An attempt at Leukemia Classification

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# Abstract

We classify genes associated Leukemia and specific sub-types of Leukemia to find gene expression patterns that exist within Leukemia patients and specific sub-types of Leukemia by examining each sub-type of Leukemia and comparing significant gene expressions. We also attempt to classify specific subtypes of Leukemia with the intent of analyzing learned patterns from the results.

# Introduction

Leukemia is a type of blood cancer that produces excess, abnormal white blood cells that inhibit the production of normal blood cells. There are 17 sub-types of Leukemia and each sub-type is characterized by a different set of regulatory genes. Instead of identifying the gene regulatory networks, we analyze the effects of these regulatory networks as we believe they can give us important clues about the impacts and causes of certain sub-types of Leukemia. With this information, we may have a better idea of the genes involved in the specific regulatory networks of certain sub-types of Leukemia, allowing for better understanding of these gene regulatory networks and the impactful genes involved in the disease.

|  |  |  |  |
| --- | --- | --- | --- |
| **Name** | **Count** | **Name** | **Count** |
| MDS | 207 | Non-Leukemia and healthy bone marrow | 73 |
| CLL | 448 | c-ALL/Pre-B-ALL with t(9;22) | 122 |
| AML complex aberrant karyotype | 52 | AML with t(8;21) | 40 |
| AML with normal karyotype + other abnormalities | 347 | ALL with hyperdiploid karyotype | 40 |
| c-ALL/Pre-B-ALL without t(9;22) | 237 | ALL with t(1;19) | 36 |
| T-ALL | 174 | Pro-B-ALL with t(11q23)/MLL | 70 |
| CML | 76 | AML with t(15;17) | 37 |
| AML with t(11q23)/MLL | 38 | AML with inv(16)/t(16;16) | 28 |
| ALL with t(12;21) | 58 | mature B-ALL with t(8;14) | 13 |

Table 1. Distribution of data

We use array-normalized data from the Microarray Innovations in Leukemia study (MILE) [1]. This dataset contains data from 2096 blood and bone marrow samples from patients and has 17,788 genes with 18 classes, 17-subtypes of Leukemia and 1 group of healthy patients.

There is a data imbalance that we will not address in this project, but we note that this may make it harder to learn the important features for classifications of smaller sized subtypes. The small number of samples for some subtypes may cause the model to fit more of the noise than the significant genes involved in the disease. We also note that with the large number of genes, it will be hard to determine the impact of specific genes and verify the results. This problem is challenging because with the rise of machine learning and deep learning, numerous different methods will likely lead to reasonable results, so it is hard to determine which method to use and how to interpret the results. Thus, we use relatively simpler methods to maintain the interpretability of the results.

# Background

Cancer classification on gene expression data using machine learning techniques is not new. There are many published papers with new techniques, and applications of old techniques to new datasets that come out every year. We surveyed a handful of them to get a better idea of approaches we could try when tackling the problem with our gene expression data.

Cascianelli et. al used PCA on the PAM50 dataset to examine whether the subtypes of breast cancer were separable from each other [2]. They found that they could not separate the subtypes by the first two principle components and hypothesized that due to this non-separability, the boundary between subtypes changes depending on the mixed traits. Using Average of Within Class Averages (AWCA), they were able to get a single number that represents a subtype. This method produced relatively decent results with around 90% accuracy. They then went on to try different machine learning approaches and found that regularized multiclass logistic regression performed the best.

Danaee et. al used stacked denoising autoencoders to deal with the high dimensions and noisy inputs of gene expression data [3]. The purpose of using an encoder is denoise the inputs and to try to find the genes that play an important role in breast cancer. They multiply the learned autoencoder weights together to get a rough sense of how the gene expression data interacts, saying that the most heavily weighted ones have the most significant impact and were the most predictive genes. By using the heavily weighted genes as the inputs to a deep learning models, they were able to achieve slightly less accuracy than with the features found using stacked denoising autoencoders but argue that it is more readily interpretable.

Mei et. al trained a stacked autoencoder to provide input to a neural network trained on a subset of the TCGA dataset to identify survival duration for patients with Acute Myeloid Leukemia [4]. They include features like age, cytogenetics, and mutations and achieve results of around 81% accuracy for predicting whether patients survived for more of less than 730 days. They mention that the main limitation to their model was the amount of training data available.

Castillo et. al try to extract differentially expressed genes that help identify different forms of Leukemia [5]. Use the minimum-Redundancy Maximum-Relevance feature selection algorithm, they train SVM, Random Forests, K-Nearest Neighbors, and Naive Bayes classifiers. Afterwards, they extract Differentially Expressed Genes (genes that help differentiate between classes) by testing p-values, log-fold change (measures change in gene expression level), and coverage (whether it helps identify between some number of classes). They conclude that K-Nearest Neighbors with a subset of gene expression data worked the best, followed by SVM and Naive Bayes, with the worst being Random Forests.

