Multiscale mobility patterns and the restriction of human mobility under lockdown

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Abstract

Strict lockdown measures have been put in place in many countries around the world to constrain human mobility in response to the unparalleled challenges posed by the COVID-19 pandemic. Here we apply network-theoretic tools to analyse a geolocalised dataset of human mobility of 16 million UK Facebook users from March to July 2020. A special emphasis lies on dynamical perspectives of network analysis and multi-scale community detection with Markov Stability analysis is performed to identify signatures for the mobility contraction in the UK. Thereby, a new quantitative criterion for the scale selection in Markov Stability analysis is proposed, which reveals different scales of mobility in a semi-automated manner. The analysis of the UK mobility network reveals a pronounced decline of human mobility under COVID-19 and suggests that local community structure has been strengthened under lockdown. In particular, human mobility does not follow along purely geographic and administrative lines but the flow-based approach allows for the identification of intrinsic mobility patterns that may inform future interventions to prevent COVID-19 transmission.

Keywords. community detection; computational social science; COVID-19; directed graphs; flow coverage; human mobility data; Markov Stability analysis; network analysis

Introduction

The emergence of COVID-19 at the end of 2019, and its subsequent global spread, prompted governments across the world to impose a range of restrictions on the daily activities of their citizens [1]. In the UK, a first nationwide ‘lockdown’ was announced on 23 March 2020, instructing the British public to stay at home except for very limited purposes. This intervention was estimated to have saved many thousands of lives in the UK [2, 3] but also produced the greatest disruption to the patterns of work and mobility of the British population in decades, leading to the temporary closure of many businesses, a steep rise in home-working, and the furlough of 30% of the UK workforce [4–8]. Over the following months, restrictions were gradually eased to allow pupils to return to school, businesses to reopen, and people to travel more freely for leisure purposes from mid-July 2020 [9].

The effect of mobility restrictions on COVID-19 transmission has been the object of much recent work [10, 11]. For example, aggregated and anonymised mobility data from Google Maps [12, 13] and mobile phones [14] have been used to refine interventions against the spread of COVID-19 [15]; to evaluate political decision-making [16, 17]; or to assess how the pandemic affects different populations unequally [12]. Additionally, Facebook Movement maps have been used to study the contraction of human mobility during the COVID-19 pandemic using combinatorial graph properties, such as efficiency and changes in percolation and connected components [18, 19].

Here, rather than considering the relationship between mobility and COVID-19 transmission, we focus on features of the economic and social geography of the UK revealed through lockdown viewed as a ‘natural experiment’ in which human activities were curtailed to a reduced radius of action for a sustained period. We use data from Facebook’s ‘Data For Good’ programme [20, 21] to construct a baseline (pre-lockdown) network of mobility flows in the UK, which we analyse across all scales using the community detection framework of Markov Stability (MS) [22–25]. Unlike most community detection algorithms, MS is formulated in terms of a graph diffusion. As a result, MS applies naturally to directed, weighted networks, such as the mobility flows here, and extracts the inherent multi-scale community structure of the graph at different levels of coarseness selected in an unsupervised manner using a quantitative criterion which is introduced in this work. The multi-scale community structure obtained with MS allows us to identify intrinsic scales of human mobility within the pre-lockdown, baseline UK mobility network in a data-driven manner.

We then use the data collected during the first UK COVID-19 lockdown (March–June 2020) to quantify the extent to which the mobility patterns under lockdown and subsequent release conform to the data-driven pre-lockdown flow communities obtained with MS, and we compare these partitions to the NUTS hierarchy of

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administrative boundaries. Our results show that the imposition of lockdown reverted the mobility patterns towards the local, small-scale flow communities already contained in the pre-lockdown network flow data. As the restrictions were lifted, mobility patterns expanded towards the coarser flow communities found in the pre-lockdown data. We then used the flow communities to quantify the distinct regional effects of the lockdown in terms of both the strength of the contraction and the time scale of recovery of mobility towards pre-lockdown levels. We also find that whilst there is agreement between the data-driven multi-scale structure of flow communities and the existing administrative units, distinctive features emerge from human patterns of mobility.

Results

Mobility networks from Facebook movement maps

Under the ‘Data for Good’ programme [21], Facebook has made available anonymised datasets that capture temporal changes in population mobility during the COVID-19 pandemic based on user-enabled location tracking. In contrast to other datasets (e.g., Google’s COVID-19 Community Mobility Reports [26]), which record local changes in visits to different categories of places (e.g., retail, recreation, work, residential), the Facebook Movement maps used here quantify frequency of movement of individuals between locations over time, allowing the construction of directed weighted networks of human mobility. This opens the direct application of the large methodological toolbox from graph theory and network analysis to such data [18, 19].

After pre-processing the data (see Methods for a full description), we use the pre-lockdown mobility data (average over 45 days before 10 March 2020) to construct a strongly connected baseline mobility network \( G \). Each node \( i \) of the graph \( G \) corresponds to a geographic tile in the UK and the directed weighted edge \((i, j)\) represents the average daily number of trips from node \( i \) to \( j \). The width of the geographic tiles varies between 4.8-6.1 km (see Supplementary Figure 1A).

We then use the time series of mobility flows during the first COVID-19 lockdown in the UK (10 March 2020–18 July 2020 inclusive, totalling \( n_{\text{days}} = 131 \) days) to build daily mobility networks \( G(n) \), indexed over the number of days \( n = 1, \ldots, n_{\text{days}} \). The daily networks \( G(n) \) are defined on the same set of nodes as \( G \) with directed weighted edges representing the number of trips at day \( n \).

Characteristics of the baseline mobility network

Figure 2A shows the baseline mobility network \( G \), a strongly connected directed graph with \( N = 3,125 \) nodes (geographic tiles) and 37,349 directed edges (trips between tiles). Let \( A \neq A^T \) denote the adjacency matrix of \( G \), where \( A_{ij} \) is the number of trips from node \( i \) to \( j \). The matrix \( A \) is very sparse, with 99.6% of its entries equal to zero. The total number of trips is \( n_{\text{total}} = \sum_{i,j} A_{ij} = 12,892,495 \), with a much larger number of intra-tile trips \( (n_{\text{intra}} = \sum_i N_i A_{ii} = 10,416,968) \) than inter-tile trips \( (n_{\text{inter}} = \sum_{i,j} A_{ij} = 2,475,527) \). The non-zero edge weights are highly heterogeneous: \( A_{ij} \in [1.4, 72252] \) with average \( \langle A_{ij} \rangle = 345.2 \) and coefficient of variation \( cv(A_{ij}) = 5.7 \).

We have also quantified the asymmetry of the baseline network. Let \( \hat{A} \) denote \( A \) without its diagonal entries, i.e., the adjacency matrix of \( \hat{G} \), the mobility graph \( G \) without self-loops. Although the network has a high degree of statistical symmetry (the regression of the non-zero elements \( \hat{A}_{ij} \) against \( \hat{A}_{ji} \) has coefficient of determination \( R^2 = 0.998 \)) there is still a significant number of asymmetric connections. This can be seen by computing the relative asymmetry

\[
\frac{|\hat{A}_{ij} - \hat{A}_{ji}|}{\hat{A}_{ij} + \hat{A}_{ji}},
\]

whose distribution is shown in Figure 1A. Note that there are 3,226 one-way connections in the network. Hence it is crucial to use an analysis framework that can deal with directed graphs, without any imposed symmetrisation, so as to capture the subtleties of the asymmetric mobility flows in our data.

