Differential IP Clustering for Vulnerability Detection using applied Machine Learning

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A thesis submitted for the degree of
Honours of Science
in
Ethical Hacking and Computer Security

April 19, 2017

This thesis is dedicated to
no one
for no special reason

Acknowledgements

I would like to take this opportunity to thank my project supervisor, Dr Xavier Bellekens, who introduced me to the topic of Machine Learning and offered guidance from the beginning through to the completion of this project. Without whom this project would not have been possible. I would also like to thank the module leader, Colin McLean, who has given me continuous advice throughout my years of study at Abertay University.

Abstract

plenty of waffle, plenty of waffle, plenty of waffle, plenty of waffle, plenty of waffle, plenty of waffle, plenty of waffle, plenty of waffle.

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Chapter 1

Introduction

This section will give a brief background and history of Machine Learning before going in to depth with the definitions and types of algorithms used in modern Machine Learning systems. An analyses of the impact Machine Learning has in the field of computer security and how it can be applied directly to penetration testing and red teaming. Research aims and objectives will be provided as well as a statement to the structure of the rest entire thesis.

1.1 Background

The term machine learning was first defined by Arthur Samuel in the year 1959 as a "Field of study that gives computers the ability to learn without being explicitly programmed" and later as "a field of study that concentrates on induction algorithms and on other algorithms that can be said to 'learn'", Kohavi & Provost (1998). Machine learning has largely evolved from several subfields of artificial intelligence, specifically, computational learning and pattern recognition but now it stands on its own with its subfield Deep Learning being at the forefront of technology. Machine learning consists of the studying and construction of algorithms that can learn from and make predictions of data, Simon (2013). The early information available for machine learning was almost entirely theoretical due to the lack of processing power at the time. One of the early pioneers was Valiant (1984) whom developed a PAC learning framework and established the theory of a learnable algorithm, Munoz (2012). Modern machine learning algorithms use many calculations from statistics, information theory, theory of algorithms, probability and functional analyses, Munoz (2012).

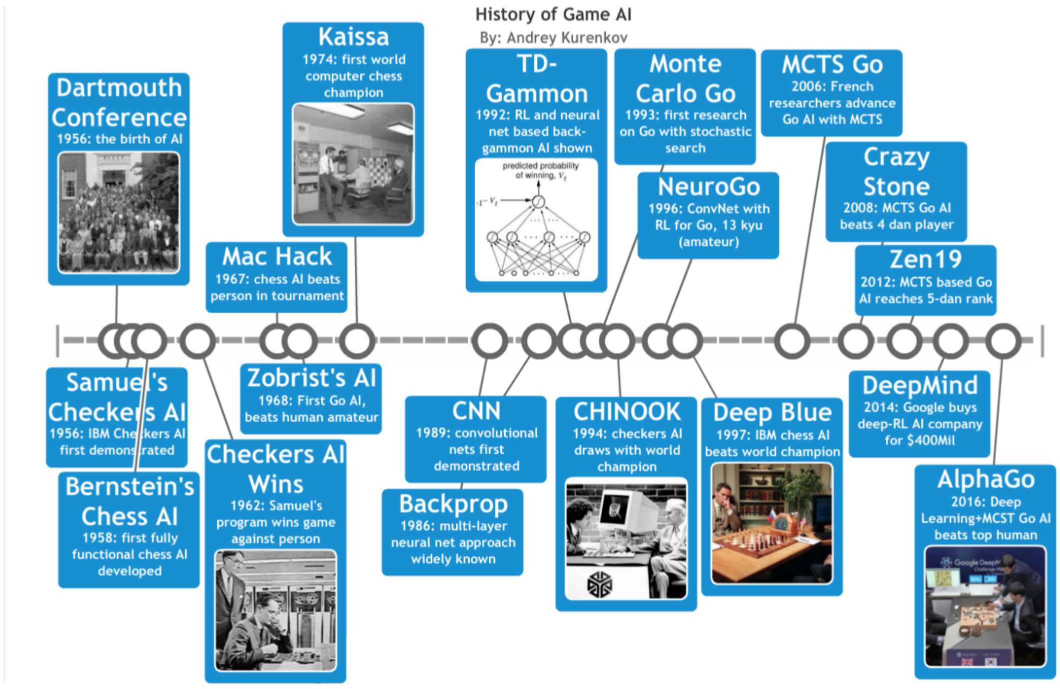

History of Game AI
By: Andrey Kurenkov
Dartmouth Conference
1956: the birth of AI
Kaissa
1974: first world computer chess champion
Mac Hack
1967: chess AI beats person in tournament
TD-Gammon
1992: RL and neural net based back-gammon AI shown
predicted probability of winning, V_t
Monte Carlo Go
1993: first research on Go with stochastic search
NeuroGo
1996: ConvNet with RL for Go, 13 kyu (amateur)
MCTS Go
2006: French researchers advance Go AI with MCTS
Crazy Stone
2008: MCTS Go AI beats 4 dan player
Zen19
2012: MCTS based Go AI reaches 5-dan rank
Samuel's Checkers AI
1956: IBM Checkers AI first demonstrated
Bernstein's Chess AI
1958: first fully functional chess AI developed
Zobrist's AI
1968: First Go AI, beats human amateur
Checkers AI Wins
1962: Samuel's program wins game against person
CNN
1989: convolutional nets first demonstrated
Backprop
1986: multi-layer neural net approach widely known
CHINOOK
1994: checkers AI draws with world champion
Deep Blue
1997: IBM chess AI beats world champion
DeepMind
2014: Google buys deep-RL AI company for $400Mil
AlphaGo
2016: Deep Learning+MCST Go AI beats top human

Figure 1.1: Timeline of artificial intelligence for games, Kurenkov (2016)

1.2 Current State of Machine Learning

In the recent years, machine learning accuracy and efficiency has increased dramatically which has caused the field to rapidly gain in popularity, especially in deep learning. One of the major reasons for this is due to the improvement in graphics processing units which in some computational tasks can outperform central processing units by an order of magnitude or more, Mattsson (2016). The rapidly growing field of deep learning could be made apparent by Googles recent self-driving car and LeNet image recognition system, however, examples of machine learning can be found in just about every field with a classification or regression problem. Some of which include: natural language processing using morphological analyses for linguistics (Black & Zernik (1994)), document classification and spam detection, better image recognition than humans (Karpathy (2011)) and beating a professional player at the complex Chinese game Go (DeepMind (2016)). Figure 1.1 illustrates the advancement of machine learning using the context of game artificial intelligence players.

The majority of projects over the past few years have focused on Deep Learning due to its performance and versatility with complex problems but also because of the media coverage with large scale projects by international corporations such as Google and Microsoft. The idea of deep learning has been around since the 1980s where a

Japanese scientist, Kunihiko Fukushima, proposed a hierarchical, multi-layered artificial neural network named Neocognitron, designed for handwritten character recognition. Neocognitron was recognised as the inspiration for convolutional neural networks, the most commonly used deep learning algorithm, LeCun et al. (2015). Deep learning attempts to model complex abstractions in data by using a multiple-level architecture most commonly compromising of artificial neural networks and non-linear transformations in its algorithms, Mattsson (2016). As such, the concepts of deep learning are extensions of regular machine learning algorithms.

In the past year a new topic has become of consider interest in the machine learning field, Automated Machine Learning, which can be considered to cover the tasks of algorithm selection, hyperparameter tuning, iterative modelling and model assessment, Mayo (2017). By the end of 2016 the python Auto-sklearn library was created based off of the scikit-learn library which encompasses these tasks, created by a team from the University of Freiburg it won the KDnuggets AutoML challenge, Matthias Feurer (2016). Using these examples, its possible to hypothesize that the future of machine learning will include automatic deep learning, however, these individual fields of machine learning are still in their infancy and far from being used together.

The computer security industry due to its nature, has many examples of machine learning implementations such as intrusion detection systems using machine learning or deep learning for anomaly detection. One of which has been commercialised under the company name Deep Instinct and advertises zero-day detection using deep learning. However, the majority are very similar and are all blue team based security solutions. Researching into Red team or penetration testing tools using machine learning resulted in a disappointing lack of tools or ideas considering the vast amount available for Blue team.

The sole documented research found for red team was for an automatic penetration testing project named Auto Red Team (ART) framework by Lu, Song of Iowa State University in 2008 which used decision trees and hard programmed exploits. This meant the entire hard programmed exploit section had to be reconstructed for each use case, this would not be ideal but also extremely time consuming. Further analyses of the ART framework can be found in the literature review of "Auto Red Team: a network attack automation framework based on decision tree". There have also been tools and libraries created to test the security of software which use machine learning models such as Deep Pwning. Deep Pwning is an open source metasploit plugin which allows the tricking of machine learning models. This field of research was named Adversarial Machine learning and the first paper of which was respectably named ”Adversarial Machine Learning” and published by ACM in 2011.

There is an extensive amount branches to machine learning and unfortunately, too many to cover in this thesis due to time constraints. Therefore, this introduction will only detail the most popular types of machines learning algorithms.

1.3 Significance of study

The increased demand for penetration testers justifies the need for more effective and advanced tools to conduct their security assessments. The goal of a penetration test being to find vulnerabilities in a system using techniques similar to that of a malicious hacker. This means malicious hackers will continue to use the most advanced methods to gain access to critical systems and thus security teams must also continue to advance their toolset to be as effective and efficient as possible. Penetration tests can last a time scale of anything between one day to several months and more advanced machine learning tools would allow for a more efficient use of this time. The large variety of machine learning models used in the blue team results in a large variety of models required to test them using adversarial machine learning as well as advanced machine learning tools, specifically for the red team in order to bring each team to the same level. Having both red team and blue team on the same level is beneficial for the industry as a whole, providing competition between both sides and to continue to strive for improvement.

This project aims to help correct this unbalance by designing and developing a proof of concept red team tool using machine learning techniques.

The application must be able to be used as an aid to a security professional during a security assessment or capture the flag hacking events in order to be classed as a red teaming tool.

This application must also be scalable and versatile to be used in varying sized network environments.

The tool will be critically analysed and recommendations of related future work will be provided.

1.4 Types of Machine learning

As mentioned above there are many different machine learning algorithms available. Each algorithm can be classed based on the problem, required output and several factors of the data set, such as whether it includes labels and the amount of values it includes. The two primary problems machine learning algorithms provide solutions to, can be put in to two categories which are not mutually exclusive and can be combined in certain use cases. These are classification and regression problems. The following describes and states the differences of these types.

