Charles University

Faculty of Social Sciences
Institute of Economic Studies

MASTER'S THESIS

Where did people die? An international assessment of a potentially positive relationship between economic development and the severity of COVID-19 outbreaks.

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Academic Year: **2022/2023**

Declaration of Authorship

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Strasbourg, April 28, 2023 Jean-Baptiste Marigo

Abstract

This paper studies the relationship between development and COVID-19 severity at the country level, expressed as total deaths per million inhabitants. The original perspective of this work is to consider that economic development factors could have a causal effect on COVID-19 deaths, instead of studying the inverse relationship. Bayesian Model Averaging procedures are used to select the most relevant predictors from a set of 21 candidate variables, using cross-sectional data from 01/01/2020 to 10/30/2022. This method solves the uncertainty issue on a topic where many potential factors could be included. In the end, four variables are selected based on their statistical significance, on the size of their standard deviation, and on other interpretability considerations. Ranked by order of importance, these predictors are the *median age*, *overweight prevalence*, *democracy index*, and *(hydroxy)chloroquine* variables, although the latter suffers from certain weaknesses. As three of these variables are characteristic of development, these robust results suggest that as a country develops, it becomes more vulnerable to outbreaks such as the COVID-19 one. This paper therefore concludes that public health policies should focus on these variables to mitigate the impact of development on the severity of future similar pandemics.

JEL Classification	I14, I15, I18, O1, O5
Keywords	Development, COVID-19, cross-country, Bayesian Model Averaging (BMA)
Title	Where did people die? An international assessment of a potentially positive relationship between economic development and the severity of COVID-19 outbreaks

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Master's Thesis Proposal

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Defense Planned:	June 2023		

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Proposed Topic:

Where did people die? An international assessment of a potentially positive relationship between economic development and the severity of COVID-19 outbreaks.

Motivation:

Now the COVID-19 crisis is hopefully coming to an end, or at least to a more stable pace, the time has come to look back at the pandemic and analyse the determinants of its dynamics. Indeed, after more than two years of outbreaks all around the world, we are left with unexplained differences across countries between their various human tolls. Furthermore, although the literature on the impact of the pandemic on the economy has rapidly proliferated, the opposite relationship remains less explored.

Beyond the papers that tackle the impact of inequality in societies in terms of vulnerability to the virus, little is known about the economic determinants of the COVID-19 damage across countries. I intend on contributing to the emerging literature on this topic by proposing to explain why or why not there is a positive relationship between the economic development of a country and the severity of its outbreaks, such as suggested by the intuitive comparison of world maps related to economic development and maps related to COVID-19 cases, hospitalisations, and deaths.

Indeed, it does not necessarily seem intuitive to think that the more developed countries could have suffered more from the pandemic. On the other hand, demographic factors could also crowd out the effects of economic development on COVID-19 outbreaks severity. Thus, there is a space for scientific research in terms of the economic determinants of the virus impact on populations across countries.

Hypotheses:

The global question of this paper would be "Where did people die?", but we can also somehow understand it as "why" did people die, in terms of which economic factors were determinants of COVID-19 outbreaks severity (cases, hospitalizations, deaths), whether related to the configuration and development of health systems in different countries and types of countries, or more generally to the economic development of countries in different regions of the world.

Thus, overlaying maps such as the HDI, GDP per capita, and death per million inhabitants per country maps already gives an idea of which hypotheses could be tested. Indeed, there seems to be potentially positive relationships (at least correlations) between some of these variables and the explained variable (COVID-19 outbreaks severity). This already yields a few possible hypotheses to test using econometrically relevant approaches:

1. Hypothesis #1: There is a positive relationship between the economic development of a country and the severity of COVID-19 outbreaks.

2. Hypothesis #2: The disparity in terms of severity of COVID-19 outbreaks between countries is in fact due to demographic differences.

3. Hypothesis #3: The different degrees of COVID-19 outbreaks severity across countries are due to socio-economic variables other than demographic variables.

Methodology:

Data on COVID outbreaks severity at the international, regional, and national scale is available on the WHO online databases, as well as on each country's national health database (although the data is likely to be less comparable in this way, it provides us with the possibility of studying each country's available data in detail).

