Original Article

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In-depth Correlation Analysis of SARS-CoV-2 Effective Reproduction Number and Mobility Patterns: Three Groups of Countries

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Objectives: Many governments have imposed—and are still imposing—mobility restrictions to contain the coronavirus disease 2019 (COVID-19) pandemic. However, there is no consensus on whether policy-induced reductions of human mobility effectively reduce the effective reproduction number (*Rt*) of severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2). Several studies based on country-restricted data reported conflicting trends in the change of the SARS-CoV-2 *Rt* following mobility restrictions. The objective of this study was to examine, at the global scale, the existence of regional specificities in the correlations between *Rt* and human mobility.

Methods: We computed the *Rt* of SARS-CoV-2 using data on worldwide infection cases reported by the Johns Hopkins University, and analyzed the correlation between *Rt* and mobility indicators from the Google COVID-19 Community Mobility Reports in 125 countries, as well as states/regions within the United States, using the Pearson correlation test, linear modeling, and quadratic modeling.

Results: The correlation analysis identified countries where *Rt* negatively correlated with residential mobility, as expected by policymakers, but also countries where *Rt* positively correlated with residential mobility and countries with more complex correlation patterns. The correlations between *Rt* and residential mobility were non-linear in many countries, indicating an optimal level above which increasing residential mobility is counterproductive.

Conclusions: Our results indicate that, in order to effectively reduce viral circulation, mobility restriction measures must be tailored by region, considering local cultural determinants and social behaviors. We believe that our results have the potential to guide differential refinement of mobility restriction policies at a country/regional resolution.

Key words: SARS-CoV-2, COVID-19, Communicable diseases, Policy, Physical distancing, Pandemics

INTRODUCTION

By November 20, 2021, over 250 million people had contracted coronavirus disease 2019 (COVID-19) with the death toll exceeding 5 million [1]. While vaccination is being rolled out en masse, lengthy mobility restrictions are still imposed as a measure to limit the spread of the virus. How efficient are mobility restrictions at limiting the disease spread? There might be multiple answers to this seemingly simple question.

To assess the impact of government mobility restriction pol-

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icies on the spread of severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2), the causative virus of COVID-19, researchers have compared changes in aggregated mobility data, such as the Google COVID-19 Community Mobility Reports [2], against changes in the effective reproduction number (*Rt*) of SARS-CoV-2 [3]. *Rt* captures dynamic changes in person-to-person viral transmission and is therefore regarded as a better measure of the speed of disease spread, both retrospectively and in real time [4], compared to cumulative or new case numbers [5]. Unlike the latter, *Rt* is insensitive to individual differences in time from infection to test and robust to temporal inaccuracies due to day-to-day variation in case reporting practices. This is particularly true when estimating the *Rt* retrospectively [6].

Multiple studies have found that policy-induced reductions of human mobility significantly decreased the *Rt* of SARS-CoV-2 [7-10]. Noland [8] noted that, in the United States, staying at home (referred to as residential mobility hereafter) was particularly effective at reducing *Rt*, and suggested that a stronger impact on *Rt* would require a larger increase in residential mobility. A similar linear negative relationship between residential mobility and *Rt* was found in a study from Turkey [7]. A time lag between changes of mobility and the corresponding changes of *Rt* was also noted [11], with marked variability between countries [12].

However, in an analysis of correlations between new cases and human mobility in 34 Organization of Economic Cooperation and Development (OECD) countries, Oh et al. [13] found that strong mobility decreases did not perform better than mild mobility decreases in terms of reducing the new case count. Furthermore, Wang et al. [11] suggested that the correspondence between mobility changes and *Rt* was rather irregular across regions and pandemic periods in Australia, relating it to the complexity of the contagion dynamics and the unmeasured confounding. Therefore, increased residential mobility might not always correlate with decreased *Rt* in all countries and regions or in all epidemic phases. The purpose of this work was to systematically characterize the relationships between the *Rt* of SARS-CoV-2 and mobility indicators in 125 countries and 52 states/regions (the United States+Puerto Rico). We hope that this research will clarify the conflicting reports on the relationship between mobility changes and *Rt* and inform decision-makers on the effectiveness of movement restriction policies at mitigating COVID-19 spread in specific countries/regions.