1.4.1 Classification

With the growth of big data, unstructured data is more prevalent than its structured counterpart. This is because, "while the amount of structured data has grown fast, the amount of unstructured data has grown much faster" Simon (2013). This creates the need for ever more efficient data analytics and is a typical classification problem for machine learning. There are many types of classification, simple types such as a linear classifier and then more complex types such as multiclass and structured classifiers. Classification is largely used in data mining and statistical analyses for these purposes. In short, classification is used when you require an input variable to be identified as part of a group or label, resulting in the full dataset being categorised. Classification can only take a finite set of values such as picking from 1 of N values. In classification, each incorrect answer is equally incorrect, compared to regression where incorrect answer can be varying levels of incorrect.

1.4.2 Regression

Regression problems are for when prediction of real continuous values is required, such as predicting stock market values and detecting the age of a person from a picture, Rossant (2014). Regression analyses involves predicting and estimating a response based on previous data and input variables. As mentioned above regression answers can have a varying level of inaccuracy as appose to binary correct or false predictions. This is due to regression using continuous values. Figure 1.2 provides a basic illustration example of these two problems.

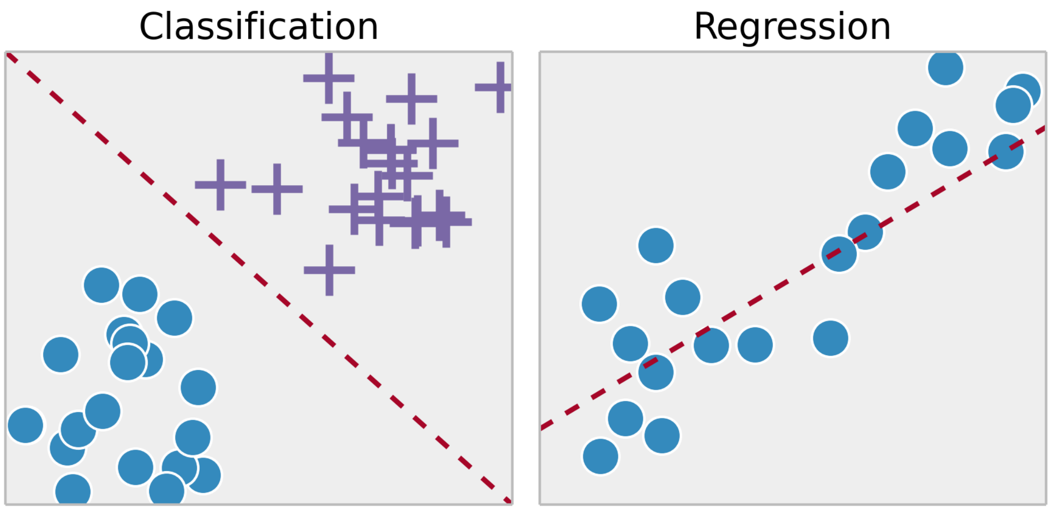


Figure 1.2: Illustration of machine learning types, Rossant (2014)

1.5 Types of Learning algorithms

The most commonly found learning methods for algorithms are supervised and unsupervised followed by semi supervised and reinforcement learning which are also fairy common. These are explained briefly as follows.

1.5.1 Supervised

In a supervised training model, the entire data-set used for training is pre-labelled so that the algorithm can use pattern analyses to predict given values after training. A use case scenario for supervised learning includes the above stock market example where current values with labels are given and the model is used to predict future labels.

1.5.2 Semisupervised

Due to the expensive nature of labelled data in most cases, semisupervised learning uses a split of labelled and unlabelled data to train the model. This is most often split unevenly with the large majority of training data being unlabelled. This model is often used in cases where the cost of labelled data-sets is simply too expensive.

1.5.3 Unsupervised

The opposite of supervised learning, where the training data-set has no labels and the model must attempt to determine the correct answer itself. This is often used as a method to determine a structure in the data given. These models can identify segments of similar attributes such as clustering. Unsupervised learning is the primary method used for this thesiss methodology.

1.5.4 Reinforcement

Reinforcement learning works similarly to heuristic algorithms in the sense that every possibility is attempted and assigned a score in which the iteration with the highest score is used as the model output. Whilst training this model the algorithm uses the highest scores iteration to modify its calculations for greater accuracy and efficiency. This model is often used in robotics as well as game design for path navigation calculation and computer player AI (artificial intelligence). The following is an example use case: A chess player AI calculates each possible move it can make using a reinforcement model for each of its turns. The model assigns a score to each move it could possible make at that point in time and weights them based on pieces acquired, future strategy prospects and defence risk. Similar models have been used for AIs mentioned in Figure 1.1.

1.6 Common Machine Learning Algorithms

As mentioned above, due to the amount of machine learning algorithms available and project time constraints, only a few of the most common algorithms will be described below.

1.6.1 Linear Regression

Linear regression predicts real values based off continuous data of two variables. It does this by using a best fit or regression line over the existing data extending in predictions. If the data does not indicate any positive or negative trends then using linear regression will likely not be a very useful model. The trend or direction of data can be calculated using correlation coefficient as follows, where $(x_2, y_1), (x_n, y_n)$ is the observed data.

$r = \frac{1}{n-1} \Sigma \left(\frac{x-\bar{x}}{s_x} \right) \left(\frac{y-\bar{y}}{s_y} \right)$

A value that is close to 1 would indicate positive correlation where -1 would indicate negative correlation. A normalised covariance calculation may also be used instead.

1.6.2 K-Nearest Neighbours

K-nearest neighbours (or KNN) is a widely used computationally expensive supervised learning model for data classification but can also be used for regression problems. The value k refers to the distance is which to weigh the number of class nodes inside. Several distance functions can be used such as Euclidean, Manhattan and Minkowski with the most common being Euclidean. Euclidian distance is the straight-line distance between the two nodes. On a two-dimensional plane it is measured using the following formula where the coordinates are $\mathbf{p} = (p1,\ p2)$ and $\mathbf{q} = (q1,\ q2)$.

$d\,(p, 1) = \sqrt{(q_1 - p_1)^2 + (q_2 - p_2)^2}$

For e.g. if k = 1 then the current node will be assigned to the same class as its nearest node, where as if k = 5 then the class with the largest number of nodes in a distance of 5 will be selected to represent the current node. KNN is not resistant to bias in data-sets and thus data must be normalised before inputted into the model. KNN models are not to be confused with K-means clustering models as they share a very loose relationship being that KNN can be used to add data into pre-existing K-means clusters known as a nearest centroid classifier.

1.6.3 K-means Clustering

K-means Clustering is an unsupervised model in which the number of clusters is specified in advance. K being the number of clusters the model will output for the given data. The value for K can be assigned manually or the optimal value can be calculated by using either the elbow method or the gap statistic, the latter of which is used and explained in the methodology section of this thesis with a practical use of K-means. The K-means algorithm itself is also known as Lloyd's algorithm and uses iterative refinement to determine the best clustering.

1.6.4 Dimensionality Reduction

Dimensionality reduction algorithms are exactly what the name suggests. With the dramatic increase in variable types and raw data size being captured leading to the invention of the term Big Data, datasets have become very large. These large datasets have become the main bottleneck for machine learning performance, especially in computationally expensive models such as KNNs and K-means. There needs to be a way to identify the significance of each variable in the data-set in order to give weights to their values for use in calculations. Principle Component Analyses (PCA) can be used for this purpose as well as for variance maximization. The PCA algorithm attempts to detect correlation between each of these variable types and uses this information to detect the vector directions of maximum variance in high-dimensional data. The algorithm then projects these maximum variance vectors into a smaller dimension whilst attempting to keep the most amount of information and greatest variance as possible. If the measurement scales of the dataset variables are not equal, then the data should be normalised prior to PCA due to the variance maximization functions of the algorithm.

1.6.5 Decision Trees

Decision trees are a classification model that uses supervised learning to calculate either categorical or continuous dependent variables. Decision trees can also be designed manually as was traditionally done. As the name suggests, the model works by splitting the data at each branch of the tree by asking questions and making decisions on each layer. The concept of decision trees is simple however they can be combined together, or include other machine learning models within its layers greatly increasing the complexity of this model.

1.6.6 Random Forests

Random decision forest is one of these complications where the model contains several decision trees built during the training stage and can also be used with unsupervised learning. These random decision forests can be used for classification or regression by simply using the mode of the results from the forest or the mean in the case of a prediction problem. They creation of this model differs from regular decision trees as the training algorithm applies bootstrap aggregating, commonly referred to as bagging, followed by feature bagging resulting in a random decision forest. Bagging increases the stability and accuracy of decision trees by reducing variance and avoiding the overfitting of data. It does this by generating additional sets data based on the given data-set which results in a larger data-set overall reducing the variance but increasing the predictivity of the model. Bagging can also be used on several other machine learning algorithms. Feature bagging also known as the random subspace method, selects random samples from the entire dataset in order to reduce the correlation between each tree in the forest. This is done to produce varied models for each tree as appose to them being very similar if they were all trained on the entire data-set. Random forests can be complicated once more by adding a neural network within its layers, or even a deep learning model such as recurrent neural networks.

1.6.7 Ariticial Neural Networks

Artificial neural networks (or ANNs) are commonly used as the bases for most deep learning algorithms such as convolutional and recurrent networks and are loosely based on the way a human brain functions. They can be used with several types of learning methods. Neural networks consist of interconnected neurons on a layered scheme in which every neuron has a function and its output can be seen by its connected neurons to then use it in their own functions. Each neural connection has an assigned weight for its output which is calculated during the training stage of the model. The layers consist of three types, an input, an output and hidden layers sandwiched between the two. The number of hidden layers in a neural network is what defines whether it is a deep learning model or not. Models with more than one hidden layer are referred to as deep learning models. How the layers are connected and the way data travels between the layers defines the type of neural network. For e.g. a recurrent neural network allows for sequences to be used for input and output unlike convolutional which can only use fixed values for these. The Google subsidiary DeepMind uses recurrent neural networks in its algorithms to create its AlphaGo AI mentioned previously.

Chapter 2

Methodology

This chapter contains an in-depth analysis of the design and implementation stages carried out during this project. Initially, the design and goals of the application will be enumerated. Subsequently an analysis of the applications infrastructure will be presented followed by an in-depth detail of the modules and submodules within the applications programming. A test case scenario will be defined and executed to provide a proof of concept. The efficiency and accuracy among other factors based on the test scenario will be analysed during the discussion chapter of this thesis.

2.1 Design

The application designs primary goal was to be able to detect vulnerable machines on a large-scale network infrastructure regardless of topology or host types by using machine learning techniques and automated tool outputs. However, there are several requirements the application must adhere to for it to be a viable tool during a security assessment. The application created for this thesis was done so strictly on a proof of concept bases.

