



Original Research Paper

Distribution and Trend Analysis of COVID-19 in India: Geospatial Approach



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Abstract

COVID-19 Coronavirus is now one of the most contagious diseases of the recently discovered and spread across the China in 2019 and has received global attention. In most COVID-19-infected individuals, respiratory symptoms should be mild to moderate and improve without the need for medical care. The risk of serious disease is higher for senior citizens and people with serious health problems, such as heart disease, diabetes, severe respiratory disease, and cancer. The World Health Organization (WHO) has formally declared the outbreak of COVID-19 to be a global pandemic. As on 11th April 2020 in India the largest number of persons testing positive for COVID-19 since the outbreak earlier month with samples of people, mostly contacts of already confirmed patients, rendering positive. In India total confirmed cases 7364, 633 are cured/discharged, with 240 deaths had been reported by the Ministry of Health and Family Welfare Government of India. The aim of the research is to analyze the spatial distribution of COVID-19 and its trends with the help of GIS software. At this time, there are no precise antibiotics or treatment options for COVID-19. Besides, several ongoing clinical studies are assessing effective treatments. The best way to protect and sluggish transmission should be well advised about the current COVID-19 virus, the disease it triggers and also how it continues to spread. Therefore, monitoring active ties using GIS spatial analysis is very important to control such as a COVID-19 virus spreading problem.

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1 INTRODUCTION

A group of pneumonia cases, triggered by recently discovered β -coronavirus, happened in Wuhan, China, in December 2019. This coronavirus was at first called the 2019 novel coronavirus (2019-nCoV) by WHO on 12 January 2020. WHO officially referred to as coronavirus disease 2019 (COVID-19) and Coronavirus Study Group (CSG) of the International Committee suggested that the current coronavirus be named SARS-CoV-2, both issued on 11 February 2020. The Chinese researchers quickly isolated SARS-CoV-2 from the

patient within such a short timeframe on 7 January 2020 and issued the SARS-CoV-2 genome sequence (Lu *et al.*, 2020). Since 1 March 2020, a total of 79,968 cases of COVID-19 have been reported in China, including 2873 deaths (WHO, 2020). The results of the study stated that the basic replication number (R_0) of SARS-CoV-2 was approximately 2.2 (Riou *et al.*, 2020) or more (range from 1.4 to 6.5) (Liu *et al.*, 2020) and that the pneumonia clusters (Chan *et al.*, 2020) add to the scientific evidence of a continuous increase in human-to-human transmission of the COVID-19 epidemic.

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SARS-CoV-2 is a β -coronavirus enclosed with an un-segmented positive-sensing RNA virus (subgenus arbecovirus, orthocoronavirinae subfamily) (Zhu et al., 2020). Coronaviruses (CoVs) were separated into four genera, with α - β - γ - δ -CoVs. α - and β -CoV are capable of infecting animals, whereas γ - and δ -CoV appear to infect animals. Earlier, six CoVs were indeed well-known as living organism-sensitive viruses, including α -CoVs HCoV-229E, HCoV-OC43, HCoV-NL63, and β -CoVs HCoV-HKU1 and with minimal pathogenicity, triggering mild breathing problems analogous to common colds. The other two recognized β -CoVs, SARS-CoV and MERS-CoV, resulted in serious and possibly fatal respiratory infections (Yin and Wunderink, 2018). It has been discovered that the SARS-CoV-2 gene sequence tends to be 96.2% similar to the CoV RaTG13 bat, even though it shares the SARS-CoV, 79.5% identity. Based on the results of virus genetic sequences and genetic analysis, bats are suspected to be a normal host of virus provenance, and SARS-CoV-2 could be transferred from bats to human beings through unidentified intermediate contestants. It is now clear that SARS-CoV-2 might use angiotensin-converting enzyme 2 (ACE2), a receptor called SARS-CoV (Zhou et al., 2020), to spread the disease.

The first outbreak of unidentified acute respiratory infections occurred in Wuhan, China, on 12 December 2019, possibly linked to the seafood market. Numerous research has proposed that the bat might be a potential pool of SARS-CoV-2 (Giovanetti et al., 2020; Paraskevis et al., 2020). Moreover, there is no current evidence that the source of SARS-CoV-2 originated in the seafood market. Somehow, bats are natural pollutants of a wide range of CoVs, such as SARS-CoV-like and MERS-CoV-like viruses (Hampton, 2005; Banerjee et al., 2019; Li et al., 2005). Not only on the genome of the virus, but COVID-19 has also been investigated throughout the genome of Bat CoV RaTG13 and reveals 96.2% of the aggregate genome sequence identity (Zhou et al., 2020), proposing that CoV bat and human SARS-CoV-2 may discuss a certain ancestor, even though bats were not commercially available in the above seafood market (Wu et al., 2020). In addition, the orientation of carbohydrate sequences and phylogenetic analysis (Liu et al., 2020) has also shown that closely related receptor residues have been identified in several species, offering additional possibilities for appropriate optimal hosts, such as pangolins and snack foods.

