Analyse Protein Model of the SARS-CoV-2 Virus using Data Mining Methods

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Abstract: Since December 2019, the SARS II Covid 19 virus pandemic worldwide, The National Centre for Biotechnology Information (NCBI) has also recorded information related to this virus in its database. This research focuses on identifying dataset the protein of the species Severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2), genus BETACORONAVIRUS, and family CORONAVIRIDAE from NCBI database by a data mining model using a classification based naïve Bayes and J48 algorithms which were recorded from December 1, 2019, to April 13, 2021, with 1.149.217 data. The dataset that has been cleaned is data of SARS II Covid 19 + virus in humans with a total record of 517.834 consisting of data on nucleotide length, nucleotide completeness, geographic location, and protein. This data used for the data training. Then we used 475 for data testing which was chosen randomly. The result is that the entire protein can be predicted using the J48 algorithm but cannot be predicted using Naive Bayes. From the data mining results, it can be concluded that the best method that can be used to predict protein in humans affected by the SARS II Covid 19 + virus is the J48 algorithm rather than the Naive Bayes algorithm.

1 INTRODUCTION

Since the pandemic occurred in December 2019, many people conducted research related to the SARS-COV-2 (Covid 19) virus. Currently, there is a very large amount of virus data in an open-source database system.

NCBI is an organization that has an open-source database system. NCBI maintains a series of databases relevant to biotechnology and biomedicine. This database is an important resource for bioinformatics tools and services which also records databases related to the SARS II Covid 19 virus from various parts of the world(Smith, 2019) (Information, 2019).

Recently, there have been major changes and improvements in the field of biomedical research which we know as biomedical. Biomedical is the basis of research related to biomedical information innovation, medical imaging technology, gene chips, nanotechnology, psycho-biomedical social models, development of biological systems that have shaped modern biomedical systems. It is closely related to the formation of the biotechnology industry in the twenty-first century, and is an important area related to medical diagnosis and human health(Kc Santosh, Zohora, 2018) (Kalsi et al., 2018). Bioinformatics is Data mining is a very effective and useful technique in the research and development of bioinformatics (Albahri et al., 2020). Data mining has attracted a great deal of attention in the research as a whole in recent years, due to the availability of big data and the need to convert that data into useful information and knowledge. Data mining, also known as Knowledge Discovery in Databases (KDD) is a field for finding new and potentially useful information from large databases (Baker, 2010).

This research will be focused on identifying dataset the protein of species Severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2), genus beta coronavirus, and family Corona VIRIDAE by implementing a data mining model using a classification based on J48 and naïve Bayes algorithms in Weka which was recorded from 1 December 2019 to April 13, 2021. The dataset that has been cleaned is data of SARS II Covid 19 + virus in humans with a total record of 517.834 consisting

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of data training and 475 data testing on nucleotide length, nucleotide completeness, geographic location, and protein class. There were 98 geographic locations, 28 protein wish nucleotide completeness used in this dataset.

This research used two algorithm classifications of data mining, i.e. J48 and naïve Bayes. Those algorithms will be compared to get the best results for making predictions of the proteins contained in the species SARS-CoV-2 in humans.

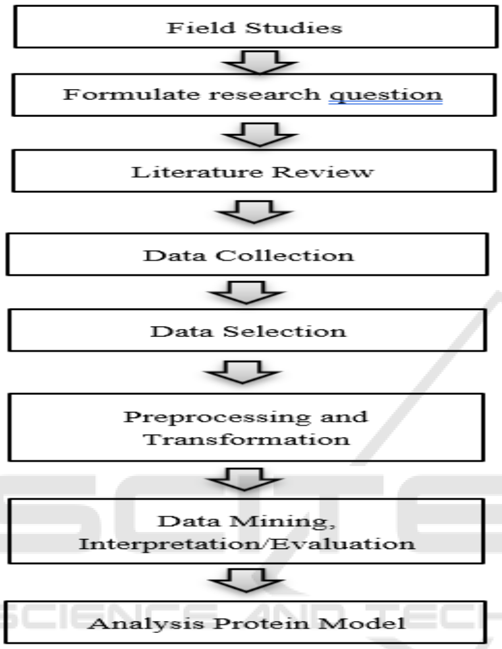

Field Studies
Formulate research question
Literature Review
Data Collection
Data Selection
Preprocessing and Transformation
Data Mining, Interpretation/Evaluation
Analysis Protein Model

Figure 1: Research Method.

2 METHODS (AND MATERIALS)

The research method can be seen in Figure 1. Each phase will discuss in this section with materials research.

2.1 Field Studies

Before starting the research, first a field survey was conducted to get a qualitative picture of the accuracy of the data to be studied.

2.2 Formulates Research Question

The formulates research question is the stage where the object of research formulates the problem, namely, how to do protein analysis of the SARS-COVID-2 using data mining method and how to predict the model protein.

2.3 Literature Review

In order to achieve the goals to be achieved, it is necessary to study literature studies related to the analysis of the SARS COV 2 virus protein and data mining (Christian, 2021).

2.4 Data Collection

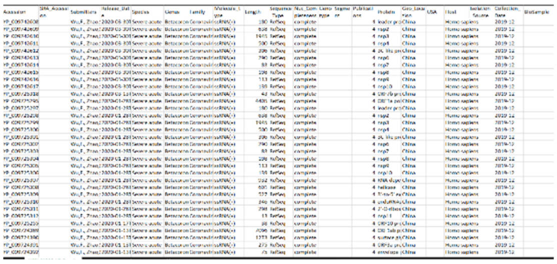
The data collection was carried out in several ways, namely the literature study method and data collection from the website of the National Centre for Biotechnology Information (NCBI). It is called the NCBI database. For this research, data was taken on December 19, 2020 until April 13, 2021 in the Comma-Separated Values (CSV) file format (Christian, 2021).

