



# A Comparative Analysis On The Efficacy Of Various Deep Learning And Machine Learning Techniques In Identifying The Different Variants Of Covid-19

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## ABSTRACT:

The current corona virus disease 2019 pandemic poses a serious danger to global public health. To evaluate its impact and guide control measures, we integrate the information on demographics, connection arrangements, illness austerity, health care accommodation and quality. Blooming community in low income nations may decrease the total risk, but insufficient healthcare capacity can have combined with more international interaction cancels this advantage. These moderation techniques that decrease but do not stop transmitting would nonetheless result in covid19 outbreaks promptly mind blogging immune systems, with significant excess fatalities in low income nations because to inadequate health care. Lower income countries have been more aggressive in their suppression efforts to date. This review provides an overview of the current state of all models for the detection and diagnosis of COVID-19 and processing based on some machine learning and deep learning techniques. According to observations, supervised machine learning techniques and deep learning techniques have an extraordinary capacity to provide accurate and efficient results for the detection and diagnosis of covid-19.

**Keywords:** COVID-19, machine learning, supervised machine learning, deep learning,

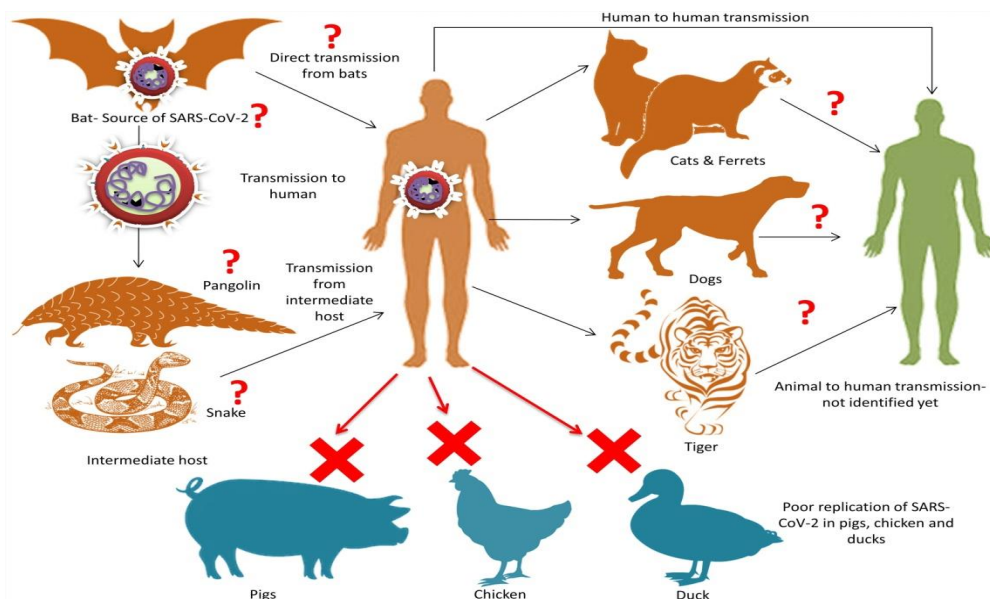
## 1. INTRODUCTION:

It is an infectious disease that damages the respiratory system and also can develop to anything ranging from a simple cold to severe diseases in individuals. This is seriously affecting the entire world because it spreads mainly from one person to other person among those who are within six feet of one another. Millions of peoples have been troubled due to this pandemic situation, some of them are sick and some are died as an outgrowth of this virus's extension. Many researchers and medical practitioners are working to stop the spread of this virus. But they are unable to stop. The 2009 HINI flu pandemic was the most contemporary pandemic to be confirmed worldwide. Because the corona virus spreads quickly from person to person and also causes severe illness, it was labeled a pandemic after 2009.

The covid19 is predicted to have an unprecedented global impact, with marginalized and vulnerable people in nations with low incomes bearing the greatest tension. Many LICs have reacted immediately and early with techniques for minimizing the spread of viruses, which may explain some of the low rates recorded in these countries thus far. Regardless of the possibly preservative holdings of developing enumerations, nearby internationally association, limited health care properties, and the prevalence of combative in low income nations necessitate long-term no pharmaceutical interventions to avoid overburdening health care capacity. For three fiscal years, the state of affairs has been continuously bad.

The current corona virus disease 2019 pandemic poses a serious danger to global public health. Lower income countries have been more aggressive in their suppression efforts to date. However, in these contexts, this will need to be maintained by high frequently in order to remain the available health capacity, with negative effects for the general healthiness, well being, and economy of these nations.

Human corona virus like severe acute respiratory syndrome corona virus (SARS CoV19) and middle east respiratory syndrome corona virus (MARS CoV19), those two are arise from animal reservoirs in the 21<sup>st</sup> century, produced a global pandemic with terrible morbidity and mortality. These corona viruses in humans are members of the Corona variance subfamily of the Corona viridian family. The virus was given the name "corona" because an electron microscope revealed a spike like feature on its outer surface. Its single stranded RNA has a diameter of 80 to 120 nm, and the length of its nucleic material ranges from 26 to 32 kbps. They are essentially separated into the genera alpha (), beta (), gamma (), and delta (). Whereas and CoV mostly affects birds, and CoV typically infects mammals.



**Fig1: Corona virus transmission from animals to humans**

The term "corona virus" refers to how the virus appears under a microscope. The virus is mainly composed of a spiked protein envelope around one genetic material core. It resembles a crown due to this feature. Latin's word corona translates to "crown". The novel corona virus is firstly invented in the city of Wuhan , china in 2019 December. In 2020 March, this Corona Virus epidemic was identified as an unrestricted spread by world health organization. The family of pathogens are termed as covid19 includes the corona viruses.

## 2. SYMPTOMS OF COVID 19:

The most frequent symptoms of this corona virus illness are Fever, cold, cough, joint pains, and respiratory issues. Peoples who are affected by the corona virus may also have symptoms like fatigue, a sore throat, soreness in muscles, loss of taste and loss of smell in addition to these symptoms. Different human beings are affected by Covid 19 illness in different ways. The superiority of those affected with this Covid 19 have slight to tolerable illness and bring back outwardly seeking medical attention.