Human-to-human transmitter, SARS-CoV-2 emanates primarily around families, along with friends and relatives who have been in direct contact with patients. It should be noted (Guan et al., 2020) that 31.3% of patients have recently travelled to Wuhan and 72.3% of patients have been able to contact Wuhan among several non-Wuhan patients. Transmission around healthcare professionals was recorded in 3.8% of COVID-19 patients received by the National Health Commission of China on 14 February 2020. On the other hand, the transmission of SARS-CoV and MERS-

CoV has been shown to arise primarily through nosocomial propagation. Health workers illnesses in 33-42% of SARS cases and distribution around patients (62-79%) have become the most prevalent pathway of disease in MERS-CoV cases (Chowell et al., 2015; Kang et al., 2017). Physical contact with optimal host animals or the use of animals has already been assumed to be the main route of propagation of SARS-CoV-2. Moreover, the sources and transmission routines of SARS-CoV-2 remain a mystery. Recent research on epidemiology, pathogenesis and clinical features of COVID-19 and ongoing treatment and scientific advances in the fight against the novel coronavirus epidemic (Guo et al. 2020), which has the potential to cause toxic encephalopathy.

Geographic Information Systems (GIS) and spatial mapping are emerging global health tools, but the degree to which they have been implemented in India for COVID-19 research is unclear. To inform researchers and program developers, this mapping review presents the scope and depth of the GIS and Spatial Analysis Studies conducted by COVID-19 in India. In particular, GIS and spatial analysis can be essential tools for knowledge, prevention, and treatment of diseases. For example, GIS technology can be used as a visualization help to map the geographical distribution of the disease, the potential risk factors and the resources available for treatment and prevention. In relation to the spatial analysis of certain information, it is possible to evaluate the risks of disease, trends in outbreaks over time and space, and hotspots of infection (Lyseen et al., 2014; Kandwal et al., 2009). Similar to each other, such methods may relate to the design, planning, and distribution of international health resources for treatment and prevention facilities and may help mitigate the impact of interference. The aim of this research is to analyze the spatial distribution of COVID-19 and its trend to predict the spread of diseases with the help of GIS software.

2 DATA AND METHODS

This study reviewed peer-reviewed research papers prepared on COVID-19 in India and concerning GIS or spatial assessment. COVID-19 related issues, except for the incidence of COVID-19, COVID-19 specific cardiovascular disease, COVID-19 health conditions, and COVID-19 preventive facilities. Research papers expressly based in India or in other parts of the world have been included. Spatial analysis approaches and the use of GIS were ambiguously defined for the uses of this analysis in order to obtain a diversity of emerging activities, i.e. they included research papers using any specialized GIS software or explicitly implementing any spatial analysis techniques (Kawo and Shankar, 2018; Shankar and Kawo, 2019; Balamurugan et al., 2020). The data used in this study is the number of COVID-19 disease patients in state-wise in India from February to 11th April obtained from the health department of India. In the present research work, distribution pattern of disease transmission is illustrated with GIS tool and

forecasts the number of patients each day the aid of Inverse Distance Weighted (IDW) and Kriging interpolation techniques.

Inverse Distance Weighted (IDW) is developed as one of the most widely known interpolation techniques. It is used to predict the values for any undetermined destination by calculating the predicted zone of the adjacent areas (Childs, 2004). It is mainly based on two inferences: first, the impact of the unknown value of a point is specifically extended to the point of close control rather than to the point of the range. Second, the extent of the impact is directly related to the inverse of the range between the points. The following equation used for the analysis (Bartier et al., 1996; Huang et al., 2011).

$$Z_p = \frac{\sum_{i=1}^n \left(\frac{Z_i}{d_i^p} \right)}{\sum_{i=1}^n \left(\frac{1}{d_i^p} \right)}$$

where, Z_p refers to the interpolated value of the unknown point, the weighting function which controls the significance of the control point Z_i and Z_i is the value observed at the control point i which represents the nearest neighborhood of the interpolated point produced and ranges from 20 to 30, n is the nearest

vicinity of the control points which is usually required to consume time, dip refers to the interpolated point, p is a weighting absolute value that is an arbitrary positive real number, p is equal to 1 in inverse distance weighting (Guan and Wu, 2008).

3 STUDY AREA

India is located in South Asia, bordered to the north by the highest mountain chain in the world, bordering the central and southern Bay of Bengal and the Arabian Sea, between Burma and Pakistan. Geographic coordinates are from 8°4' N to 37° 6' N latitude and 68° 7' E to 97° 25' E longitude, with a total area of 3287590 km². The capital of India is New Delhi, and the major cities in the nation are Mumbai, Delhi, and Kolkata. India is the 7th largest country in the world. India's population is one billion, making it the second-most densely populated nation after China (Figure 1 and Table 1). It is more than three times the population of the US, but only about a third of its area. The most populous state in India is Uttar Pradesh and the least populous state in India is Sikkim, with the population map shown in figure 1 and table 1. India is the biggest democratic country in the world. The country is mainly an agricultural nation, although it has a huge iron and steel industry and supplies all kinds of manufactured goods.