To reveal the structure of directed graphs, a natural tool is to use a diffusive process on the network, which, as it evolves dynamically, uncovers graph substructures and its topology. Our method of Markov Stability (see Methods) uses such a graph diffusion to extract the multi-scale community structure of the baseline network. The transition probability matrix \( M \) of the discrete-time random walk on \( \hat{G} \) is:

\[
M = D_{\text{out}}^{-1} \hat{A},
\]

where \( D_{\text{out}}^{-1} \) denotes the pseudo-inverse of \( D_{\text{out}} = \text{diag}(d_{\text{out}}) \), the diagonal matrix of out-strengths \( d_{\text{out}} = \hat{A} \mathbf{1}_N \). A key aspect of this diffusive process is its stationary distribution \( \pi \), which fulfills \( \pi = \pi M \) and exists for our strongly connected graph \( \hat{G} \) (see Methods). The stationary distribution \( \pi \) is an \( N \)-dimensional vector and each of its components \( \pi_i \) can be thought of as a centrality measure for node \( i \) [27]. A high value of \( \pi_i \) means that the random walk on \( \hat{G} \) is expected to visit node \( i \) often [28]; hence node \( i \) has high centrality. Indeed, Figure 2A shows that urban areas have high centrality.
We find that the random walk on the baseline network $G$ is close to being time-reversible, i.e. the probability of following a particular trajectory from node $i$ to $j$ is almost equal to the probability of going back on the same trajectory from $j$ to $i$. This can be seen because the random walk fulfills approximately the detailed balance condition (7), since $\| \Pi M - \Pi M^T \|_F / \| \Pi M \|_F = 0.03$, where $\Pi = \text{diag}(\pi)$ and $\| \cdot \|_F$ denotes the Frobenius norm [29]. This near time-reversibility coincides with the intuition that most journeys in the mobility network are based on commuting travel patterns. It is worth noting that time-reversibility does not contradict the asymmetry of $G$ because reversibility describes behaviour only at stationarity.

**Evolution of human mobility under COVID-19**

We then studied the temporal changes in the number trips (total, inter-tile, intra-tile) over the lockdown period by analysing the daily networks $G(n)$, $n = 1, ..., n_{\text{days}}$. Figure 1B shows the percentage change in the number of intra-tile and inter-tile trips as compared to the pre-lockdown baseline movement data. Whilst the total number of trips remains largely unchanged after the onset of restrictions on 24 March 2020, the number of inter-tile trips decreased sharply at the beginning of lockdown reaching a minimum of 11.02% of baseline values on 12 April 2020 followed by a steady increase steadily towards 47.37% of baseline values at the end of the study period on 18 July 2020. In contrast, the number of intra-tile trips increased after the introduction of mobility restrictions to a maximum of 136.64% of baseline on 12 April 2020 before decreasing steadily to 108.42% of baseline on 18 July 2020. There is a weekly oscillatory pattern (weekdays/weekends) in the number of trips. Yet the pattern is different between inter- and intra-tile trips: the number of intra-tile trips is higher on weekends than weekdays, although to a smaller degree than the reverse effect observed for inter-tile trips.

Overall, the observed temporal behaviour reflects a general redistribution of inter-tile toward intra-tile trips after mobility restrictions were imposed, as a result of long-distance travel and commuting being strongly reduced and human mobility reverting to local neighbourhoods under lockdown. We next investigated if the observed restriction of human mobility to local regions of a smaller scale during lockdown was already prefaced in the fine flow communities present in the Markov Stability analysis of the baseline network.

**Markov Stability analysis of the baseline mobility network**

We use the continuous-time random walk with rate matrix $Q = M - I$ and $M$ as defined in (2) in the context of the baseline mobility network $G$, multi-scale community detection with Markov Stability analysis reveals the different scales of human mobility by simulating individual travel on the network with a random walk. As a random walker remains in smaller communities for shorter Markov scales and explores bigger communities for larger Markov scales, so does a travelling individual. Again, the Markov scales are denoted by $t$ and they should not be confused with the index $n$ of the time series of observed daily networks $G(n)$. An efficient implementation of Markov Stability analysis based on the Louvain algorithm is performed on the baseline network for 300 Markov scales, equidistantly ranging from $t = -2$ to $t = 3$ in logarithmic scale. The most relevant Markov scales are chosen according to the local minima of the quantitative criterion $\psi(t)$ (with small variability to hit the local minima of NVI(t)) as detailed in the Methods section. Only the partition corresponding to the smallest Markov scale at the margin of the domain corresponds to a dip in the $\text{NVI}(t)$ on the very first plateau in the number of communities.
The selection of Markov scales is visualised in Figure 2B-C and leads to six partitions corresponding to scales $t_1 = -1.48$, $t_2 = -0.49$, $t_3 = 0.27$, $t_4 = 0.86$, $t_5 = 1.38$ and $t_6 = 2.57$.

Figure 2: **Markov Stability analysis on baseline network.** A Node centrality in the baseline network with respect to the stationary distribution $\pi$ of the diffusion process that drives Markov Stability analysis. B Multi-scale community detection is performed with Markov Stability analysis on the baseline network. The block structure in the heatmap for \( NVI(t, t') \) and dips in the \( NVI(t) \) mark relevant partitions. The dashed red lines correspond to the most relevant Markov scales as selected by the criterion $\psi(t)$ with small variations to hit the local minima of \( NVI(t) \). C Selection of relevant Markov Stability scales as the local minima of the criterion $\psi(t)$ that is the root mean-square of \( NVI(t, t') \) and the block size $|NVI(t, t')|$.

The partition results are explored for the selected most relevant Markov scales and statistical characteristics of the community structures are summarised in Supplementary Table 1. One can observe that small Markov scales correspond to fine partitions with a large number of small communities and large Markov scales lead to coarse partitions of few but large communities. A visualisation of the Markov Stability partitions in Supplementary Figure 2 reveals that the communities clearly correspond to geographic areas, although only the mobility flows between abstract nodes were used, without any additional geographic information available for the tiles. One can also observe that the partitions corresponding to the most relevant Markov scales have a strong quasi-hierarchical structure. As Markov Stability analysis does not superimpose a hierarchical structure, this is an intrinsic feature of the baseline network resulting from different levels of human mobility.

