ORIGINAL RESEARCH

# Whether County Lockdown Could Deter the Contagion of COVID-19 in the USA

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School of Mathematics and Statistics, Baise University, Baise Clty, Guangxi Province, People's Republic of China **Aim:** Whether to lock down a country or not during COVID-19 pandemic becomes a vital issue, since it affects people's daily life. The objective of this research is to design a measurement that could be utilised to predict the efficacy of a lockdown decision.

**Methods:** One would expect that the effectiveness of lockdown lies in the assumption that the virus spreads from one area to another area in a rippling way. If the virus spreads in a radiating way, then lockdown should be an effective countermeasure to contain the pandemic. On the other hand, if it spreads indiscernibly or randomly, then a lockdown decision would have lesser or little effect on the containment. We mainly combine graphs and metric to compute correlation matrices, which would measure whether the virus spreads in a rippling way. The metric used is to measure the boundary (or county) distances between counties. We take 3073 counties and equivalents in the USA and explore the property of contagion with respect to distance. The distance between any two counties is measured by the number of neighbours (or counties) between them. Then, we study the relation between contagion and distances. The relation between distance (complexity of neighbouring) and confirmed cases (contagion) is further explored.

**Results:** Then, we study the relation between contagion and distances. The relation between distance (complexity of neighbouring) and confirmed cases (contagion) could be explored. Our research shows county lockdown in the USA plays no important role in containing the spread of coronavirus for the time being.

**Conclusion:** Rippling effect in the USA regarding COVID-19 is not significant. This indicates other robust approaches or policies should be taken into consideration, rather than a simple lockdown policy.

Keywords: COVID-19, transport, lockdown, neighbouring, graph, minimal distance

### Introduction

Since the COVID-19 pandemic has caused a lot of deaths, tracking the contagion and containing the spread has become an important global issue. The pandemic affects all sorts of people, regardless of their ages.<sup>1</sup> The transmissibility and severity of the pandemic have also caused a huge concern about risk management,<sup>2</sup> since the strength of the healthcare system would be put into its ultimate test.<sup>3</sup> Many countries have adopted preventive measures or containing approaches to combat such pandemic – among them, lockdown probably is the measure taken the most despite its controversy. Lockdown would bring some psychological issues,<sup>4</sup> educational problems,<sup>5</sup> and so on,<sup>6</sup> despite the fact that other alternatives are also adopted.<sup>7–9</sup> Decisions of lockdown might

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© 2021 Chen. This work is published and licensed by Dove Medical Press Limited. The full terms of this license are available at https://www.dovepress.com/terms.php and hereby accept the Terms. Non-commercial uses of the work are permitted without any further permission from Dove Medical Press Limited, provided the work is properly attributed. For permission for commercial use of this work, please see paragraphs 4.2 and 5 of our Terms (http://www.dovepress.com/terms.php). affect the trajectory of contagion of COVID-19.12,13 Though some claim they are very effective,<sup>14</sup> some regard them controversial.<sup>15</sup> Henceforth, some systematic approaches and models are applied in studying the effect of lockdown.<sup>10,11</sup> In addition to some criteria for lockdown decision,<sup>16</sup> one also needs to consider the timing of lockdown.<sup>17</sup> Too early lift of the lockdown might cause a second wave of pandemic, while a delayed one might further deteriorate the economy and normal daily life. In order to evaluate a lockdown decision, one needs to delve into the spreading mechanisms of COVID-19. If it spreads in a pattern that ripples from areas to their neighbouring areas, then one could expect that a lockdown might deter the rippling spread and contain the virus; if not, then one could also anticipate that a lockdown decision would produce little effect on the containment. Such rippling effect is witnessed by studying the spreading behaviours between all the bordering areas. The main objective of this paper is to study the property of such spread in the USA during some period of time.<sup>18</sup> We study 3073 Counties and Equivalents in the USA to understand whether lockdown in the county scale is an effective approach for the time being. We devise a systematic mechanism to answer this question by combining the graph theory and metric, in particular the minimal distances between nodes, in one framework. The Counties are identified with nodes (or vertices) of a network (or tree). The number of neighbours from one county to another is associated with the edges. Then a metric of minimal edge is applied to calculate the distance between two counties. This distance will reveal the number of bordered counties between any two counties - the higher the value, the more the bordered counties between the two given counties. The basic idea is if a county has more bordered counties, then it would have higher contacting rate of the virus – if the rippling effect really presents. We will trace the relation between contagion and distance to identify whether the rippling effect really exists in the USA. Henceforth, the values of distances will serve our independent variables. Then we measure the similarity of evolution (from a period of 169 days) between counties via correlation matrix. These values will serve our dependent variable. The relation between distance (complexity of neighbouring) and confirmed cases (contagion) could be explored. Our research shows there is little rippling effect of COVID-19 between neighbouring counties in the USA. This result shall reach a conclusion that a county lockdown decision in the USA plays no important role in containing the spread of coronavirus for the time being. This result also

