

**Integrated Deep Learning and Bayesian Classification
for Prioritization of Functional Genes in
Next-Generation Sequencing Data**

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A thesis submitted to the
Department of Biochemistry
National University of Singapore
in partial fulfilment for the
Degree of Bachelor of Science with
Honours in Life Sciences

Life Sciences Honours Cohort
AY2015/2016 S1

DECLARATION

I hereby declare that this thesis is my original work and it has been written by me in its entirety. I have duly acknowledged all the sources of information which have been used in the thesis.

This thesis has also not been submitted for any degree in any university previously.

Chan Khai Ern Edwin

04 April 2017

Acknowledgements

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Abstract

1 Introduction

1.1 Next Generation Sequencing in Personal Genomics Pipelines

Identification of functionally important mutations is a critical step in enabling personal genomic pipelines. Recently, there has been great interest in using a persons genome to help doctors treat and diagnose disease (Rehm, 2017;Angrist, 2016). The fundamental intuition is that sequencing the person’s genome can help doctors and clinicians narrow down important disease subtypes and progression. This enables doctors to better diagnose the disease, as well as prepare targeted medication to treat the specific disease. This is of particular interest now, especially since it is possible to sequence an exome for about \$1,000 - a price similar to most other clinical procedures. In this sequencing, also known as Next-Generation Sequencing(NGS), a sample of the patients genome is sequenced in parallel to enable a rapid whole-exome sequence (Metzker, 2010; Mardis, 2008).

However, there are still two critical steps that prevent this data from being used treat and diagnose patients. Firstly, we need to be able to obtain high confidence mutations from this sequencing data, and secondly there needs to be a method to prioritise these mutations for clinicians and doctors. For the first problem we have to be able to find out mutations in the persons genome that is different from a reference genome. This step is termed in literature as variant calling as it involves the discovery (calling) of genes (variants) that differ from a reference genome. However, current variant callers still tend to have low concordances for variants called (O’Rawe et al., 2013; Cornish and Guda, 2015), primarily due to differences in variant calling algorithms and assumptions. The second problem, ranking of mutations is critical as these variant callers do not take into account the importance of each variants. Thus, an additional step must be taken to attempt to find out which might be the most important genes for clinicians. This is critical a clinician should be able to obtain variants that are of clinical significance without having to sieve through literature to manually pick out genes that important. This would allow them to narrow their search to the most likely candidate dates, and then be able to embark on the most ideal treatment pathway.

In this paper, we describe a machine learning approach to solve these two problems - specifically using deep learning to validate high confidence variant calls, and using Bayesian networks to filter variants and prioritise their importance.

1.2 Variant Calling in Personal Genomics Pipelines

Here, it is useful to analyse variant calling and the problems that make it difficult. Variant calling in NGS data primarily involves the use of various statistical and mathematical methods to discover variants, or mutations, in the genome (Nielson et al., 2011). Calling variants allows the analysis of deviations and differences between the genome of interest and a standard human genome. However, this is not a trivial problem as for every call involves the analysis of a complex amount of information (Zook et al., 2014). This comes from the large amount of information that is created from NGS data - because sequencing is done by mapping a large number of reads together, calling specific mutations becomes a difficult problem. For example, if we look a typical pileup of a variant call involves, we can visualise the complexities that go into a variant call.

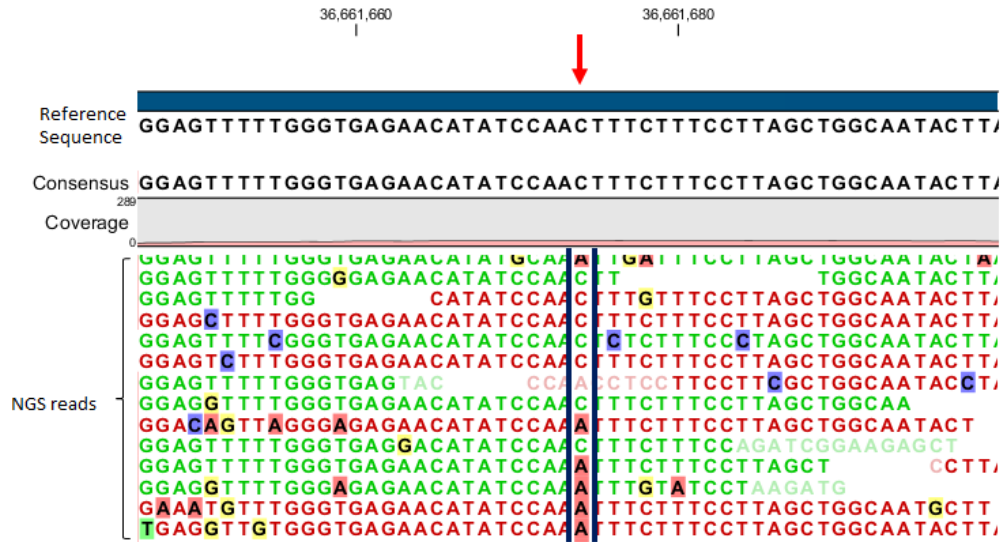


Figure 1: Variant Calling Pileup - Due to noise and errors in sequencing and variant mapping, it is sometimes difficult properly call variants. Figure adapted from: CLC Genomics Workbench 9.5, Figure 29.8

As can be seen from the graph, at any location there might be a number of reads with a competing bases. Some reads might have been wrongly mapped, while other reads might

be sequenced wrongly. The difficulty for the variant caller then is to be able to look at these types of reads and form a decision on whether it should be called as a variant or not (Davey et al., 2011; O’Rawe et al., 2013). Furthermore, because the variant callers do not have differential methods and algorithms depending on the types of sequencing machine used, it is difficult for them to make good decisions in all types of variant calls due to differences in noise, bias and error structures. Thus, there are still areas for improvement in current variant calling methods, including dealing with different classes of mutations, as well as reducing the number of false positives (Mohiyuddin, et al., 2015; Gzsi et al., 2015).

Both these problems fundamentally result from assumptions and implementations of variant callers - certain algorithms are more sensitive and accurate in calling certain classes of mutations, but suffer from inaccuracies in calling other variant types and edge cases. Probabilistic haplotype generating callers (such as GATK’s haplotype caller and FreeBayes) tend to be more accurate for SNPs and indels (McKenna et al. 2010; Garrison & Marth, 2012). They perform de-novo local assembly, where they rebuild small portions of the genome, and subsequently use bayesian analysis to determine the existence of variants. Specifically, they generate short haplotypes of local regions from sampled sequences, and determine (based on the haplotypes and prior probabilities in the reference genome) whether a variant should be called. However, these methods can only handle limited window sizes, preventing the detection of larger structural variants. For these we have to rely on other tools that examine larger segments of the genome (Ning et al., 2009) or use libraries of known mutation regions, and study these breakpoints to check if any mutations have occurred (Gerstein et al., 2015). Due to the heterogeneity in mutations as well as the presence of errors and noise, no single caller works best for all classes of mutations, pointing towards a variant calling framework that aggregates data from multiple callers.

1.3 Deep Learning in Variant Calling Methodology

Thus, one large hurdle to overcome in enabling personal genomic pipelines is the generation of high quality variant calls. Indeed, studies have shown low concordances between variant callers themselves, due to their specific implementations and algorithms (Mohiyuddin, et al., 2015; Gzsi et al., 2015). If we consider that each variant caller samples from the same

genome but with a different statistical technique, then we can see each variant caller as a mode of data that provides us with a unique piece of information on the genome. Thus, we can generate more accurate calls by aggregating the multi-modal data from various callers, allowing us to cross validate the variants called using multiple techniques.

The simplest approach to aggregate data is concordance - if multiple variant callers are able to call a variant, it is most likely to be accurate. However, the recall of such a tool would be poor due to the differential sensitivity of callers to edge cases, resulting in a lot of false negatives as true variant calls might only be picked up by one or two calling methodologies. This would defeat the purpose of using multiple callers in the first place, as the strength of a combinatorial approach lies in tapping into the sensitivities of different callers. More sophisticated efforts have since been done to use machine learning methods such as Support Vector Machines as a way to integrate variant calling information (Gzsi et al., 2015), and the authors showed that SVMs presented an improvement over concordance based methods. However, with the advent of deep learning techniques and libraries, which have been shown be able to integrate complex multi-modal information to solve problems (Ng et al., 2015), we hypothesize that deep learning can also be used to integrate the information from variant callers.

Deep learning is a method of machine learning that involves deep stacks of artificial neural networks. These neural networks were inspired by the way our synapses work in the brain, and are represented in silico by input/output nodes that fire when a certain threshold is reached. Thus, these neural networks are able to simulate learning - by learning from labelled data correlations between inputs and outputs, these networks are able to predict outputs if given a new input.

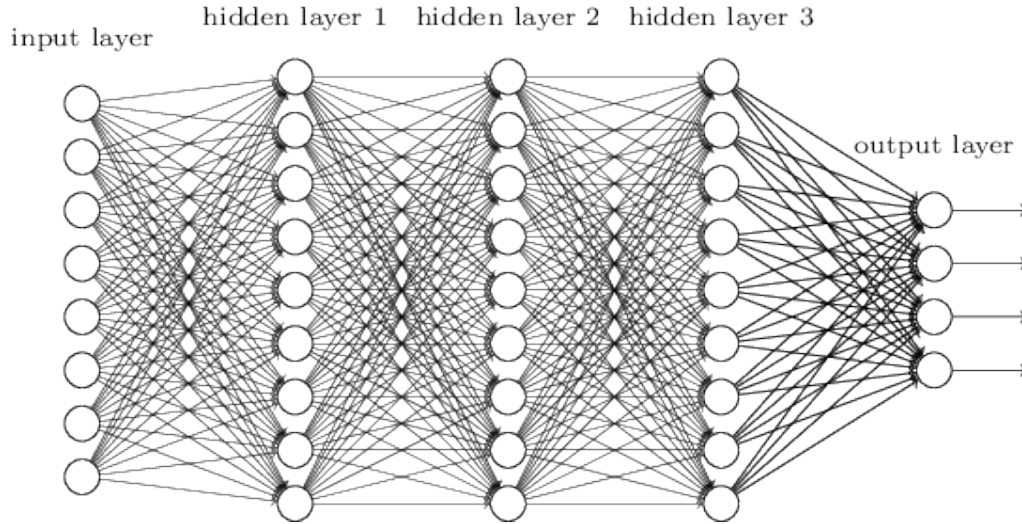


Figure 2: A Neural Network with 1 input layer, 3 hidden layers and 1 output layer. This represents a densely connected neural network, where each node is connected to every node of the preceding and subsequent layers. At each node, linking functions can be defined to connect the input and output.

Figure 1 depicts a sample neural network with 5 layers, with 8 data points as input, and 3 data points as output. In such a network, we would train it by providing the input data and output data, and letting the network learn how to integrate the inputs to create a network of activations that can be used to produce the corresponding output. In variant calling, deep learning will allow us to predict based on variant calling features and data whether a variant is valid and exists, or is erroneous. This will allow us to draw of the diversity of data with different variant callers, through letting the network learn which patterns will result in a valid call and which patterns are actually false positives. It will also allow us to tap on the differential sensitivity of different callers, as the neural network is able to learn which callers work best for which types of mutations. Thus, such a combinatorial approach will allow us to improve the accuracy and precision of variant calling.

1.4 Bayesian Networks in Gene Prioritisation

The second problem of enabling personal genomic pipelines is gene prioritisation. The problem of gene prioritisation arises because there are a multitude of data sources we can draw on to analyse how important a gene is. The possible approaches include studying previously characterised variants and their phenotypic effects on a person, studying how

the mutation itself will affect protein function through studying the likelihood of amino acid mutation for conserved regions and so on. These functional annotations can be done with the tool ANNOVAR, but the fundamental problem here is integrating such information in a systematic manner that is clear and understandable to clinicians. Clinicians may not be so familiar with the tools and functional annotation pipelines, but yet in order for them to trust such a ranking system they have to be able to intuitively understand how it works. As such, to solve this problem, we use Bayesian networks to integrate the information from functional annotations as well as the confidence of a call (how likely it is real) to provide a ranking system for how likely the gene is going to be important. Bayesian networks were chosen for this ranking system as it is understandable and yet have proven stable in terms of solving decision making problems (Pourret et al., 2008; Jensen et al., 1996). Bayesian networks have been applied in medical treatment decision making (Windecker et al., 2014), ecological studies (Johnson et al., 2014) and even predictive epidemiology (Su et al., 2014). A Bayesian network is a network that records the probabilities of events, and based on conditional probabilities and observations it updates the final likelihood of an event. This can be seen in Figure 2.

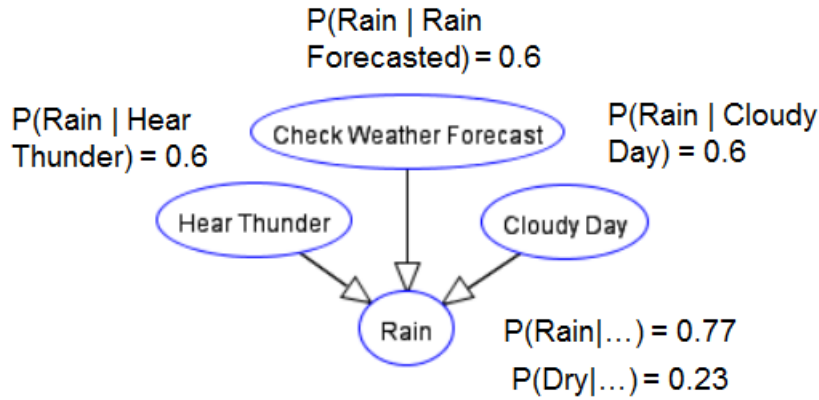


Figure 3: A Sample Bayesian Network for Rain Prediction.

Here, we would like to predict how likely it is to rain. Thus, we record observations (we hear thunder, check the weather forecast, notice it is a cloudy day) and updating the likelihood of rain happening based on the conditional probabilities of $P(\text{Rain} | \text{Hear Thunder})$... and so on. This model of learning was chosen because a Bayesian Network closely mimics the way Humans think - we observe events and form co-relational and causative predictions based on those events. This is advantageous over deep learning as in deep learning we are

unable to interrogate the system to intuitively understand what the network is learning from - it has high predictive power but is essentially a black-box. The Bayesian network allows clinicians and doctors to see what are the components that went into gene ranking and prioritisation, and even change the probabilities, weightage or add more observation nodes based on their own diagnosis and treatment models and ideas. Ultimately, this enables the doctors and clinicians to be able to have confidence in the software as they are able to analyse and understand how it works. This also allows them to be able to explain their methodology and treatment plans clearly to the patient, making the diagnosis and treatment process clear, understandable and transparent.

1.5 Aims and Research Structure

In this paper, we describe the deep learning to validate high confidence variant calls, and using Bayesian networks to filter variants and prioritise their importance. Specifically, we will validate the use of deep learning to validate true variants in both real and simulated datasets. Subsequently, we will build a Bayesian network based on functional annotations to prioritise mutations and test our network on a real patient's cancer genome.

2 Materials and Methods

2.1 Overall Analysis Structure

For our research, we describe two main pipelines - the first pipeline will be used for training and optimisation of a neural network, and the second pipeline uses a trained neural network to perform variant validation and prediction. The first pipeline involves using a training dataset, performing alignment, variant calling and deep learning network training and prediction on the dataset. This allows us to generate a set of predictions which we can validate against the ground truth. The second analysis pipeline is meant for real datasets with no ground truth. For this pipeline, we will perform alignment and variant calling, and then filter it with a pre-trained network. Finally, we apply the Bayesian network analysis to predict genes in this dataset.

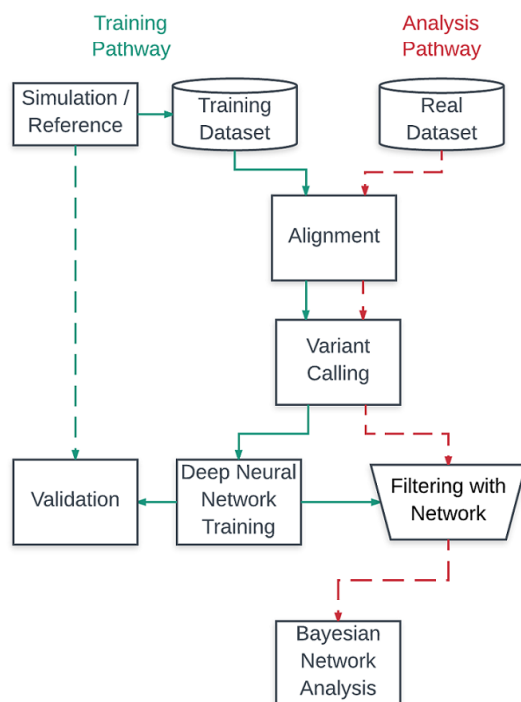


Figure 4: Overall Analytical Pipelines - Pipelines were implemented using the Groovy Domain Specific Language, NextFlow

2.2 Artificial Datasets

Artificial genomes present a simple way to simulate NGS data with perfectly known ground truth variants to test our neural network. For our simulator, we used Mason, a genome mu-

tation software written in C++ (SeqAn version 2.3.1) to mutate the hg19 reference genome from UCSC (Karolchik et al., 2014). We used indel rates of 0.00002 and SNP rates of 0.00008 to generate sufficient truth variants for analysis, which comprise 229253 SNPs and 57257 indels.

After generating a ground truth model, we simulated sequence reads with error rates and ground truth variants(Figure 5). For error rates, we used published data from Schirmer et al. (2016) as the input to Mason - the general substitution error rate used was 0.0004 per base in the genome, and the insertion and deletion error rate per base was $5 * 10^{-6}$.

2.3 Alignment and Variant Calling

To perform alignment of simulated and real sequences, the Burrows Wheeler Aligner (Li, 2013), version 0.7.13, was used. Default settings were used, with the mem option which is known to work well with longer sequences. After alignment, variant calling was performed. Variant callers used were FreeBayes (v1.0.2-16), GATK Haplotype Caller (v3.7-0) and Unified Genotyper (v3.7-0), Samtools (v1.3.1) and finally Pindel (v2.3.0)(Garrison & Marth, 2012; McKenna et al. 2010, DePristo et al. 2011; Li H, et al., 2009; Ye et al., 2009). All callers were used at their default settings.