**A posteriori** comparison of Markov Stability partitions to NUTS administrative divisions

Obtained Markov Stability partitions are compared to the administrative and geographic Nomenclature of Territorial Units for Statistics (NUTS) regions in the UK. These regions exist at three hierarchical levels, where NUTS1 regions are built upon NUTS2 regions that again consist of NUTS3 regions. In the UK, NUTS1 is generally equivalent to the regions of England while Scotland, Wales and Northern Ireland are treated as whole nations. NUTS2 level generally consists of groups of counties and NUTS3 represents individual counties and groups of smaller unitary authorities. Each tile in the baseline network is assigned by a majority rule to the NUTS3 region...
with which it shares the largest area.

\begin{figure}[h]
\centering
\includegraphics[width=\textwidth]{figure3.png}
\caption{Similarity between Markov Stability partitions and NUTS regions. We can \textit{a posteriori} relate administrative NUTS regions to their most similar Markov Stability partitions as measured by the NVI. A NUTS3 regions correspond to $t_1 = 1.48$, NUTS2 regions correspond to $t_2 = -0.49$ and NUTS3 regions correspond to $t_4 = 0.86$. B The similarity between Markov Stability partitions and NUTS regions is measured with the NVI. Minima are marked by vertical pink lines and indicate highest similarity of a Markov partition to NUTS region. They correspond closely to the most relevant Markov scales marked by vertical red lines.}
\end{figure}

The similarity between the NUTS regions and Markov Stability partitions over different scales is measured with the Normalised Variation of Information (NVI) metric introduced in the Methods section and one can observe from Figure 3B that each NUTS level corresponds to one of the previously selected Markov Stability partitions: NUTS1 corresponds to Markov scale $t_1 = -1.48$, NUTS2 to $t_2 = -0.49$ and NUTS3 to $t_4 = 0.86$. This suggests that the optimal partitions of mobility flows obtained through Markov stability capture the fine, medium and coarse scale of NUTS regions in the UK. The quasi-hierarchical structure of the Markov Stability partitions also mirrors the different levels of NUTS regions. However, there are still significant deviations of the Markov Stability partitions from the NUTS regions, as visualised in Figure 3A. For example on the level of NUTS1 regions, Greater London is separated from the rest of the South for administrative reasons, whereas in terms of flows almost the whole South East of England forms one community for $t_4 = 0.86$. Similarly, Wales is connected very strongly via flows to the South West of England at $t_4 = 0.86$, which is not reflected in the NUTS1 regions. As suggested by the lower NVI value, the correspondence between the finer Markov partition at scale $t_1 = -1.48$ and NUTS3 regions is stronger.

After quantifying similarities between Markov Stability partitions and NUTS regions, we show that our Markov Stability partitions compare favourably under different performance measures. Markov Stability partitions and NUTS regions are compared along the established correspondence at fine ($t_1 = -1.48$ and NUTS3), medium ($t_2 = -0.49$ and NUTS2) and coarse ($t_4 = 0.86$ and NUTS1) level with different performance measures. We compute the Total Flow Coverage (TFC) and Inter-tile Flow Coverage (IFC) at community level and the Nodal Containment (NC) at node level as introduced in the Methods section and Figure 4A-C visualises the variability of these measures with boxplots. From the figure we observe that the Markov Stability partitions perform better for each measure and have lower variability indicating a better fit to human mobility than the administrative
NUTS regions.

Figure 4: **Performance of Markov Stability partitions as compared to NUTS regions.** Markov Stability partitions and NUTS regions are compared at fine ($t_1 = -1.48$ and NUTS3), medium ($t_2 = -0.49$ and NUTS2) and coarse ($t_4 = 0.86$ and NUTS1) level with different performance measures. Boxplots visualise the variability for the A TFC and B IFC computed at community level and C the NC computed at node level. The means are indicated by solid dots. We observe that the Markov Stability partitions perform better for each measure and have lower variability indicating a better fit to human mobility than the administrative NUTS regions.

To further analyse the heterogeneity in the NC at node level we compute the difference in the NC measure between Markov Stability partitions and NUTS regions for the three different levels of granularity. The top panel in Figure 5A-C visualise the spatial heterogeneity of the difference in the NC measure where a positive value indicates that the node has a higher NC value in the respective Markov partition. The bottom panel shows histograms for the difference in the NC values. Across much of the country, differences in NC between Markov Stability and NUTS partitions are small with larger positive or negative values generally located at the boundaries between communities of either partition. Generally, areas where NC in the Markov Stability partition is higher than the NUTS partition correspond to locations where the boundaries of NUTS partitions pass through conurbations or between closely connected towns or cities. A prominent example is that of Greater London in Panel C of Figure 5, where NC is higher in the Markov Stability partition than the corresponding NUTS1 partition across the entire boundary of the Greater London NUTS1 partition. This reflects the larger size of Greater London’s Markov Stability partition to include its wider commuter belt.

Figure 5: **Spatial analysis of nodal containment.** The difference in the NC measure at node level between Markov Stability partitions and NUTS regions is visualised in A at fine ($t_1 = -1.48$ and NUTS3), in B at medium ($t_2 = -0.49$ and NUTS2) and in C at coarse ($t_4 = 0.86$ and NUTS1) level. The top panel shows the spatial heterogeneity of the difference in the NC measure where a positive value indicates that the node has a higher NC value in the respective Markov partition and a negative value indicates a higher NC value in the respective NUTS partition. The bottom panel shows histograms for the difference in the NC values.
Identifying signatures for mobility restrictions

After determining flow communities in the baseline network, one can analyse their response under COVID-19 and in reaction to social distancing and stay-at-home rules. One would expect that the mobility reverts to more local communities under lockdown measures and for quantifying this hypothesis the TFC and IFC for mobility contained in a community as compared to journeys leaving the community is used.

From Figure 6 it can be observed that the relative TFC and IFC of each Markov partition are increasing with lockdown and slowly reverting to equilibrium afterwards. The response curves for the relative TFC and IFC of each Markov partition are analysed by fitting an activation response function stimulated by an exponential shock as described in the Supplementary Information. Acceptable fits of the response function to the evolution of network features allow to quantify the shock amplitude $\alpha$, the expected decay time of the shock $\lambda$ and the expected recovery time $\beta$ of stabilising at a possibly new equilibrium $x_{\infty}$.

**Figure 6:** Relative Flow Coverage of Markov Stability partitions. A Relative Total Flow Coverage and B relative Inter-tile Flow Coverage for each Markov partition over days. The solid lines show the empirical values and the dashed lines are the optimal fits of the respective response functions to the moving mean of the empirical data with a window size of seven days.

The relative TFC returns to normal (i.e. 100%) with an expected recovery time $\frac{1}{\beta}$ of 120 to 160 days, whereas the relative IFC stabilises at a new equilibrium of increased IFC values for some Markov Stability partitions and has a shorter recovery time of about 25 to 90 days. Table 1 displays the response parameters of the relative TFC and IFC for different Markov Stability partitions. The findings show that fine partitions experience the strongest increase in coverage with high values of $\alpha$. This supports the hypothesis that smaller communities can explain mobility flows after lockdown, because people revert to local neighbourhoods under COVID-19 constraints. The expected decay time of the shock $\frac{1}{\lambda}$ is very similar across all Markov times for the relative TFC with about 14 days and for the relative IFC with about 25 days.

