

# Patient Triaging for COVID-19

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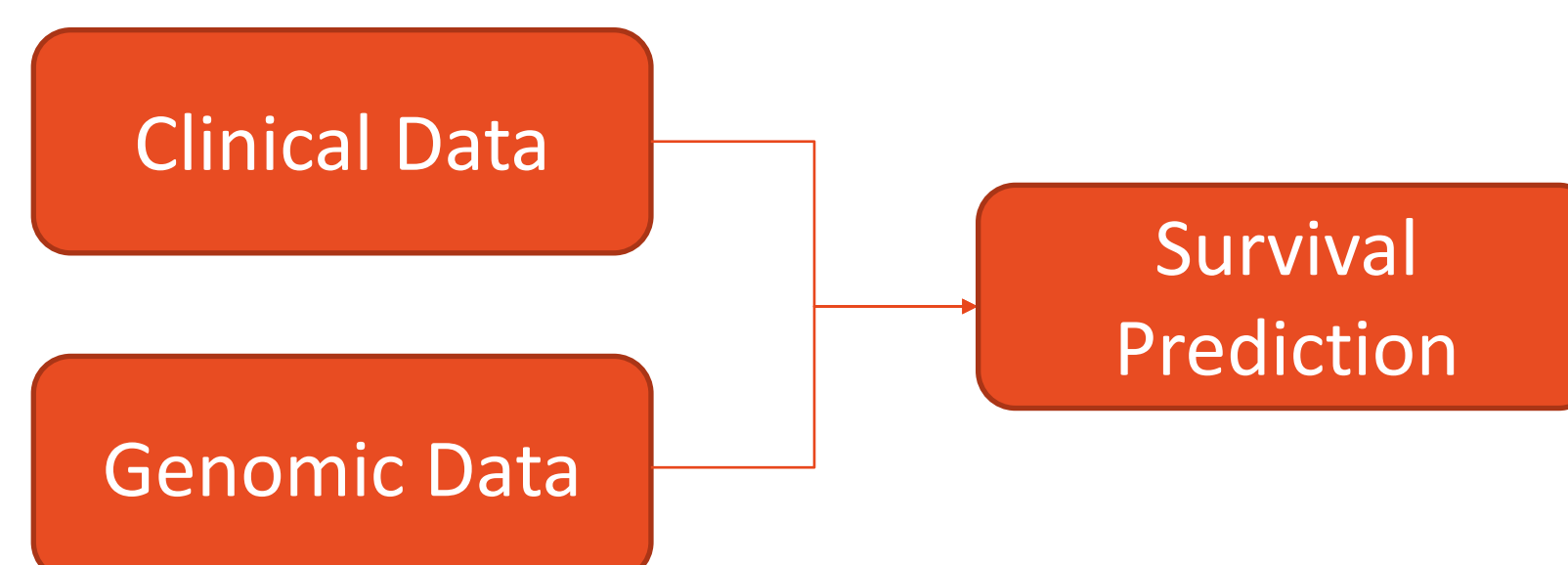
## Introduction

Patient triaging is the process of determining the priority of patients' treatment based on severity of the disease/illness. Automation of patient triaging has many benefits –

- Important in Clinical Settings. Help in clinical decision making.
- Can you used to automate certain stages of treatment (specially during covid-19 with shortage of doctors).

Patient triaging can be done with clinically measurable parameters as input (from blood tests, liver function test, kidney function test etc.) along with the time of infection and end status (alive/deceased).

Addition of genomic features such as long non-coding RNA, can give better accuracy to the trained model and identification of such features is of importance to improving automated triaging.



## Objectives

1. To develop a patient triaging model based on clinical parameters.
2. To identify genomic features which have a potential to improve performance of the model.

