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Investigating infection pattern of viral bioaerosols: A case study of COVID-19 in Lagos, Nigeria

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Abstract. The dynamics of viral bioaerosols are unknown; hence, its detection and control may be complicated. In this study, the structural analysis of Influenza A, SARS Coronavirus, and IBV Coronavirus was adequately discussed. The infection pattern of the SARS coronavirus was further investigated using the dataset from Nigeria Centre for Disease Control (NCDC), Nigeria, and 'Ourworldindata' for datasets in parts of China. The artificial neural network (ANN) tool was used to determine the COVID-19 infection in Lagos. It was observed that many unaccounted COVID-19 patients are roaming the region. It is recommended that the Lagos government embark on compulsory house-to-house testing to detect potential COVID-19 carriers.

1. Introduction

Bioaerosols are a subcategory of particles released from natural and marine conditions into the atmosphere. They involve the dispersion of living and non-living fragments [1]. Bioaerosols may include morbific or non-morbific, live or dead microbes, sub-atomic weight (HMW) allergens, bacterial endotoxins, mycotoxins, peptidoglycans, β (1→3)- glucans, dust, etc. Bioaerosols rely on various biotic and abiotic factors, which incorporate climatic conditions, bright (UV) light, temperature, and moisture. Bioaerosols found over marine comprise of microorganisms, while those found over natural conditions are wealthy in microbes, parasites, and pollen. Bioaerosols can extend in size from 10-nanometer infection particles to 100 micrometers of dust grains [2]. Pollen grains are the biggest bioaerosols and are more averse to stay suspended noticeable all around over a significant period due to their weight. At present, there is little research on the particular elevation resistance of various bioaerosols. However, the transmission of the viral bioaerosols gives a fair understanding of its transport patterns [3].

An excellent example of viral bioaerosols is measles, tuberculosis, and aspiratory aspergillosis, and it is transmitted via airborne to a new host. Coronavirus belonged to the family of the virus. However, it has its effects on the body, it disables and affects the respiratory organs of the system, weakens it before finally paralyzing the whole respiratory organ it also causes enteric, hepatic, and neurological diseases. According to WHO, coronavirus has been in existence. Researched have found out that coronavirus originates from animals, e.g., bats, rodents, rabbits, and other wild animals. This virus exists in these animals, and when humans get in contact or consume these animals, the virus is then transmitted to the human body, then after, the infected person can then transmit it just by mere contact with the person or by air. Many coronavirus cases have been traced to eating different animals like bats, snakes, rats, and rodents since the Chinese people eat these in their quest to try new food.

Coronavirus is divided into four subdivisions, i.e., Alpha (229E, NL63), Beta (OC43, HKU1, MERS-CoV, SARS-CoV, 3. 2019-nCoV), Gamma and Delta. However, it was discovered that gamma and delta coronavirus does not affect humans. In 2002, severe acute respiratory syndrome

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coronavirus (SARS-CoV) was discovered in Guangdong, China [4]. In 2012, Middle East respiratory syndrome coronavirus (MERS-CoV) was discovered in Saudi Arabia [5]. On 15 January 2020, the World Health Organisation (WHO) reported two new cases of MERS-CoV in the United Arab Emirates [6]. The new strand of coronavirus is the 2019-nCoV, or Covid-19 is a novel virus discovered in Wuhan China in December 2019. The sizes of coronaviruses are between 65 and 125 nm in diameter. They are very minute and can be deposited in the human lung within short movements [7]. The novel coronavirus SARS-CoV-2 can survive in the air for several hours in fine particles known as aerosols and can be detected up to 3 hours after aerosolization and can infect cells throughout that period [11].

2. Methodology

The structural database was obtained from the protein database. Influenza A, SARS coronavirus, and IBV coronavirus were examined using their crystal structure. The samples were further analyzed using computational tools. The computational tool is to obtain specific parameters such as unit cell volume, number of atoms, and number of bonds. This parameter would help us understand the infection pattern of the virus. Secondly, the data of the daily infection rates were obtained from the Nigeria Centre for Disease Control (NCDC) in Nigeria. Also, the datasets from China was obtained from 'Ourworldindata'. The analysis of the data was performed using an artificial neural network (ANN).