The symptoms of corona virus disease can be classified based on severity are three categories:

- The dynamite typicaldiagnostics include a high temperature, tickle in throat and cold.
- Body caution, sore head, flux, pain in the neck, loss of zest and flavor, rashes on film of body and blemish on hooks and phalanx are categorized into less common symptoms.
- Serious symptoms include respiratory conditions, chest discomfort, high blood pressure, and loss of speech or immobility.

This virus seems to have the possibility of affecting society. Three kinds of persons are particularly at a greater prospect of developing inflexible covid 19 syndrome. Senior Citizens (people over 70 years of age), Physically sedentary individuals, Individuals with severe chronic diseases, include De-bates, Acute myocardial infarction, Chronic respiratory disease, Malignancy, Diastolic Pressure, Chronic liver diseases.

### 3. VARIANTS OF COVID 19 :

Due to adaptive alterations in the aggressive phenom, the pythonic capabilities of such a virus can fluctuate over time. Even an individual amino acid substitution can have a significant impact on a virus scope to avoid the exempt classification, making it more difficult to develop a vaccine to defend in opposition to the virus. SARS CoV 2, like other Ribonucleic acid viruses, is subject to patrimonial growth as it develops mutations over time in response to its new human hosts. As a consequence, several variations even distinct from its ancestral strains emerge. Routine genetic sensing of sprouting segments edibles the discovery of new SARS CoV 2 genomic variations spreading in society, particularly it is a national wide pandemic. The genetic development of SARS CoV 2 was relatively modest due to the early pandemic's establishment of the globally dominant mutation D614G.

Remaining mutations of SARS CoV 2 have emerged since then they detected some of them are known as alternatives of concern by the reason of their imaginable harm to the stamina of people. VOCs have been associated to the potentiality to evade finding, an expansion in transformation, a decrease in elimination by antibiotic created by common inoculation, or a reduction in the effectiveness of therapies or immunizations. According to the WHO's etymological announcement, 5 SARS CoV 2 variants had been invented from the start of this pandemic, before until 11<sup>th</sup> December, 2021.

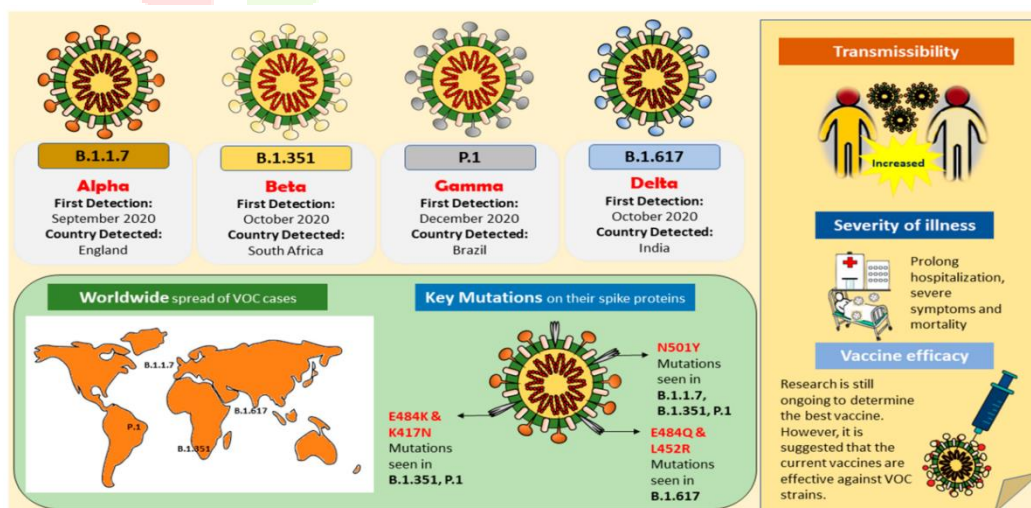


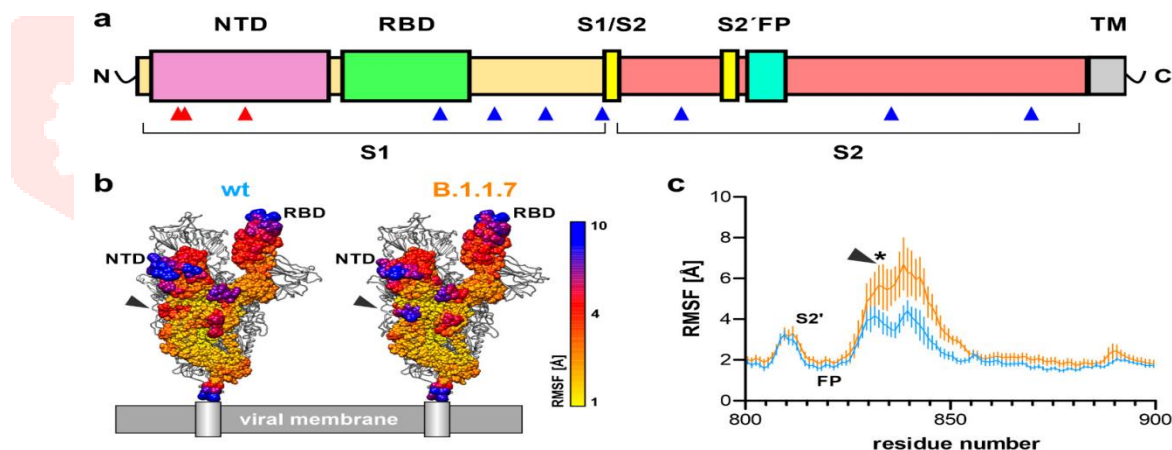
Fig 2: How CORONA Virus Mutations Can Takes Place

Describes that how corona virus mutations can take place and where the first detection is observed in each country and also tells that how transmissibility will increase and severity of illness, how effectively vaccine works on each mutation.

### 3.1. ALPHA (B 1.1.7):

In the United States of Kingdom, the concern Alpha B 1.1.7 initial mutation is identified in December 2020. A SARS CoV2 variation of concern was the alpha variant (B.1.1.7). According to estimations, it was 40 to 80 percent more contagious than the SARS CoV2. This variant was first identified in November 2020 from a sample collected in UK in the month September, and by December, right when infections were on the rise, it was spreading rapidly. Because it had more changes than usual, the variation stood out.