In Figure 6A it can be seen that changes in relative TFC are most pronounced for the most granular partition at $t_1 = -1.48$. Figure 7B shows the weekly TFC over the study period for each community produced from this most granular partition ($t_1 = -1.48$). In week 11 of 2020, two weeks before the introduction of mobility restrictions, more than 95% of trips started and ended in the same community for 130 of the 201 communities (64.7%). This increases to 186 of 201 communities (92.5%) by week 15. Therefore, at this fine community structure, mobility in many communities is highly contained within the same community in the absence of mobility restrictions. With the imposition of mobility restrictions, it is those communities with the lowest pre-restriction containment that experience the greatest increase in containment of flow within communities, and who most quickly have less contained flow as restrictions ease.

Figure 7A shows the spatial distribution of the weekly TFC of single communities in the most granular Markov Stability partition two weeks before the imposition of mobility restrictions (week 11), two weeks after mobility restrictions (week 15) and at the end of the study period (week 29). In communities located in London and the urban north west of England, fewer trips start and end in the same community compared to more rural parts of the country. By week 15, this spatial variation is attenuated as the number of trips between communities is reduced. As restrictions ease towards the end of the study period, fewer trips start and end in the same community in Greater London than elsewhere, mirroring the distribution seen in Week 11. Supplementary Figure 3 shows the spatial distribution of weekly TFC for the other Markov Stability communities.
Figure 7: Distribution of weekly TFC in the most granular Markov Stability partition. A The weekly TFC of each community in the most granular Markov Stability partition ($t_1 = -1.48$) is visualised by heatmaps at prior to lockdown (Week 11), two weeks after the start of lockdown in the UK (week 15) and in the final week of included data (Week 29). Maps for the other five partitions can be found in the Supplementary Information. B The weekly TFC of single communities in the most granular Markov Stability partition is computed over the study period. The vertical red line shows the week of the introduction of national lockdown measures on 24rd March 2020.

Table 1: Response parameters for relative TFC and IFC of Markov Stability partitions. The table shows point estimates and 95% Confidence Intervals for the response parameters $\alpha$, $\beta$, $\lambda$ and $m$ corresponding to the relative TFC and IFC of the different Markov Stability partitions, as well as the equilibrium point $x_8$ with respect to the baseline value in percentage. The CVRMSE is a measure of the model quality and the BIC values are computed for models $x_1$ and $x_2$ as introduced in the Supplementary Information.
Discussion

This study aims to explore daily changes in the movement of individuals following the emergence of COVID-19 pandemic in the UK. Through applying unsupervised graph-based clustering methods to geospatial movement data before COVID-19, we were able to identify local flow communities over a range of scales. The analysis reveals that mobility flows are suppressed under COVID-19 and individual movement reverts to local communities. For each of the stable partitions produced from Markov Stability, we find an increase in the percentage of trips that are contained within the communities identified compared to the baseline mobility network. The extent to which flow coverage changes over time varies between communities, and is most pronounced in the most granular community \( t_1 = -1.48 \) where its temporal trajectory (Figure 6) mirrors the change of the number of trips seen in Figure 1B. Changes to TFC are less pronounced for coarser communities, where the majority of trips at baseline already occurred within the boundaries of the community. The opportunity for flow to be further contained following lockdown is therefore limited.

In the dynamic framework of Markov Stability analysis, this means that the post-lockdown communities correspond to a diffusion with smaller time horizon and exploratory capacity. This suggests that signatures for a later mobility contraction are already contained in the baseline mobility network and can be uncovered by the multi-scale community detection with Markov Stability analysis. While partitions corresponding to larger Markov scales explain the normal commuting flows, partitions of smaller Markov scales indicate the suppressed flow communities under COVID-19. Formulated in this way, Markov Stability analysis could be used for the prediction of communities under external suppression of flows.

In a sense, the processes of national lockdown and Markov Stability are somewhat analogous. In the case of national lockdown, trips that are not necessary, whether for leisure or for business, are restricted, while shorter necessary trips closer to home persist to a greater extent. Similarly, in Markov Stability, a probabilistic Markov process operates over a network whose edges are weighted according to the number of trips occurring between tiles prior to lockdown. Therefore, when assigning communities of tiles, it is those tiles with the strongest connections to one another that are assigned to the same community. Shorter Markov scales, therefore, correspond to the greater constriction of free movement observed during lockdown, while longer Markov scales partition the UK into larger communities which incorporate trips that occur less frequently and are generally over longer geographic distances.

In finding intrinsic scales to the patterns of human mobility, our paper also contributes to the wider study of human mobility in the computational social sciences [30]. In a recent study, spatial containers have been deduced from very granular GPS traces to characterise the different ‘scales of human mobility’ [31] and in this study scales correspond to the characteristic size of the containers that are organised in a nested hierarchy specific to each individual. In our work, we also showcase a multi-scale organisation of human mobility but deduce a semi-hierarchical community structure on a population level instead. Moreover, the scales of our communities determined with Markov Stability analysis correspond to the characteristic time a continuous random walk remains within communities with a high probability.

In the UK, regional mobility restrictions were introduced in place of national restrictions in the Autumn of 2020 [32]. Individual local authorities were assigned to different tiers of restrictions based on a range of factors including local COVID-19 incidence and hospital capacity. Instead of assigning restrictions at a granular, local authority level, restrictions were largely imposed at a coarser level involving multiple adjacent local authorities and conforming to historic counties or regions. In our study we find that while existing administrative geographies, in this case NUTS regions, exist at a scale similar to unsupervised partitions derived from Markov Stability, there is significant disagreement in their boundaries. As such, applying mobility restrictions at the level of existing administrative geographies may not be an adequate reflection of existing patterns of mobility. Imposition of such measures may therefore have different effects on communities according to the extent to which their unrestricted patterns of movement are contained within, or cross the boundaries of administrative geographies.

As new COVID-19 variants emerge, the potential for localised outbreaks of new strains remains a possibility in the UK and elsewhere for months to come and effective strategies for the confinement of the pandemic are necessary [33]. While regionalised strategies have been attempted in the UK and elsewhere, our findings indicate that the patterns of movement of the population of the UK may not neatly align with the boundaries of administrative geographies. In such a regionalised model, it is intended to contain the spread of COVID-19 within a defined geography while allowing social and economic activity outside of the region to remain relatively unaffected. In doing so, it is crucial to ensure that the boundaries around which such restrictions are introduced impose as little friction to the underlying patterns of everyday individual movement as possible.

Our study suggests that Markov Stability analysis can serve as tool for designing a regionalised mobility restriction model that takes into account the everyday individual movement. In particular, computations suggest that COVID-19 infections are correlated stronger within the communities of Markov Stability partitions than within administrative NUTS regions. These considerations are of special importance for bottom-up approaches to confine the spread of the pandemic as popularised in the #ZeroCovid campaign that proposed a strict lockdown
with a just distribution of social burdens [33, 34].

The data used in this study is aggregated from around 16 million Facebook users in the UK that enable location sharing, which is over 20% of the total population of the UK. However, the observed sample of the population might still not be representative of the general UK population and it is necessary to study how Facebook users that enable location services differ from the rest of the population, in order to account for this sampling bias [20]. Moreover, pairs of tiles with fewer than 10 trips within an 8-hour period are suppressed to prevent individual identification. This suppression of low frequency connections between tiles may alter the overall connectedness of the mobility network, however, such connections account for a comparatively small number of the total trips made from each tile, and are not expected to greatly alter the configuration of the communities derived from Markov Stability in this study.

