

# Prediction of Patients at High Risk and Associated Risk Factors in Mucormycosis

Shradha Jain and Yatender Kumar

**Abstract** — Mucormycosis is a deadly fungal disease which showed its severity again during the COVID19 pandemic. Mucormycosis was first detected in the year 1847 and since then, many parts of the world including India has seen a rise in mucormycosis cases especially, with the onset of COVID19. CAM which is also known as COVID Associated Mucormycosis is also a cause of concern, since its arrival has led to an increase in the number of mucormycosis cases along with the mortality rate. Mucormycosis can prove to be a dangerous fatal disease, as the person suffering from mucormycosis can die within 3-4 days, if the person is not treated early. WHO has also suggested that the early diagnoses of mucormycosis is crucial for mucormycosis detection in patients for timely treatment and improved survival rate. ML techniques have proven efficient when we want to develop a detection model and, in this case, can also be used to calculate high risk factors among mucormycosis. Here, we present an artificial intelligence-based model to predict the patients at high risk and associated crucial risk factors in mucormycosis since it is important that patients at high risk can be warned in advance. The model assesses COVID-associated mucormycosis also so that patients suffering from COVID19 or patients who have even recovered from COVID19 can benefit from the same.

**Index Terms**— Mucormycosis, Machine Learning, Artificial Intelligence, Diagnoses.

## I. INTRODUCTION

Mucormycosis also commonly known as Black fungus saw its first case in the year 1847 reported by Sluyter. It was named mucormycosis in the year 1957 by Baker [1]. Mucormycosis is caused by a group of molds commonly found in the air, soil, manure, decaying fruits or vegetables and can also be found in the mucus of healthy people.

Mucormycosis is a highly dangerous disease that has proven its disastrous nature during the second wave of COVID19. With the surge in COVID19 cases, humanity saw a rise of cases in

mucormycosis too. Cases were rising at unprecedented rates. In countries like India, Mucormycosis was creating havoc due to the rising COVID19 Cases. The cases seen in CAM have proven to be associated with high mortality [2][3][4]. The intracranial involvement in mucormycosis is also associated with the increase in mortality rate up to 90%.[5] The government of India even declared Mucormycosis as an epidemic. During COVID19 the hospitalizations were overwhelmed and to look for a crucial diagnostic solution, it may add a layer of relief to this problem.[6] It is crucial to look for the early diagnosis of Mucormycosis in order to identify the patients at risk so the patients at high risk can be warned.[7] This research proposes an Artificial intelligence-based Model which will predict patients at high risk and the associated high-risk factors.

## II. RELATED WORK

Covid has proven to be associated with increase in number of mucormycosis cases [8].

Mucormycosis is a fungal infection that is more commonly observed in individuals with underlying medical conditions and weakened immune systems, and rarely seen in healthy individuals. Some of the medical conditions that may increase the risk of developing mucormycosis include Diabetes Ketoacidosis (DKA), the most prevalent disease Diabetes Mellitus, Neutropenia, or Drug Abuse [9].

This infection can affect different parts of the body such as the sinuses, lungs, orbit, gastrointestinal tract, skin, and central nervous system. In 1950, Smith and Krichner conducted research on mucormycosis that is still considered as the gold standard work in this area [10] Their study included findings such as black, necrotic turbinate's that could be easily mistaken for dried or crusted blood, ptosis of eyelid, proptosis of the eyeball, and complete Ophthalmoplegia.

In the year 2019 a multinational survey was being carried out to study suspected cases of mucormycosis in India prior to COVID19[11]. It was founded that 18% of cases had DKA and 57% of patients had un-controlled DM. In another study [12] it was found out that rhino-orbital (67.7%) cases were most common followed by pulmonary (13.3%) and cutaneous type (10.5%). If there is a delay of just 12 hours, disseminated mucormycosis can become severe and potentially fatal. This is

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since approximately 50% of mucormycosis cases are diagnosed during post-mortem autopsies. [13]. The predisposing factors associated with mucormycosis in Indians include DM (73.5%), malignancy (9.0%) and organ transplantation (7.7%) [14]. A study from Europe has found that the most significant causes were haematological malignancies [15], while it showed that he calls it in India, Iran, Middle East, North Africa, and Mexico that was turning out to be more disastrous.