By January 2021, more than half of the SARS CoV2 DNA sequencing work had been completed in the UK. This prompted questions about how many additional significant variations might be travelling around the world without being noticed. On February 2<sup>nd</sup>, 2021, Public Health England reported the discovery of a limited number of B 1.1.7 VOC 202012/01 genomes with E484K mutations, which they named VOC 202102/02. One of the alterations N501Y is also present in beta and gamma versions. The World Health Organization stated on May 31<sup>st</sup>, 2021, that the variant of concern will be given the title Alpha for use in public communications.

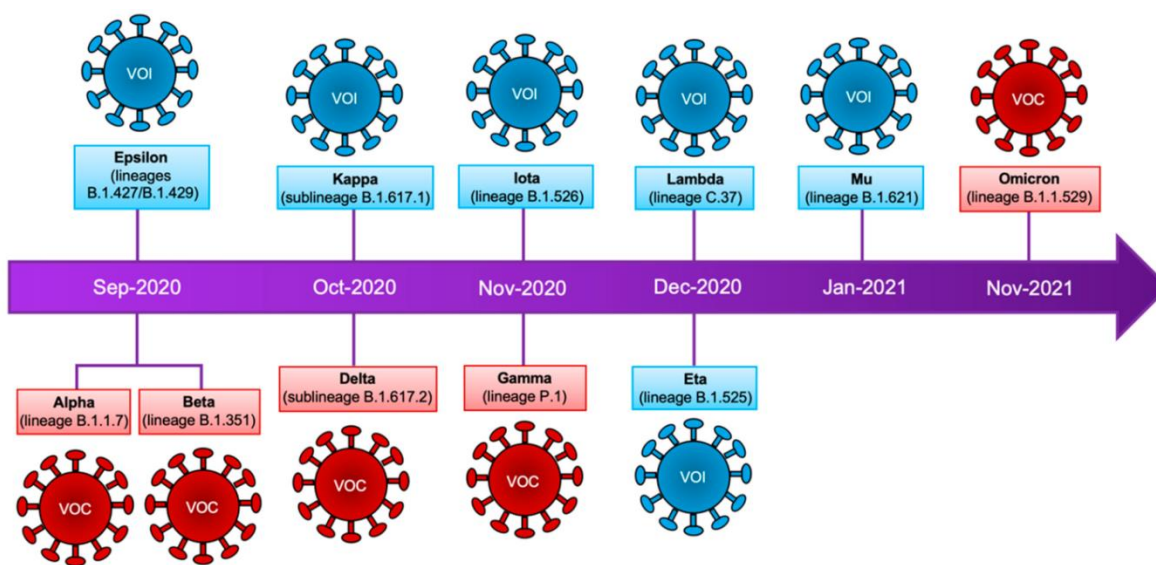


**Fig 3: ALPHA Variant spike mutations**

### 3.2. Beta (B 1.351):

In the south Africa, the concern Beta (B 1.351) initial mutation is identified in December 2020. The SARS CoV2, was a variation that had a beta version (B 1.351). It has been one among a number of SARS CoV2 types and was initially considered to be particularly important. In South Africa's Eastern Cape province, it was discovered for the first time in Nelson Mandela Bay in October 2020. On December 18<sup>th</sup>, 2020, the health department of that country revealed its discovery. According to phylogeographic research, this variation

appeared around July or August of 2020. The world health organization designated the variation as a **Beta variant**.



**Fig 4: How Beta variant takes mutations to delta and gamma**

**Three alterations in the genealogy B 1.351 genome's peak region are of special relevance. K417N, E484K, N501Y.**

**Five additional spike variants that possess less worry in Beta variant mutations. They are L18F, D80A, D215G, R246I, A701V.**

With the exceptions of the alterations beyond the fasten domain, it also has the K1655N, SGF 3675 to 3677 deletions, P71L, and T205I mutations. The three alterations N501Y (a shift from asparagine's (N) to tyrosine (Y) in amino acid position 501), K417N, and E484K in the virus's receptor binding domain were discovered to be responsible for the variant's improved capacity to attach to human cells. Two of these changes E484K and N501Y can be found in the raptor bounden motif of the raptor-bounden domain. The raptor bounden motif is simply called as RBM and raptor bounden domain is called as RBD. Similarly, the N501Y variation has been discovered in UK. The Alpha form does not contain the mutations K417N and E484K, which are both found in the Beta version. Moreover, Beta is deficient in the 69 to 70del gene that is present in the other variant.

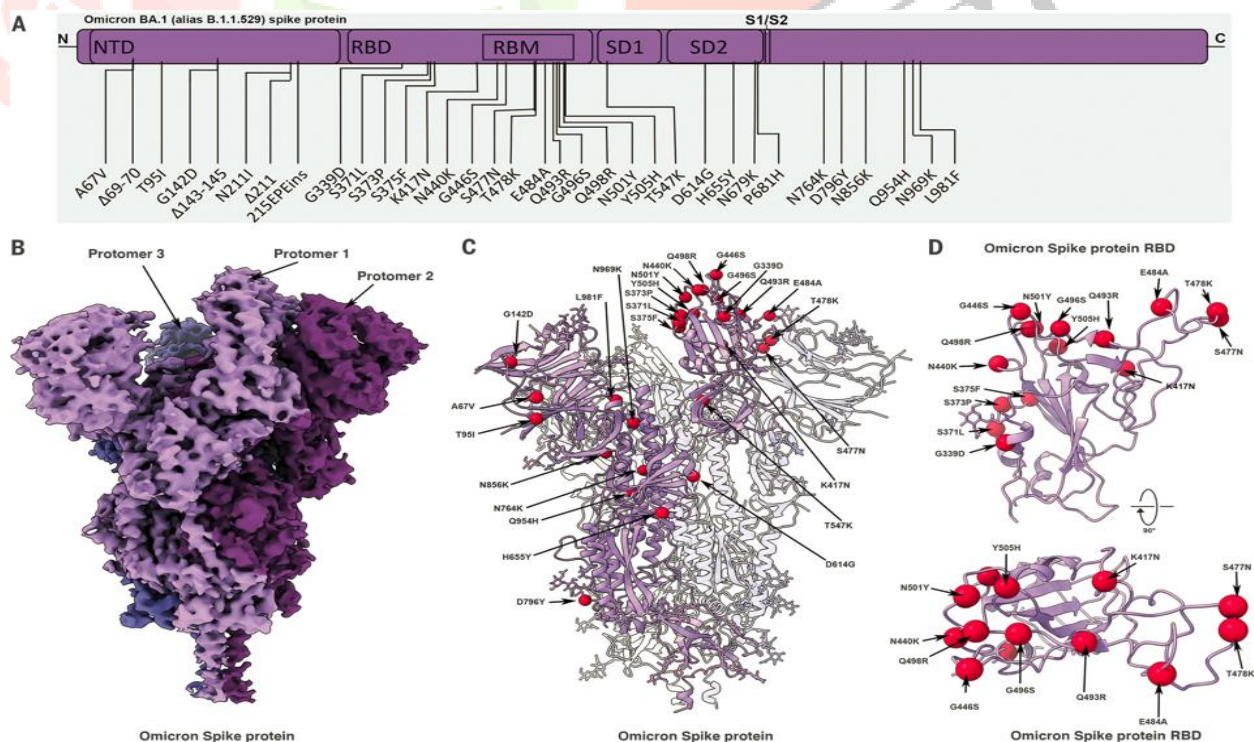
### 3.3. GAMMA (P.1):

