# A CoronaVirus Disease-2019 Prediction Model Based on Bayesian Belief Network

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Abstract: Coronavirus is a type of virus that belongs to the family of (+)ssRNA Virus that causes a disease called Coronavirus Disease 2019 (COVID-19) which gives rise to severe acute respiratory conditions. Due to its mode of transmission, contact with respiratory droplets during coughing or sneezing and physical contact with infected persons has resulted to over 160,000 recorded deaths worldwide and counting within few months of the outbreak; hence, the disease was declared a pandemic by World Health Organization in February, 2020. In recent past, several systems have been developed to diagnose this pandemic disease, but they generated a lot of false negative during testing and were unable to detect COVID-19 and its overlapping symptoms. Hence, in this paper, we proposed and simulated a Bayesian Belief Network model to predict Coronavirus Disease 2019. The model was designed using Bayes Server and tested with data collected from COVID-19 medical repository. The model had a 99% prediction accuracy.

Keywords: Coronavirus; COVID-19; Prediction; Bayesian Belief Network

# 1.0 Introduction

The human body is the framework of a human being which comprises of cells, tissues, organs, and organ systems that is structured from the simplest to the most multifaceted as stated by [1]. Conversely, all the above-listed components of the body work in synergy with one another for optimal functionality of the human body. Despite the operational functionalities these body components exhibit, they are subject to anomalies caused by disease causing organisms.

[2] defined disease as a disarray in structure or function in humans, animals and plant, particularly one that creates explicit indications affecting a precise part within the body of the living organism. In addition, diseases can be categorized into two major type namely communicable and non-communicable diseases.

Non-communicable diseases (NCD) are diseases that are not transmissible from one person to another such as Parkinson's disease, autoimmune diseases, strokes, most heart diseases, cancers and chronic kidney disease just to name a few which may be chronic or acute but are non-infectious as avowed by [3].

In [4], a communicable disease (CD) was defined as a form of disease that is transmitted from one person to another. The transmission of this disease occurs via bacteria or viruses that are airborne, through contact of blood and various types of body fluids from an infected person. This disease is regarded as pandemic due to its mode of spread; hence, termed as a contagious disease. Examples of such disease are hepatitis, tuberculosis etc.

In [5], it was stated that the main cause of CDs (infectious diseases) are pathogenic microorganisms such as bacteria, fungi, parasites and viruses, with the disease going viral from one person to another in a direct or indirect mode. Of all the CDs causing organisms, diseases caused by viruses are the most frightening of all.

Viruses are submicroscopic transmittable agents that duplicate itself solitary inside living cells of an organism as affirmed by [6]. Viruses have the ability to infect all forms of living organisms such as plants, animals, microorganisms and humans.

In [7], it was stated that viruses are also located in every ecosystem on planet earth and are categorized as the most abundant form of biological entity. However, viruses can be classified into 7 main groups namely dsDNA virus (e.g. Adenoviruses, Herpesviruses, Poxviruses), ssDNA virus (e.g.Parvoviruses), dsRNA virus (e.g.Reoviruses), dsDNA-

RT viruses (e.g. Hepadnaviruses), (-)ssRNA virus (e.g.Orthomyxoviruses, Rhabdoviruses), ssRNA-RT viruses (e.g. Retroviruses) and (+)ssRNA virus (e.g. Coronaviruses, Picornaviruses, Togaviruses) respectively.

Of all the above-listed examples of viruses, Coronavirus which is a member of the (+)ssRNA virus family is the most dreadful of all.

Coronavirus is defined as a class of virus formerly called novel Coronavirus (2019-nCoV) and now called severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) that causes an ailment called Coronavirus disease 2019 (COVID-19) as stated by [8,9].



Figure 1: Coronavirus

In [10], it was stated that the symptoms of this disease are fever, cough, sore throat, tiredness, aches, sneezing, nasal congestion, malaise, diarrhea, septic shock, pneumonia and difficulty in breathing. In addition, the level of sternness of COVID-19 ranges from mild, moderate, severe, and critical level with the symptoms of the disease varying in people, with some persons showing no symptoms whatsoever, hence being categorized as been asymptomatic while individuals with the infection are classified as symptomatic persons who are the major carrier of the infection. Also, asymptomatic persons can also transmit the disease if they come in contact with the virus. The transmission of the disease can occur through contact with respiratory droplets during coughing or sneezing from asymptomatic and symptomatic persons.

Furthermore, persons who are advanced in age that has existing ailments such as respiratory diseases, diabetes, cardiovascular diseases and people who their immune systems are destabilized stand a high chance of contacting this disease; with the disease having an incubation period of 2 to 14 days in humans after contact with the said virus.