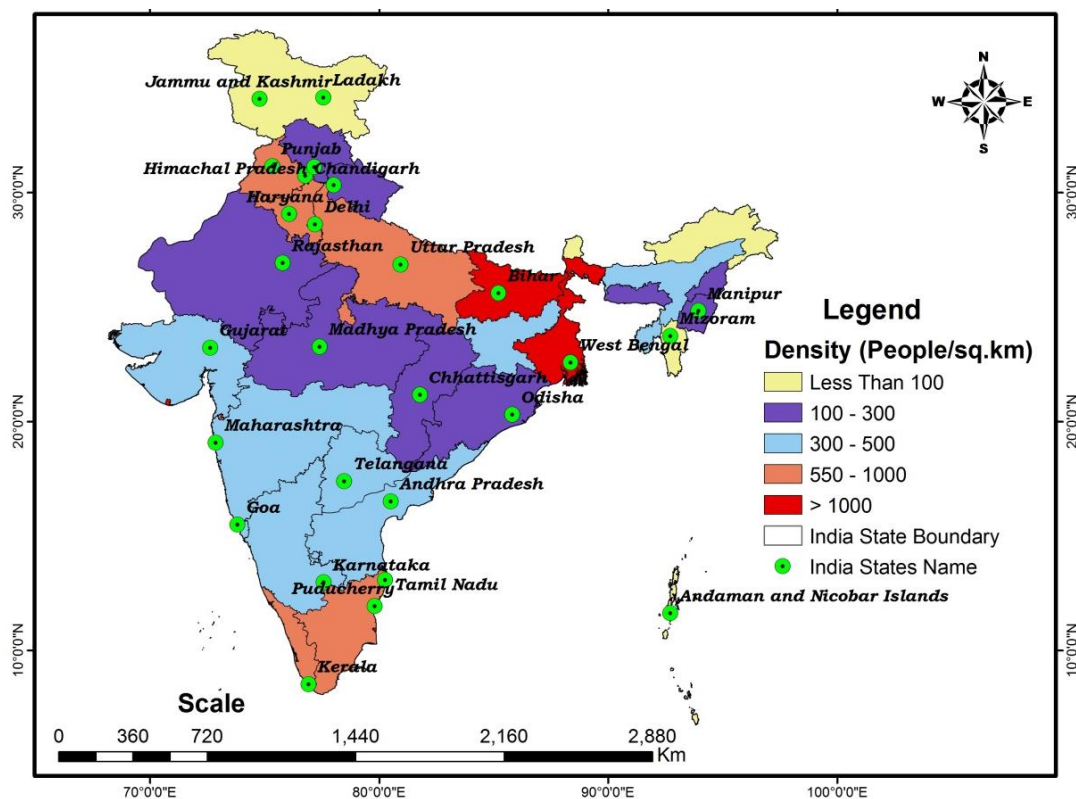


Figure 1. Distribution of population

Table 1. State-wise population (2011)

Sr. No	Name of state/UT	Population	Sr. No	Name of state/UT	Population
1	Jammu and Kashmir	12548926	19	Lakshadweep	64473
2	Andaman and Nicobar	380581	20	Madhya Pradesh	72597565
3	Andhra Pradesh	49386799	21	Maharashtra	112372972
4	Arunachal Pradesh	1382611	22	Manipur	2721756
5	Assam	31169272	23	Meghalaya	2964007
6	Bihar	103804637	24	Mizoram	1091014
7	Chandigarh	1055450	25	Nagaland	1980602
8	Chhattisgarh	25540196	26	Orissa	41947358
9	Dadra and Nagar Haveli	585764	27	Pondicherry	1247953
10	Daman and Diu	585764	28	Punjab	27704236
11	Delhi	16787941	29	Rajasthan	68621012
12	Goa	1457723	30	Sikkim	607688
13	Gujarat	60383628	31	Tamil Nadu	72138958
14	Haryana	25353081	32	Tripura	3671032
15	Himachal Pradesh	6864602	33	Uttar Pradesh	199812341
16	Jharkhand	32966238	34	Uttarakhand	10116752
17	Karnataka	61130704	35	West Bengal	91347736
18	Kerala	33387677	36	Telangana	35286757

4 RESULTS AND DISCUSSIONS

4.1 Current Status

Novel Coronavirus or COVID-19 cases in India are well over 7364 as of 11th April 2020 (Table 2). The state-wise confirmed COVID-19 cases in India shown in this table. The first three cases reported by India in Kerala appear to be every student returning from Wuhan, China. The number of reported cases in the world increased during March, mostly due to people with travel records to the affected locations. The number of cases in the world as a whole has increased. On 10th March, the total number of cases increased to 50. The first survivor of the virus in Saudi Arabia was a 76-year-old man on 12th March, who crossed more than one hundred on 15th March, five hundred on 24th March, one thousand one hundred and seventeen on 30th March, and seven thousand three hundred and sixty four on 11th April (Table 2). The total number of recently confirmed cases augmented rapidly from March 30 to April 11, 2020. Maharashtra is followed by Delhi, Tamil Nadu with a maximum number of cases of coronavirus. As of 11th April the death and discharge (cured) given in Table 2. Maharashtra having 110, Madhya Pradesh 33, Gujarat 19, and Delhi 13 deaths and cured cases are 188 in Maharashtra, 123 cases in Kerala and 44 in Tamil Nadu.

4.2 Spatial Distribution COVID-19

In this work, interpolation using Inverse Distance Weighted (IDW) makes clear the conclusion that objects

similar to each other are more similar than those further apart. IDW uses the calculated values (cases) of the prediction site to estimate the value for each undetermined site. The values determined nearest to the location of the forecast have a greater impact on the expected value than those further away. IDW assumes that each measured point imposes a time-decreasing local effect. Using values from nearby weighted locations, the IDW approach calculates the average value for unsampled locations. The weights were commensurate with the proximity of the points sampled to the non-sampled location and the IDW power coefficient could be specified.

