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PREDICTION OF THE SUPPORTIVE VACCINE TYPE OF THE COVID-19 FOR PUBLIC HEALTH

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Abstract: The novel corona virus SARS-Cov-2 caused the COVID-19 pandemic and mostly deteriorated the respiratory system. This paper aims to predict the supportive vaccine type (RNA, Non-replicating viral vector, DNA, Inactivated, Protein subunit) of COVID-19 for the human being by the rough set's novel process. The Rough set is an approach to identify patterns in uncertainty. The vaccine dataset, vaccine name, number of tested cases, age, randomize, and vaccine types of COVID-19 have been taken to overcome this disaster. By the rough set method, the supportive vaccine pattern is predicted, and it is observed that the vaccine based on RNA is highly supported to the human beings compared to the others. Extensive tests explained the Pfizer vaccine (RNA) is 95% effective, Moderna (mRNA) is 94.1%, while the Oxford/AstraZeneca (Non-replicating) one is 62%. It shows that the efficiency obtained by the rough set is accurate. A data-intensive computer-based analysis is given for the medical system. Furthermore, we present an extended record of sources that will support the scientific bioinformatics society to attain various sorts of a database linked to SARS-CoV-2 and advances to associate with COVID-19 treatment.

Keywords: COVID-19; vaccine; RNA; DNA; rough sets.

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1. INTRODUCTION

A novel corona-virus outbreak has started on 29 December 2019 in Wuhan (China). After, it has progressively expanded to the various countries of the world. Based on its dangerous expansion in the world, the WHO declared a Public Health Emergency of International Concern [WHO India Report 1] [WHO India Report 7][1]. The most common symptoms of COVID-19 are fever, dry cough, breathing difficulty, sore throat, or diarrhea [**MoHFW, Government of India 25 March 2020 Awareness materials**] [2]. The COVID-19 is considered zoonotic in starting from bats to intermediate animals to people [3], and its introduction is geographically connected with the ambiguity of the seafood business in Wuhan [4]. However, in the Indian scenario, the zoonotic transmission is zero as the cases are only imported from foreign countries. So, only Human-to-human transfer of COVID-19 has been established through respiratory droplets [5], and asymptomatic infection [6]. To restrain the diseases, global administration has directed the dissolution of essential functions to prevent the corona-virus disease.

The corona 2019 virus is a dangerous condition for human beings and created an enormous hazard to health. A global multilevel interaction with plenty of circumstances varying from physical to financial factors forces the advancement of extremely modern mathematical models for the sound presentation of infectious dynamics of diseases (i. e., COVID-19). To control the outbreak of diseases, the government has ordered the ending of vital functions through lockdown to restrict the corona-virus disease. The corona virus COVID-19 is affecting 213 countries and territories around the world [7]. The corona virus's major impact can be seen in South America, Asia, North America, Europe, and Africa.

Most cities and whole countries have been put under lockdown by restraints on journeys and gatherings. These steps and the cessation of foreign boundaries and worldwide tour limitations have had a notable financial influence, ending in an explicit deterioration [8]. The mandated social distancing in a region curbed the corona virus every day new cases [9]. To check the virus's spread and find the supportive vaccine type, we testify strict standards by the rough set method.

Developing a vaccine against COVID-19 is one of the most pressing challenges of our time [1]. Various attempts are in advancement to deliver a vaccine for COVID-19. The procedures involve the standard inactivated vaccines (seven teams are acting upon this, including two inactivated vaccines in clinical tests), the protein subunit and virus-like particle vaccines (VLP) (twenty-eight teams toward the subunit vaccines, regularly upon the spike protein and five on VLPs), viral vector-based vaccines (approximately twenty-five teams including one in the clinical trial), and the latest RNA and DNA based vaccines (twenty teams by one of every kind in clinical trials) [10].Every strategy has its benefits and limitations, and each procedure is being advanced concurrently to form an efficient vaccine [11].The model should be viewed as a base for additional development. We bypass fitting models to data in a standard system. Alternatively, we adopt a simple model structure to explain what factors might be required. For example, to obtain excellent fitting representation, one must incorporate a time-varying summary, induced by the availability of medicinal stocks, dispensary functions, and developing examination/recording systems. Therefore, it would be challenging given a comparatively small interval and some other hidden parameters to be determined.