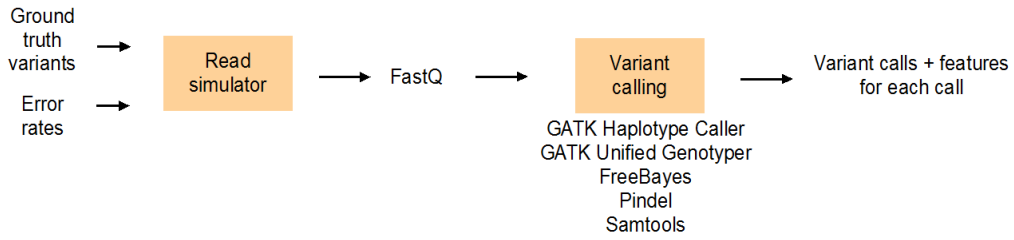


Figure 5: Pipeline for simulation of artificial genome for analysis

2.4 Feature Engineering

In order to train a neural network, features in the form of numerical vectors must be used as an input. We subset our features into three broad sets, which are base-specific information, sequencing error and bias information features, and calling and mapping quality. Here we describe the computation of the features - please see Appendix 5.2 for an more in-depth explanation on their usage and interpretation.

Base Information

Shannon Entropy

Shannon Entropy captures the amount of information contained inside the allele sequences.

It is calculated using the equation :

$$H(X) = - \sum_{i=1}^n P(x_i) \log_2 P(x_i) \quad (1)$$

where $P(x_i)$ is the prior probability of finding each base at each position. This prior probability is calculated in two ways - over the entire genome, over a region of space around the allele (10 bases plus the length of the allele in our calculations).

Kullback Leibler Divergence

The Kullback-Leibler Divergence feature is similar to Shannon entropy, but instead we use this to measure the informational change converting from the reference to the allele sequence. The Kullback-Leibler Divergence is calculated as follows :

$$D_{KL}(P||Q) = - \sum_{i=1}^n P(x_i) \log_2 \frac{P(x_i)}{Q(x_i)} \quad (2)$$

where $Q(x_i)$ is the prior probability of finding each base at each position based on the genomic region around the allele, while $P(x_i)$ is the posterior probability of finding a specific base inside the allelic sequence.

Base Quality

Base quality refers to the Phred score probability that the called allele is wrong. It is given by the equation :

$$P = 10^{-\frac{Q}{10}}$$

Where P is the Base Quality and Q is the probability that the allele called is wrong. This is a number computed by the sequencing machine based on the quality of the base samples provided.

Sequencing Biases and Errors

GC content

This feature comprises the percentage GC content of reference genome for at least 10 bases around the mutation site.

Longest homozygous run

This feature comprises the longest similar string of bases in the reference genome, for at least 10 bases around the mutation site.

Allele Count and Allele Balance

This feature is an output from Haplotype Caller and Unified Genotyper, and describes the total number of alleles contributing to a call and the balance between reference and alternate alleles reads.

Calling and Mapping Qualities

Genotype Likelihood

The genotype likelihood provides the phred-scaled likelihood scores of how confident the caller is in determining that it is a homozygous or heterozygous call, and is provided by all variant callers.

Read Depth

Mapped read depth refers to the total number of bases sequenced and aligned at a given reference base position. It is provided by all variant callers.

Quality by Depth

Quality by Depth is computed by dividing the quality score against allele depth, to obtain an average score of allele quality. This is provided by Haplotype Caller and Unified Genotyper.

Mapping Quality

Mapping quality is a score provided by the alignment method and gives the probability that a read is placed accurately. It is provided by all variant callers except Pindel.

2.5 General Programming, Pipelining and Mathematical Computations

The general programming platform used was Python (v2.7). Python was chosen due to its access to various important libraries, including NumPy, SciPy, Pomegranate and PyVCF. NumPy was used to prepare input vectors for deep learning training, SciPy was used to perform Principal Component Analysis and Synthetic Minority Oversampling Technique Methods (See Appendix 5.3 for more information). Finally, PyVCF was used to parse the VCF files into python objects for easy manipulation. Comparison of VCF file entries, which are each individuals mutations, was also performed using python dictionary lookups. This method was chosen due to a high number of lookups required, and a fast $O(1)$ constant time required for each lookup.

General pipelining and chaining of programmes was done using NextFlow and Bash scripts. NextFlow is a Groovy Based Domain Specific Language (DSL) that provides easy writing of parallel pipelines with an accessible unix interface. Nextflow was used to run the overall pipelines and control input and output of abstracted core modules, which are in turn either python scripts or Bash shell scripts. This ensures that results are easily replicable and can be later implemented as a single analytic pipeline for clinical use.

2.6 Deep Learning and Bayesian Networks

For our deep learning networks, we used the Keras library (v1.1.1) with a TensorFlow backend (v0.11.0). TensorFlow (Abadi et al., 2015) was chosen due to its distributed computation and queue management system that enabled better performance in training on a CentOS-7 compute cluster compared to other backends. For more explanation on the algorithms underpinning deep learning, see Appendix 5.1 for more information.

Pomegranate (a Python library) was used to generate and compute the probabilistic model and ranking system for our Bayesian Network. The preparation of the probabilistic model and the truth-tables required was done using Python scripts, and subsequently used as input in pomegranate.

2.7 Patient Derived Xenograft Mouse Model Development and Sequencing

[TO CLARIFY] To test the Bayesian ranking system, we used a patient derived xenograft mouse model. Athymic mice with the FOX mutation were grown for X number of days, and subsequently a tumour is grafted onto the mouse's body. Subsequently, the tumour was sequenced on an Illumina MiSeq platform and used for analysis.

3 Results and Discussion

3.1 Generation of Artificial Datasets

Using a genome mutation software, we generation a mutated genome (using the hg19 genome from ucsc (Karolchik et al., 2014) as a reference) with over 300,000 random mutations spread over the chromosomes as can be seen below in Figures 3 and 4.

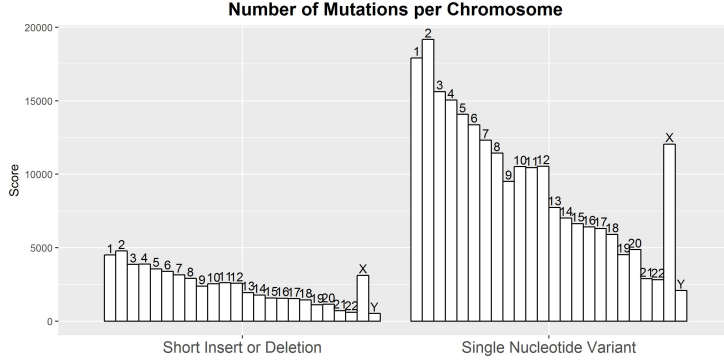


Figure 6: Number of ground truth mutations (variants) created in each chromosome

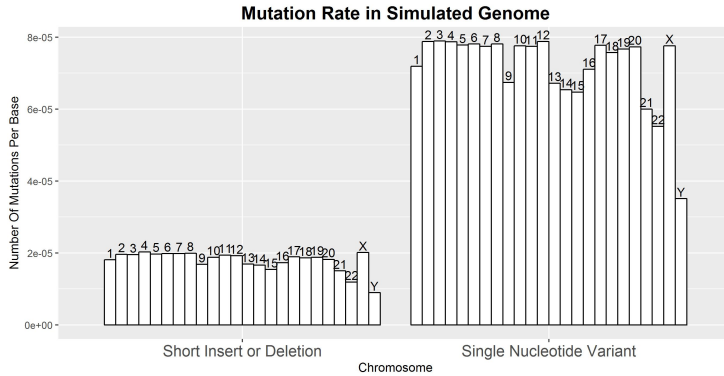


Figure 7: Mutation rate per base in each chromosome

Artificial genomes are a good method to analyse deep learning networks on as the ground truth, which are the truth variants inside the genome, are already known. This allows accurate verification of prediction schemes and is a commonly used method to test next generation sequencing related software (Escalona, Rocha & Posada, 2016). This is primarily because it is difficult to obtain complete truth datasets for real genomes as due to the inhibitory cost of checking every variant called via Sanger sequencing. Thus, artificial genomes present a simple way to simulate NGS data with perfectly known ground truth variants to test our validation platform.

3.2 Feature Engineering

Subsequently, we engineered a set of 19 features to use as input data for our variant callers, using data obtained from the variant callers themselves as well as engineering other features from the dataset. A summary of the features used in the training can be found in Table 1 and a description of the full list of features can be found in Appendix 5.2. Features were engineered based on obtaining information for the main aspects of variant calling, which includes the information contained in the sample bases (Base Quality, Entropy, Kullback-Leibler divergence etc), the confidence we have in the calling and alignment (Read Depth, Mapping Quality etc) and finally possible biases in the sequencing machine (Allele Balance, Allele Count, GC content).

Table 1: Feature Engineering Table

Features	Shannon Entropy (Reference, Alternate and KL- Divergence)	Base Composition (Homopolymer Run, GC content)	Read Depth	Mapping Quality	Base Quality	Allele Balance	Quality by Depth	Allele Count	Genotype Likelihoods
Free Bayes	+	+	+	+	+	+			+
Haplotype Caller	+	+	+	+	+		+	+	+
Unified Genotyper	+	+	+	+	+	+	+	+	+
Pindel	+	+	+						+
Samtools	+	+	+	+	+	+			+

3.3 Variant Callers

Variant callers were chosen for our deep learning neural network based on their orthogonal calling and reference methodologies - we wanted to maximise the range of variant callers in order to optimise the information that the neural network receives (See Table 2). We used two haplotype based callers, FreeBayes (Garrison & Marth, 2012) and GATK Haplotype Caller (McKenna et al. 2010, DePristo et al. 2011), two position based callers GATK unified Genotyper and Samtools (Li H, et al., 2009) and finally Pindel, a pattern growth based caller (Ye et al., 2009). All callers have been well studied and are commonly used in variant calling pipelines (Sandmann et al., 2017, Hwang et al., 2015 Xie et al., 2014 and Liu et al., 2013).

Table 2: Table Comparing Methods and Features of Different variant callers.

	GATK Unified Genotyper	Samtools	GATK Haplotype Caller	Free Bayes	Pindel
Calling Method	Uses a list of mapped reads, calling model is probabilistic with increased priors at regions with known SNPs	Uses a list of mapped reads, calling model is probabilistic. Does not assume sequencing errors are independent and has less hard filters compared to Unified Genotyper	Uses Hidden Markov Models to build a likelihood of haplotypes which are then used to call variants	Uses a posteriori probability model to build a set of haplotypes to represent mutations, calling model is probabilistic with population based priors	Locates regions which were mapped with indels or only one end was mapped, and then performs a pattern growth to find inserts and deletions. Shown to be able to identify medium length indels missed by other callers in real samples (Spencer et al., 2013)
Reference and Mapping Method	Position based caller that realigns fragments and analyses each position to call SNPs and indels	Position based caller that uses mapped sequences to call SNPs and indels.	Analyses regions where there is high likelihood of mutation based on activity score, and builds a De Bruijn-like graph that reassembles reads (Haplotypes) in that region	Dynamic sliding window based reference frame, using algorithms to determine window size for analysis. Does not require precise alignment, unlike other callers	Focuses on Unmapped regions, regions known to have insert and deletions or regions with only one end mapped.

INSERT CONCORDANCE GRAPHS

3.4 Network Architecture

Before training our deep learning network, we tested out various neural network architectures to see which architecture would perform the best for our set of input features.

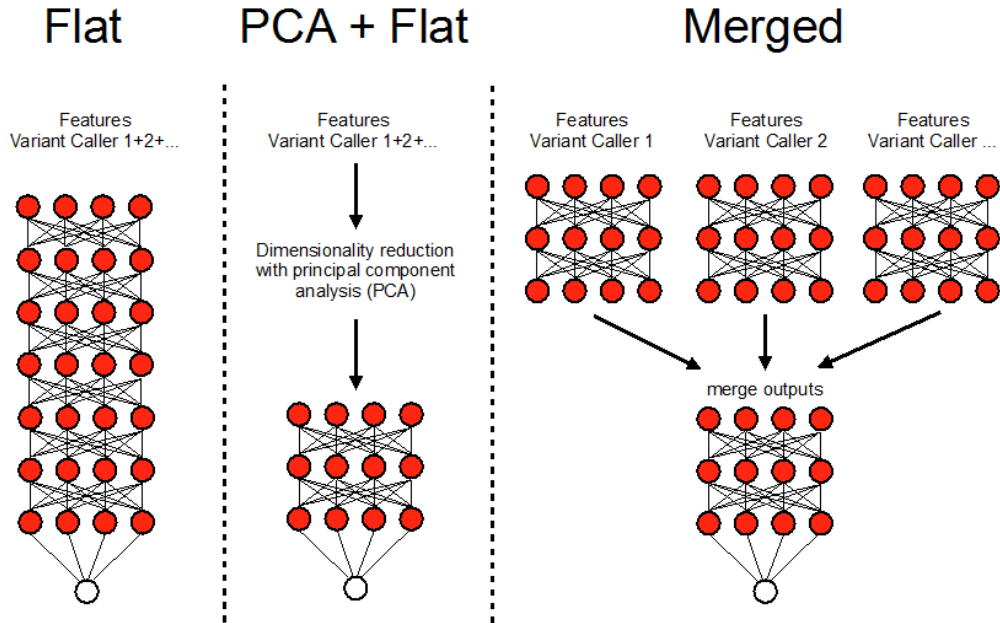


Figure 8: Different Designs for Neural Network Architecture

We first explored the flat architecture (Figure N), which contains stacks of fully connected layers with multiple nodes (initially 7 layers, with 80 nodes per layer). This is the simplest architecture, where all the features are loaded onto a single vector, and this entire vector is used as an input to train the neural network. We next explored the PCA + flat architecture which had the same neural network architecture but before the input data was fed into the network, a Principal Components Analysis was done to reduce the dataset to 8 principal components which was then used as input data for the neural network (please see Appendix 5.3 for more details of the PCA analysis). Principal components analysis is a dimensionality reduction technique that enables a compressed representation of data. Each principal component is an linear summation of the original function in the form

$$\begin{aligned}
 PC_1 &= \beta_{1,1} * X_1 + \beta_{2,1}X_2 + \dots + \beta_{n,1}X_n \\
 &\dots \\
 &\dots \\
 PC_i &= \beta_{1,i} * X_1 + \beta_{2,i}X_2 + \dots + \beta_{n,i}X_n
 \end{aligned}$$

which enables a few principal components to capture a high amount of variance in the dataset. Finally, the last architecture we tested was the merged network this network had a set of layers (initially 5 layers, 24 nodes per layer) that learns from each caller alone, and then the outputs from each of these layers are subsequently merged and used to make a prediction.

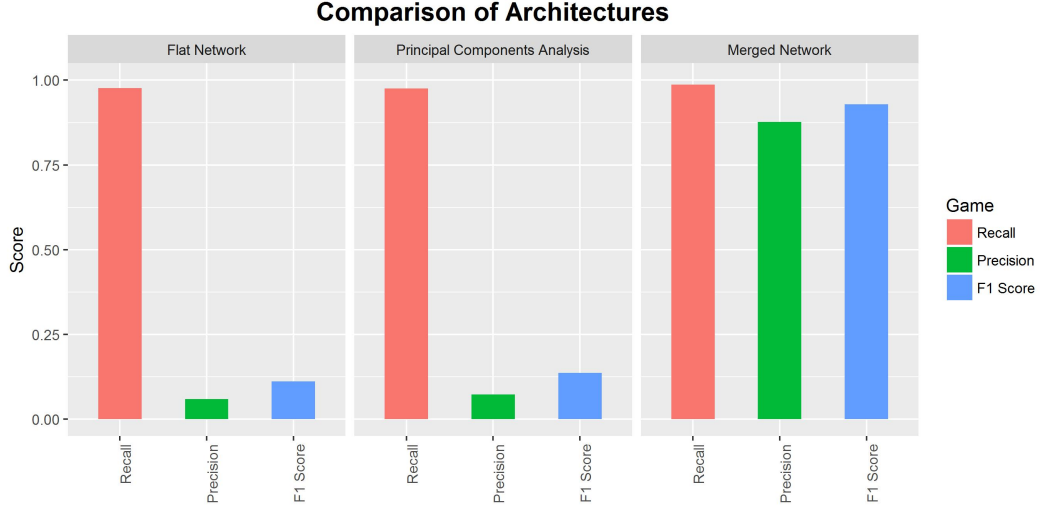


Figure 9: Analysis of Different Neural Network Architecture

Initially, with the flat network, the precision rate was very low at 0.059 with an F1 score of 0.112, indicating that the neural network was unable to learn from the input feature set. We suspected that this was due to high dimensionality in the dataset, which led to our second architecture design, the PCA with flat analysis. Principal components analysis has been shown to be able to successfully improve learning in high dimensionality datasets (Chen et al., 2014; Van Der Maaten, Postma & Van den Herik, 2009). However, the precision and F1 score for the PCA architecture was also low at 0.0735 and 0.137. Ultimately both failed to learn, indicating to us that perhaps the features from each of the callers had to be analysed separately before being passed into a separate neural network that did the final score computations. With this merged network, we managed to obtain a precision and F1 score (0.877 and 0.929) that was far better than the previous two architectures. Interestingly, the recall scores for all three architectures were around the same (± 0.01), indicating the main learning point for the neural network was removing false positive calls.

3.5 Network Tuning and Optimisation

Next, we systematically optimised and tuned the deep learning neural network to maximise its predictive ability. In tuning our network, we also sought to study how the various hyperparameters as well as the datastructure affected our network's ability to learn from the data. In particular, we focused on four issues - the number of layers, optimiser choice, learning rate choice and finally sample balancing. These four issues are known to be critical

in deep learning networks (Ruder et al., 2016; LeCun, Bengio & Hinton, 2015; Yan et al., 2015; Sutskever et al., 2013) and would likely be critical to the success of a neural network.

A. Number of Layers

Firstly, we studied how many layers should be in the neural network. The number of layers is critical as it determines what kind of information and the representation of data that can be captured by the neural network. Choosing the number of layers is important as sufficient layers are needed to obtain the complex data representation needed for learning, but too many layers might result in the vanishing gradient problem. We started off with a neural network architecture as shown below, and began to vary the number of layers in at each point.