4.3 Prediction of COVID-19 Disease Spread Pattern

Interpolation using IDW has been obtained with the aim of predicting the spread of disease in India. This map shows the number of patients and the extended disease zone across the country. As per IDW, the pattern of COVID-19 diseases in the seven classes is 0 to 150, 151 to 250, 251 to 350, 351 to 450, 451 to 700, 701 to 1000 and > 1000 shown in Figure 2. These classes are at risk of exposing the spatial spread of the disease in relation to different states, based on population and environmental factors that may control the distribution of the patient. The highest number of patients returning on board, including families, friends, and relatives in close contact with incubation carriers, is reported daily as an observational analysis.

Table 2. State-wise breakdown of total confirmed cases of COVID-19 in India

Sr. No	Name of state/UT	Confirmed cases	Cured/discharged	Death
1	Jammu and Kashmir	207	6	4
2	Andaman and Nicobar	11	0	0
3	Andhra Pradesh	363	7	6
4	Arunachal Pradesh	1	0	0
5	Assam	29	0	1
6	Bihar	60	0	1
7	Chandigarh	18	7	0
8	Chhattisgarh	18	9	0
9	Dadra and Nagar Haveli	0	0	0
10	Daman and Diu	0	0	0
11	Delhi	903	25	13
12	Goa	7	1	0
13	Gujarat	308	31	19
14	Haryana	117	29	3
15	Himachal Pradesh	28	6	1
16	Jharkhand	14	0	1
17	Karnataka	207	31	6
18	Kerala	364	123	2
19	Lakshadweep	0	0	0
20	Madhya Pradesh	435	0	33
21	Maharashtra	1574	188	110
22	Manipur	2	1	0
23	Meghalaya	0	0	0
24	Mizoram	1	0	0
25	Nagaland	0	0	0
26	Orissa	40	2	1
27	Pondicherry	5	1	1
28	Punjab	132	5	11
29	Rajasthan	553	21	3
30	Sikkim	0	0	0
31	Tamil Nadu	911	44	8
32	Tripura	1	0	0
33	Telangana	473	43	7
34	Uttar Pradesh	431	32	4
35	Uttarakhand	35	5	0
36	West Bengal	116	16	5
Total		7364	633	240

* Ministry of Health, India (11th April 2020).

India could be the next global hotspot for infectious diseases of the COVID-19 virus. For this research COVID-19 prediction IDW map suggests that extreme cases will be conforming next two months >1000 cases in the following states are Maharashtra and Tamil Nadu. Maharashtra is the largest urbanization in the country, close to the Mumbai financial center and the stock market. The largest spread of infectious disease with COVID-19 cases has been increased daily. Where the observed increase in patients is concentrated primarily

in these states, there is a need for more prevalence, with some major distributions ranging from 451 to 1000 being Delhi, Gujarat, Telangana, Uttar Pradesh (city) and Rajasthan (city). The moderate range of spread ratio is observed in the following states: Karnataka, Kerala, Andhra Pradesh, Madhya Pradesh, with a range of 251 to 450 might to be affected more cases in future. The lowest range 0 to 250 is observed in Odisha, Manipur, Haryana and Jammu & Kashmir, Bihar, Chhattisgarh, Chandigarh and Mizoram for patients in the center of

the city. The death and cured prediction distribution of the COVID-19 map in India as shown in Figure 3 and 4, respectively. In cases of death, the area around Maharashtra is more extremely dangerous and the area around Madhya Pradesh and Gujarat is moderately risky and the rest of the states are less than 20. In cases of healing, the area around Maharashtra, Kerala, and South Tamil Nadu is more healing and the areas around Telangana, Karnataka, Uttar Pradesh, Ladakh, and Gujarat are moderately cured and the cases are less cured in the center of Tamil Nadu and the rest of the states. Some diseases move quickly between people. However, the exposure behavior of each disease differs from another depending on regional or space factors,

environmental conditions, etc. No specific drugs for the prevention or treatment of coronavirus disease (COVID-19).

This analysis may provide valuable information to support government monitoring and predicting spread of virus across small and large areas. The WHO announced that the outbreak of Novel Coronavirus Disease (COVID-19) was a pandemic and reiterated its call for immediate action by governments to step up their response to diagnose, identify and mitigate spread to save lives. In this context, the Government of India will take all necessary precautions to ensure that we are well prepared to face the challenge and threat posed by the growing pandemic of COVID-19 Corona Virus.