On the other hand, it is also possible to access aggregated data on GDP per capita, HDI, or other economic development indicators on the World Bank online database, as well as once again on many governments' national databases. It could also be relevant to explore economic inequality as a determinant of COVID-19 outbreaks severity, using aggregated data from the World Inequality Database (WID).

Other sources such as Our World in Data can also provide us with additional data for many countries and regions of the world, both in terms of COVID-19 and economic development data.

1. Hypothesis #1: There is a positive relationship between the economic development of a country and the severity of COVID-19 outbreaks.

To test this hypothesis, it could be quite intuitive to use aggregated and comparable data on different economic development variables such as GDP per capita, or the HDI, and to econometrically check whether they have any explanatory power over the "severity" of COVID-19 outbreaks, using proxies such as COVID-19 deaths, hospitalisations per million inhabitants, or even the positivity of tests. However, one must be sure that the data is comparable, especially since tests were used in very different ways depending on countries, making it harder even for available online databases to build a comparable aggregated set of data.

2. Hypothesis #2: The disparity in terms of severity of COVID-19 outbreaks between countries is in fact due to demographic differences.

Data on demographics can be found on multiple online databases such as from the WHO, from the OECD, the Institute for Health Metrics and Evaluation (IHME), for example. They can provide us with the age structure of the population for each country, which will allow us to test for any relationship between demographic differences and COVID-19 outbreaks severity difference.

Although the awaited result is very intuitive, the next step would be to check whether adding the age structure variable does crowd out the effect of economic development on the explained variable.

3. The different degrees of COVID-19 outbreaks severity across countries are due to socio-economic variables other than demographic variables.

If the introduction of demographic variables does not crow out all the effect of the economic development variable, then it is possible that other socio-economic predictors help to explain the impact on COVID-19 severity. Otherwise, there could also be non-socio-economic variables that play an important role, which can be used as controls if identified.

Expected Contribution:

The results of this paper could be part of the foundation of the growing literature on the assessment of the COVID-19 outbreaks and their related causes and consequences, including in terms of economic determinants.

I intend to prepare to lay the ground for further questioning in terms of the dynamics and mechanisms of COVID-19 as a virus evolving in different societies, with different economic development levels and socio-economic characteristics.

Outline:

Literature review:

On topics related to the determinants of COVID-19 outbreaks severity, not necesseraily only in terms of its economic determinants, but also in terms of other potentially relevant variables, that could be used as control variables.

Analysis of the role played by economic development

This part would aim at verifying whether the level of economic development, such as measured by the GDP per capita or the HDI variables, is a positive and important determinant of the severity of the COVID-19 outbreaks or not.

The influence of demographic characteristics

Characteristics such as the age structure of a population are very likely to impact the severity of the outbreaks across countries. Furthermore, it is also possible that it crowds out the effects of economic variables on the explained variable.

Different socio-economic characteristics

Variables other than demographic factors could still be hidden by the economic development one. The aim would be to disentangle these effects and identify those predictors, as well as other non socio-economic factors which we could use as controls.

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Introduction

Many papers evaluate the impact that the COVID-19 crisis had on the economy across countries. However, since the World Health Organisation (WHO) declared a pandemic on 11th March 2020, few studies have tried to identify whether country characteristics could explain the differences in COVID-19 cases and deaths between states. Such characteristics should be related to the degree of development of countries, as the latter is closely linked to public health. Indeed, ground-breaking studies on less developed countries such as the ones that led Banerjee, Duflo and Kremer to be awarded the Nobel Memorial Prize in Economic Sciences (KVA, 2019) have revealed the dramatic consequences of underdevelopment, including in terms of public health. However, the development economics literature has also proved that beyond being a component of development on its own, health is also crucial in supporting progress in fields such as education and economic growth. To this extent, Todaro & Smith (2015, p.382) also write that health plays a dual role as both input and output of economic development. This means that developed countries should be more protected against epidemics, whether in their spreading or their ability to cause physical harm, for example in terms of lethality. These measures of the impact of a disease on a population are further referred to as the degree of *severity*. Thus, the severity of COVID-19 waves should be approximated with proxies such as COVID-19 cases, hospitalisations, or deaths, for example. Nevertheless, it appears that less developed countries were *spared* by the COVID-19 pandemic compared to more developed countries. For example, the two maps of the cumulative number of COVID-19 deaths on the 8th of October 2022 (Mathieu et al., 2020/2022) and of the pre-crisis Human Development Index (HDI) of countries in 2019 (Roser, 2014/2022) intuitively suggest that such a correlation does exist. To this extent, the COVID-19 pandemic would directly contradict the development economics literature on the relationship between development and health. Todaro & Smith (2015, p.412) qualify AIDS, malaria, and parasitic worms as the "three major scourges of the developing world", as part of the "disease burden" that less developed countries bear. In this case, it could be that the COVID-19 pandemic was in fact the *scourge* of the developed world.

