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Data interpretation and visualization of COVID-19 cases using R programming

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ABSTRACT

Background: Data analysis and visualization are essential for exploring and communicating medical research findings, especially when working with COVID records.
Results: Data on COVID-19 diagnosed cases and deaths from December 2019 is collected automatically from www.statista.com, datahub.io, and the Multidisciplinary Digital Publishing Institute (MDPI). We have developed an application for data visualization and analysis of several indicators to follow the SARS-CoV-2 epidemic using Statista, Data Hub, and MDPI data from densely populated countries like the United States, Japan, and India using R programming.
Conclusions: The COVID19-World online web application systematically produces daily updated country-specific data visualization and analysis of the SARS-CoV-2 epidemic worldwide. The application will help with a better understanding of the SARS-CoV-2 epidemic worldwide.

1. Introduction

The first case of COVID originated in China on Dec 29 and Jan 3, 2020, when fifty people developed pneumonia-like symptoms [1,[2]]. Before the Chinese New Year, Wuhan was a significant transport hub [3,4]. Several new cases of COVID infections were reported daily after that, resulting in the World Health Organization declaring COVID 19 an epidemic [5]. Although 43% of hospitalized patients showed fever symptoms, more than 80% of COVID patients showed fever in hospital and quarantine facilities. Sometimes, these diseases may not get detected based on symptoms alone [6,7]. COVID 19 disease primarily manifests as diarrhea, cough, and shortness of breath [9]. We cannot, therefore, assume that patients without fever will not find COVID infection. Early symptoms of diarrhea may occur in 3%–5% of patients [8]. Those suffering from mild symptoms must isolate themselves for 14 days from the first infection. In this situation, patients who experience difficulty breathing and have chest infections should see a doctor right away [10]. During this time, doctors encourage patients to rest and rebuild their immune system by taking them into quarantine [11].

Only 5% of patients suffer from ARDS (Acute Respiratory Distress Syndrome), a condition in which a virus extends into the air sack with water, making breathing and purifying red blood cells more complex [12]. In cases of severe lung damage, the oxygenation process, which removes blood from the patient and filters it before returning it to the patient, may be necessary [13]. Heart patients, kidney patients, diabetes patients, long-term pharmaceutical users experience more severe symptoms than those younger [14]. Despite this, we are concerned about halting the spread at the community level. Everyone speaks about flattening the curve, which is slowing its spread so that the hospital system can deal with it more quickly rather than having to manually pick it out in a fixed period to prevent the entire hospital system from becoming like a country without toilet paper [15,16].

Table 1 shows that the total number of COVID cases in India has reached 720346, with 22510 new cases discovered every day in 0607/202 records. Overall, there have been 1704 COVID-related deaths in India. The number represents 4% of all active cases in India. A total of 613 deaths per day out of 8944 patients out of 260022 active cases. In the same way, a country like India has tested 9969662 people out of 13 million people living there.

The interactive map of Table 1 is available for free at https://www.statista.com/statistics/1103458/india-novel-coronavirus-covid-19-cases-by-state/, describes the most interactive rather than tabular records when compared to both the given table and the chart presented here. The graph shows states having the highest or lowest number of new

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Table 1
India state data statistics.

States	India	Gujarat	Uttar Pradesh	Maharashtra	Delhi	Tamil Nadu
Status	22,500	735	929	5,368	1,379	3,827
Conformed	7,20,346	36858	28636	2,11,987	1,00,823	1,14,978
Active	2,59,926	8574	8718	87682	25620	46836
Status	15,256	423	348	3,522	749	3,793
Recovery	4,40,150	26323	19109	1,15,262	72088	66571
Status	473	17	24	204	48	61
Death	473	17	24	204	48	61
Status	10 M	6.3K	25.9K	22.6K	13.9K	34.8K
Total	138019747	418.5K	890K	1.1 M	657.4K	1.4 M

COVID cases. Likewise, trend and pattern line graphs and charts provide more information than tabular statistics, as shown in the preceding table.

Compared to the fact table and figure comparisons above, map visualization is one of the most effective tools for presenting data. Despite this, the theory behind flattening the curve ensures that the balance between hospital ventilators, quarantine medicine systems, and human control in every country is maintained. The hospital system can accommodate everyone if the spread is gradual [4]. As a result of 1918's influenza and pneumonia outbreaks in Philadelphia, the mortality rate rose sharply during October [17], enabling a flat curve. As of now, the primary control of COVID 19 is considered social distance [18].

Consequently, flattening the curve consists of 20 s of handwashing, 6 feet of social distancing, and wearing a mask unless necessary. However, health workers and those who suffer from symptoms should also wear the mask. Vaccines and antiviral medicines have developed. However, several clinical trials on appropriate vaccines are currently underway. The best way to stop the spread of the disease is to disengage socially to flatten the curve and manage our health care system globally [19]. Twenty-eight vaccines are currently under the testing phase by the WHO [20]. Since healthy individuals are vaccinated, vaccination must be more precise. It should also be very safe to use and require a considerable amount of time to produce. As part of the development process, 20 to 80 people will be evaluated for the medications in the first phase, followed by 100–300 healthy participants in the second phase [21]. If there are no harmful substances detected, a license should grant for production, with appropriate precautions for refrigeration. This process requires time. The production is scheduled accordingly for vaccinating the people [22]. For example, the production of the Ebola vaccine took four years. Tests conducted on mice, rabbits, monkeys, and even people in the future. The substance does not cause harm and generates *messenger ribonucleic acid* (mRNA). In addition, if all of the trials prove to be successful, the World Health Organization (WHO) hopes to shorten the process. The viral infection of COVID-19 is the result of SARS-Cov-2 (Severe Acute Respiratory Syndrome). Coronavirus 2 is similar to the SARS coronavirus, which caused an outbreak in 2002 [23].