METHODS

Data Source and Pre-processing

Country/region-specific mobility indicators were obtained from Google COVID-19 Community Mobility Reports [2]. Google reports anonymized position data from users who have Location History activated on their mobile phones [14]. Positions are classified as: retail stores, restaurants, and recreation places in general (referred to as "retail" below); grocery stores and pharmacies (grocery); transit stations (transit); residential places (residential); parks and natural spaces (parks); and workplaces (work). These positions are referred to as "mobility indicators" throughout the article. For each country/region, the dataset consists of daily percentages of changes in each mobility indicator, from the median value of the same weekday during the 5-week baseline period (January 3 to February 6, 2020). For days with missing mobility data, linear interpolation between the previous and next days with available data was used. Incidence data of SARS-CoV-2 infections (reported as daily new cases) was obtained from the GitHub COVID-19 repository of Johns Hopkins University (github.com/CSSEGISandData/COVID-19) [1]. We focused on the pre-vaccination and pre-variants-of-concern phase of the pandemic (from February 15 to December 31, 2020), using days as the time unit. For each country, pre-pandemic days (those in which the number of cumulated cases was <2) were excluded from the analysis. Likewise, countries that reported fewer than 60 days of new cases and mobility data were excluded, leaving a final dataset of 125 countries and 52 United States states/regions.

The *Rt* was computed for each country and each day retrospectively from the case incidence data over the entire period using the R package EpiEstim [15]. In our computations of *Rt*, we used the serial interval derived from a meta-analysis of 64 studies (mean, 5.15 days; 95% confidence interval [CI], 4.73 to 5.57) [16]. The time-series for *Rt*, new cases, cumulative cases, and mobility indicators are provided as Supplemental Material 1.

Statistical Analysis

For each country/region and mobility indicator, the data pre-processing described above yielded 60-316 *Rt*/indicator pairs, 1 per day of observation (with a median of 299 days of observation across countries/regions). Supplemental Material 2 presents the corresponding data as scatter plots with mobility indicators and *Rt* shown on the x and y axes, respectively.

For each country, *Rt*/mobility indicator correlations were defined as the R coefficient of the Pearson test for linear correlations, yielding 1 number (the *Rt*/mobility indicator covariance) per country per *Rt*/mobility indicator pair:

$$R = \frac{\sum_{d=1}^{D}[(Rt(d) - \overline{Rt}) * (M(d) - \overline{M})]}{\sqrt{\sum_{d=1}^{D}(Rt(d) - \overline{Rt})^2} * \sqrt{\sum_{d=1}^{D}(M(d) - \overline{M})^2}}$$

where *M* is a mobility indicator, *D* is the number of data days (d) with *Rt*/mobility scored for this country, and $\overline{Rt}$ and $\overline{M}$ are, respectively, the *Rt* and *M* averages over the observation period (*D* days). This coefficient characterizes the linear correlations between mobility indicators and the *Rt* coefficient computed for the same day (+1: perfect correlation; -1: perfect anti-correlation). However, it is theoretically possible that the *Rt* determination could yield time-lagged estimates of the reproduction number. To mitigate the effects of time lags in *Rt* determination, we also computed correlations between mobility indicators and time-lagged *Rt* coefficients, with a time lag from 1 day to 30 days:

$$R(d_0) = \frac{\sum_{d=1}^{D}[(Rt(d + d_0) - \overline{Rt}) * (M(d) - \overline{M})]}{\sqrt{\sum_{d=1}^{D}(Rt(d) - \overline{Rt})^2} * \sqrt{\sum_{d=1}^{D}(M(d) - \overline{M})^2}}$$

where d_0=1…30 is the time lag (in days) between the mobility indicator *M* and *Rt* in the covariance estimation [4,17]. This analysis yielded, for each country and mobility indicator, a curve $R(d_0)$ showing the R coefficient of the linear Pearson test as a function of the time lag.

In several countries, the *Rt* versus mobility scatter plots (either same day or time-lagged) showed non-monotonic distributions of the daily *Rt*/mobility values, translating into poor fits of the data with the Pearson correlation coefficient and the linear relationships between *Rt* and mobility variables (i.e., data fitted to a linear model $R_t = a * M + b$, where a and b are fitting parameters). In these instances, the data were fitted with the simplest model that accounted for non-monotonic correlations: a quadratic model $R_t = a * M^2 + b * M + c$, where a, b, and c are fitting parameters (Supplemental Material 2).

When specified, *Rt*/mobility indicator correlations were corrected for autocorrelations using the standard procedure. First, the residuals (ε) of the original *Rt* versus mobility indicator linear fit (Pearson) were subjected to the Durbin and Watson test [18,19] evaluating the null hypothesis (ρ=0) in a model with time-correlated residuals between a day (d) and the day preceding it: $\varepsilon(d) = \rho * \varepsilon(d-1) + w$, where w corresponds to white noise. When applicable (null hypothesis rejected), the Durbin and Watson test [18,19] returned the coefficient ρ that fits the residual correlations the best. The ρ-corrected residuals were poorly correlated, indicating that the autocorrelations in our data had predominantly a first-order autoregressive AR(1) structure. We next used the Cochrane and Orcutt [20] procedure to correct the input time series $R_t(d)$ and mobility indicators $M(d)$, defining autocorrelation-free time-series: $R_t^*(d) = R_t(d) - \rho * R_t(d-1)$, and $M^*(d) = M(d) - \rho * M(d-1)$, that were finally used to compute the autocorrelation-corrected *Rt*/mobility correlations as defined above for $R_t(d)$ and $M(d)$.