This paper gives a picture of the supportive vaccine type (RNA, Non-replicating viral vector, DNA, Inactivated, Protein subunit) of COVID-19, viral-human protein intercommunications, and the current status of vaccine and novel mediation progress.

2. STUDY DESIGN

The design of this study is a prediction of the supportive vaccine type of Covid-19. In work, we concentrated on the various vaccines of COVID-19 and successively for the effectiveness of the vaccine type (RNA, Non-replicating viral vector, DNA, Inactivated, Protein subunit) of COVID-19.

3. ROUGH SET METHOD

The rough set describes the matter from information to the broad concept of the data's cryptic patterns. Every knowledge system includes two platforms: (i) estimate of dubious conditions, (ii) utilization of assessed patterns to project outcomes. The rough set showed an impressive biomedical study area, including various applications, by employing different approaches and estimates [12-16].

3.1 WHY THE ROUGH SET METHOD

The rough set describes the matter from information to the broad sense of selection of features and recognizing a pattern in the data [12-16]. The Rough Set Exploration System (RSES) [16] is an essential mechanism for finding decision rules. Therefore, here the features and the pattern of vaccines are dealt with using the rough set. The 34 decisional rules are generated, and based on these rules, the supported vaccine type was found.

3.2 DECISION RULES FOR KNOWLEDGE STRUCTURE

The data analysis by the rough set is an information system named as a knowledge structure. A knowledge structure $IS = (Z, P)$, where Z and P are finite sets objects and characteristics, respectively. All characteristic $p \in P$, a set W_p, of its states described the region of p [17-18]. Any subset Q of P determines a binary relation $Ind(Q)$ on Z, is identified as a similarity connection and characterized by, $(u, v) \in Ind(Q)$ iff $p(u) = p(v)$ for every $p \in P$, where $p(u)$ shows the value of the specific $'p'$ for segment $'u'$ [17-18]. An equivalence relationship is $Ind(Q)$. The collection of all identical classes of $Ind(Q)$, i.e., a portion-controlled by Q, is shown by Z/Q [17-18].

In a data frame of the knowledge structure, is expressed by $IS = (Z, E, F)$, where E and F are condition and decision characteristics, respectively [17-18]. By each $Q \subseteq P$ and from combinations of characteristic-value (p, w) where $p \in Q$ and $w \in W_p$, codes of $For(Q)$ are

formed. Each $\alpha \in For(Q)$ by $\| \alpha \|_{IS}$ indicates all objects $u \in Z$ satisfying α viewed as follows [17-18]:

$\| (p, w) \|_{IS} = \{u \in Z : \mathrm{p}(w) = u)\}$, for every $p \in Q$ and $w \in W_p$

Let $Decision(IS)$ be a collection of regulations in the knowledge structure $IS = (Z, E, F)$ follows [17-18]:

1) If $\bigcup_{Y \in Z/F} E_*(Y) = \| \bigvee_{\alpha \to \beta \in Decision^+(S)} \alpha \|$ where $Decision^+(IS)$ the collection of all specific decision are rules from $Decision(IS)$, then the collection of regulations $Decision(IS)$ sustain the confidence of the knowledge structure *IS = (Z, E, F)*.

2) If $\alpha \to \beta \in Desicion(IS)$ and $\sup_{IS}(\alpha, \beta) \neq 0$ then the rule $\alpha \to \beta$ is possible in a knowledge structure (*IS*).

3.3 RULES BY THE ROUGH SET

The collection of a dataset of vaccine which is in the development phase [15] (Table 1) is used to describe the model as further relevant because we only require the attributes phase of the vaccine, vaccine name, number of tested cases, age, randomize, and vaccine type (RNA, Non-replicating viral vector, DNA, Inactivated, Protein subunit). We noticed this preliminary data in the precise form. The data is sound and very proper for working in the model.