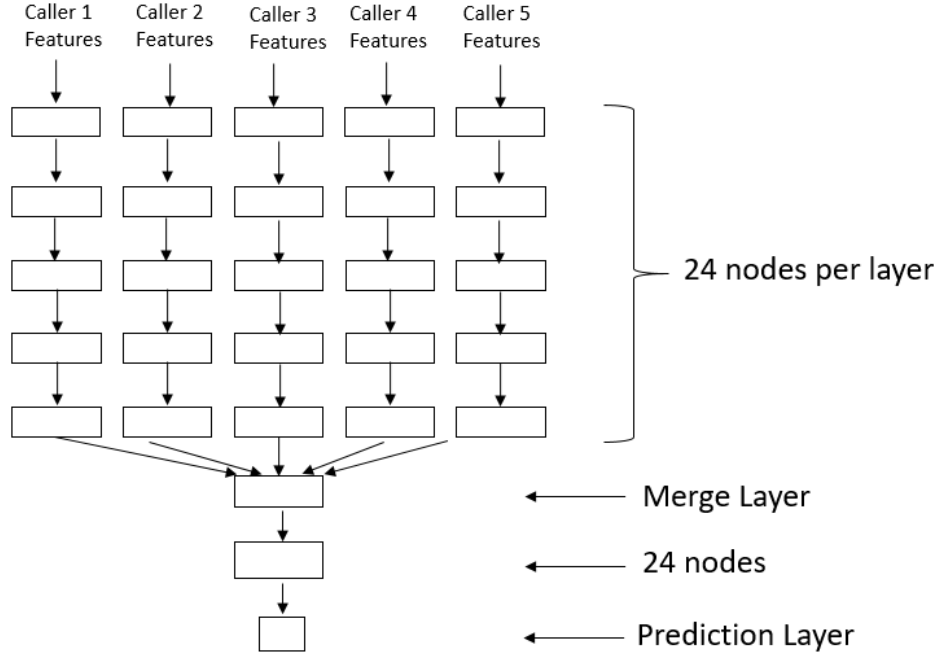


Figure 10: Basic Merge Network Structure

For all layers, the LeakyReLU activation function was used. The LeakyReLU is a refinement of the ReLU activation function, and both are well documented activation functions that have been shown to work well in deep neural networks (LeCun, Bengio & Hinton, 2015; Maas, Hannun & Ng, 2013). We noticed that changing the number of layers after the merge layer did not significantly vary the output, and so we focused on changing the number of layers before the merge layer. We studied 6 different neural network structures (4 layers to

9 layers).

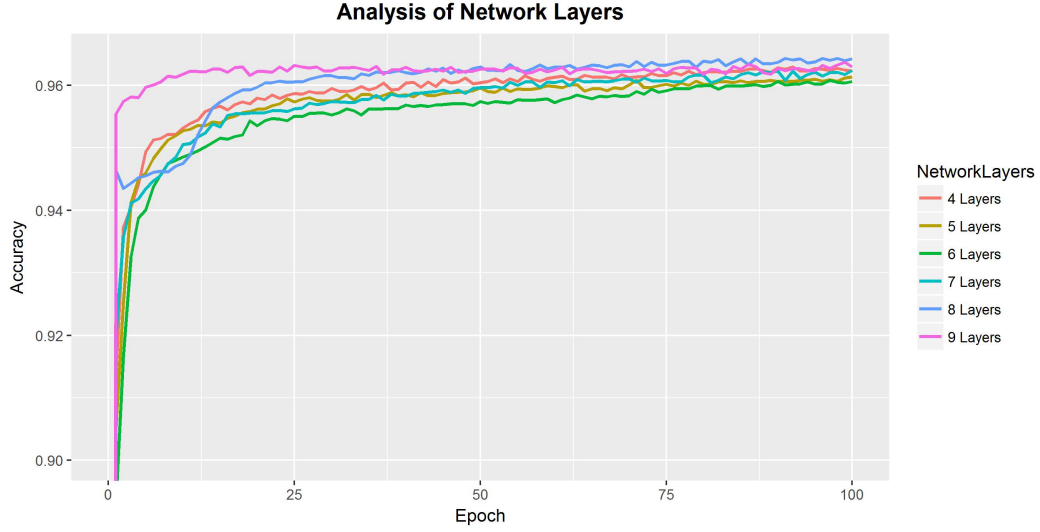


Figure 11: Analysis of Different Number of Layers On Training Accuracy

From analysing the accuracies of the different layers, we find that 8 layers seem the best at learning from the input data. We note that all the layers follow the same rough trend of accuracy, indicating they are all able to learn from the dataset. We decided on the 8 layer network as it seemed best able to learn from the input dataset, with a final accuracy of 0.964 that is about 0.001 higher than other layers. A final design feature used was to add two dropout filters at the last two layers before merging in order to prevent overfitting in data. Dropout filters have been shown to be an effective in preventing overfitting of data (Srivastava et al., 2014). Another active step taken to prevent overfitting was to ensure random separation of test, validation and training datasets.

B. Optimiser and Learning Rates

Next, we sought to choose the best optimiser and learning rate for our dataset. Both optimisers and learning rates have been well studied and known to be important in neural network training (Ruder et al., 2016; Sutskever et al., 2013). Optimiser choice is critical as the optimisers determine how the weights and gradients are updated in the network, thus playing an integral part in learning. We studied 3 well-known optimisers for use in our network, ADAM, RMSprop and Stochastic Gradient Descent (SGD). ADAM is an adaptive learning rate optimiser that is known to be well suited in large dataset and parameter

problems (Kingma & Ba, 2014). RMSprop is another adaptive learning rate optimiser that unpublished, but has been shown to work well for real experimental datasets (Tieleman & Hinton, 2012). SGD is the simplest learning model with no adaptive learning rate, but is a useful model because it is the easiest to understand mathematically and has also been shown to solve deep learning problems (Kingma & Ba, 2014). For more information on the mathematical foundations of backpropagation, please see Appendix 5.1. For the three optimisers, we ran tests to study the accuracy of the neural network running on each optimiser to predict true variants (Figure 11).

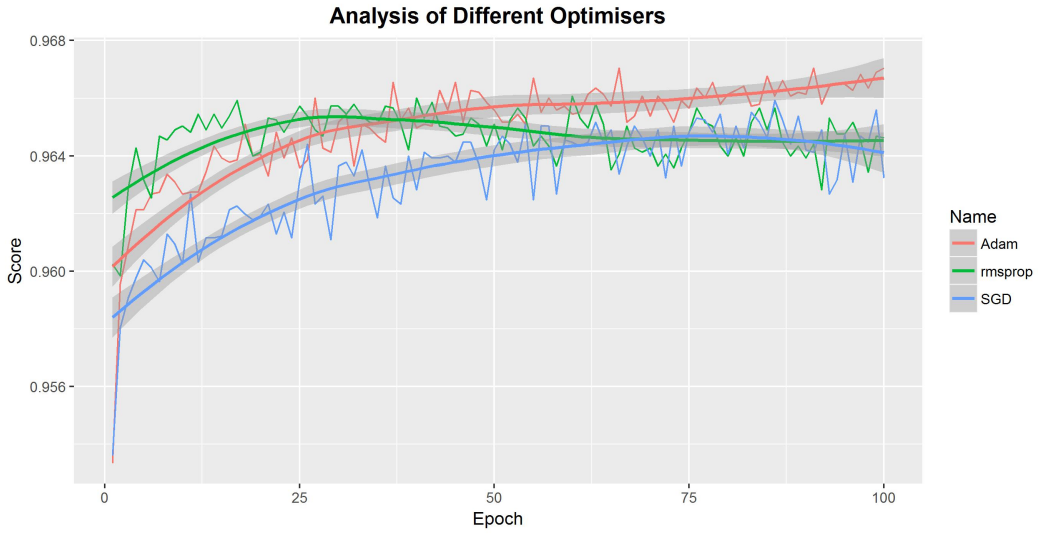


Figure 12: Optimiser accuracies for training at each epoch. Due to the noise in accuracies, the overall momentum of the dataset, calculated as a sliding window average is shown. The 95% confidence interval is also shown.

The adaptive rate optimisers, Adam and RMSprop obtained the highest accuracies of 0.9670 and 0.9660 while SGD reached a maximum accuracy of 0.9569, very close to that of RMSprop. Interestingly adaptive rate optimisers seemed to have complex learning trajectories, while SGD has a very stable learning rate. This makes sense as adaptive learning rates allow greater gradient descents when the error is high, and decreasing the learning rate at smaller errors. This allows Adam and RMSprop to learn at variable rates based on the current gradients. For SGD, it appears that while it takes a while to learn the true minima, it eventually still reaches about the same minima as RMSprop. In the end, we chose Adam as our optimiser as the final accuracy discovered by Adam was noted to be higher than RMSprop and SGD, and we note a stable learning curve for Adam, indicating it is able to learn and update the gradients in the neural network to learn from input data.

Then, we also looked at various initial learning rate for Adam (Figure 12), and found that the most stable learning could be found at a learning rate of 10^{-5} . This initial learning rate is critical as it determines the first few gradient descents which enable stable adaptive learning throughout the epochs (Sutskever et al., 2013). At any larger learning rates (10^{-4} and below), a very high amount of noise was observed, indicating that the learning rate was too high resulting in minima finding errors. At smaller learning rates (10^{-6} and above), the final accuracy after 100 epochs (0.9639) was lower than the learning rate at 10^{-5} (0.9672). Thus, we chose 10^{-5} to be our learning rate.

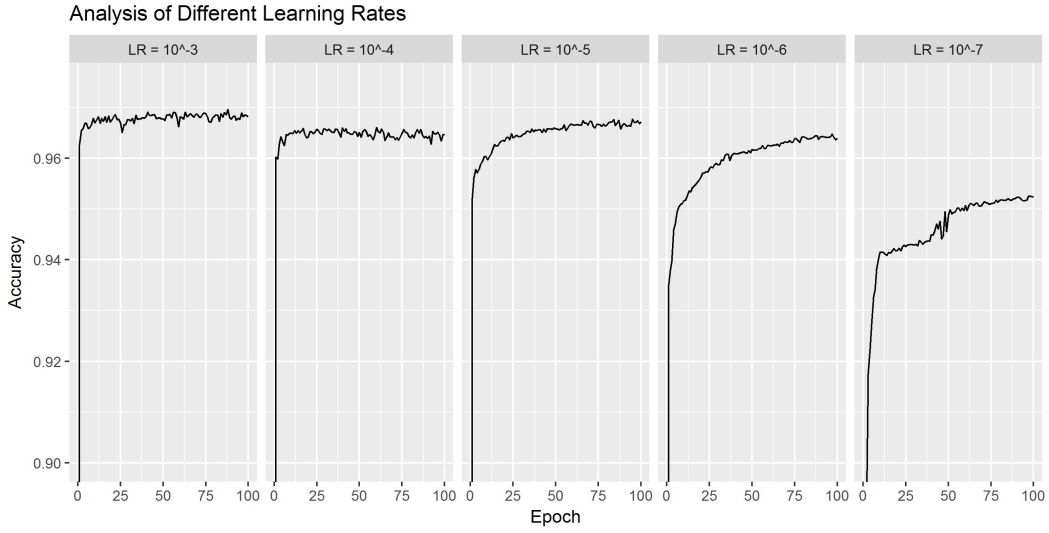


Figure 13: Training Accuracies over Each Epoch for Different Learning Rates

C. Sample Balancing

Our final concern was sample balancing - the simulated dataset contained an imbalance of positive training examples versus negative training examples. In total, there were 286569 positive training examples and 4547919 negative training examples. Such an sample imbalance has been known to affect learning adversely (Yan et al., 2015; Lopez et al., 2012). Thus, we sought to study two methods of sample balancing, undersampling and oversampling. Our data was skewed with a high amount of negative training samples and a low number of positive train samples. Thus, undersampling was implemented by removing negative training examples until the number of negative training examples was equal to the number of positive training examples. In oversampling, the Synthetic Minority Oversampling Technique (SMOTE) was done, which uses nearest neighbours to create more data points for the positive training example (see Appendix 5.3 for more details). Figure 13

shows the metrics for each sampling technique.

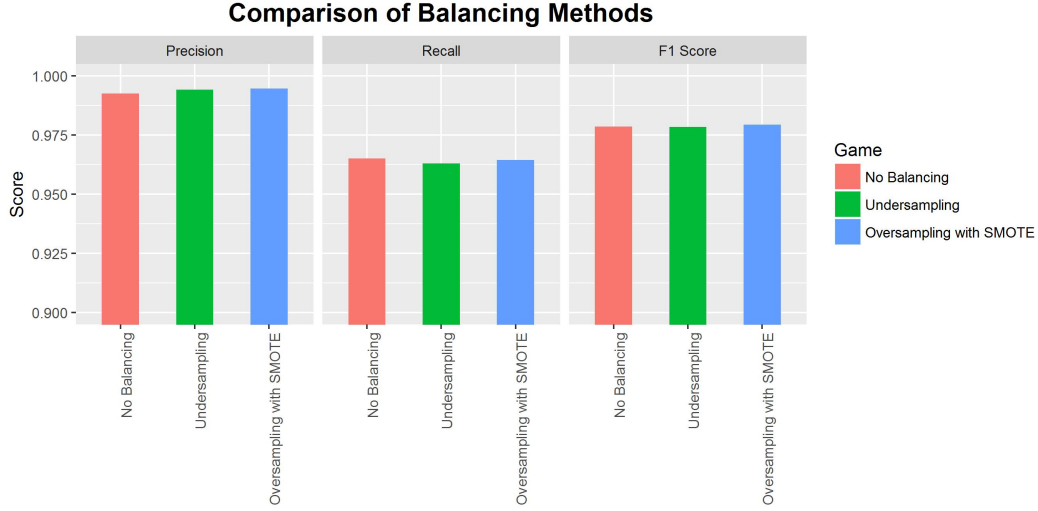


Figure 14: Effect of Sample Balancing on Prediction Ability

Interestingly, we note that overall, undersampling, oversampling and no sampling at all had very small effects on precision, recall and the final F1 score. This could be due to clear boundary separation within positive and negative class examples as well as good representative datapoints within the positive training example class. This prevents the imbalanced data from having too much of an effect on variant prediction and classification. Still, we note that oversampling techniques resulted in a marginally higher F1 score (0.001 higher than undersampling and no sampling), and since ensuring that datasets are balanced is a recommended protocol to prevent further bias downstream, we used SMOTE oversampling to produce extra positive training class examples for all analysis pipelines.

3.6 Benchmarking of Optimised Network with Mason Datasets

From optimisation steps, we finalised the network architecture as seen in Figure 9, but with 8 layers before the merge layer. We chose the learning rate to be 10^{-5} , and the optimiser used was Adam. With this network, we benchmarked the neural network against the single variant callers, as well as concordance callers, which are an integration of the outputs of the 5 variant callers. Specifically, the n-concordance variant callers are defined as the set of calls that any n callers agree upon - so 1-concordance includes all the calls made by all callers and 4-concordance includes all the calls made by any 4 callers. The metrics we use to determine how well the neural networks perform is via precision, recall and F1 score

(their derivation can be found in appendix 5.3).

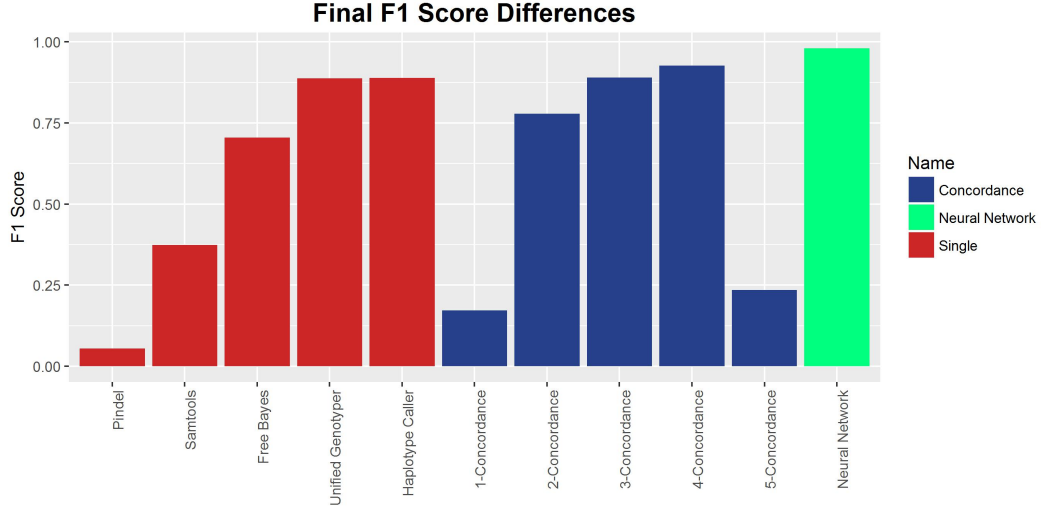


Figure 15: Overall Comparison of Variant Callers

In terms of overall F1 score, we see that the neural network was able to outperform single and concordance-based callers. This provides strong evidence that the neural network is able to learn from the input features whether the variant call is real or not, validating its usage in variant calling. The final F1 score obtained by the best single variant caller was Haplotype caller at 0.888, the best concordance caller had an F1 score of 0.927 while the neural network achieved an F1 score of 0.980. To study whether the increase in F1 score is due to improvements in precision or recall, we studied the exact precision, recall and F1 scores of the top 2 variant callers as well as the best single variant caller versus the neural network. We find that the neural network is more precise than both, but the recall is rather similar.

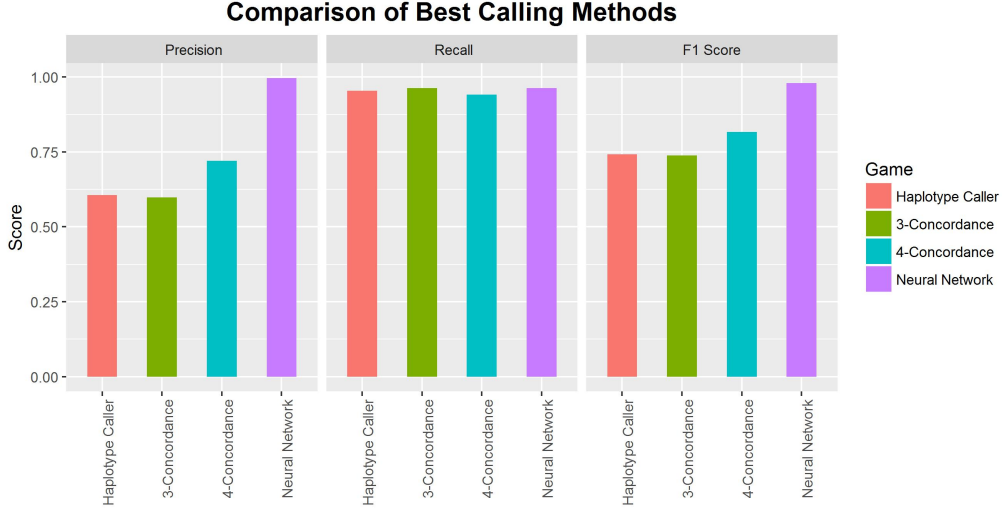


Figure 16: Comparison of Best Variant Callers in terms of Precision, Recall and F1 Score

We find that the neural network is more precise than all four callers, with the neural network had a high precision of 0.995 compared to only 0.917 for 4 concordance. This is a 20 fold decrease in the number of false positives, or about 23,000 more false positive calls in the 4 concordance network compared to the neural network. Interestingly, the recall of all the callers was high in the range of 0.90 to 0.95, indicating that while all were able to pick out most of the truth class variables, the main errors came from a high number of false positives that were also called as true mutations. Thus, this provides strong evidence that the neural network is able to sieve out false positives within the dataset and stably predict whether a mutation is true.