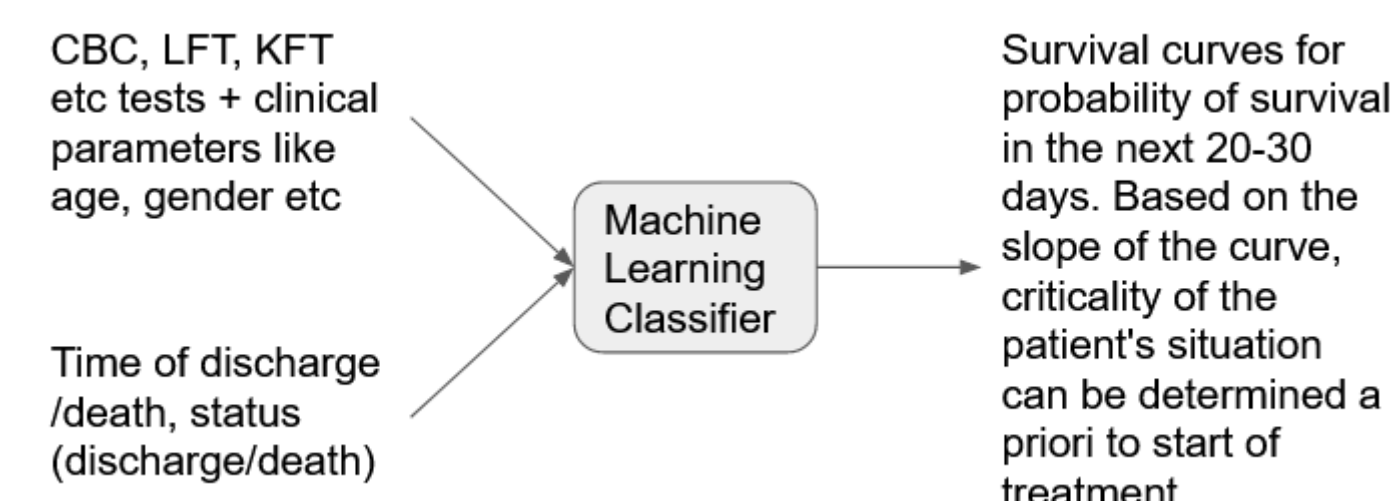
## Results

A dataset containing 375 samples (315 train, 60 test) was used to train the baseline model. The classification of samples into high risk and low risk was done using logistic regression with L1 penalty and gave the following results -

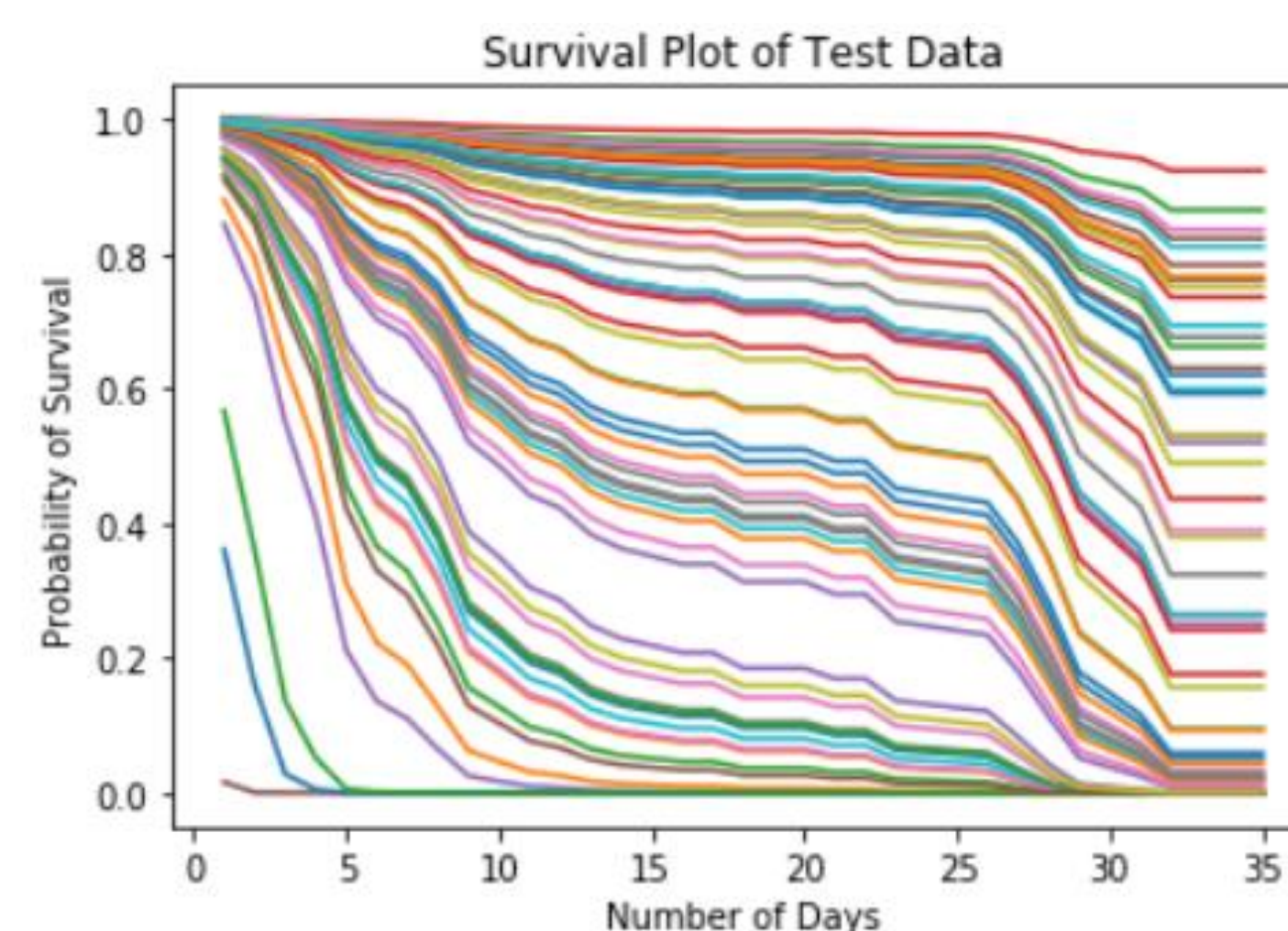
Actual Labels	Predicted	
	0	1
0	26	4
1	2	28

Test accuracy = 0.90  
Train accuracy = 0.92

Similarly, to generate survival curves for each patient (i.e. probability of survival over time), Cox Regression with elastic net penalty was used.