The first outbreak of COVID-19 was reported in Wuhan, China in December, 2019 with the reported confirmed cases worldwide standing at over 2.3 million and 160,000 recorded deaths worldwide and counting in year 2020. Furthermore, it was affirmed that this disease affects people of all ages ranging from a day old to above 80 years in respective of the sex, with patients above 10 years having a grand total mortality rate of 28.7 percent as stated by [11,12].

In [13], a pronouncement was made by the World Health Organization (WHO) changing the name of the coronavirus disease to COVID-19 in January, 2020 and following the outbreak of the virus, the disease was declared a pandemic in February, 2020.

Despite the pandemic nature of COVID-19, clinical methods have been utilized in diagnosing this disease such as chest X-ray, computed tomography (CT) scan, lung ultrasound, whole genome sequencing and real-time reverse transcriptase PCR (rRT-PCR). However, this usage of the aforementioned diagnostic methods exposes patients to high radiation which has side effects such as vomiting, bleeding, fainting; isolation and sequencing sometimes negatively influence test results of genomic sequencing and PCR (rRT-PCR) testing which can lead to false results due to the contamination of deoxyribonucleic acid (DNA). Hence, a lot of false positives are produced as a result of usage of the above-listed methods due to the overlapping symptoms this disease has with other respiratory tract diseases.

Moreover, with the growth in artificial intelligence, several machine learning techniques has been utilized in diagnosing COVID-19 in the works of [14, 15, 16, 17,18,19,20, 21 and 22] but they generated a lot of false negative during testing and were unable to detect COVID-19 due to the overlapping symptoms the disease shares with some respiratory tract diseases.

In this paper, Bayesian Belief Network (BBN) was utilized in diagnosing COVID-19 with its symptoms. BBN is a multifaceted probabilistic network that merges expert knowledge and experimental datasets. It plans a route for cause and effect associations between variables and trains them with probability that indicates the level in which one

variable is likely to sway another. In this paper, BBN was our technique of choice because of its capability to make predictive inference.

#### 2. Related Works

Several studies have been conducted on diagnosing Coronavirus Disease 2019 (COVID-19) using Artificial Intelligence.

In [14], a system that utilized a deep learning technique called conventional neural network (CNN) and computed tomography (CT) to diagnose COVID-19 in patients was designed. The system showed the capability of diagnosing COVID-19 patients with Influenza-A viral pneumonia early with 86.7% detection rate. However, the use of CT exposes patients to high radiation while CNN is exceedingly expensive to train, requires large data to perform very well and time-consuming. The system also failed to diagnose respiratory tract diseases with overlapping symptoms with COVID-19.

In [15], a system based on conventional neural network (CNN) with chest X-ray images to predict COVID-19 in patients was proposed. The system demonstrated the ability to predict the disease with a 98% accuracy. However, the system required a lot of data to execute properly with the system results obtained from the learning process usually difficult to comprehend and the X-ray images produced are not always best images. Furthermore, the system also failed to diagnose respiratory tract diseases with overlapping symptoms with COVID-19.

In [16], an artificial intelligence system to diagnose COVID-19 was developed. The system employed deep conventional neural networks and predicted COVID-19 with a 94.98% prediction accuracy. However, the system required large data to train the network, the network is slow with each training step taking longer to execute. In addition, the system also failed to diagnose respiratory tract diseases with overlapping symptoms with COVID-19.

In [17], a system to diagnose COVID-19 that utilized conventional neural network (CNN), transfer learning and Xray Images was proposed. The system predicted COVID-19 with accuracy of 96.78%. However, the system also failed to diagnose respiratory tract diseases with overlapping symptoms with COVID-19; the neural network learning process is time-consuming, expensive to train and the X-ray images do not provide 3-Dimensional information.

In [18], deep conventional neural network (CNN) and chest X-ray images were employed to design a system called COVID-Net to detect COVID-19. The system predicted COVID-19 cases with a 92.4% detection accuracy based on the COVIDx dataset. Despite the high detection accuracy, the system neural network was capital and time intensive and the system also failed to diagnose respiratory tract diseases with overlapping symptoms with COVID-19.

In [19], a system that utilized a deep learning technique to diagnose COVID-19 was developed. The system had 80% sensitivity and 81% in specifying COVID-19 cases in patients. Nevertheless, the system failed to specify other respiratory tract diseases having overlapping symptoms with COVID-19; the solution derived from the neural network is difficult to comprehend and the learning process of the network is time-consuming and capital intensive.

A hybrid machine learning system that utilized convolutional neural network (CNN), support vector machine (SVM), and Random Forest to diagnose COVID-19 was developed in [20]. The system detected COVID-19 cases early with a 95.2% detection accuracy. However, the system neural network is difficult to interpret, requires large data to train, time and capital intensive and utilizes a lot of memory to execute the network. The SVM algorithm is not suitable for handling vast datasets and solving a target problem that has overlapping features while Random Forest Algorithm is not easily interpretable and requires a lot of time during creation of large trees for learning. Also the system also failed to diagnose respiratory tract diseases with overlapping symptoms with COVID-19.