The Google COVID-19 Community Mobility Reports [2] and Johns Hopkins University [1] datasets provided detailed data for the 51 United States states and the unincorporated territory of Puerto Rico. We took advantage of this increased resolution within the United States to compute, in addition to the country-wide correlations, same-day and time-lagged correlations for each state/territory independently using the same methodology as for countries.

We used R version 4.04 (https://www.R-project.org) for all computations. Correlations and time-lagged correlations were also computed using our custom analysis scripts written in MATLAB version R2019b (https://www.mathworks.com/) and the results were confirmed (data not shown).

Ethics Statement

This study needed no ethical review since the observations concerned countries, not identified persons.

RESULTS

We curated daily country/region-specific SARS-CoV-2 infections incidence data [1] and human mobility data [2] from public databases, and computed the effective viral reproduction index *Rt* and 6 mobility indicators for each country/region and each day retrospectively over the entire analysis period (February 15 to December 31, 2020; see Figure 1, Methods for details, and Supplemental Material 1).

Mobility and *Rt* data were aggregated for 125 countries, as well as 52 United States states/regions (51 states+Puerto Rico), yielding for each country/region, and for each mobility indicator pair or *Rt*/mobility indicator pairs, scatter plots representing the daily data (Supplemental Material 2). Next, these data were used to compute statistical correlations (Pearson correla-