The dataset [15] of the vaccine, vaccine name, number of tested cases, age, randomize, and vaccine type (RNA, Non-replicating viral vector, DNA, Inactivated, Protein subunit) COVID-19 with time (days) taken from 30 January 2020 to 25 October 2020. By using Rough Set Exploration System (RSES 2.2.2) [16], the rules are generated (Table 2), and it is observed the vaccine based on RNA supported by eight decision rules, seven rules support non-replicating vaccine, six rules support inactivated vaccine, five rules support protein-based vaccine, and DNA and other supported by four rules. Table 3 shows the statistics of the rules generated by the RSES2. Fig. 1 shows the number of rules supporting decision classes from the ruleset.

TABLE 1. The collection of a dataset of vaccine which is in the development phase [15]

Phase	**Name**	**Type**	**Number of tested cases**	**Age (years)**	**Randomized**
Phase I/II/III	BioNTech BNT162	RNA	32000	18-85	Yes
Phase III	Moderna mRNA-1273	RNA	30000	18	Yes
Phase III	WIBP vaccine	Inactivated	15000	18	Yes
Phase II/III	Oxford AZD1222/ChAdOx1-S	Non-replicating viral vector	10260	5	Yes
Phase III	Sinovac vaccine	Inactivated	8870	18	Yes
Phase I/II	BIBP/Sinopharm BBIBP-CorV	Inactivated	2128	3	Yes
Phase I/II	Oxford AZD1222/ChAdOx1-S	Non-replicating viral vector	2000	18-65	Yes
Phase III	Oxford AZD1222/ChAdOx1-S	Non-replicating viral vector	2000	18-55	Yes
Phase I/II	WIBP vaccine	Inactivated	1264	6	Yes
Phase I/II	Bharat Covaxin/BBV152	Inactivated	1125	65	Yes
Phase I/II	Oxford AZD1222/ChAdOx1-S	Non-replicating viral vector	1090	18-55	Yes
Phase I/II	Zydus Cadila DNA vaccine	DNA	1048	18-55	Yes
Phase I/II	CAMS vaccine	Inactivated	942	18-59	Yes
Phase II	AZLB protein subunit vaccine	Protein subunit	900	18-59	Yes
Phase I/II	Sinovac vaccine	Inactivated	744	18-59	Yes
Phase I/II	Cansino Ad5-nCoV	Non-replicating viral vector	696	18-84	Yes
Phase II	Moderna mRNA-1273	RNA	600	18	Yes
Phase II	Cansino Ad5-nCoV	Non-replicating viral vector	508	18-60	Yes
Phase I/II	CAMS vaccine	Inactivated	471	60	Yes
Phase I/II	Sinovac vaccine	Inactivated	422	60	Yes
Phase I	Imperial LNP-nCoVsaRNA	RNA	300	18-75	Part

SUPPORTIVE VACCINE TYPE OF THE COVID-19

Phase I/II	BioNTech BNT162	RNA	200	18-55	No
Phase I/II	Genexine GX-19	DNA	190	18-50	Yes
Phase I/II	Aivita AV-COVID-19	Other	180	18	Yes
Phase I	Medicago VLP vaccine	Other	180	18-55	Yes
Phase I/II	KBP-COVID-19	Protein subunit	180	18-70	Yes
Phase I	Curevac CVnCoV	RNA	168	18-60	Yes
Phase I	PLA-AMS vaccine	RNA	168	18-80	Yes
Phase I/II	Inovio INO-4800	DNA	160	19-64	Yes
Phase I	Moderna mRNA-1273	RNA	155	18-55	No
Phase I	Clover SCB-2019	Protein subunit	150	18-75	Yes
Phase I	BioNTech BNT162	RNA	144	18	Yes
Phase I	Novavax SARS-CoV-2 rS	Protein subunit	131	18-59	Yes
Phase I	Inovio INO-4800	DNA	120	18	No
Phase I	University of Queensland vaccine	Protein subunit	120	18-55	Yes
Phase I	Symvivo bacTRL-Spike	Other	112	19	Yes
Phase I	Cansino Ad5-nCoV	Non-replicating viral vector	108	18-60	No
Phase I/II	Altimmune T-COVID	Non-replicating viral vector	100	35	Yes
Phase I	SGMI aAPC	Other	100	0.5-80	No
Phase I	SGMI LV-SMENP-DC	Other	100	0.5-80	No
Phase I/II	Arcturus ARCT-021	RNA	85	21-80	Yes
Phase I	Gamaleya Gam-COVID-Vac (Lyo)	Non-replicating viral vector	76	18-60	No
Phase I	AZLB protein subunit vaccine	Protein subunit	50	18-59	Yes
Phase I	Vaxine protein subunit vaccine	Protein subunit vaccine	40	18-65	Yes
Phase I	AnGes AG0301-COVID19	DNA	30	20-65	No
Phase I	Immunitor V-SARS inactivated plasma	Other	20	18-65	No