The application was designed with the following requirements in mind:

Text progress output with multiple verbosity settings allowing for an experienced tester to understand what the application is doing at any point in time during execution. This is critical as tools used during an assessment on live networks must not hinder or damage the network or its hosts in any way as to disrupt an organisations business.

Several input type parameters for which the tester can utilise based on the current information known about the network. Such as only using one type of scan file and manually selecting the clustering model.

Several output options including visually in the form of graphs and to a dot type file to be used with other industry applications and reports.

Manual overriding of variables via parameters in order to allow for the application to be scripted and modified by the tester. This will increase the efficiency of using the tool and provide advanced customisation of the algorithms within the application.

Highly versatile with working conditions and configurability. The programming of the application to be highly documented allowing a tester to fix and modify the application code to suit the operations needs. By using a primarily interpreted language as appose to compiled one would allow for this, as well as making the application portable without extra code. For these purposes, the Python programming language was chosen. With the majority of modern tools and scripts used by penetration testers haven been written in Python due to its versatility, reliability and portability, it further enforces this choice.

2.1.1 Application Brief

The application requires several parameters to run and has three different global modes; manual, assisted and automatic. These modes can either be run with Nmap, Nessus or both inputs with the majority of the use case scenarios requiring both. The application will then parse these inputs, process the data in several ways and cluster the information based on feature similarities. Output includes the full details of each cluster within the clustering. If using both inputs the application will combine the data from each and subtract large similarity clusters. By doing this, the application will determine the most unique hosts within the topology and display them in a new clustering. The unique hosts will, based on probability, be the most vulnerable on the network and should be prioritised by a tester during the manual assessment. This is due to the model prioritising the vulnerabilities each scanner detects then appends them to the pre-existing host set, thus rendering that host more unique than the others.

An example output of the application when using **twin input automatic mode** can be found in text form using maximum verbose level at Appendix B.1.1 and a Figure of the graphing interface GUI at Appendix B.1. The data-set used for these examples were Nessus and Nmap scan XML outputs generated from a fictional network. Due to the sensitive nature of the data included within these scans such as SSH keys and vulnerability codes, there are no publicly available data-sets.

The difference between modes and parameters will be explained within the next section *infrastructure analyses.*

2.2 Infrastructure

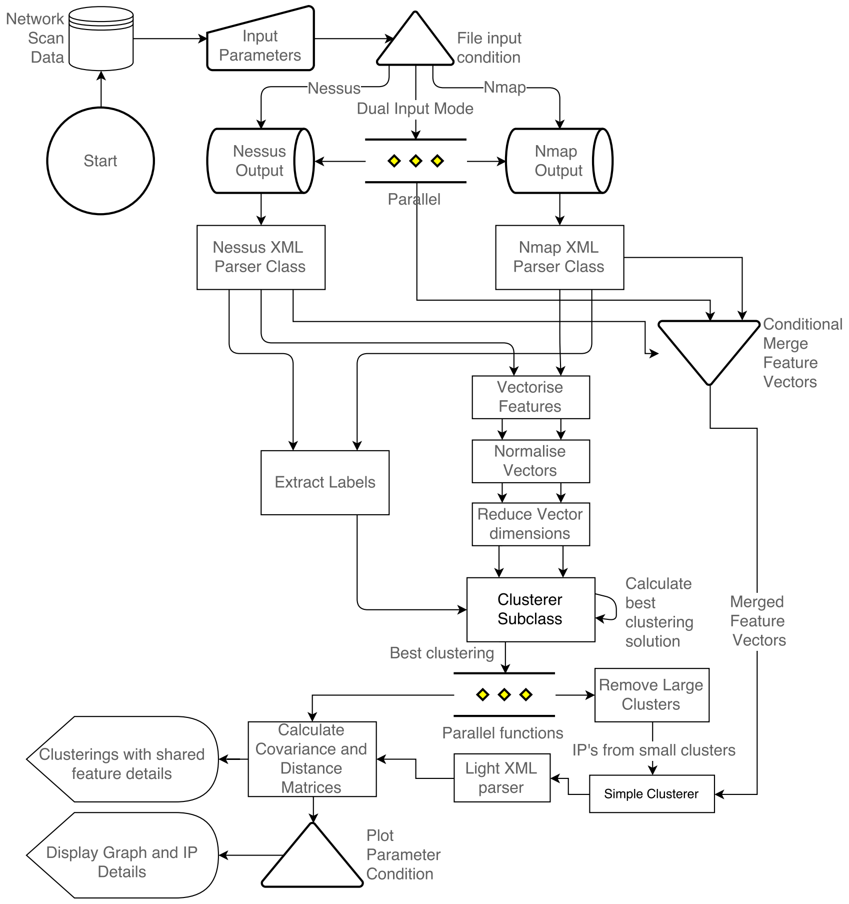


Figure 2.1: Application infrastructure data flow diagram

Figure 2.1 shows the applications primary class infrastructure when in automatic mode. The infrastructure diagram has been created using standard flow diagram symbols to provide understanding of the process types. The application has been programmed for python version 2.7 interpreters and therefore will not have complete functionality without modification for python 3.0 and above. Due to time constraints placed upon this thesis the library NMAP-Cluster, Blackhat USA (2016), was used to conserve time.

In order to execute this application, it is important to have the correct library dependences. This is done via the python package manager PIP and a requirements file, found in Appendix A.1, by executing the command:

```
Pip install -r requirements.txt
```

The following sections include detailed descriptions of the processes symbolised within the infrastructure Figure 2.1. Beginning from the start circle and ending at the display modules.

2.2.1 Usage and Parameters

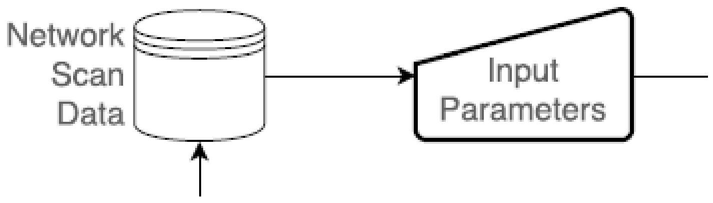


Figure 2.2: Network scan data and input parameter modules from infrastructure diagram at Figure 2.1

The modules shown in Figure 2.2 are those used to store the network scan data and process the applications input parameters. The Network Scan Data module refers to the XML output of an Nmap scan, Nessus proprietary export file or both. These must be in their respectable formats in order for the parser to recognise them. The files must also be referenced in their correct positional arguments when executing the application such as mentioned in the application usage in Appendix A.2.

The manual input parameters module on Figure 2.2 refers to the parameters that the application requires to select the correct run configuration. This is required because the application has no execution graphical user interface (GUI), the lack of which was decided for several reasons. Such as allowing for scripting, verbose output and terminal pipe operation commands. This type of interface is generally preferred by professionals due to the speed and reliability it provides over a standard GUI. The graphing stage of the application does however, provide a GUI to allow for manipulation of the graphs in multiple ways. The application usage found in Appendix A.2 includes a full description of the possible parameters. The parameters are passed into the data processing section of the application explained in the next session. The three possible run modes are explained in a later section ??.

2.2.2 Data Processing

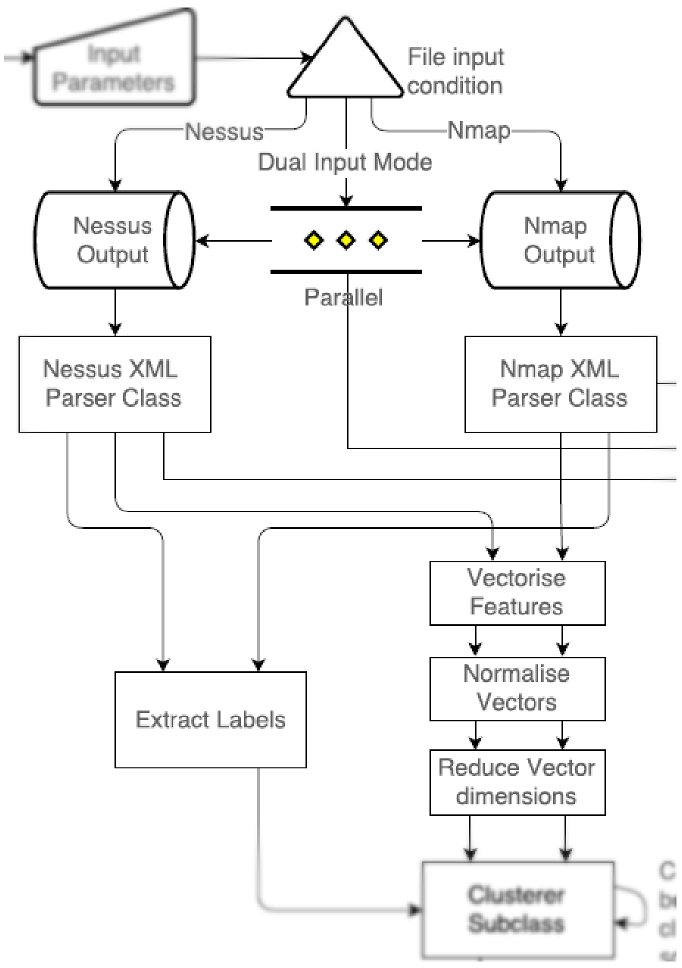


Figure 2.3: The data processing section from the infrastructure diagram at Figure 2.1 with the irrelevant modules blurred out

Figure 2.3 displays the data processing section of the application, an analysis of this section is provided in the following paragraphs.

Depending on the files specified within the input parameters, the application will either feed the Nessus, Nmap or both XML files into the parser classes. These parser classes will take the data from each file and transform it into IP addresses and features which are then passed individually into vectorizers. Vectorization is required for the features to be understood by the clustering algorithm. Vectorization refers to the general process of turning a collection of text (in this case machine attributes) into numerical feature vectors. It is important to note that data from each scanner file is kept separate until the final process. The vectorization class is short and concise due to it having only two purposes, to call the parsers and vectorise the returned results. More information on the vectorization of each file as well as the raw python class code can be found in Appendix A.4.

Once the data has been vectorised it must be normalised in order to avoid large value bias when using dimensionality reduction algorithms such as PCA. Data normalization scales the values to within the same range whilst keeping the data variance and eliminating the bias problem. This is programmed immediately after vectorisation in the applications initialisation class found in its raw code form at Appendix A.3.