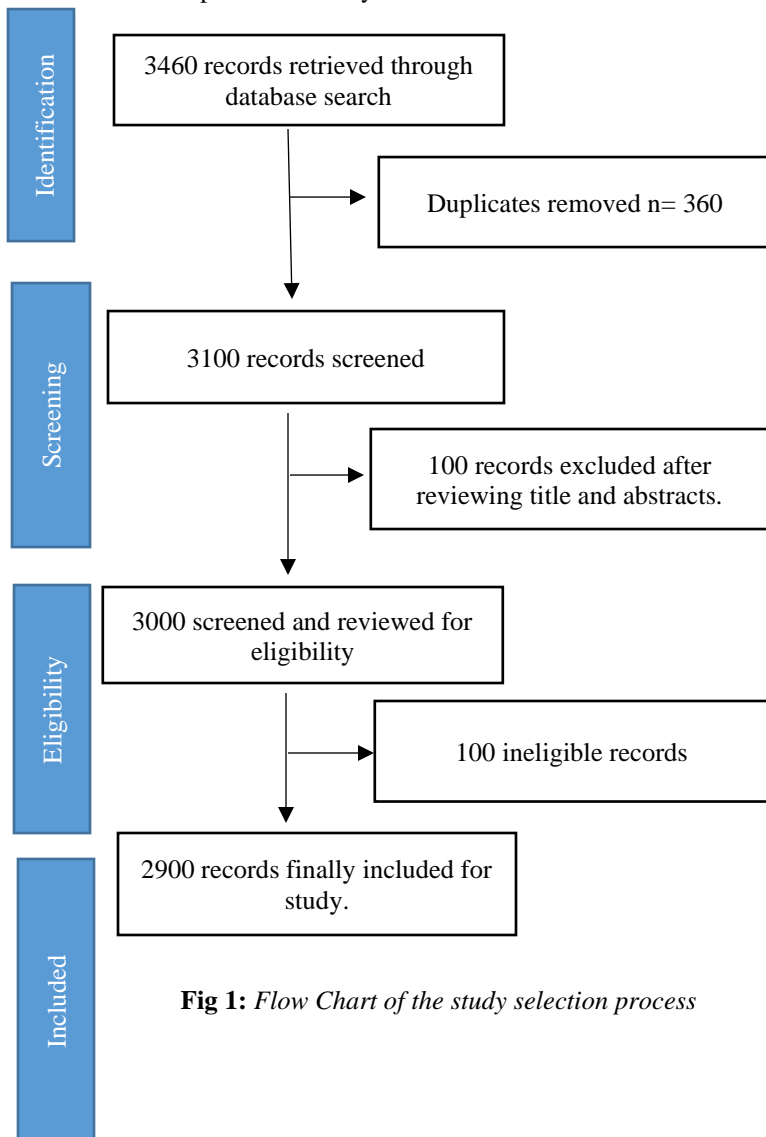
There have not been many investigations made to diagnose mucormycosis early, and WHO has repeatedly stressed on the fact that it is crucial to detect mucormycosis at an early stage to combat the high mortality of mucormycosis and to detect the fatal disease early.

Since it is crucial to look for more data and to look for different risk factors in with presentations from different part of the world and to establish a relationship between risk factors and mucormycosis.

### III. METHOD

#### 3.1 Data Collection and Pre-Processing

A systematic an extensive literature search was carried out in electronic databases like Google Scholar, PubMed to obtain details of the cases that reported mucormycosis cases, suspected and confirmed both cases were considered. CAM cases consist a crucial part of the study and were also included for the same.



**Fig 1: Flow Chart of the study selection process**

The search words include ‘mucormycosis,’ ‘zygomycosis,’ ‘COVID-19,’ ‘SARS CoV-2,’ ‘black fungus,’ ‘Zygomycosis,’ ‘Mucorales,’ ‘Rhizopus,’ ‘Rhizomucor’.