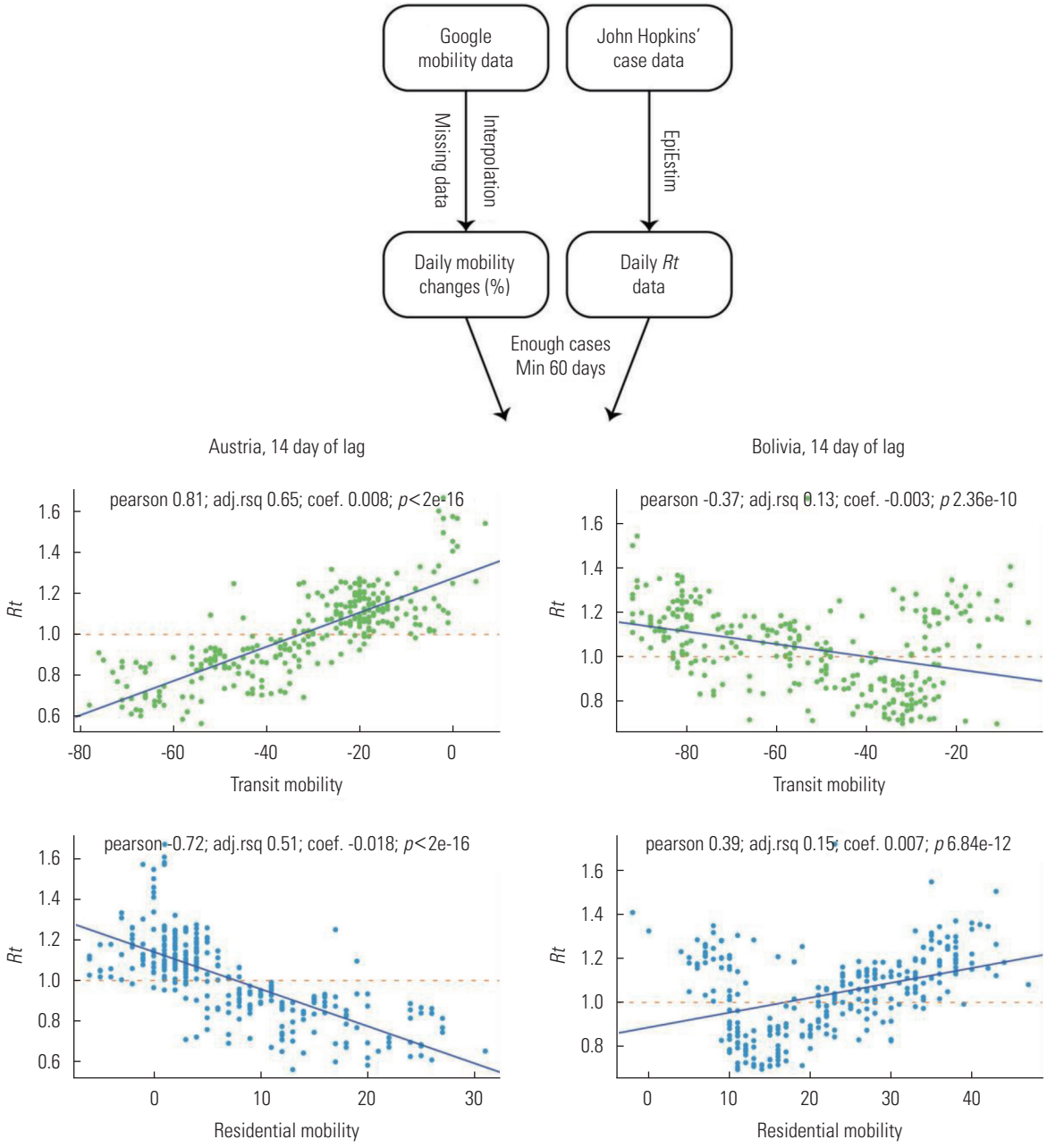

Figure 1. A methodology to probe correlations between effective reproduction number (*Rt*) and mobility indicators. Schematics showing our analysis pipeline (see Methods for details). Same-day and time-lagged *Rt* versus mobility indicators scatter plots (bottom) were tested for linear correlations (R from the Pearson test, adjusted R-squared from the linear regression model, beta coefficient of the mobility indicator from the linear regression equation, *p*-value from the linear regression model). Shown are the *Rt* versus transit mobility (top) and *Rt* versus residential mobility (bottom) scatter plots for 2 exemplary countries, Austria (left, group 1), and Bolivia (right, group 2), with a time lag of 14 days. The dotted orange horizontal line represents the level of *Rt*=1, below which disease spread is halted.

tion coefficient [R]; Figure 1 and Methods) between mobility indicators and mobility indicators/*Rt* for the entire analysis period (Figure 2 and Supplemental Material 3) or for particular subperiods when indicated (Supplemental Material 4). Correlations were computed both across variables estimated at the same time point ("same-day" correlations, Supplemental Material 2) or as a function of a time-lag between mobility indicators and mobility indicators/*Rt* (Figure 2 and Supplemental