This study also assumes that rates of utilisation of the Facebook app, and the activation of location sharing within the app remain constant over the study period. Changes to the number of users, or the demographic distribution of those users may lead to the changes in mobility observed being mediated in part by changes in app adoption and location sharing. The impact of this limitation is somewhat mitigated by the derivation of communities by Markov Stability from baseline data, rather than post-pandemic movement information.

A further limitation of this study is that it does not distinguish between weekdays and weekends. Differences in patterns of movement on weekdays and weekends are observed in Figure 1B and Figure 6. It is likely that better representation of mobility patterns could be achieved through separate weekday and weekend models, however the aim of this study was to examine general mobility trends over time, rather than to isolate variation with respect to weekdays or weekends. Additionally, this study explores changes in patterns of movement within and between communities over time, but does not correlate this with social, demographic and economic features of these communities, however this has been explored in other studies examining mobility changes during the pandemic [13, 35, 36].

Lockdown measures imposed due to the COVID-19 pandemic resulted in large scale changes in individual patterns of movement in the UK. Applying Markov stability analysis, a graph based and multiscale clustering method, to a national, longitudinal mobility dataset we find that patterns of movement during lockdown were contained within smaller geographic communities than before the pandemic. The structure of these localities could be identified from pre-pandemic movement data, indicating that the effect of this and future lockdown circumstances on individual movement may be predicted in advance of implementation. Imposition of localised restrictions on mobility based on communities identified in this study rather than administrative regions may reduce the social and economic frictions of future localised lockdown measures.

Identifying flow communities on different scales allows to measure the impact of COVID-19 on mobility contraction at local, regional and national levels over time, thereby providing a data-driven, unsupervised insight into the scale at which lockdown measures restricted mobility most, and when.

## Methods

### Data aggregation for directed mobility graphs from Facebook data

Facebook Mobility Maps [20, 21] provide movement between geographic tiles as codified by the Bing Maps Tile System, a multi-level grid over the rectangular Open Street Map Web Mercator projection encoded by 12-digit quadkeys [37]. The width of the tiles varies with latitude, getting larger towards the equator. For the UK, there are 5,436 geographic tiles with widths between 4.8-6.1 km (see Supplementary Figure 1A). The dataset provides the number of trips within each tile and to any other tile at intervals of 8 hours starting at 00:00 Coordinated Universal Time (UTC), 08:00 UTC and 16:00 UTC each day. The data is anonymised by Facebook prior to release using proprietary aggregation methods, including addition of small amounts of random noise, spatial smoothing, and dropping counts of less than 10 trips within an 8-hour period to avoid identifiability.

As our baseline, we use pre-lockdown mobility data consisting of the tile-level movement for each day of the week averaged over the 45 days before the start of the daily mobility data on 10 March 2020. We also use time series data of mobility flows from 10 March 2020 to 18 July 2020 inclusive, totalling \( n_{\text{days}} = 131 \) days, and representing the first COVID-19 lockdown in the UK. In this study period a total of 1,831,647,077 trips occurred between tiles located within the UK. From the time series data, we build daily mobility networks \( G(n) \), indexed over the number of days \( n = 1, ..., n_{\text{days}} \) starting from 10 March 2020. Each node \( i \) in network \( G(n) \) corresponds to a geographic tile of the UK and the directed weighted edge \((i, j)\) from node \( i \) to \( j \) at day \( n \) represents the number of trips from node \( i \) to \( j \) at day \( n \). Similarly, the baseline network \( G \) is obtained by averaging the daily trips between each pair of tiles over the 45 days prior to the start of the lockdown.

Recall that a subgraph \( \hat{G} \) of the directed network \( G \) is a weakly connected component (WCC) of \( G \) if each pair of nodes is connected by an undirected path, whereas in a strongly connected component (SCC) each pair of nodes is connected by a directed path [27]. For any given graph \( G \), one can then find the largest weakly connected component (LWCC) and the largest strongly connected component (LSCC).
Multiscale community detection in directed graphs with Markov Stability

The directed graph of baseline mobility flows is analysed using Markov Stability (MS), a multiscale community detection framework that uses graph diffusion to detect communities in the network at multiple levels of resolution. MS is naturally applicable to directed graphs. We provide definitions and a summary of the formalism in the subsections below. For a fuller explanation of the ideas underpinning the method and several applications to social and biological networks, see [22–25, 38–40].

Diffusive processes on graphs

Consider a directed weighted graph $G$ with $N$ nodes and no self-loops. Let $A \neq A^T$ be the $N \times N$ adjacency matrix of $G$ and $d_{\text{out}} = A \mathbf{1}_N$ be the vector of out-strengths, where $\mathbf{1}_N$ is the $N$-dimensional vector of ones. Let us also define $D_{\text{out}} = \text{diag}(d_{\text{out}})$, the diagonal matrix containing the out-strengths on the diagonal.

The transition probability matrix $M$ of a discrete-time random walk on $G$ is:

$$M = D_{\text{out}}^{-1}A,$$

where $D_{\text{out}}^{-1}$ denotes the pseudo-inverse of $D_{\text{out}}$. The matrix $M$ defines a discrete time Markov chain on the finite state space defined by the nodes of $G$ [41]:

$$p_{t+1} = p_t M$$

where $p_t$ is a $1 \times N$ probability vector with components equal to the probability of the random walk hitting the respective node at (discrete) time $t$. Clearly, $p_t \mathbf{1}_N = 1$, $\forall t$, because $p_t$ is a probability vector. While $p_t$ defines the distribution of the Markov chain at each time $t$, we denote by $X_t$ the random process that follows this distribution.

A Markov chain on a finite state space is [41]:

- **irreducible** when there is a positive probability to jump from an arbitrary state $i$ to another state $j$ in a finite number of steps;
- **aperiodic** when the number of steps necessary to return from state $i$ to itself with positive probability has no fixed period;
- **ergodic** when it is both irreducible and aperiodic.

A stationary distribution $\pi$ of the Markov chain fulfills:

$$\pi = \pi M,$$

where $\pi$ is a $1 \times N$ probability vector, which corresponds to a dominant left eigenvector of $M$ with eigenvalue 1. When the Markov chain is ergodic, it has a unique stationary distribution $\pi$.

The random walk defined by $M$ is said to have the detailed-balance property [28] if its stationary distribution $\pi$ fulfills

$$\pi_j M_{ij} = \pi_i M_{ij}, \quad \forall i, j = 1, ..., N$$

which can be rewritten as a matrix equation

$$\Pi M = M^T \Pi,$$

where $\Pi = \text{diag}(\pi)$ denotes the diagonal matrix with $\pi$ on the diagonal. A Markov chain $X_t$ with stationary distribution $\pi$ that fulfills the detailed balance equation (6) is called reversible, since the distribution of the Markov chain up to each time $t$ is equal to the distribution of the time-reversed Markov chain, i.e.

$$(X_0, X_1, ..., X_t) \overset{d}{=} (X_t, X_{t-1}, ..., X_0),$$
when $X_0$ is distributed according to the stationary distribution $\pi$.