According to reports, bat in Wuhan, China, was the primary source of human infection. Later, it spread to other parts of the world. There were 903826 cases worldwide and 45335 deaths in April 2020. Around 5% of the total cases were fatal [9]. In addition, many cases were asymptotic carriers of the Coronavirus, which resulted in an exact death rate of 0.7% for the total number of cases, according to the study [24]. Reports from CDC expect the number of people affected by these diseases to grow, with up to 25% of the population showing symptoms. With a proper health care system and protective equipment, a curve plot on the y-axis represents the full potential of the health care system to combat COVID-19. Because of this, the data presented in various official sources only show the records that need some visualization plot for better future action.

2. Methodology and data analysis using R programming

Records of COVID-19 updated within 24 h after the pandemic is declared. This study focuses on the interactive presentation of these figures and data. The data sources for this research include https://datahub.io/core/covid-19 # resources-covid-19_zip [25] and https://www.mdpi.com/2079-9292/9/5/827/htm [26]. Generating graphical outputs from raw open-source records and manage and organize the raw data to create data presentations. After loading various libraries *(leaflet), (tidy verse), (ggmap), (htmltools), (leaflet. extras), (maps), (ggplot2), (mapproj), (mapdata), (spData)* on the R console, the world city data with 15493 records on 11 variables is stored in the data. The *tidier* data format changed by using the *tbl_df* function.

However, the most modern R package readr provides several functions *(read_delim(), read_tsv() and read_csv())*, which are faster than R base functions and import data into R as a ***tbl_df*** (pronounced as "*tibble diff*").

```
Tokyo 35.7 140.  Japan   JP   JPN Tokyo? "primary~     35676000   1.39e9
York  40.7 -73.9 United States US USA   New York       19354922   1.84e9
Dhaka  23.7 90.4 Bangladesh  BD BGD   Dhaka"primary   12797394 1.05e9
```

A data structure containing city name, asci name, longitude-latitude name, and population of the capital city is available open-source on https://datahub.io/core/world-cities. As shown below, the data frame looks like to access one variable in a dataset, use the dollar sign "$".

To create a new table from combining multiple vectors, use the function ***data_frame():***

#str(data) output shows variables, data type, and few records of the data

```
$ city: chr “Tokyo" "New York" "Mexico City" "Mumbai"
 $ city_ascii: chr “Tokyo" "New York" "Mexico City" "Mumbai"
 $ lat: num 35.7 40.7 19.4 19 -23.6
 $ long: num 139.8 -73.9 -99.1 72.9 -46.6
 $ country: char “Japan" "United States" "Mexico" "India"
 $ iso2: char “JP" "US" "MX" "1"
 $ iso3: char “JPN" "USA" "MEX" "IND"
 $ admin_name: chr “Tokyo?" "New York" "Ciudad de México" "Maharashtra"
 $ capital: chr “primary" "" "primary" "admin"
 $ population: int 35676000 19354922 19028000 18978000 18845000 15926000 14987000
14787000 12815475 12797394
 $ id: int 1392685764 1840034016 1484247881 1356226629 1076532519 1356872604
1156073548 1356060520 1840020491 1050529279t
```

Variables are categorized using the structure command, which describes their properties. In the *tidverse* command, data is filtered via *shift-ctrl-m*, using the United States data only depending on the information required for the selected country, as described below.

#Using Dplyr library, the Filter function used to filter the data of the country United States

Data represent the world by country and its subregions. Then use the settings *ink=map data ('world', region=c ('Nepal', 'China')* to plot the map of that country. Inbuilt *ggplot2* functions typically plot three-country maps, as in the selection below. This *Rmarkdown* file use to test Choropleth's plot on the Japan map from the map data package. Maps include regions only, not subregions.

```
> uss=data% >% filter (country=='United States')
```

In the same way, the world map records with longitude, latitude group, and region stored in the w variable as *w=map data ('world')*. Based on the pattern below, the structure appears like the one below.

#Structure of Map Data

The *ggplot* command uses longitude and latitude groups with filled-in region names, and the polygon supports the black border of each county. Like the U.S., each state's data is taken from the world data of each state and matched and grouped with a geographical map. The *ggplot2*, one of the core members of the *tidyverse*, accesses the datasets by running the

```
long      lat group order region sub region
1 -69.89912 12.45200     1      1 Aruba      <NA>
…………………
6 -70.05088 12.59707     1      6 Aruba      <NA>
```