The Gamma form of the variant SARS CoV2 is one of the variants that implements covid19 (P1). This SARS CoV2 variant virus is referred to as lineage P1. It possesses 17 amnestied novelties, and 10 of these are present in the spike protein. Three variants of these alterations are E484K, N501Y, and K417T have been noted as particularly concerning. On January 6<sup>th</sup>, 2021, the Japanese National Institute of Infectious Disorders (NIID) of Japan recognized the first case of this SARS CoV2 variant. In 4 vacationers who had possess just returned from such a four-day excursion to Brazil's Amazonas. Following that, it came to be known that Brazil

was using it. The World Health Organization's suggested condensed naming system identifies P1 as a Gamma variant, which is generally accepted.

According to a report from May 2020, the Amazonian region's capital city of Manaus has already seen widespread infection with a significant experience of SARS Co antibiotic. Nevertheless, earliest year of 2021, gamma triggered a widespread outbreak throughout the city. A study published in Science Magazine found that human beings who are effected by B 1.1.28 infection will have a greater possibility of dying and a reduced likelihood of transmission. The 2 transparent subversions are 28 AM 1 and 28 AM 2, in which both of them are originated separately within same Brazilian Amazonas region and make up the Gamma variant, share the K417T, N501Y and E484K variations. Gamma variant is apparently contrasting against the Zeta type (ligeneology P2), which, while extensively dispersed in Brazil as well, varies significantly from Gamma. Zeta, who solely carries the E484K mutation, does not have any of the other two mutations.

Early sources indicated that the Brazilian Lineage B 1.1.248 had two unique and independent forebears, P1 and P2. After that, B 1.1.248 was demoted to B 1.1.28 and invisible its consequences on the point of a branch. P1 has also been known as B 1.1.28.1, while P2 has also been known as VUI-202101/01 and B1.1.28.2. Just three sublevels are allowed under the PANGO Lineage name convention, hence B 1.1.28.1 and B 1.1.28.2 are referred to as P1 and P2, respectively. Genome information from four samples that included the new variation was provided with GISAID under the ID range from **EPI ISL 792680** to **EPI ISL 792683** once it was detected.



**Fig 5: Three alterations in the lineage B.1.351 genome's peak region are of special relevance.**

### 3.4. Delta (B1.617.2) :

Delta divergent of covid19 is First proclaimed in India late days of December 2020. Currently, 8 percent of interpreted corona virus cases in the UK are linked to Sub Delta Variant (AY 4.2). The variant might be 10 percent more contagious than the most common Delta variety in the UK. The spike contains two unique mutations, Y145H and A222V.

### 3.5. Omicron (B1.1.529):

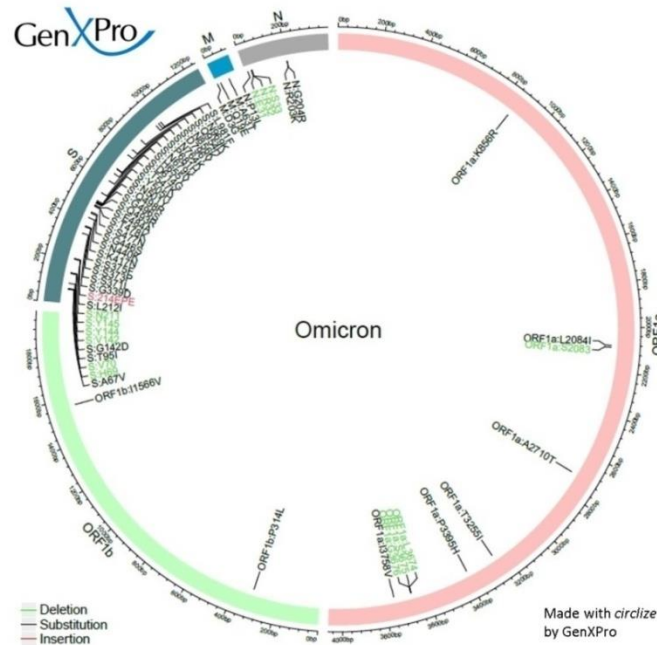
In 2021 November, the omicron variant has been first noticed in South Africa. Except for the Delta variant, which justifies the spike molecule's compatibility for ACE 2 resets to improve their ability, all five observed VOCs like Alpha, Beta, Gamma, Delta, and Omicron have been some genetic defects in the RBD and the NTD. This will facilitate all the attachments of the virus and its successive access into manage cells. Similarly, with NBD, RBD provides as the main destination for neutralization and encourages the construction of antibodies in resonance to immunizations or antiserum. The two novel folios claim the N501Y alteration of individual particle will increases the compatibility of RBD and ACE2 by over 10 times compared to the original pressure(N501-RBD). It's fascinating to observe that the binding efficiencies of the N417/K848/Y501 RBD and ACE2 modified Beta and Gamma variants are significantly subordinate those of N501Y RBD and ACE2. The changes discovered in Omicron variant is pretended later.

Ongoing emergence of each novel variant severe acute respiratory strains threatens the outstanding procession finished up to now in irresolute the enlargement of SARS Cov19 despite the swift creation of covid19 vaccinations and ongoing mass immunization events, which include suggestions for vaccine renewals. The main goal of this review paper is to provide a comprehensive discussion of these novel versions of concern, the most recent adult covid19 treatments, and the efficacy of the various covid19 antiseptics that are presently accessible.