2.5 Data Selection

The NCBI database has a lot of data that can be researched, but at the selection stage the data is determined in relation to the severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) protein in humans. The selected column of NCBI database consists of the Accession, SRA Accession, Submitters, Release Date, Species, Genus, Family, Molecule Type, Length, Sequence Type, Nucleotide Completeness, Genotype, Segment, Publications, Protein, Geography Location, USA, Host, Isolation Source, and Collection Date classes.

2.6 Preprocessing and Transformation

In the preprocessing stage, data cleaning will be carried out. The entire data collection is 1,149,217 data. There were many empty data and useless data, then we cleaned and become 517.834 data training and 475 data testing which consists of the Length, Nucleotide Completeness, Protein, Geography Location, Host, and Isolation Source classes. The data sample can be seen in Figure 2.



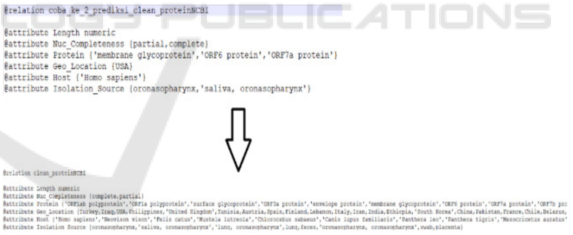
Accession	SRA_Accession	Submitters	Release_Date	Species	Genus	Family	Molecule_type	Length	Sequence Type	Nuc_Completeness	Genotype	Segment	Publications	Protein	Geo_Location	USA	Host	Isolation Source	Collection_Date	BioSample
YP_009742608		Wu,F., Zhao	2020-03-30	Severe acute	Betacoron	Coronavirid	ssRNA(+)	180	RefSeq	complete			1	leader pro	China		Homo sapiens		2019-12	
YP_009742609		Wu,F., Zhao	2020-03-30	Severe acute	Betacoron	Coronavirid	ssRNA(+)	638	RefSeq	complete			4	nsp2	China		Homo sapiens		2019-12	
YP_009742610		Wu,F., Zhao	2020-03-30	Severe acute	Betacoron	Coronavirid	ssRNA(+)	1945	RefSeq	complete			1	nsp3	China		Homo sapiens		2019-12	
YP_009742611		Wu,F., Zhao	2020-03-30	Severe acute	Betacoron	Coronavirid	ssRNA(+)	500	RefSeq	complete			1	nsp4	China		Homo sapiens		2019-12	
YP_009742612		Wu,F., Zhao	2020-03-30	Severe acute	Betacoron	Coronavirid	ssRNA(+)	306	RefSeq	complete			4	3C-like pro	China		Homo sapiens		2019-12	
YP_009742613		Wu,F., Zhao	2020-03-30	Severe acute	Betacoron	Coronavirid	ssRNA(+)	290	RefSeq	complete			1	nsp6	China		Homo sapiens		2019-12	
YP_009742614		Wu,F., Zhao	2020-03-30	Severe acute	Betacoron	Coronavirid	ssRNA(+)	83	RefSeq	complete			1	nsp7	China		Homo sapiens		2019-12	
YP_009742615		Wu,F., Zhao	2020-03-30	Severe acute	Betacoron	Coronavirid	ssRNA(+)	198	RefSeq	complete			4	nsp8	China		Homo sapiens		2019-12	
YP_009742616		Wu,F., Zhao	2020-03-30	Severe acute	Betacoron	Coronavirid	ssRNA(+)	113	RefSeq	complete			4	nsp9	China		Homo sapiens		2019-12	
YP_009742617		Wu,F., Zhao	2020-03-30	Severe acute	Betacoron	Coronavirid	ssRNA(+)	139	RefSeq	complete			1	nsp10	China		Homo sapiens		2019-12	
YP_009725318		Wu,F., Zhao	2020-01-13	Severe acute	Betacoron	Coronavirid	ssRNA(+)	43	RefSeq	complete			4	ORF7b pro	China		Homo sapiens		2019-12	
YP_009725295		Wu,F., Zhao	2020-01-28	Severe acute	Betacoron	Coronavirid	ssRNA(+)	4405	RefSeq	complete			4	ORF1a pol	China		Homo sapiens		2019-12	
YP_009725297		Wu,F., Zhao	2020-01-28	Severe acute	Betacoron	Coronavirid	ssRNA(+)	180	RefSeq	complete			1	leader pro	China		Homo sapiens		2019-12	
YP_009725298		Wu,F., Zhao	2020-01-28	Severe acute	Betacoron	Coronavirid	ssRNA(+)	638	RefSeq	complete			4	nsp2	China		Homo sapiens		2019-12	
YP_009725299		Wu,F., Zhao	2020-01-28	Severe acute	Betacoron	Coronavirid	ssRNA(+)	1945	RefSeq	complete			4	nsp3	China		Homo sapiens		2019-12	
YP_009725300		Wu,F., Zhao	2020-01-28	Severe acute	Betacoron	Coronavirid	ssRNA(+)	500	RefSeq	complete			1	nsp4	China		Homo sapiens		2019-12	
YP_009725301		Wu,F., Zhao	2020-01-28	Severe acute	Betacoron	Coronavirid	ssRNA(+)	306	RefSeq	complete			4	3C-like pro	China		Homo sapiens		2019-12	
YP_009725302		Wu,F., Zhao	2020-01-28	Severe acute	Betacoron	Coronavirid	ssRNA(+)	290	RefSeq	complete			4	nsp6	China		Homo sapiens		2019-12	
YP_009725303		Wu,F., Zhao	2020-01-28	Severe acute	Betacoron	Coronavirid	ssRNA(+)	83	RefSeq	complete			1	nsp7	China		Homo sapiens		2019-12	
YP_009725304		Wu,F., Zhao	2020-01-28	Severe acute	Betacoron	Coronavirid	ssRNA(+)	198	RefSeq	complete			4	nsp8	China		Homo sapiens		2019-12	
YP_009725305		Wu,F., Zhao	2020-01-28	Severe acute	Betacoron	Coronavirid	ssRNA(+)	113	RefSeq	complete			4	nsp9	China		Homo sapiens		2019-12	
YP_009725306		Wu,F., Zhao	2020-01-28	Severe acute	Betacoron	Coronavirid	ssRNA(+)	139	RefSeq	complete			1	nsp10	China		Homo sapiens		2019-12	
YP_009725307		Wu,F., Zhao	2020-01-28	Severe acute	Betacoron	Coronavirid	ssRNA(+)	932	RefSeq	complete			4	RNA-depe	China		Homo sapiens		2019-12	
YP_009725308		Wu,F., Zhao	2020-01-28	Severe acute	Betacoron	Coronavirid	ssRNA(+)	601	RefSeq	complete			4	helicase	China		Homo sapiens		2019-12	
YP_009725309		Wu,F., Zhao	2020-01-28	Severe acute	Betacoron	Coronavirid	ssRNA(+)	527	RefSeq	complete			1	3'-to-5' ex	China		Homo sapiens		2019-12	
YP_009725310		Wu,F., Zhao	2020-01-28	Severe acute	Betacoron	Coronavirid	ssRNA(+)	346	RefSeq	complete			4	endoRNAs	China		Homo sapiens		2019-12	
YP_009725311		Wu,F., Zhao	2020-01-28	Severe acute	Betacoron	Coronavirid	ssRNA(+)	298	RefSeq	complete			4	2'-O-ribos	China		Homo sapiens		2019-12	
YP_009725312		Wu,F., Zhao	2020-01-28	Severe acute	Betacoron	Coronavirid	ssRNA(+)	13	RefSeq	complete			1	nsp11	China		Homo sapiens		2019-12	
YP_009725255		Wu,F., Zhao	2020-01-17	Severe acute	Betacoron	Coronavirid	ssRNA(+)	38	RefSeq	complete			4	ORF10 pro	China		Homo sapiens		2019-12	
YP_009724389		Wu,F., Zhao	2020-01-13	Severe acute	Betacoron	Coronavirid	ssRNA(+)	7096	RefSeq	complete			4	ORF1ab p	China		Homo sapiens		2019-12	
YP_009724390		Wu,F., Zhao	2020-01-13	Severe acute	Betacoron	Coronavirid	ssRNA(+)	1273	RefSeq	complete			1	surface gl	China		Homo sapiens		2019-12	
YP_009724391		Wu,F., Zhao	2020-01-13	Severe acute	Betacoron	Coronavirid	ssRNA(+)	275	RefSeq	complete			4	ORF3a pro	China		Homo sapiens		2019-12	
YP_009724392		Wu,F., Zhao	2020-01-13	Severe acute	Betacoron	Coronavirid	ssRNA(+)	75	RefSeq	complete			4	envelope	China		Homo sapiens		2019-12	