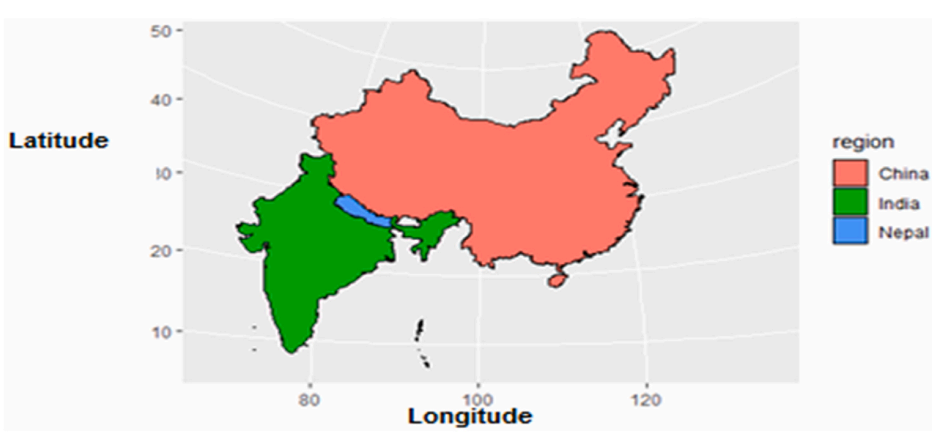


Fig. 1. Country maps of China, India, and Nepal.

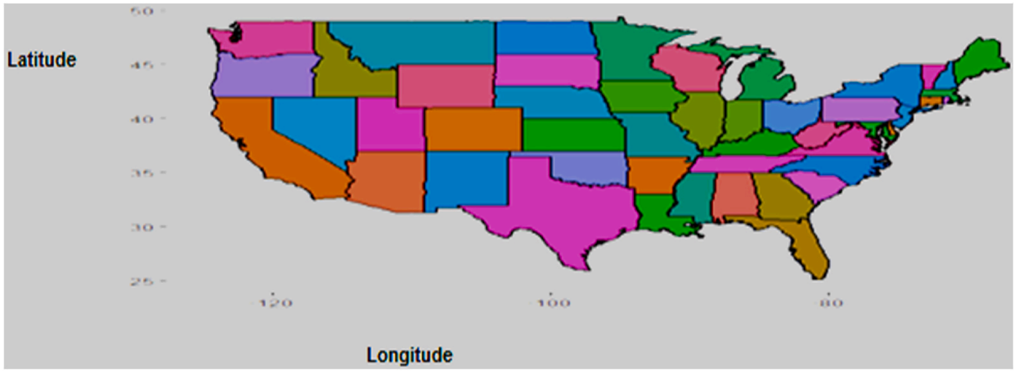


Fig. 2. U.S. State maps.

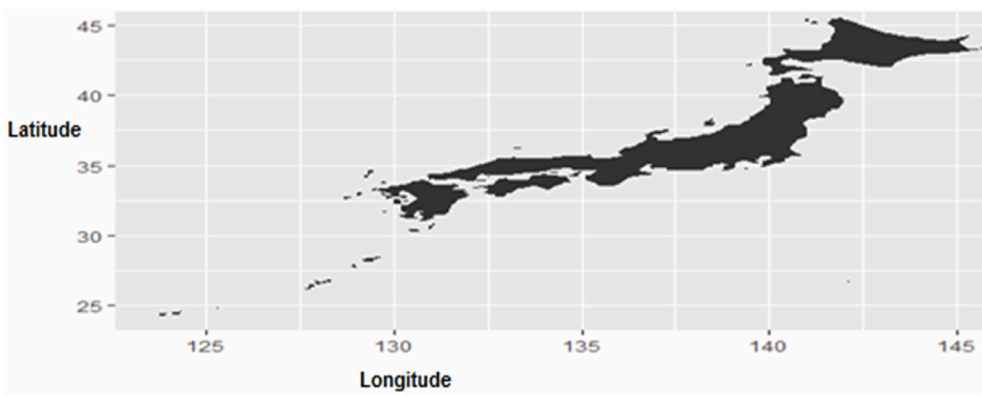


Fig. 3. Japan country map.

below code:

#Plot the data

```
> usa=map_data('state')
ggplot (usa, aes (x=long, y=lat, group=group, fill=region)) geom_polygon(color='black')
guides(fill=F) are plotted as base map for covid data prediction.
```

The system provides a user-friendly web-based interface for viewing COVID-19 data and metrics. World, country and regional maps are color-coded to represent various selectable infection attributes at those locations. Clicking on any given location brings up a set of pages that provide details about that location—from raw statistics to charts to advanced metrics and commentary. The user interface provides several ways to navigate, such as Map View, Trend View, Stats View, Hotspots View. Below is a detailed introduction to each view (see Figs. 1 and 2).

Application libraries like a library *(ggfortify)*, library *(mapdata)*, library *(maps)*, and library *(ggplot2)* Fig. 3 depicts the map of Japan from the world2 data set plotted with jpg **-ggplot2: map_data ('world2', 'japan')*. It contains 1097 observations with six variable geographic points (see Figs. 4–6).

#Structure of Map Data

```
#Code
$ long: num 124 124 124 124 124 ...
 $ lat: num 24.3 24.3 24.3 24.3 24.3 ...
 $ region: chr “Japan" "Japan" "Japan" "Japan" ...
 $ sub region: chr “Iriomote Jima" "Iriomote Jima" "Iriomote Jima" "Iriomote Jima" ...
```