echoes other research of invalidity of lockdown in western European countries.<sup>19</sup>

### **Methods**

### **Basic Settings**

Let G = (N, E) be an undirected graph, where N is a set of nodes (or vertices) and E is a set of edges. Let  $n \in N$  be arbitrary. If n = k, then no edge is assumed. Let Ch(p, q)denote all the paths (or chains) connecting nodes p and q in G. Let  $l_1 * l_2$  denote the concatenation (a new path) of path  $l_1$  and path  $l_2$ . Let  $|l_1|$  denote the length of the path  $l_1$ . For a path P, we use  $P_{end}$  to denote its endpoints.

**Definition 2.1.** (fix neighbours) Let  $B_{=k}$  (n) denote the set of all the nodes m, in which there are exactly k edges lying between n and m, ie,

 $B_{=k}(n) := \{m \in N: \exists P \in Ch(n, m) \text{ s.t. } |P| = k, P_{end} = \{n, m\}\}.$ 

Observe that 
$$B_{=0}(n) = \{n\}$$
 and  $B_{=k+1}(n) = \bigcup_{m \in B_k(n)} B_{=1}(m)$ 

**Definition 2.2.** Let  $B_{\leq k}$  (*n*) denote the set of all the nodes *m*, in which there are at most *k* edges lying between *n* and *m*, ie,

 $B_{\leq k}(n) := \{ m \in N : \exists P \in Ch(n, m) \text{ s.t. } |P| \leq k, P_{end} = \{ n, m \} \}.$ 

**Definition 2.3.** (minimal nodes with length k) Let  $B_k^*(n)$  denote the set of all the nodes m, in which there are exactly k edges lying between n and m and there is no path with length less than k that could serve a path between n and m, ie,  $B_k^*(n) := \{m \in N: \exists P \in Ch (n, m) \text{ s.t. } |P| = k, P_{end} = \{n, m\}, Ch(n, m) \cap \prod_{\leq k-1}(n) = \emptyset\}$ ,

where  $\Pi_{k-1}(n)$  is the set of all the paths whose initial node is n and whose length is k - 1.

Observe that  $B_k^*(n) \cap B_h^*(n) = \emptyset$ , but in general  $B_{=k}(n) \cap B_{=h}(n) = \emptyset$  does not hold, if  $k \neq h$  for all  $k, h \leq |l^*(n)|$ .

**Definition 2.4.** (accumulated minimal nodes with length k) Define

$$\Im_k^*(n) := \bigcup_{i=1}^k B_i^*(n)$$

Observe that  $\Im_k^*(n) = B_{\leq k}(n)$ .

**Claim 1.** (characterization) For any given  $n \in N$ , the node set *N* could be partitioned via the following inductive procedures:

Proof. It follows immediately from the definitions.

**Definition 2.5.** (chain distance) Let  $p, q \in N$  be arbitrary. Define  $\delta(q, p)$  the minimal length of all the paths between p and q, ie,  $\delta(p, q) = \min\{l: l \in Ch(p, q)\}$ .

**Claim 2.** (distance function)  $\delta$  is a distance function on *G*.

Proof. Since no edge is assumed for a node to itself, it suffices to show the triangle property. Let  $p, q, r \in N$  be arbitrary. Let  $l_1$  be a minimal path in Ch(p, q) and  $l_2$  be a minimal path in Ch(q, r). Then  $l_1 * l_2 \in Ch(q, r)$ , ie,  $\delta(p, q) + \delta(q, r) = |l_1| + |l_2| \ge d(p, r)$ .