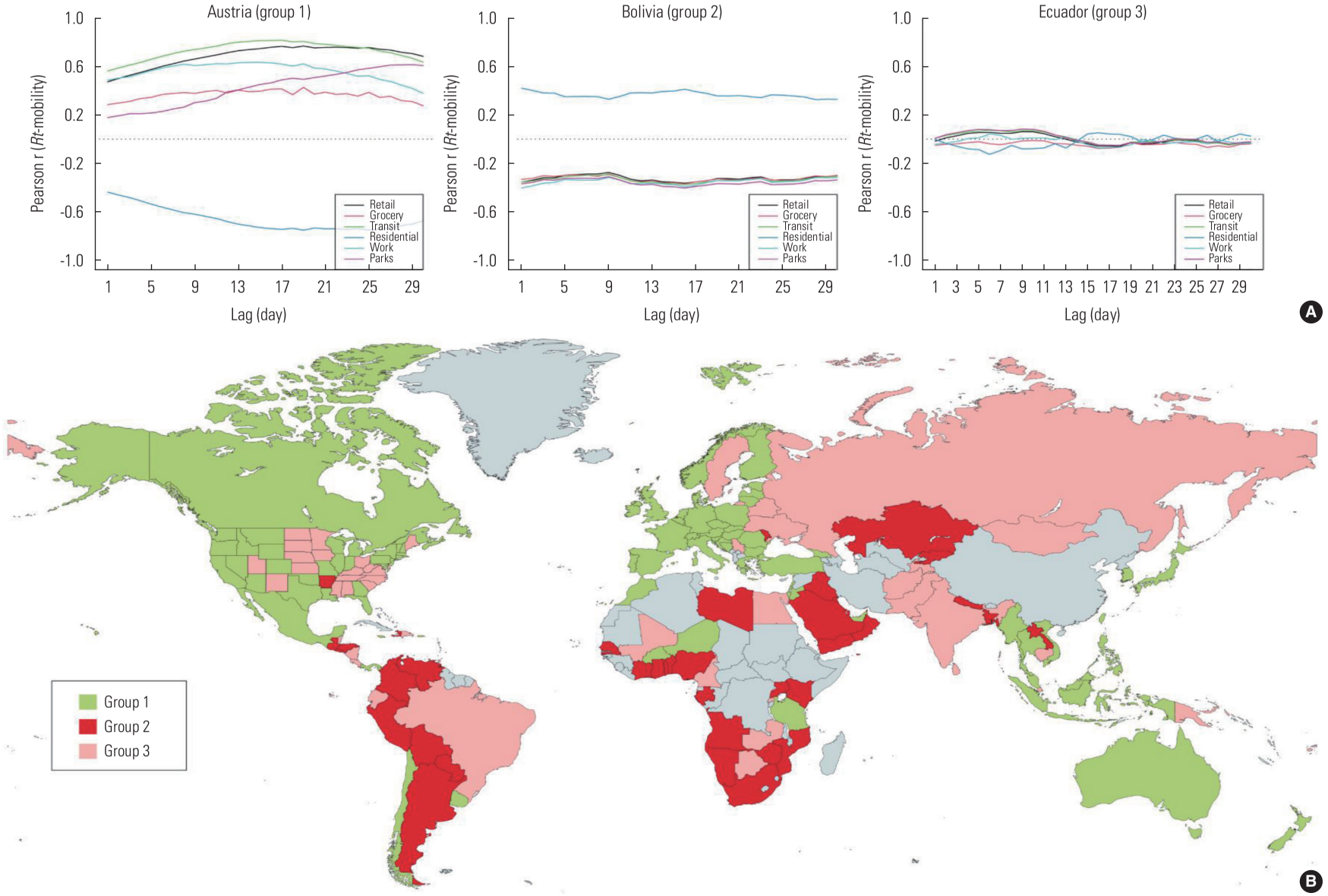

Figure 2. Contrasting effective reproduction number (*Rt*) versus residential mobility correlations identifies 3 groups of countries. (A) *Rt* versus mobility indicators (Pearson R coefficient; *y*-axis, as output by the Pearson tests) as a function of time-lag (*x*-axis) for 1 exemplary country of each group: Austria (left, group 1), Bolivia (middle, group 2), and Ecuador (right, group 3). All mobility indicators are shown with the indicated colors. (B) Map of the world showing countries/regions in group 1 (negative *Rt* vs. residential mobility, green), group 2 (positive *Rt* vs. residential mobility, red), and group 3 (complex patterns, pink). The map was generated with mapchart.net. Countries/regions where data were not available or insufficiently documented are shown in gray (see Methods).

Materials 3 and 4).

After establishing the impact of autocorrelations and the comprehensiveness of the mobility indicators (Supplemental Materials 5 and 6), we analyzed the correlations between *Rt* and mobility indicators with a time lag from 0 days to 30 days [4,17]. In most countries, the sign of the Pearson correlation coefficient for *Rt* versus residential mobility was independent of the time lag, and minimal variations of the correlation coefficient modulus were observed (Figure 2A). The correlations of *Rt* versus other mobility indicators were often opposed to that of *Rt* versus residential mobility, in agreement with residential mobility being systematically anti-correlated with other mobility indicators.

Based on these observations, 3 groups of countries emerged: (1) Group 1: countries with *negative Rt* versus residential mobility correlations regardless of the time lag (Supplemental Material 3). This correlation pattern will be referred to hereafter as "normal". These countries included, as previously published, the United States [8], Turkey [7], and many others, mostly in Europe, North America, and Asia, including South and East Asia (58 countries; Figure 2B, green; Table 1; and Supplemental Material 7). (2) Group 2: countries with *positive Rt* versus residential mobility correlations regardless of the time lag (Supplemental Material 3). This correlation pattern will be referred to as "inverted". These countries included many Central/South American, African/Caribbean countries, and some others (39 countries; Figure 2B, red; Table 1; and Supplemental Material 7). (3) Group 3: other countries showing a time lag-dependent sign of the *Rt* versus residential mobility correlations ("inconclusive"). Countries belonging to this third group were scattered all over the globe (28 countries; Figure 2B, pink; Table 1; and Supplemental Material 7). Many United States states/regions also displayed group 3-like correlations (Figure 2B).

For all groups, time-series autocorrelations in *Rt* and residential mobility strongly contributed to *Rt* versus residential mobility correlations. Indeed, removing first-order correlations using the Cochrane and Orcutt [20] procedure with an autocorrelation parameter determined by the Durbin and Watson test [18,19] strongly attenuated the magnitude of the Pearson coefficient for *Rt* versus residential mobility, but generally not its sign (Supplemental Material 5). Hence, *Rt* versus residential mobility correlations stemmed from complex, time-correlated processes in viral transmission.

The existence of groups 2 and 3 *per se* contradicted the commonsense belief that increasing residential mobility (to the detriment of other types of mobility, Supplemental Material 2), should correlate with a *drop* in SARS-CoV-2 reproduction number. While this was true for group 1 countries, our data showed that for many countries, increased residential mobility correlated with an *increase* in *Rt*. Hence, strict policies reinforcing residential mobility could be counter-productive in reducing viral spread.