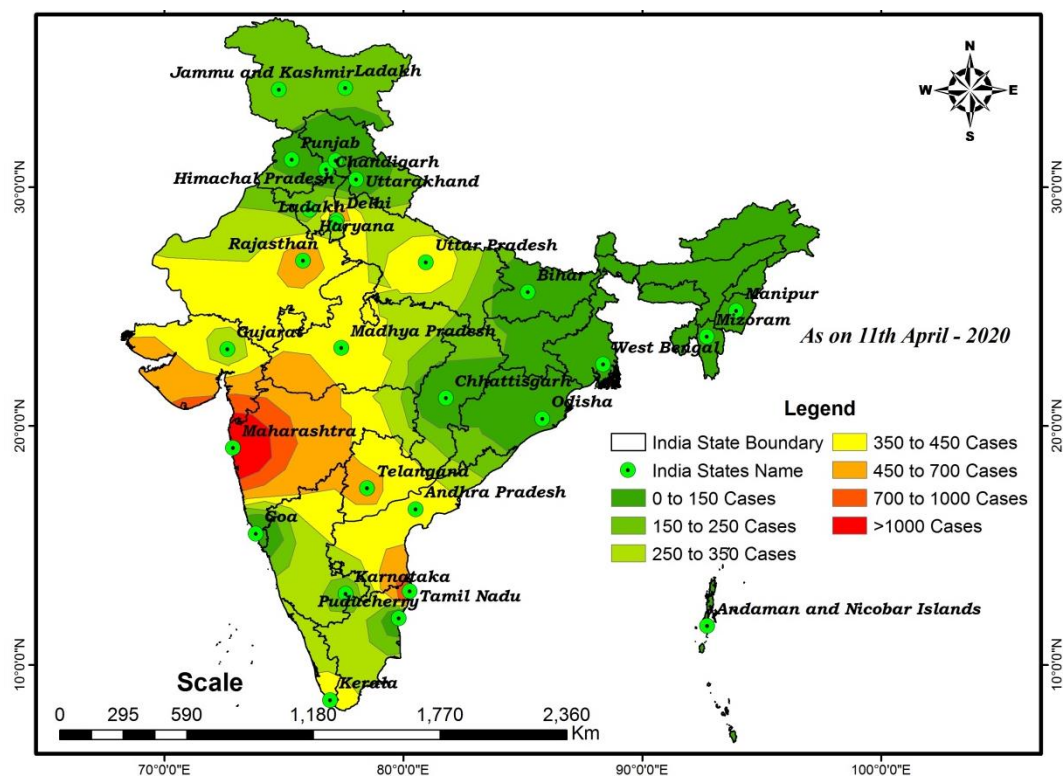


Figure 2. COVID-19: Distribution of estimated confirmed patients

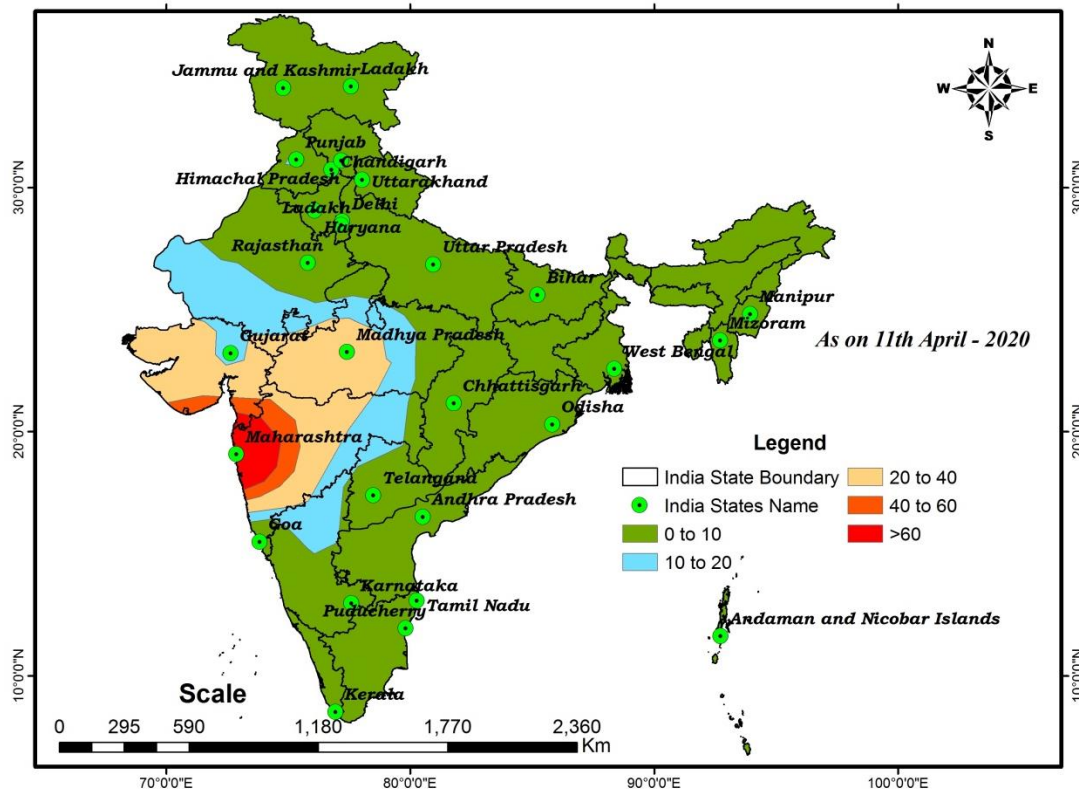


Figure 3. COVID-19: Distribution of estimated deaths

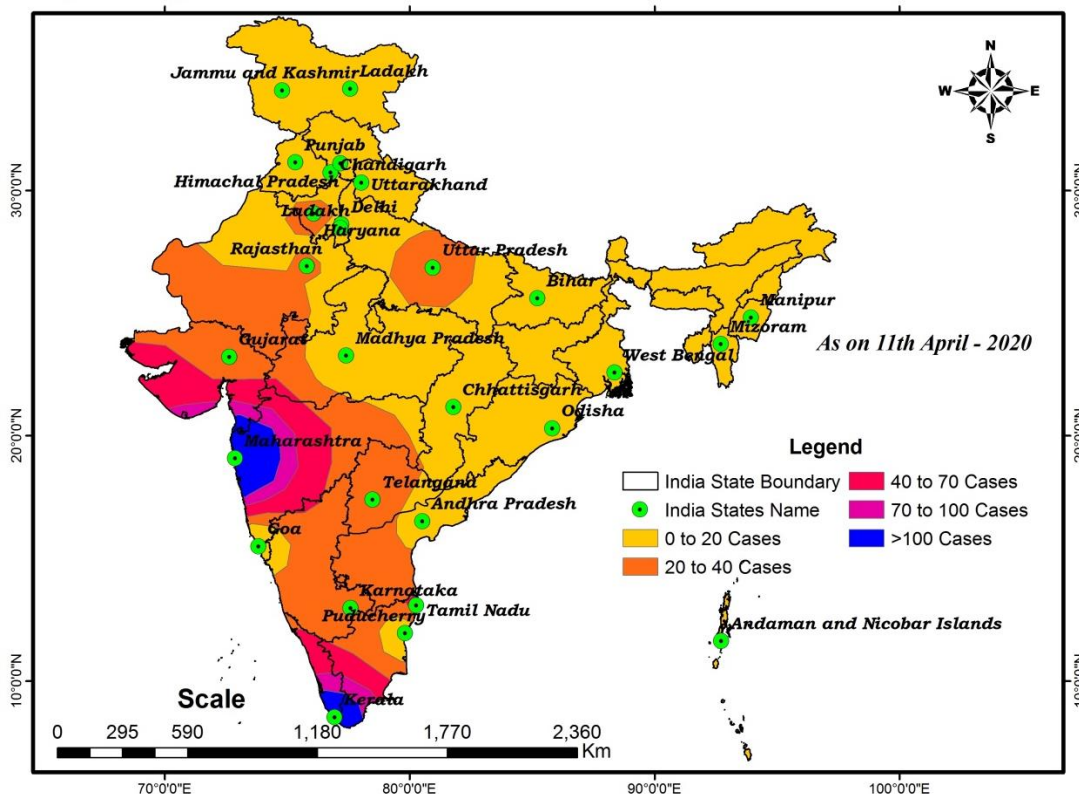


Figure 4. COVID-19: Distribution of estimated cured/discharged patients

5 CONCLUSIONS

This study was conducted on diseases that have spread to the pattern of spatial distribution in India. GIS-based spatial techniques provided a perspective for simplifying and measuring the outbreak status of COVID-19 diseases in particular areas and provided a basis for future surveys of environmental factors responsible for the imminent threat of disease. Analysis of spatial distribution patterns may provide valuable information to support government monitoring and the predicting spread of the virus across small and large areas. As a result, a GIS-based spatial distribution using the IDW method was performed in this article to identify potential disease risk assessments in India. The IDW analysis of the spatial interpolation layers and the apparent weight of the conditioning factors were also prepared. Validation results revealed the strength and effectiveness of the proposed method for detecting and predicting the potential for disease risk assessment in India. The results of this study may be appropriate for the associated agencies to carry out a comprehensive assessment of the spread of the virus and environmental control in the study area. In addition, the method not only prohibits the predictive mapping of satisfactory zones for different parts of the country, but also permits the demonstration of the level of uncertainty in the forecast that could be directly applicable to other countries with associated distance and density characteristics.

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ABBREVIATIONS

2019-nCoV: Novel Coronavirus-2019; **ACE2:** Angiotensin-Converting Enzyme 2; **COVID-19:** Coronavirus Disease-2019; **CSG:** Coronavirus Study Group; **GIS:** Geographic Information System; **HCoV:** Human Coronavirus; **IDW:** Inverse Distance Weighting; **MERS-CoV:** Middle East Respiratory Syndrome Coronavirus; **SARS-CoV-2:** Severe Acute Respiratory Syndrome Coronavirus-2; **UT:** Union Territory; **WHO:** World Health Organization.

CONFLICT OF INTEREST

The authors declare that they have no conflict of interest.