TABLE 2. Rules for the pattern of the supportive vaccine types

S. No.	Matches	Rules
1	2	(Randomize=Yes) & (Phase=Phase I) & ("Number Tested Cases"=168) => ("Vaccine Type"= {RNA (2))
2	2	(Randomize=Yes) & (Phase=Phase I/II) &(Age=18-59) => ("Vaccine Type"= {Inactivated (2)})
3	2	(Randomize=Yes) & (Phase=Phase I/II) &(Age=60) => ("Vaccine Type"= {Inactivated (2)})
4	2	(Age=18-60) & (Phase=Phase I) &(Randomize=No) => ("Vaccine Type"= {Non-replicating (2)})
5	2	(Randomize=Yes) & (Phase=Phase I) &(Age=18-59) => ("Vaccine Type"= {Protein (2)})
6	2	(Phase=Phase I) &(Randomize=No)&("Number Tested Cases"=100)=>("Vaccine Type"= {Other (2)})
7	1	(Randomize=Yes) &(Age=18) &(Phase=PhaseIII)&("Number Tested Cases"=30000) =>("Vaccine Type"={RNA (1)})
8	1	(Randomize=Yes)&(Age=Â18)&(Phase=PhaseII)=>("Vaccine Type"={RNA (1)})
9	1	(Phase=Phase I)&("Number Tested Cases"=300)=>("Vaccine Type"={RNA (1)})
10	1	(Randomize=Yes)&(Phase=Phase I/II/III)=>("Vaccine Type"={RNA (1)})
11	1	(Phase=Phase I/II)&("Number Tested Cases"=200)=>("Vaccine Type"={RNA (1)})
12	1	(Phase=Phase I)&("Number Tested Cases"=155)=>("Vaccine Type"={RNA (1)})
13	1	(Randomize=Yes)&(Phase=Phase I)&("Number Tested Cases"=144)=>("Vaccine Type"={RNA (1)})
14	1	(Randomize=Yes)&(Phase=Phase I/II)&("Number Tested Cases"=2128)=>("Vaccine Type" = {Inactivated (1)})
15	1	(Randomize=Yes)&(Phase=PhaseIII)&(Age=Â18)&("Number Tested Cases"=15000)=>("Vaccine Type"={Inactivated (1)})
16	1	(Randomize=Yes)&(Phase=PhaseI/II)&("Number Tested Cases"=1264)=>("Vaccine Type"={Inactivated (1)})
17	1	(Randomize=Yes)&(Phase=PhaseIII)&("Number Tested Cases"=8870)=>("Vaccine Type" = {Inactivated (1)})
18	1	(Randomize=Yes)&(Phase=PhaseI/II)&("Number Tested Cases"=2000)=>("Vaccine

