectrometry techniques that can differentiate between healthy and cancerous tissue to localize tumours for removal in real-time during the surgical procedure. The major hurdle is that there exists a time delay between the tissue classification signal from the mass spectrometer and when the tissue is burnt by the electro-cautery. Once this time delay can be classified and localized, we will be able to feed backwards in time the mass spectrometer signal in order to spatially localize what classification the previously burned tissue is. In order to do this, we need to determine a synchronized temporal state between the mass spectrometer and the cautery so that we know the two machines are synchronized temporally.

The synchronization between the two data streams occurs in a software called Slicer. The mass spectrometer data stream can provide real-time streaming to slicer. However, we need to know when the cautery is beginning to burn tissue (cut through it). If we can determine what state the cautery is in, then we can determine whether or not it is burning tissue. The four states of the cautery are: cut - air, cut - tissue, coag - air, and coag - tissue.

Our goal was to figure out a way to determine the state of the cautery tool in real time. There were many restrictions on what technological tool we were allowed to use. Since the operating rooms and surgical protocols are tightly regulated, we needed a non-invasive method of data extraction. Therefore, we chose to use an oscilloscope that attached to the grounding wire on the cautery at the end of iKnife which removes any confrontation with the surgeon during their operation. The oscilloscope streams a voltage signal from the cautery into Slicer.

Depending on the state the cautery is in, the voltage signal is different. By training a machine learning model to differentiate between voltage signals, we can use the the model to differentiate between voltage signals in real-time thus telling us what state the cautery is in. This will then allow us to know the exact moment the cautery tool touches down on the patient begins burning tissue, passing vapour to the iKnife for processing, and then for streaming to Slicer. Since we know the ground zero (0) temporal state, we can calculate the delay, and stream the data backwards in time to the spatial location of the burn.

We used a Support Vector Machine to classify the cautery states. Our model produced an accuracy of 100% with an ROC curve of 1.00. This meant that with our current voltage states, we are able to classify every incoming signal.

Our future work will consist of combining spatial tracking with temporal tissue data localization into a fully operational navigated iKnife. This means that the surgeon will be able to use the cautery tool and in real time know what tissue they are burning, be it muscle, fat, skin, or tumour. Our direct next step will be to build a module in Slicer, written in Python, that will synchronize our data streams. After this, we will need to extrapolate the data to determine the different factors that cause the time delay. Finally, we will combine all the metrics and system and implement them on real patients.

The main application for this system will be for breast cancer surgery. The preferred approach is breast conserving surgery which maximizes patient retention of healthy breast tissue while removing all of the tumour tissue. However, since the breast deforms during surgery and the tumour can change shape, often excess tumour is left behind. Therefore, creating a narrow healthy tissue margin around the tumour will ensure that all tumour tissue is removed. However, if we were unable to localize the tumour in 3-dimensions and fail to know what tissue we are cutting through, we could unknowingly slice through the healthy margin barrier and leave tumour in the patient. Thus, by combing 3-dimensional tracking with real-time iKnife tissue classification, we could ensure that we are aware of where the tumour is, where we are in space, and remove all tumour from the patient.

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