

How political choices shaped Covid connectivity: the Italian case study

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1 How political choices shaped Covid connectivity: the
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13 **Abstract**

The importance of implementing new methodologies to study the ever-increasing amount of Covid-19 data is apparent. The aftermath analysis of these data could inform us on how specific political decisions influenced the dynamics of the pandemic outbreak. In this paper we use the Italian outbreak as a case study, to study six different Covid indicators collected in twenty Italian regions. We define a new object, the Covidome, to investigate the network of functional Covid interactions between regions. We analyzed the Italian Covidome over the course of 2020, and found that Covid connectivity between regions follows a sharp North-South community gradient. Furthermore, we explored the Covidome dynamics and individuated differences in regional Covid connectivity between the first and second waves of the pandemic. These differences can be associated to the two different lockdown strategies adopted for the first and the second wave from the Italian government. Finally, we explored to what extent Covid connectivity was associated with the Italian geographical network, and found that Central regions were more tied to the structural constraints than Northern or Southern regions in the spread of the virus. We hope that this approach will be useful in gaining new insights on how political choices shaped Covid dynamics across nations.

14 *Keywords:* Covidome, network science, data analysis, modularity, Dynamic
15 functional connectivity

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16 **Introduction**

17 The Covid-19 pandemic has produced an impressive amount of epidemio-
18 logical data, collected all over the world [1]. Each country collected their data
19 following different protocols depending on its respective national health service.
20 In Italy, with twenty administrative regions independent on Health, Covid-19
21 data were made available at regional and national level through the Italian De-
22 partment of Civil Protection, [2]. The Italian Covid-19 collected data consists of
23 time series or Covid indicators, such as: the number of hospitalized individuals
24 in intensive care units (ICU), hospitalized individuals with symptoms, individu-
25 als in home isolation, new positives, discharged healed and deceased individuals.
26 All of them are available for all twenty Italian regions [2]. In the aftermath of
27 the pandemic, these data provide a benchmark to investigate the effects of two
28 distinct political decisions that were taken during the first and second wave of
29 the Sars-Cov-2 spread, one at the beginning and the other at the end of 2020,
30 respectively [3]. Specifically, the first Italian lockdown was a quite severe na-
31 tionwide lockdown, whereas the second one was region-wide, tailored on each
32 specific regional health situation [4].

33 The first Covid-19 pandemic wave took most countries and their leaders
34 by surprise. The immediate reaction resulted in more severe policy interven-
35 tions such as: travel bans, self-isolation, quarantines and stay-at-home orders;
36 public-gathering and event restrictions; school, restaurant, and non-essential
37 business closures; up to complete lockdowns [5]. The adopted restrictions were
38 different between countries, but also, at a smaller scale, between regions and/or
39 provinces/states. This differentiation eventually led to different results depend-
40 ing on the political decisions made [6]. Apart from improving the current epi-
41 demiological models for the SARS-CoV-2 transmission, researchers also focused
42 on proposing alternative solutions to severe lockdown choices, in view of a po-
43 tential second (and third) wave, [7]-[9] by reducing some restrictions. These
44 "soft lockdown" measures were also adopted by the Italian government, during
45 the second wave of the pandemic.

46 In this work we tap into the link between these policy decisions and the
47 network dynamics of the Sars-Cov-2 spread in Italy. In order to do so, inspired
48 by methodology commonly used in brain network analysis [10], we introduce and
49 analyze the "Covid functional connectome", i.e. the *Covidome*, which is closely
50 related to the covariance matrix of a specific Covid indicator. For instance,
51 two Italian regions that share a similar trend in the number of hospitalized in
52 ICU will have high values in its correspondent Covidome values, and viceversa.
53 In essence, the Covidome provides a summary picture of the pairwise "Covid
54 connectivity" between nodes (the regions) of the Italian network, during the
55 pandemic.

56 We use this representation to explore the Covidome community structure, in
57 order to learn more about the hidden interactions between Italian regions dur-
58 ing the spread of the Covid-19 pandemic [11]-[13]. We found a specific North-
59 South separation in two distinct "Covid functional" community, across almost
60 all Covid indicators. Furthermore, using sliding window analysis, we found that

61 Covid connectivity changed consistently across Northern, Central and Southern
62 Italy, with major differences spiked by the regionwide lockdown for the second
63 wave, on 4th of November 2020, and the more severe first lockdown, on 10th of
64 March 2020. Notably, the measures introduced short before the second differ-
65 entiated lockdown, i.e. the obligation to wear masks in open and closed public
66 spaces (on 13th of October 2020), the closure of major non essential activi-
67 ties (on 24th of October 2020), etc., have led to evident concrete results. In
68 fact, Covid connectivity started decreasing already before the effective date of
69 the second lockdown for all the time series considered, differently from the first
70 lockdown where the correlation values started decreasing after the effective date.
71 Finally, we investigate whether Covidomes related to the structural network of
72 Italy (i.e. its geography). We found that Covid connectivity relates strongly to
73 the structure more to central areas of Italy than to the Northern and Southern
74 regions.