Characteristics of each patient were retrieved and assessed on various endpoints. We collected 440 mucormycosis patient’s dataset, and an additional 2460 patient’s dataset that were not diagnosed with mucormycosis. The dataset was tabulated to be used in the machine learning algorithm

The data set consist of 2900 samples including patients who have suffered from COVID19. There are 2900 patients in the sample size including 440 mucormycosis patients. This study has also included patients who have suffered from corona virus and have been subsequently infected with mucormycosis then. The study consists of confirmed as well as suspected mucormycosis cases. The data set comprises of patients from different parts of the world like India, Australia, USA, Oman, Turkey, France, Chile, Iran, China, Taiwan, Mexico, Egypt and other parts of the world.

The original data was raw and unstructured, it was collected from various verified sources and it originally contained 64 features which was later filtered out to ensure that our model is unbiased. The categorical features are binary encoded, and after selecting the features, 36 features are included like:

Nominal features:

- Gender,
- symptoms such as headache,
- fever,
- Cough, shortness of breath,
- Loss of vision,
- Facial swelling,
- Nausea,
- Skin lesions.
- Mucormycosis: Confirmed/Suspected

Presence of COVID was also evaluated

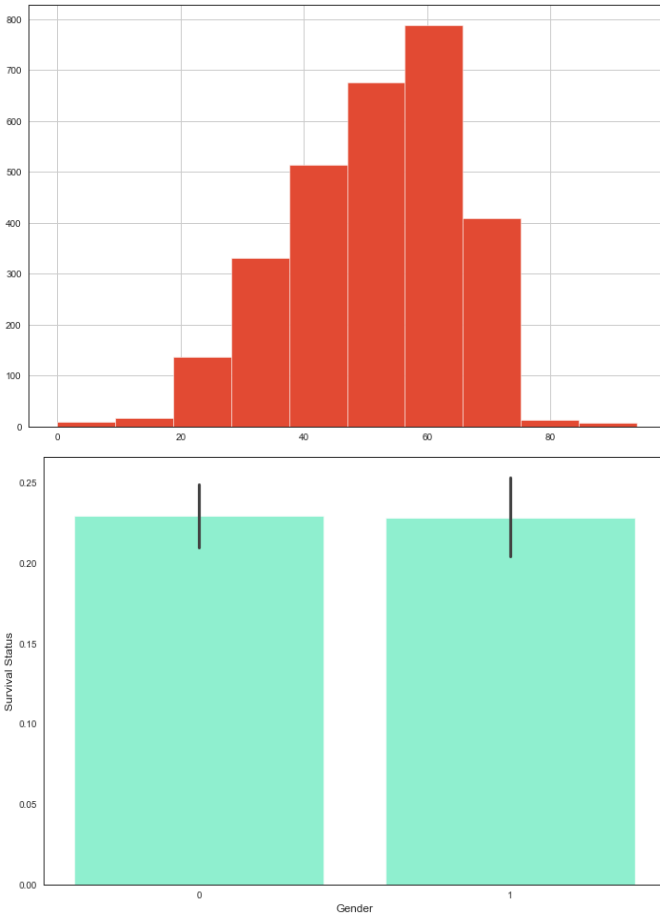
Comorbidities include diseases like diabetes, diabetes ketoacidosis, chronic kidney disease, hypertension, leukemia, cancer, drug abuse, heart disease, asthma, others. Healthy patients were also considered as a data point

Survival rate: dead or alive.

Numerical features:

- Age.

The data was divided into training dataset and testing dataset and 5-fold cross validation was applied to the dataset. The reason, we chose this size is to find the result without any bias and to select features that could possibly tell us the risk factors.



**Fig 2: (Top panel) Bar graph of Age of patients. (Bottom panel) Density graph of Gender and survival status of subjects**

The patients were mostly in the age group 40-60. The mean age of the patients was found to be 51 years.

### 3.2 Modelling

We trained logistic regression model from the Scikit library in python and used XG boost from the respective XGboost library. Similarly, models such as GBM, LGBM, SVM were also used. Random Forest and Decision Trees were also used to evaluate performance measure. To prevent underfitting and overfitting we trained our model to be able to perform well even on the unseen data. We used 5-fold Cross Validation technique to obtain a precise result.