3.7 Benchmarking of Network with NA Datasets

After verification of the neural network architecture, optimised parameters and ability to learn with a simulated dataset, we sought to analyse a real dataset to set the validity of the neural network in validating variants. We studied the NA12878 Genome In a Bottle dataset (Zook et al., 2014), which has been used in other variant calling validation pipelines (Talwalkar et al., 2014; Linderman et al., 2014) and contains a set of high confidence variant calls which we can use as ground truth for training and validation. This set of high confidence variant calls are obtained from multiple iterations of orthogonal sequencing methods (using Solid, Illumina platforms, Roche 454 sequencing and Ion torrent technologies). The usage of multiple platforms enables an intersection of variants that can

be considered as the ground truth. We then sought to see if our neural network can predict the ground truth better than single or concordance based variant callers.

We applied the same methodology to the sequences as with the simulated data and then used our neural network to predict the true variants.

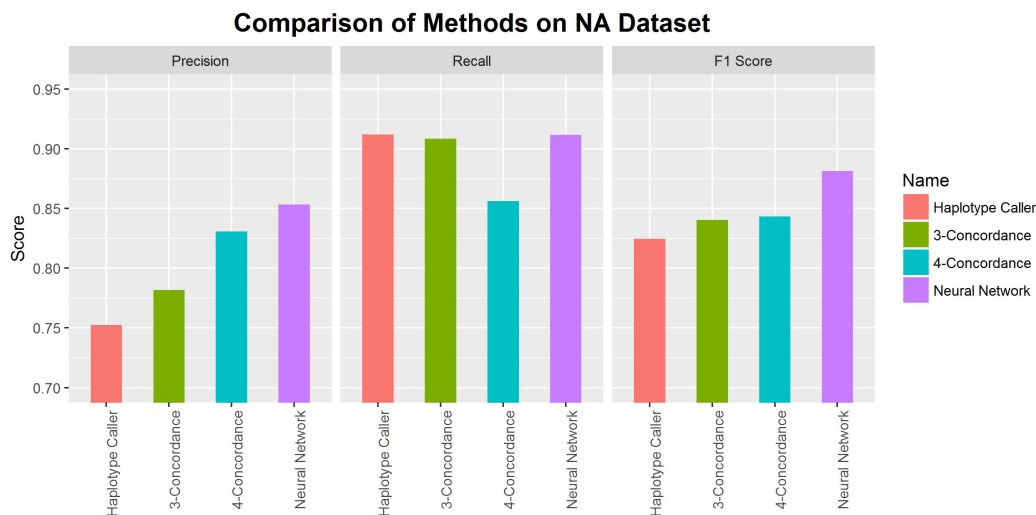


Figure 17: Comparison of Variant Callers

As can be seen from the figure, the neural network was able to predict with the highest precision (0.859) when compared the best single caller, haplotype caller (0.752) and the 2 best concordance callers, 3-concordance (0.782) and 4-concordance (0.830). In terms of recall, the neural network had a higher recall (0.911) compared to the 4 concordance caller (0.856). Thus, we see that in the NA dataset, the neural network compared with the 4 concordance network is able to call 2650 true variants that were missed by 4 concordance and still had 1228 less false positives. This means the neural network was more aggressive in making calls, yet more of the calls were correct. Compared to the three concordance caller, the neural network had 4253 less false positives. Ultimately when we looked at the F1 score, the neural network was able to outperform concordance variant callers by at least 0.04 and single callers by 0.06. This validates our neural network pipeline in a real genomic dataset and indicates that network is able to learn from the input features.

3.8 Analysis of gene importance using Bayesian Ranking systems

After validation of high confidence calls, we sought to enable a clear and understandable ranking of genes. We first build a Bayesian network analysis using known functional annotations from ANNOVAR. These were subsequently used to compute the Bayesian probability ranking, which is shown in Figure 17 below.

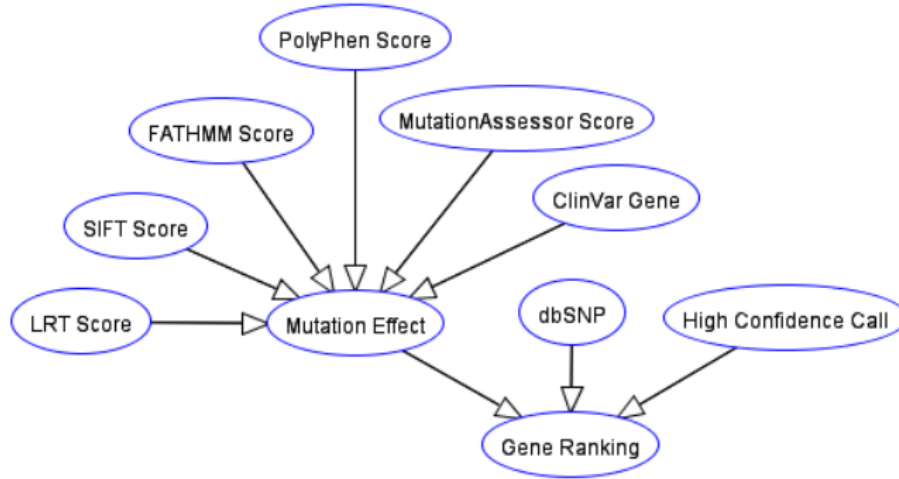


Figure 18: Final Bayesian Network used in Analysis

This network structure was chosen as we wanted to use three different sets of information to update the probability of the gene being important. Firstly, the confidence of the call should matter in how important it is - the more likely a gene is real, the more important it should be. Secondly, the rank should also be determined by how common the variation is, based on studying known SNP polymorphism rates. If it is a common SNP, then the ranking should be downgraded as it is less likely to be a driver mutation. Finally, we sought to predict the overall effect of mutations via an ensemble of mutation effect predictors. These predictors use different methods to predict the average effect of that mutation - based on statistical methods like position specific substitution matrixes and Hidden Markov Models to study the effect of a mutation on protein structure and function. We also used the ClinVar database, a curated repository of known Human variants and their resulting phenotypes. These scores were then aggregated to update the probability of the mutation effect.

Figure 19: Table of Functional Annotations obtained from ANNOVAR

Annotation Name	Information Type	Method	Scoring Method
Likelihood Ratio Test	Deleterious Mutation Score	Likelihood Ratio Test of each amino acid is evolving neutrally to the alternative model of evolution under negative selection	Score normalised to [0,1] and used directly in Bayesian Network
MutationAssessor	Deleterious Mutation Score	Mutation rate of homologous sequence subfamilies	Score normalised to [0,1] and used directly in Bayesian Network
SIFT	Deleterious Mutation Score	Position Specific Scoring Matrixes with conserved Sequences	Score normalised to [0,1] and used directly in Bayesian Network
PolyPhen2	Deleterious Mutation Score	naïve Bayes classifier on various multiple sequence alignments methods of homologous proteins and protein structure-based features	Score normalised to [0,1] and used directly in Bayesian Network
FATHMM	Deleterious Mutation Score	Hidden Markov Model used to score MSA based on protein homologous sequences	Score normalised to [0,1] and used directly in Bayesian Network
ClinVar Genes	Known Pathogenic Genes	Database lookup of curated set of relationship between variant calls and human phenotype	Higher Probability of Importance if known pathogenic variant
dbSNP138	Common Single Nucleotide Polymorphisms	Database lookup of curated set of known Human SNPs	Lower Probability of Importance if known common variant

Based on scores provided, we report the update the conditional probabilities using the probabilities chain rule - for the first level, this is given as

$$P(Impt|(Del \cap Uncom \cap High Conc)) = \frac{P(Impt \cap Del \cap Uncom \cap High Conc)}{P(Del \cap Uncom \cap High Conc)} \quad (3)$$

P(Impt) refers to the probability of the gene being important,
P(Del) refers to the probability of the gene being deleterious,
P(Uncom) refers to the probability of the gene being uncommon and
P(High Conc) refers to the probability of the gene being a high confidence call.
Further calculations can be found and derivations can be found in Appendix A

To compute the final probabilities, the software pomegranate was used. This simplifies the node drawing and probabilistic updates of the final ranking scores.

3.9 Validation of Bayesian Network Ranking on PDX dataset

To study the effectiveness of our bayesian network ranking system, we sequenced and analysed a patient derived xenograft (PDX) tumour genome. This tumour genome was grafted onto the immunocompromised mouse from a patient with a known cancer - Diffuse Large B Cell Lymphoma (DLBCL). We chose to analyse lymphoma as lymphoma is a well-known and studied disease model with a well-defined disease progression. The patient derived xenograph model also allows in vivo studies of the tumour in its environment, and serves as a good model for sequencing and analysis. After sequencing the PDX genome, we put it through our full analysis pipeline, which involves identifying high confidence mutations

using the neural networks and then ranking these genes using the bayesian network ranking.

Figure 19 shows the top 30 genes by probability.

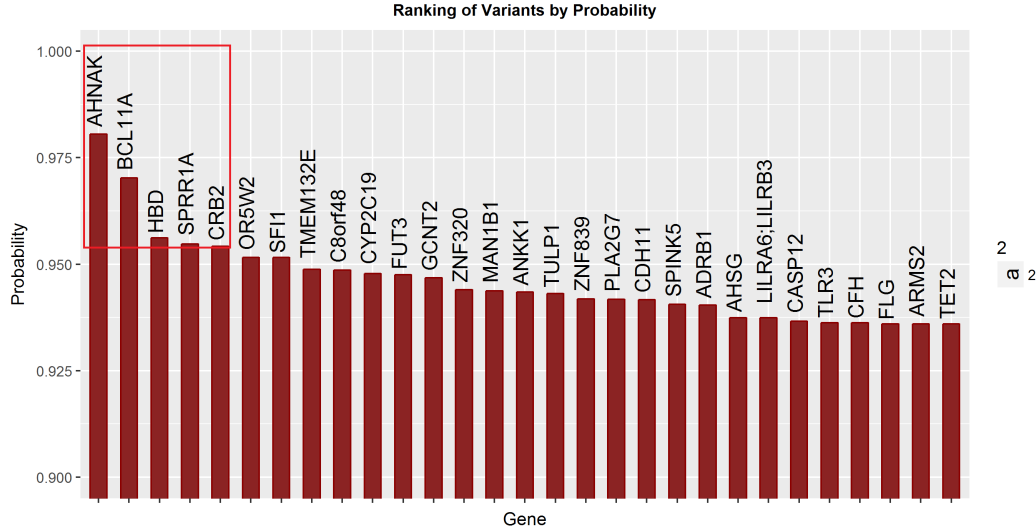


Figure 20: Top 30 genes from Bayesian Ranking Algorithm

Figure 21: Table of Top 5 important genes from Bayesian Ranking

Gene	Full Name	Known Involvement in Lymphoma or Cancer	Evidence	Mutation Location	Predicted Mutation Type
AHNK	Neuroblast Differentiation-Associated Protein (Desmoyokin)	<ul style="list-style-type: none"> Known tumour suppressor via modulation of TGFβ/Smad signalling pathway Known to be downregulated in cell lines of Burkitt lymphomas 	Lee et al., 2014; Amagai et al., 2004; Shtivelman et al., 1992	chr11 - 62293433 T -> C	non synonymous SNV
BCL11A	B-Cell CLL/Lymphoma 11A	<ul style="list-style-type: none"> Known proto-oncogene in DLBCL Overexpression of BCL11A was found in 75% of primary mediastinal B-cell lymphomas (a subset of DLBCLs) 	Weniger et al., 2006; Schlegelberger et al., 2001; Satterwhite et al., 2001	chr2 - 60688580 C -> G	non synonymous SNV
HBD	Hemoglobin Subunit Delta	<ul style="list-style-type: none"> Shown to be expressed by aggressive glioblastoma cell lines 	Allalunis-Turner et al., 2013	chr11 - 5255274 G -> A	stop-gain
SPRR1A	Small Proline Rich Protein 1A (Cornifin-A)	<ul style="list-style-type: none"> Known to be expressed in DLBCL and expression has been shown to correlate with 5 year survival rate 	Liu et al., 2014	chr1 - 152957961 G -> C	non synonymous SNV
CRB2	Crums 2, Cell Polarity Complex Component	<ul style="list-style-type: none"> Cell polarity and cytoskeletal reorganisation is known to affect B-cell lymphoma migration and invasiveness Development of B-cell lymphoma has also been noted in Crb2-related syndrome (bi-allelic mutation of Crb2) 	Slavotinek, 2015; Gold et al., 2010	chr9 - 126135887 T -> C	non synonymous SNV

Studying the top 5 genes, we found that four of these five genes have been implicated on lymphomas or other cancers. AHNK is a known tumour suppressor and has been known to be downregulated inlines of Burkitt Lymphoma. BCL11A is a known proto-oncogene in DLBCL, and has been found to be overexpressed in 75% of primary mediastinal B-cell Lymphomas, a subset of DLBCL. SPRR1A, the fourth gene ranked in terms of importance,

has been shown to be expressed in DLBCL and its expression has been shown to strongly correlate with 5 year survival rate (Figure 21). Finally development of B-cell lymphoma has been noted in Crb-2 related syndrome, which is a bi-allelic mutation of CRB2. Interestingly, the last of the high ranked genes was noted to be a subunit of Hemoglobin. While there is no strong evidence for the role of Hemoglobin in DLBCL, it has been shown to be expressed in aggressive glioblastoma lines, indicating a possible previously unknown role in cancer. This gives us high confidence that the bayesian ranking network is able to pick up important and relevant mutations. Without such a ranking system, we would have to look through over 70 thousand genes, without a way to systematically study their call confidence, as well as their probability of having an effect.

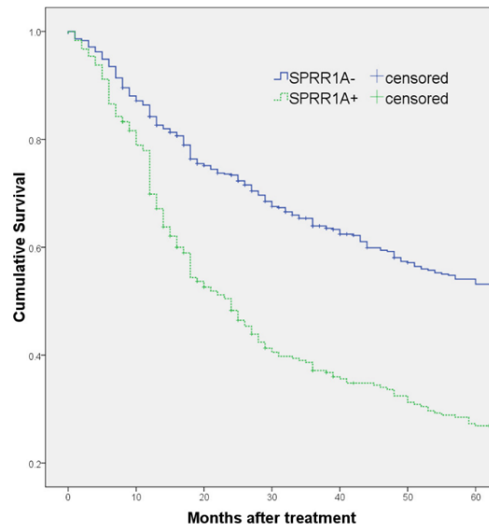


Figure 22: 5 year survival curve of patients with SPRR1A+ and SPRR1A- patients with DLBCL. Source : Zhang et al. (2014), Figure 2.

To aggregate the data from our Bayesian Ranking system, we did a Circos plot for the top 300 genes picked up by our gene ranking system. A Circos enables easy visualisation and analysis of large genome datasets, enabling quick understanding and comprehension of results. From the Circos Plot (Figure 22), we find several interesting gene families that might also be relevant in B-Cell Lymphoma. These include several Toll-Like Receptors (TLRs), TLR3 (chr4,rank 26) and Tlr1(chr4,rank 77) as well as interleukin receptors IL4R (chr16,rank 37) and IL1 β (chr2,rank 196). TLRs are of significant interest in cancer due to their involvement in the caspase pathway, and interleukins are also important in cancer due to their importance in mediating inflammation and immune response. Thus,

we show that our Bayesian network can be used by Clinicians to quickly interrogate the information from functional annotations and database lookups to understand the disease specifics.

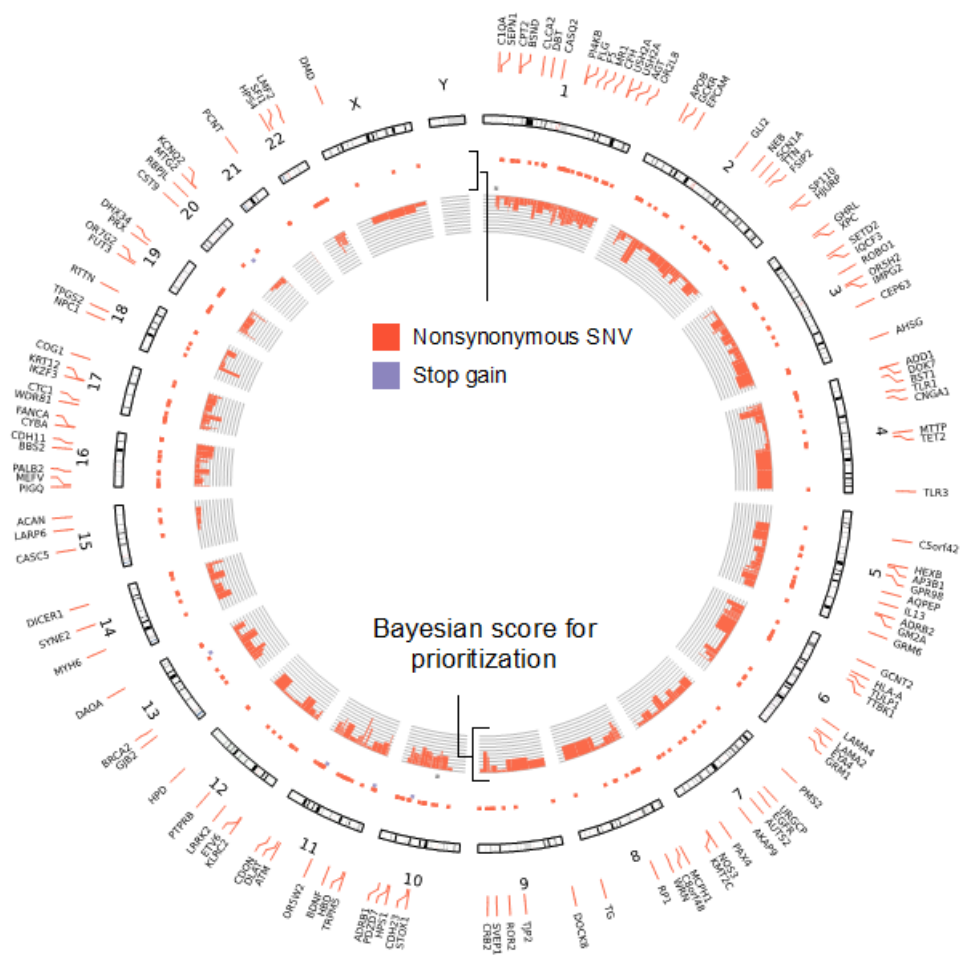


Figure 23: Circos plot of top 300 ranked genes from Bayesian network ranking. In this Circos plot, the outer track indicates the top ranked genes and their positions on the chromosome. The inner track describes the type of mutation that was observed - most mutations were non synonymous SNVs, with a few stop-gain mutations. The innermost track shows the relative probabilities of each ranked gene.