The major difference between each scanner used is that the Nessus output values include vulnerabilities over Nmap which has superior information on the services and ports of the machine. By using both, the optimal range of information can be achieved, however, this introduces the problem of overfitting which PCA has countered. For more information on PCA refer to dimensionality reduction section 1.6.4 in the introduction. It is possible to greatly modify the output of the two scanners by either using scripts with Nmap or custom plugins for Nessus. Due to the modularity of the application, these modifications to the scanners will not affect the parsers and therefore can be used safely. PCA is also implemented within the initialisation class which can be found in Appendix A.3. Once PCA is complete, the still separated feature vectors are sent to the clusterer subclass and possibly the conditional merger. The following section will explain the conditional merger of which is represented by symbol in Figure 2.4.

2.2.3 Small Combined Cluster

The conditional process of merging the feature vectors, referred to by the symbol in Figure 2.4, is executed at this stage, condition dependant on whether dual input

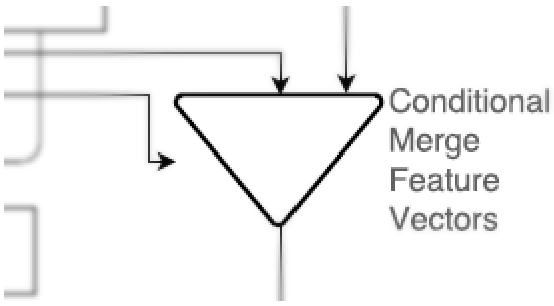


Figure 2.4: Conditional merge vectors process module from the infrastructure diagram at Figure 2.1

mode has been selected when initialising the applications parameters. However, this path must then pause until the main cluster subclass (as represented by the symbol in Figure 2.5.) has completed in order to use its clustering outputs. Once this has occurred, each clustering will be duplicated and the large clusters with greater than three IP addresses will be removed from the clustering. This value can be changed based on the network size however the value of three was found to be optimal for networks of size 10 to 1000 from the algorithm tuning stage. The result of each is combined then re-clustered and the remaining IPs passed through a simpler file parser (compared to that of the ones previously used) to retrieve the information in an un-vectorised text format. This is done to display individual machine information for the end user within the graphing interface. The main cluster subclass mentioned previously is explained in the following section.

2.2.4 Clustering Algorithm

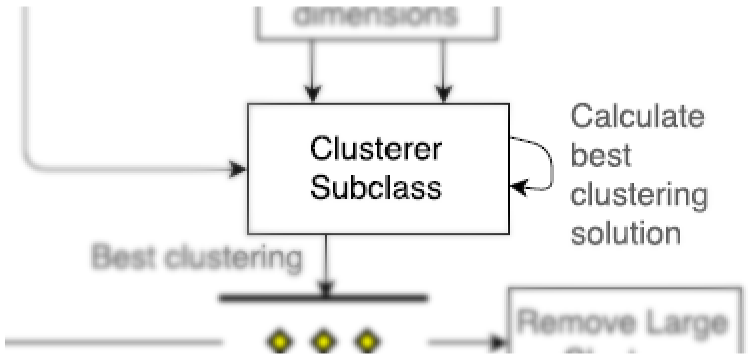


Figure 2.5: Representation of clusterer subclass from infrastructure diagram Figure 2.1 spotlighted

The Clusterer subclass represented in the infrastructure diagram by the symbol in Figure 2.5 above is where the majority of the calculations are done within the application. This includes the three different modes; manual, assisted and automatic. The raw python code for this module can be found in Appendix A.5. *INCOMPLETE*

2.2.5 Covariance and Distance Matrices

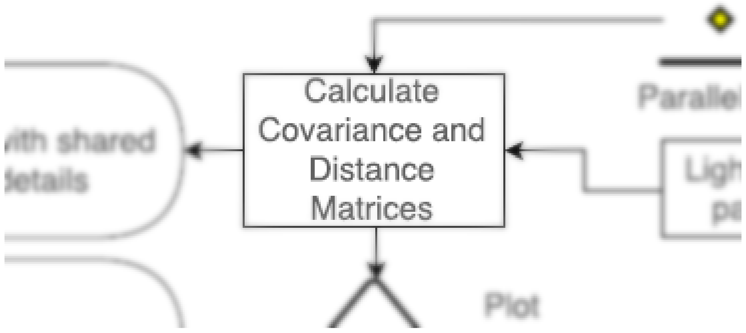


Figure 2.6: Representation of covariance and distance matrices function from infrastructure diagram Figure 2.1 spotlighted

Covariance and distance matrices are calculated just before displaying the graphing interface. The function symbol is shown in Figure 2.6 above. The output from these functions can be found at the end of the text output, an example is shown in Appendix B.1.1. This is shown for the simple purpose of giving a technical user the knowledge of the used data-set. Specifically, the covariance matrix shows how related the centroids for each clustering are to each other. Whilst the Distance matrix shows the distance between each clustering centroid. These calculations are done for each clustering in the current mode (e.g. three times if using twin mode) however, they only shown in verbose level one and above.

2.2.6 Display Modules

The application will display the main output at the end of its execution as shown in the infrastructure diagram with the symbol from Figure 2.7. The application will show a running output as the calculations are performed providing that the verbosity level is set to one or higher. The verbosity parameter will only effect the text output and not the graphing interface of the application. Without verbose output selected the text output will only show the cluster details (for both formats if using twin mode) *INCOMPLETE*

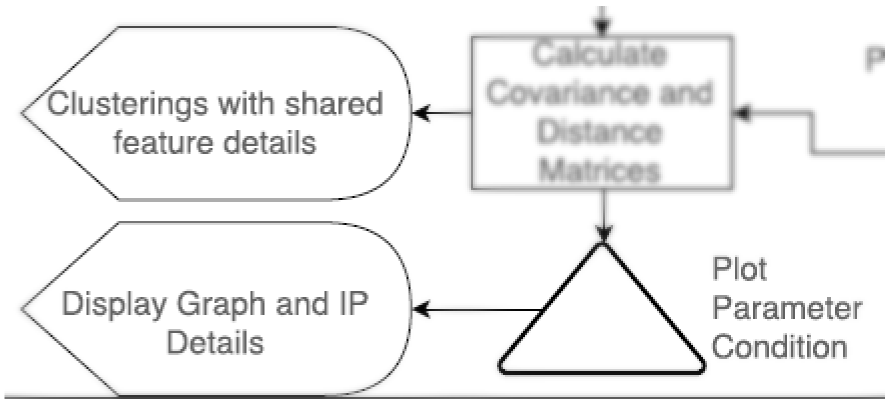

Clusterings with shared feature details
Calculate Covariance and Distance Matrices
Display Graph and IP Details
Plot Parameter Condition

Figure 2.7: Representation of the display modules from infrastructure diagram Figure 2.1 with irrelevant modules blurred out

Modes and parameters. Usage examples.

TODO notes

- complete cluster sub class description and display description such as Gap statistic- http://web.stanford.edu/ hastie/Papers/gap.pdf and The elbow method
- Modes and parameters. Usage examples. - describe them in depth
- mathematical model
- POC testing, what was done. Validate results

2.3 Proof of Concept Testing

Appendix A

Code

A.1 Requirements python file

```
backports-abc==0.4
bokeh==0.12.1
certifi==2016.8.8
cycler==0.10.0
futures==3.0.5
Jinja2==2.8
MarkupSafe==0.23
matplotlib==1.5.1
numpy==1.11.1
pyparsing==2.1.8
python-dateutil==2.5.3
pytz==2016.6.1
PyYAML==3.11
requests==2.11.0
scikit-learn==0.17.1
scipy==0.18.0
singledispatch==3.4.0.3
six==1.10.0
tornado==4.4.1
tabulate==0.7.7
```

A.2 Application Usage Parameters

The following includes the usage and parameter definitions for the application.

```
usage: cluster.py [-h] [-s {manual,automatic,assisted}]
                  [-c {kmeans,dbscan,agglomerative}]
                  [--metric {euclidean,cosine,jaccard}] [-N] [-n N_CLUSTERS]
                  [-e EPSILON] [-m MIN_SAMPLES] [-cent] [-t] [-tp twinpath]
```

```
                 [-p] [-v]
                 path [path ...]
Cluster NMap/Nessus Output
positional arguments:
  path                  Paths to files or directories to scan
optional arguments:
  -h, --help            show this help message and exit
  -s {manual,automatic,assisted}, --strategy {manual,automatic,assisted}
  -c {kmeans,dbscan,agglomerative}, --method {kmeans,dbscan,agglomerative}
  --metric {euclidean,cosine,jaccard}
  -N, --nessus          use .nessus file input
  -n N_CLUSTERS, --n_clusters N_CLUSTERS
                        Number of kmeans clusters to aim for
  -e EPSILON, --epsilon EPSILON
                        DBSCAN Epsilon
  -m MIN_SAMPLES, --min_samples MIN_SAMPLES
                        DBSCAN Minimum Samples
  -cent, --centroids    plot only centroids graph, requires the use of "-p"
  -t, --twin            use both input formats to calculate vulnerable single
                        clusters, use with -tp and -N
  -tp twinpath, --twinpath twinpath
                        path to nmap xml if using twin clustering
  -p, --plot            Plot clusters on 2D plane
  -v, --verbosity       increase output verbosity
```