We next investigated whether there are optimal mobility patterns with respect to their correlation with the lowest possible *Rt*. For this purpose, we directly reanalyzed the scatter plots of *Rt* versus mobility indicators (Supplemental Material 2).

We specifically considered countries from groups 2 and 3. For many of these countries, the *Rt*/residential mobility scatter plot could not be accurately fitted with a linear model, explaining the often-low R score modulus in the Pearson test. This was due to a U-shaped distribution of daily data in the *Rt*/residential mobility scatter plots for these countries (Supplemental Material 2). The use of the simplest non-linear model, a quadratic model, strongly improved the fitting of this data, as exemplified in Figure 3. Minimal *Rt* values often correlated with partial changes in mobility indicators (15-30% increase in residential mobility, and a 20-50% decrease in other mobility indicators). This result indicates that in many countries, partial mobility restrictions might be more efficient in reducing the *Rt* of SARS-CoV-2.

DISCUSSION

An efficient assessment of the impact of governmental mobility restriction policies to mitigate COVID-19 spread requires a better understanding of the complex interplay between mobility and the *Rt* of SARS-CoV-2. Conflicting reports have indicated that this interplay could be country-dependent or region-dependent [7-12], calling for a systematic investigation of the correlations between the SARS-CoV2 *Rt* and human mobility at the country level. In this study, we examined correlations between *Rt* and a comprehensive set of mobility indicators provided by Google COVID-19 Community Mobility Reports, at the global scale in 125 countries and 52 United States states/regions, from February 20 to December 31, 2020. We examined, in-depth, the sign and linearity of the correlations between *Rt* and 6 mobility indicators. Our approach resembled the methodology used by Oh et al. [13], but used the *Rt* as a metric to quantify disease spread, as recommended in the literature [5,6], and also extended the analyses well beyond

Table 1. Correlations between the effective reproduction number and residential mobility distinguish 3 groups of countries and United States regions

Group 1		Group 2		Group 3	
Countries (n=58)	**States/Regions (n=31)**	**Countries (n=39)**	**States/Regions (n=1)**	**Countries (n=28)**	**States/Regions (n=20)**
Australia	Alaska	Angola	Arkansas	Afghanistan	Alabama
Austria	Arizona	Argentina	-	Belarus	Delaware
Barbados	California	Bahrain	-	Belize	Dis. of Columbia
Belgium	Colorado	Bangladesh	-	Botswana	Iowa
Bosnia and Herzegovina	Connecticut	Benin	-	Brazil	Kansas
Bulgaria	Florida	Bolivia	-	Cambodia	Kentucky
Burkina Faso	Georgia	Cabo Verde	-	Cameroon	Maine
Burma	Hawaii	Colombia	-	Costa Rica	Minnesota
Canada	Idaho	Cote d'Ivoire	-	Dominican Republic	Mississippi
Chile	Illinois	El Salvador	-	Ecuador	Nebraska
Croatia	Indiana	Gabon	-	Egypt	New Mexico
Czechia	Louisiana	Ghana	-	Fiji	North Carolina
Denmark	Maryland	Guatemala	-	India	North Dakota
Estonia	Massachusetts	Haiti	-	Mali	Ohio
Finland	Michigan	Honduras	-	Mongolia	South Carolina
France	Missouri	Iraq	-	Nicaragua	South Dakota
Georgia	Montana	Kazakhstan	-	Pakistan	Tennessee
Germany	Nevada	Kenya	-	Papua New Guinea	Utah
Greece	New Hampshire	Kuwait	-	Russia	Virginia
Hungary	New Jersey	Kyrgyzstan	-	Rwanda	West Virginia
Indonesia	New York	Laos	-	Serbia	-
Ireland	Oklahoma	Libya	-	Singapore	-
Israel	Oregon	Moldova	-	Sri Lanka	-
Italy	Pennsylvania	Mozambique	-	Sweden	-
Jamaica	Puerto Rico	Namibia	-	Tajikistan	-
Japan	Rhode Island	Nepal	-	Trinidad and Tobago	-
Jordan	Texas	Nigeria	-	Ukraine	-
Latvia	Vermont	Oman	-	Zambia	-
Lebanon	Washington	Paraguay	-	-	-
Lithuania	Wisconsin	Peru	-	-	-
Luxembourg	Wyoming	Qatar	-	-	-
Malaysia	-	Saudi Arabia	-	-	-
Mauritius	-	Senegal	-	-	-
Mexico	-	South Africa	-	-	-
Morocco	-	Togo	-	-	-
Netherlands	-	Uganda	-	-	-
New Zealand	-	Venezuela	-	-	-
Niger	-	Yemen	-	-	-
Norway	-	Zimbabwe	-	-	-
Panama	-	-	-	-	-
Philippines	-	-	-	-	-
Poland	-	-	-	-	-
Portugal	-	-	-	-	-
Romania	-	-	-	-	-
Slovakia	-	-	-	-	-
Slovenia	-	-	-	-	-
South Korea	-	-	-	-	-
Spain	-	-	-	-	-
Switzerland	-	-	-	-	-
Taiwan	-	-	-	-	-
Tanzania	-	-	-	-	-
Thailand	-	-	-	-	-
Turkey	-	-	-	-	-
United Arab Emirates	-	-	-	-	-
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Vietnam	-	-	-	-	-