2.1. The structural pattern of viral bioaerosols

The 2019-nCoV pathogen is referred to as SARS-CoV-2. Researches have shown that the genome of the SARS-CoV-2 is similar to the previous human coronavirus [8]. Five structural genes describe the structural proteins of SARS-CoV-2, i.e., spike (S), envelope (E), membrane (M), nucleocapsid (N), and orf1ab genes. SARS-CoV-2 is characterized by several unidentified non-structural open reading frames [9]. It is proposed in this study that the unidentified non-structural frames have vital physical meaning that may not be significant biological fields. For example, influenza A was captured Thierry et al. [10]. Further analysis shows that it has a unit-cell volume of 3014097.472761 Å^3. Within the unit cell volume, there were120002 atoms, 121380 bonds, and 22242 polyhedral. The elements were mainly nitrogen, carbon, oxygen, sulfur, and phosphorus.

In like manner, Egloff et al. [12] worked on the crystal structure of SARS coronavirus NSP9. Its unit-cell volume is 939985.871573 Å^3. Within the unit cell volume, there were 33696 atoms, 33798 bonds, and 6003 polyhedra. The elements were mainly nitrogen, carbon, oxygen, and sulfur. Jayaram et al. [13] worked on the crystal structure of the infectious bronchitis virus (IBV) coronavirus nucleocapsid. It is also called the avian coronavirus, a respiratory pathogen of chickens that causes severe economic losses in the poultry. This pathogen also affects the gut, kidney, and reproductive systems of chickens. Its unit-cell volume is 348530.977136 Å^3. Within the unit cell volume, there were 13242 atoms, 13286 bonds, and 2444 polyhedra. The elements were mainly nitrogen, carbon, oxygen, and sulfur. The axial dimension for each element of all the virus is the same as presented in Table 1.

Table 1 Axial dimension of examined viruses

Axes	a1	a2	a3	a4	a5	c
N:	11.893780	3.277479	1.858092	0.858927	0.912985	-11.804902
C:	2.657506	1.078079	1.490909	-4.241070	0.713791	4.297983
O:	2.960427	2.508818	0.637853	0.722838	1.142756	0.027014
S:	6.372157	5.154568	1.473732	1.635073	1.209372	0.154722
P:	1.950541	4.146930	1.494560	1.522042	5.729711	0.155233
Axes	b1	b2	b3	b4	b5	bc
N:	0.000158	10.232723	30.344690	0.656065	0.217287	9.360000
C:	14.780758	0.776775	42.086843	-0.000294	0.239535	6.646000
O:	14.182259	5.936858	0.112726	34.958481	0.390240	5.803000

S:	1.514347	22.092528	0.061373	55.445176	0.646925	2.847000
P:	0.908139	27.044953	0.071280	67.520190	1.981173	5.130000

It is observed that influenza A had an extra element, i.e., phosphorus. Also, SARS coronavirus is almost three times larger than influenza A and IBV coronavirus in volume, the number of atom, and bonds. Hence, one of the reasons it has very high infection rates. Hence, if a unit-cell volume is mixed with atmospheric aerosols, there will be a more potent danger because atmospheric aerosol can be suspended in the atmosphere for more than three days [15].

2.2. Infection trend in Lagos Nigeria

Lagos is the commercial capital of Nigeria. Its population is estimated to be over 14,368,332 people [16]. The first confirmed case of SARS-CoV-2 in Nigeria was announced on 27 February 2020 in Lagos [17]. Ever since, the trend of the infection has risen unpredictably. In this section, the trends of the COVID-19 infection in Lagos were traced using the artificial neural network (ANN), whose set-up is displayed in Figure 1. The input file was the COVID-19 dataset in Lagos for the first 37 days. The target of the analysis was the common dataset from three towns in China (i.e., Zhejiang, Anhui, Jiangxi) whose infection rates are similar to Lagos. The hidden layer is fifty. The three datasets are displayed in Figure 2, i.e. China infection data, Lagos infection data, and the ANN infection trend.