75 We believe that the innovation of analyzing Covid-19 time series as a com-
76 plex structure of networked systems might help in the interpretation of the
77 key political decisions in the aftermath. Currently, the community is missing
78 straightforward methods apt at plugging the data from the tracking systems into
79 mathematical tools [14], which can help in a better understanding of the key
80 political decisions, at different levels of spatial granularity [15]. We hope that
81 this approach will be useful in analyzing epidemiological data in general, and
82 that this study might open up new research avenues able to gain new insights
83 on how political choices can shape pandemic outbreaks.

84 **Materials and methods**

85 In this section we will first introduce the time series (i.e., Covid indica-
86 tors) used for this study, and detail the Italian outbreak and political decisions
87 made to prevent it. Secondly, we will introduce the Covid connectivity matrix
88 ("Covidome") and give an overview of the network approaches employed.

89 *Data and outbreak details*

90 The data used in this paper was collected by the Italian Department of Civil
91 Protection and is freely available on a Github directory [2]. We analyzed differ-
92 ent time series starting from 24 February 2020 until 7 January 2021 (few days
93 after vaccine campaign started). All the considered time series are available for
94 each Italian region. We focused on 6 different Covid indicators, such as: 1)
95 the number of hospitalized individuals in ICU; 2) number of hospitalized indi-
96 viduals with symptoms; 3) number of individuals in home isolation; 4) number
97 of new positives; 5) number of discharged healed; and 6) number of deceased
98 individuals.

99 On February 20, 2020 the first severe patient was tested positive for SARS-
100 Cov-2 at hospital of Codogno, Italy. Since this first episode a rapidly increasing
101 number of patients have been identified, especially in the Northern part of the
102 country. Italy was one of the most affected European country and was the first

103 to implement drastic measures in the attempt to contain the disease. Below we
104 list the most relevant dates for Italy (see [4] for more details):

- 105 – Lockdown of the Northern regions on March 8, 2020, which was followed
106 by complete lockdown of Italy within a few days (10 March), including
107 travel restrictions and a ban on public gatherings.
- 108 – On March 21, the Italian government closed all non-essential businesses
109 and industries, and restricted movement of people unless was strictly nec-
110 essary.
- 111 – On March 31, the president of the Italian National Institute of Health
112 announced that the pandemic had reached its peak in the country, which
113 corresponded to the start of the outbreak plateau. The news was confirmed
114 also by the head of the Civil Protection Department.
- 115 – On April 20, Italy saw the first fall in the number of active cases.
- 116 – Covid-19 cases started to decline in May 2020, thanks to the two-months
117 lockdown. Freedom of movements was re-established on May 4 and other
118 not essential activities re-opened later that month.
- 119 – On October 13 the obligation to wear masks, in both open and closed
120 spaces, returns, and on October 14, cases of Covid-19 positives exceeded
121 the peak of the March infections.
- 122 – On October 18 new restrictions were applied with the possibility of dis-
123 tance learning for both high schools and universities depending on the
124 regional epidemiological situation.
- 125 – On October 24, major non essential activities were closed and distance
126 learning political decisions were reapplied.
- 127 – On November 4, the Italian Prime Minister announced a new lockdown,
128 dividing the country into three zones depending on the severity of the
129 pandemic, corresponding to red, orange and yellow regions. Moreover,
130 a national curfew from 10 PM to 5 AM was implemented, as well as
131 compulsory weekend closing for shopping malls, and online education in
132 high schools.
- 133 – From December 21 to January 6 further movement restrictions were im-
134 plemented in order to prevent an increase in cases during the Christmas
135 holidays period, and to block movement between regions.

136 *Introducing the Covidome*

We here define a "Covid connectivity network" (or *Covidome*). This network consists of 20 nodes, which corresponds to the Italian regions. For each of the six different aforementioned Covid indicators, the edge between region pairs is

defined by its Pearson’s correlation coefficient. Specifically, for two Covid time series X and Y , and n time points, this coefficient is defined as:

$$r_{X,Y} = \frac{\sum_{i=1}^n (x_i - \bar{x})(y_i - \bar{y})}{\sqrt{\sum_{i=1}^n (x_i - \bar{x})^2 \sum_{i=1}^n (y_i - \bar{y})^2}}. \quad (1)$$

137 Once computed all the edges values we get six Covid-19 adjacency matrices, of
 138 dimension 20×20 , that, for simplicity, will be referred to as Covidome through-
 139 out the text. In a nutshell, the Covidome represents a second-order statistic
 140 of the regional Covid trend reported by the time series evolution. In fact, it is
 141 closely related to the covariance matrix of the Covid indicators across Italian
 142 regions. Therefore, for each time series, high values in the Covidome will inform
 143 on two regions following the same trend in Covid dynamics, and viceversa. We
 144 will see in this paper how this information is tightly linked to the political decision
 145 made during 2020 to fight the pandemic spread. Please also see Fig.1-B
 146 for an example of Covidome corresponding to the hospitalized individuals with
 147 symptoms time series (Fig.1-A).