Figure 2: Preprocessing Data Sample.

Each class will be described in this section (Information, 2019).

- **Length** records how long the sequence of SARS-COV-2 protein.
- **<u>Nuc_completeness</u>** stands for nucleotide completeness where data stored is data that explains completeness or some of the descriptions listed for the data. If the data has a molecular description / information, the data is considered **complete**, but if the data does not have a molecular description / information, the data will be considered **partial**.
- **Protein** stored data protein of SARS-CoV-2 virus in each location that was inserted into the NCBI database. According to the phylogenetic tree, there are three core variants, with minor variations in their amino acid sequences. The most primitive ("ancestral") variant is designated 'A'. Two newer variants are designated B and C, respectively. Geographically, A and C are prevalent outside East Asia, whereas B has a predominant presence in East Asia (Biswas et al., 2020) (Mohanty et al., 2020). Gene arrangement in the viral genome has been determined through sequencing. Two untranslated regions (UTR) flank the coding region at both 5′ and 3′ ends. Genes in the coding region, from 5′ end to 3′ end are Open Read Frame ab (ORF1ab), spike (S), envelope (E), membrane (M), and nucleocapsid (N). Several other ORFs are also present between S (Spike) and N (nucleocapsid) genes. ORF1ab is the largest of the genes (Noorimotlagh et al., 2020) and is further subdivided into ORF1a and ORF1b. The ORF1ab gene encodes more than 15 nonstructural proteins including RNA-dependent RNA polymerase (RdRP) and helicase (Wu et al., 2020)(Mohanty et al., 2020). The ORF1ab also encodes the pp1ab protein that contains 15 nsps (nsp1-nsp10 and nsp12-nsp16). The pp1a protein encoded by the orf1a gene also contains 10 nsps (nsp1-nsp10). The accessory genes are distributed among the structural genes" (Noorimotlagh et al., 2020) (Wu et al., 2020).
- Geolocation stands for "The geographic location" of each country of origin of humans infected with the SARS-COV2 virus which is inserted into the NCBI database. There were many countries inserted into the database.
- Host record human or animal in which a parasite or commensal organism lives of SARS-CoV-2 virus. The data written in Latin that contains homo sapiens (human), CANIS LUPS FAMILIARIS (dog), CHLOROBEUS SABEUS (green monkey), FELIS CATUS (cat), MESOCRICETUS AURATUS (Suriah hamster), MUSTELA LUTREOLA (Europe Cerpelai), NEOVISION VISON (American Cerpelai), PANTHERA LEO (lion), dan PANTHERA TIGRIS (tiger). In this research we used just humans for host value.
- Isolation source record the protein was taken from the SARS-CoV-2 virus that contains the ORONASOPHARYNX (part of the throat behind the oral cavity), placenta (a temporary organ that connects the mother and fetus), feces (body waste removed from the intestine), lung (a large organ located in the chest cavity at both sides of the heart), saliva (saliva), and swabs (taking using a cotton swab or gauze that takes a substance from the surface of the body or a hole).
  - Isolation Source is in the form of data that covers where the protein is taken from the SARS-CoV-2 virus. Data Isolation Source is written in medical terms which contains the ORONASOPHARYNX (part of the throat behind the oral cavity), placenta (a temporary organ that connects the mother and fetus), feces (body waste removed from the intestine), lung (a large organ located in the chest cavity at both sides of the heart), saliva (saliva), and swabs (taking using a cotton swab or gauze that takes a substance from the surface of the body or a hole).