This variant is a SARS CoV2 variant and it was originally expressed to the world health organization on Nov 24th, 2021 through the system for bionomics Survayance in South Africa. Since its initial discovery in Botswana, it has developed into one of the most common variety globally. After the initial BA.1 variation, Omicron has a large number of sub variants, including BA2, BA3, BA4 and BA5. later 2022 October, two BA5 subordinates known as BQ1 and BQ.1.1 has been quickly spreading.

A three dose covid19 vaccination gives protection in opposition to serious sickness and rehabilitation due to BA1 and BA2. Indemnity responses to BA2 are equivalent to those to BA1. By the month of June 2022, an advanced vertex in covid19 illness is developed because the BA4 and BA5 variations have huge conterminous than earlier subordinates in three dose vaccinated persons.

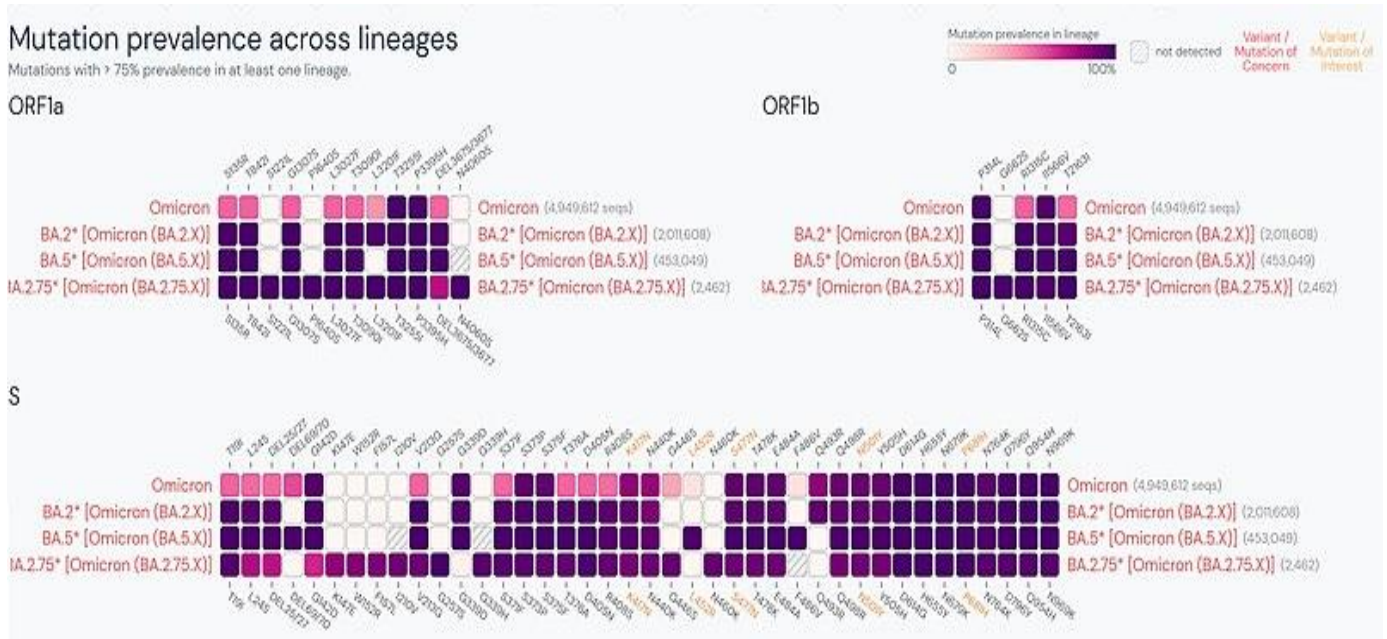




**Fig 6: The Omicron variant's genomic sequence.**

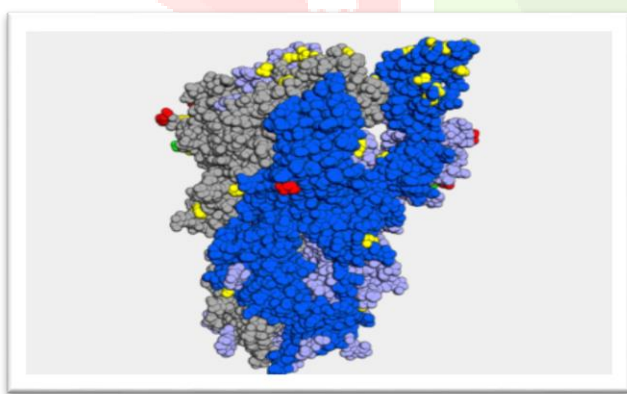
More than any other SARS CoV 2 variation before it, Omicron (BA1) had about 50 mutations as of June 2022, 32 of which were linked to the spike protein that the majority of vaccines focus on to counterbalance this type of virus. By the month of December in 2021, huge number of alterations were invented and those have not been seen in earliest mutations. The variation had 30 amended revisions, among those three are inconsequential eliminations, and one is inconsequential addition as per April 2022, 15 revisions of those are in the receptor binding domain(RBD).

Numerous methods have been used to identify Omicron sub variants, and new ones are constantly being discovered. The Omicron variation is currently linked to 310 Pango lineages. The authoritative subordinate is known as BA.1, while the 2 additional subordinates are called as BA.2 and BA.3. The middle of 2022 saw the discovery of BA.4 & BA.5 in a number of different countries.