In [21], an expert system for diagnosing COVID-19 was designed using Clips and Delphi expert system languages. The system diagnosed COVID-19 symptoms at a fast rate using an inference engine which relies on expert knowledge. The system results showcased high detection accuracy. However, the system also failed to diagnose respiratory tract diseases with overlapping symptoms with COVID-19, cost of implementation and maintenance of the system is quite high. Also, there is a level of difficulty in creating inference rules which may results in providing wrong diagnosis of diseases.

#### 3. Bayesian Belief Network

Bayesian Belief Network (BBN) is directed acyclic graphical model that employs probability to illustrate conditional dependencies that prevail amongst nodes on a graph [22]. It is a complex probabilistic network that merges expert knowledge and experimental datasets. It plans out route of cause and effect relationships between variables and encodes them with probability that signify the amount in which one variable is probable to sway another. Bayesian Belief Network is based on the Bayes theorem which relies on probability.

The Bayes theorem is represented in the mathematical equation below:

$$P(a|b) = \frac{P(b|a)P(a)}{P(b)}$$
(1)

Where,

P(a) is the probability of event "a" happening without any information about event "b". It is called the "Prior".

P(a/b) is the conditional probability of event "a" happening given that event "b" has already occurred. It is otherwise called the "Posterior".

P(b/a) is the conditional probability of event "b" happening given that event "a" has already occurred. It is called the "Likelihood".

P(b) is the probability of event "b" happening without any information about event "a". It is called the "Marginal Likelihood".

The Naive Bayes classifiers are often represented as a type of directed acyclic graph (DAG). The Directed Acyclic Graph (DAG) comprises of vertices representing random variables and arrows connecting pairs of nodes.

Figure 2 shows a pictorial representation of a Bayesian Belief Network.



Figure 2: A Pictorial Representation of a Bayesian Belief Network

Some advantages of this model are: it is pretty fast in making inferences, the resulting probabilities are easy to interpret, the learning algorithm is quite simple to comprehend and the model adequately combines with utility functions to make optimal inferences. In this paper, we intend to detect COVID-19 using Bayesian Belief Network (BBN). A model consisting of 47 nodes where each node represents a form of disease ailment will be designed using Bayes Server. A COVID-19 dataset will be used to train and test the system. Using the Pareto Principle, 80% of the dataset will be used to train the model while the remainder will be used in testing the model. The aim of the model is to achieve a high level of detection accuracy with the use of the overlapping symptoms of COVID-19.

# 4. Methodology

#### Simulation, Result and Discussion

The dataset used in training, testing and predicting COVID-19 was retrieved from [23]. The dataset consist of 47 disease ailments and each ailment has a value which represents the probability of such disease ailment causing Coronavirus Disease 2019 (COVID-19).

The ailments are Aches, Aorta Disease, Arrhythmias, Breathlessness, Bronchiolitis, Bronchitis, Cardiomyopathy, Cardiovascular Disease, Chest Cough, Cold, Continuous Fever, Congenital Heart Disease, Coronary Artery Disease, Cough, COVID-19, Deep Vein Thrombosis, Diabetes, Diarrhea, Dry Cough, Epiglottitis, Fever, Heart Failure, Intermittent Fever, Layrngotracheitis, Lower Respiration Infection, Malaise, Marfan Syndrome, Nasal Congestion,

Neutropenic Fever, Pel-Ebstein Fever, Pharyngitis, Post-Viral Cough, Pneumonia, Pulmonary Embolism, Quartan Fever, Quotidian Fever, Remittent Fever, Septic Shock, Sneezing, Sinusitis, Sore Throat, ssRNA Virus, Tertian Fever, Tiredness, Upper Respiration Infection, Viral Hemorrhagic Fever and Whooping Cough respectively. Figure 3 below shows a sample the dataset.