Then the data transformed to the Attribute Relation File Format (ARFF) using the WEKA application see figure 3.



```
@relation coba_ke_2_prediksi_clean_proteinNCBI

@attribute Length numeric
@attribute Nuc_Completeness {partial,complete}
@attribute Protein {'membrane glycoprotein','ORF6 protein','ORF7a protein'}
@attribute Geo_Location {USA}
@attribute Host {'Homo sapiens'}
@attribute Isolation_Source {oronasopharynx,'saliva, oronasopharynx'}
```

```
@relation clean_proteinNCBI

@attribute Length numeric
@attribute Nuc_Completeness {complete,partial}
@attribute Protein {'ORF1ab polyprotein','ORF1a polyprotein','surface glycoprotein','ORF3a protein','envelope protein','membrane glycoprotein','ORF6 protein','ORF7a protein','ORF7b pro
@attribute Geo_Location {Turkey,Iraq,USA,Philippines,'United Kingdom',Tunisia,Austria,Spain,Finland,Lebanon,Italy,Iran,India,Ethiopia,'South Korea',China,Pakistan,France,Chile,Belarus,
@attribute Host {'Homo sapiens','Neovison vison','Felis catus','Mustela lutreola','Chlorocebus sabaeus','Canis lupus familiaris','Panthera leo','Panthera tigris','Mesocricetus auratus'
@attribute Isolation Source {oronasopharynx,'saliva, oronasopharynx','lung, oronasopharynx',lung,feces,'oronasopharynx, oronasopharynx',swab,placenta}
```

Figure 3: Data Transformation in ARFF Format.

2.7 Data Mining and Interpretation/ Evaluation

After preprocessing, data is ready for mining procedure and extracting the knowledge. We called data mining.

2.7.1 Data Mining

At this stage, the classification of data mining task was selected by applying the Naïve Bayes and J48 algorithms. The 517.834 of data training will be discussed next.

Data Training. Classification data training of SARS-Cov-2 virus protein consists of 12 classification proteins. They are envelope protein, membrane glycoprotein, nucleocapsid phosphoprotein, ORF1a polyprotein, ORF1ab polyprotein, ORF3a protein, ORF6 protein, ORF7a protein, ORF7b protein, ORF8 protein, ORF10 protein and surface glycoprotein. The total of each protein can be seen in Table 1. The most protein of SARS-COV2 is surface glycoprotein.

Table 1: Data Training of Total Protein.,

No	Protein	Total
1	Envelope protein	43.567
2	Membrane glycoprotein	43.804
3	Nucleocapsid phosphoprotein	43.766
4	ORF1a polyprotein	43.833
5	ORF1ab polyprotein	43.852
6	ORF3a protein	43.740
7	ORF6 protein	43.463
8	ORF7a protein	43.460
9	ORF7b protein	43.270
10	ORF8 protein	37.636
11	ORF10 protein	43.363
12	surface glycoprotein	44.080
Grand Total		517.834

Table 2 illustrates the total nucleotide completeness protein of the SARS-Cov2 class. The most were partial nucleotide completeness of surface glycoprotein.

Table 2: Data Training of Nucleotide Completeness Protein.

No	Protein	Nucleotide completeness		Total
		Complete	Partial	
1	Envelope protein	20.384	23.183	43.567
2	Membrane glycoprotein	20.384	23.420	43.804
3	Nucleocapsid phosphoprotein	20.384	23.382	43.766
4	ORF1a polyprotein	20.379	23.454	43.833
5	ORF1ab polyprotein	20.361	23.491	43.852
6	ORF3a protein	20.348	23.392	43.740
7	ORF6 protein	20.371	23.092	43.463
8	ORF7a protein	20.373	23.087	43.460
9	ORF7b protein	20.366	22.904	43.270
10	ORF8 protein	19.856	17.780	37.636
11	ORF10 protein	20.379	22.984	43.363
12	Surface glycoprotein	20.385	23.695	44.080
Total		243.970	273.864	517.834

The data collected from 58 geolocations, namely Argentina, Austria, Bahrain, Bangladesh, Belarus, Benin, Brazil, Cambodia, Cameroon, Chile, China, Ecuador, Egypt, Ethiopia, Finland, France, Gabon, Georgia, Germany, Ghana, Guatemala, Hong Kong, India, Iran, Iraq, Italy, Japan, Jordan, Kazakhstan, Lebanon, Mali, Malta, Mexico, Morocco, Myanmar, New Zealand, Pakistan, Peru, Philippines, Poland, Portugal, Puerto Rico, Russia, Saudi Arabia, Sierra Leone, South Korea, Spain, Sweden, Switzerland, Taiwan, Thailand, Tunisia, Turkey, United Kingdom, Uruguay, USA, Venezuela and West Bank. Most of the data come from the USA, as many as 493.154 rows. The surface glycoprotein for each geolocation illustrates in Table 3. The USA is still the country which has the most surface glycoprotein. The total was 41.787.