**Table 1**  
Machine learning algorithms and their main features.

ML Algorithm	Basic Idea	Features
RF	Dt ensemble method	Really efficient for highly complex problems
LGBM	Tree Based algorithm	Fast execution with reliable results
SVM	Hyperplane Optimization	Highly accurate model
Decision Tree	Tree structured algorithm	Considers all possible outcomes of a decision and makes the best optimum choice
XGB	Decision tree based	Finds More accurate Model
GBM	Decision tree based	Finds more reliable model
Logistic Regression	Supervised Learning Method	Efficient to train, perform well on datasets

## IV. RESULTS

### 4.1 Training details

The dataset was divided into training set and testing set. The model was evaluated for 5-fold cross validation to evaluate for accurate results. The results obtained by different models was evaluated for performance measure.

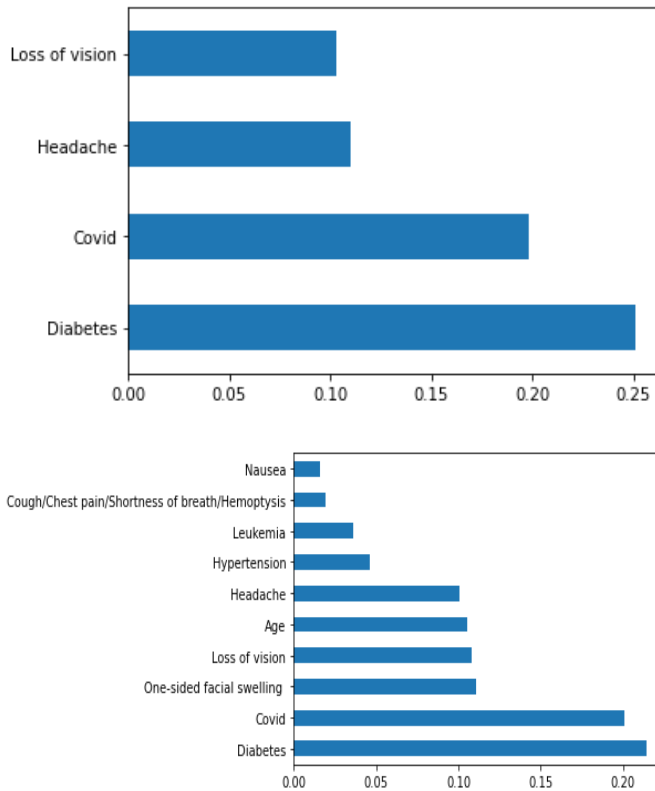
Decision tree obtained accuracy of 0.93 shared by Random Forest too. LGBM and XGBoost achieved accuracy of 0.93. Models such as logistic regression and GBM also achieved good accuracy of 0.92 followed by SVM which achieved accuracy of 0.91. The results indicate that the model can successfully predict the high risk of mucormycosis in a patient.

### Results

The results obtained which tell us about the risk factors involved are predominantly showed here.

The top 4 risks observed included Diabetes, Prescence of COVID, headache, Loss of vision which could signify that the patient is at high risk of mucormycosis.

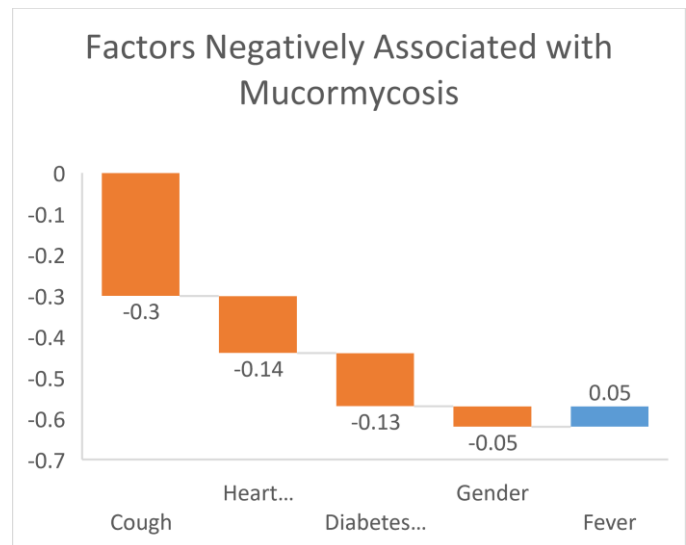
Top 10 associated risk factors of mucormycosis involve Diabetes, headache, Loss of vision, Age, Headache, hypertension, Leukemia, Cough and Nausea. Risk factors that are negatively associated with mucormycosis include Fever.