4 Discussion

We demonstrate the validation of high confidence variant calls using a deep learning neural network on both real and simulated datasets, and we also show that a Bayesian network is able to rank and prioritise genes in a systematic way so as to obtain important genes. We then compared our results with other methods like VariantMetaCaller(using Support Vector Machines) and BAYSIC(using Bayesian Latent Analysis) (Gzsi et al., 2015; Cantarel et al., 2014).

Both methods were used to analyse and predict variants for NA12878 data, but due to differences in metrics, processes and datasets, absolute comparison of precision and recall is difficult. Thus, it is more suitable to study the looking at relative improvements seen when using each method. VariantMetaCaller increased SNP prediction by 0.04 and indel prediction by 0.07 in terms of the Area Under Prediction Recall Curve (AUPRC) metric when compared to their best single variant caller. BAYSIC noted a 0.03 increase in SNP prediction and 0.05 increase in indel prediction compared to the best single variant caller. This is comparable to our own results of a 0.06 increase in both indel and SNP prediction for the NA dataset compared to the best single variant caller. However, we used the F1 score metric, instead of the AUPRC metric. Thus, while their results provide evidence of precision improvements at all levels of recall (Fawcett et al., 2006), our results provide evidence that at the optimal threshold for each specific caller, we can show an F1 score improvement of 0.06. This metric is more relevant in clinical practice as we are mainly interested in the optimal operating conditions where precision and recall are maximised and not the fringe conditions. Fawcett (2006) also mentions this problem, as he notes that 'It is possible for a high-AUC classifier to perform worse in a specific region of ROC space than a low-AUC classifier'. Here, AUC refers to the Area Under Curve, another term for the AUPRC, and ROC refers to the Receive Operator Characteristics graph (Egan, 1976) which is the curve that the AUPRC uses.

Thus, one definite step moving forward is to incorporate VariantMetaCaller and BAYSIC into our pipelines as negative controls, and measure using the same dataset and same processes whether deep learning is able to outperform these two methods using the same comparison methods and metrics. Intuitively, we believe that deep learning will be able

to edge out improvements as deep learning is able to form complex representations of the data to learn from that Support Vector Machines are unable to do (LeCun et al., 2015; Schmidhuber, 2015) Furthermore, evidence from our flat and dense network architecture shows that putting all the features in a single vector and using that to performing machine learning might not be the best method as it is difficult to learn features from it. Finally, deep learning has been shown to outperform other methods in terms of data prediction and classification.

However, one large limitation in the overall approach of measuring each of the methods against the NA12878 dataset is that the high confidence calls provided is not the ground truth. Zook et al.(2014) themselves note estimate a possible false negative or positive that for every 30 million bases in the NA12878 dataset. This is due to true variants that are not inside the high confidence dataset because of errors in one sequencing machine, or genomic regions that cause all sequencing machines to have similar biases and noise. Hence, this would result in misclassification and wrongly called false negative and false positive results, thus skewing the classification results. To solve this problem, a lot of effort has to be put in to obtain a set of verified truth variants via gold standard Sanger sequencing (Tsiatis et al., 2014), but this might be prohibitively expensive for a large sample of mutations. Still, this would have to be done for us to have a good set of truth variables to test prediction software with before such software can be considered for use in actual treatment and diagnosis.

For the Bayesian Network analysis, it is more difficult to benchmark our results for gene prioritisation. This is because currently used platforms include gene panels (Olek and Berlin, 2002) or manual literature look-ups of disease related genes, such as using the Clin-Var database. While gene panels work well in a clinical setting, with NGS data it is hoped that as much information about a person’s genome as possible can be used in treatment and diagnosis (Meldrum et al., 2011). Using a gene ranking system instead of just looking at a set of implicated genes might allow doctors to find out tease out possible homologs or interacting agents that might be related to the known deleterious genes (perhaps in the gene panel) and integrate that into their treatment and diagnosis. One interesting extension

we would definitely like to move into in the future is to be able to integrate a druggable genome into the network, enabling the prioritisation of genes who have possible candidate drug targets. This method would look up a drug-gene interaction database, for example DGIdb (Griffith et al., 2013), and use the results to inform the importance of a gene. This would enable doctors to notice further possible drug candidates that would work very well on the gene profile of the patient that they might not have considered previously, thus increasing their scope of possible treatment options and augmenting their skills.

Other directions in the future include being able to include extra variant callers which will provide it with even more feature data, enabling it to make better predictions. We would also like to move everything onto a web interface such that it is accessible for use in terms of both variant validation and gene prioritisation. This would enable easy access to both the validation and prioritisation pipelines.

Thus, in this paper, we have shown the use of deep learning neural networks to successfully validate variants in both real and simulated datasets. We also show that using a Bayesian network is able to identify important genes within a lymphoma disease sample.

5 Appendixes

5.1 Neural Network Learning

Machine learning is underpinned by two key phases, the feed-forward phase and the back-propagation phase. The feedforward phase describes the computation of a prediction, and during this phase the input features are used to compute the final output prediction. For a simple network below :

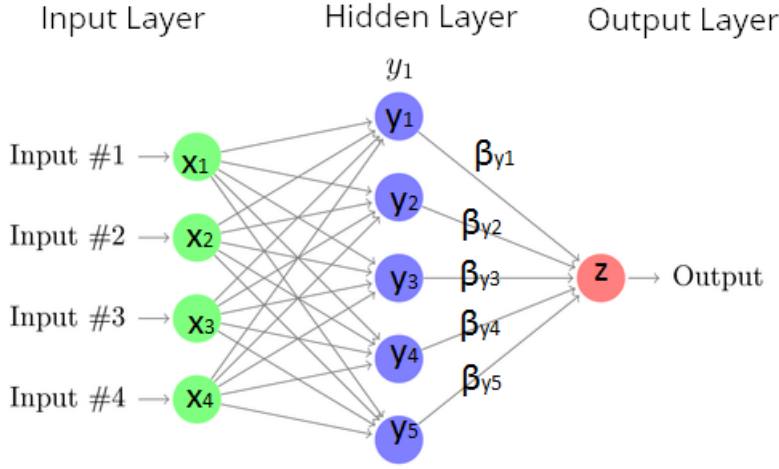


Figure 24: Example neural networks with nodes and weights

The final prediction, z is computed with the equation :

$$z = \beta_{y1} * y_1 + \beta_{y2} * y_2 + \beta_{y3} * y_3 + \beta_{y4} * y_4 + \beta_{y5} * y_5 \quad (4)$$

Where β indicates the weights linking each output to the input of z and each of the y_i terms are also computed in the same manner from the x_i layer. At each node (x,y,z) , there is also the existence of an activation function that modifies the input of the node to compute an output. Commonly used activation functions include the rectified linear unit (ReLU), sigmoid functions like hyperbolic tangent and logistic function,

$$S(T) = \frac{1}{1 + e^{-t}} \quad (5)$$

Thus, the final prediction can be seen as a summation of all weights multiplied by the activation output of each node. In theory, we can expand each of the y_i terms in equation (2) to

include the y_i layer activation function as well as rewrite the y_i layer inputs in terms of the sum of outputs and weights from the x_i layers. This complex integration of terms allows for the neural network to form complex continuous decision boundaries as the neural networks can compute sophisticated non-linear prediction functions despite being a fundamentally linear model.

After a prediction is made, we then have to check whether it is correct, and change our weights if an erroneous prediction was made (Figure 24).

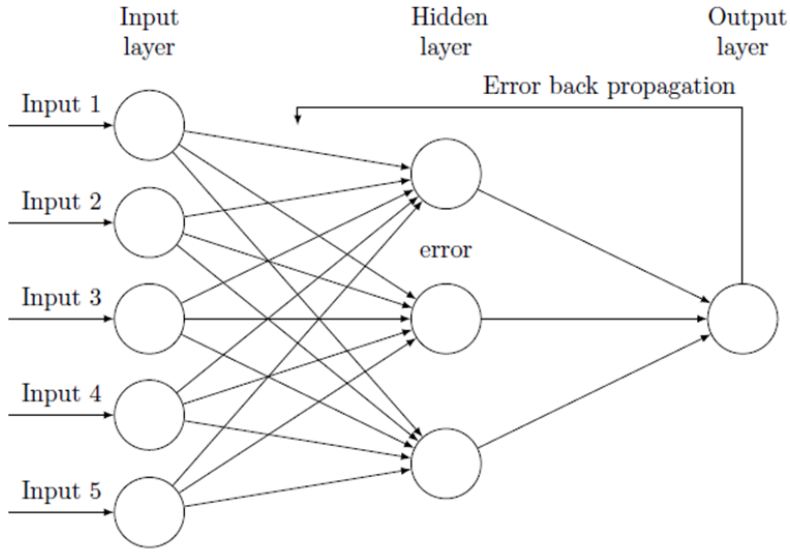


Figure 25: Backpropagation of Error Terms

This is the backpropagation step, which involves backpropagating the error terms from the output layers to the input layer and updating the weights at each node based on the differential relationship between the error and each specific gradient. Specifically, this is governed by the optimiser functions which have been mentioned earlier - one example of such an function is the Stochastic Gradient Descent function, which is

$$\beta_{yi}^n = \beta_{yi}^{n-1} - \alpha \frac{\partial E_n(\beta)}{\partial \beta_i} \quad (6)$$

Here, each β term indicates a gradient, α is a constant for the learning rate and $\frac{\partial E_n(\beta)}{\partial \beta_i}$ is the term used to modify the weight of the gradient based on the cost function $E_n(\beta)$. The idea used in all backpropagation functions is gradient descent, where the contribution of the

gradient term to the error is computed and the gradient is changed by an amount in order to reduce the future contribution of the gradient to that error. Here it is useful to consider what the cost function $E_n(\beta)$ is. It is essentially the error rate when a set of gradients is used to perform predictions, as it measures how many accurate predictions were made and how many wrong predictions were made. For a binary class predictor (which is what we are using, only true and false), this is given by the equation

$$E(\beta) = -\frac{1}{n} \sum_{i=1}^n \sum_{j=1}^2 y_{ij} \log(p_{ij}) \quad (7)$$

where y_{ij} indicates the empirical observed probabilities of each class label while $\log(p_{ij})$ is the theoretical probabilities of each class label. From this term, we see that if the neural network predicts something with a high probability (y_{ij} is high) and it is false (p_{ij} is low) so then $\log(p_{ij})$ is a big negative number, and so the cost function will very high. On the other hand, if y_{ij} and p_{ij} is high then the entropy will be close to zero, indicating a correct prediction. Since each of the prediction terms can be rewritten in terms of the gradient (rewrite z in terms βy_i and so on, we can theoretically compute the contribution of each gradient to the cost function to see how the cost function changes as the gradient changes. Thus, this is what gradient descent does - it tries to see how the cost function changes as each gradient changes, then attempts to move the gradient in the direction that minimises the error term. This is best seen in the graph below where the gradient, or specifically the partial differentiation of the cost function with regards to each gradient is used to move the gradient to a new position so as to minimise the error term. Thus, machine learning is in essence a minimisation problem - we want to find a set of weights that minimises the cost function, and because the cost function describes how many predictions we made correctly, this is also training our network to accurately predict outputs from inputs.

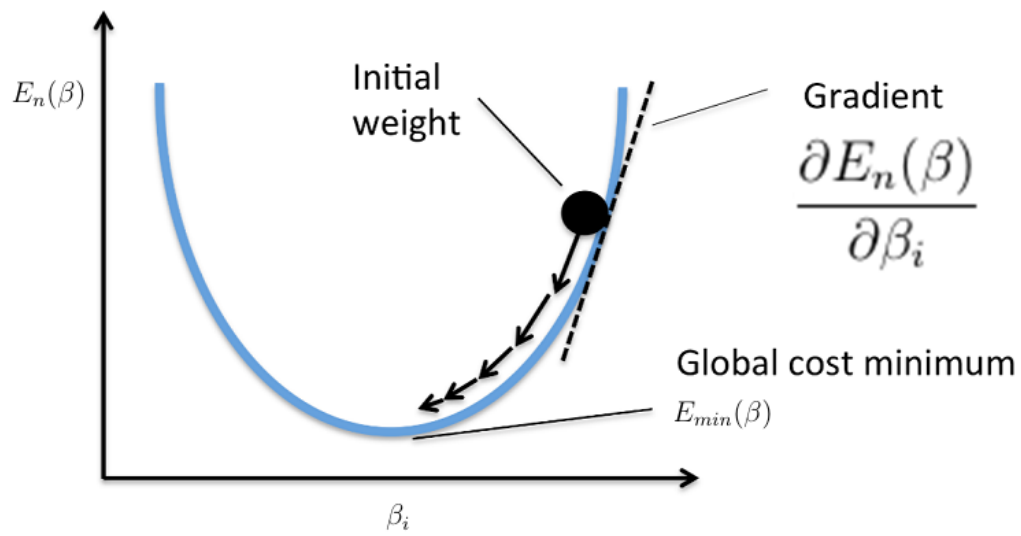


Figure 26: Gradient Descent

5.2 Feature Engineering

We subset our features into three broad sets, which are base-specific information, sequencing error and bias information features, and calling and mapping quality. Base information tells us base specific properties, including information contained in the base as well as the quality of sequenced bases in the samples. Sequencing error and bias features attempt to tease out potential biases in sequencing, including features such as GC content, longest homopolymer run and as well as allele balances and counts. Finally, calling and mapping quality scores provide information on the mapping and calling confidence of the variant callers, and includes features such as genotype confidence and mapping quality. In all, these sets of information provide information on the key aspects of variant calling - specifically the properties of the bases in the samples, the characteristics of the sequencing process and finally the variant calling and mapping algorithms.

Base Information

Shannon Entropy

Shannon Entropy captures the amount of information contained inside the allele sequences. It is calculated using the equation :

$$H(X) = - \sum_{i=1}^n P(x_i) \log_2 P(x_i) \quad (8)$$

where $P(x_i)$ is the probability of finding each base at each position. Thus, we calculate the entropy by summing up the probabilities/ $\lg(\text{probabilities})$ at each position. This prior probability is calculated in two ways and both are used as features - firstly, the overall genome base probabilities are calculated over the entire genome, and thus the entropy is related to the probability of finding a base at any position in the genome. The second way prior probability is calculated is to take a region of space around the allele (10 bases plus the length of the allele in our calculations) and use those probabilities to calculate the entropy of the allelic sequence. Intuitively, it attempts to find out the amount of information contained within the allelic sequence and hopefully the neural network is able to use the information to determine the validity of a mutation.

Kullback Leibler Divergence

The Kullback-Leibler Divergence feature is similar to Shannon entropy, but instead we use this to measure the informational change converting from the reference to the allele sequence. The Kullback-Leibler Divergence is calculated as follows :

$$D_{KL}(P||Q) = - \sum_{i=1}^n P(x_i) \log_2 \frac{P(x_i)}{Q(x_i)} \quad (9)$$

where $Q(x_i)$ is the prior probability of finding each base at each position based on the genomic region around the allele, while $P(X_i)$ is the posterior probability of finding a specific base inside the allelic sequence. Thus, the KL divergence describes the informational gain when the probabilities from Q is used to describe P. Intuitively, since we know the base probabilities of the region, we can then study the probabilities observed in the reference allelic sequence and see how well $Q(X_i)$ probabilities is able to approximate $P(X_i)$ probabilities.

Base Quality

Base quality refers to the Phred score probability that the called allele is wrong. It is given by the equation :

$$P = 10^{-\frac{Q}{10}}$$

Where P is the Base Quality and Q is the probability that the allele called is wrong. This is a number computed by the sequencing machine based on the quality of the base samples provided, and tells us how much confidence the sequencing machine has in calling that base.

Sequencing Biases and Errors

GC content

This feature computes the calculated GC content of reference genome, which may affect sequencing results and accuracy as regions with a GC content are known to be more difficult to sequence. This is because of the greater strength of GC bonds, resulting in errors and biases in sequencing (Benjamini & Speed, 2012).

Longest homozygous run

Homopolymer runs (AAAAAAAA) are known to cause sequencer errors (Quail et al.,2012), and might be a factor in determining in whether a variant is true. This because long homopolymers provide the same type of signal to the sequencing machine, resulting in a difficult in estimating the magnitude of the signal or rather how many bases are in that homopolymer, resulting in errors and wrongly called variants. The reference sequence region including the allele was checked for homopolymer runs.

Allele Count and Allele Balance

Allele count gives the total number of alleles in called phenotypes, while allele balance gives the ratio of final allele called over all other alleles called(reference allele for heterozygous calls, or other alleles for homozygous calls). Both these features give us information of possible biases in the sequencing machine.

Calling and Mapping Qualities

Genotype Likelihood

The genotype likelihood provides the phred-scaled likelihood scores of how confident the caller is in determining that it is a homozygous or heterozygous call, and for the homozygous calls whether it is a more likely to be a bi-allelic mutation or no mutation at all. This feature thus gives us the confidence of the caller in determining if one or two alleles have mutated.

Read Depth

Mapped read depth refers to the total number of bases sequenced and aligned at a given reference base position. The read depth tells us how many reads contributed to a specific call, and thus provides information on how much evidence there is for the variant call

Quality by Depth

Quality by Depth is computed by dividing the quality score against allele depth, to obtain an average score of allele quality. This composite feature provides information on the information provided by each read supporting the call

Mapping Quality

Mapping quality is originally a score provided by the alignment method and gives the probability that a read is placed accurately. The variant callers compute a overall mapping quality of the reads that provide evidence for a variant call which is given in this feature. A low mapping quality means that there are multiple positions where the reads contributing to this variant call could have gone, and thus providing evidence that this might not be an accurate call due to poor mapping.

5.3 Mathematical and Statistical Tools

A. Derivation of F1 Score

The F1 score is a useful measure as it can measure both the precision as well as the recall of a predictor. For a binary predictor with a binary truth class(Figure 26), we can obtain 4 types of results - true positives, true negatives, false positives and false negatives.