		Type"={Non-replicating (1)})
19	1	(Randomize=Yes)&(Phase=PhaseI/II)&("Number Tested Cases"=1090)=>("Vaccine Type"={Non-replicating (1)})
20	1	(Randomize=Yes)&(Phase=PhaseI/II)&("Number Tested Cases"=696)=>("Vaccine Type"={Non-replicating (1)})
21	1	(Randomize=Yes)&(Phase=PhaseII/III)=>("Vaccine TypeNon-replicating (1)})
22	1	(Randomize=Yes)&(Phase=PhaseIII)&("Number Tested Cases"=2000)=>("Vaccine Type"={Non-replicating (1)})
23	1	(Randomize=Yes)&(Phase=PhaseII)&("Number Tested Cases"=508)=>("Vaccine Type"={Non-replicating (1)})
24	1	(Phase=PhaseI/II)&(Randomize=Yes)&("Number Tested Cases"=1048)=>("Vaccine Type"={DNA (1)})
25	1	(Phase=PhaseI/II)&(Randomize=Yes)&("Number Tested Cases"=190)=>("Vaccine Type"={DNA (1)})
26	1	(Phase=PhaseI)&(Randomize=No)&("Number Tested Cases"=120)=>("Vaccine Type"={DNA (1)})
27	1	(Phase=PhaseI/II)&("Number Tested Cases"=160)=>("Vaccine Type"={DNA (1)})
28	1	(Randomize=Yes)&(Phase=PhaseI)&("Number Tested Cases"=150)=>("Vaccine Type"={Protein (1)})
29	1	(Randomize=Yes)&(Phase=PhaseI)&("Number Tested Cases"=120)=>("Vaccine Type"={Protein (1)})
30	1	(Randomize=Yes)&(Phase=PhaseII)&("Number Tested Cases"=900)=>("Vaccine Type"={Protein (1)})
31	1	(Randomize=Yes)&(Phase=PhaseI/II)&("Number Tested Cases"=180)&(Age=18-70)=>("Vaccine Type"={Protein (1)})
32	1	(Phase=PhaseI)&(Randomize=Yes)&("Number Tested Cases"=180)=>("Vaccine Type"={Other (1)})
33	1	(Phase=PhaseI)&("Number Tested Cases"=112)=>("Vaccine Type"={Other (1)})
34	1	(Phase=PhaseI/II)&("Number Tested Cases"=180)&(Age=Â18)=>("Vaccine Type"={Other (1)})

TABLE 3. Statistics of rules among decision classes

Statistics		Distribution of regulations among decision classes	
Total rules: 34 Total attributes: 5 **Rule Strength** Min: 1 Max: 2 Average: 1.2	**Rule Range:** Min 2 Max 4 Average 2.9	**Decision class**	**Count**
		RNA	8
		Inactivated	6
		Non-replicating	7
		Protein	5
		Other	4
		DNA	4

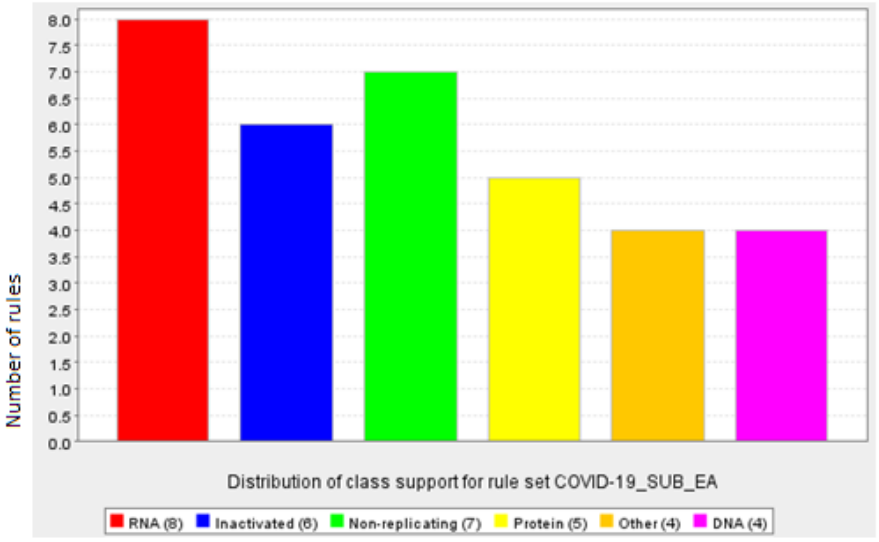

FIGURE 1. The number of rules supporting decision classes from the rule set generated by the rough set