**Example 1.** Suppose a geographical structure is shown in Figure 1. Then we could compute some results as listed in Table 1.

The minimal path might not be unique. As the nodes and the complexity of the geographical structures increase, one needs to devise a systematic approach to compute the values of  $\delta$ .

### Reachability Operators

Let  $BIN_k$  denote the set of all the binary vectors whose length are k. Let

Table I Comparison for Algorithms Partitioning

$B_{=0}(C_4) = B_{=0}^*(C_4) = \Im_{=0}^*(C_4)$	{C <sub>4</sub> }
$B_1(C_4) = \bigcup \{ B_{=1}(m) : m \in B_{=0}^*(C_4) \}$	{ <i>C</i> <sub>3</sub> , <i>C</i> <sub>7</sub> }
$B_{=1}^*(C_4) = B_{=1}(C_4) - \mathfrak{T}_{=0}(C_4)$	{ <i>C</i> <sub>3</sub> , <i>C</i> <sub>7</sub> }
$\Im_1^*(C_4) = \Im_0^*(C_4) \cup B_{=1}^*(C_4)$	$\{C_3, C_4, C_7\}$
$B_{=2}(C_4) = \cup \{B_{=1}(m) : m \in B_{=1}^*(C_4)\}$	$\{C_1, C_3, C_4, C_5, C_7, C_8, C_{10}\}$
$B_{=2}^*(C_4) = B_{=2}(C_4) - \Im_{=1}(C_4)$	$\{C_1, C_5, C_8, C_{10}\}$
$\Im_2^*(C_4) = \Im_1^*(C_4) \cup B_{=2}^*(C_4)$	$\{C_1, C_3, C_4, C_5, C_7, C_8, C_{10}\}$
$B_{=3}(C_4)$	$(C_1, C_2, C_3, C_5, C_6, C_7, C_8, C_9, C_{10}, C_{11})$
$B_{=3}^*(C_4) = B_{=3}(C_4) - \mathfrak{T}_2(C_4)$	$\{C_2, C_6, C_9, C_{11}\}$
$\Im_3^*(C_4) = \Im_2^*(C_4) \cup B_{=3}^*(C_4)$	{C <sub>1</sub> , C <sub>2</sub> , C <sub>3</sub> , C <sub>4</sub> , C <sub>5</sub> , C <sub>6</sub> , C <sub>7</sub> , C <sub>8</sub> , C <sub>9</sub> , C <sub>10</sub> , C <sub>11</sub> }

 $\vec{u} = (a_1, a_2, \dots, a_k), \vec{v} = (b_1, b_2, \dots, b_k) \in BIN_K$  be arbitrary.

Definition 2.6. (And Operator) Define

 $\vec{u} \wedge \vec{v} := (\min\{a_1, b_1\}, \min\{a_2, b_2\}, \cdots, \min\{a_k, b_k\}).$ 

Definition 2.7. (Or Operator) Define



Figure I A geographical structure: neighbouring.

$$\vec{u} \lor \vec{v} := (max\{a_1, b_1\}, max\{a_2, b_2\}, \cdots, max\{a_k, b_k\}).$$

**Definition 2.8.** (Negative Operator) Define  $-\vec{u} := (1 - a_1, 1 - a_2, \dots, 1 - a_n)$ .

We use the notation  $\vec{U} - \vec{V}$  to denote the binary vector  $\vec{U} + (-\vec{V})$ . Now we devise an algorithm to fast implement Claim 1.