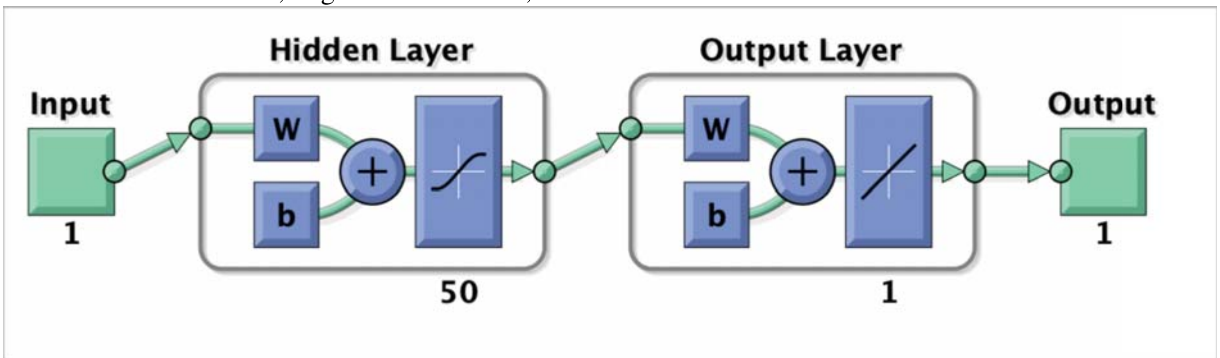

Figure 1: Artificial neural network (ANN) set-up

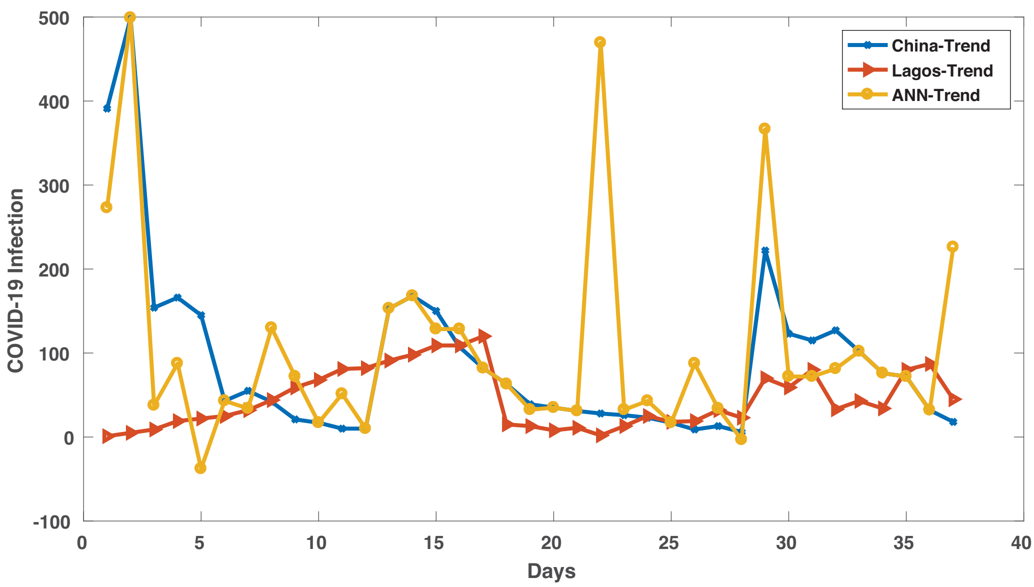

Figure 2: COVID-19 infection trends

It is observed that the COVID-19 infection results in Lagos do not show the reality of the actual state of infection. First, the testing laboratory was not conducting testing by the geographical survey. The testing was done on request. Secondly, the number of infected persons cannot be known because there is no medical database in the metropolis that monitors the health records of patients in the state. Third, the uncoordinated sales of drugs from different pharmaceutical stores make it difficult to monitor drug consumption in the metropolis. With the challenges mentioned above, the actual state of COVID-19 infection cannot be known. However, the Lagos dataset for the following dates, i.e., 16th, 24th, 25th, 26th, 28th, 30$^{th.}$ 31st, 32nd, 35th, and 36th, showed similarity the ANN trend. Three cases in the trend showed wide variance, i.e., 23rd, 27th, 29th, and 37th showed days were COVID-19 infections should be more. The linear regression of the training, validation, test, and cumulative parameters are presented in Figure 3.

