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.

2010 AMS Subject Classification: 92B05, 92B15.
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 \( \alpha \in \text{For}(Q) \) by \( \| \alpha \|_{IS} \) indicates all objects \( u \in Z \) satisfying \( \alpha \) viewed as follows [17-18]:

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

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

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

2) If \( \alpha \rightarrow \beta \in \text{Decision}(IS) \) and \( \text{sup}_{IS}(\alpha, \beta) \neq 0 \) then the rule \( \alpha \rightarrow \beta \) 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       |
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| Phase I/II   |            |        |
|--------------|------------|--------|
| 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=Phase III) & ("Number Tested Cases"=30000) => ("Vaccine Type"= {RNA (1)}) |
| 8      | 1       | (Randomize=Yes) & (Age=Â18) & (Phase=Phase II) => ("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=Phase III) & (Age=Â18) & ("Number Tested Cases"=15000) => ("Vaccine Type"= {Inactivated (1)}) |
| 16     | 1       | (Randomize=Yes) & (Phase=Phase I/II) & ("Number Tested Cases"=1264) => ("Vaccine Type"= {Inactivated (1)}) |
| 17     | 1       | (Randomize=Yes) & (Phase=Phase III) & ("Number Tested Cases"=8870) => ("Vaccine Type"= {Inactivated (1)}) |
| 18     | 1       | (Randomize=Yes) & (Phase=Phase I/II) & ("Number Tested Cases"=2000) => ("Vaccine Type"= {Inactivated (1)}) |
|   | Type               |
|---|-------------------|
| 19 | (Randomize=Yes) & (Phase=Phase I/II) & ("Number Tested Cases"=1090) => ("Vaccine Type"={Non-replicating (1)}) |
| 20 | (Randomize=Yes) & (Phase=Phase I/II) & ("Number Tested Cases"=696) => ("Vaccine Type"={Non-replicating (1)}) |
| 21 | (Randomize=Yes) & (Phase=Phase II/III) => ("Vaccine Type"={Non-replicating (1)}) |
| 22 | (Randomize=Yes) & (Phase=Phase III) & ("Number Tested Cases"=2000) => ("Vaccine Type"={Non-replicating (1)}) |
| 23 | (Randomize=Yes) & (Phase=Phase II) & ("Number Tested Cases"=508) => ("Vaccine Type"={Non-replicating (1)}) |
| 24 | (Phase=Phase I/II) & (Randomize=Yes) & ("Number Tested Cases"=1048) => ("Vaccine Type"={DNA (1)}) |
| 25 | (Phase=Phase I/II) & (Randomize=Yes) & ("Number Tested Cases"=190) => ("Vaccine Type"={DNA (1)}) |
| 26 | (Phase=Phase I) & (Randomize=No) & ("Number Tested Cases"=120) => ("Vaccine Type"={DNA (1)}) |
| 27 | (Phase=Phase I/II) & ("Number Tested Cases"=160) => ("Vaccine Type"={DNA (1)}) |
| 28 | (Randomize=Yes) & (Phase=Phase I) & ("Number Tested Cases"=150) => ("Vaccine Type"={Protein (1)}) |
| 29 | (Randomize=Yes) & (Phase=Phase I) & ("Number Tested Cases"=120) => ("Vaccine Type"={Protein (1)}) |
| 30 | (Randomize=Yes) & (Phase=Phase II) & ("Number Tested Cases"=900) => ("Vaccine Type"={Protein (1)}) |
| 31 | (Randomize=Yes) & (Phase=Phase II) & ("Number Tested Cases"=180) & (Age=18-70) => ("Vaccine Type"={Protein (1)}) |
| 32 | (Phase=Phase I) & (Randomize=Yes) & ("Number Tested Cases"=180) => ("Vaccine Type"={Other (1)}) |
| 33 | (Phase=Phase I) & ("Number Tested Cases"=112) => ("Vaccine Type"={Other (1)}) |
| 34 | (Phase=Phase I/II) & ("Number Tested Cases"=180) & (Age=Â¹18) => ("Vaccine Type"={Other (1)}) |
TABLE 3. Statistics of rules among decision classes

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

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]:

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

$$s_{c^*}(s_o) = \bigcup_{z \in c_o} \{ s_c(z) : s_c(z) \cap s_o \neq \emptyset \}$$

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 $s_c N_{s_c}(s_o) = \emptyset$ then $s_o$ is crisp or exact with respect to $s_c$; and if $s_c N_{s_c}(s_o) \neq \emptyset$, $s_o$ 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            |

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

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

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
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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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