This paper aims to find out whether country determinants of development did act as positive factors of COVID-19 severity at the national level. Should such a relationship exist, this study then attempts to identify these country characteristics and to estimate the magnitude of their effects on the response variable. Thus, three hypotheses are tested in this paper. First, this study evaluates whether direct components of development are positively associated with an increase in COVID-19 severity. Second, the potential role of demographic differences, such as the age structure of a population, is explored. Indeed, such predictors could act as intermediary variables between economic development and COVID-19 severity. Third, this paper also checks whether other additional factors can explain the variations of the response variable

observed at the country level. Compared to the existing literature on this topic, this study thus chooses an original perspective with respect to the direction of causality that is assessed between development and COVID-19 severity. Furthermore, while some authors have tried to explore this relationship, many have stopped at assessing a correlation. In this paper, the choice of the data collection period ensures that the temporal sequence of the explanatory variables with respect to the response variable only allows the effects of the desired causality relationship to be estimated. Additional theoretical arguments that stem from the commonly assumed relationship between economic development factors and epidemics further support the existence of causation beyond correlation. On the other hand, as it has already been proved in the literature that statistically significant results can be found despite the limited number of countries for which data is available, this paper uses cross-sectional data. Compared to time series, this approach is more fitted to explaining the impact of pre-crisis factors on the outcome, although the results for post-outbreak variables are more difficult to interpret. The use of Bayesian Model Averaging (BMA) procedures as a methodological choice also adds to the quality of the results as it allows for the uncertainty issue to be solved. Indeed, it is likely that the number of determinants of a pandemic severity at the country level is very high. To this extent, many candidate variables in the literature could be used in a regression model to study this relationship. The chosen approach allows for many predictors to be included in the analysis, as the BMA method can be used to run all possible linear regression model combinations of the candidate covariates. These procedures thus compute statistics related to their statistical significance as well as weighted coefficients. In the end, this method yields results that provide strong evidence on which explanatory variables should be selected in a linear regression model specification, and allows for very accurate coefficients to be estimated. The initial set of candidate predictors is built based on the selection of the most relevant variables highlighted in the literature, and on the identification of other potential parameters that had not been yet included in this type of work. Stojkoski et al. (2022) already studied the correlates that could explain country differences in COVID-19 deaths and cases using a BMA approach. However, their work only focuses on the first wave of COVID-19 and use a smaller sample whose composition is less random than in this paper. To this extent, it is possible that their results are not representative of all countries. In this study, the sample suffers less from the non-random exclusion of countries and uses actualised COVID-19 severity data on the 01/01/2020 – 10/30/2022 period. Furthermore, the composition of the data allows for the results to be generalisable to the population of large continental countries, above the one-million inhabitants threshold. Finally, a total of 8 BMA settings is used, based on different parameters. First, these settings can differ in terms of the inclusion or exclusion of data on inequality, which also has consequences on the sample size. Second, a BMA configuration can also include post-outbreak predictors, referred to as *government response* variables such as the use of restrictions, early treatments or vaccination campaigns. Finally, different types of BMA procedures either use a