A.3 Initialization Class

The following contains the raw code for the primary initializer class of file 'cluster.py' in the application parent folder. It is used to start the application using parameters from the usage, in Appendix A.2. The code has been thuroughly commented with the intention of being modified by a potential tester for individual operational requirements. This is further enforced by the application being entirely modular with each module able to be modified without harming the others. The cluster subclass has been removed from this code and placed in A.5 in order to promote the legibility of this appendix thus must not be executed direction without concatination with the afore mentioned subclass first.

```python
import logging

from sklearn.preprocessing import normalize

from clusterer_parts.optimal_k_k_means import optimalK
from clusterer_parts.analysis import get_common_features_from_cluster,
    get_common_feature_stats
from clusterer_parts.clustering import cluster_with_dbscan,
    cluster_with_kmeans, precompute_distances, \
    cluster_with_agglomerative, cluster_interactive, get_centroids,
        cluster_single_kmeans, get_k
from clusterer_parts.display import print_cluster_details,
    generate_dot_graph_for_gephi, create_plot, \
    create_plot_centroids, create_plot_only_centroids, twin,
        remove_large_clusters
from clusterer_parts.optimizing import sort_items_by_multiple_keys
from clusterer_parts.reduction import pca
from clusterer_parts.validation import validate_clusters,
    get_average_distance_per_cluster
from clusterer_parts.vectorize import vectorize
import numpy as np
from tabulate import tabulate
firstpass = True

if __name__ == "__main__":
    import argparse

    parser = argparse.ArgumentParser(description=u'Cluster NMap/Nessus
        Output')

    parser.add_argument('path', metavar='path', type=str, nargs='+',
        default=None,
                        help="Paths to files or directories to scan")

    parser.add_argument('-s', '--strategy', default="automatic",
        choices=["manual", "automatic", "assisted"])
    parser.add_argument('-c', '--method', default="kmeans",
        choices=["kmeans", "dbscan", "agglomerative"])
    parser.add_argument('--metric', default="euclidean",
        choices=["euclidean", "cosine", "jaccard"])
    parser.add_argument('-N', '--nessus', default="false", required=False,
        action='store_true',
                        help='use .nessus file input')

    parser.add_argument('-n', '--n_clusters', type=int, default=2,
        help='Number of kmeans clusters to aim for')
    parser.add_argument('-e', '--epsilon', type=float, default=0.5,
        help='DBSCAN Epsilon')
    parser.add_argument('-m', '--min_samples', type=int, default=5,
        help='DBSCAN Minimum Samples')
    parser.add_argument('-cent', '--centroids', default=False,
        required=False, action='store_true',
                        help='plot only centroids graph, requires the use of
                            "-p"')
    parser.add_argument('-t', '--twin', default=False, required=False,
        action='store_true',
                        help='use both input formats to calculate vulnerable
                            single clusters, use with -tp and -N')
    parser.add_argument('-tp', '--twinpath', metavar='twinpath', type=str,
        required=False,
                        help='path to nmap xml if using twin clustering')

    parser.add_argument('-p', '--plot', default=False, required=False,
        action='store_true',
                        help='Plot clusters on 2D plane')

    parser.add_argument("-v", "--verbosity", action="count",
        help="increase output verbosity")
    args = parser.parse_args()

    logging.basicConfig(format='\%(asctime)s \%(process)s \%(module)s
        \%(funcName)s \%(levelname)-8s :\%(message)s',
                        datefmt='\%m-\%d \%H:\%M')

    if args.verbosity == 1:
        logging.getLogger().setLevel(logging.INFO)
    elif args.verbosity > 1:
        logging.getLogger().setLevel(logging.DEBUG)

    if (args.twin == False):

        # Vectorize our input
        logging.info("Vectorizing Stage")
        vector_names, vectors, vectorizer = vectorize(args.path,
            args.nessus)
        logging.debug("Loaded {0} vectors with {1}
            features".format(len(vector_names), vectors.shape[1]))
        logging.info("Vectorizing complete")

        # normalise vectors first before passing them through PCA. PCA uses
            2 dimensions
        logging.info("Normalising the vectors")
        normalized_vectors = normalize(vectors)
        logging.info("Reducing vectors to two dimensions with PCA")
        reduced_vectors = pca(normalized_vectors)
        logging.debug(
            "reduced to {0} vectors with {1}
                dimensions".format((reduced_vectors.shape[0]),
                reduced_vectors.shape[1]))
```

```
# Cluster the vectors
logging.info("Clustering")
labels = cluster(vector_names, vectors, reduced_vectors,
    normalized_vectors, vectorizer, args.strategy,
                 args.method, args.n_clusters, args.epsilon,
                     args.min_samples, args.metric)
logging.info("Clustering Complete")
# Test cluster validity
overall_score, per_cluster_score = validate_clusters(vectors,
    labels)

# Analysis relevant to the person reading results
universal_positive_features, universal_negative_features,
    shared_features = get_common_features_from_cluster(
    vectors, labels, vectorizer)

# logging.debug("Shared features: {0}".format(shared_features))

# Reduce results and relevant information to per cluster data
cluster_details = {}
for cluster_id in per_cluster_score.keys():
    cluster_details[cluster_id] = {
        "silhouette": per_cluster_score[cluster_id],
        "shared_positive_features":
            shared_features[cluster_id]['positive'],
        # "shared_negative_features":
            shared_features[cluster_id]['negative'],
        "ips": [vector_names[x] for x in xrange(len(vector_names))
            if labels[x] == cluster_id]
    }
print "Note: shared features does not retain keys from XML and
    therefore wont always be human readable."
print_cluster_details(cluster_details, shared_features)

if args.plot:
    # only kmeans centroids for now
    if no_clusters.startswith("kmeans") :
        logging.debug("Getting centroids using reduced vectors:")
        # global centroidskmeans
        # take just cluster number from result string
        n_clusters = no_clusters.split("=", 1)[1]
        n_clusters = int(n_clusters.rsplit(')', 1)[0])
        logging.debug("nclusters: " + str(n_clusters))

        centroidskmeans = get_centroids(reduced_vectors, n_clusters)
        logging.debug("attempting to plot the following centroids:\n
            " + str(centroidskmeans))

        # covariance
        x = centroidskmeans[:, 0]
        y = centroidskmeans[:, 1]
        X = np.vstack((x, y))
        cov = np.cov(X)
        logging.info("Centroids Covariance Matrix:\n
            {0}".format(cov))

        # print similarity distance between centroids
        matrix = precompute_distances(centroidskmeans,
            metric=args.metric)
        matrixTable = tabulate(matrix)
        logging.info(
            "distance matrix between centroids using metric: {0}
                :\n{1}".format(args.metric, matrixTable))

        if args.centroids:
            create_plot_only_centroids(reduced_vectors, labels,
                vector_names, centroidskmeans, n_clusters)
        else:
            create_plot_centroids(reduced_vectors, labels,
                vector_names, centroidskmeans, n_clusters,
                                 cluster_details)

    # manually selected kmeans though arguments
    elif args.method == "kmeans" and args.strategy != "automatic":
        if get_k()>0:
            centroidskmeans = get_centroids(reduced_vectors, get_k())
        else:
            centroidskmeans = get_centroids(reduced_vectors,
                args.n_clusters)

        logging.debug("attempting to plot the following centroids:
            \n" + str(centroidskmeans))

        # covariance
        x = centroidskmeans[:, 0]
        y = centroidskmeans[:, 1]
        X = np.vstack((x, y))
        cov = np.cov(X)
        logging.info("Centroids Covariance Matrix:\n
            {0}".format(cov))

        # print similarity distance between centroids
        matrix = precompute_distances(centroidskmeans,
                metric=args.metric)
            matrixTable = tabulate(matrix)
            logging.info(
                "distance matrix between centroids using metric: {0}
                    :\n{1}".format(args.metric, matrixTable))

            if args.centroids:
                if get_k() > 0:
                    create_plot_only_centroids(reduced_vectors, labels,
                        vector_names, centroidskmeans, get_k())
                else:
                    create_plot_only_centroids(reduced_vectors, labels,
                        vector_names, centroidskmeans, args.n_clusters)
            else:
                if get_k() > 0:
                    create_plot_centroids(reduced_vectors, labels,
                        vector_names, centroidskmeans, get_k(),
                                          cluster_details)
                else:
                    create_plot_centroids(reduced_vectors, labels,
                        vector_names, centroidskmeans, args.n_clusters,
                                          cluster_details)
        else:
            logging.debug("plotting standard graph")
            create_plot(reduced_vectors, labels, vector_names)
    # Write DOT diagram out to cluster.dot, designed for input into
        Gephi (https://gephi.org/)
    with open("cluster.dot", "w") as f:
        f.write(
            generate_dot_graph_for_gephi(precompute_distances(vectors,
                metric=args.metric), vector_names, labels))

elif args.twin == True and args.strategy == "automatic":

    logging.debug("twin flag enabled")
    logging.debug("tp: {0} , path: {1}".format(args.twinpath,
        args.path))

    # Vectorize our input for nessus
    logging.info("Vectorizing Stage for Nessus")
    Nvector_names, Nvectors, Nvectorizer = vectorize(args.path,
        args.nessus)
    logging.debug("Loaded {0} vectors with {1}
        features".format(len(Nvector_names), Nvectors.shape[1]))
    logging.info("Vectorizing complete\n")

    # Vectorize our input for nmap
```

```
logging.info("Vectorizing Stage for nmap")
twinpath = list()
twinpath.append(args.twinpath)
vector_names, vectors, vectorizer = vectorize(twinpath, False)
logging.debug("Loaded {0} vectors with {1}
    features".format(len(vector_names), vectors.shape[1]))
logging.info("Vectorizing complete\n")

# normalise vectors first before passing them through PCA. PCA uses
    2 dimensions
# nessus
logging.info("Normalising the nessus vectors")
Nnormalized_vectors = normalize(Nvectors)
logging.info("Reducing vectors to two dimensions with PCA")
Nreduced_vectors = pca(Nnormalized_vectors)
logging.debug(
    "reduced to {0} vectors with {1}
        dimensions".format((Nreduced_vectors.shape[0]),
        Nreduced_vectors.shape[1]))
logging.info("Normalising complete\n")

# normalise vectors first before passing them through PCA. PCA uses
    2 dimensions
# nmap
logging.info("Normalising the nmap vectors")
normalized_vectors = normalize(vectors)
logging.info("Reducing vectors to two dimensions with PCA")
reduced_vectors = pca(normalized_vectors)
logging.debug(
    "reduced to {0} vectors with {1}
        dimensions".format((reduced_vectors.shape[0]),
        reduced_vectors.shape[1]))
logging.info("Normalising complete\n")

# Cluster the vectors
logging.info("Clustering Nessus")
Nlabels = cluster(Nvector_names, Nvectors, Nreduced_vectors,
    Nnormalized_vectors, Nvectorizer, args.strategy,
                  args.method, args.n_clusters, args.epsilon,
                      args.min_samples, args.metric)
logging.info("Clustering Complete\n\n")
# Test cluster validity
Noverall_score, Nper_cluster_score = validate_clusters(Nvectors,
    Nlabels)

# Cluster the vectors
logging.info("Clustering Nmap")
```

```
labels = cluster(vector_names, vectors, reduced_vectors,
    normalized_vectors, vectorizer, args.strategy,
                 args.method, args.n_clusters, args.epsilon,
                     args.min_samples, args.metric)
logging.info("Clustering Complete\n\n")
# Test cluster validity
overall_score, per_cluster_score = validate_clusters(vectors,
    labels)

# Analysis relevant to the person reading results
# nessus
Nuniversal_positive_features, Nuniversal_negative_features,
    Nshared_features = get_common_features_from_cluster(
    Nvectors, Nlabels, Nvectorizer)

# Analysis relevant to the person reading results
# nmap
universal_positive_features, universal_negative_features,
    shared_features = get_common_features_from_cluster(
    vectors, labels, vectorizer)

# Reduce results and relevant information to per cluster data
# nessus
Ncluster_details = {}
for cluster_id in Nper_cluster_score.keys():
    Ncluster_details[cluster_id] = {
        "silhouette": Nper_cluster_score[cluster_id],
        "shared_positive_features":
            Nshared_features[cluster_id]['positive'],
        "ips": [Nvector_names[x] for x in xrange(len(Nvector_names))
            if Nlabels[x] == cluster_id]
    }
print "Note: shared features does not retain keys from XML and
    therefore wont always be human readable."
print "Printing Nessus cluster details\n"
print_cluster_details(Ncluster_details, Nshared_features)

print "\n\n"

# Reduce results and relevant information to per cluster data
cluster_details = {}
for cluster_id in per_cluster_score.keys():
    cluster_details[cluster_id] = {
        "silhouette": per_cluster_score[cluster_id],
        "shared_positive_features":
            shared_features[cluster_id]['positive'],
        # "shared_negative_features":
            shared_features[cluster_id]['negative'],
        "ips": [vector_names[x] for x in xrange(len(vector_names))
            if labels[x] == cluster_id]
    }
print "Printing Nmap cluster details\n"
print_cluster_details(cluster_details, shared_features)

if args.plot:
        # Nmap
        logging.debug("Getting centroids using reduced vectors for
            Nmap:")
        # take just cluster number from result string
        n_clusters = Nno_clusters.split("=", 1)[1]
        n_clusters = int(n_clusters.rsplit(')', 1)[0])
        logging.debug("nclusters: " + str(n_clusters))

        centroidskmeans = get_centroids(reduced_vectors, n_clusters)
        k = get_k()
        logging.debug("attempting to plot the following centroids:\n
            " + str(centroidskmeans) + "\n\n")

        # Nessus
        logging.debug("Getting centroids using reduced vectors for
            Nessus:")
        # take just cluster number from result string
        logging.debug("nclusters: " + str(Nno_clusters))

        Nn_clusters = no_clusters.split("=", 1)[1]
        Nn_clusters = int(Nn_clusters.rsplit(')', 1)[0])
        logging.debug("nclusters: " + str(Nn_clusters))

        Ncentroidskmeans = get_centroids(Nreduced_vectors,
            Nn_clusters)
        logging.debug("attempting to plot the following centroids:\n
            " + str(Ncentroidskmeans) + "\n\n")
        Nk = get_k()

        # covariance for Nmap
        x = centroidskmeans[:, 0]
        y = centroidskmeans[:, 1]
        X = np.vstack((x, y))
        cov = np.cov(X)
        logging.info("Nmap Centroids Covariance Matrix:\n
            {0}".format(cov))

        # covariance for Nessus
        Nx = Ncentroidskmeans[:, 0]
```

```
Ny = Ncentroidskmeans[:, 1]
NX = np.vstack((Nx, Ny))
Ncov = np.cov(NX)
logging.info("Nessus Centroids Covariance Matrix:\n
   {0}".format(Ncov))

# print similarity distance between centroids
# Nessus
matrix = precompute_distances(centroidskmeans,
   metric=args.metric)
matrixTable = tabulate(matrix)
logging.info(
    "distance matrix between centroids using metric for
       Nmap: {0} :\n{1}".format(args.metric, matrixTable))

# print similarity distance between centroids
# Nmap
Nmatrix = precompute_distances(Ncentroidskmeans,
   metric=args.metric)
NmatrixTable = tabulate(Nmatrix)
logging.info(
    "distance matrix between centroids using metric for
       Nessus: {0} :\n{1}".format(args.metric,
       NmatrixTable))

small_ips = remove_large_clusters()

logging.info("IP's from clusters with less than 3 IP's:\n
   {0}".format((small_ips)))


#creates large array with 2nd dimension as large enough to
   hold both feature vectors
nesmap = np.zeros((len(small_ips),
    (Nvectors.shape[1]+vectors.shape[1])))


#for each single ip
for index in range(len(small_ips)):
    # for each ip in vectors
    features = 0
    for index2 in range(vectors.shape[0]):
        #if ip is equal to vector ip
        #logging.debug("if {0} = {1}
           ".format(small_ips[index], vector_names[index2]))
        if small_ips[index] == vector_names[index2]:
           #logging.debug("ip is equal to vector ip")
```

```
                #for every one of this vectors features
                for index3 in range(vectors.shape[1]):
                    #assign its features to single ip vector
                    nesmap[index,features] = vectors[index2,
                        index3]
                    features +=1
                break

        for index2 in range(Nvectors.shape[0]):
            #logging.debug("if {0} = {1}
                ".format(small_ips[index], Nvector_names[index2]))
            if small_ips[index] == Nvector_names[index2]:
                #logging.debug("ip is equal to vector ip")
                for index3 in range(Nvectors.shape[1]):
                    #append nessus features onto nmap features
                    nesmap[index,features] = Nvectors[index2,
                        index3]
                    features += 1
                break

logging.debug("Loaded {0} vectors with {1}
    features".format(nesmap.shape[0], nesmap.shape[1]))
small_normalized_vectors = normalize(nesmap)
logging.info("Normalizing input and reducing vectors to two
    dimensions with PCA")
final = pca(small_normalized_vectors)

logging.info("Resulting single IP vectors:\n
    {0}".format(final))

Smatrix = precompute_distances(final, metric=args.metric)
SmatrixTable = tabulate(Smatrix)
logging.info(
    "distance matrix between centroids of small combined
        clusters: {0} :\n{1}".format(args.metric,
        SmatrixTable))
clusterz = cluster_single_kmeans(final, 2)

logging.info("Writing recommended attack IP's to targets.txt
    for exploitation\n {0}")
f = open('targets.txt', 'w')
for index in range(len(small_ips)):
    f.write('{0}\n'.format(small_ips[index])) # python will
        convert \n to os.linesep
f.close() # you can omit in most cases as the destructor
    will call it
```

```
            twin(reduced_vectors, labels, vector_names, centroidskmeans,
               n_clusters, cluster_details, Nreduced_vectors, Nlabels,
               Nvector_names, Ncentroidskmeans, Nn_clusters,
               Ncluster_details, small_ips, final, clusterz, twinpath)

    else: print "not yet implemented #todo"
```