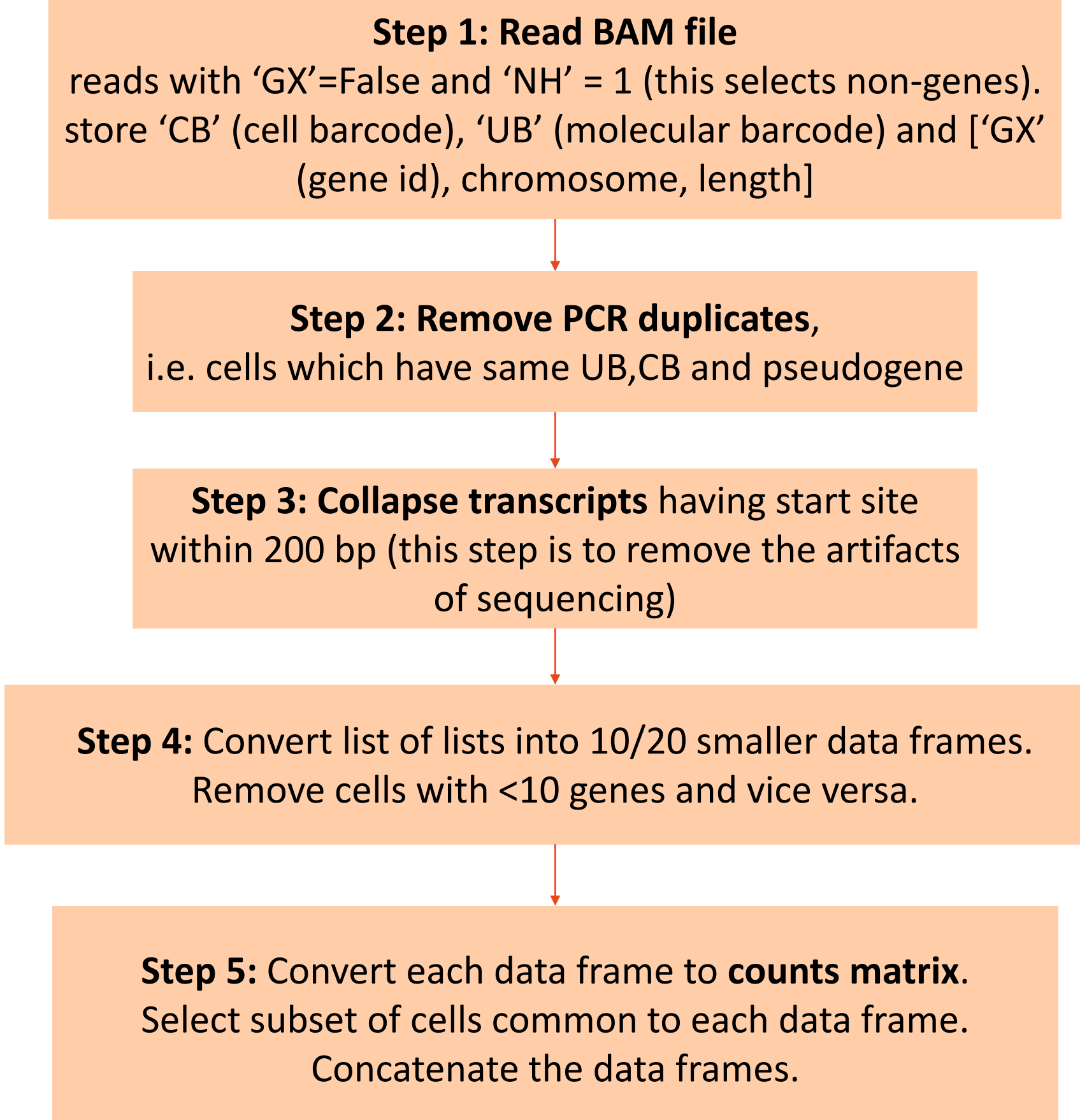


Survival curves for the test set are as follows -



Test concordance = 0.83  
Train concordance = 0.85

## Pipeline for Genomic Feature identification



## Future Work

Clinical and Experimental Studies designed based on the identified genomic features are under way at AIIMS Delhi. Data is getting generated for COVID-19, which will be analysed as soon as it is available, and incorporated into the model.

## Acknowledgement

I would like to thank LV Subramaniam and Saurabh Raje from IBM research for their insights to speed up the algorithm for identifying important genomic features.