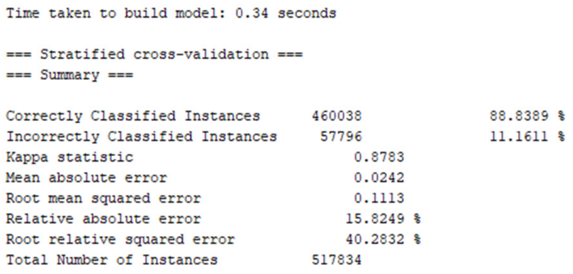
Table 3: The distribution data of surface glycoprotein based on geolocation.

No	Geo Location	Total
1	USA	41.787
2	Chile	370
3	Bangladesh	299
4	Egypt	281
5	Pakistan	205
6	Iran	199
7	Ghana	77
8	Hong Kong	70
9	Turkey	68
10	Italy	64
11	Philippines	60
12	Tunisia	59
13	Austria	55
14	Mexico	48
15	Saudi Arabia	46
16	Argentina	43
17	China	34
18	Jordan	27
19	Portugal	22
20	Russia	22
21	Spain	17
22	India	16
23	West Bank	16
24	South Korea	15
25	Lebanon	13

Table 4: The distribution data of surface glycoprotein based on geolocation (cont.).

No	Geo Location	Total
26	Benin	12
27	Finland	11
28	Sierra Leone	11
29	Gabon	10
30	Guatemala	10
31	Malta	10
32	Japan	9
33	Myanmar	9
34	Georgia	7
35	Iraq	7
36	Poland	7
37	Uruguay	7
38	France	6
39	Taiwan	6
40	Peru	5
41	Bahrain	4
42	Brazil	4
43	Ecuador	4
44	Ethiopia	4
45	United Kingdom	4
46	Venezuela	4
47	Germany	3
48	Mali	2
49	Thailand	2
50	Belarus	1
51	Cambodia	1
52	Cameroon	1
53	Kazakhstan	1
54	Morocco	1
55	New Zealand	1
56	Puerto Rico	1
57	Sweden	1
58	Switzerland	1
Total		44.080

The distribution data about the length protein of SARS-Cov2 will not be discussed in this paper, because of the need to separate sessions. Using data mining method, the classification data training used k-fold cross-validation according to protein class. The value k is 10. After performing 10 folds cross-validation using WEKA application, then a classification pattern model will be created. The pattern model will then be stored for data testing. And the summary of the J48 and Naïve Bayes classification pattern models illustrates in Figure 4 and Figure 5.



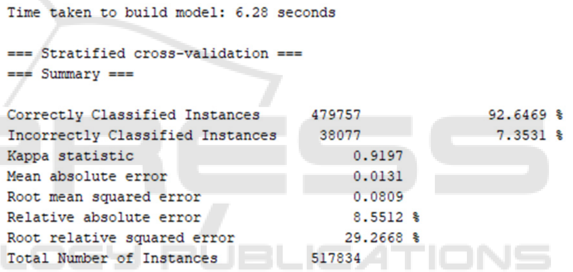
```
Time taken to build model: 0.34 seconds

=== Stratified cross-validation ===
=== Summary ===

Correctly Classified Instances      460038               88.8389 %
Incorrectly Classified Instances     57796               11.1611 %
Kappa statistic                          0.8783
Mean absolute error                      0.0242
Root mean squared error                  0.1113
Relative absolute error                 15.8249 %
Root relative squared error             40.2832 %
Total Number of Instances           517834
```

Figure 3: Summary of Naïve Bayes Algorithm.

Figure 4 shows the results of the Naïve Bayes algorithm classification, the accuracy of the correctly classified data amounted to 88.8% and the incorrect classification amounted to 11.1%.



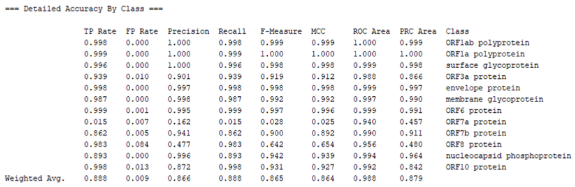
```
Time taken to build model: 6.28 seconds

=== Stratified cross-validation ===
=== Summary ===

Correctly Classified Instances      479757               92.6469 %
Incorrectly Classified Instances     38077                7.3531 %
Kappa statistic                          0.9197
Mean absolute error                      0.0131
Root mean squared error                  0.0809
Relative absolute error                  8.5512 %
Root relative squared error             29.2668 %
Total Number of Instances           517834
```

Figure 4: Summary of J48 Algorithm.

Figure 5 shows the results of the J48 algorithm classification, the accuracy of the data that is classified correctly is 92.6% and the incorrect classification is 7.3%.