REFERENCES

Balamurugan, P., Kumar, P. S. and Shankar, K., 2020. Dataset on the suitability of groundwater for drinking and irrigation purposes in the Sarabanga River region,

- Tamil Nadu, India, Data in brief, 29,105255. DOI: <https://doi.org/10.1016/j.dib.2020.105255>
- Banerjee, A., Kulcsar, K., Misra, V., Frieman, M. and Mossman, K., 2019. Bats and Coronaviruses. *Viruses*, 11(1), 41. DOI: <https://doi.org/10.3390/v11010041>
- Bartier, P. M. and Keller, C. P., 1996. Multivariate interpolation to incorporate thematic surface data using inverse distance weighting (IDW). *Computers and Geosciences*, 22(7), 795-799. DOI: [https://doi.org/10.1016/0098-3004\(96\)00021-0](https://doi.org/10.1016/0098-3004(96)00021-0)
- Chan, J. F., Yuan, S., Kok, K. H., To, K. K., Chu, H., Yang, J., Xing, F., Liu, J., Yip, C. C.-Y., Poon, R.W.-S., Tsoi, H.W., Lo, S. K.-F., Chan, K.H., Poon, V. K.-M., Chan, W.-M., Ip, J.D., Cai, J.P., Cheng, V.C.-C., Chen, H., Hui, C. K.-M. and Yuen, K. Y., 2020. A familial cluster of pneumonia associated with the 2019 novel coronavirus indicating person-to-person transmission: A study of a family cluster. *Lancet*, 395(10223), 514-23. DOI: [https://doi.org/10.1016/S0140-6736\(20\)30154-9](https://doi.org/10.1016/S0140-6736(20)30154-9)
- Childs, C., 2004. Interpolating surfaces in ArcGIS spatial analyst. *ArcUser*, July-September, 3235, 569.
- Chowell, G., Abdirizak, F., Lee, S., Lee, J., Jung, E., Nishiura, H. and Viboud, C., 2015. Transmission characteristics of MERS and SARS in the healthcare setting: A comparative study. *BMC Med*, 13, 210. DOI: <https://doi.org/10.1186/s12916-015-0450-0>
- Giovanetti, M., Benvenuto, D., Angeletti, S. and Ciccozzi, M., 2020. The first two cases of 2019-nCoV in Italy: Where they come from?, *J. Med Virol*, 92(5), 518-521. DOI: <https://doi.org/10.1002/jmv.25699>
- Guan, W. J., Ni, Z. Y., Hu, Y., Liang, W. H., Ou, C. Q., He, J. X., Liu, L., Shan, H., Lei, C.-L., Hui, D. S. C., Du, B., Li, L. -J., Zeng, G., Yuen, K.-Y., Chen, R., Tang, C., Wang, T., Chen, P., Xiang, J., Li, S., Wang, J., Liang, Z., Peng, Y., Wei, L., Liu, Y., Hu, Y., Peng, P., Wang, J., Liu, J., Chen, Z., Li, G., Zheng, Z., Qiu, S., Luo, J., Ye, C., Zhu, S., and Zhong, N., 2020. Clinical characteristics of coronavirus disease 2019 in China. *N Engl J Med*, 1-13. DOI: <https://doi.org/10.1056/NEJMoa2002032>
- Guan, X. and Wu, H., 2008. Parallel optimization of IDW interpolation algorithm on multicore platform. *Geoinformatics 2008 and Joint Conference on GIS and Built Environment: Advanced Spatial Data Models and Analyses*, 2008. *International Society for Optics and Photonics*, 71461Y. DOI: <https://doi.org/10.1117/12.813163>
- Guo, Y. R., Cao, Q. D., Hong, Z. S., Tan, Y. Y., Chen, S. D., Jin, H. J., Tan, K. S., Wang, D. Y. and Yan, Y., 2020. The origin, transmission and clinical therapies on coronavirus disease 2019 (COVID-19) outbreak - An update on the status. *Military Medical Research*, 7(1), 11. DOI: <https://doi.org/10.1186/s40779-020-00240-0>
- Hampton, T., 2005. Bats may be SARS reservoir. *JAMA*, 294(18), 2291. DOI: <https://doi.org/10.1001/jama.294.18.2291>
- Huang, F., Liu, D., Tan, X., Wang, J., Chen, Y. and He, B., 2011. Explorations of the implementation of a parallel IDW interpolation algorithm in a Linux cluster-based parallel GIS. *Computers and Geosciences*, 37(4), 426-434. DOI: <https://doi.org/10.1016/j.cageo.2010.05.024>
- Kandwal, R., Garg, P. K. and Garg, R. D., 2009. Health GIS and HIV/AIDS studies: Perspective and retrospective.