- 1. Label *N* by  $N = (n_1, n_2, \dots, n_{|N|})$  (or simply  $N = (1, 2, \dots, |N|)$ ).
- Convert a geographical structure into an adjacency matrix with a cell value 1 if the two nodes are connected directly and 0 if not; the reachability of a node itself is declared to be 0; define n ∈ BIN<sub>|N|</sub> (or) B<sub>=1</sub>(n) to implement B<sub>=1</sub>(n).
- 3.  $\vec{B}_{=0}(n) = \vec{B}_{=0}^*(n) = \Im_{=0}^*(n) = (0, 0, \dots, 0, 1, 0, \dots, 0)$  where 1 appears in the labelled-n element
- 4.  $\vec{B}_{=k+1}(n) = \bigvee_{m \in \overrightarrow{B}_{=k}(n)} \vec{B}_{=1}(m)$ , where  $m \in \overrightarrow{B}_{=k}(n)$  denotes all the nodes corresponding to the values 1 in the vector;

5. 
$$\vec{B}_{=k+1}^{*}(n) = \vec{B}_{=k+1}(n) - \vec{\Im}_{=k}^{*}(n);$$
  
6.  $\vec{\Im}_{=k+1}^{*}(n) = \vec{\Im}_{k}^{*}(n) \lor \vec{B}_{=k+1}^{*}(n);$ 

**Example 2.** This geographical structure could be converted into an adjacency matrix by setting  $N = \{C_1, C_2, \dots, C_{11}\}$  and *E* be specified by the immediate successors as shown in *Figure 2*.

Hence, we have  $[0]_{C4} = \{C_4\}, [1]_{C4} = \{C_3, C_7\}, [2]_{C4} = \{C_1, C_5, C_8, C_{11}\}, [3]_{C4} = \{C_2, C_6, C_9, C_{11}\}.$ 

Furthermore, we have  $\vec{B}_{=0}(n) = \vec{B}_{=0}^*(n) = \vec{\mathfrak{S}}_{=0}^*(n) = (0, 0, 0, 1, 0, 0, 0, 0, 0, 0)$  and  $\vec{B}_{=1}(C_4) = (0, 0, 1, 0, 0, 0, 0, 1, 0, 0, 0, 0, 0, 0, 0, 0, 0)$  and  $\vec{B}_{=1}(C_4) = \vec{\mathfrak{S}}_{=0}^*(n) = (0, 0, 1, 0, 0, 0, 0, 1, 0, 0, 0, 0);$  by the same token  $\vec{B}_{=2}(C_4) = \vec{B}_{=1}(C_3) \lor \vec{B}_{=1}(C_7) = (1, 0, 0, 1, 1, 0, 1, 0, 0, 0, 0) \lor (0, 0, 1, 1, 1, 0, 0, 1, 0, 1, 0) = (1, 0, 1, 1, 1, 0, 1, 1, 0, 1, 0), \vec{B}_{=2}^*(C_4) = \vec{B}_{=2}(C_4) - \vec{\mathfrak{S}}_{=1}^*(C_4) = (1, 0, 1, 1, 1, 0, 1, 1, 0, 1, 0) - (0, 0, 1, 0, 0, 0, 1, 0, 0, 0, 0) = (1, 0, 0, 1, 1, 0, 0, 1, 0, 1, 0).$ 

Though convenient to perform computations based on this, it consumes too much memory and computational resources. We use the first characterization to implement our algorithms. For any vector  $\vec{v}$ , we use  $\vec{v}(j)$  to denote its jth element. We use  $||\vec{v}||_E$  to denote its Euclidean norm. Let  $\{\alpha_j: 1 \le j \le n\}$  be a set of positive real numbers.

	$C_1$	$C_2$	$C_3$	$C_4$	$C_5$	$C_6$	$C_7$	$C_8$	$C_9$	$C_{10}$	$C_{11}$
$C_1$	(0	1	1	0	1	1	0	0	0	0	0)
$C_2$	1	0	0	0	0	1	0	0	0	0	0
$C_3$	1	0	0	1	1	0	1	0	0	0	0
$C_4$	0	0	1	0	0	0	1	0	0	0	0
$C_5$	1	0	1	0	0	1	1	1	0	0	0
$C_6$	1	1	0	0	1	0	0	1	1	0	1
$C_7$	0	0	1	1	1	0	0	1	0	1	0
$C_8$	0	0	0	0	1	1	1	0	1	1	1
$C_9$	0	0	0	0	0	1	0	1	0	0	1
$C_{10}$	0	0	0	0	0	0	1	1	0	0	1
$C_{11}$	0	0	0	0	0	1	0	1	1	1	0 /

Figure 2 Adjacency matrix.