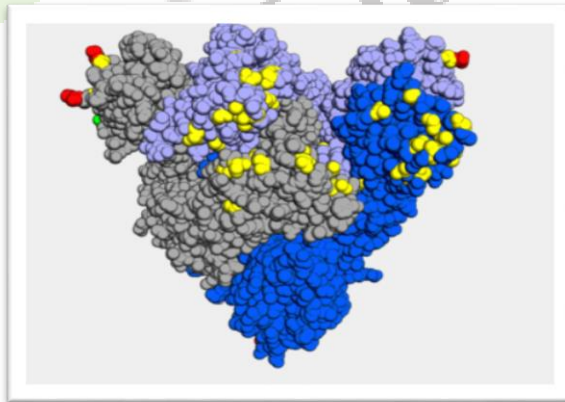


**Fig 7: Across Omicron lineages, mutation frequency.**

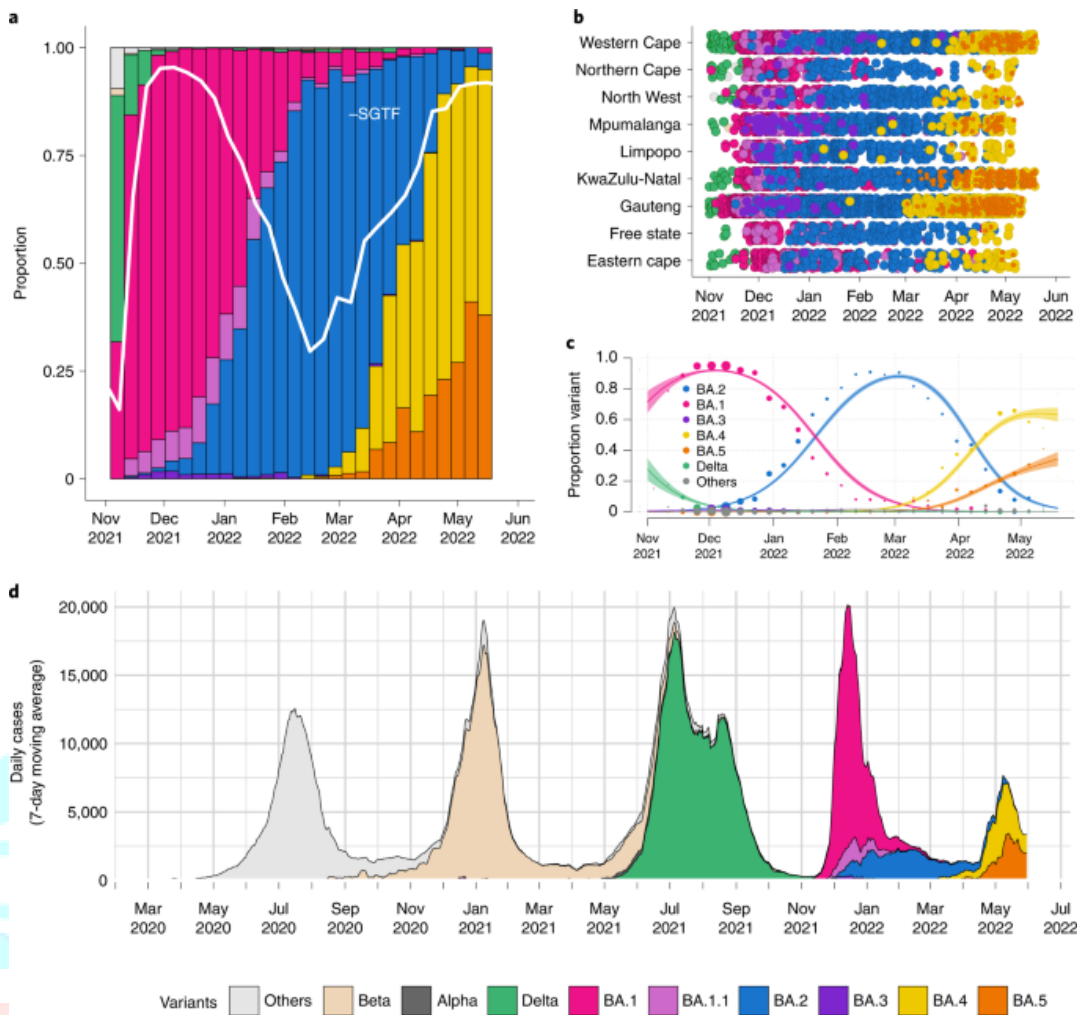
The ORF1a, ORF1b, and S genes of the Variants of Concern Omicron lines are compared for the prevalence of mutations. Particularly the aspect of mutations for an extractions are consonant changes or eliminations that appears in more than 75 percent of the genes in that lineage. They differ greatly yet also have a lot of mutations in common. In general, 32 mutations are shared by BA1 & BA2, whereas 28 mutations are contrasting. The initial BA.1 has been divided into two sections, the first of which is BA1.1 (or B 1.1.529.1.1), which is distinguished by the presence of the R346K mutation. All Omicron sub variants are still detected ascovid19 by standard PCR and fast testing, but additional analysis are required to identify the subordinates from one to another and from the othercovid19 variations.



**Fig 8: Side view**



**Fig 9: Top view**



**Fig 10:** All Omicron lineages have a high mutation rate.

**Literature searching strategy and article selection:**

**Table 1:** Supervised, un-supervised machine learning and deep learning for analyzing the COVID-19 disease that included articles with the related details of the Dataset, author name, year of publication, the data set, aim of study and used method in the study

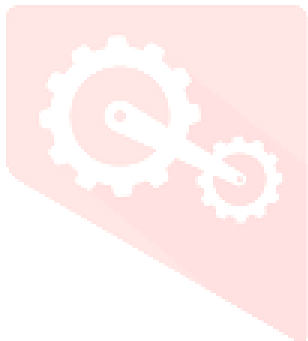
S.No	Author/Reference	Year	Aim of The Study	Dataset/ Population	Tasks and Algorithms/ Model
1	Khanday et al. [61]	2020	Detection	GitHub 212 reports	Classification Logistic Regression and Naive Bayes
2	NursultanMakhanov et al., [82]	2022	Classification & Detection	CT-Scan & RT-PCR Records	CNN, RNN, GANs, LSTMs
3	Alina sirbu et al.,[80]	2021	detection, diagnosis & prognosis	lung X-ray and CT Scan of 265 patients	Classification, logistic regression and genetic algorithm
4	Luca et al. [63]	2020	Detection	85 chest X-rays	Classification K-nearest neighbors classifier (k-NN)
5	Constantin et al. [63]	2020	Detection	152 datasets of COVID-19patients, 500 chest CTs	ClassificationsConvolutional Neural Network(CNN)
6	Ramjeetsingh yadav et al.,[78]	2020	Detection	1,52,25,252	Regression analysis model and RMSE
7	Dan et al. [67]	2020	Detection and Diagnosis	6995 patients in Sheba Medical Center	Classifications Artificial Neural Network (ANN)