uniform prior or a *dilution* prior based on whether the effects of multicollinearity are taken into account or not in the estimation process. These elements are further described in the methodology section. The robustness of the results can therefore be assessed across the outputs of the 8 BMA settings used in this paper. In the end, 6 of the initial set of 21 candidate variables are selected based on their statistical significance and on the size of their standard deviation. However, only 4 of them can then be reliably interpreted, due to certain limitations. Among them, the ones whose coefficient magnitude, statistical significance, and robustness are the highest are the *overweight prevalence* (%) and the *median age* (years) of a population. As their estimates are positive, this means that both increases in overweight prevalence and in the age of a population aggravate the outcome in terms of COVID-19 severity. Second, it also appears that the *democracy index* predictor has a positive, important, and fairly robust impact on COVID-19 fatalities per million at the country level. Finally, as part of the *government response* group, the *(hydroxy)chloroquine* early treatment variable has a non-negligeable negative effect on the response variable, although its robustness to changes in the BMA configuration is limited. The *overweight prevalence*, *median age*, and *democracy* variables are all characteristics of development, to some extent. These results therefore have serious implications for future national and global public health issues. Indeed, as countries develop, it is likely that they become more vulnerable to pandemics such as the COVID-19 one. Although this conclusion seems to contradict the development economics literature, it is in fact likely that the nature of this virus is different from diseases as AIDS and malaria, which would explain the difference in findings in this study. This still means that as countries develop, they should become more vulnerable to pandemics that target older and overweight segments of the population. Furthermore, compared to non-democratic decision-making, deliberative processes appear to be less efficient in quickly implementing effective responses to fight against a pandemic. Therefore, the results in this paper suggest that future public health policies should focus on targeting the most vulnerable segments of a population. This conclusion is all the more important as development is associated with more democratic country characteristics, and therefore to more vulnerability to this type of outbreak. Finally, the *(hydroxy)chloroquine* predictor also suffers from the potential undesired effects of double causality. Indeed, the variables of the *government response* group do not use pre-crisis data, which means that temporal sequence considerations blur the causality relationship with the response variable. Still, elements suggest that the *(hydroxy)chloroquine* predictor should not be as affected as other covariates of the same category, such as the *stringency* variable, which measures the degree of restrictions used by government during the pandemic. Finally, the coefficient of the *population mean* (thousands) predictor is inconsistent with the literature. To this extent, no plausible and reliable interpretation has been found to explain the statistical significance, negativity, magnitude, and moderate robustness of its coefficient. This weakness is a limitation of this work, which could either be due to an omitted variable bias, or to the inability to find strong

theoretical ground for this variable's results. The different steps of this analysis are organised as follows.

In a first section, previous works on this topic are summarised, with special attention on the results that have already been found, the different relevant variables to include in the analysis, as well as the existing available methods that can be used (I). The second section explains in detail the final methodology followed to carry out this research, including in terms of theoretical background, choice of variables, as well as data collection and transformation (II). Finally, this paper ends with a third section in which the final results are presented, criticised, interpreted, and discussed. Thus, they are compared to already existing findings, and their implications with respect to national and global health policy issues are explored (III).

I - Literature review

1) Findings

Although we mentioned that few papers have tried to specifically study the role of development characteristics as determinants of the severity of COVID-19 waves, some authors did conclude on the existence or absence of such a relationship.

In a paper that studies the change in new COVID-19 cases to Gross Domestic Product (GDP) per capita for European countries during the first wave of the pandemic, Drydakis & Pardhan establish that there is a negative correlation between the two variables. To do so, they use a linear regression model, and also add key additional variables such as public expenditure and life expectancy to disentangle any hidden effects (Drydakis & Pardhan, 2021, p.4). This result corresponds to the development economics idea that countries that are more developed suffer less from public health issues, including in terms of the spread of a disease. On the contrary, Toya and Skidmore use a set of six multivariate regressions and find that "it is surprising that countries with higher income […] were affected more severely because epidemics are more likely in highly populated lower incomes countries where access to clean water and sanitation is a challenge" (Toya & Skidmore, 2021, p.5). Here, income is expressed in GDP per capita, which directly contradicts the results found by Drydakis & Pardhan, although the two papers do not study the same population of countries. Still, these differences already highlight the fact that the sign of the coefficient estimate of the development variable requires special attention.

Moreover, other authors also find the opposite relationship between economic development and the severity of COVID-19 waves, this time using different proxy variables than GDP per capita. For example, Liu et al. (2020, p.3) discover an "unexpected" positive effect of development on

the severity of the COVID-19 outbreak in Italy. Indeed, they run a multiple logistic regression of COVID-19 cases and deaths on HDI, controlling for the effects of other economic and health predictors such as the average annual gross salary or the number of people with a chronic disease per hundred people. Doing so, they find a statistically significant coefficient for the Human Development Index ($p < 0.001$), such that a "0.1 increase in HDI results in […] 9.78 exponential increase in death odds" (Liu et al, 2020, p.3). Thus, and although additional variables such as the number of people with a chronic disease partially disentangle the effects hidden behind the HDI variable for developed countries, they still find a positive relationship between development and their COVID-19 severity variable.