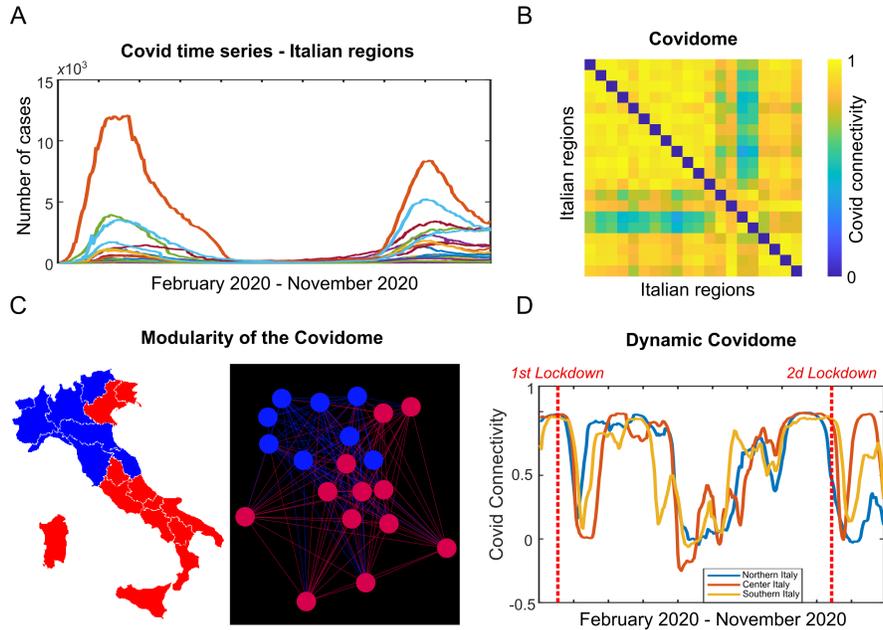


Figure 1:

148 *Covidome modularity*

149 We used the Newman and Girvan modularity score [11] to investigate the
 150 community structure of the Covidome. Given a network and a partition (mod-

151 ularity solution), the modularity score Q introduced in [11] is:

$$Q_{score} = \frac{1}{2E} \sum_{ij} \left(A_{ij} - \gamma \frac{k_i k_j}{2E} \right) \delta(m_i, m_j), \quad (2)$$

152 where E is the number of edges in the network, A_{ij} is the adjacency matrix of
153 the network (in this case binary undirected obtained from the Covidome), k_i
154 and k_j are the degree of nodes i and j respectively, γ the resolution parameter
155 and $\delta(m_i, m_j)$ is the Kronecker delta between community m_i and m_j . We used
156 the Louvain algorithm [13] to obtain the optimal partition of the Covidome.
157 To improve the robustness of the Louvain solution, we used the consensus cluster-
158 ing procedure introduced by Lancichinetti and Fortunato [12], by running
159 Louvain 100 times and finding the optimal community solution obtained from
160 the consensus matrix [10] over the 100 runs. Please see Fig.1-C for an example
161 of the community structure of the Covidome computed from the hospitalized
162 individuals with symptoms time series. Finally, we also computed a Covid "al-
163 legiance matrix", that is the probability that each region pair belonged to the
164 same module across all Covid indicators. This matrix provides quantitative in-
165 sights on whether two regions had similar Covid outbreaks (as reported by the
166 six aforementioned indicators or time series) during the pandemic.

167 *Dynamic Covidome analysis*

168 In order to better understand the link between the Covid-19 dynamics and
169 the political decisions made, we performed sliding window analysis on the Covid
170 indicators, inspired but techniques commonly used in Network Neuroscienc [10].
171 In a nutshell, we computed Covidome "snapshots" (or dynamic Covidomes) at
172 shorter time intervals within a sliding window of fixed length. We chose a three
173 week window with a step (slide) of one day, to explore the Covidome dynamics at
174 different time interval across 2020 (please see also the videos in Supplementary
175 material). In order to investigate local differences in the dynamic Covidomes we
176 first subdivided the Italian map in three main areas corresponding to Northern,
177 Central and Southern Italy (see Fig.S1 for the geographical subdivision of the
178 Italian regions), and then we evaluated the fluctuation of the mean value of
179 the dynamic Covidomes (i.e., average of their upper triangular) across sliding
180 windows (see Fig.1-D).