- Journal of biomedical informatics*. 42(4),748-55. DOI: <https://doi.org/10.1016/j.jbi.2009.04.008>
- Kang, C. K, Song, K. H, Choe, P. G, Park, W. B, Bang, J. H, Kim, E. S, Park, S. W., Kim, H. B., Kim, N. J., Cho, S., Lee, J.-K., and Oh, M., 2017. Clinical and epidemiologic characteristics of spreaders of middle east respiratory syndrome coronavirus during the 2015 outbreak in Korea. *J Korean Med Sci*. 32(5), 744-9. DOI: <https://doi.org/10.3346/jkms.2017.32.5.744>
- Kawo, N. S. and Shankar, K., 2018. Groundwater quality assessment using water quality index and GIS technique in Modjo River Basin, Central Ethiopia. *Journal of African Earth Sciences*, 147, 300-311. DOI: <https://doi.org/10.1016/j.jafrearsci.2018.06.034>
- Li, W., Shi, Z., Yu, M., Ren, W., Smith, C., Epstein, J. H., Wang, H., Cramer, G., Hu, Z., Zhang, H., Zhang, J., McEachern, J., Field, H., Daszak, P., Eaton, B., T., Zhang, S. and Wang, L.-F., 2005. Bats are natural reservoirs of SARS-like coronaviruses. *Science*. 310(5748), 676-9. DOI: <https://doi.org/10.1126/science.1118391>
- Liu, Y., Gayle, A. A., Wilder-Smith, A. and Rocklöv, J., 2020. The reproductive number of COVID-19 is higher compared to SARS coronavirus. *J Travel Med*. 27(2), taaa021. DOI: <https://doi.org/10.1093/jtm/taaa021>
- Liu, Z., Xiao, X., Wei, X., Li, J., Yang, J., Tan, H., Zhu, J., Zhang Q., Wu, J. and Liu, L., 2020. Composition and divergence of coronavirus spike proteins and host ACE2 receptors predict potential intermediate hosts of SARS-CoV-2. *Journal of Travel Medicine*, 1-4. DOI: <https://doi.org/10.1002/jmv.25726>
- Lu, R., Zhao, X., Li, J., Niu, P., Yang, B., Wu, H., Wang, W., Song, H., Huang, B., Zhu, N., Bi, Y., Ma, X., Zhan, F., Wang, L., Hu, T., Zhou, H., Hu, Z., Zhou, W., Zhao, L., Chen, J., Meng, Y., Wang, J., Lin, Y., Yuan, J., Xie, Z., Ma, J., Liu, W. J., Wang, D., Xu, W., Holmes, E. C., Gao, G. F., Wu, G., Chen, W., Shi, W. and Tan, W., 2020. Genomic characterisation and epidemiology of 2019 novel coronavirus: Implications for virus origins and receptor binding. *Lancet*, 395 (10224), 565-74. DOI: [https://doi.org/10.1016/S0140-6736\(20\)30251-8](https://doi.org/10.1016/S0140-6736(20)30251-8)
- Lysean, A.K., Nohr, C., Sorensen, E.M., Gudes, O., Geraghty, E.M., Shaw, N.T. and Bivona-Tellez, C., 2014. A review and framework for categorizing current research and development in health related Geographical Information Systems (GIS) studies. *Yearb Med Inform*. 9, 110-24. DOI: <https://doi.org/10.15265/TY-2014-0008>
- Paraskevis, D., Kostaki, E. G., Magiorkinis, G., Panayiotakopoulos, G., Sourvinos, G. and Tsiodras, S., 2020. Full-genome evolutionary analysis of the novel corona virus (2019-nCoV) rejects the hypothesis of emergence as a result of a recent recombination event. *Infect Genet Evol*. 79, 104212. DOI: <https://doi.org/10.1016/j.meegid.2020.104212>
- Riou, J. and Althaus, C.L., 2020. Pattern of early human-to-human transmission of Wuhan 2019 novel coronavirus (2019-nCoV), December 2019 to January 2020. *Euro Surveill*. 25(4), 2000058. DOI: <https://doi.org/10.2807/1560-7917.ES.2020.25.4.2000058>
- Shankar, K. and Kawo, N. S., 2019. Groundwater quality assessment using geospatial techniques and WQI in North East of Adama Town, Oromia Region, Ethiopia. *Hydrospatial Analysis*, 3(1), 22-36. DOI: <https://doi.org/10.21523/gcj3.19030103>
- WHO [World Health Organization], 2020. Coronavirus disease (COVID-2019) situation reports. Accessed 5 Mar 2020.
- Wu, F., Zhao, S., Yu, B., Chen, Y.M., Wang, W., Song, Z.G., Hu, Y., Tao, Z.-W., Tian, J. H., Pei, Y.-Y., Yuan, M. L., Zhang, Y. L., Dai, F.-H., Liu, Y., Wang, Q.-M., Zheng, J.-J., Xu, L., Holmes, E. C. and Zhang, Y.-Z., 2020. A new coronavirus associated with human respiratory disease in China. *Nature*. 579, 265-269. DOI: <https://doi.org/10.1038/s41586-020-2008-3>
- Yin, Y. and Wunderink, R. G., 2018. MERS, SARS and other coronaviruses as causes of pneumonia. *Respirology*. 2018; 23(2), 130-7. DOI: <https://doi.org/10.1111/resp.13196>
- Zhou, P., Yang, X.L., Wang, X.G., Hu, B., Zhang, L., Zhang, W., Si, H., Zhu, Y., Li, B., Huang, C.-L., Chen, H.-D., Chen, J., Luo, Y., Guo, H., Jiang, R.-D., Liu, M. Q., Chen, Y., Shen, X.-R., Wang, X., Zheng, X.-S., Zhao, K., Chen, Q.-J., Deng, F., Liu, L.-L., Yan, B., Zhan, F.-X., Wang, Y.-Y., Xiao, G.-F., and Shi, Z. -L., 2020. A pneumonia outbreak associated with a new coronavirus of probable bat origin. *Nature*. 579, 270-273. DOI: <https://doi.org/10.1038/s41586-020-2012-7>
- Zhu, N., Zhang, D., Wang, W., Li, X., Yang, B., Song, J., Zhao, X., Huang, B., Shi, W., Lu, R., Niu, P., Zhan, F., Ma, X., Wang, D., Xu, W., Wu, G., Gao, G. F. and Tan, W., 2020. A novel coronavirus from patients with pneumonia in China, 2019. *N Engl J Med*. 382(8), 727-33. DOI: <https://doi.org/10.1056/NEJMoa2001017>