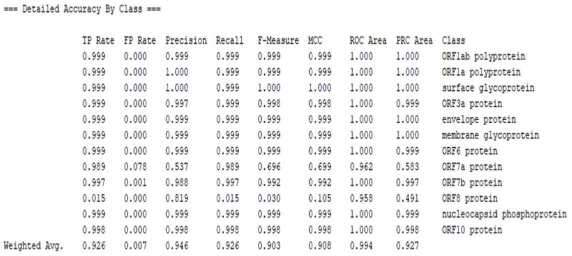


```
=== Detailed Accuracy By Class ===

                 TP Rate  FP Rate  Precision  Recall   F-Measure  MCC      ROC Area  PRC Area  Class
                 0.998    0.000    1.000      0.998    0.999      0.999    1.000     0.999     ORF1ab polyprotein
                 0.999    0.000    1.000      0.999    1.000      1.000    1.000     1.000     ORF1a polyprotein
                 0.996    0.000    1.000      0.996    0.998      0.998    0.999     0.998     surface glycoprotein
                 0.939    0.010    0.901      0.939    0.919      0.912    0.988     0.866     ORF3a protein
                 0.998    0.000    0.997      0.998    0.998      0.998    0.999     0.997     envelope protein
                 0.987    0.000    0.998      0.987    0.992      0.992    0.997     0.990     membrane glycoprotein
                 0.999    0.001    0.995      0.999    0.997      0.996    0.999     0.991     ORF6 protein
                 0.015    0.007    0.162      0.015    0.028      0.025    0.940     0.457     ORF7a protein
                 0.862    0.005    0.941      0.862    0.900      0.892    0.990     0.911     ORF7b protein
                 0.983    0.084    0.477      0.983    0.642      0.654    0.956     0.480     ORF8 protein
                 0.893    0.000    0.996      0.893    0.942      0.939    0.994     0.964     nucleocapsid phosphoprotein
                 0.998    0.013    0.872      0.998    0.931      0.927    0.992     0.842     ORF10 protein
Weighted Avg.    0.888    0.009    0.866      0.888    0.865      0.864    0.988     0.879
```

Figure 5: Detailed result of Naïve Bayes algorithm.

Figure 6 shows the detailed results of the accuracy based on the SARS-CoV-2 protein classification class with the Naïve Bayes algorithm.



```
=== Detailed Accuracy By Class ===

                 TP Rate  FP Rate  Precision  Recall   F-Measure  MCC      ROC Area  PRC Area  Class
                 0.999    0.000    0.999      0.999    0.999      0.999    1.000     1.000     ORF1ab polyprotein
                 0.999    0.000    1.000      0.999    0.999      0.999    1.000     1.000     ORF1a polyprotein
                 0.999    0.000    1.000      0.999    1.000      1.000    1.000     1.000     surface glycoprotein
                 0.999    0.000    0.997      0.999    0.998      0.998    1.000     0.999     ORF3a protein
                 0.999    0.000    0.999      0.999    0.999      0.999    1.000     1.000     envelope protein
                 0.999    0.000    0.999      0.999    0.999      0.999    1.000     1.000     membrane glycoprotein
                 0.999    0.000    0.999      0.999    0.999      0.999    1.000     0.999     ORF6 protein
                 0.989    0.078    0.537      0.989    0.696      0.699    0.962     0.583     ORF7a protein
                 0.997    0.001    0.988      0.997    0.992      0.992    1.000     0.997     ORF7b protein
                 0.015    0.000    0.819      0.015    0.030      0.105    0.958     0.491     ORF8 protein
                 0.999    0.000    0.999      0.999    0.999      0.999    1.000     0.999     nucleocapsid phosphoprotein
                 0.998    0.000    0.998      0.998    0.998      0.998    1.000     0.998     ORF10 protein
Weighted Avg.    0.926    0.007    0.946      0.926    0.903      0.908    0.994     0.927
```

Figure 6: Detailed result of J48 algorithm.

Figure 7 shows the detailed results of the accuracy based on the SARS-CoV-2 protein class with the J48 algorithm. The following is a detailed explanation about of the accuracy (Zhu et al., 2010):

a. TP (True Positive) Rate: The true positive rate refers to positive data that is considered correct by the classifier.
b. FP (False Positive) Rate: A false positive rate refers to negative data that is incorrectly labelled as positive.
c. Precision: Precision can be thought of as a measure of the accuracy of what percentage of data label as positive is actually.
d. Recall: A measure of how complete the correct identified percentage rate is.
e. F-Measure: an alternative to measure precision and recall with F-measure.
f. MCC: Matthews Correlation Coefficient is a measure of the coefficient relationship between classifications to predict. MCC returns a value between -1 (indicating a failed prediction) to +1 (indicating a perfect prediction).
g. ROC Area: Receiver Operating Characteristics Area is a test used as a criterion for measuring the ability of classification performance, the concept of ROC Area can be interpreted if the data has 2 classes and each has a data, what is the percentage of correct predictions if the data from the two classes are predicted. ROC Area is considered as one of the important outputs where the optimal ROC area results are close to 1, and 0.5 is proportional to the "random prediction".
h. PRC Area: If the ROC Area shows an overview of how classifiers are performing in general, Precision-Recall Curves are useful for measuring how classifiers are performing in one class.

For now, we will not discuss accuracy here. The accuracy will be discussed in other sessions.

Data Testing. From the data training, the USA is the geolocation with the most data in the NCBI database, so test data testing will be used from the USA which is taken randomly. There were 475 data testing that chosen random from geolocation USA in this phase ready to proceed. The data that has been determined then will be loaded into Microsoft Excel to replace with a question mark as a prediction class. The data consists of 12 proteins of SARS-Cov2 which have complete or partial value for nucleotide completeness.