# **Results** Data Analysis

We use R program 4.0 version to help us implement the procedures in this section.

# Procedures

In this section, we list the procedures based on the basic settings in Section 2. These procedures would help us detect whether a rippling effect exists between neighbouring counties in the USA or not.

- 1. After downloading and compiling the files, we use DT for the 3073 counties and their neighbouring Counties and COV ID to read data from the confirmed cases from January 12 until July 8 (or 169 days in total) for the 3073 Counties. The read results are presented in Table 2.
- 2. Then we rename and label the 3073 fips (Counties) by number 1 to 3073. An explicit way of labelling for the confirmed cases could

Table 2 Raw Data DT: Neighbouring Counties

be found in Table 3. Similarly, the renaming of DT., which is implicitly associated in a matrix RDT, is not presented here.

- 3. Based on RDT, we start to calculate the distance matrix DIS, whose size is 3073 by 3073. The calculation of the distance matrices comes directly from Section 2; the resulting distance matrix is presented in Table 4. The values of distance matrix will serve the range of our independent variable.
- 4. Compute the first order and second order of COVID, respectively, to obtain the net increase (decrease). Both are presented in Table 5, where the upper one represents the first order via Matrix SCOVID; the lower one represents the second order via matrix SSCOVID. One observes that the cell value 0.001 indeed is used to replace the original 0 to avoid the computational problems;
- 5. Based on Table 5, we could compute the correlation matrix for all the counties and the

Ct.	Nb.	Ct.	Nb.	 Ct.	Nb.	Ct.	Nb.
1001	1001	1003	1003	 55,117	26,105	55,119	55,017
1001	1021	1003	1025	 55,117	26,127	55,119	55,019
1001	1047	1003	1053	 55,117	55,015	55,119	55,069
1001	1051	1003	1097	 55,117	55,039	55,119	55,073
1001	1085	1003	1099	 55,117	55,071	55,119	55,099
1001	1101	1003	1129	 55,117	55,089	55,119	55,107
		1003	12,033	 55,117	55,117	55,119	55,119

Label	Fips	I	2	3	4	 166	167	168	169
1	1001	0	0	0	0	 615	618	644	651
2	1003	0	0	0	0	 881	911	997	1056
3	1005	0	0	0	0	 352	356	360	366
4	1007	0	0	0	0	 193	197	199	201
3070	55,113	0	0	0	0	 12	12	13	14
3071	55,115	0	0	0	0	 86	86	86	87
3072	55,117	0	0	0	0	 229	236	245	255
3073	55,119	0	0	0	0	 15	15	16	17

County	I	2	3	•••	3071	3072	3073
I	0	4	3		32	31	33
2	4	0	5		32	31	33
3	3	5	0		35	34	36
3071	32	32	35		0	3	2
3072	31	31	34		3	0	5
3073	33	33	36	• • •	2	5	0

results are presented in Table 6 (or Matrix

CORRE); the upper part represents the correlation matrix for SCOVID, and the low one repre-

sents the correlation matrix for SSCOVID. These

values serve the range of our dependent

6. Based on DIS and CORRE, we could plot the

7. Based on the plot, we could decide whether to

further apply statistical techniques or not.

graphs as shown in Figure 3.

Table 4	Distance	Matrix	for	Counties
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variables.

# Implementation: Preliminary

The downloaded neighbouring information for the counties is presented in Table 2, in which "Ct." stands for County; "Nb." stands for Neighbouring Counties; and the cell values are the fips (Federal Information Processing Standards) for the Counties in the USA. In order to facilitate numerical computation, we rename the 3073 Counties names by the number 1 to 3073. The distance matrix is listed in Table 4.

# Implementation: Distance Matrix

For the confirmed cases of COVID-19, we extract data from date January 22 to July 8 (169 days in total). The raw data are presented in Table 4.

## Implementation: First and Second Order

Here we compute the first order and second order of COVID-19, respectively, to obtain its net increase (decrease). The results are presented in Table 5.