Beatleases)	BindvieRis	Branchikis	Cardiorryspethy	Cardievascolar	Chest Cough	Celt	Congenital	Contineus Feret	Coronary Artery	Cough	COVID-18	Degr Vein Thrombosis
1.81	-6.459	1.11	0.379	-0.355	0.987	0.00774	-3.42	1.18	1.11	0.648	0.319	0.275
0.567	-0,0655	-0.0148	-0,0444	-1.58	-0.408	0.548	-4.627	-0.199	-0.456	4.22	1.44	0.213
0.243	-0.413	0.644	-0.397	0.915	-0.572	1.636	0.317	-0.527	1.596	2.27	0.285	1.363
0.125	0.148	-0.302	0.255	-0.795	0.483	4	0.542	1.07	-2.83	0.10	1,78	1.18
0.532	8.833	4.57	0.0600	-6.134	0.283	-0.804	1.38	-1.58	1306	2.06	0.252	8.779
0.361	8,0853	1.31	0.780	-0.136	1.72	-0.23	111	0.155	8.325	-0.409	-1.07	6121
0.419	0.254	-0.728	6.23	-5.645	-0.17	1.05	4.29	1.48	137	0.863	-1.05	1.143
-0.43	1.595	1.15	-0.578	1.51	-0.575	9.522	-645	-0.38	4.753	-4.05	0.010.03	4.258
1.07	-0.008	0.428	0.684	-8.297	-0.995	-0.388	-0.627	0.508	1.61	-0.395	0.3.23	-6.380
-0.0862	1.0798	1.53	0.799	1.43	-0.686	-2.57	1.02	0.687	1945	-0.54	-0.88	4.39
2.07	1.597	-0.437	0.309	0.00687	-0.718	-0.375	0.806	-0.282	1.1	0.314	1.38	1.928
0.642	-0,488	4.21	6.0911	-8.852	1.64	\$78	1.22	3.8	6.118	4.31	13	-0.018
0.862	-0.631	0.46	-0,781	-8.257	-0.963	-3.63	0.695	-0.532	8.500	-0.934	-0.1#L	1.52
-1.00	0.239	0.611	-0.448	1.41	0.257	-1.11	-0.612	0.333	-0.58	-2.28	0.332	0.0529
0.0907	-5.32	-0.51	0.0636	2.56	0.3.37	-241	4199	0.416	\$532	-0.0131	2.69	-12
0.611	-0.89	-1.41	-1.14	-8,7,27	-1.65	-1.67	-8.215	1.02	-8.815	-0.434	-0.887	8,729
1.82	1.37	-0.169	-1.18	6.174	1.29	2.4	-4.969	2.15	8.842	-0.865	1.51	1.387
-2.68	-0.044	-1.19	8,28	-8.1.72	1.65	0.000205	2.11	-0.045	-6.314	0.182	-4.15	12
1.04	1.01	1.18	0.00388	-0.332	-1.9	-0.348	9398	0.378	8/878	-0.651	0.32	-1.31
1.4	-0,334	-9.108	1.04	0.817	-0.627	0.222	-6.425	-0.412	-0.364	1,89	-0.790	0.302
-0.487	1.34	0.30	1.62	0.367	-0.06L4	-0.00	9.131	0.962	8.265	0.583	0.005	0.617
0.892	-6.8325	0.685	6.368	-8-8732	0.728	-0.286	0.437	0.558	4,767	1.67	6.211	1.36
0.525	8.423	2,03	-0.543	0.724	0.212	0.859	0.389	2,02	-2.22	-1.47	0.028	-1.41
-0.06	-0.873	0.283	-1.71	3.433	-0.742	-0.375	4.5	0.93	4.34	-28	0.0925	4.630

#### Figure 3: Snapshot of Dataset

The Bayesian Belief Network model was designed using Bayes-Server platform. The Bayesian Belief Network (BBN) for predicting COVID-19 was designed such that the nodes on the network are linked based on the probability of a disease ailment resulting to another. In our model for a case to be denoted as a COVID-19 case, there would have be contact with several or all of the following disease ailments; Aches, Aorta Disease, Arrhythmias, Breathlessness, Bronchiolitis, Bronchitis, Cardiomyopathy, Cardiovascular Disease, Chest Cough, Cold, Continuous Fever, Congenital Heart Disease, Coronary Artery Disease, Cough, COVID-19, Deep Vein Thrombosis, Diabetes, Diarrhea, Dry Cough, Epiglottitis, Fever, Heart Failure, Intermittent Fever, Layrngotracheitis, Lower Respiration Infection, Malaise, Marfan Syndrome, Nasal Congestion, Neutropenic Fever, Pel-Ebstein Fever, Pharyngitis, Post-Viral Cough, Pneumonia, Pulmonary Embolism, Quartan Fever, Quotidian Fever, Remittent Fever, Septic Shock, Sneezing, Sinusitis, Sore Throat, ssRNA Virus, Tertian Fever, Tiredness, Upper Respiration Infection, Viral Hemorrhagic Fever and Whooping Cough respectively.

Figure 4 shows the BBN model for detecting COVID-19 and its symptoms.



Figure 4: Bayesian Belief Network Model for Detecting COVID-19 with its symptoms.

So, to mathematically represent our model we have:

$$= \prod_{i=1}^{47} P(Disease_i | Parents(Disease_i))$$

Where,

Disease: Node with a Disease Ailment Parents (Disease<sub>i</sub>) = Nodes that converge on Disease Ailment<sub>i.</sub>

The dataset was used to train and test the model. Upon completion of training and testing the BBN model, the test data converged at time series 2. The log likelihood value for each case was recorded. Figure 5 shows the BBN model convergence of COVID-19 and its symptoms at Iteration Count 2.