3.4 THE MECHANISM USED FOR THE ROUGH SET

The rough set data analysis is an information system. Let a data frame comprising information $I_N = (c_o, c_c)$, where c_o is the collection of objects and c_c is the collection of characteristics, $s_o \subseteq c_o$ and $s_c \subseteq c_c$. The two sets $s_{c*}(s_o)$ and $s_c^*(s_o)$ represent the lower and upper estimate of s_o, respectively, and described as follows [12-14] [17-18]:

$$s_{c*}(s_o) = \bigcup_{z \in c_o} \{s_c(z) : s_c(z) \subseteq s_o\}$$

$$s_c^*(s_o) = \bigcup_{z \in c_o} \{s_c(z) : s_c(z) \bigcap s_o \neq \phi\}$$

The set

$$s_c N_{s_c}(s_o) = s_c^*(s_o) - s_{c*}(s_o)$$

is described as the boundary area of s_o [12-14].

If $s_c N_{s_c}(s_o) = \phi$ then s_o is crisp or exact with respect to s_c; and if $s_c N_{s_c}(s_o) \neq \phi$, s_o is rough or inexact with respect to s_c [12-14] [19-27].

3.5 ACCURACY OF THE METHOD

The rough set applications utilized today are considerably more extensive than before, basically in the drug zones, investigation of database traits, and process control. The rough set has a few covers with different strategies for information examination, e.g., cluster investigation, fuzzy sets, statistics, proof hypothesis, and others, yet very well may be seen in its rights as a free control [12-14]. The rough set method found that vaccines based on RNA supported by eight rules and large trials showed the Pfizer vaccine (RNA) was 95% effective, Moderna (mRNA) is 94.1%, while the Oxford one was 62% [28]. It shows that the accuracy found by the rough set method was 95%. Therefore, the rough set method is a powerful tool for finding the hidden pattern. Table 4 and Fig. 2 show the number of people fully vaccinated against COVID-19 till 09 February 2021. Table 5 shows the COVID-19 vaccine doses administered by the manufacturer

till 09 February 2021.

TABLE 4. The number of people fully vaccinated against COVID-19 till 09 February 2021 [29]

Country	Fully vaccinated population
United States	9840000
Israel	2220000
Italy	1210000
Germany	1020000
Spain	838782
United Kingdom	516392
Poland	482146
France	294120
Romania	263213
Indonesia	221453
Argentina	190203
Mexico	84218

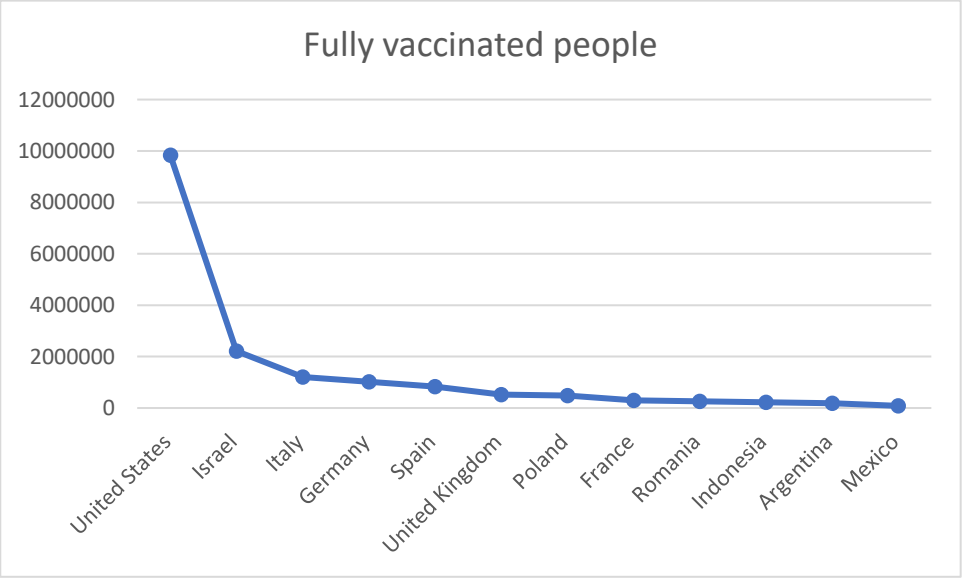

FIGURE 2. The number of people fully vaccinated against COVID-19 till 09 February 2021.