8	Joep et al. [68]	2020	Detection and Diagnosis	319 patients	Classification Logistic regression
9	mustafaGhad er et al., [75]	2021	Detection and diagnosis	radiographic imaging	Not mentioned
10	Hoyt et al. [63]	2020	Detection and Diagnosis	290 patients	Classification Logistic Regression
11	María.et al. [71]	2020	Detection	Food for each of the 170 countries	Clustering K-means clustering
12	Apostolopoulos et al., [56]	2020	Detection	455	MobileNetV2
13	Yigrem.et al. [73]	2020	Detection	244 samples	Classification Logistic Regression
14	Abolfazl et al. [74]	2020	Detection	US Centers for Disease and Control and Johns Hopkins University. Database of 57 candidate	Classification Artificial Neural Networks (ANN)
15	F. A. Saiz and I. Barandiaran, [58]	2020	Detection	1500	VGG-16 SDD
16	Ni et al., [20]	2020	Detection	14531	Convolutional MVP-Net and 3D U-Net
17	Mei et al., [54]	2020	Diagnosis	905	Inception_ResNet_V2
18	Rahimzadeh& Attar, [22]	2020	Diagnosis	images (open source) 337 images	Xception and ResNet50V2
19	L.J.Muhammad et al., [76]	2020	Detection	651247	SVM,Naïve Bayes
20	Ardakani et al., [24]	2020	Detection	194	AlexNet, VGG-16, VGG-19, SqueezeNet, GoogLeNet, etc.
21	Li et al., [59]	2020	Diagnosis	4356 CT exams from 3322 patients	ResNet-50 as backbone of main model
22	Li et al., [25]	2020	Automatic diagnosis	2914	MobileNetV2

23	Togaçar et al., [44]	2020	Diagnosis	Two open sources (n = 295)	SqueezeNet and MobileNet
24	Song et al., [27]	2020	Detection	227	BigBiGAN
25	Das et al., [49]	2020	Screening (diagnosis)	6845	Truncated inception net
26	Butt et al., [29]	2020	Classification (diagnosis)	618	ResNet-18
27	Loey and et al., [30]	2020	Diagnosis (Classification)	306	GoogLeNet
28	Pathak et al., [51]	2020	Classification (detection)	852	ResNet-50
29	El Asnaoui and Chawki, [32]	2020	Diagnosis	6087	Inception_ResNet_V2
30	Martínez et al., [48]	2020	Detection	240	NASNet2
31	Jaiswal et al., [35]	2020	Detection	2492 (open source)	DenseNet201
32	N Dey et al., [37]	2020	Diagnosis	5856	CovXNet
33	Waheed et al., [52]	2020	Detection	1124	ACGAN3 , VGG-16
34	Ko et al., [39]	2020	Diagnosis (differentiate)	3993 patients	ResNet-50
35	Wu et al., [46]	2020	Screening (diagnosis)	495	ResNet-50
36	Vaid et al., [42]	2020	Detection	181	VGG-19
37	Ucar&Korkmaz, [43]	2020	Classification (diagnosis)	Public	Deep Bayes SqueezeNet
38	Sethy et al., [26]	2020	Diagnosis	381	ResNet-50
39	Khan et al., [45]	2020	Detection and diagnosis	Two datasets (n = 1300)	Xception

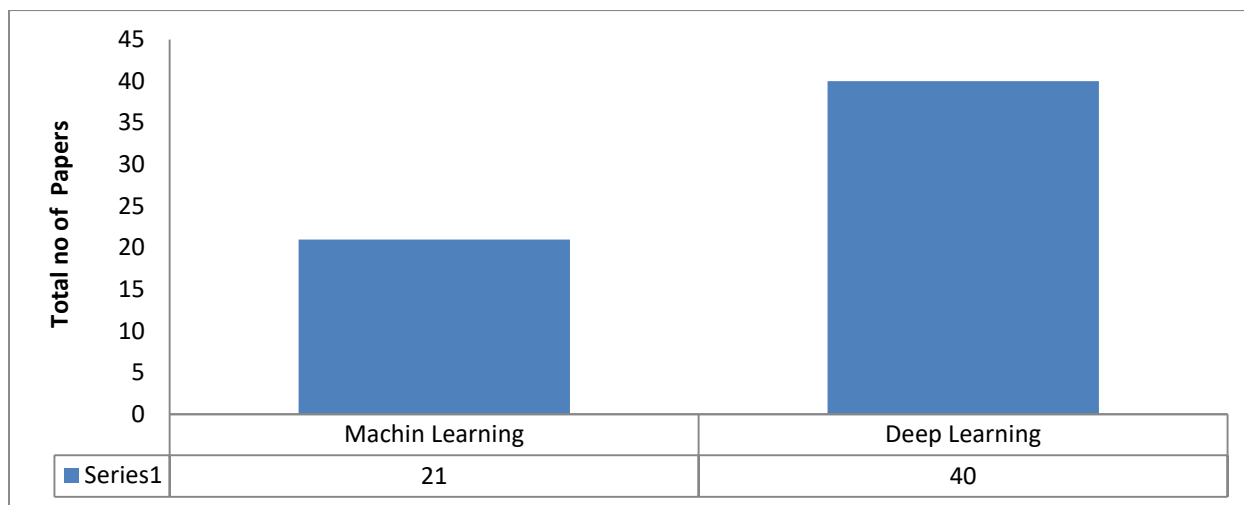
40	Wu et al., [40]	2020	Screening (diagnosis)	495	VGG-19
41	Yi et al., [47]	2020	Classification (detection)	88	Not mentioned
42	Yang et al., [33]	2020	Detection	295	DenseNet
43	Brunese et al., [28]	2020	Detection	6,523	VGG-16
44	Hasan et al., [50]	2020	Diagnosis (classification)	321	LSTM neural network classifier
45	Ozturk et al., [31]	2020	Automated detection	2 databases	DarkNet
46	Singh et al., [38]	2020	Classification (diagnosis)	Not mentioned	Not mentioned
47	Pereira et al., [53]	2020	Diagnosis (classification)	1144	Inception-V3
48	Wang et al., [21]	2020	Diagnosis and prognosis	5372 (two datasets) 11302	DenseNet121-FPN
49	Brunese et al., [55]	2020	Detection and diagnosis	6523	VGG-16
50	Shinwoo et al. [72]	2020	Detection	790 Korean immigrants	Classifications Artificial Neural Network (ANN)
51	Elaziz et al., [57]	2020	Detection	2 databases (open source)	MobileNet
52	chaoling Huang et al., [60]	2020	Detection	X-Ray of 41 people	supervised learning
53	Christopher et al. [69]	2020	Detection and Diagnosis	368 independent variables	Classifications Naive Bayes
54	Panwar et al., [23]	2020	Fast detection	(open source)	VGG-16