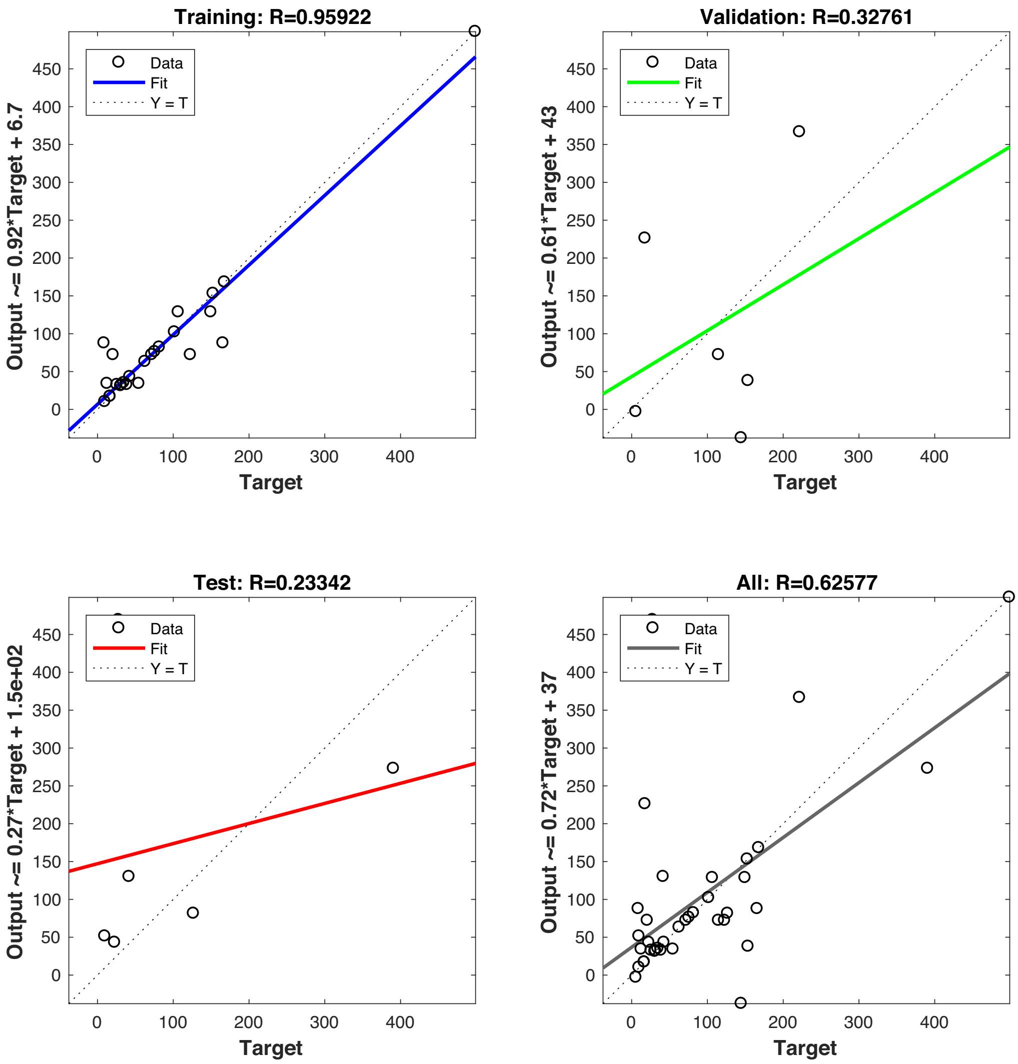

Figure 3:Regressional analysis of ANN processes

In the work, 70% of the dataset was trained. 15% of the dataset was validated, and 15% of the dataset was tested. The training showed an R-square of 96%, meaning that the dataset was adequately trained during the process. The validation and testing process was < 32%. This result is due to the volume of the dataset used for the validation and training. However, the cumulative R-square was 63% showing that the acquired ANN trend was excellent. Hence, the accuracy of the ANN trend can be relied upon. The poly-fit of the processes is displayed in Figure 4. The function fit featured the training targets, training outputs, validation targets, validation output, test targets, test outputs, errors, and fit. The result is tallied with the results discussed in Figure 2. Fifteen error points were heightened. This shows that the Lagos dataset had 41% error due to human error and negligence. This result means that for each passing day, the COVID-19 infection patterns have been deprived of 41% accuracy. The recent campaign of the regional government on voluntary location further supported the assertion that the COVID-19 results