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X 4/17/000/11/51/52 44	A R		-346 047084436557	2004/03545472977
E Charmina survert read	el with selected	6		Copy statistics

Figure 5: Bayesian Belief Network Model for COVID-19 Convergence at Time Series 2.

Figures 6, 7, 8, 9, 10, 11,12 and 13 shows log likelihood batch query chart for predicting COVID-19 with its symptoms, association/strengths of nodes of the model, feature importance chart for nodes in the model, the insample anomaly detection chart, association plot showing relation of ssRNA Virus leading to a COVID-19 infection case and its probabilities, the log likelihood graph for detecting COVID-19 with its symptoms, The mesh query plot for the loglikelihood of a disease causing ailment (ssRNAVirus) being the reason for a COVID-19 Infection and COVID-19 detection results chart respectively. The result generated from the simulation indicated that the network was able to predict 99% COVID-19 on the dataset accurately and it had a loglikelihood of 16.5 on the test dataset.

	Date values Date values Date 7 guary arm	21	n (	Ster 1 Ster 1 Sector 1	Ratio -	Assesso Tea	Dearen P   Ingeloity	North T			
	Logiathood	Likelihood	Participant	ProtectureRealities	Fredictic COUD-ED	PediciDirecting	Fedst7neurena	Predict Breathing regist	PrefetCold	ProtectCought	fudeeceCoort
Quey 0	41	A REAL	649	114	178	1	1000	5/101	17 Million	1000	11
ValanceGreating Va *	43	10	0.168	0,818	0.89	9,821	0048	8.127	0,89	0.364	41
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Lounno te	43	0.000302	0.RM	0.0633	0.623	9,225	6.362	8,35,6	0.31	0.420	a
	-5.8	0.00003	0.479	0.658	8.417	0.757	8,773	8.427	0.095	0.298	47
Trial Competition	48	2,88.46	0.808	0.001	0.66	8.28	0.384	\$.28	0.248	0.38	41
Federal State Days Te La	-3.46	0.360578	0,846	0.968	6.153	0.063	LONER	8.413	0.052	0.773	41
Anteroper Printed For Ma	34	0.8154	0.047	508.0	0.528	0.479	0323	8.789	0.947	0.983	41
Internet out that the	-6.45	6.06257	0.322	0.018	0.368	0.479	6.979	8.58	0.366	0.0638	47
and a second sec	-2.9	0.0148	0.318	0.408	0.967	0.972	0.0015	8.044	0.407	0,107	47
ARE CREEKED IN	75.8	0.00294	0.001	0.998	0.367	5.987	1.645	1.054	0.839	0.907	47
Weight	-7.00	0.000808	0.59	0.482	0.0028	0.621	8.658	142	0.355	0.6553	47
mentioned in	4.18	0.000279	0.8348	0.483	0.239	0.001	6.379	6.897	0.38	0.35	a.
in a state of the state	4.00	0.0034	0.298	0.0185	1.47	0.0677	8.038	8.788	9.307	0.861	47
and the second second second	6.23	0.0000.00	0.038	0.061	0.613	9.457	8,198	136	0.258	0.628	41
demention of the	-7.05	0.0004017	0.0350	0.825	0.55	0.344	8.821	8.484	0.289	Out t	41
otest of	3.64	0.000205	0.849	0.956	0.256	0.0235	8463	8.238	6.814	0.054	£
Septa Shock	-00.2	3294-01	0.501	0.828	8/47	0.798	6.073	1.743	0.135	0.128	41
adaption by h	8.05	0.00811	0.064	0.052	0.215	8.401	6.252	8.0445	8381	6325	41
And an and a state of the state	-840	6,316-85	0.465	0.008	0.478	0.0838	8,321	8.400	0.561	0.438	47
a a classification of Age	-8.22	0.003.09	0.494	0.859	0.0464	0.588	1.294	8.074	0.647	0.968	41
contraction to	414	0.0150	0.6%	osat	0.3	6.384	8.157	8.415	0.828	0.228	47
State Law 24	-1.04	0.000363	0.417	0.472	0.000	2.951	0.646	8.642	0.0499	0.847	47
Darres -	8.00	0.000011	0.415	0.158	0.005	5.441	8.757	1.179	6.0973	0.05	47
Manager and	1.00	0.000001	1.124	4941	B 165	4.000	0.120	8.101	0.401	William .	40

Figure 6: The Loglikelihood Chart Batch Query for Predicting COVID-19 with Its Symptoms

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(2)

This loglikelihood chart batch shows the result of the test data.