A.4 vectorization class - vectorize.py

The following contains the raw code for the vectorize.py class. This class is called by the main cluster.py class at appendix A.3 in order to extract the information from the scan files as well as vectorize that information to be returned to the primary class.

```
import logging
from parsing import parsers
from parse_nessus import Nparsers
from single_ip_parsing_nmap import single_ip_parsers
import numpy as np


class Vectorizer:
    """
    This class handles the vectorizing of input
    It additionally stores all pseudo vectors until we are ready for the
       finished vectors
    """

    def __init__(self):
        self.tokenized_strings = []
        self.pseudo_vectors = {}

    def add_string_to_ip(self, ip, string):
        if ip not in self.pseudo_vectors:
            self.pseudo_vectors[ip] = []

        if string not in self.tokenized_strings:
            self.tokenized_strings.append(string)

        s_id = self.tokenized_strings.index(string)
        self.pseudo_vectors[ip].append(s_id)

    def parse_input(self, input_string, n):
    ##n boolean value refers to nessus input only
        if (n==True):
            for parser in Nparsers:
```

```
            if parser.can_parse_input(input_string):
                results = parser.parse_input(input_string)
                for key in results.keys():
                    for s in results[key]:
                        self.add_string_to_ip(key, s)
        else:
            for parser in parsers:
                if parser.can_parse_input(input_string):
                    results = parser.parse_input(input_string)
                    for key in results.keys():
                        for s in results[key]:
                            self.add_string_to_ip(key, s)

    def output_vectors(self):
        vector_names = []
        vectors = np.zeros((len(self.pseudo_vectors.keys()),
            len(self.tokenized_strings)), dtype=np.float)

        for ip_index, ip in enumerate(self.pseudo_vectors.keys()):
            vector_names.append(ip)
            for s_index in self.pseudo_vectors[ip]:
                # Just set it to one, we want to ignore any case we see a
                    value more than once
                vectors[ip_index, s_index] = 1

        return vector_names, vectors


def vectorize(files_to_vectorize, n):
    vectorizer = Vectorizer()
    for file_path in files_to_vectorize:
        with open(file_path, "r") as f:
            vectorizer.parse_input(f.read(), n)

    vector_names, vectors = vectorizer.output_vectors()

    return vector_names, vectors, vectorizer

def parse_single_ips(files_to_vectorize, ips):
    for file_path in files_to_vectorize:
        with open(file_path, "r") as f:
            for parser in single_ip_parsers:
                #logging.debug("vectorisor selecting single ips")
                results = parser.parse_input(f.read(), ips)
                return results
```