When, as in our case, the transition matrix $M$ is obtained from a graph adjacency matrix, the above conditions for the Markov chain can be translated to graph properties. In particular, it is well known that a necessary and sufficient condition for the irreducibility of the Markov chain defined by a graph-based transition matrix $M$ (3) is that the graph $G$ is strongly connected [42]. The assumption of aperiodicity is harder to interpret but requires that the graph is non-bipartite or does not consist of a circle. Under these conditions, the Markov chain defined by equation (3) is ergodic, and its unique stationary distribution $\pi$ is often referred to as eigenvector centrality in the network literature [27].

There is an associated continuous-time process associated with the above random walk. Let us define the rate matrix

$$Q = M - I,$$

(9)

where $I$ is the $N \times N$ identity matrix. Note that $L = -Q$ represents the so called random walk normalised Laplacian. We then consider the continuous-time Markov process $X(t)$ with semi-group $P(t)$ governed by the forward Kolmogorov equation

$$\frac{dP(t)}{dt} = P(t) Q,$$

(10)

which has the solution

$$P(t) = e^{tQ}.$$

(11)

When the Markov process is ergodic, $P(t)$ converges in total variation to its unique stationary distribution $\pi$ [43].

### Markov Stability as a cost function for clustering algorithms

The dynamics of the Markov chain with transition matrix $M$ defined on the nodes of the graph can be exploited to get insights into properties of the graph $G$ itself.

Let $P(t)$ be the semi-group of a Markov process as defined in equation (11) with stationary distribution $\pi$ on a graph with adjacency matrix $A$. Following [24], each partition of the graph into $c$ communities corresponds to a $N \times c$ indicator matrix $H$ with $H_{ij} \in \{0, 1\}$ and $H_{ij} = 1$ denotes that node $i$ is part of community $j$. Define now the clustered autocovariance matrix for partition $H$ as

$$R_t(H) = H^T [\Pi P(t) - \pi^T \pi] H.$$  

(12)

The diagonal elements of $R_t(H)$ correspond to the probabilities that the Markov process starting in one community $j$ does not leave the community up to time $t$, whereas the off-diagonal elements correspond to the probabilities that the process has left the community in which it started by time $t$. Note at this point that $t$ is an internal time of the Markov process that needs to be clearly distinguished from physical time like the number of days in our later applications with the Facebook mobility data. To avoid confusion, it is customary in Markov Stability analysis to refer to $t$ as the Markov scale rather than time. Following these observations, one defines the Markov Stability of a partition $H$ by

$$r_t(H) = \min_{0 \leq s \leq t} \text{Tr} [R_s(H)] \approx \text{Tr} [R_t(H)],$$

(13)

as a dynamical quality measure of the partition for each Markov scale $t$. The approximation is supported by numerical simulations that suggest that $R_t(H)$ is monotonically decreasing in $t$. Markov Stability allows to determine optimal partitions for the graph and each scale of its associated Markov process. The objective is to find a partition $H(t)$ that maximises Markov Stability up to a time horizon $t$ for the Markov process on the graph such that

$$r_t(H(t)) = \max_{H} r_t(H).$$

(14)

The Markov Stability serves as a cost function for clustering algorithms but its optimisation is known to be NP-hard. However, expressing Markov Stability in terms of the modularity [44] for another directed graph [24] allows to use efficient algorithms developed for modularity optimisation like the Louvain algorithm [45]. Optimising Markov Stability for different Markov scales $t$ then leads to a series of partitions $H(t)$. For small Markov scales, the Markov process can only explore very local neighbourhoods which leads to a fine partition, whereas increasing the Markov scale also widens the horizon of the Markov process and larger areas are explored to obtain coarser partitions [24]. Hence, the notion of a community as detected by Markov Stability analysis is strictly based on the spread of a diffusion on the network. In particular, Markov Stability analysis is able to identify non clique-like communities, which are likely present in heterogeneous mobility networks [46].
Normalised Variation of Information as similarity measure of partitions

In order to assess the quality of partitions produced by the optimisation algorithm and across different Markov scales \( t \), it is necessary to introduce a similarity measure for partitions. Following [47] and [48], consider two different partitions \( H(t) \) and \( H(t') \) with potentially different numbers of communities and let \( P(j) \) denote the probability that an arbitrary node of \( G \) is part of community \( j \) in partition \( H(t) \). Similarly, let \( P(j, k) \) denote the joint probability that an arbitrary node in \( G \) simultaneously falls into communities \( j \) of partition \( H(t) \) and \( k \) of partition \( H(t') \). Based on these probabilities one can define as usual the information entropy \( \mathcal{H}(t) \), the joint information entropy \( \mathcal{H}(t, t') \) and the Mutual Information (MI) \( \text{MI}(t, t') \) between the partitions \( H(t) \) and \( H(t') \).

Moreover, one obtains the Variation of Information (VI) from these measures as follows:

\[
\text{VI}(t, t') = \mathcal{H}(t) + \mathcal{H}(t') - 2\text{MI}(t, t').
\]

The VI is proven to be a metric on the space of partitions with upper bound \( \log(N) \) [49] and a Normalised Variation of Information (NVI) can be defined by:

\[
\text{NVI}(t, t') = \frac{\text{VI}(t, t')}{H(t)}
\]

which fulfills \( \text{NVI}(t, t') \leq 1 \). The NVI is also a metric and low values indicate a high similarity between the partitions [48]. Previously, the Variation of Information was normalised with \( \log(N) \) for applications in Markov Stability [24], but NVI is advantageous as it is a universal similarity metric [50]. This essentially means that, if the partitions \( H(t) \) and \( H(t') \) are similar under any non-trivial metric, then they are also similar under NVI [48].

A new quantitative criterion for scale selection in Markov Stability analysis

After obtaining optimised partitions for a sequence of \( m \) Markov scales \( t_0, t_1, \ldots, t_{m-1} \), the most relevant scales have to be chosen [24]. Those should be robust to the optimisation algorithm and persistent across scales. For each Markov scale \( t \), the robustness with respect to the optimisation algorithm can be evaluated by repeating the Louvain optimisation (300 scales in our study) with different random initialisation and computing the average NVI for the ensemble of optimised partitions (or a random and sufficiently large sample of the ensemble) that will be called NVI(\( t \)). The optimised partition in the ensemble that maximises the Markov Stability \( \psi(t) \) is chosen to be the optimal partition for scale \( t \).

The persistence across scales can now be assessed by computing the NVI for all pairs of such optimal partitions corresponding to scales \( t \) and \( t' \) that will be called NVI(\( t, t' \)). This yields an \( m \times m \) symmetric matrix NVI(\( t, t' \)), which by convention is displayed ‘upside down’ with NVI(\( t_0, t_0 \)) in the bottom left and NVI(\( t_{m-1}, t_{m-1} \)) in the top right. In the lack of a fully developed statistical criterion, a relevant Markov scale \( t \) was previously chosen based on the heuristic that it should be located in a distinctive block of low values in the NVI(\( t, t' \)) and correspond to a dip in the NVI(\( t \)), as low values in the Normalised Variation of Information indicate high similarity [24].