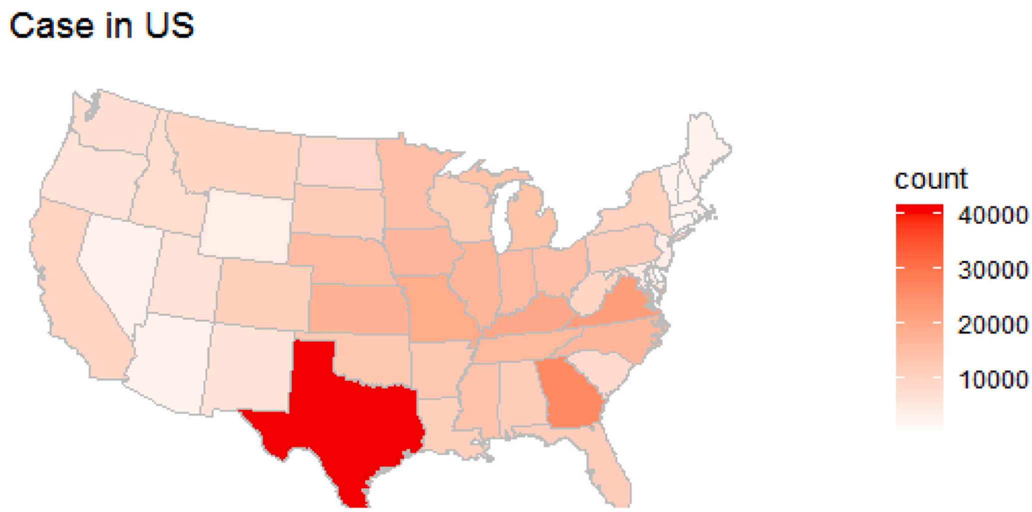


Fig. 4. Covid data in the U.S.

#Japan Map plotted using *ggplot* library

> *ggplot (jp, aes (x = long, y = lat, group = group)) geom_polygon ()*

The above maps illustrate the COVID data of country and city records. In addition to the open-source COVID-19 data, a zip file [25] with data projections for country-wise and state-wise records was also available. The COVID data is read into a file whose structure resembles data. As shown below, data frame 528282 records 13 variables from 58 states in the U.S.

#Structure of data of Covid confirmed cases

In many cases, the data format of collected data can be converted from the first format with qualifying digits to numeric data variables after converting longitude and latitude and rounding their data management values.

#Data filtered to the U.S. & summarised by Province. States using its count

```
$ UID: int 16 16 16 16 16 16 16 16 16 16 ...
 $ iso2: Factor w/ 6 levels "AS","GU","MP”, 1 1 1 1 1 1 1 1 1 1 ...
 $ iso3: Factor w/ 6 levels "ASM","GUM","MNP”, 1 1 1 1 1 1 1 1 1 1 ...
 $ code3: in 16 16 16 16 16 16 16 16 16 16 ...
 $ FIPS: in 60 60 60 60 60 60 60 60 60 60 ...
 $ Admin2: Factor w/ 1902 levels "","Abbeville”, 1 1 1 1 1 1 1 1 1 1 ...
 $ Let: num -14.3 -14.3 -14.3 -14.3 -14.3 ...
 $ Combined Key: Factor w/ 3261 levels "Abbeville, South Carolina, US”, 57 57 57 57 57
57...
 $ Date: Factor w/ 162 levels "1/22/2020","1/23/2020”, 1 2 3 4 5 6 7 8 9 10
 $ Case: int 0 0 0 0 0 0 0 0 0 0 ...
 $ Long: num -170 -170 -170 -170 -170 ...
 $ Country. Region and Province. State: Factor of 58 states of US which structure as
UID iso2 iso3 code3 FIPS Admin2 Lat Combined_Key Date Case Long Country. Region
1    16 AS    ASM     16    60 ""    -14.3 American Sa~ 1/22~     0 -170. US
2    16 AS    ASM     16    60 ""    -14.3 American Sa~ 1/23~     0 -170. US
```

```
6 8.41e7 US    USA     840 NA Weber~ 41.3 Weber-Morga~ 7/1/~ 1004 -112. US
> us=ct %>% filter (Country. Region =='US')
> cc=us %>% group_by (Province. State) %>% summarise (count=n ()) %>%
arrange(desc(count))
```

Prepare a map data set, a *summary,* and an *arranger* used after filtering the records of a single country, such as the United States (U.S.). Therefore the COVID records of the United States (U.S.) can be viewed using the filter with the group with the help of command on 06/07/2020, which includes the counts of 56 states from the United States (U.S.) and the corresponding COVID cases in decreasing order, as shown below.

#Check Province. State summarised records. Convert Province. State Names to Lower Case

In order to complete the merge operation, map information and COVID cases combine and merge into a standard index as the name of the state and region, while the lower case finishes for the map data organization. The *data1 = merge (ss, cc, by.x='region', by.y='Province. State')* command groups combine, region, longitude, latitude, group, order, sub-region with COVID counted. In the same way, the tabular information selects only the essential records for the map, eliminating unnecessary data.

```
#Output
1 Texas        41472
2 Georgia      26082
3 Virginia     21870
4 Kentucky     19764
------------------
6 Kansas       17334
> cy$Province.State=tolower (cy$Province.State)
```

However, another table has street information listed in lower cases, so the lower function changed to the lower cases below.