### Implementation: Correlation

By Table 5, we compute the correlation matrix for all the Counties as shown in Table 6. We could

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			1				1		
Label	Ι	2	3	4		165	166	167	168
I	0.001	0.001	0.001	0.001		24	3	26	7
2	0.001	0.001	0.001	0.001		18	30	86	59
3	0.001	0.001	0.001	0.001		2	4	4	6
4	0.001	0.001	0.001	0.001		3	4	2	2
3070	0.001	0.001	0.001	0.001		0.001	0.001	I.	I.
3071	0.001	0.001	0.001	0.001		3	0.001	0.001	I
3072	0.001	0.001	0.001	0.001		5	7	9	10
3073	0.001	0.001	0.001	0.001		0.001	0.001	I	I
Label	I	2	3	4	• • •	164	165	166	167
Label	<b>I</b> 0.001	<b>2</b> 0.001	<b>3</b> 0.001	<b>4</b> 0.001		<b>164</b>	<b>165</b> -21	<b>166</b> 23	<b>167</b> 19
Label I 2	I 0.001 0.001	2 0.001 0.001	<b>3</b> 0.001 0.001	<b>4</b> 0.001 0.001	· · · · · · ·	164 I 0.001	165 21 12	166 23 56	<b>167</b> -19 -27
Label 1 2 3	I 0.001 0.001 0.001	2 0.001 0.001 0.001	<b>3</b> 0.001 0.001 0.001	<b>4</b> 0.001 0.001 0.001	•••• ••• •••	164 I 0.001 0.001	165 21 12 2	166 23 56 0.001	167 -19 -27 2
Label 1 2 3 4	I 0.001 0.001 0.001 0.001	2 0.001 0.001 0.001 0.001	3 0.001 0.001 0.001 0.001	4 0.001 0.001 0.001 0.001	···· ···· ···	164 I 0.001 0.001 2	165 21 12 2 1	166 23 56 0.001 -2	167 -19 -27 2 0.001
Label 1 2 3 4 	I 0.001 0.001 0.001 0.001 	2 0.001 0.001 0.001 0.001 	3 0.001 0.001 0.001 0.001 	4 0.001 0.001 0.001 0.001 	· · · · · · · · · · · ·	164 I 0.001 0.001 2 	165 -21 12 2 1 	166 23 56 0.001 -2 	167 -19 -27 2 0.001 
Label 1 2 3 4  3070	I 0.001 0.001 0.001 0.001  0.001	2 0.001 0.001 0.001 0.001  0.001	3 0.001 0.001 0.001 0.001  0.001	4 0.001 0.001 0.001 0.001  0.001	· · · · · · · · · · · · · · ·	164 I 0.001 0.001 2  0.001	165 -21 12 2 1  0.001	166 23 56 0.001 -2  0.999	167 19 27 2 0.001  0.001
Label  1 2 3 4 3070 3071	I 0.001 0.001 0.001 0.001  0.001 0.001	2 0.001 0.001 0.001 0.001  0.001 0.001	3 0.001 0.001 0.001 0.001  0.001 0.001	4 0.001 0.001 0.001 0.001  0.001 0.001	···· ···· ···· ···	164 I 0.001 0.001 2  0.001 I	165 -21 12 2 1  0.001 -2.999	166 23 56 0.001 -2  0.999 0.001	167 -19 -27 2 0.001  0.001 0.999
Label  1 2 3 4 3070 3071 3072	I 0.001 0.001 0.001 0.001  0.001 0.001 0.001	2 0.001 0.001 0.001 0.001 0.001 0.001 0.001	3 0.001 0.001 0.001 0.001  0.001 0.001 0.001	4 0.001 0.001 0.001 0.001  0.001 0.001 0.001	· · · · · · · · · · · · · · ·	164 I 0.001 0.001 2  0.001 I 4	165 -21 12 2 1  0.001 -2.999 2	166 23 56 0.001 -2  0.999 0.001 2	167 19 27 2 0.001  0.001 0.999 1