In the same way, Mirahmadizadeh et al. find a positive relationship between development and COVID-19 deaths, stating that "HDI and its components had positive correlation with […] the cumulative incidence rate of death" (Mirahmadizadeh et al., 2022, p.1). Although the authors only use Spearman correlations, they find once again statistically significant coefficient estimates ($p < 0.001$) for their development variables, using the HDI as well as its components, such as mean years of schooling, life expectancy, and gross national income (GNI). However, they note that "although the HDI is higher in high income countries, these countries may also have better reporting and surveillance systems" (Mirahmadizadeh et al., 2022, p.1). COVID-19 cases should be more sensitive to such reporting issues compared to other measures such as COVID-19 deaths. To this extent, this shortcoming should be a point of attention to consider in the choice of variables.

At this stage, it appears that the authors that did study the role of socio-economic determinants as factors of COVID-19 cases or deaths have found conflicting results. However, the positive or negative character of the correlation relationship between the different development variables and the severity of COVID-19 waves could in fact depend on the choice of the proxy variables, as well as of the additional variables. For example, it already appears that the GDP per capita variable and the HDI variable do not seem to have the same relationship with the different COVID-19 severity proxy variables, although they are both directly related to the concept of economic development. To this extent, the choice of the explained variable, the explanatory variables, and the additional predictors used to disentangle effects is likely to be key to finding the most meaningful and accurate results.

2) Variables

In order to assess and characterise any potential causal relationship between economic development and the severity of COVID-19 waves, it is essential to define the most relevant

proxy variables to work with. To this extent, it is important to assess which variables have already been found in the literature to have an effect on COVID-19 severity at the country-level. These predictors can then be used in this paper either as explanatory variables directly related to development or as additional variables to disentangle effects.

A variety of covariates could be chosen as parameters of the severity of COVID-19 waves, whether they are health, economic, social, political, environmental variables, etc. For example, Drydakis & Pardhan (2021, p.1) use many additional variables, such as "lockdown policies", "public expenditure in health", "hospital beds", "social support", "demographic features", or even "economic exposure".

On the other hand, Chang et al. (2022, p.2) classify their variables into four groups: "demographic-geographic, political-legal, socio-economic, and health factors". Indeed, it appears that most of the predictors used in the literature on country level determinants of COVID-19 severity can be categorised in one of these groups. To this extent, the demographic-geographic, the political-legal and the health factors predictors should be used as additional variables in the study of the effect of development on COVID-19 severity. On the other hand, it should be more relevant to use socio-economic factors as proxy variables for the economic development of a country. However, some variables such as life expectancy, for example, should be given special attention, for they could both be considered either as health or economic development variables.

The available papers that study the relationship between development and the severity of the COVID-19 pandemic at the national level use many variables that correspond to the three concepts of COVID-19 severity, development, or additional variables.

First, cases or deaths are generally chosen as the explained variable. For example, Liu et al. (2020), Drydakis & Pardhan (2021), Chang et al. (2022), Toya & Skidmore (2021), Farzanegan et al. (2021), Mirahmadizadeh et al. (2022), Stojkoski et al. (2022) all use COVID-19 cases as a possible explained variable, while Liu et al. (2020), Toya & Skidmore (2021), Farzanegan et al. (2021), Davies (2021), Mirahmadizadeh et al. (2022), Chang et al. (2022), Stojkoski et al. (2022) use COVID-19 deaths as the explained variable. For the explanatory variables, these authors mostly use the HDI, GDP per capita in purchasing parity power, or other socio-economic predictors such as income inequality, or tourism indicators.

Second, several additional variables are used in the literature, following the four types of variables such as highlighted by Chang et al (2022, p.2). In the demographic-geographic category, the authors generally use population size, population density, and the median age of the population, while they use freedom, democracy, and corruption indicators for the political-legal group. Lastly, health variables such as obesity or overweight prevalence, and healthcare

infrastructure such as the number of hospital beds are chosen as additional variables. Multiple studies suggest that these predictors have an important role to play in explaining COVID-19 severity across countries. For example, as Stojkoski et al. (2022, p.8) study the determinants of country differences in terms of COVID-19 infections and deaths, they find that "the sole variable strongly related to the coronavirus deaths is the overweight prevalence". Thus, it is likely that the health predictors are important additional variables to be included in order to effectively disentangle the effects hidden behind the development variable.