181 **Results**

182 The results reported in the next section are related to two complementary
183 Covid indicators, such as the number of hospitalized individuals with symptoms
184 and the number of new positives (with the exception of the Covid allegiance
185 matrix, computed across all six time series, see Methods for details). For the
186 results related to the remaining four Covid indicators (i.e., hospitalized individ-
187 uals in intensive care units, individuals in home isolation, discharged healed and
188 deceased individuals, respectively) please see the Supplementary material.

189 *Consensus modularity and allegiance matrix*

190 The modularity analysis on the Covidome for the hospitalized with symp-
191 toms and new positives (Fig.2-A and 2-B) subdivided Italy into two different
192 modules, with a prominent North-South gradient, for both the hospitalized with
193 symptoms and new positives indicators. The results for the remaining four time
194 series are reported in Fig.S4 (Supplementary material). Starting from the six
195 different consensus matrices, obtained for each time series, we can compute the
196 Covid "allegiance matrix" (Fig.2-C, first panel). That is, the probability for two
197 regions of being in the same community across all Covid indicators. For both
198 within-indicator modularity, as well as for the allegiance matrix, the Covidome
199 network is mainly split into a North-South community pattern, with some ex-
200 ceptions: specifically, FVG (Friuli Venezia Giulia) and Veneto are included in
201 the "Southern" module for the hospitalized with symptoms, whereas for new
202 positives the "Northern" community spreads over to Abruzzo and Campania,
203 and then "Southern" incorporates Emilia Romagna and Marche in its commu-
204 nity. Note that the allegiant community structure preserve the North-South
205 gradient (with the exception of FVG). Interestingly, two regions had the lowest
206 within-module allegiant score: Veneto and Umbria. That is, these regions swing
207 between community affiliations depending on the considered Covid indicator.

208 Note that the division of the Italian Covidome into two different modules is
209 robust with different values of the resolution parameter γ in (2) in the $[0.95, 1]$
210 range, as well as when choosing different threshold values on the Covidome
211 matrix in the percentiles between 40% and 10% (Fig. S3).

212 *Dynamic Covidome via sliding window analysis*

213 The modularity analysis refers to the Covidomes computed over the pan-
214 demic period ranging from the 24th of February, 2020 to the 7th of January,
215 2021. In order to better investigate the associations between Covid connectiv-
216 ity and political decisions, we decided to perform a sliding window analysis, by
217 computing Covidome snapshots in overlapping time windows of 21 days (see
218 Methods for details). The results for the hospitalized individual with symp-
219 toms and the new positives Covid time series are reported in Fig.3, whereas the
220 dynamic Covidome changes in time are represented in videos 1 and 2 (see Sup-
221plementary material). We analyzed the dynamic Covidomes evolution for these
222 two time series, with respect to four important dates in the pandemic policy
223 changes: 10th of March (first national lockdown); 4th of May (restoration of
224 freedom of movement); 14th of October (new Covid-19 positives exceeded the
225 peak of the March infections); 4th of November (lockdown differentiated by re-
226 gions). It is worth noting that a day before the third date, the 13th of October,
227 the obligation to wear masks in open and closed public spaces was introduced.
228 This is a key date in terms of the political decisions made (see Material and
229 methods section). The mean value of the dynamic Covidome is depicted in
230 Fig.3-A, for three different Italian areas corresponding to Northern, Center and
231 Southern Italy; Fig.3-B shows the nodal eigenvector centrality of the dynamic
232 Covidomes averaged across Northern, Central and Southern Italy.