In this study, we propose a semi-automated approach to scale selection in Markov Stability analysis that formalises these heuristics. At first, the block structures in NVI(\( t, t' \)) is quantified via thresholding and counting. This can be achieved by counting the number of entries in the primary diagonal ‘above’ a Markov scale \( t \), whose values are under a certain threshold \( \delta > 0 \) and in our study \( \delta = 0.1 \) is used. Note that a \( m \times m \) matrix has \( 2m + 1 \) primary diagonals and so the diagonal ‘above’ Markov scale \( t_i \) is defined as the \( 2i \)-th diagonal. Let the diagonal count for a Markov scale \( t \) as described above be denoted by \( |\text{NVI}(t, \cdot)| \). Counting the number of diagonal entries allows to identify the centers of mass in the block structure of the matrix NVI(\( t, t' \)), in contrast to a simple horizontal count. Diagonal counting is advantageous over horizontal counting, as one often wants to perform Markov Stability iteratively with a higher resolution in the neighbourhood of previously identified relevant scales.

To formulate a criterion \( \psi(t) \) that combines the information of NVI(\( t \)) and \( |\text{NVI}(t, \cdot)| \), it is practical to first smooth both functions with a triangular moving mean of a sufficiently large window size (in our study 10% of the number of Markov scales \( m \) is chosen) and to then normalise both functions by their respective maximal value (without changing their names for clarity). One can now define the criterion \( \psi(t) \) by the root mean-square

\[
\psi(t) = \sqrt{\frac{\text{NVI}(t)^2 + (1 - |\text{NVI}(t, \cdot)|)^2}{2}},
\]

which assumes that both ingredients have the same importance, and otherwise choose a convex combination. Note that \( 1 - |\text{NVI}(t, \cdot)| \) in the equation is again normalised without change of notation. For a better comparison with its ingredients, \( \psi(t) \) is also normalised by its maximal value (again without changing the name).

Align with the selection heuristic described above, the most relevant Markov scales are then defined by the local minima of \( \psi(t) \). Suppose that \( \psi(t) \) has \( l \) local minima \( t_1, t_2, \ldots, t_l \), then the partitions \( H_{t_1}, H_{t_2}, \ldots, H_{t_l} \) are the most relevant Markov Stability partitions that correspond to the intrinsic scales of the network.

Note that the scales at the margins of the domain of \( \psi(t) \) can not be properly assessed with the proposed criterion, because they are cut off by the moving window. In this case, the number of communities \( n_c(t) \) in
the optimal partition at scale $t$ serves as a useful heuristic for the selection of relevant Markov scales, because persistent scales should correspond to a plateau in $n_c(t)$, where the number of communities does not change. There are strong correlations between the number of communities $n_c(t)$ and the similarity across scales $NVI(t,t')$, but again a thorough analysis is still missing.

Measures for Flow Coverage

Consider the the adjacency matrix of mobility flows $A_n$ at day $n$ and a $N \times c$ indicator matrix $H$ for a partition corresponding to $c$ communities. Then $(H^T A_n H)_{kl}$ denotes the daily mobility flow from community $k$ to community $l$. Similar to [51, 52], we define the Total Flow Coverage (TFC) of community $k$ as the fraction of flow preserved within the community given by:

$$TFC(k, H; A_n) = \frac{(H^T A_n H)_{kk}}{\sum_k (H^T A_n)_{ki}},$$

where the denominator is the total amount of flow emerging from community $k$. Hence, the TFC quantifies the ability of a community to cover the flows emerging from its nodes. Furthermore, one can define the TFC of the whole partition $H$ by:

$$TFC(H; A_n) = \frac{\text{Tr}(H^T A_n H)}{\sum_k (H^T A_n)_{ki}} = \frac{\text{Tr}(H^T A_n H)}{\sum_k (A_n)_{ki}}.$$  \hspace{1cm} (19)

Recall that the multiscale community detection algorithm of Markov Stability analysis leads to a series of partitions $H(t)$ for each Markov scale $t$. After selecting the $l$ most relevant Markov scales $t_1, ..., t_l$, one can compute the evolution of the TFC over days for each of the partitions $H(t_1), ..., H(t_l)$.

One might be interested in only quantifying the inter-tile flows contained within communities, which is possible by using matrix $\hat{A}_n$ (referring to $A_n$ with zero diagonal) in equation (18) or (19) and this yields the Inter-tile Flow Coverage (IFC) for a single community or the whole partition, respectively. Moreover, one can normalise IFC($\cdot; A_n$) or IFC($\cdot; \hat{A}_n$) with the respective baseline values TFC($\cdot; A$) or IFC($\cdot; \hat{A}$) (where $\hat{A}$ refers to $A$ with zero diagonal), to obtain a measure for the relative change of Total or Inter-tile Flow Coverage from baseline to day $n$. In the following, the relative TFC or IFC of a partition $H$ will be be denoted by IFC($H$) or IFC($\hat{A}$) for simplicity. E.g., the formula for the IFC($H$) is given by:

$$\text{IFC}(H) := \frac{\text{IFC}(H; \hat{A}_n)}{\text{IFC}(H; A)} = \frac{\text{Tr}(H^T \hat{A}_n H)}{\text{Tr}(H^T A H)} \frac{\sum_k (\hat{A})_{ki}}{\sum_k (A)_{ki}}.$$  \hspace{1cm} (20)

If one is interested in the weekly evolution of the TFC or IFC, one can simply replace the daily adjacency matrices in in equations (18) and (19) with weekly adjacency matrices.

Measures for Nodal Containment

Consider now the adjacency matrix $\hat{A}$ of the baseline network without self-loops and a partition given by a $N \times c$ indicator matrix $H$. We introduce a measure of nodal containment (NC) that quantifies the proportion of baseline flows emerging from a node $i$ that remain within its community given by:

$$\text{NC}(i, H; \hat{A}) = \frac{(\hat{A}H)_{iC(i)}}{d_i},$$  \hspace{1cm} (21)

where $C_i \in \{1, 2, ..., c\}$ denotes the community of node $i$ and $d_i = (B 1_N)_i$ its out-degree. The NC is clearly related to the IFC: While NC measures containment from a node-centered perspective, IFC measures the ability of a community to cover flows from a community-centered perspective.

To compare the performance of two partitions $H$ and $\tilde{H}$ at a node level one can compute the difference of the NC measure for each node $i$ given by $\text{NC}(i, H; \hat{A}) - \text{NC}(i, H; \tilde{A})$. While positive values indicate that $H$ better contains the flows emerging from $i$, negative values indicate that $\tilde{H}$ performs better for node $i$.

Data availability

The mobility data is available from Facebook upon reasonable request via https://dataforgood.fb.com Shape files for the NUTS regions in the UK are available from the Open Geography Portal https://geoportal.statistics.gov.uk/
Code availability

Code for Markov Stability analysis can be found at https://github.com/michaelschaub/generalizedLouvain and for a Python wrapper see https://github.com/barahona-research-group/PyGenStability

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Ethics approval and consent to participate

This study was limited to aggregate data obtained from the Facebook Data for Good programme and therefore formal ethics approval was not required.