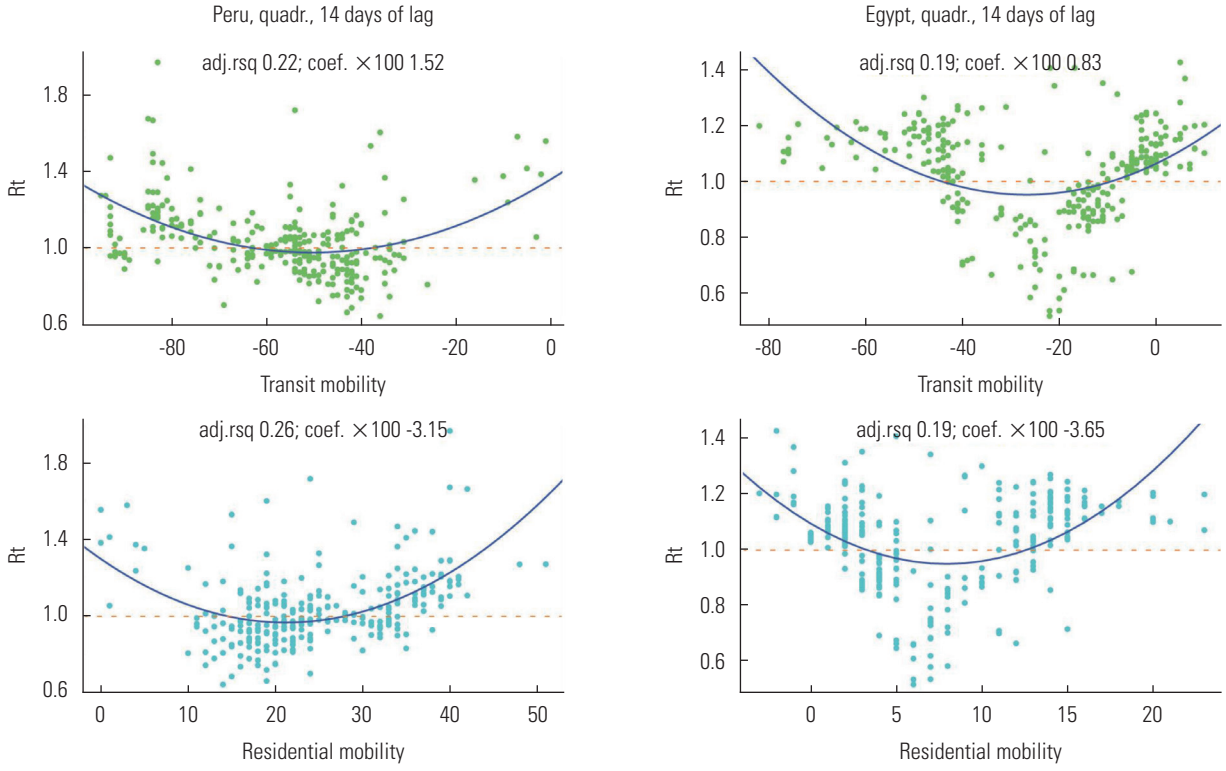

Figure 3. Minimal effective reproduction number (*Rt*) values correlate with intermediate mobility restrictions. *Rt* versus transit mobility (top) and *Rt* versus residential mobility (bottom) scatter plots for two exemplary countries, Peru (left, group 2) and Egypt (right, group 3), with a time lag of 14 days. Data were fitted with a quadratic model (adjusted R-squared from the quadratic regression model, beta coefficient [multiplied by 100] of the first-level mobility indicator factor in the quadratic regression equation), which outperformed the linear Pearson model for these countries. The dotted orange horizontal line represents the level of *Rt*=1, below which disease spread is halted.