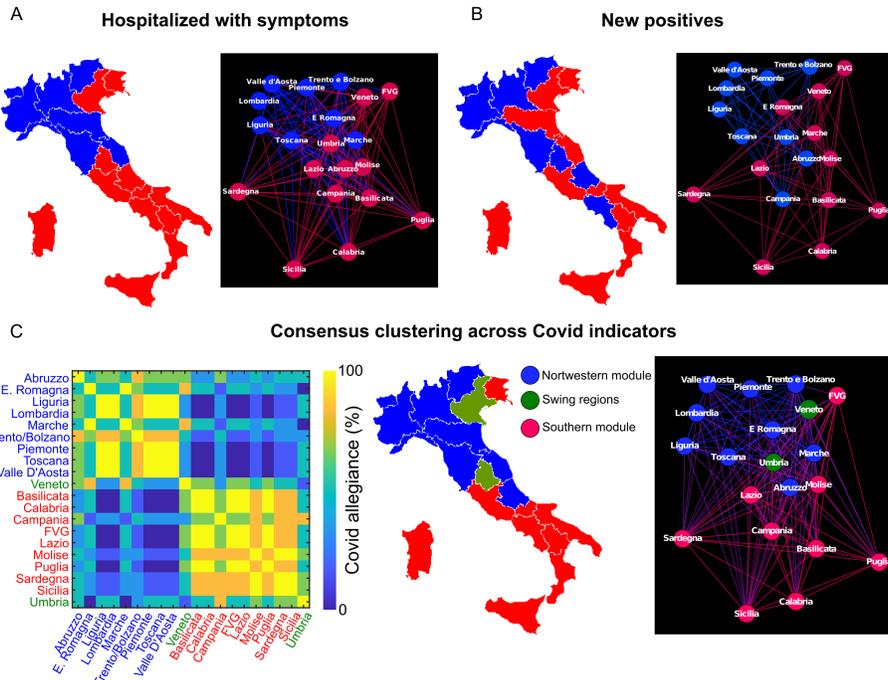


Figure 2:

233 In order to compare the two different political choices made during the first
 234 and second wave respectively, we consider the time series introduced in Fig.3
 235 on two different time intervals. The first one considering 10 days before and
 236 30 days after 10th of March, called W_1 , while the second one corresponding to
 237 4th of November, called W_2 . For both W_1 and W_2 we compute the minimum
 238 and maximum values for Northern, Central and Southern areas, respectively. In
 239 Table 1 we represented this values for all the mean dynamic Covidome time series
 240 introduced in Fig.3. Note that the maximum values for the new positives time
 241 series for W_2 does not correspond to the absolute maximum values of the second
 242 wave, due to the fact that this values fall short before the considered range. This
 243 could be due to the wearing mask measure introduced on 13th of October, as well
 244 as the measures taken on 18th and 24th of October, before the second lockdown
 245 started. Analyzing the results related to hospitalized individuals with symptoms
 246 indicator we can see how the minimum value of the Northern time series in W_2
 247 is much lower, and negative, than the one of W_1 . The three minimum values
 248 in W_2 correspond to 14 – 19 days after the second lockdown, differently from
 249 18 – 30 days in W_1 . Another important difference between the first and second
 250 lockdown is the clear difference in between the time windows shortly after W_1
 251 and W_2 , respectively. In fact, for the differentiated lockdown, corresponding
 252 to the second wave, we have that the correlation between Northern regions
 253 (max = 0.3585) increase less than Southern (max = 0.7548) and Central (max
 254 = 0.9824) regions, respectively. This result cannot be seen for the first lockdown
 255 where all three the time series in the time window short after W_1 reach values
 256 close to 1. Analyzing the results related to new positives time series, in the same
 257 ranges of time introduced before, we can see that only the minimum values stays
 258 in W_1 and W_2 respectively, moreover these values are reached from 5 to 10 days
 259 after the first lockdown while from –5 to 4 days before and after the second
 260 lockdown, respectively. From the eigenvector centrality time series Fig. 3-B we
 261 can see how for a short interval of time before and after the lockdown days all
 262 three Northern, Central and Southern regions remain almost constants for the
 263 hospitalized individuals with symptoms while there is a higher variability in the
 264 interval of time shortly after the first and second lockdown respectively.

	W_1 (HS)		W_2 (HS)		W_1 (NP)		W_2 (NP)	
	min	max	min	max	min	max	min	max
Northern	0.1595	0.9551	-0.0283	0.9305	0.0789	0.8141	0.2934	0.4296
Central	0.0063	0.9795	-0.0072	0.9803	0.2834	0.8805	0.3714	0.7378
Southern	0.0811	0.9522	0.1358	0.9650	0.1596	0.7824	0.1867	0.5443

Table 1:

265 In Supplementary material are reported the results about mean dynamic
 266 Covidomes and eigenvector centrality for the remaining time series, see Fig.S5.

267 *Covidome and structural connectome*

268 As our last result we analyzed the dynamic correlation between Covidome
 269 and structural connectome of Italy, in order to understand if and how Covid-19
 270 data trend and the geographical distribution of the Italian regions were related.
 271 To this aim, we decided to correlate the dynamic Covidome snapshots (top row
 272 of Fig.4-A and Fig.4-C) with the structural connectome obtained by computing
 273 the arclength of the geographical coordinates (latitude and longitude) between
 274 two different Italian regions (bottom row of Fig.4-A and Fig.4-C). Fig.4-B and
 275 Fig.4-D depict the temporal correlation between dynamic Covidomes and struc-
 276 tural connectome for Northern, Center and Southern Italy areas. Please see
 Supplementary material for the results on the remaining time series (Fig.S6).