A.5 Clustering Algorithm subclass

The following code consists of the clustering algorithm used for all the modes within the application. It uses the provided parameters to decide between these modes as well as calls several other subclasses for code modularity.

```
def cluster(
        vector_names,
        vectors,
        reduced_vectors,
        normalized_vectors,
        vectorizer,
        strategy="automatic",
        cluster_method="kmeans",
        n_clusters=2,
        epsilon=0.5,
        min_samples=5,
        metric="euclidean",
):
    """
    Clustering options:

    Manual:
     The user supplies all required information to do the clustering. This
         includes the clustering algorithm and
     hyper parameters,
     if no cluster count is provided the gap_statistic method will be used
         to calculate the optimal cluster count

    Assisted:
     The user assists the algorithm by suggesting that some samples should
         or should not be clustered together

    Automatic:
     The multiple clustering strategies and parameters are used in an
         attempt to get the best clusters

     finds the least amount of clusters with atleast one shared feature

     only uses gap statistic for small IP clusters
    """

    global centroidskmeans, centroidagglo, centroiddbs, no_clusters,
        Nno_clusters, Ncentroidskmeans
```

```
if strategy == "manual":
    no_clusters = ""
    if cluster_method == "kmeans":
        #centroidskmeans = get_centroids(reduced_vectors,
            n_clusters=n_clusters)
        #logging.debug("centroids for kmeans:
            {0}".format(centroidskmeans))
        k, gapdf = optimalK(vectors, nrefs=3,
            maxClusters=reduced_vectors.shape[0])
        return cluster_with_kmeans(reduced_vectors, n_clusters=k)

    elif cluster_method == "dbscan":
        return cluster_with_dbscan(reduced_vectors, epsilon=epsilon,
            min_samples=min_samples, metric=metric)

    elif cluster_method == "agglomerative":
        return cluster_with_agglomerative(reduced_vectors,
            n_clusters=n_clusters, metric=metric)

    else:
        # Unknown clustering method
        raise NotImplementedError()

elif strategy == "assisted":
    """
    To display a information about a vector to a user, you can use the
        following:
    display_vector_index_details(vector_index, vectors, vector_names,
        vectorizer)
    """

    return cluster_interactive(reduced_vectors, vectorizer, vectors,
        vector_names)
elif strategy == "automatic":
    results = []
    smallest_cluster_count = vectors.shape[0]
    # centroids works for only kmeans atm
    for cluster_method in [
        #todo add agglo and dbscan back in after they can return
            centroids.
        "kmeans" # ,
        # "agglomerative",
        # "dbscan",
    ]:
        if cluster_method == "kmeans":
            #this method is called X-means clustering
            logging.debug("Starting prospective KMeans clusterings")
```

```
move_to_next_method = False
# start at 2 clusters and end at smallest_cluster_count
for n_clusters in xrange(2, smallest_cluster_count):
    logging.debug("Trying
       {0}".format("kmeans(n_clusters={0})".format(n_clusters)))
    labels = cluster_with_kmeans(reduced_vectors,
       n_clusters=n_clusters)
    overall_score, per_cluster_score =
       validate_clusters(vectors, labels)
    mean_distance =
       get_average_distance_per_cluster(vectors, labels)[0]

    tsp, msp, msn = get_common_feature_stats(vectors,
       labels, vectorizer)

    # If any cluster has 0 shared features, we just ignore
       the result
    if msp <= tsp:
        logging.debug("Not all clusters are informative (a
           cluster has 0 shared features) ")
        continue
    if len(set(labels)) > smallest_cluster_count:
        move_to_next_method = True
        # logging.debug("len(set(labels)): {0} >
           smallest_cluster_count:
           {1}".format(len(set(labels)),
           smallest_cluster_count))
        break
    if len(set(labels)) < smallest_cluster_count:
        smallest_cluster_count = len(set(labels))
    #too verbose
    # logging.debug(repr((
    #        overall_score,
    #        min(per_cluster_score.values()),
    #        mean_distance,
    #        labels,
    #        len(set(labels)),
    #        tsp,
    #        msp,
    #        msn,
    #        "kmeans(n_clusters={0})".format(n_clusters)
    #    )))
    results.append(
        (
            overall_score,
            min(per_cluster_score.values()),
            mean_distance,
                        labels,
                        len(set(labels)),
                        tsp,
                        msp,
                        msn,
                        "kmeans(n_clusters={0})".format(n_clusters)
                    )
                )
            if move_to_next_method:
                continue

        if cluster_method == "agglomerative":
            logging.debug("Starting prospective Agglomerative
                clusterings")
            move_to_next_method = False
            for n_clusters in xrange(2, smallest_cluster_count):
                logging.debug("Trying
                    {0}".format("agglomerative(n_clusters={0})".format(n_clusters)))
                labels = cluster_with_agglomerative(reduced_vectors,
                    n_clusters=n_clusters, metric=metric)
                overall_score, per_cluster_score =
                    validate_clusters(vectors, labels)
                mean_distance =
                    get_average_distance_per_cluster(vectors, labels)[0]

                tsp, msp, msn = get_common_feature_stats(vectors,
                    labels, vectorizer)

                # If any cluster has 0 shared features, we just ignore
                    the result
                if msp <= tsp:
                    logging.debug("Not all clusters are informative (a
                        cluster has 0 shared features) ")
                    continue
                if len(set(labels)) > smallest_cluster_count:
                    move_to_next_method = True
                    break
                if len(set(labels)) < smallest_cluster_count:
                    smallest_cluster_count = len(set(labels))

                logging.debug(repr((
                    overall_score,
                    min(per_cluster_score.values()),
                    mean_distance,
                    labels,
                    len(set(labels)),
                    tsp,
                msp,
                msn,
                "agglomerative(n_clusters={0})".format(n_clusters)
            )))
            results.append(
                (
                    overall_score,
                    min(per_cluster_score.values()),
                    mean_distance,
                    labels,
                    len(set(labels)),
                    tsp,
                    msp,
                    msn,
                    "agglomerative(n_clusters={0})".format(n_clusters)
                )
            )
        if move_to_next_method:
            continue

    if cluster_method == "dbscan":
        logging.debug("Starting prospective DBSCAN clusterings")
        distance_matrix = precompute_distances(vectors,
            metric=metric)
        min_distance =
            sorted(set(list(distance_matrix.flatten())))[1]
        max_distance =
            sorted(set(list(distance_matrix.flatten())))[-1]
        num_steps = 25.0
        step_size = float(max_distance - min_distance) /
            float(num_steps)
        epsilon = min_distance
        while True:
            logging.debug("Trying
                {0}".format("dbscan(epsilon={0})".format(epsilon)))
            labels = cluster_with_dbscan(reduced_vectors,
                epsilon=epsilon, min_samples=1,
                                        distances=distance_matrix)
            if len(set(labels)) == 1 and list(set(labels))[0] == 0:
                break
            overall_score, per_cluster_score =
                validate_clusters(vectors, labels)
            mean_distance =
                get_average_distance_per_cluster(vectors, labels)[0]

            tsp, msp, msn = get_common_feature_stats(vectors,
                labels, vectorizer)
            # If any cluster has 0 shared features, we just ignore
                the result
            if msp <= tsp:
                logging.debug("Not all clusters are informative (a
                    cluster has 0 shared features) ")
                epsilon += step_size
                continue

            logging.debug(repr((
                overall_score,
                min(per_cluster_score.values()),
                mean_distance,
                labels,
                len(set(labels)),
                tsp,
                msp,
                msn,
                "dbscan(epsilon={0})".format(epsilon)
            )))
            results.append(
                (
                    overall_score,
                    min(per_cluster_score.values()),
                    mean_distance,
                    labels,
                    len(set(labels)),
                    tsp,
                    msp,
                    msn,
                    "dbscan(epsilon={0})".format(epsilon)
                )
            )
            epsilon += step_size

# Choose best clustering result based on the following attributes
sorted_results = sort_items_by_multiple_keys(
    results,
    {
        # 0: True, # AVG Silhouette
        # 1: True, # Min Silhouette
        # 2: False, # Average distance
        4: False, # Number of clusters
        # 6: True,  # Min common features per cluster
    },
    {
        # 0: 1,
                # 1: 1,
                # 2: 1,
                4: 1,
                # 6: 1
            }
        )
        # logging.debug(sorted_results)
        best_result = results[sorted_results[0][0]]
        # logging.debug(best_result)

        best_method = best_result[-1]
        best_silhouette = best_result[0]
        best_labels = best_result[3]
        global firstpass
        if firstpass:
            no_clusters = best_result[-1]
            firstpass = False
        else:
            Nno_clusters = best_result[-1]

        # no_clusters = best_result[-1]

        logging.info("Best clustering method: {0} (adjusted silhouette ==
            {1})".format(best_method, best_silhouette))
        return best_labels

    else:
        # Unknown strategy
        raise NotImplementedError()
```

Appendix B

Example Application Output

B.1 Fictional Small Network Output

This output was generated by running the application in automatic, verbosity level 2, twin input with graph plotting mode. The command used to execute the application with this configuration is as follows:

```
cluster.py -s automatic -vv -p -t -N -tp ../cw.xml ../cw.nessus
```

The network in which the scans were taken place is an entirely fictional and uses four machines in the scope. This scope is described below.

Table B.1: Fictional Network Scope and Machine Descriptions

192.168.0.1	Windows 2008 server running Apache 2 web server with MySQL database. Hosting a DNS server. Domain Controller for UADTARGETNET domain running Lightweight Directory Access Protocol NETBIOS name: SERVER1
192.168.0.2	Windows 2008 server running empty web server and hosting a DNS server running Lightweight Directory Access Protocol NETBIOS name: SERVER2
192.168.0.10	Windows 7 Professional 7600 (Windows 7 Professional 6.1) NETBIOS name: CLIENT1
192.168.0.11	Windows 7 Professional 7600 (Windows 7 Professional 6.1) NETBIOS name: CLIENT2