3.6 F-MEASURE OF THE MODEL

The likely cases of the true positive, true negative, false positive, and false negative denoted by T_P, T_N, F_P, and F_N, respectively. The T_P and T_N are the accurately recognized positive and negative occasions. An F_P happens when the result is anticipated, indeed, when it is not flawed. An F_N occurred when the result expected not when it is really yes.

TABLE 5. COVID-19 vaccine doses administered by manufacturer

S. No.	Manufacturer	No. of people vaccinated
1.	Moderna (mRNA)	20.07 Million
2.	Pfizer/BioNTech (RNA)	22.25 Million
3.	Oxford/AstraZeneca (Non-replicating)	29.21 Million

$$\text{Precision } (P) = \frac{T_P}{T_P + F_P} = \frac{40.204}{40.204 + 18.11} = 0.6894$$

$$\text{Recall } (R) = \frac{T_P}{T_P + F_N} = \frac{40.204}{40.204 + 11.09} = 0.7838$$

$$\text{F-measure} = 2 \times \frac{P \times R}{P + R} = 2 \times \frac{0.5404}{1.4732}$$

$$= 0.7336$$

4. RESULTS

The COVID-19 pandemic extends to increase; there is a thriving need for speedy testing of the virus. In current times, speedy molecular analyses applying computerized platforms have earned swift permissions from governing administrations. Every strategy has its benefits and limitations, and each procedure is being advanced concurrently to form an efficient vaccine [11].

The dataset [15] of the vaccine, vaccine name, number of tested cases, age, randomize, and vaccine type of COVID-19 with time (days) taken. By using Rough Set Exploration System

(RSES 2.2.2) [16], it was observed that eight decision rules support the RNA based vaccine; seven rules support non-replicating vaccine, six rules support inactivated vaccine, five rules support protein-based vaccine, and DNA and other supported by four rules. The rules for the pattern of the supportive vaccine types are given in Table 2. The statistics of rules among decision classes are given in Table 3.

5. Discussion and Conclusion

The corona 2019 virus is a dangerous condition for human beings and created an enormous hazard to health [30] [31]. A global multilevel interaction with plenty of circumstances varying from physical and financial factors forces the advancement of extremely modern mathematical models for the sound presentation of infectious dynamics of diseases (i. e., COVID-19) that would start to the establishment of efficient fundamental approaches and restriction strategies for eradicating the disease.

The first vaccine to start clinical trials is the mRNA vaccine. An RNA-based vaccine utilizes the spike protein biogenetic code implanted in particular lipid-based nanoparticles for inoculation into the body [8-32]. It was developed at a thunderbolt pace by Moderna Therapeutics, previously acting on SARS-CoV and MERS-CoV vaccines readjusted to SARS-CoV-2. After showing potential in the animal trial, the initial phase I trial of the vaccine commenced on 16 March 2020 in collaboration with the NIH on forty-five fit people between 18 and 55 years [8] [11].

Many other mRNA-based vaccines like Pfizer, BNT162 by BioNTech, CureVac are in various steps of progress. The vaccine that has enrolled clinical trials in China was developed by CanSino Biologics, producing a vaccine for Ebola. Additionally, the Ad5-nCoV vaccine (based on the S protein) is based on their adenovirus vaccine principles and is undergoing phase I clinical trials in healthy individuals between 18–60 years of age in [8] [33].

Several efforts are in progression to produce a vaccine for COVID-19. The systems involve the standard inactivated vaccines, the protein subunit and virus-like particle vaccines (VLP), viral vector-based vaccines, and the latest RNA and DNA based vaccines [10]. The individual

procedure has its advantages and weaknesses, and each procedure is being advanced concurrently to form an efficient vaccine [11].

In work, we concentrated on the various vaccines of COVID-19 and successively for the effectiveness of the vaccine type (RNA, Non-replicating viral vector, DNA, Inactivated, Protein subunit) of COVID-19. This work advances to bioinformatics associated with COVID-19 treatment. This research is useful for the bioinformatics society.

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CONFLICT OF INTERESTS

The authors declare that there is no conflict of interests.

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