#Sample records after converting to lower case

```
1 diamond princess        162
2 grand princesses        162
---------------
6 Virgin Islands          162
```

As shown below, the state information provides the state for the state, providing longitude, latitude, grouping order, region long lat grouping order, and subregion long lat grouping order.

```
15594 -106.3295 41.00659    63 15594 Wyoming     <NA>
................................
15599 -109.0511 40.99513    63 15599 Wyoming     <NA>
```

#Required fields selected after subsetting the summarised data

```
Using keeps <- c("region","long","lat","group","count") and data1 = data1[keeps] commands.
region long lat group count
1 alabama -87.46201 30.38968 1 11178
```

In the case of integer types with the region, longitude, latitude, group, and count, the following records of 15537 observations based on five variables chosen for map plotting: This includes *11178 11178* as outlined below:

#Data is plotted on U.S. map using *ggplot* library

```
ggplot(data1,aes(x=long,y=lat,group=group,fill=count)) geom_polygon(color='gray')
coord_map('polyconic') scale_fill_gradient2(low='white',high='red') theme_void()
ggtitle('Covid Case in US').
```

The command displays the U.S. map mapped with the number of COVID cases ranked higher and lower levels. In a legend scale, the color indicates the highest to the lowest state. As a result, the output is more than adequate to present tabular data using the statistics above, like India's tabular records. According to the legend on the left, there are a total of 79 cases with fading colors. Interactive maps of COVID record data could easily be visualized using clusters. Through using multiple map providers, the leaflet packet connects the online world map. Marker clusters, for example, add tiles that are circular markers with names and colors that add to a map.

#Data plotted using *leaflet* library on U.S. map

```
> dataf %>% leaflet () %>% addTiles () %>% addCircleMarkers (radius = 2, label =
~htmlEscape(city), color = 'red', clusterOptions = markerClusterOptions ())
```

Using a *leaflet*, *addTiles* with circle markers, and describing each state's respective locations help plot a map of COVID cases in each state. Viewing the state aggregate features of the country's map in zoomed-in mode.

By highlighting the boundaries of maps, planners can better judge what measures should consider. Using the zoom in and zoom out feature, the *leaflet* with added tiles could plot COVID total cases state-wise and city-wise with the border area location of the open street base maps. In the following manner, COVID data from many states and cities shall be share interactively.

3. Discussion

The COVID-19 pandemic is challenging our society and economy in an unprecedented way. Overall, the U.S. response to containing COVID-19 may not have been as effective as other countries, like Japan and India. These studies may have been due to insufficient or delayed testing and a lack of alternative monitoring tools near the pandemic's beginning [27]. Early warning and detection may represent a critical opportunity for India, Japan, and the U.S. to track the rate of respiratory illness and quickly institute policies to prevent or at least mitigate a future outbreak.

The study recommended that the COVID-19 diagnosis and prognosis models adhere to transparent and open-source reporting methods to reduce bias and encourage real-time application. Secondly, with the help of the system, it provides a user-friendly web-based interface for viewing COVID-19 data and metrics. World, country and regional maps are color-coded to represent various selectable attributes of the infection at those locations with latitude and longitude values for the countries like India, Japan, and the U.S.

Real-time epidemiologic data is critical to managing different aspects of a pandemic. For instance, this data can help public health authorities forecast demand/surge models, thereby allowing public or private organizations to reposition resources or reallocate personnel quickly. These are corroborating data that should consider in combination with other indicators, such as the officially reported number of newly positive laboratory tests, disease-related hospitalizations, and disease-related deaths.