		Predicted Class	
		Yes	No
Actual Class	Yes	True Positive	False Negative
	No	False Positive	True Negative

Figure 27: Confusion Matrix

True positives are positive predictions that are made that are actually positive class labels, while false positives are positive predictions that are made that have negative class labels. Similarly, true negatives are negative predictions that have negative class labels, while false negatives are negative predictions that are actually positive class labels. From this, we can define two equations, precision and recall. Precision is defined as (8) while recall is defined as (9).

$$Precision = \frac{True\ Positive}{True\ Positive + False\ Positive} \quad (10)$$

$$Recall = \frac{True\ Positive}{True\ Positive + False\ Negative} \quad (11)$$

Precision tells us how likely a positive prediction made will be true, while recall tells us how much of the truth class positive predictions the predictor is able to encompass. Thus, a predictor can have a high precision but low recall (makes few predictions but are very accurate) or a high recall and low precision(makes a lot of predictions that capture all truth variables, but have a lot of false positives as well). In genomics, both types of errors are not desired - we would want all the predictions to be true (precision), while not losing out on any important mutations (recall). Thus, we use the composite metric, the F1 score, that

looks at the overall precision and recall of a predictor. It is defined as follows :

$$F1\ Score = \frac{2 * Precision * Recall}{Precision + Recall} \quad (12)$$

B. Principal Components Analysis (PCA)

Principal Components Analysis (PCA) is a commonly used tool for dimensionality reduction. It was first proposed by Pearson in 1901 (Pearson, 1901) and has been commonplace in many data analytics and signal processing methodologies (Jolliffe, 2002). PCA works by attempting to discover orthogonal principal components (PCs) that are able to represent the original data. Specifically, this means that the PCs are able to capture variance in the datasets. This is done by finding the Eigenvalues and Eigenvectors of the dataset, with the eigenvectors representing a linear combination of all input variables and the eigenvalues representing the amount of variance that that eigenvector is able to represent. Ultimately, we select n eigenvectors that is able to represent a percentage of variance in our dataset. Because each eigenvector is orthogonal, they are able to capture the variance in the dataset. For our analysis, we decided to use 8 principal components - we took the limit as the last principal components that was able to represent at least 0.5% of variance in the dataset.

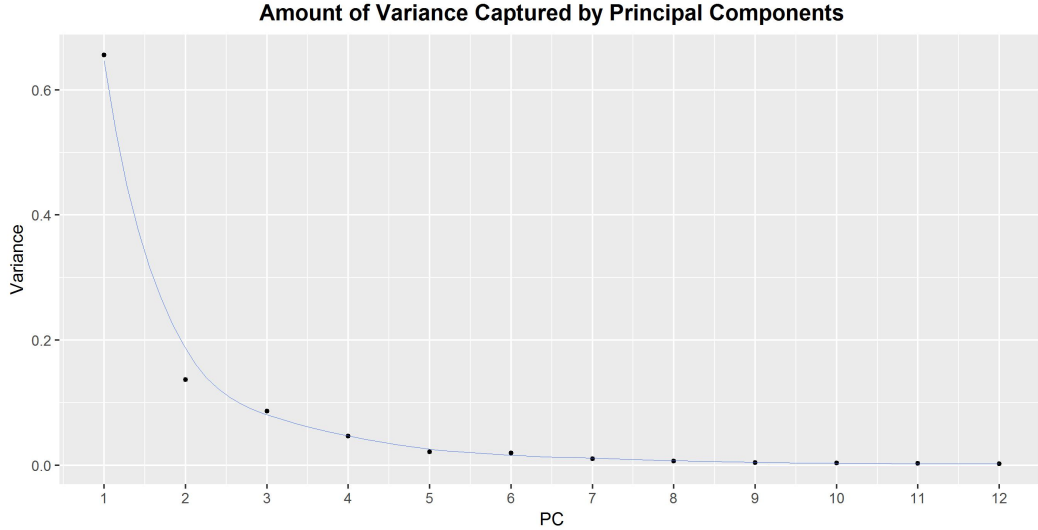


Figure 28: Variance captured by first 12 principal components

To carry out PCA, we used the preprocessing step SciPy to normalise all the input vectors to mean 0 and standard deviation 1. Subsequently, we perform principal components

decomposition to obtain the eigenvector transformed representation of the dataset, and their corresponding eigenvalues. We then fit 8 of the principal components that explained the largest amount of variance into the neural network to study if it is able to learn from the compressed representation of the input features.

B. Synthetic Minority Overrepresentation Technique (SMOTE) SMOTE is a statistical technique described in by Chawla et al. (2002) to overcome problems with imbalanced datasets that are common in machine learning. SMOTE oversamples the training class with less variables in a way that tries not to replicate data points (that makes certain data points over-represented) without creating new invalid training training examples. It does this by taking the intersection of two nearest data points of the same training class. This can be seen in Figure 28.

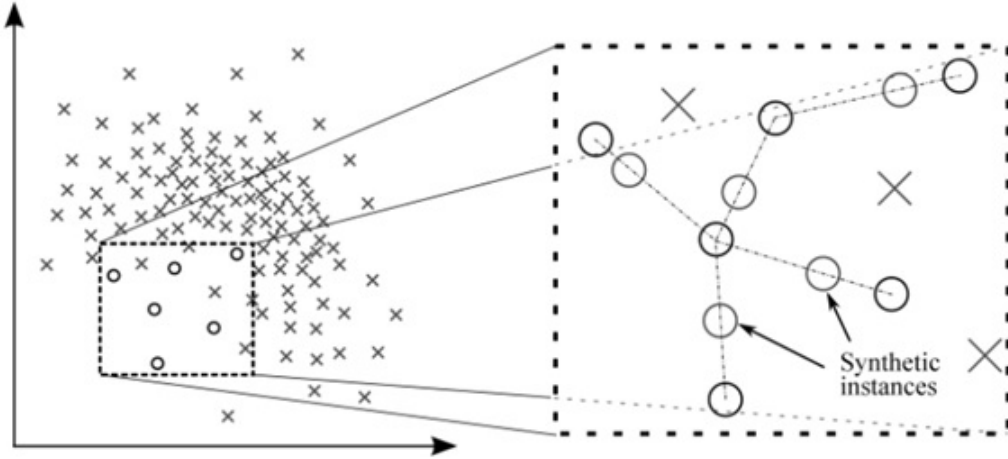


Figure 29: SMOTE oversampling algorithm

In doing so, it creates a more generalised representation of the sample class with less training examples, without replicating certain datapoints and without creating invalid data. This enables intelligent oversampling of the dataset to balance out the positive and negative feature classes. SMOTE has been shown to be valid for other datasets including sentence boundary detection (Liu et al., 2006) and data mining (Chawla, 2005).

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7 Relevant Code

3 code segments are provided to clarify the implementation of generating the matrixes for deep learning, deep learning networks and finally bayesian networks. Other code segments not shown include the code base for parsing vcf input into features, concordance generators, NextFlow and Bash code used to simulate and process genomic data as well as to control deep learning and analytic pipelines, and other python helper scripts (e.g. comparing two VCF files, analysis with pre-trained network).

7.1 generate_matrixes.py

```
1  #This python script generates the set of matrixes to be used in deep learning, and then calls the main
   ↪ method that trains the deep learning network.
2  #Input : a directory that contains all the vcf files for processing, as well as a truth file.
3  #Output : np.arrays of features from generate_matrixes with accompanying truth labels, feature set lengths,
   ↪ a dictionary of vcf object records, as well as the list of relevant sample features for easy reference
4  #Notes :
5  #Vcf files should be labelled with vcf and truth file should be labelled with truth.
6  #No other file should be present in the folder
7  #Overall Strategy :
8  #Generate a dictionary of lists, where the keys are mutations, and the value is contains a matrix
   ↪ containing information of all five callers
9  #Secondly, for each mutation label, check if it is inside the truth file or not. The truth is preloaded
   ↪ into a dictionary
10 #Finally, pass the set of features with accompanying truth labels to the neural network
11 #The main datastructure used are python dictionaries, which allows O(1) dictionary lookup times
12
13 import os
14 import time
15 from ANNgenerateresults import * #this file contains all the main methods for actual neural network
   ↪ training
16 from methods import * #this file contains all the methods for parsing each VCF entry into a numerical list
   ↪ of features
17
18 #set of useful files that contains processed data to be saved
19 LIST_OF_INPUTS_NAME = '/ANN/samplelist.p'
20 TRUTH_DICTIONARY_NAME = '/ANN/truthdict.p'
21 CALLER_LENGTH_FILE_NAME = '/ANN/callerlengths.txt'
22 VCF_LIST_FILE_NAME = '/ANN/vcf_list.p'
23 SCORES_NAME = '/ANN/scores.txt'
24 Y_DATA_NAME = '/ANN/myydata.txt'
25 X_DATA_NAME = '/ANN/myXdata.txt'
26
27 #Initialise NUMBER_OF_CALLERS
28 NUMBER_OF_CALLERS = 5
29
30
```



```

31 # This method follows the typical input output processing pipeline
32 # It takes in the user input, and loads it into local variables.
33 # It then executes another method, main_analyse_samples_and_truth on the loaded variables
34 # Finally, it then saves files into a directory determined by the final variables, and calls the next step
    ↪ of the pipeline
35 # the neural network training, which is main_gather_input_execute_prep_output
36
37 def load_and_save_data(user_input):
38     user_input = vars(user_input)
39     input_samples, referencepath, output_location = load_references(user_input) # load user input
40     my_x_dataset, my_y_dataset, list_of_samples, truth_dictionary, length_of_caller_outputs, \
41     vcf_record_list = main_analyse_samples_and_truth(input_samples, referencepath)
42     save_files(output_location, my_x_dataset, length_of_caller_outputs,
43               list_of_samples, truth_dictionary, vcf_record_list, my_y_dataset)
44     orig_stdout = sys.stdout #save print statements into stdout
45     f = file(str(output_location) + SCORES_NAME, 'w')
46     sys.stdout = f
47     main_gather_input_execute_prep_output(length_of_caller_outputs, truth_dictionary, my_x_dataset,
    ↪ my_y_dataset, list_of_samples, output_location, vcf_record_list)
48
49 # This method first prepares a dictionary of truth to be checked against. It then initialises
50 # a dictionary of samples with all the keys, each key being a variant call, and then fills it up each key
    ↪ with data from each caller
51 # subsequently, it removes dictionary entries that are the wrong size, and then checks whether
52 # each entry in the dictionary is true or not by looking up the truth dictionary
53 # subsequently it performs array balancing, and converts the data to np.array, as well as the dictionary of
    ↪ truth
54 # and list of called samples
55
56 def main_analyse_samples_and_truth(path, referencepath):
57     os.chdir(path)
58     truthdict = generate_truth_list(path)
59     print "truth dictionary generated at time :", time.time() - start
60     callerlengths, list_of_called_samples, vcf_list = generate_input(path, referencepath)
61     print "samples generated at time :", time.time() - start
62     clean_truth_array, cleaned_sample_array = check_predicted_with_truth(list_of_called_samples,
    ↪ truthdict)
63     print "samples checked with truth at time :", time.time() - start
64     cleaned_sample_array = np.array(cleaned_sample_array, np.float64)
65     clean_truth_array = np.array(clean_truth_array)
66     return cleaned_sample_array, clean_truth_array, list_of_called_samples, truthdict, callerlengths,
    ↪ vcf_list
67

```

```

68  # This method generates the truth dictionary, by iterating through the vcf file, parsing all the vcf
    ↪ entries and appending them all as keys in the dictionary
69
70  def create_truth_dictionary(generated_truth_dictionary, truth_file):
71      vcf_reader = vcf.Reader(open(truth_file, 'r'))
72      for record in vcf_reader:
73          if "GL" in record.CHROM:      #Ignore non-regular chromosomes in our dataset
74              continue
75          templist = []
76          for item in record.ALT:
77              templist.append(str(item).upper())      #Alternates might be a list, so they have to be
    ↪ saved as a immutable tuple
78          generated_truth_dictionary[(str(record.CHROM), str(record.POS), str(record.REF).upper())] =
    ↪ tuple(templist)
79
80  # This method generates the input dictionary, by first initialising the keys of the dictionary by iterating
    ↪ through the vcf file once, and then
81  # Iterating through the vcf file again and parsing all the entries as input vectors
82
83  def generate_input(path, referencepath):
84      reference_dictionary = get_reference_dictionary_for_entropy(referencepath)
85      base_entropy = get_ref_entropy(referencepath)
86      full_dictionary = get_dictionary_keys(path)
87      list_of_called_samples, callerlengths, vcf_list = fill_sample_dictionary(base_entropy,
    ↪ full_dictionary, path, reference_dictionary)
88      return callerlengths, list_of_called_samples, vcf_list
89
90
91  # This method goes through all the training variant calling files and extracts unique calls as keys in the
    ↪ sample dictionary
92
93  def get_dictionary_keys(path):
94      sample_dictionary = {}
95      for vcf_file in os.listdir(path):
96          if ignore_file(vcf_file):
97              continue
98          vcf_reader = vcf.Reader(open(vcf_file, 'r'))
99          sample_dictionary = create_dictionary_keys(vcf_reader, sample_dictionary)
100      return sample_dictionary
101
102  #This method ensures the feature vector is in the right order - the entries must always be in the order fb,
    ↪ hc, ug, pindel and st.
103
104  def create_list_of_paths(path):

```

```

105     list_of_paths = [0] * NUMBER_OF_CALLERS
106     for vcf_file in os.listdir(path):
107         if ignore_file(vcf_file):
108             continue
109         if "fb" in vcf_file:
110             list_of_paths[0] = vcf_file
111         if "hc" in vcf_file:
112             list_of_paths[1] = vcf_file
113         if "ug" in vcf_file:
114             list_of_paths[2] = vcf_file
115         if "pind" in vcf_file:
116             list_of_paths[3] = vcf_file
117         if "st" in vcf_file:
118             list_of_paths[4] = vcf_file
119     return list_of_paths
120
121     # This method goes through all the training variant calling files and fills each entry in a sample
122     ↪ dictionary
123     # with data. If it is empty, it returns an array of length n, where n is the number of variables
124     # that same caller would have provided.
125     # Each caller has a different amount of variables because it contains different datasets
126
127     def fill_sample_dictionary(base_entropy, sample_dictionary, path, reference_dictionary):
128         callerlengths = [0] * number_of_callers
129         index = 0
130         total_mode_value = 0
131         list_of_paths = create_list_of_paths(path)
132         for vcf_file in list_of_paths:
133             index += 1
134             opened_vcf_file = vcf.Reader(open(vcf_file, 'r'))
135             removaldict = iterate_over_file_to_extract_data(base_entropy, sample_dictionary,
136                                                             reference_dictionary, opened_vcf_file, vcf_file)
137             mode_value = get_mode_value(removaldict)
138             add_length_to_caller_lengths_based_on_file_name(vcf_file, mode_value, callerlengths)
139             refill_dictionary_with_zero_arrays_for_each_file(sample_dictionary, index, mode_value)
140             total_mode_value += mode_value
141             list_of_passed_samples, vcf_list = add_mode_values_into_list_of_samples(sample_dictionary,
142                                         ↪ total_mode_value)
143         return list_of_passed_samples, callerlengths, vcf_list
144
145     # this method fills the dictionary with empty arrays with the same length as the ones that were supposed to
146     ↪ be added

```

```

146 def refill_dictionary_with_zero_arrays_for_each_file(full_dictionary, index, length_of_data_array):
147     empty_set = []
148     for i in range(length_of_data_array):
149         empty_set.append(0)
150     for item in full_dictionary:
151         checksum = len(full_dictionary[item][0])
152         if checksum < index:
153             arbinfo = empty_set
154             full_dictionary[item][0].append(arbinfo)
155
156
157 # this method iterates through all the files to extract data from each sample. It uses methods from the
158 # methods.py function, which parses each record for data.
159
160 def iterate_over_file_to_extract_data(base_entropy, sample_dictionary, recorddictionary, vcf_reader1,
    ↪ vcf_file):
161     removaldict = {}
162     for record in vcf_reader1:
163         if "GL" in str(record.CHROM):
164             continue
165         sample_name = get_sample_name_from_record(record)
166         sample_data = getallvalues(record, recorddictionary, base_entropy, vcf_file)
167         sample_dictionary[sample_name][0].append(sample_data)
168         sample_dictionary[sample_name][1] = record
169         create_removal_dict(sample_data, removaldict)
170     return removaldict
171
172 # this method counts the mode number of entries in the dictionary. Due to certain vcf files having multiple
    ↪ possible number of entries for a field, this will create an error
173 # as the size of the input arrays should always be constant. Thus, any sample that does not fit the array
    ↪ should be removed.
174 # TO-DO See if a better implementation can be done that doesn't reduce data available
175
176 def create_removal_dict(sample_data, removaldict):
177     count = 0
178     count += len(sample_data)
179     if count not in removaldict:
180         removaldict[count] = 1
181     else:
182         removaldict[count] += 1
183
184
185 # this method prepares the reference genome dictionary for use in entropy calculations
186

```

```

187 def get_reference_dictionary_for_entropy(reference_path):
188     record_dictionary = SeqIO.to_dict(SeqIO.parse(reference_path, "fasta"), key_function=get_chr)
189     return record_dictionary
190
191 # this method ensures that the files inputed are correct
192
193 def ignore_file(vcf_file):
194     if "vcf" not in vcf_file or "truth" in vcf_file:
195         return True
196     return False
197
198 # this method creates the set of keys for the dictionary
199
200 def create_dictionary_keys(vcf_reader, sample_dictionary):
201     for record in vcf_reader:
202         if "GL" in str(record.CHROM):
203             continue
204         sample_name = get_sample_name_from_record(record)
205         sample_dictionary[sample_name] = [], [] # fullname has become a key in fulldictionary
206     return sample_dictionary
207
208 # standard method that returns a tuple of the variant call object with the chromosome, position, reference
↪ and tuple of alternates
209
210 def get_sample_name_from_record(record):
211     templist = []
212     for item in record.ALT:
213         templist.append(str(item).upper())
214     sample_name = (str(record.CHROM), str(record.POS), str(record.REF).upper(), tuple(templist))
215     return sample_name
216
217 # this method sets the length of the input neural networks
218
219 def add_length_to_caller_lengths_based_on_file_name(vcf_file, caller_length, callerlengths):
220     if "fb" in vcf_file:
221         callerlengths[0] = caller_length
222     if "hc" in vcf_file:
223         callerlengths[1] = caller_length
224     if "ug" in vcf_file:
225         callerlengths[2] = caller_length
226     if "pind" in vcf_file:
227         callerlengths[3] = caller_length
228     if "st" in vcf_file:
229         callerlengths[4] = caller_length