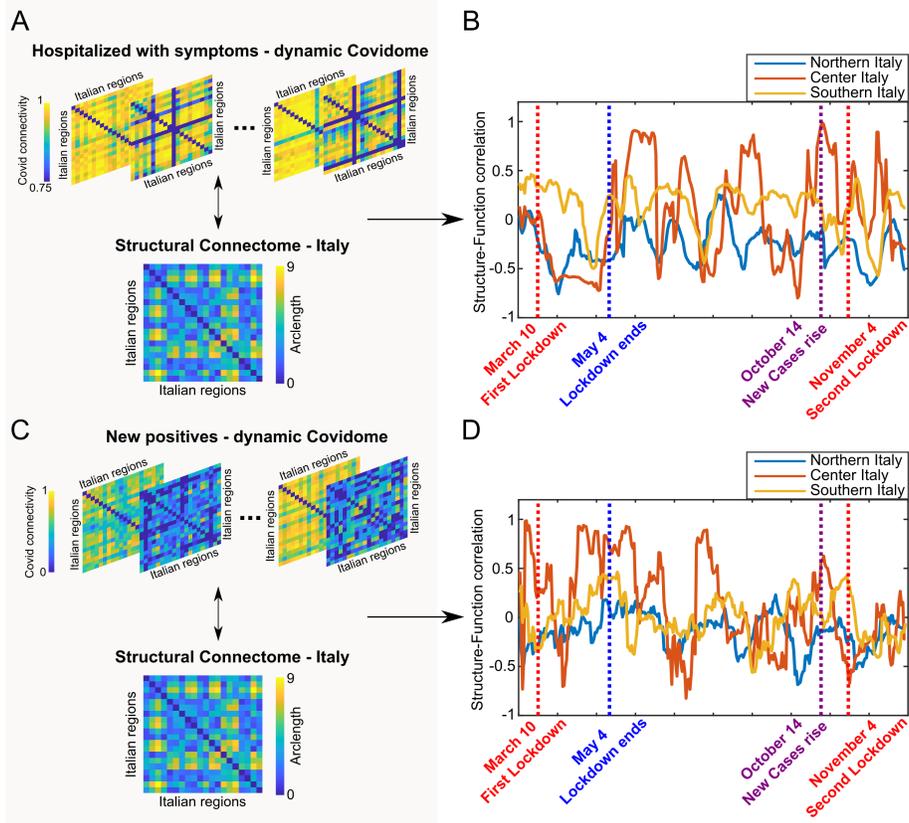


Figure 4:

277 We once more consider W_1 and W_2 introduced before in order to quantify
 278 the results from Figs.4-B and D and analyze if two different lockdowns resulted
 279 in different functional-structural Covid correlation. Furthermore, there is also
 280 an evident change between the three time series fluctuation in time. As can
 281

282 be seen in Table 2 (for hospitalized with symptoms) the Northern regions, in
 283 both W_1 and W_2 , are negative correlated in mean that remain negative also
 284 considering the corresponding standard deviation (std), while Central regions
 285 passes from a negative mean in W_1 with lower std in absolute value to a positive
 286 one in W_2 , with higher std. For Southern regions there is a positive mean value
 287 in W_1 and a negative one for W_2 . Moreover for new positives both Northern and
 288 Southern has negative mean correlation values, while Central regions, positive in
 289 the first wave and negative in the second one, respectively. The higher variability
 290 (std= 0.437) can be seen in W_1 for new positives in Central regions while the
 lower one (std= 0.078) for Northern regions, for the same time interval.

	W_1 (HS)		W_2 (HS)		W_1 (NP)		W_2 (NP)	
	mean	std	mean	std	mean	std	mean	std
Northern	-0.328	0.244	-0.380	0.182	-0.209	0.078	-0.263	0.146
Central	-0.328	0.282	0.2019	0.303	0.225	0.437	-0.257	0.205
Southern	0.317	0.094	-0.086	0.296	-0.056	0.156	-0.016	0.279

Table 2:

291

292 Discussion

293 In this study we employed network science tools [10], [24] to study Covid-
 294 19 pandemic data one year after the Italian outbreak. Specifically, we decided
 295 to compute and study Covid connectivity (i.e., the Covidome), that is, the
 296 covariance matrix of the Covid pandemic network, across six different indicators
 297 (number of hospitalized in ICU, hospitalized with symptoms, individuals in
 298 home isolation, new positives, discharged healed and deceased). The aim was
 299 to study whether its dynamics was related to the political choices made. We have
 300 found that: (i) the Covidome community structure shows a well defined North-
 301 South pattern; (ii) dynamic Covidome fluctuations stem from the effects of the
 302 two different preventive measures during the first and the second waves, in the
 303 early and towards the end of 2020, respectively; (iii) the association between
 304 Covidome and structural constraints for mobility depends on the differences
 305 between the two different lockdowns: one nationwide, the other more localized
 306 regionally. Below follows the in-depth analysis of these findings.