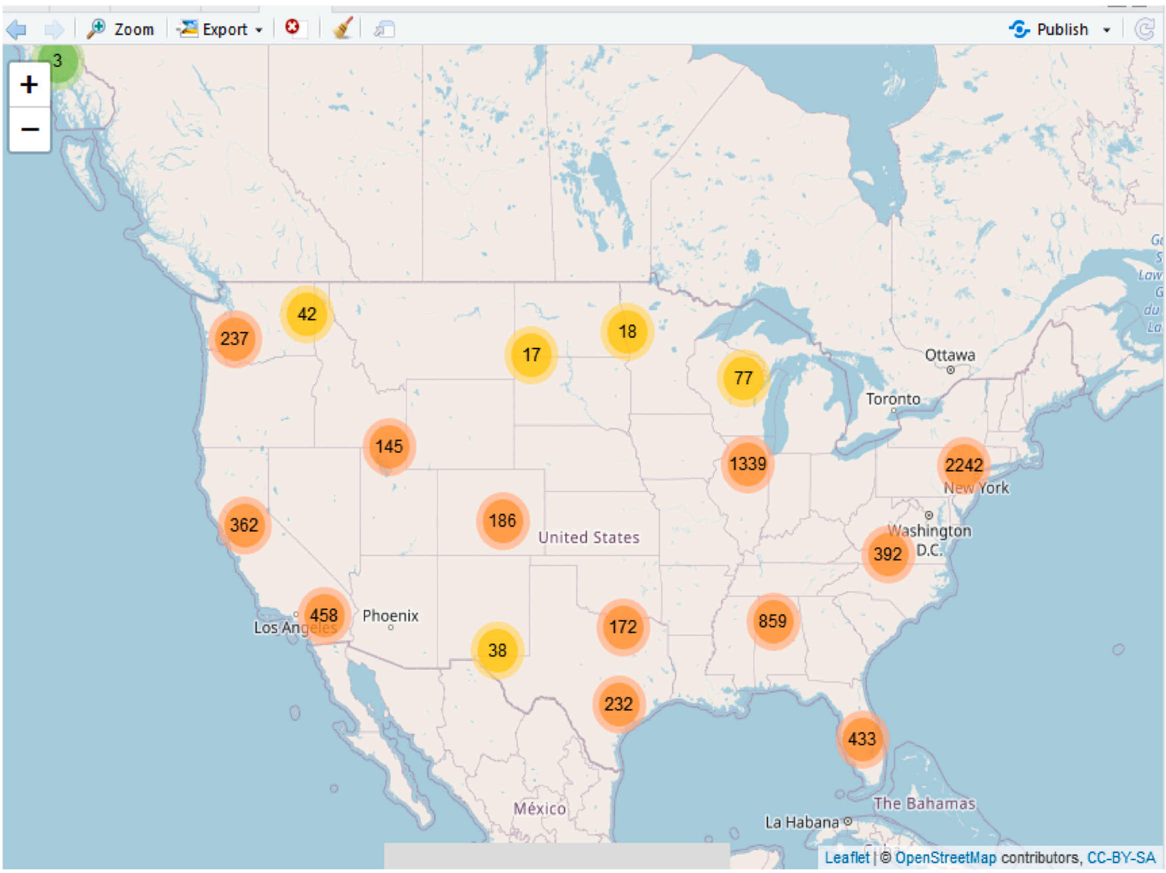
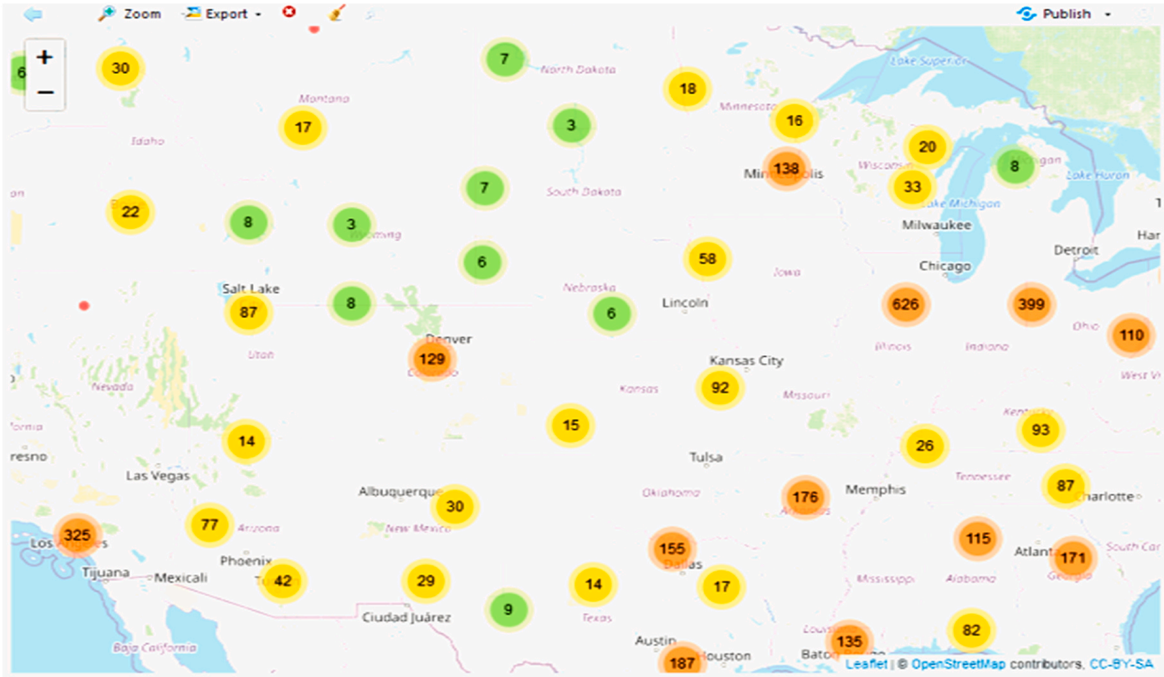


Fig. 5. Covid maps with respective data of the U.S.



Using a *leaflet*, *addTiles* with circle markers, and describing each state's respective locations help plot a map of COVID cases in each state. Viewing the state aggregate features of the country's map in zoomed-in mode.