Competing interests

The authors declare that they have no competing interests.

Author contributions

The computations in this study were performed by DS and JC. All authors contributed to the writing of this manuscript.
Supplementary Information for
Multiscale mobility patterns and the restriction of human mobility under lockdown

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1 Supplementary note: Linear model for activation response functions

In order to model the response of a system to an activation function \( R(s) \), one can formulate a linear ODE for the weakly activated response \( x_s^p \) at time \( s \) by

\[
\frac{dx}{ds}(s) = -\beta [x(s) + 1] + \alpha R(s), \quad x(0) = 1,
\]

where the activation rate \( \alpha \in \mathbb{R} \) and the deactivation rate \( \beta > 0 \) determine the properties of the subject under a stimulus or shock [1]. The value \( x(0) = 1 \) reflects a positive baseline value that is disturbed by the shock, where \( \alpha > 0 \) leads to an increase with respect to the baseline value and \( \alpha < 0 \) to a decrease. The expected relaxation time of the system is given by \( \frac{1}{\beta} \). Assume an exponentially decaying stimulus

\[
R(s) = e^{-\lambda s} + m
\]

with decay rate \( \lambda > 0 \) and constant stimulus \( m \in \mathbb{R} \), whose expected decay time is given by \( \frac{1}{\lambda} \). Then the solution of equation (1) can be obtained from the Variation of Constants formula as

\[
x(s) = \frac{\alpha}{\beta - \lambda} (e^{-\lambda s} - e^{-\beta s}) + m \frac{\alpha}{\beta} (1 - e^{-\beta s}) + 1.
\]

Let in the following denote by \( x_1(s) \) the response function (3) with \( m = 0 \) and by \( x_2(s) \) the response function with \( m \neq 0 \). A constant stimulus of \( m = 0 \) corresponds to the modelling assumption that the system will go back to its initial state, as \( \lim_{s \to \infty} x_1(s) = 1 \). However, one might be interested in a model that allows for a new equilibrium point and in the case of a constant stimulus \( m \neq 0 \), the solution (3) converges to the new equilibrium

\[
x_2(x) := \lim_{s \to \infty} x_2(s) = m \frac{\alpha}{\beta} + 1 \neq 1.
\]

In this study, the response curves for the relative TFC and IFC of each Markov partition are analysed by fitting the activation response function \( x(s) \) from equation (3) with the Levenberg-Marquardt algorithm [2]. For \( n \) data points \((\hat{s}_i, \hat{x}_i)\) with \( i = 1, ..., n \), the Levenberg-Marquardt algorithm efficiently minimises the sum of squares

\[
\chi^2 = \sum_{i=1}^{n} (x(\hat{s}_i) - \hat{x}_i)^2.
\]

In order to account for weekly oscillations in the relative TFC and IFC, the response functions are fitted to a triangular moving mean of the time series with a window size of seven days. This makes sense for a comparison with the baseline network, which is also obtained by averaging mobility data over a whole week. Due to their scale dependence, the abstract sum of squares \( \chi^2 \) or the mean-square error (MSE) given by

\[
\text{MSE} = \frac{\chi^2}{n}
\]

are often no meaningful holistic performance measures [3]. As an alternative, the coefficient of variation of the root mean-square error (CVRMSE) given by

\[
\text{CVRMSE} = \frac{\sqrt{\text{MSE}}}{\bar{x}}
\]

\[
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with the mean \( \bar{x} = \frac{1}{n} \sum_{i=1}^{n} \tilde{x}_i \) defines an unbiased and scale-independent performance measure that is reliable for the quality assessment of non-linear models [3]. In order to decide between models \( x_1 \) and \( x_2 \) that differ in the number of variable model parameters \( q \), one can apply model selection criteria like the Bayesian information criterion (BIC) that have a strong statistical foundation [4]. Under the assumption of independently Gaussian distributed residuals, the BIC is given by

\[
\text{BIC} = n \ln(\text{MSE}) + q \ln(n)
\]

and the model \( x_i \) is chosen, which minimises the BIC value [5]. Apart from determining the best parameter estimates \( \hat{\alpha}, \hat{\beta}, \hat{\lambda} \) and \( \hat{m} \) (note that \( m \) is only a variable parameter if model \( x_2 \) was chosen), one can also calculate joint 95% confidence intervals (CIs) with the F-Test [6]. The equilibrium point for the response function is estimated according to equation (4) as \( \hat{x}_x = \hat{m} \frac{\hat{\alpha}}{\hat{\beta}} + 1 \). In order to determine a 95% CI for \( x_x \), one can naively combine the 95% CIs of the the parameters \( \alpha, \beta \) and \( m \), which is only a rough approximation as the parameters are not mutually independent. The python package LMFIT [7] is used for the non-linear least-squares minimisation and the computation of the BIC criterion and the confidence intervals.

2 Supplementary results

![Figure 1: Geographic tiles in the Facebook Movement map. A](image)

A Visualisation of the geographic 12-digit tiles for which movement data is available in the Facebook Movement maps. Overlaid is the UK border. One can observe that the bounding box for the Movement maps contains tiles outside the UK. B The mobility network is a directed network and the nodes in the LSCC are coloured in green, the remaining nodes in the LWCC in blue and all other nodes in grey. Most of the grey nodes are unconnected to the rest of the network. C The geographic tiles in the LSCC are spread over most NUTS3 regions in the UK.
Table 1: **Statistics for communities in Markov Stability partitions.** The number of communities, the minimal number of nodes in each community, the three quartiles Q1, Q2 and Q3 and the maximal community size are displayed for the partitions corresponding to the most relevant Markov scales $t$.

| $t$   | Number of communities | min | Q1 | Q2 | Q3 | max |
|-------|------------------------|-----|----|----|----|-----|
| -1.48 | 201                    | 1   | 7  | 13 | 22 | 59  |
| -0.49 | 63                     | 4   | 33 | 44 | 61 | 169 |
| 0.27  | 32                     | 10  | 67 | 87 | 116| 246 |
| 0.86  | 18                     | 42  | 86 | 132| 233| 404 |
| 1.38  | 13                     | 9   | 126| 263| 313| 590 |
| 2.57  | 6                      | 190 | 253| 365| 835| 997 |

Figure 2: **Quasi-hierarchical structure of Markov Stability partitions.** Small Markov scales correspond to fine partitions and large Markov scales to coarse partitions. One can observe a quasi-hierarchical structure of the partitions, which is not superimposed by the algorithm but a feature of the data. The boxplots display statistics for community sizes in the respective partitions. Note that there is no consistency of the colours throughout different Markov scales.
Figure 3: **Spatial distribution of weekly TFC in the six Markov Stability partitions.** The spatial location of each community is shown in the leftmost column. The weekly TFC of each community in each Markov stability partition is visualised by heatmaps prior to lockdown (Week 11), two weeks after the start of lockdown in the UK (Week 15) and in the final week of included data (Week 29).
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