**Fig 3:** (*Top panel*) Top 4 high risk factors associated with mucormycosis. (*Bottom panel*) Top 10 risk factors associated with mucormycosis

Factors	Coefficient
Cough	-0.30
Heart Disease	-0.14
Diabetes Ketoacidosis	-0.13
Gender	-0.05
Fever	0.05

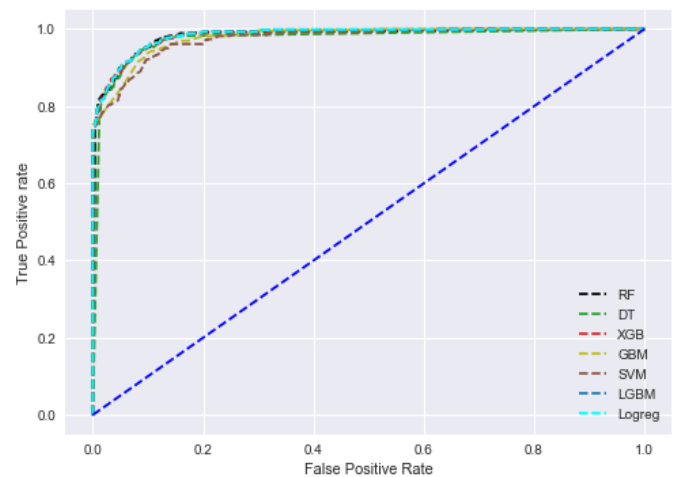
**Table 2:** Factors Negatively affecting Mucormycosis.



**Fig 4:** Factors Negatively associated with mucormycosis

These are some of the factors who have shown a negative correlation with the risk of mucormycosis.

In our study, it was shown that the person suffering from covid were positively affected by mucormycosis.

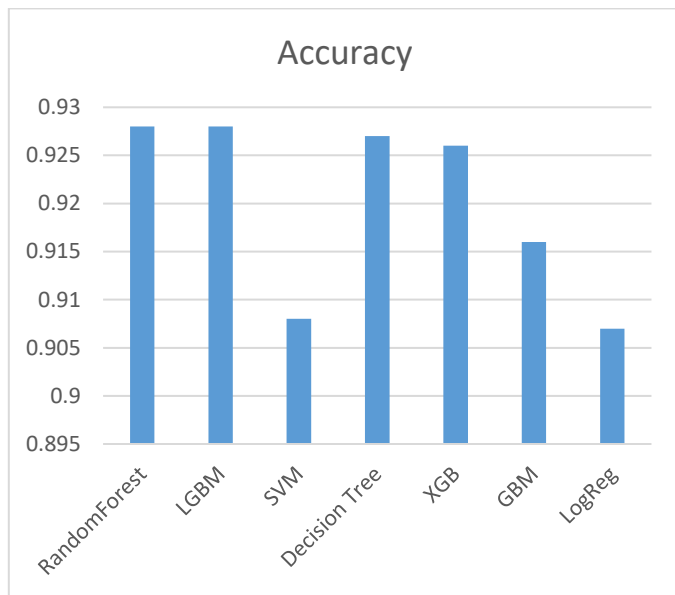


**Fig 5:** ROC Curves of Different models.

Furthermore, the ROC curve and all other graphs are shown are given in Table 1. ROC curve is useful in evaluating the different testing and training accuracies obtained for the given models.

## 4.2 Model Comparison

Different models are evaluated for accuracy.