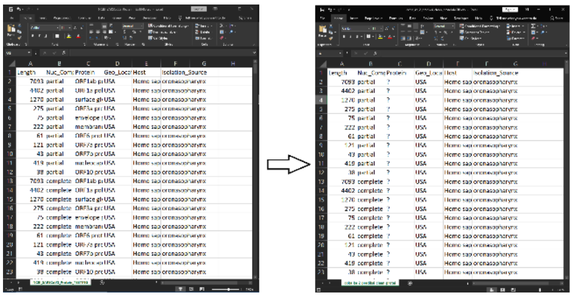
Nucleotides, which are nucleic acid monomers (building blocks) that form deoxyribonucleic acid (DNA) and ribonucleic acid (RNA), which function as a repository of genetic information. Nucleotides have three component characteristics, namely heterocyclic nitrogenous bases, pentose sugars, and phosphate groups. Nucleotide molecules whose phosphate groups undergo hydrolysis are called nucleosides. Bases and pentose sugars that makeup nucleotides are heterocyclic compounds. The heterocyclic nitrogen bases that make up the nucleotides are purines and pyrimidines. There are four nitrogen bases which are the building blocks of DNA, namely adenine (A), guanine (G), cytosine (C), and thymine (T). Meanwhile, the formers of RNA are adenine (A), guanine (G), cytosine (C), and uracil (U). Adenine and guanine are purine-type nitrogen bases while cytosine, thymine, and uracil are pyrimidine derivatives(National Human Genome Reasearch Institute National Human Genome Reasearch Institute, 2014). If the nucleotide component is complete then the class of nucleotide completeness has “complete” value, otherwise it is “partial” (see data in Table 4).

Table 5: Data Testing.

Protein	Nucleotide Completeness		Total
	Complete	Partial	
Envelope protein	15	27	**42**
Membrane glycoprotein	15	27	**42**
Nucleocapsid phosphoprotein	15	26	**41**
ORF1a polyprotein	15	27	**42**
ORF1ab polyprotein	15	27	**42**
ORF3a protein	15	26	**41**
ORF6 protein	15	27	**42**
ORF7a protein	15	27	**42**
ORF7b protein	15	26	**41**
ORF8 protein	4	13	**17**
ORF10 protein	15	26	**41**
Surface glycoprotein	15	27	**42**
Total	**169**	**306**	**475**

2.8 Interpretation/ Evaluation

The next process is to load the J48 and Naïve Bayes classification models that were made in the previous stage. After loading the classification model, the test data can be predicted with the option Re-evaluate the model on the current test set (see Figure 8 and Figure 9).

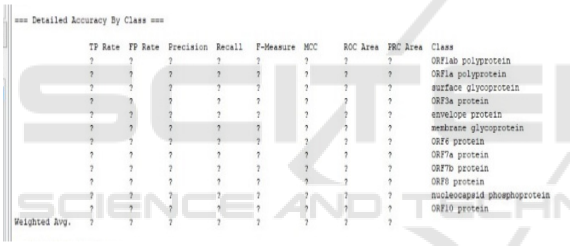


	Length	Nuc_Com	Protein	Geo_Loca	Host	Isolation_Source
2	7093	partial	ORF1ab p	USA	Homo sap	oronasopharynx
3	4402	partial	ORF1a pol	USA	Homo sap	oronasopharynx
4	1270	partial	surface gl	USA	Homo sap	oronasopharynx
5	275	partial	ORF3a pr	USA	Homo sap	oronasopharynx
6	75	partial	envelope p	USA	Homo sap	oronasopharynx
7	222	partial	membran	USA	Homo sap	oronasopharynx
8	61	partial	ORF6 prot	USA	Homo sap	oronasopharynx
9	121	partial	ORF7a pro	USA	Homo sap	oronasopharynx
10	43	partial	ORF7b pro	USA	Homo sap	oronasopharynx
11	419	partial	nucleocap	USA	Homo sap	oronasopharynx
12	38	partial	ORF10 pro	USA	Homo sap	oronasopharynx
13	7093	complete	ORF1ab p	USA	Homo sap	oronasopharynx
14	4402	complete	ORF1a pol	USA	Homo sap	oronasopharynx
15	1270	complete	surface gl	USA	Homo sap	oronasopharynx
16	275	complete	ORF3a pr	USA	Homo sap	oronasopharynx
17	75	complete	envelope p	USA	Homo sap	oronasopharynx
18	222	complete	membran	USA	Homo sap	oronasopharynx
19	61	complete	ORF6 prot	USA	Homo sap	oronasopharynx
20	121	complete	ORF7a pro	USA	Homo sap	oronasopharynx
21	43	complete	ORF7b pro	USA	Homo sap	oronasopharynx
22	419	complete	nucleocap	USA	Homo sap	oronasopharynx
23	38	complete	ORF10 pro	USA	Homo sap	oronasopharynx

	Length	Nuc_Com	Protein	Geo_Loca	Host	Isolation_Source
2	7093	partial	?	USA	Homo sap	oronasopharynx
3	4402	partial	?	USA	Homo sap	oronasopharynx
4	1270	partial	?	USA	Homo sap	oronasopharynx
5	275	partial	?	USA	Homo sap	oronasopharynx
6	75	partial	?	USA	Homo sap	oronasopharynx
7	222	partial	?	USA	Homo sap	oronasopharynx
8	61	partial	?	USA	Homo sap	oronasopharynx
9	121	partial	?	USA	Homo sap	oronasopharynx
10	43	partial	?	USA	Homo sap	oronasopharynx
11	419	partial	?	USA	Homo sap	oronasopharynx
12	38	partial	?	USA	Homo sap	oronasopharynx
13	7093	complete	?	USA	Homo sap	oronasopharynx
14	4402	complete	?	USA	Homo sap	oronasopharynx
15	1270	complete	?	USA	Homo sap	oronasopharynx
16	275	complete	?	USA	Homo sap	oronasopharynx
17	75	complete	?	USA	Homo sap	oronasopharynx
18	222	complete	?	USA	Homo sap	oronasopharynx
19	61	complete	?	USA	Homo sap	oronasopharynx
20	121	complete	?	USA	Homo sap	oronasopharynx
21	43	complete	?	USA	Homo sap	oronasopharynx
22	419	complete	?	USA	Homo sap	oronasopharynx
23	38	complete	?	USA	Homo sap	oronasopharynx

Figure 7: Re-evaluation data.