In Experiment 1: the value of Predict(COVID-19) was 0.779 compared to 0.77910982681692, Predict(Fever) was 0.458 compared to 0.458435315306961, Predict(ssRNAVirus) was 0.562 compared to 0.561698365897675, Predict(Sneezing) was 0.697 compared to 0.697023577631117, Predict(Pneumonia) was 0.0426 compared to 0.0426169752371289, Predict(Breathlessness) was 0.945 compared to 0.94470472768411, Predict(Cold) was 0.666 compared to 0.665730880418207, Predict(Cough) was 0.946 compared to 0.946256042291144 and an EvidenceCount of 47 which is the number of evidence available for prediction of COVID-19 in Experiment 1. Experiment 2: the value of Predict(COVID-19) was 0.99 compared to 0.989634818722027, Predict(Fever) was 0.458 compared to 0.458435315306961, Predict(ssRNAVirus) was 0.815 compared to 0.81537985759412, Predict(Sneezing) was 0.827 compared to 0.8266910590975, Predict(Pneumonia) was 0.646 compared to 0.645606697475363, Predict(Breathlessness) was 0.127 compared to 0.1266977928753, Predict(Cold) was 0.146 compared to 0.146071005660792, Predict(Cough) was 0.164 compared to 0.164043253117239 and an EvidenceCount of 47 which is the number of evidence available for prediction of COVID-19 in Experiment 2. Experiment 3: the value of Predict(COVID-19) was 0.633 compared to 0.633002047545645, Predict(Fever) was 0.396 compared to 0.396265075715765, Predict(ssRNAVirus) was 0.592 compared to 0.592275621871613, Predict(Sneezing) was 0.237 compared to 0.236894752780365, Predict(Pneumonia) was 0.392 compared to 0.392282715489759, Predict(Breathlessness) was 0.216 compared to 0.215622928127693, Predict(Cold) was 0.31 compared to 0.310040299655906, Predict(Cough) was 0.921 compared to 0.920528220657181 and an EvidenceCount of 47 which is the number of evidence available for prediction of COVID-19 in Experiment 3. Furthermore, this experiment continues up to Experiment number 100. Hence, the system results showed a 0.01% value difference between the prediction results and original test data of 100% resulting to 99% prediction accuracy.

Associations given evidence	Ū							
X	Y	Mutual Information	Symmetric	For X Given V	For Y Given X	Entropy X	Entropy	ē.
Acheil	(COVID-19)	2.765-16	1.425-15	1146-15	1.88E-15	0244	0.048	e
Preumonia)	(COVID-19)	2.22E-16	1.4E-15	1.316-15	1.5E-15	0.169	0.148	
Neutropenic Fever)	(Faver)	2.225-16	1166-15	1.09E-15	1.296-15	0.203	0.18	
Tertan Fever)	(Feven	2.08E-16	1388-15	1.718-15	1158-15	0.122	0.18	į,
Whasping Caugh)	(Cough)	1.94E-16	8.26E-16	9.685-15	7.215-16	0,201	0.269	
Sore Throat!	(COVID-19)	1.946-16	1128-15	9.8E-16	1.818-15	0.198	0.148	
Quarter Fever)	(Fexet)	1.94E-16	1195-15	1325-15	1.08E-15	0.147	0.5E	
Autominis)	(COVID-19)	1.67E-16	8-80-18	8.75-18	1.138-15	0.249	0.548	
Upper Respiration Infectio	Kough	1.67E-16	9.13E-16	1756-15	6.186-16	0:0952	0.269	
Breathlessness)	(COVID-19)	1.538-16	1.348-15	1.96-15	1.038-15	0.0804	0.148	
Nexal Congestion)	(COVID-19)	1.395-16	8,588-16	7,96-16	9.398-16	0.175	0.148	
Pel-Ebstein Feirer)	(Fevel)	1.396-16	7.55E-16	7.4E-16	7.7E-16	0.188	0.18	
intermittent Fever)	(Fever)	1.115-16	6.875-16	7.78E-16	6.165-16	0.143	0.1B	
Cardiovascular Disease)	COVID-19	9716-17	9.038-10	1448-15	6.57E-16	0.0574	0145	
Coronary Artery Disease)	(Cardiovescular Disease)	6.945-17	7.16E-16	5.485-16	1.035-15	0.127	0.0674	
Pulmonary Embolism)	(Cardiovascular Disease)	0	0	9	0	0.149	0.0674	
Sneezing)	(COVID-19)	0	0	0	0	0.125	0.548	
Cardomooamul	(Cardioussoder Disease)	0.	0	0	0	0.166	0.0674	ļ!

Figure 7: The Association/Strengths Chart of Nodes of the model.

The Association/Strength chart shows the association that exist amongst nodes given evidence of a node event occuring. This chart consists of Mutual Information, Symmetric Information, For (X Given Y), For (Y Given X), Entropy X and Entopy Y respectively.

Mutual Information: specifies the relationship with nodes directly connected to one another and assigned a value (e.g. the mutual relationship that coexist between COVID-19 and Aches nodes and has a value of  $2.78e^{-16}$ .