OECD countries. Our methodology allowed us to identify novel, unexpected *Rt* versus mobility correlations that have the potential to guide the refinement of mobility restriction policies differentially across countries. For instance, we discovered that 3 groups of countries could be distinguished in terms of the sign of the correlations between *Rt* and residential mobility: countries with *negative Rt* versus residential mobility correlations ("normal" correlations; group 1, e.g. the United States [8] and Turkey [7], or most OECD countries in agreement with Oh et al. [13]); countries with *positive Rt* versus residential mobility correlations ("inverted" correlations, group 2), which have never been reported in a peer-reviewed publication, to the best of our knowledge; and countries with more complex correlation patterns ("inconclusive" correlations, group 3). While *Rt*/mobility correlations were often linear, particularly for group 1 countries, for many group 2-3 countries, they were U-shaped, indicating an optimal level above which increasing residential mobility is counterproductive. Finally, we also observed (some) variability within United States regions, and we stress that repeating our approach at a regional resolution within countries could provide a finer-grained understanding of the factors that govern the *Rt* versus residential mobility correlations.

Since this study was solely based on correlation analyses, it does not allow conclusions to be drawn on what caused the inverted correlations. However, based on the regional variability within the United States data, we highly doubt the possibility that factors such as the overall population density, the health system/case reporting system capacities, and the climate could explain the inverted correlations on their own. In contrast, population repartition/lifestyle seemed to play a role since most rural United States states/regions belonged to group 3, while more urban/industrial states/regions belonged to group 1. The gross domestic product per capita (GDPpc) or the Human Development Index (HDI), could also play a role, since group 1 was enriched in countries with high GDPpc/HDI; nonetheless, these

parameters alone are not sufficient to fully explain the distribution of countries across the 3 groups, though they can contribute to the variable extent (Supplemental Material 6). Confining populations at home in some countries led to an increase in viral spread within familial units, where social distancing was not used. This interpretation of the data would give weight to sociological factors, such as the size of the familial unit or the interpersonal distance, in the *Rt* versus residential mobility correlations. Data for the mean personal distance between strangers, acquaintances, and close relations have been published for 42 countries [21]. It would be informative to extend these measurements to cover all 125 countries analyzed in our study and systematically analyze the links between interpersonal distances and *Rt* versus residential mobility correlations.

We stress that in order to make relevant comparisons of the viral spread versus mobility correlations across countries, we have restricted our analysis to 2020 data (i.e., prior to mass vaccination). One consequence is that our dataset does also not account for potential effects of the Delta/Omicron variants, or other variants of concern, on *Rt* versus mobility correlations. While this means that our findings are unlikely to be biased by the difference in contagion dynamics between the new variants and the original SARS-CoV-2 strain, it also means that similar analyses of disease spread versus mobility data after December 2020 would be required to account for the particularities of variants of concerns. *Rt* computations might also be confounded by isolated events affecting contagion at a broad scale, such as superspreading events. However, such events are likely impactful in very early stages of the pandemic as demonstrated in Korea by Lim et al. [22], while our conclusions are based on data aggregated until the end of 2020, well after the pandemic rise in most countries. Hence, we believe that our results, based on a comprehensive analysis over a long time period, are robust against isolated early pandemic events. It is, yet, in theory possible that superspreading events played a role in the association of positive correlations between *Rt* and residential mobility in group 1, particularly in early stages of the pandemic. Moreover, our analysis was limited to correlation analyses, and therefore is not sufficient to draw conclusions on the causes of opposite sign *Rt*/mobility correlations in different countries/regions. Our analysis of the variability within United States data makes it possible to rule out certain geographic or demographic factors as being the sole sources of positive *Rt*/mobility correlations, yet our analysis overlooks sociological or ethnic/genetic factors. In particular, it is possible that the link between movement restriction and disease spread is affected by other mitigation measures and individual behaviors that would have strong national specificities.

In conclusion, in this work, we have identified 3 groups of countries where correlations between the SARS-CoV-2 *Rt* and residential mobility were qualitatively opposite during the first year of the pandemic, or where minimal *Rt* values correlated with intermediate mobility restrictions. Our results underline the importance of systematically characterizing *Rt* versus mobility correlations at a regional/national resolution, in order to understand the country-specific range of mobility control that minimizes the *Rt* and optimally adjust movement restriction policies to mitigate COVID-19 spread. Our work took a first step at closing this gap. We believe that our results could guide the refinement of mobility restriction policies differentially across countries in the future.

SUPPLEMENTAL MATERIALS

Supplemental materials are available at https://doi.org/10.3961/jpmph.21.522.

CONFLICT OF INTEREST

The authors have no conflicts of interest associated with the material presented in this paper.

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The R code used for analysis can be found here: https://github.com/mounirsetti/COVID-19-Rt-and-Mobility-Patterns.

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AUTHOR CONTRIBUTIONS

Both authors contributed equally to conceiving the study, analyzing the data, and writing this paper.

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