Using the WEKA application, the result of evaluation using J48 and Naïve Bayes algorithm illustrated in Figure 9.



```
=== Detailed Accuracy By Class ===

                 TP Rate  FP Rate  Precision  Recall   F-Measure  MCC      ROC Area  PRC Area  Class
                 ?        ?        ?          ?        ?          ?        ?         ?         ORF1ab polyprotein
                 ?        ?        ?          ?        ?          ?        ?         ?         ORF1a polyprotein
                 ?        ?        ?          ?        ?          ?        ?         ?         surface glycoprotein
                 ?        ?        ?          ?        ?          ?        ?         ?         ORF3a protein
                 ?        ?        ?          ?        ?          ?        ?         ?         envelope protein
                 ?        ?        ?          ?        ?          ?        ?         ?         membrane glycoprotein
                 ?        ?        ?          ?        ?          ?        ?         ?         ORF6 protein
                 ?        ?        ?          ?        ?          ?        ?         ?         ORF7a protein
                 ?        ?        ?          ?        ?          ?        ?         ?         ORF7b protein
                 ?        ?        ?          ?        ?          ?        ?         ?         ORF8 protein
                 ?        ?        ?          ?        ?          ?        ?         ?         nucleocapsid phosphoprotein
                 ?        ?        ?          ?        ?          ?        ?         ?         ORF10 protein
Weighted Avg.    ?        ?        ?          ?        ?          ?        ?         ?
```

Figure 8: Re-evaluation data of J48 and Naïve Bayes algorithm sample in WEKA.

2.9 Analysis Protein Model

The result of prediction protein using the J48, and Naïve Bayes Algorithm summarized in Table 5 and Table 6. Using the J48 algorithm the most wrong prediction was ORF7a protein and when using Naïve Bayes algorithm there was no ORF7a protein in prediction.

Table 6: Summarize protein model prediction using J48 Algorithm.

No	Protein	Prediction		Total
		FALSE	TRUE	
1	Envelope protein		42	**42**
2	Membrane glycoprotein		42	**42**
3	Nucleocapsid phosphoprotein		41	**41**
4	ORF1a polyprotein		42	**42**
5	ORF1ab polyprotein		42	**42**
6	ORF3a protein	1	41	**42**
7	ORF6 protein		42	**42**
8	ORF7a protein	15	42	**57**
9	ORF7b protein		41	**41**
10	ORF8 protein		1	**1**
11	ORF10 protein		41	**41**
12	Surface glycoprotein		42	**42**
Total		**16**	**459**	**475**

Table 7: Summarize protein model prediction using Naïve Bayes Algorithm.

No	Protein	Prediction		Total
		FALSE	TRUE	
1	Envelope protein		42	42
2	Membrane glycoprotein		42	42
3	Nucleocapsid phosphoprotein		41	41
4	ORF1a polyprotein		42	42
5	ORF1ab polyprotein		42	42
6	ORF3a protein		41	41
7	ORF6 protein		42	42
8	ORF7b protein		41	41
9	ORF8 protein	42	17	59
10	ORF10 protein		41	41
11	Surface glycoprotein		42	42
Total		**42**	**433**	**475**

3 RESULT AND DISCUSSION

The results of protein analysis can be seen from Table 5. The protein summary prediction model uses the J48 Algorithm. We can see that there are 12 proteins predicted using the J48 algorithm, namely Envelope protein, membrane Glycoprotein, Nucleocapsid phosphoprotein, ORF1a polyprotein, ORF1ab protein, ORF3a protein, ORF6 protein, ORF7a protein, ORF7b protein, ORF8 protein, ORF10 protein, and Surface glycoproteins. From the 12 proteins, not all proteins were predicted correctly. For ORF3a protein and ORF7a protein, not all were successfully predicted. From the 42 ORF3a proteins, 1 protein could not predictable. And from the 57 ORF7a proteins, there were 15 proteins that could not be predicted. The summary of 12 protein predictions using the J48 algorithm were 496 proteins which correct predictions.

It can also be seen from Table 6. Summarizing the predictions of the protein model using the Naïve Bayes Algorithm. We can see that there are 11 proteins that were predicted using the Naïve Bayes Algorithm are proteins that were also predicted by the J48 algorithm. There is only 1 protein that cannot be predicted using Naive Bayes, namely ORF7a protein. And the ORF8 protein was not predictable at all, there were 42 unpredictable proteins out of 59 proteins. And if recap, obtained 433 proteins from the 11 types of proteins that were successfully predicted using the Naive Bayes algorithm.

The result of the data testing prediction shows in Table 7. The J48 algorithm produces a lot of correct predictive data like the original data than the Naïve Bayes Algorithm. The ORF7a protein can be predicted using the J48 algorithm with many false predictions but cannot be predicted using the Naïve Bayes algorithm. The comparison between the two algorithms summarizes in Table 7.

Table 8: Result of Data Testing Prediction.

RESULT	ALGORITHM	
	J48	NB
TRUE	459	433
FALSE	16	42

4 CONCLUSIONS

The conclusion of this study is that to analyse the SARC-COV2 protein, data mining methods can be used by applying the J48 and Naive Bayes algorithms. When comparing the two algorithms, it can be proposed using the J48 algorithm, because all proteins can be predicted even though there are still prediction errors for the ORF1a protein. Meanwhile, when using the Naive Bayes algorithm, the ORF1a protein cannot be predicted at all. For future research, the J48 algorithm can be compared with other algorithms besides Naive Bayes. It will hope that the predictions can get even better results.

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