Label	I	2	3	4	•••	3070	3071	3072	3073
1	1.00	0.61	0.71	0.63		0.30	0.57	0.63	0.52
2	0.61	1.00	0.55	0.66		0.29	0.37	0.64	0.53
3	0.71	0.55	1.00	0.72		0.26	0.59	0.62	0.44
4	0.63	0.66	0.72	1.00		0.23	0.45	0.61	0.56
3070	0.30	0.29	0.26	0.23		1.00	0.28	0.22	0.23
3071	0.57	0.37	0.59	0.45		0.28	1.00	0.45	0.22
3072	0.63	0.64	0.62	0.61		0.22	0.45	1.00	0.39
3073	0.52	0.53	0.44	0.56		0.23	0.22	0.39	1.00
Label	I	2	3	4	•••	3070	3071	3072	3073
1	1.00	0.16	0.06	-0.22		0.18	0.17	-0.08	0.05
2	0.16	1.00	0.24	0.37		0.06	0.03	0.19	0.19
3	0.06	0.24	1.00	0.24		012	0.15	0.10	-0.01
		0.21	1.00	0.24		-0.13	0.15	0.19	0.01
4	-0.22	0.37	0.24	1.00		-0.13 -0.17	0.13	0.19	0.24
4	-0.22 	0.37	0.24	1.00		-0.13 -0.17 	0.13	0.19	0.24
4  3070	-0.22  0.18	0.37	0.24  -0.13	1.00  -0.17	· · · · · · ·	-0.13 -0.17  1.00	0.10	0.19 0.20  -0.02	0.24  0.10
4  3070 3071	-0.22  0.18 0.17	0.37  0.06 0.03	0.24  -0.13 0.15	0.24 1.00  -0.17 0.10	· · · · · · ·	-0.13 -0.17  1.00 0.13	0.13 0.10  0.13 1.00	0.19 0.20  -0.02 0.08	0.24  0.10 -0.05
4  3070 3071 3072	-0.22  0.18 0.17 -0.08	0.37  0.06 0.03 0.19	0.24  -0.13 0.15 0.19	0.24 1.00  -0.17 0.10 0.20	· · · · · · · · · ·	-0.13 -0.17  1.00 0.13 -0.02	0.13 0.10  0.13 1.00 0.08	0.19 0.20  -0.02 0.08 1.00	0.01 0.24  0.10 -0.05 -0.15

Table 6 Correlation for SCOVID and SSCOVID

further visualise the correlations against distances in Figure 3. In this figure, one could easily observe that the physical distance and correlation do not form a recognisable pattern and are very divergent in forming a relation. This also indicates there is no clear rippling effect between the counties.

# Conclusion

Lockdown is a controversial global issue. It always has advantages and disadvantages among all sorts of research or policies. The essential part of lockdown or not depends on the effectiveness of such measure – which in turn relies on the rippling spread of the virus. In this article, we sample county data in the USA for a period of time and utilise our minimal metric, which takes the number of bordered counties into consideration, to study the relation between the contagion of COVID-19 and the distances. Our result shows that the spread of virus in the USA is not related to the rippling type of spreading. To some degree, this indicates a lockdown in county scales would not be an effective containing approach at this stage. This shall shed some light on how to effectively adopt other methods to deter the contagion of this virus. There are some limitations, shortcomings and future work. Firstly, we do not take the gender, age, etc., into consideration. Hence, our conclusion only applied to the general public. However, some lockdown policies might benefit some groups from the contagion. Secondly, we do not really tackle the qualitative properties of the lockdown, but only focus on the numeric values. This might be a shortcoming by overlooking the exact content and procedures capsulised in a lockdown policy. Thirdly, this study focuses solely on USA territories. In order to grasp a much comprehensive picture about lockdown policy again contagion of COVID-19, lockdown policies and effect in other countries should also be compared. In this study, we mainly use chain metric as our distance function. Other structural metrics<sup>20</sup> could be also applied in the future work. In addition, if the lockdown policy does not work, one should further explore the underlying reasons for the failure: whether it is people who are reluctant to comply with the rules or whether the viruses are clever enough to detour around the lockdown policies.<sup>21</sup>



Figure 3 SCOVID against Neighbouring Distance.

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### Disclosure

The author declares that there are no conflicts of interest regarding the publication of this paper.

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