Symmetric Information: shows nodes that are around the axis of the location of Aches and COVID-19 nodes in the model and having a value of 1.42e-<sup>15</sup> showing it is quite further away from ths two nodes.

For (X Given Y): shows the probability of Event X(Aches) happening given there is evidence that an event Y(COVID-19) has already occurred and having a value of  $1.14e^{-15}$ 

For (Y Given X): ): shows the probability of event Y(COVID-19) happening given there is evidence that an event (Aches) has already occurred and having a value of  $1.88e^{-15}$ 

Entropy X: is the degree of disorderness or randomness of X in the model and having a value of 0.244.

Entropy Y: is the degree of disorderness or randomness of Y in the model and having a value of 0.148.

Target variable				
COMD-19				
Celculate Significance level 0.05	=			
Variable	1-positie -	Feature	Mutual information	
Tirednesi	0.983	10	0.0334	
Epigkottikis	0.955	35	0.0205	
Centinous Fever	0.952	14	0.0203	
Contraction of the second s	0.00		0.011	
Cardiomyopathy	0.903	0	0.0647	
Neutropenic Fever	C(15)	10	0.0132	
Aurte Disease	CARS1	13	0.00979	
Remittent Fever	0.820	- 8	0.0093	
Lower Respiration Infection	0.513	- 11	0.00894	
Brochicktie	0073	- 四	0.00755	
Upper Respiration Infection	0,72	10	0.00752	
Aches	<b>1</b> 746	13	0.00673	
Laryngotracheitis	E 699	- 10	0.90554	
Martan Syndrome	2.695	85	0.00545	
Cough	.684	11	0.00522	
Disconsta	643	25	0.00430	

Figure 8: The Feature Importance Chart for Nodes in the Model

The Feature Importance Chart shows p-value of the variable (nodes), Feature and Mutual information in reference to the COVID-19 Node.

The p-value signifies the likelihood (probability) of the nodes being the cause of a COVID-19 infection.

The Feature box is checked if that particular node is fully involved in the cause of a COVID-19 infection.

The Mutual information shows the relationship with nodes directly connected to one another (i.e. in this case the direct relationship of the nodes with the COVID-19 node) and assigned a value.

The Significance Level signifies the margin of error in the detection of COVID-19.

Options.			
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6374773737718996 0	2		
0.603058811885335 0	N.		
0,813477195133176 0	12.		
0.618819163467002 0	(X)		
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0.6171690400305 0	186 I		
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0.707195886881248 0	12 C		

Figure 9: The In-sample Anomaly Detection Chart

The In-sample Anomaly Detection Chart shows 100 experimental results of detecting COVID-19. Each Case is assigned an ID(Identification value) which is the value of the Predict(COVID-19) in Fig.6. The IsAnomaly checkbox is checked to identify that each case is a confirmed case of COVID-19 infection. The 100 cases of COVID-19 has a case count value of 49.497 (weighted) which signifies the importance of the cases leading to a COVID-19 infection and 99 case count value signifies the number of cases in the pool of data available to the

system for detection of COVID-19 excluding the COVID-19 column in the dataset pool. The tolerance is the margin of error that could be encoutered as regards to the detection of the COVID-19.



Figure 10: Association Plot showing relation of ssRNAVirus leading to a COVID-19 Infection Case and its Probabilities

The association plot shows the relation of how contact with ssRNA Virus leads a COVID-19 infection case. In this plot, 100 experimental cases were taken into consideration with each colored point in the graph classified as a case and assigned a probability which is stationed on the right of the graph. The ssRNA Virus on the Y-axis is plotted against COVID-19 on the X-axis.

However, there are four severity levels of the COVID-19 which are mild, moderate, severe, and critical level respectively.

Mild Level: This level ranges from -0.5 to -0.1 on Y-axis and -0.1024 to 1.122 on X-axis and has 5 colored points (cases). This signifies that the 5 colored points in this region represent 5 cases of COVID-19 infection with the severity level categorized as being Mild.

Moderate Level: This level ranges from 0 to 0.5 on Y-axis and -0.1024 to 1.312 on X-axis and has 37 colored points (cases). This signifies that the 37 colored points in this region represent 37 cases of COVID-19 infection with the severity level classified as being Moderate.

Severe Level: This level ranges from 0.5 to 1 on Y-axis and -0.1024 to 1.329 on X-axis and has 55 colored points (cases). This signifies that the 55 colored points in this region represent 55 cases of COVID-19 infection with the severity level categorized as being Severe.

Critical Level: This level ranges from 1 to 1.5 on Y-axis and -0.1024 to 0.8976 on X-axis and has 3 colored points (cases). This signifies that the 3 colored points in this region represent 3 cases of COVID-19 infection with the severity level classified as being Critical.