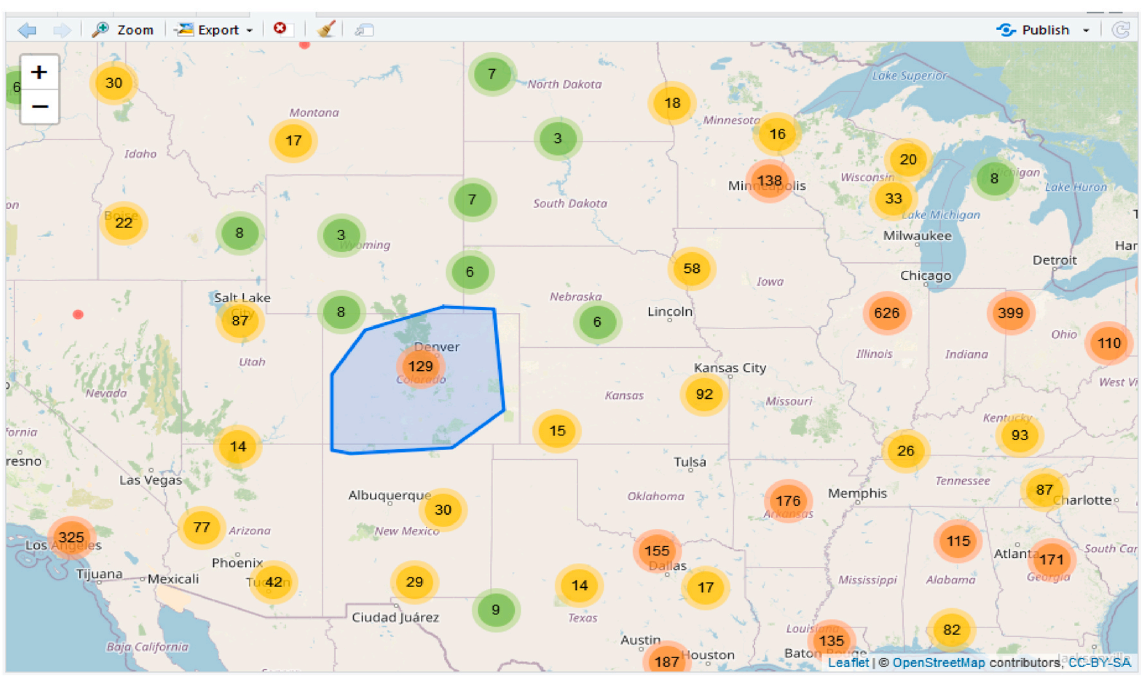


Fig. 6. Interactive geographic map of U.S.

4. Conclusion

In this paper, we have studied COVID data interpretation and visualization using open-data sources for larger countries like the USA and India to understand better how COVID is spreading nationwide and internationally. An effective tool for updating country-specific analysis and visualizing epidemiological indicators of the COVID-19 epidemic, COVID19-World aims to fill a gap in the field by presenting a set of valuable tools for the current global COVID-19 epidemic. Through the web application, a better understanding of the epidemiological development in each country can be obtained and help with country-specific surveillance.

Despite promising results, some additional suggestions could enhance the performance of the algorithms and make them more useful, for example, by strengthening the datasets of several health centers throughout the country or by ensuring that all details in the screening are filling with accuracy.

Declaration of competing interest

The authors declare that they have no known competing financial interests or personal relationships that could have appeared to influence the work reported in this paper.