is not adequately captured for planning and public awareness. If this trend persists, it means that high spikes of COVID-19 would characterize future results. The sinusoidal nature of the fit suggests that the COVID-19 infection via airborne is controlled by temperature and humidity.

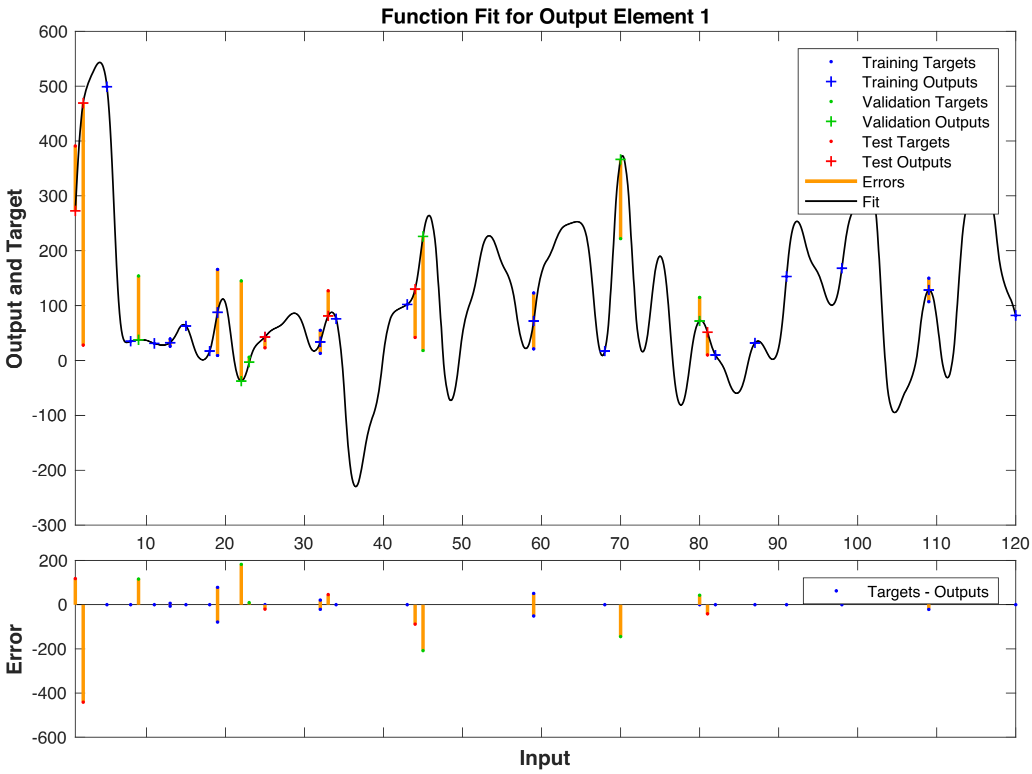

Figure 4: Function fit for input and output elements

Conclusion

The studies have shown that structurally, the differences between viral bioaerosols are the unit-cell volume, number of atoms and bonds, and chemical component. This factor is responsible for their functionality as it was established that they all have the same axial dimension. This revelation shows that with over 2500 bonds, the bioaerosols can recombine in the atmosphere to extend its lifespan or duration of flight. The sinusoidal nature of the fit suggests that the COVID-19 infection via airborne is controlled by temperature and humidity. The unaccounted number of COVID-19 patients in Lagos are accumulating by the day. It is therefore recommended that the government of Lagos should embark on compulsory house-to-house testing to detect potential COVID-19 carriers.

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