Figure 11: The Loglikelihood Graph for Detecting COVID-19 with its Symptoms

This loglikelihood graph for detecting COVID-19 shows the residual values on the vertical axis plotted against the loglikelihood values on the horizontal axis which are independent variables. A residual value is a measure of how much a regression line vertically misses a data point. Regression lines are the best fit of a set of data. The lines are categorized as averages; a few data points will fit the line and others will miss.

In this graph, it shows that 100 experimental cases resulted in value of 16.5, 16.2, 16, 14.6, 14.5, 14.45...... and 2 respectively.

Ideally, residual values should be equally and randomly spaced around the horizontal lines. Taking a view of the system' experimental results values obtained from the horizontal lines on the graph, it can be seen that the point where the highest residual value and the loglikelihood independent variable attained meets at -15.88 on the horizontal line with 18 being the highest value that can be reached on the vertical line.

The residual value attained is 16.5 and loglikelihood independent value is -15.88, the difference between both values is 0.62 which is the predicted value.

Hence, in this system the highest residual value, a loglikelihood independent value can attain is 18. With 18, being the 100 % residual value mark, to get our prediction accuracy percentage, we have highest residual value subtracted from predicted value i.e. 100% -0.62= 99.38% residual loglikelihood percentage value.



Figure 12: The Mesh Query Plot for the Loglikelihood of a Disease Causing Ailment (ssRNAVirus) Being the Reason for a COVID-19 Infection.

The mesh query plot shows the loglikelihood/likelihood of a node in this case ssRNA Virus (ssRNAVirus) being a cause of a confirmed COVID-19 infection. The Node (COVID-19) is plotted on the Y-axis and the other node ssRNA Virus (ssRNAVirus) plotted along the X-axis.

In this context, the Red contour signifies the likelihood of an ssRNA Virus being a major of cause of COVID-19 infection with the contour ranging from interval (-1.600 to 1.600) on the Y-axis and interval (-1.500 to 1.500) on the X-axis.

The Yellow contour shows the loglikelihood of an ssRNA Virus being the reason of a COVID-19 infection with the contour ranging from interval (-0.592 to 0.620) on the Y-axis and interval (-1.115 to 0.965) on the X-axis.

After training of the model, the model was tested and produced results of COVID-19 detection which is showed in figure 13 below.

Cosph	Barreing		Paramete	Breathlessness	Nasal Congestion	Malaise	Cold	Heart Falm	Lower Hesp Intention	Cardiovascular Disease	Seer Threat	Opper Heisp Infection	Brunebitis	SSENA Vice	Prob. of COND-III	COND IN DUIL
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Figure 13: COVID-19 Detection Results Chart

This chart shows the probabilities of 15 ailments namely Cough, Sneezing, Fever, Pneumonia, Breathlessness, Nasal Congestion, Malaise, Cold, Heart Failure, Lower Respiratory Infection, Cardiovascular Disease, Sore Throat, Upper Respiratory Infection, Bronchitis and ssRNA Virus respectively.

This detection results showed the probability of having all the aforementioned ailments leading to a COVID-19 Infection is denoted as:

P(COVID-19| Cough, Sneezing, Fever, Pneumonia, Breathlessness, Nasal Congestion, Malaise, Cold, Heart Failure, Lower Respiratory Infection, Cardiovascular Disease, Sore Throat, Upper Respiratory Infection, Bronchitis and ssRNA Virus)= 0.620975926.

The detection results showed all levels of severity status of COVID-19 Infection such as Mild, Moderate, Severe, Critical and the status of having none of the ailments categorized as asymptomatic.

From the experiment it can be seen that our model has a higher residual log likelihood value which is 16.5 and a prediction accuracy of 99.38%.

Comparing the 99.38% prediction accuracy of our model with the experiments conducted by [16, 17 and 18] which are 94.98%, 96.78% and 92.4% respectively, it is obvious our model has a better prediction accuracy. The higher prediction accuracy achieved by our model could be due to the range of the dataset used in training and testing the model as well as its ability to predict the overlapping symptoms other respiratory tract diseases shares with COVID-19 which aided the high detection accuracy of the said disease.

# 5. Conclusion

COVID-19 infection is very difficult to detect due to the overlapping symptoms the disease shares with other respiratory tract diseases. To predict this disease, health professionals need to improve on the existing techniques utilized in detecting COVID-19.

In this paper, we utilized a Bayesian Belief Network model to predict COVID-19 and its symptoms. The network had 47 nodes with each node representing an exclusive ailment. The model was trained and tested and it had an accuracy of 99.38% in predicting COVID-19 with its symptoms. The system can be deployed in health facilities and COVID-19 isolation centers to help provide information which will be used to detect the virus. It will also bring

about improvement in the following areas: COVID-19 prediction, COVID-19 detection and Diagnosis of respiratory tract diseases with similar symptoms as COVID-19.

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