307 *Geographical gradients of the Covidome community structure*

308 We observed a sharp subdivision between North and South of Italy, persis-
 309 tent across time series and corresponding Covidomes (Fig.2 A-B and Fig.S4,
 310 Fig.2-C). It is worth noting that this geographical pattern is obtained purely
 311 from the community structure of the Covidome, hence without considering any
 312 explicit geographical information. Nonetheless, there are few regions that do not
 313 participate to the North-South gradient: Friuli Venezia Giulia (FVG), a North-
 314 ern region that gets assigned to the Southern module (Fig.2 A-B-C); Veneto

315 and Umbria, respectively a Northern and a Central region, oscillate between the
316 Northern and Southern module across Covid indicators, therefore denominated
317 as “swing regions” (Fig.2-C). The fact that FVG Covidome behavior is more
318 related to the one of the Southern regions is not surprising. In fact, the regional
319 administration imposed severe restrictions, such as banning public gathering,
320 schools closure, mandatory quarantine for people from epidemiological risk ar-
321 eas, etc., valid already from 1st of March when the virus wasn’t circulating yet
322 in this region [16]. Such sever regulations were adopted as well in the South
323 of Italy. Moreover, Umbria being a swing region might be linked to two main
324 political decisions: the first is that the first official document on the restrictions
325 due to Covid-19 was already introduced on 26th of February, a couple of days
326 after the Codogno case, [23]; the second, that on 4th of March more severe re-
327 strictions were introduced, since in the second wave Umbria was more affected
328 than in the first one. Furthermore, its central position between Northern and
329 Southern modules might also be related to its “swing region” behavior. In fact,
330 from the Figs. 2-A,B and Fig.S4 one can notice that Umbria region is in the
331 ”Northern” module for new positives, home isolation and discharged healed in-
332 dividuals and in the ”Southern” module for the remaining three time series.
333 Similarly, the oscillation of Veneto across community may be due to the fact
334 that one of the first Italian outbreaks happened in Vo’ which was, quickly, com-
335 pletely isolated from the rest of the region when the first cases appeared [17],
336 and on the other side, to the massive control of the people, [17]-[19], that might
337 have helped in identifying people infected with Sars-Cov-2 before reaching the
338 hospitals with more severe symptoms. In fact from Figs. 2-A,B and S4 it can
339 be seen that Veneto region is in the ”Northern” module for hospitalized in ICU
340 and deceased individuals time series, while it falls in the ”Southern” module for
341 the remaining four indicators. We further tapped into the link between policy
342 regulations and Covidomes, by analyzing the dynamics of the Covidomes and
343 its relationship with the italian structural network.

344 *Nationwide versus region-wide lockdown impact on Covid connectivity*

345 The Italian region mostly affected by Covid-19 was Lombardia, followed
346 by other Northern regions, especially in the first wave of the pandemic, at
347 the beginning of 2020. In the second wave, at the end of 2020, the pandemic
348 spread over the entire country. The political decisions made during that year
349 were different between the two pandemic waves, with a more severe national
350 lockdown at the beginning of 2020, followed by a region-specific lockdown for the
351 second wave. These two different political approaches propagate into the Italian
352 Covidome dynamics. Fig.3 shows that the average minimum values for dynamic
353 Covidomes of the hospitalized individuals with symptoms appear at distance of
354 18, 30 and 23 days after 10th of March (first lockdown) for Northern, Central and
355 Southern areas. In contrast, during the second lockdown the decrease happens
356 at 17, 19 and 14 days after the 4th of November. Interestingly, the mean value of
357 dynamic Covidome increases after the second lockdown, and it is higher for the
358 Central Italian regions, followed by Southern and Northern Italy, respectively.
359 It is evident from these findings that a lockdown leads to low Covidome values

360 between regions across all Covid indicators, with the exception of discharged
361 healed and deceased individuals: this might due to the fact that these time
362 series represent the cumulative numbers in time, hence there is no first and
363 second wave trend as the time series are only increasing. Notably, the drop in
364 the dynamic Covidome values soon after the lockdowns appears with a certain
365 delay with respect to the effective dates of the hospitalized individuals with
366 symptoms, and no delay for new cases. The reason for this different behavior is
367 two-fold: first, the information at each time point in Fig.3 represents a window
368 of three weeks; second, it was shown that there is an intrinsic delay of 3 and
369 10.4 days, depending on the age of the patient, from the day a person shows
370 symptoms to Sars-Cov-2 and needs to be hospitalized [22].