55	Alison et al.,[77]	2020	Detection	stanford university test samples data	AUROC logistic regression, root mean square algorithm
56	Lamiaa et al. [63]	2020	Detection	COVID-19 5000 cases	Regression Linear Regression model
57	Auriel et al.,[79]	2022	Detection	80 Participants with 124 test cases	Classification and AUC
58	Varun et al. [63]	2020	Detection and Diagnosis	184,319 reported cases	Classifications Convolutional Neural Networks (CNN)
59	YazeedZoabi et al.,[81]	2021	Detection and diagnosis	51,831 records of RT-PCR	gradient-boosting ML model & decision tree baselearners
60	Burdick et al. [62]	2020	Detection and Diagnosis	United States health systems 197 patients	Classification Logistic Regression
61	MatjazKukar et al., [83]	2021	Detection and diagnosis	blood tests of 5333 patients and CT-Scan & RT-PCR records	Machine Learnig models



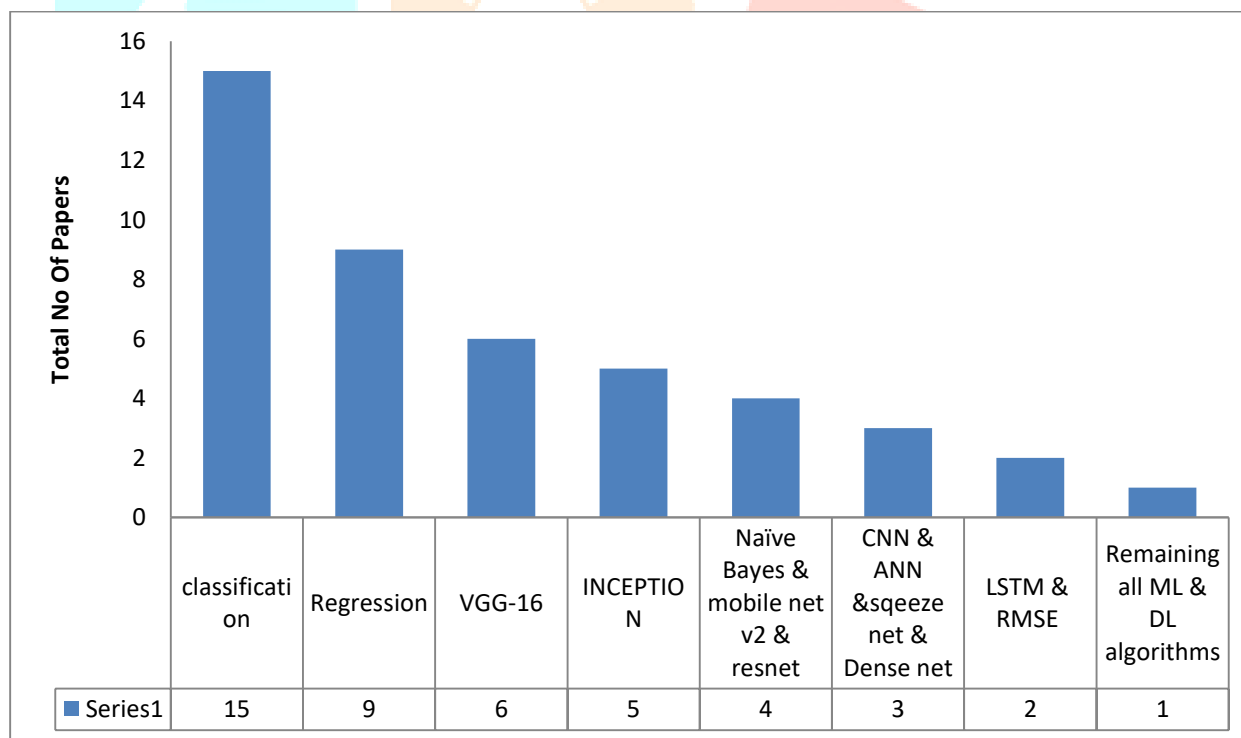


#### 4. Results:



**Fig 11: Distribution of Machine Learning and Deep Learning types**

According to Fig. 11, deep learning and its techniques are mostly used in 40 articles out of 61 articles. The majority of studies used both machine learning methods which were in 21 articles whereas deep learning methods in 40 articles.



**Fig 12: Distribution of Machine Learning and Deep Learning Algorithms**

According to Fig.12, classification technique is most frequently used in detection and diagnosis of Covid-19. Out of 61 articles, classification is used in 15 papers. Regression techniques used in 9 paper out of which are 16. The next priority is that given to VGG algorithm that out of 61 articles VGG is used in 6 articles. Naïve Bayes, Mobile Net & ResNet are used in 4 articles, and then CNN, ANN, Squeeze Net & Dense Net are used in 3 articles, LSTM & RMSE are applied in 2 articles and finally remaining

algorithms and techniques like RNN, GAN, Genetic Algorithm, KNN, Clustering, K-Means are applied in least count in various articles.

## 5. Conclusion:

In this research, we focused on 61 published articles that applied Machine Learning and Deep Learning applications in COVID-19 disease for various purposes with many different algorithms. Both ML & DL techniques shows best result in detection and diagnosis of covid-19 disease. With incorporation of DL algorithm in the equipment of radiology centers, it will be possible to achieve a faster, cheaper and safer diagnosis of disease. DL is one of the most powerful computing tools in diagnosis and developers should be careful to avoid overfitting and to maximize the generalizability and usefulness of covid-19 DL diagnosis models. These models must be trained on large and heterogeneous datasets to cover all the availability data space. In general, this research results explored that Deep Learning is more accurate to detect and diagnosis the covid19 cases which were above 65.57% when compared to the Machine Learning was 34.42%. As a result, Ref. [39] will shows best results as sensitivity as 99.58%, specificity as 100% and accuracy as 99.87% by using Deep Learning Techniques.

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