B.1.1 Text Output

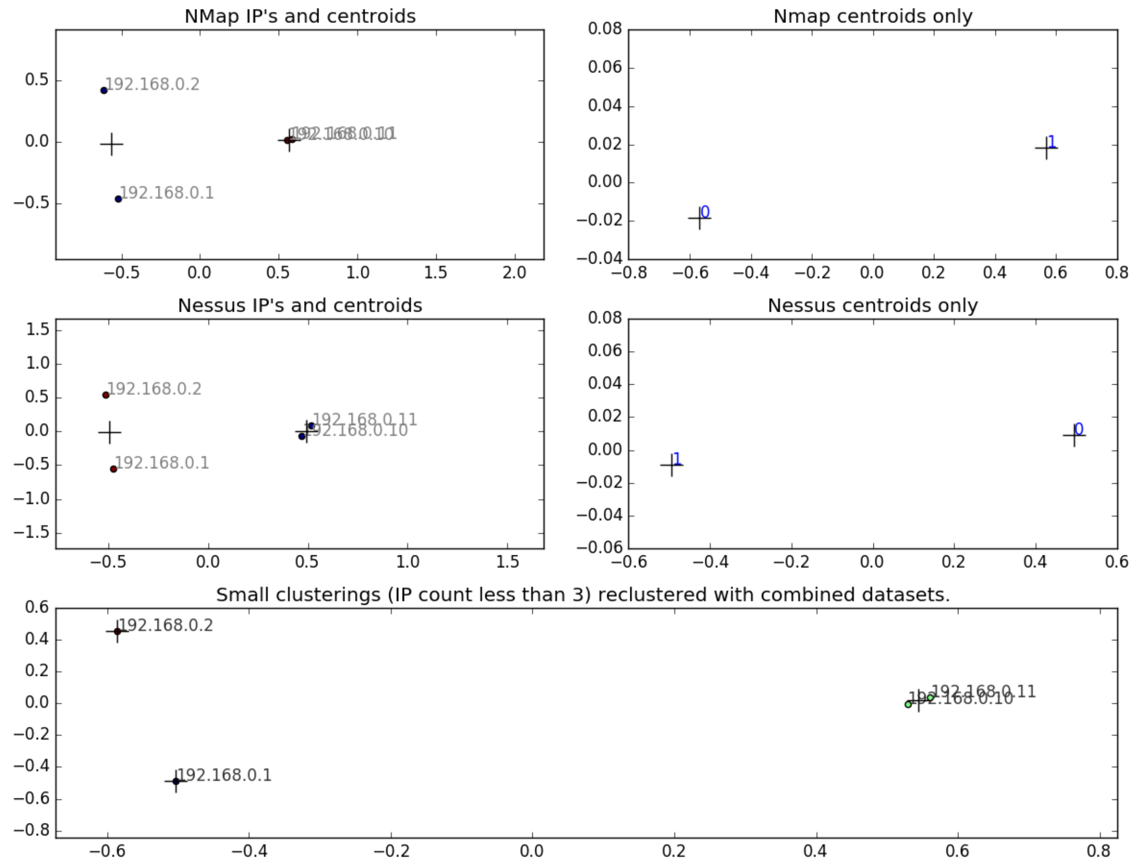
```
04-19 01:32 19624 cluster <module> DEBUG :twin flag enabled
04-19 01:32 19624 cluster <module> DEBUG :tp: ../cw.xml , path: ['../cw.nessus']
04-19 01:32 19624 cluster <module> INFO :Vectorizing Stage for Nessus
04-19 01:32 19624 parse_nessus parse_input INFO :Parsing Nessus XML * BETA *
no of IP's taken from nessus: 4
04-19 01:32 19624 parse_nessus parse_input INFO :Done Nessus parsing
04-19 01:32 19624 cluster <module> DEBUG :Loaded 4 vectors with 45 features
04-19 01:32 19624 cluster <module> INFO :Vectorizing complete

04-19 01:32 19624 cluster <module> INFO :Vectorizing Stage for nmap
no of IP's taken from NMAP: 4
04-19 01:32 19624 cluster <module> DEBUG :Loaded 4 vectors with 81 features
04-19 01:32 19624 cluster <module> INFO :Vectorizing complete

04-19 01:32 19624 cluster <module> INFO :Normalising the nessus vectors
04-19 01:32 19624 cluster <module> INFO :Reducing vectors to two dimensions with PCA
04-19 01:32 19624 cluster <module> DEBUG :reduced to 4 vectors with 2 dimensions
04-19 01:32 19624 cluster <module> INFO :Normalising complete

04-19 01:32 19624 cluster <module> INFO :Normalising the nmap vectors
04-19 01:32 19624 cluster <module> INFO :Reducing vectors to two dimensions with PCA
04-19 01:32 19624 cluster <module> DEBUG :reduced to 4 vectors with 2 dimensions
04-19 01:32 19624 cluster <module> INFO :Normalising complete

04-19 01:32 19624 cluster <module> INFO :Clustering Nessus
04-19 01:32 19624 cluster cluster DEBUG :Starting prospective KMeans clusterings
04-19 01:32 19624 cluster cluster DEBUG :Trying kmeans(n_clusters=2)
04-19 01:32 19624 cluster cluster DEBUG :Trying kmeans(n_clusters=3)
04-19 01:32 19624 cluster cluster INFO :Best clustering method: kmeans(n_clusters=2) (adjusted
     silhouette == 0.176059056707)
04-19 01:32 19624 cluster <module> INFO :Clustering Complete


04-19 01:32 19624 cluster <module> INFO :Clustering Nmap
04-19 01:32 19624 cluster cluster DEBUG :Starting prospective KMeans clusterings
04-19 01:32 19624 cluster cluster DEBUG :Trying kmeans(n_clusters=2)
04-19 01:32 19624 cluster cluster DEBUG :Trying kmeans(n_clusters=3)
04-19 01:33 19624 cluster cluster INFO :Best clustering method: kmeans(n_clusters=2) (adjusted
     silhouette == 0.441640409673)
04-19 01:33 19624 cluster <module> INFO :Clustering Complete


Note: shared features does not retain keys from XML and therefore wont always be human readable.
Printing Nessus cluster details

Cluster ID: 0
Silhouette Score: 0.299967117317
IPs: 192.168.0.10, 192.168.0.11

    Shared Features:
    general-purpose
    windows
    445
    cpe:/o:microsoft:windows_7:::professional
    Mon Apr 03 11:25:23 2017
    Microsoft Windows 7 Professional
    9
    5355



Cluster ID: 1
Silhouette Score: 0.0521509960965
IPs: 192.168.0.1, 192.168.0.2

    Shared Features:
    Mon Apr 03 11:25:06 2017
    cpe:/o:microsoft:windows
    general-purpose
    windows
    53
    23
    445



cluster ID : amount of IP's
0 : 2
1 : 2



Printing Nmap cluster details

Cluster ID: 0
Silhouette Score: 0.213624573736
IPs: 192.168.0.1, 192.168.0.2

    Shared Features:
    tcp23opentelnet
    tcp42opentcpwrapped
    tcp53opendomain
    tcp80openhttp
    tcp88openkerberos-sec
    tcp135open
    tcp139open
    tcp389open
    tcp445open
    tcp464open
    tcp593open
    tcp636opentcpwrapped
    tcp3268open
    tcp3269opentcpwrapped
    tcp49152open
    tcp49153open
    tcp49154open
    tcp49155open
    tcp49157open
    tcp49158open



Cluster ID: 1
Silhouette Score: 0.66965624561
IPs: 192.168.0.10, 192.168.0.11

    Shared Features:
    tcp135openmsrpcMicrosoft Windows RPC
    tcp139opennetbios-ssnMicrosoft Windows 98 netbios-ssn
    tcp445openmicrosoft-dsMicrosoft Windows 10 microsoft-ds
    tcp49152openmsrpcMicrosoft Windows RPC
    tcp49153openmsrpcMicrosoft Windows RPC
    tcp49154openmsrpcMicrosoft Windows RPC
    tcp49175openmsrpcMicrosoft Windows RPC
    tcp49176openmsrpcMicrosoft Windows RPC



cluster ID : amount of IP's
0 : 2
1 : 2
04-19 01:33 19624 cluster <module> DEBUG :Getting centroids using reduced vectors for Nmap:
04-19 01:33 19624 cluster <module> DEBUG :nclusters: 2
04-19 01:33 19624 clustering get_centroids DEBUG :K = 0
```

```
04-19 01:33 19624 cluster <module> DEBUG :attempting to plot the following centroids:
 [[-0.56736301 -0.01841586]
 [ 0.56736301 0.01841586]]


04-19 01:33 19624 cluster <module> DEBUG :Getting centroids using reduced vectors for Nessus:
04-19 01:33 19624 cluster <module> DEBUG :nclusters: kmeans(n_clusters=2)
04-19 01:33 19624 cluster <module> DEBUG :nclusters: 2
04-19 01:33 19624 clustering get_centroids DEBUG :K = 0

04-19 01:33 19624 cluster <module> DEBUG :attempting to plot the following centroids:
 [[-0.49416507 -0.0089938 ]
 [ 0.49416507 0.0089938 ]]


04-19 01:33 19624 cluster <module> INFO :Nmap Centroids Covariance Matrix:
 [[ 0.64380156 0.02089695]
 [ 0.02089695 0.00067829]]
04-19 01:33 19624 cluster <module> INFO :Nessus Centroids Covariance Matrix:
 [[  4.88398234e-01  8.88884549e-03]
 [  8.88884549e-03  1.61776945e-04]]
04-19 01:33 19624 cluster <module> INFO :distance matrix between centroids using metric for Nmap:
     euclidean :
------- -------
0       1.13532
1.13532 0
------- -------
04-19 01:33 19624 cluster <module> INFO :distance matrix between centroids using metric for Nessus:
     euclidean :
-------- --------
0        0.988494
0.988494 0
-------- --------
04-19 01:33 19624 cluster <module> INFO :IP’s from clusters with less than 3 IP’s:
 [’192.168.0.1’ ’192.168.0.10’ ’192.168.0.11’ ’192.168.0.2’]
04-19 01:33 19624 cluster <module> DEBUG :Loaded 4 vectors with 126 features
04-19 01:33 19624 cluster <module> INFO :Normalizing input and reducing vectors to two dimensions
     with PCA
04-19 01:33 19624 cluster <module> INFO :Resulting single IP vectors:
 [[-0.50300301 -0.49063882]
 [ 0.52888708 -0.00269094]
 [ 0.56066029 0.03834554]
 [-0.58654436 0.45498422]]
04-19 01:33 19624 cluster <module> INFO :distance matrix between centroids of small combined
     clusters: euclidean :
-------- --------- --------- --------
0        1.14144   1.18794   0.949306
1.14144  0         0.0518992 1.20568
1.18794  0.0518992 0         1.22052
0.949306 1.20568   1.22052   0
-------- --------- --------- --------
04-19 01:33 19624 clustering cluster_single_kmeans INFO :Calculating gap statistic value, this can
     take a while...

04-19 01:33 19624 clustering cluster_single_kmeans INFO :gap statistics recommends number of
     clusters: 3

04-19 01:33 19624 clustering cluster_single_kmeans DEBUG :No K value specified, using Gap Statistic

04-19 01:33 19624 cluster <module> INFO :Writing recommended attack IP’s to targets.txt for
     exploitation
 {0}
04-19 01:33 19624 display twin DEBUG :twin cluster plot.
04-19 01:33 19624 single_ip_parsing_nmap parse_input DEBUG :found ip 192.168.0.1
04-19 01:33 19624 single_ip_parsing_nmap parse_input DEBUG :found ip 192.168.0.2
04-19 01:33 19624 single_ip_parsing_nmap parse_input DEBUG :found ip 192.168.0.10
04-19 01:33 19624 single_ip_parsing_nmap parse_input DEBUG :found ip 192.168.0.11
```

```
04-19 01:33 19624 display twin DEBUG :{'192.168.0.2': ['"Microsoft Windows 7 SP0 - SP1, Windows
    Server 2008 SP1, Windows 8, or Windows 8.1 Update 1. Prediction accuracy: 100"'], '192.168.0.1':
    [], '192.168.0.10': ['"Microsoft Windows 7 SP0 - SP1, Windows Server 2008 SP1, Windows 8, or
    Windows 8.1 Update 1. Prediction accuracy: 100"'], '192.168.0.11': ['"Microsoft Windows 7 SP0 -
    SP1, Windows Server 2008 SP1, Windows 8, or Windows 8.1 Update 1. Prediction accuracy: 100"']}
```

B.1.2 Graphing Interface Output

The Figure B.1 below shows the example graphing interface output using the configuration mentioned previously in Appendix B.1.



Recommended attack vectors:
192.168.0.2 : "Microsoft Windows 7 SP0 - SP1, Windows Server 2008 SP1, Windows 8, or Windows 8.1 Update 1. Prediction accuracy: 100"
192.168.0.1 : OS detection failed, Didn't receive UDP response
192.168.0.10 : "Microsoft Windows 7 SP0 - SP1, Windows Server 2008 SP1, Windows 8, or Windows 8.1 Update 1. Prediction accuracy: 100"
192.168.0.11 : "Microsoft Windows 7 SP0 - SP1, Windows Server 2008 SP1, Windows 8, or Windows 8.1 Update 1. Prediction accuracy: 100"

Figure B.1: Example of graphing interface GUI from a fictional network to be used in conjunction with text output at ??

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