Krivtsov et. al outlines procedures on how to extract the gene expression data and utilize some form of either hierarchical or K-means clustering and use permutation analysis to determine significance for the purpose of profiling Leukemia Stem Cells [6]. They use the GenePattern software to distinguish marker genes that would distinguish the two groups, comparing means, using a signal-to-noise statistic, and evaluating significance. This was the only study read that seemed to have extracted and recorded the data themselves instead of taking the data from a database.

These papers showed that there were many ways to approach the problem of cancer classification using gene expression data and have inspired us to take a somewhat similar approaches, with an emphasis on finding DEGs or significant features.

# Results and Methods

[Describe what experiments you performed, how you collected the data and how you analyzed results, etc.]

## Methods

We take a multifaceted approach to this problem of identifying DEGs and classifying Leukemia sub-types. We use a 90/10 train/test split to leave some data for evaluation purposes.

To look for significant features within each Leukemia sub-type, we perform Welch’s t-test using the training data and compare each sub-type against the “Non-Leukemia and healthy bone marrow” patients. Then we apply the Bonferroni correction with and to correct for multiple hypotheses. Afterwards, we determine the similarity of significant features between Leukemia sub-types to get a better idea of how similar the selected genes were between Leukemia sub-types, so we looked at the Jaccard similarity (a set similarity metric) between the selected significant features between Leukemia sub-types. We then look up some of the top shared features to confirm the pattern was also observed by others.

Afterwards, we attempt to classify the Leukemia sub-types by using multi-class Logistic Regression, which uses a 1 vs. all classification scheme and has a model with learned weights for each classification. We focus on using L1 regularization because we believe that not all gene expressions are relevant to determining whether someone has a specific sub-type of Leukemia or not. We varied our training by using all of the features and just using the combined significant features we found, along with three normalization schemes: not normalizing, normalizing by the training data, and normalizing by the healthy patients in the training data. The same normalization schemes are applied when evaluating the model. We use 5-fold cross-validation to get a general idea of the generalizability of our different models. We then look at the similarity between learned weights of the learned models as well as the learned weights themselves to examine the most impactful genes found by the model.

We conclude by comparing the classification accuracy of logistic regression with K-Nearest Neighbors.

We believe that our approach will work well on this problem because it allows us to tackle the problem of identifying the significant genes from multiple directions to arrive at a better understanding of how the different genes interact and what are significant indicators of each sub-type of Leukemia. Our initial methods differ from existing methods in that we perform our analysis on the 17 sub-types of Leukemia, while previous research we have seen only does this analysis among 4 sub-types of Leukemia [5] and do not focus on the similarities of the significant features. Our latter methods do not differ much from existing methods in that it focuses on using a machine learning algorithm as a means of obtaining determining significant features.

We evaluate our ability to locate significant features by checking some of the genes against existing research to confirm that these patterns were also observed by other researchers. This leaves us with many genes that could be involved in the gene regulatory networks that may or may not have been observed by other researchers that could be a focus on future research on specific gene regulatory networks for specific sub-types of Leukemia. We evaluate our classification results on the top-1 and top-5 accuracy because there are 18 total classes, and we want to see how close our model is at predicting the correct class.

## Results

After selecting out the significant features for each sub-type of Leukemia, we found a total of 1,408 significant features. We also examined the Jaccard similarity [table omitted for space reasons, but it can be found [here](https://github.com/nowei/leukemia-classification/blob/main/features/jaccard.png)] of the found significant features and learned that MDS seemed to be the most different sub-type of Leukemia from the other sub-types. This may require some more investigation in the future. The number of labels that share a particular significant feature range from 1 to 16, so we can look at a handful of the top shared and least shared labels for significant genes and look for them in existing research.

|  |  |  |  |
| --- | --- | --- | --- |
| Gene | Description | # of shared labels | Observed in |
| 10487\_at | CAP1 | 16 | [7] |
| 1116\_at | CHI3L1 | 15 | [8] |
| 116362\_at | RBP7 | 15 | [9] |
| 10123\_at | ARL4C | 15 | [10] |
| 1118\_at | CHIT1 | 15 | [11] |
| 114880\_at | OSBPL6 | 1 (MDS) | [12] |
| 100128907\_at | hypothetical protein LOC100128907 | 1 (MDS) | Not found |
| 10006\_at | ABI1 | 1 (CLL) | [13] |
| 100128309\_at | hypothetical protein LOC100128309 | 1 (CLL) | Not found |
| 100129015\_at | hypothetical protein LOC100129015 | 1 (CLL) | Not found |

Table 2. Table of selected results from the search for significant features

We observe that some hypothetical proteins were marked as significant genes, so further studies could be carried out. There are likely other genes that have not been observed in studies, studying these genes might give us a better idea of how to distinguish some of

* + A clear justification of your evaluation criteria.
  + What do you use as evaluation criteria and why?

## Interpretation

* + Why do you think that your method(s) performed in certain ways?
  + How does your method work compared to alternative approaches?
  + What is the implication of your results with respect to solving your problem?

# Conclusion

### Discussion

* + How is the computational challenge addressed?
  + Future direction (possible next steps)

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