371 Note that the dynamic Covidome fluctuations should always be interpreted
372 together with the historical process of the pandemic spread. For instance, we
373 observed two sharp correlation drops (Fig.3): one, shortly after the lockdown,
374 when the virus slowed down due to the prevention measurements taken; the
375 second one, during the summer, when no restriction on traveling were imposed.
376 This is probably due to the fact that people gathered outside, diminishing the
377 probability of getting infected. Recent studies also found a negative correlation
378 between the external temperature and the spreading of the virus [20]-[21].
379 Hence, two similar drops might have different meanings, depending on the po-
380 litical choices adopted and the level of diffusion of the pandemic.

381 *Dynamic Covidome and structural connectome correlation*

382 From the functional-structural correlation results (Fig.4-B) one can notice
383 that the Covid connectivity of the Northern regions is generally poorly corre-
384 lated to the structure, whereas the Central regions change from high to low
385 correlation ($\simeq [-1, 1]$) during the pandemic outbreak, and finally the South-
386 ern regions vary their structure-function correlation in smaller interval than the
387 Central regions ($\simeq [-0.5, 0.5]$). During the first wave the dynamic Covidomes
388 of the hospitalized with symptoms (Fig.4-B) of the Southern regions are positively
389 correlated with the structural connectome. Northern and Central regions, how-
390 ever, both show little or no correlation with the geographical Italian network
391 during the first wave. The scenario changes completely when one analyzes the
392 hospitalized with symptoms during the second wave. The Covid connectivity
393 of the Central regions co-varies with interregional distance in a larger range, as
394 opposed to the Northern regions where the functional-structural correlation is
395 always negative.

396 For what concerns the structure-function associations between dynamic Covidomes
397 of new positive cases (Fig.4-D), it is noticeable a larger variability ($\simeq [-1, 1]$) for
398 the Central regions, whereas this range gets smaller for Northern and Southern
399 areas. The variability for central regions decrease in the second differentiated
400 lockdown. These results also confirm the score of the Central regions in the
401 Covid allegiance matrix. As can be seen in Table 2, for new positives, in the
402 first wave there is a negative functional-structural correlation average for the
403 Northern and Southern regions, respectively, which is maintained across the
404 second wave.

405 Two hypothesis can be postulated to explain the structure-function differ-
406 ences across lockdowns: one relates to the fact that the virus outbreak originated
407 in the North and hit the Southern region with a larger delay, due to the closure
408 of the borders; the second is that, during the second wave, the political deci-
409 sions aimed at reducing the mobility from and to the "at risk" regions helped in
410 "disconnecting" the Covidome dynamics from the Italian geographical network,
411 hence keeping the functional-structural correlation mean negative.

412 *Limitations and future directions*

413 This study has some limitations. The use of the Pearson's correlation coef-
414 ficient as a metric to compute the Covidomes might be limited. Further studies
415 should explore more advanced methods or directed measurements, based on in-
416 formation theory and time series analysis, or even, for a deeper analysis, on
417 Graph Signal Processing tools [26]-[27]. Another limitation, that can also bring
418 to further analysis, is the computation of the structural connectome based on
419 the geographical arclength between regions. It will be interesting to see how the
420 Covidome relates to the structural connectome based on mobility data [25], or
421 even the one extracted from the Italian public transportation network data.

422 The Covidome methodology presented here and applied to the Italian case
423 study can be easily adapted to other countries with a federal state organization,
424 or more generally at the European level, depending on the granularity detail
425 of study. Besides the aforementioned limitations, we think that the use of this
426 simple tools might inform on the link between the temporal information inherent
427 to Covid time series and the efficiency of the political decisions of each nation's
428 governments,

429 *Conclusions*

430 We here presented a first investigation of the functional network of Covid-19
431 pandemic (Covidome), across different indicators. We show that dynamics and
432 structure of the Covidomes is dependent of the political choice made by the Ital-
433 ian government, suggesting that the Covidome might serve as a good indicator
434 to infer region-to-region spreading during the pandemic. This approach seems
435 promising based on these preliminary findings, and we hope that it can help in
436 shedding light on the complex system generated by Covid-19.

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443
444 **Data and Code availability** The code (in MATLAB) used for this analy-
445 sis, together with some sample Covidomes, will be made available upon accep-
446 tance of the manuscript on EA EPFL webpage and a git repository.

447 **Author Contributions** IMB processed the data; IMB and EA conceptu-
448 alized the study; IMB designed the framework and performed the connectivity
449 analyses; IMB and EA interpreted the results and wrote the manuscript.

450 **Conflict of interest**

451 The authors declare no conflict of interest.

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