```

```

230
231 # this method wraps the create truth dictionary method and is used to checking that the dictionary file has
    ↳ the correct name
232
233 def generate_truth_list(path):
234     generated_truth_dictionary = {}
235     for truth_file in os.listdir(path):
236         if "truth" not in truth_file:
237             continue
238         create_truth_dictionary(generated_truth_dictionary, truth_file)
239     return generated_truth_dictionary
240
241 # this method takes in the mutation (in a tuple) and checks if that mutation exists in the truth dictionary
242 # A mutation exists if the chromosome, reference and position of the variant call is correct, AND one of
    ↳ the alternate alleles it contains
243 # is also an alternate allele in the truth dataset
244
245 def check_sample_against_truth_dictionary(tuple_name, final_truth_list, truth_dictionary):
246     temp_tuple = (tuple_name[0], tuple_name[1], tuple_name[2])
247     if temp_tuple in truth_dictionary:
248         for alternate in tuple_name[3]:
249             if alternate in truth_dictionary[temp_tuple]:
250                 final_truth_list.append(1)
251             return
252     final_truth_list.append(0)
253     return
254
255 # This method loads the paths of the files into local variables
256
257 def load_references(user_input):
258     file1 = user_input['input'][0]
259     referencepath = user_input['reference']
260     output_location = user_input['output']
261     return file1, referencepath, output_location
262
263 # This method saves all the processed data into files that can be used for other purposes later or loaded
    ↳ natively instead of doing the processing again
264
265 def save_files(output_location, x_array, length_of_caller_outputs, sample_list, truth_dict,
    ↳ vcf_dictionary_file,
266                 y_array=[]):
267     file2 = output_location
268     x_data_file_name = str(file2) + str(X_DATA_NAME)
269     np.save(x_data_file_name, x_array)

```

```

270     vcf_file_name = str(file2) + str(VCF_LIST_FILE_NAME)
271     caller_length_file_name = str(file2) + str(CALLER_LENGTH_FILE_NAME)
272     truth_dictionary_name = str(file2) + str(TRUTH_DICTIONARY_NAME)
273     list_of_inputs_name = str(file2) + str(LIST_OF_INPUTS_NAME)
274     np.save(caller_length_file_name, length_of_caller_outputs)
275     with open(list_of_inputs_name, 'wb') as samplesave1:
276         pickle.dump(sample_list, samplesave1)
277     with open(truth_dictionary_name, 'wb') as samplesave2:
278         pickle.dump(truth_dict, samplesave2)
279     with open(vcf_file_name, 'wb') as samplesave3:
280         pickle.dump(vcf_dictionary_file, samplesave3)
281     if y_array != []:
282         y_data_file_name = str(file2) + str(Y_DATA_NAME)
283         np.save(y_data_file_name, y_array)
284
285     # This method takes in two dictionaries, a dictionary of truth mutations and a dictionary of sample
286     ↪ mutations,
287     # checks whether each of the sample variables are inside the truth dictionary
288     # and returns 2 arrays, an array of samples and an array of accompanying truth labels
289
290     def check_predicted_with_truth(passed_list_of_samples, dictionary_of_truth=[]):
291         final_array_of_samples = []
292         final_truth_list = []
293         for item in passed_list_of_samples:
294             if dictionary_of_truth:
295                 check_sample_against_truth_dictionary(item[0], final_truth_list, dictionary_of_truth)
296             temp_array = []
297             for row in item[1]:
298                 temp_array.extend(row)
299             final_array_of_samples.append(temp_array)
300         if dictionary_of_truth:
301             return final_truth_list, final_array_of_samples
302         return final_array_of_samples
303
304     # This method ensures that only the variables that have the modal number of features are used
305     # in neural network training to ensure all array sizes are the same
306
307     def add_mode_values_into_list_of_samples(full_dictionary, mode_value):
308         list_of_passed_samples = []
309         vcf_list = []
310         for key in full_dictionary:
311             second_count = 0
312             for item in full_dictionary[key][0]:
313                 second_count += len(item)

```

```

313         if second_count != mode_value:
314             continue
315         list_of_passed_samples.append([key, full_dictionary[key][0]])
316         vcf_list.append(full_dictionary[key][1])
317     return list_of_passed_samples, vcf_list
318
319     # This method gets the modal number of features from a modal dictionary
320
321     def get_mode_value(removaldict):
322         curr = 0
323         mode_value = 0
324         for new_key in removaldict:
325             if removaldict[new_key] > curr:
326                 curr = removaldict[new_key]
327                 mode_value = new_key
328         return mode_value
329
330     # This method iterates through the dataset to create a modal dictionary which contains a key-value pair of
331     ↪ (number of features - number of times seen).
332     # The mode number of features is kept
333
334     def iterate_through_dictionary_to_find_mode_size(full_dictionary):
335         removaldict = {}
336         samples = 0
337         for key in full_dictionary:
338             samples += 1
339             if samples == sample_limit:
340                 break
341             count = 0
342             for item in full_dictionary[key]:
343                 count += len(item)
344             if count not in removaldict:
345                 removaldict[count] = 1
346             else:
347                 removaldict[count] += 1
348         return removaldict
349
350     if __name__ == "__main__":
351         np.seterr(divide='raise', invalid='raise')
352         parser = argparse.ArgumentParser(description="train neural net")
353         parser.add_argument('-i', '--input', help="give directories with files", nargs='+')
354         parser.add_argument('-d', '--debug', help="look at matrixes built")
355         parser.add_argument('-r', '--reference', help="")

```



```

356     parser.add_argument('-o', '--output', help="")
357     paths = parser.parse_args()
358     start = time.time()
359     load_and_save_data(paths)

```

7.2 train_network.py

```

1  #This script is called by the generate_matrixes.py script and contains the implementation of the neural
   ↪ network.
2  #Input : np.arrays of features from generate_matrixes with accompanying truth labels, feature set lengths,
   ↪ a dictionary of vcf object records, as well as the list of sample features
3  #Output : A VCF file containing all the filtered entries by the neural network, as well the list of
   ↪ accompanying scores
4  #Overall Strategy :
5  #Perform SMOTE oversampling of the input features, and then use the features to train the neural network
6  #After training, perform validation on test dataset, and subsequently prepare a vcf file with filtered
   ↪ entries
7
8
9  #import all necessary components
10 import argparse
11 import cPickle as pickle
12 import sys
13 import numpy as np
14 import vcf
15 from imblearn.over_sampling import SMOTE
16 from keras.callbacks import *
17 from keras.layers import Dense, Dropout, Activation
18 from keras.layers.advanced_activations import LeakyReLU
19 from keras.layers.normalization import BatchNormalization
20 from keras.models import Sequential
21 from keras.models import load_model
22 from keras.optimizers import RMSprop
23 from sklearn.metrics import *
24 from sklearn.model_selection import train_test_split
25
26
27 #set constants
28 PCA_COMPONENTS = 8
29 STEP_INCREMENT = 10
30 RECURSION_LIMIT = 0.0002
31 VERBOSE = 1
32 seed = 1337
33

```

```

34  # Initialise random seed for reproducibility
35  np.random.seed(seed)
36
37  #Prepare file names for saving
38  vcf_file_name = "/ANN/truevcf.vcf"
39  keras_model_name = "/ANN/model"
40  model_truth_name = "/ANN/modeltruths.txt"
41  model_predictions_name = "/ANN/modelpredictions.txt"
42  original_vcf_reader = "/data/backup/metacaller/stage/data/version6.3a/hc.vcf.normalisedtrain.vcf"
43
44  # this method takes in a path and returns training matrixes for the ANN
45  # The path should contain n caller vcf files and 1 truth file
46  # vcf files should be labelled with vcf and truth file should be labelled with truth
47  # no other file should be present in the folder
48  def main_gather_input_execute_prep_output(array_sizes, dict_of_truth_input, fullmatrix_sample,
    ↪ fullmatrix_truth, list_of_samples_input, save_location, vcf_dictionary):
49      calculated_prediction_actual, calculated_truth_actual = train_neural_net(20, 10, fullmatrix_sample,
    ↪ fullmatrix_truth,
    ↪ save_location, array_sizes)
50      get_all_relevant_scores(calculated_prediction_actual, calculated_truth_actual, dict_of_truth_input,
    ↪ list_of_samples_input, vcf_dictionary, save_location)
51
52  # This method counts the number of false negatives inside the input sample
53
54  def count_false_negative(calculated_prediction_actual, calculated_truth_actual):
55      count_false_negative = 0
56      for i in range(len(calculated_prediction_actual)):
57          if calculated_prediction_actual[i] == 0 and calculated_truth_actual[i] == 1:
58              count_false_negative += 1
59      return count_false_negative
60
61  # this is the wrapper function for the recursive hill climbing algorithm to get the best f1 score
62  # It starts from a low threshold value, and marginally increases the threshold until it is unable to find
63  # any better F1 scores. It then reports the threshold, F1 score and produces the filtered callset
64
65  def get_all_relevant_scores(calculated_prediction_actual, calculated_truth_actual, dict_of_truth_input,
66                             list_of_samples_input, vcf_list, outputpath):
67      print "Here are some predictions", calculated_prediction_actual[:100]
68      print "here are some truths", calculated_prediction_actual[:100]
69      f1_score_left = get_scores(calculated_prediction_actual, calculated_truth_actual, 0.0,
    ↪ list_of_samples_input, dict_of_truth_input)
70      guess_f1_final_score, guess_f1_final = recursive_best_f1_score(calculated_prediction_actual,
    ↪ calculated_truth_actual, dict_of_truth_input, list_of_samples_input, 0.0, f1_score_left, 0.2)

```

```

71     get_scores(calculated_prediction_actual, calculated_truth_actual, guess_f1_final,
72               ↪ list_of_samples_input, dict_of_truth_input, VERBOSE)
73
74     produce_vcf_file(calculated_prediction_actual, guess_f1_final, list_of_samples_input, vcf_list,
75                     ↪ outputpath)
76
77     # This method produces the vcf file through filtering with the neural network threshold calls
78
79     def produce_vcf_file(calculated_prediction_actual, guess_f1_final, list_of_samples_input, vcf_list,
80                         ↪ outputpath):
81         prediction = []
82         for item in calculated_prediction_actual:
83             if item > guess_f1_final:
84                 prediction.append(1)
85             else:
86                 prediction.append(0)
87         list_of_records = []
88         for i in range(len(list_of_samples_input)):
89             if prediction[i] == 1:
90                 list_of_records.append(vcf_list[i])
91         vcf_reader = vcf.Reader(filename=original_vcf_reader)
92         vcf_writer = vcf.Writer(open(outputpath + vcf_file_name, 'w'), vcf_reader)
93         for record in list_of_records:
94             vcf_writer.write_record(record)
95
96     # This method is the recursive function that attempts to find the threshold that produces the best f1
97     ↪ score. It does this
98     # by iterating through steps of thresholds (0.2, 0.02 and 0.002) until no better F1 score can be found for
99     ↪ a marginal increase in threshold.
100     # It then returns the best F1 score and the threshold
101
102     def recursive_best_f1_score(calculated_prediction_actual, calculated_truth_actual, dict_of_truth_input,
103                                list_of_samples_input, guess, guess_score, step):
104         if step <= RECURSION_LIMIT:
105             return guess_score, guess
106         new_guess = guess + step
107         new_guess_score = get_scores(calculated_prediction_actual, calculated_truth_actual, new_guess,
108                                     list_of_samples_input, dict_of_truth_input)
109         if new_guess_score > guess_score:
110             return recursive_best_f1_score(calculated_prediction_actual, calculated_truth_actual,
111                                             dict_of_truth_input,
112                                             list_of_samples_input, new_guess, new_guess_score, step)
113         return recursive_best_f1_score(calculated_prediction_actual, calculated_truth_actual,
114                                         dict_of_truth_input,
115                                         list_of_samples_input, guess, guess_score, step / STEP_INCREMENT)

```

```

108
109 # this method uses pre-loaded data to train the neural network. It is optional and only used when this
    ↪ python script is called natively and not imported
110
111 def load_references(input_paths):
112     input_paths = vars(input_paths)
113     fullmatrix_sample = np.load(input_paths['input'][0])
114     fullmatrix_truth = np.load(input_paths['input'][1])
115     with open(input_paths['input'][3], 'rb') as fp1:
116         list_of_samples_input = pickle.load(fp1)
117     with open(input_paths['input'][4], 'rb') as fp2:
118         dict_of_truth_input = pickle.load(fp2)
119     array_sizes = np.load(input_paths['input'][5])
120     with open(input_paths['input'][6], 'rb') as fp3:
121         vcf_dictionary = pickle.load(fp3)
122     orig_stdout = sys.stdout
123     f = file(str(input_paths['input'][3]) + '.txt', 'w')
124     sys.stdout = f
125     return array_sizes, dict_of_truth_input, fullmatrix_sample, fullmatrix_truth, list_of_samples_input,
    ↪ input_paths, vcf_dictionary
126
127 # this method solves the double false negative problem that is created due to the neural network prediction
    ↪ scheme
128
129 def remove_duplicated_false_negative(prediction_list, truth_list, false_negatives):
130     count = 0
131     removal_list = []
132     for i in range(len(prediction_list) - 1, -1, -1):
133         if count == false_negatives:
134             break
135         if prediction_list[i] == 0 and truth_list[i] == 1:
136             removal_list.insert(0, i)
137             count += 1
138     for index in removal_list:
139         prediction_list.pop(index)
140         truth_list.pop(index)
141     return prediction_list, truth_list
142
143 # this method takes in the binary truth and predicted samples and calculates the true positive rate, false
    ↪ positive rate, recall, precision and f1 score
144
145 def get_scores(actual_predictions, actual_truth, value, sample_list, truth_dictionary, verbose=0):
146     temp_actual_truth = list(actual_truth)
147     prediction = []

```

```

148     for item in actual_predictions:
149         if item > value:
150             prediction.append(1)
151         else:
152             prediction.append(0)
153     false_negatives = count_false_negative(actual_predictions, actual_truth)
154     finalpredictionnumbers, finaltruthnumbers = add_negative_data(sample_list, truth_dictionary,
        ↪ prediction, temp_actual_truth)
155     finalpredictionnumbers, finaltruthnumbers = remove_duplicated_false_negative(finalpredictionnumbers,
        ↪ finaltruthnumbers, false_negatives)
156     final_f1_score = f1_score(finaltruthnumbers, finalpredictionnumbers)
157     if verbose:
158         print_scores(actual_truth, final_f1_score, finalpredictionnumbers, finaltruthnumbers, prediction,
            ↪ value)
159     return final_f1_score
160
161     # default method for printing all relevant scores
162
163     def print_scores(actual_truth, final_f1_score, finalpredictionnumbers, finaltruthnumbers, prediction,
        ↪ value):
164         false_positive_before_adjust, true_negative_before_adjust = perf_measure(actual_truth, prediction)
165         print "false positive is :", false_positive_before_adjust
166         print "true negative is :", true_negative_before_adjust
167         print "precision score is :", precision_score(actual_truth, prediction)
168         print "recall score is :", recall_score(actual_truth, prediction)
169         print "F1 score is : ", f1_score(actual_truth, prediction)
170         final_false_positive, final_true_negative = perf_measure(finaltruthnumbers, finalpredictionnumbers)
171         print "final false positive is :", final_false_positive
172         print "final true negative is :", final_true_negative
173         print "final precision score is :", precision_score(finaltruthnumbers, finalpredictionnumbers)
174         print "final recall score is :", recall_score(finaltruthnumbers, finalpredictionnumbers)
175         print "threshold is", value
176         print "final F1 score is : ", final_f1_score
177
178     # This method looks at the set of predicted samples and the set of truths and adds the false negatives to
        ↪ the predicted sample.
179
180     def add_negative_data(list_of_samples, dict_of_truth, array_of_predicted, array_of_truth):
181         dict_of_samples = generate_sample_dictionary(array_of_predicted, list_of_samples)
182         list_of_truth = generate_list_of_truth(dict_of_truth)
183         new_array_of_predicted = list(array_of_predicted)
184         new_array_of_truth = list(array_of_truth)
185         original_length = len(new_array_of_predicted)
186         for item in list_of_truth:

```

```

187         fillnegative(item, dict_of_samples, new_array_of_predicted, new_array_of_truth)
188     print "number of false data samples are", (len(new_array_of_predicted) - original_length)
189     return new_array_of_predicted, new_array_of_truth
190
191     # This method generates a list of truth variant calls from a dictionary of truth variant calls.
192
193     def generate_list_of_truth(dict_of_truth):
194         list_of_truth = []
195         for key in dict_of_truth:
196             mytuple = dict_of_truth[key]
197             temptuple = []
198             for item in mytuple:
199                 temptuple.append(item)
200             list_of_truth.append([key[0], key[1], key[2], temptuple])
201         return list_of_truth
202
203     # This method generates a dictionary of sample variant calls from a list of sample variant calls.
204
205     def generate_sample_dictionary(array_of_predicted, list_of_samples):
206         dict_of_samples = {}
207         for i in range(len(list_of_samples)):
208             item = list_of_samples[i]
209             if array_of_predicted[i] == 0:
210                 continue
211             new_key = (item[0][0], item[0][1], item[0][2])
212             new_value = item[0][3]
213             if new_key not in dict_of_samples:
214                 dict_of_samples[new_key] = new_value
215             else:
216                 dict_of_samples[new_key] = list(dict_of_samples[new_key])
217                 dict_of_samples[new_key].extend(new_value)
218                 dict_of_samples[new_key] = tuple(dict_of_samples[new_key])
219                 # print dict_of_samples[new_key]
220         return dict_of_samples
221
222     # Actual method to calculated false positive, false negative rates
223
224     def perf_measure(y_actual, y_hat):
225         true_positive = 0
226         false_positive = 0
227         false_negative = 0
228         true_negative = 0
229
230         for i in range(len(y_hat)):

```

```

231         if y_actual[i] == 1 and y_hat[i] == 1:
232             true_positive += 1
233     for i in range(len(y_hat)):
234         if y_hat[i] == 1 and y_actual[i] == 0:
235             false_positive += 1
236     for i in range(len(y_hat)):
237         if y_actual[i] == 1 and y_hat[i] == 0:
238             false_negative += 1
239     for i in range(len(y_hat)):
240         if y_hat[i] == 0 and y_actual[i] == 0:
241             true_negative += 1
242
243     print "true positives :", true_positive
244     print "false positives :", false_positive
245     print "false negatives :", false_negative
246     print "true negatives :", true_negative
247
248     true_positive = float(true_positive)
249     false_positive = float(false_positive)
250     false_negative = float(false_negative)
251     if false_positive == 0 and true_positive == 0:
252         false_positive_rate = 0
253     else:
254         false_positive_rate = false_positive / (false_positive + true_positive)
255     if false_negative == 0 and true_positive == 0:
256         true_negative_rate = 0
257     else:
258         true_negative_rate = false_negative / (false_negative + true_positive)
259
260     return false_positive_rate, true_negative_rate
261
262
263     # comparator method that takes a tuple and checks whether it is in the dictionary of samples, if it is not,
264     ↪ then add a false negative call to the dataset
265
266 def fillnegative(tuple1, sampledict, arrayofsamples, arrayoftruths):
267     tuple2 = (tuple1[0], tuple1[1], tuple1[2])
268     if tuple2 in sampledict:
269         for ALT in tuple1[3]:
270             if ALT in sampledict[tuple2]:
271                 return
272     arrayofsamples.append(0)
273     arrayoftruths.append(1)