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References

[1] Lin S, Pan H, Wu H, Yu X, Cui P, et al. Epidemiological and clinical characteristics of 161 discharged cases with coronavirus disease 2019 in Shanghai, China. BMC Infect Dis 2020 Oct 20;20(1):780. https://doi.org/10.1186/s12879-020-05493-7. PMID: 33081711; PMCID: PMC7573864.
[2] Sanche S, Lin YT, Xu C, et al. The novel coronavirus, 2019-nCoV, is highly contagious and more infectious than initially estimated. medRxiv 2020. https://doi.org/10.1101/2020.02.07.20021154.
[3] Wu JT, Leung K, Leung GM. Nowcasting and forecasting the potential domestic and international spread of the 2019-nCoV outbreak originating in Wuhan, China: a modelling study. Lancet 2020 Feb 29;395(10225):689–97. https://doi.org/10.1016/S0140-6736(20)30260-9. Epub 2020 Jan 31. Erratum in: Lancet. 2020 Feb 4;: PMID: 32014114; PMCID: PMC7159271.
[4] Lai S, Bogoch I, Ruktanonchai N, Watts A, Lu X, et al. Assessing spread risk of Wuhan novel coronavirus within and beyond China, January-April 2020: a travel network-based modelling study. 2020.02.04.20020479 medRxiv 2020 Feb 5. https://doi.org/10.1101/2020.02.04.20020479. PMID: 32511631; PMCID: PMC7276059.
[5] Jandrić P. Postdigital research in the time of covid-19. Postdigit Sci Educ 2020;2: 233–8. https://doi.org/10.1007/s42438-020-00113-8.
[6] Breslin N, Baptiste C, Gyamfi-Bannerman C, et al. Coronavirus disease 2019 infection among asymptomatic and symptomatic pregnant women: two weeks of confirmed presentations to an affiliated pair of New York City hospitals. Am J Obstet Gynecol MFM 2020 May;2(2):100118. https://doi.org/10.1016/j.ajogmf.2020.100118. Epub 2020 Apr 9. PMID: 32292903; PMCID: PMC7144599.
[7] Huang L, Zhang X, Zhang X, Wei Z, Zhang L, et al. Rapid asymptomatic transmission of COVID-19 during the incubation period demonstrating strong infectivity in a cluster of youngsters aged 16-23 years outside Wuhan and characteristics of young patients with COVID-19: a prospective contact-tracing study. J Infect 2020 Jun;80(6):e1–13. https://doi.org/10.1016/j.jinf.2020.03.006. Epub 2020 Apr 10. PMID: 32283156; PMCID: PMC7194554.
[8] Pan L, Mu M, Yang P, Sun Y, Wang R, Yan J, Li P, Hu B, et al. Clinical characteristics of COVID-19 patients with digestive symptoms in Hubei, China: a descriptive, cross-sectional, multicenter study. Am J Gastroenterol 2020 May;115 (5):766–73. https://doi.org/10.14309/ajg.0000000000000620. PMID: 32287140; PMCID: PMC7172492.
[9] Wu Z, McGoogan JM. Characteristics of and important lessons from the coronavirus disease 2019 (COVID-19) outbreak in China: summary of a report of 72 314 cases from the Chinese center for disease control and prevention. J Am Med Assoc 2020 Apr 7;323(13):1239–42. https://doi.org/10.1001/jama.2020.2648.PMID:32091533.
[10] Jin YH, Cai L, Cheng ZS, Cheng H, Deng T. Zhongnan Hospital of Wuhan University Novel Coronavirus Management and Research Team, Evidence-Based Medicine Chapter of China International Exchange and Promotive Association for Medical and Health Care (CPAM). A rapid advice guideline for the diagnosis and treatment of 2019 novel coronavirus (2019-nCoV) infected pneumonia (standard version). Mil Med Res 2020 Feb 6;7(1):4. https://doi.org/10.1186/s40779-020-0233-6. PMID: 32029004; PMCID: PMC7003341.
[11] Mofijur M, Fattah IMR, Alam MA, et al. Impact of COVID-19 on the social, economic, environmental and energy domains: lessons learnt from a global pandemic. Sustain Prod Consum 2021 Apr;26:343–59. https://doi.org/10.1016/j.spc.2020.10.016. Epub 2020 Oct 14. PMID: 33072833; PMCID: PMC7556229.
[12] Zheng J. SARS-CoV-2: an emerging coronavirus that causes a global threat. Int J Biol Sci 2020 Mar 15;16(10):1678–85. https://doi.org/10.7150/ijbs.45053. PMID: 32226285; PMCID: PMC7098030.
[13] Stawicki SP, Jeanmonod R, Miller AC, Paladino L, et al. The 2019-2020 novel coronavirus (severe Acute respiratory Syndrome coronavirus 2) pandemic: a Joint American College of Academic International Medicine-World Academic Council of Emergency Medicine Multidisciplinary COVID-19 working group consensus paper. J Global Infect Dis 2020 May 22;12(2):47–93. https://doi.org/10.4103/jgid.jgid_86_20.PMID:32773996. PMCID: PMC7384689.
[14] Andersen AL, Hansen ET, Johannesen N, Sheridan A. Pandemic, shutdown and consumer spending: Lessons from Scandinavian policy responses to COVID-19. 2020. arXiv preprint arXiv:2005.04630.
[15] Laverty MS, Bannish EB. Exploring modeling by programming: insights from numerical experimentation. 2020.
[16] Roldan E, Biasiotto G, Magro P, Zanella I. The possible mechanisms of action of 4-aminoquinolines (chloroquine/hydroxychloroquine) against Sars-Cov-2 infection (COVID-19): a role for iron homeostasis? Pharmacol Res 2020 Aug;158:104904. https://doi.org/10.1016/j.phrs.2020.104904. Epub 2020 May 13. PMID: 32430286; PMCID: PMC7217799.
[17] Sharma A, Ghosh D, Divekar N, Gore M, Gochhait S, Shireshi S. Comparing the socio-economic implications of the 1918 Spanish flu and the COVID-19 pandemic in India: a systematic review of literature. Int Soc Sci J 2021. https://doi.org/10.1111/issj.12266.
[18] Chhikara BS, Rathi B, Singh J, et al. Corona virus SARS-CoV-2 disease COVID-19: infection, prevention and clinical advances of the prospective chemical drug therapeutics: a review on Corona Virus Disease COVID-19, epidemiology, prevention, and anticipated therapeutic advances. Chem Biol Lett 2020;7(1): 63–72.
[19] Dancer SJ. Controlling hospital-acquired infection: focus on the role of the environment and new technologies for decontamination. Clin Microbiol Rev 2014 Oct;27(4):665–90. https://doi.org/10.1128/CMR.00020-14. PMID: 25278571; PMCID: PMC4187643.
[20] Thevarajan I, Nguyen THO, Koutsakos M, et al. Breadth of concomitant immune responses prior to patient recovery: a case report of non-severe COVID-19. Nat Med 2020 Apr;26(4):453–5. https://doi.org/10.1038/s41591-020-0819-2. PMID: 32284614; PMCID: PMC7095036.
[21] Woestenberg PJ, King AJ, Van Benthem BHB, Leussink S, Van der Sande MAB, Hoebe CJPA, Bogaards JA. Medical microbiological laboratories and the public health services. Bivalent vaccine effectiveness against anal human papillomavirus positivity among female sexually transmitted infection clinic visitors in The Netherlands. J Infect Dis 2020 Mar 28;221(8):1280–5. https://doi.org/10.1093/infdis/jiz187.PMID:31100134.
[22] Schwartz DA, Graham AL. Potential maternal and infant outcomes from (Wuhan) coronavirus 2019-nCoV infecting pregnant women: lessons from SARS, MERS, and other human coronavirus infections. Viruses 2020;12(2):194. https://doi.org/10.3390/v12020194. Published 2020 Feb 10.
[23] Bairoliya N, Imrohoroglu A. Macroeconomic consequences of stay-at-home policies during the COVID-19 pandemic. 2020.
[24] Ali I, Alharbi OML. COVID-19: disease, management, treatment, and social impact. Sci Total Environ 2020 Aug 1;728:138861. https://doi.org/10.1016/j.scitotenv.2020.138861. Epub 2020 Apr 22. PMID: 32344226; PMCID: PMC7175909.
[25] Kariv A. COVID-19 and compartmental models in epidemiology. 2020.
[26] Alamo T, Reina DG, Mammarella M, Abella A. Covid-19: open-data resources for monitoring, modeling, and forecasting the epidemic. Electronics 2020;9(5):827. https://doi.org/10.3390/electronics905082.
[27] Schneider EC. Failing the test - the tragic data gap undermining the U.S. Pandemic response. N Engl J Med 2020;383(4):299–302.