**Fig 6:** Accuracy of different models

S. No	Method	Accuracy
1	Random Forest	0.93
2	LGBM	0.93
3	SVM	0.91
4	Decision Tree	0.93
5	XGB	0.93
6	GBM	0.92
7	Logistic Regression	0.92

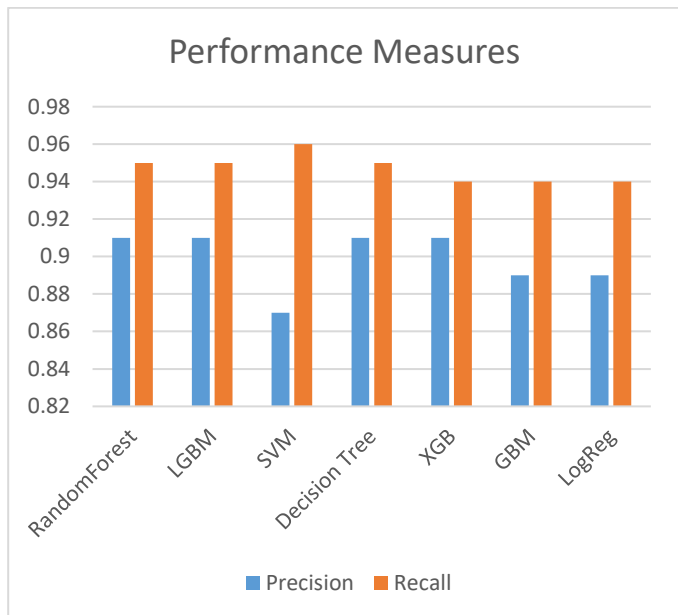
**Table 3:** Accuracy Measure of different models.

### 4.3 Classification Report

Algorithm	Precision	Recall
Random Forest	0.91	0.95
LGBM	0.91	0.95
SVM	0.87	0.96
Decision Tree	0.91	0.95
XGB	0.91	0.94

GBM	0.89	0.94
Logistic Regression	0.89	0.94

**Table 4:** Comparison of different models used in evaluating the model performance.

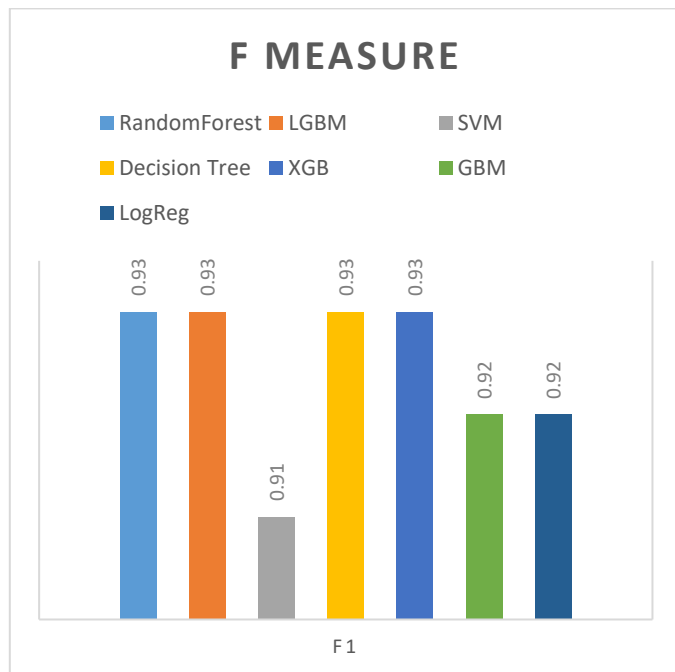


**Fig 7:** Performance measures of different models

F measure

Algorithm	F measure
Random Forest	0.93
LGBM	0.93
SVM	0.91
Decision Tree	0.93
XGB	0.93
GBM	0.92
Logistic Regression	0.92

**Table 5:** Comparison of different models used in evaluating the model performance.



**Fig 8:** *F measure of different models*

## V. CONCLUSION

This paper finds the solution to one of the major problem whose solution to find was also prompted by WHO, to look for diagnostic methods. The artificial intelligence model provides us with a solution that finally is able to tell based on parameters whether the person will be at high risk of mucormycosis or not. This paper is also successfully able to tell us the factors which are positively associated with mucormycosis. The potential risk factors are also described which will further strengthen our understanding of risk of mucormycosis.

## VI. FUTURE WORK

The models propose to detect patients at high risk of having mucormycosis and intent to warn them in advance. This can be used as a diagnostic measure and can be used for early diagnoses of mucormycosis which would be really helpful. This model included patients from different parts of the globe. For the future, the patients discharging rate can be calculated. Patients can be looked for amphotericin and remdesivir taken and can look for the association between the inhibition of mucormycosis with number of days associated.

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