```

```

274 # main method that performs neural network training. This method takes in the sample matrices, the truth
    ↪ variables, a save file location, number of epochs,
275 # size of input arrays and the minibatch training size. It first performs SMOTE on the input dataset, then
    ↪ splits it into training and test dataset. It then
276 # initialises the deep learning layers, compiles the neural network and uses the input data to fit the
    ↪ network. The best set of weights at any point is saved
277 # to a file and reloaded at the end of the fitting. After training, the neural network is used to predict
    ↪ the original un-oversampled dataset
278
279 def train_neural_net(mybatch_size, mynb_epoch, myX_train, myy_train, location, arraysize):
280     number = int(reduce(lambda x, y: x + y, arraysize))
281     X_resampled, y_resampled = do_smote_resampling(myX_train, myy_train)
282     X_train, X_test, y_train, y_test = train_test_split(X_resampled, y_resampled,
283                                                         test_size=0.2, random_state=seed)
284
285     batch_size = mybatch_size
286     nb_epoch = mynb_epoch
287
288     final_model = Sequential()
289     final_model.add(BatchNormalization(input_shape=(number,), axis=1))
290     final_model.add(Dense(24, activation='linear'))
291     final_model.add(LeakyReLU(alpha=0.05))
292     final_model.add(Dense(6, activation='linear'))
293     final_model.add(LeakyReLU(alpha=0.05))
294     final_model.add(Dense(1, activation='linear'))
295     final_model.add(Activation('sigmoid'))
296     print (final_model.summary())
297     rmsprop = RMSprop(lr=0.000003, rho=0.9, epsilon=1e-08, decay=0.0)
298     final_model.compile(loss='binary_crossentropy',
299                       optimizer=rmsprop,
300                       metrics=['accuracy'])
301
302     filepath = location + "/best_weights.hdf5"
303     checkpoint = ModelCheckpoint(filepath, monitor='val_acc', verbose=1, save_best_only=True, mode='max')
304     callbacks_list = [checkpoint]
305     model_history = final_model.fit([X_train], y_train, batch_size=batch_size, nb_epoch=nb_epoch,
306                                   validation_split=0.2, verbose=2, callbacks=callbacks_list)
307     final_model = load_model(location + "/best_weights.hdf5")
308     print model_history.history['val_acc'], model_history.history['val_acc']
309     print model_history.history['val_loss'], model_history.history['val_loss']
310     np.save(location + "/best_weights.hdf5", model_history.history['val_acc'])
311     np.save(location + "/best_weights.hdf5", model_history.history['val_loss'])
312     scores = final_model.evaluate([X_test], y_test)
313     print scores
314     final_prediction_array_probabilities = final_model.predict([myX_train])

```



```

314     final_prediction_array_probabilities = np.squeeze(final_prediction_array_probabilities)
315     save_model_details(final_model, final_prediction_array_probabilities, myy_train, location)
316
317     return final_prediction_array_probabilities, myy_train
318
319     # Method to perform SMOTE oversampling
320
321     def do_smote_resampling(myX_train, myy_train):
322         sm = SMOTE(kind='regular')
323         where_are_NaNs = np.isnan(myX_train)
324         myX_train[where_are_NaNs] = 0
325         X_resampled, y_resampled = sm.fit_sample(myX_train, myy_train)
326         return X_resampled, y_resampled
327
328     # this method saves the details of the neural network
329
330     def save_model_details(final_model, save_model_probabilities, trutharray, location):
331         name1 = location + model_predictions_name
332         name2 = location + model_truth_name
333         name3 = location + keras_model_name
334         np.save(name1, save_model_probabilities)
335         np.save(name2, trutharray)
336         final_model.save(name3)
337
338     # this method gets the array size of the features used
339
340     def get_sizes(array_sizes):
341         fb_size = array_sizes[0]
342         hc_size = array_sizes[1]
343         ug_size = array_sizes[2]
344         pindel_size = array_sizes[3]
345         st_size = array_sizes[4]
346         return fb_size + hc_size + ug_size + pindel_size + st_size
347
348
349     # this method uses a map function to filter data such that each merge layer gets the correct set of data
350
351     def prep_input_samples(array_sizes, x_training_data):
352         count = 0
353         X_fb = np.array(map(lambda x: x[count:array_sizes[0]], x_training_data))
354         count += array_sizes[0]
355         X_hc = np.array(map(lambda x: x[count:count + array_sizes[1]], x_training_data))
356         count += array_sizes[1]
357         X_ug = np.array(map(lambda x: x[count:count + array_sizes[2]], x_training_data))

```

```

358     count += array_sizes[2]
359     X_pindel = np.array(map(lambda x: x[count:count + array_sizes[3]], x_training_data))
360     count += array_sizes[3]
361     X_st = np.array(map(lambda x: x[count:count + array_sizes[4]], x_training_data))
362     count += array_sizes[4]
363     return X_fb, X_hc, X_ug, X_pindel, X_st
364
365
366 if __name__ == "__main__":
367     parser = argparse.ArgumentParser(description="train neural net")
368     parser.add_argument('-i', '--input', help="give directories with files", nargs='+')
369     input_path = parser.parse_args()
370     array_sizes, dict_of_truth_input, fullmatrix_sample, fullmatrix_truth, \
371     list_of_samples_input, paths, vcf_dictionary = load_references(input_path)
372     main_gather_input_execute_prep_output(array_sizes, dict_of_truth_input, fullmatrix_sample,
    ↪     fullmatrix_truth, list_of_samples_input, paths, vcf_dictionary)

```

7.3 compute_bayesian.py

```

1  #This script takes in a VCF file with functional annotation already done, and computes the bayesian network
   ↪ using the annotations. It produces a sorted list of vcf entries in a text file, with accompanying
   ↪ annotation scores
2  #Input : VCF file with functional annotation
3  #Output : A sorted list of vcf entries with accompanying annotation scores, redirected from stdout to a
   ↪ file
4  #Overall Strategy :
5  #First extract all the features from the vcf files and then perform feature-wise normalisation.
6  #Subsequently, prepare the bayesian network by creating edges, nodes, preparing prior distributions
7  #Finally use features to update the bayesian network to obtain final probabilities for importance
8  #Report a list of sorted probabilities for easy ranking
9
10 import matplotlib
11 import vcf
12
13 matplotlib.use('Agg')
14
15 from pomegranate import *
16
17 #main method for loading references into local variables
18
19 def load_reference(paths):
20     paths = vars(paths)
21     input = paths['input']
22     opened_vcf_file = vcf.Reader(open(input, 'r'))
23     name3 = input + "finalscores.txt"

```

```

24     # orig_stdout = sys.stdout
25     # f = file(name3 + '.txt', 'w')
26     # sys.stdout = f
27     return opened_vcf_file
28
29     #method for getting functional annotation scores
30
31     def get_scores(record):
32         list_of_important_mutations = [record.INFO['SIFT_score'], record.INFO['LRT_score'],
33                                       record.INFO['MutationAssessor_score'],
34                                       record.INFO['Polyphen2_HVAR_score'], record.INFO['FATHMM_score']]
35
36         if 'NN_prediction' in record.INFO:
37             NN_prediction = record.INFO['NN_prediction'][0]
38         else:
39             NN_prediction = -1
40
41         list_of_important_mutations = map(lambda x: x[0], list_of_important_mutations)
42         list_of_important_mutations = map(lambda x: None if x == None else float(x),
43                                           ↪ list_of_important_mutations)
44
45         return NN_prediction, list_of_important_mutations
46
47     #main method that controls I/O - it gets the input, applies the main function and then prepares the output
48
49     def main(paths):
50         vcf_object = load_reference(paths)
51         full_list_of_scores = analyse_main(vcf_object)
52         prepare_output(full_list_of_scores)
53
54     #this method controls the processes applied to the vcf file - for each record, it extract the list of
55     ↪ scores,
56
57     # normalises it, compute probabilities, sorts it and then return output
58
59     def analyse_main(vcf_object):
60         full_list_of_scores = extract_list_of_scores(vcf_object)
61         apply_feature_wise_normalisation(full_list_of_scores)
62         compute_network_and_probabilities(full_list_of_scores)
63         full_list_of_scores.sort(key=lambda x: x[4], reverse=True)
64         return full_list_of_scores
65
66     # since print is redirected to stdout, print function is used to store output
67
68     def prepare_output(full_list_of_scores):
69         for item in full_list_of_scores:
70             print item[2], item, item[2].INFO['Gene.refGene']

```

```

66  # wrapper function used to create bayesian network for all records
67
68  def compute_network_and_probabilities(full_list_of_scores):
69      for record in full_list_of_scores:
70          network = create_network_and_compute_probabilities(record)
71          compute_record(network, record)
72
73  # this function applies a featurewise normalisation of all features to a range of 0-1, and flip scores
74  # for certain features
75
76  def apply_feature_wise_normalisation(full_list_of_scores):
77      for i in range(6):
78          min_num = 1000000
79          max_num = -1000000
80          for item in full_list_of_scores:
81              if item[1][i] != None:
82                  min_num = min(min_num, item[1][i])
83                  max_num = max(max_num, item[1][i])
84          for item in full_list_of_scores:
85              if item[1][i] != None:
86                  value = ((item[1][i] - min_num) / (max_num - min_num) + 0.2) / 1.3
87                  item[1][i] = value
88              else:
89                  item[1][i] = 0.5
90          if i == 0 or i == 5:
91              for item in full_list_of_scores:
92                  if item[1][i] != None:
93                      item[1][i] = -item[1][i]
94
95  # extract list of of scores from each record, including all functional annotations, clinvar scores and
96  ↪ dbSNP
97
98  def extract_list_of_scores(vcf_object):
99      count = 0
100     full_list_of_scores = []
101     for record in vcf_object:
102         count += 1
103         nn_prediction, list_of_scores = get_scores(record)
104         if not list(filter(lambda x: x != None, list_of_scores)):
105             continue
106         get_clinvar_scores(list_of_scores, record)
107         snp_present = get_db_snp_scores(record)
108         full_list_of_scores.append([float(nn_prediction), list_of_scores, record, snp_present])
109     return full_list_of_scores

```

```

109
110 # Compute the Bayesian Network by assuming observations and attaching mapped probabilities (0,1) to
    ↪ P(X=True | Y=True)
111
112 def compute_record(network, record):
113     beliefs = network.predict_proba({'Real Gene': 'True', 'ClinVar': 'True', 'PolyPhen': 'True', 'LRT':
    ↪ 'True', 'MutationAssessor': 'True', 'SIFT': 'True', 'FATHMM_gene': 'True', 'rs_gene': 'True'})
114     # print "\n".join("{}\t{}".format(state.name, belief) for state, belief in zip(network.states,
    ↪ beliefs))
115     # get the probability that the gene is important
116     prob_gene_important = beliefs[2].values()[1]
117     beliefs = map(str, beliefs)
118     record.append(prob_gene_important)
119     record.append(record[2].INFO['snip138'])
120     record.append(record[3])
121
122 # If snp is present in db-snp, attach probability of importance to 0.3, else 0.7
123
124 def get_db_snp_scores(record):
125     snp_present = 0.7
126     if record.INFO['snip138'][0] != None:
127         snp_present = 0.3
128     return snp_present
129
130 # If snp is present in clinvar, attach probability of importance to 0.7, else 0.3
131
132 def get_clinvar_scores(list_of_scores, record):
133     if record.INFO['clinvar_20150629'][0] != None:
134         list_of_scores.append(0.7)
135     else:
136         list_of_scores.append(0.3)
137
138 # wrapper method to create the bayesian network and compute probabilities
139
140 def create_network_and_compute_probabilities(record):
141     ClinVar_gene, FATHMM_gene, LRT_gene, MutationAssessor_gene, MutationTaster_gene, PolyPhen2_gene,
    ↪ SIFT_gene, functional_gene, importgene, real_gene, rs_gene = initialise_distributions(
142         record)
143     # set up states
144     s1, s10, s11, s2, s3, s4, s5, s6, s7, s8, s9 = generate_states(ClinVar_gene, FATHMM_gene, LRT_gene,
    ↪ MutationAssessor_gene, MutationTaster_gene, PolyPhen2_gene, SIFT_gene, functional_gene,
    ↪ importgene, real_gene, rs_gene)
145     # set up network
146     network = add_edges_bake_network(s1, s10, s11, s2, s3, s4, s5, s6, s7, s8, s9)

```

```

147     return network
148
149     # method to create the edges in the network
150
151     def add_edges_bake_network(s1, s10, s11, s2, s3, s4, s5, s6, s7, s8, s9):
152         network = BayesianNetwork("Gene Prediction")
153         network.add_states(s1, s2, s3, s4, s5, s6, s8, s9, s10, s11)
154         network.add_edge(s1, s3)
155         network.add_edge(s2, s3)
156         network.add_edge(s4, s2)
157         network.add_edge(s5, s2)
158         network.add_edge(s6, s2)
159         network.add_edge(s7, s2)
160         network.add_edge(s8, s2)
161         network.add_edge(s9, s2)
162         network.add_edge(s10, s2)
163         network.add_edge(s11, s3)
164         network.bake()
165         return network
166
167     # method that generates the nodes in the bayesian network
168
169     def generate_states(ClinVar_gene, FATHMM_gene, LRT_gene, MutationAssessor_gene, MutationTaster_gene,
170         ↪ PolyPhen2_gene,
171         SIFT_gene, functional_gene, importgene, real_gene, rs_gene):
172         s1 = State(real_gene, name="Real Gene")
173         s2 = State(functional_gene, name="Functional Gene")
174         s3 = State(importgene, name="Important Gene")
175         s4 = State(ClinVar_gene, name="ClinVar")
176         s5 = State(PolyPhen2_gene, name="PolyPhen")
177         s6 = State(LRT_gene, name="LRT")
178         s7 = State(MutationTaster_gene, name="MutationTaster")
179         s8 = State(MutationAssessor_gene, name="MutationAssessor")
180         s9 = State(SIFT_gene, name="SIFT")
181         s10 = State(FATHMM_gene, name="FATHMM_gene")
182         s11 = State(rs_gene, name="rs_gene")
183         return s1, s10, s11, s2, s3, s4, s5, s6, s7, s8, s9
184
185     #methods to initialise prior distributions in bayesian network
186
187     def initialise_distributions(record):
188         ClinVar_gene = DiscreteDistribution({'True': 0.5, 'False': 0.5})
189         PolyPhen2_gene = DiscreteDistribution({'True': 0.5, 'False': 0.5})
190         LRT_gene = DiscreteDistribution({'True': 0.5, 'False': 0.5})

```

```

190     MutationTaster_gene = DiscreteDistribution({'True': 0.5, 'False': 0.5})
191     MutationAssessor_gene = DiscreteDistribution({'True': 0.5, 'False': 0.5})
192     SIFT_gene = DiscreteDistribution({'True': 0.5, 'False': 0.5})
193     FATHMM_gene = DiscreteDistribution({'True': 0.5, 'False': 0.5})
194     rs_gene = DiscreteDistribution({'True': 0.5, 'False': 0.5})
195     import_cdp = get_cdp(3, [(record[0] + 0.2) / 1.3, record[3], 0.8])
196     functional_cdp = get_cdp(6, record[1])
197     functional_gene = ConditionalProbabilityTable(functional_cdp, [ClinVar_gene, PolyPhen2_gene, LRT_gene,
198                                                                MutationAssessor_gene,
199                                                                SIFT_gene, FATHMM_gene])
200     real_gene = DiscreteDistribution({'True': 0.5, 'False': 0.5})
201     importgene = ConditionalProbabilityTable(import_cdp, [real_gene, rs_gene, functional_gene])
202     return ClinVar_gene, FATHMM_gene, LRT_gene, MutationAssessor_gene, MutationTaster_gene,
203         ↪ PolyPhen2_gene, SIFT_gene, functional_gene, importgene, real_gene, rs_gene
204
205     # method that builds the cdp table. n is the number of input variables, probability list gives the
206     ↪ probability
207
208     # that the i-th X variable is true P(Xi=True).
209
210     def get_cdp(n, prob_list):
211         temp_list = create_true_false_matrix(n)
212         calculate_probabilities(n, prob_list, temp_list)
213         return temp_list
214
215     # Generates a True False matrix using binary counting logic, critical for input in bayesian network
216
217     def create_true_false_matrix(n):
218         temp_list = []
219         for i in range(0, 2 ** n):
220             temp_row = []
221             for j in range(n):
222                 number_2 = i // (2 ** (n - j - 1))
223                 number_1 = number_2 % 2
224                 if number_1 == 0:
225                     temp_row.append('False')
226                 else:
227                     temp_row.append('True')
228             temp_list.insert(0, temp_row + ['False'])
229             temp_list.insert(0, temp_row + ['True'])
230         return temp_list
231

```

```

232 # calculates the probabilities, taking in the true list as well as a list of probabilities. The key here is
233 # the probability that the mutation is true is related to the scores given by mutation taster etc..
234 # ie  $P(X \text{ is imp } | X \text{ is Clinvar}) = P(X \text{ is Clinvar})$ 
235
236 def calculate_probabilities(n, prob_list, temp_list):
237     for i in range(0, 2 * (n + 1), 2):
238         true_row = temp_list[i]
239         true_probability = 1
240         false_probability = 1
241         for k in range(0, n, 1):
242             if true_row[k] == 'True':
243                 true_probability *= prob_list[k]
244                 false_probability *= 1 - prob_list[k] # probability that mutation is false is 1 minus
                # mutation is true
245             else:
246                 true_probability *= 1 - prob_list[k]
247                 false_probability *= prob_list[k]
248         final_true_probability = true_probability / (true_probability + false_probability)
249         final_false_probability = false_probability / (true_probability + false_probability)
250         temp_list[i].append(final_true_probability)
251         temp_list[i + 1].append(final_false_probability)
252
253 if __name__ == "__main__":
254     parser = argparse.ArgumentParser(description="train neural net")
255     parser.add_argument('-i', '--input', help="give directories with files")
256     paths = parser.parse_args()
257     main(paths)

```