A fifth category of variables could be covered by an environmental category such as the one used once again by Stojkoski et al. in their 2022 paper, which contains predictors like weather or air pollution. Including such covariates could further help crowd out the effects of any intermediary predictors in the relationship between the economic development variable and the severity of COVID-19 waves. Indeed, this addition would be useful as the literature on the Environmental Kuznets Curve (EKC) suggests that economic development is an important parameter of the pollution level or quality of the environment. However, it is still not clear how this relationship evolves once a certain development threshold is reached (Gambhir & Murthy, 2017). To this extent, air pollution and its consequences on human health as well as the vulnerability of a population to respiratory diseases could also be included in the analysis.

Finally, it would make sense to consider variables such as the ones related to tests, vaccination, the use of medical treatments, but also the promotion of social distancing or the use of curfews and lockdowns as part of a *government response* variables group. To this extent, it is possible to include predictors such as the Oxford COVID-19 government response index, which is defined as "a composite measure that combines the daily effect of policies on social distancing, testing and contact tracing in an economy" (Stojkoski et al., 2022, p.3).

3) Approach

Mirahmadizadeh et al.'s paper is a global level ecologic study, where "all studied variables are aggregate variables" (2022, p.2), which means that the approach focuses on the characteristics of the population at a macro level rather than at the individual level. This perspective should therefore be the most relevant to conduct a cross-country analysis of the relationship between economic development and the severity of COVID-2019 waves.

In their 2021 paper, Drydakis & Pardhan find statistically significant results, although their cross-country analysis sample of 38 countries is quite small. This means that using cross-sectional data of countries instead of time series or panel data still has the potential to yield

significant results despite the limited sample size of this type of study. Doing so, the authors are confronted with the different reporting delays between countries, whether in terms of COVID-19 cases or deaths. As they are working on a sample that ends on 31st May 2020, and thus whose period is quite short, this issue might have a serious consequence on their final coefficient estimates. To avoid this bias, the authors chose to "calculate the change in the numbers of new COVID-19 cases between two dates, which were 2 months apart, i.e., 1st April and 31st May 2020" (Drydakis & Pardhan, 2021, p.3). This solution should not be necessary however on a larger sample that goes from the beginning of the pandemic to late 2022, as reporting delay differences at the end of the sample should not weigh as much as they do for the relatively short period studied by Drydakis & Pardhan. Moreover, this issue should be less important for the number of confirmed COVID-19 deaths compared to the number of cases. Indeed, the latter should be affected by differences in the use of tests between countries, which are not likely to be randomly determined.

On the other hand, Farzanegan et al. (2020, p.688) use data on international tourism using the average log number of arrival and departures of international tourists from 2010 to 2019. Using an average for such variables is a way to avoid that the final coefficient estimates are affected by unrepresentative data. Proxy variables for economic development such as the HDI or GDP per capita could indeed yield biased estimates if their corresponding cross-sectional data for a given year is an outlier on the last five-year period, for example. Using an average approach or at least checking that the data of a given year is representative of the variable's trend on the past few years are ways to solve this issue.

It is worth noting that Farzanegan et al. are not the only ones to use a logarithmic transformation on the data. Indeed, Stojkoski et al. (2022, p.2) write that "the log transformation of the COVID-19 infections/deaths p.m.p [per million people] reduces the skewness of the original data and makes the dependent variable real-valued and continuous". When dealing with COVID-19 infections or deaths data, this is therefore a way to overcome the exponential trends that the spread of the virus follows during a wave at the country level. Thus, their linear model approach better fits the transformed data, and allows for a better analysis of any potential relationship between the explained variable and the independent variables.

In terms of additional predictors, the covariates included in the *government response* category are likely to suffer from an endogeneity problem. This is highlighted by Chang et al. (2022, p.1) when they write that "a response measure (e.g., lockdowns and vaccination) may enable countries to lower the number of COVID-19 cases and deaths. Conversely, countries with greater COVID-19 cases and deaths are more likely to adopt such a measure". To this extent, these covariates might suffer from a simultaneity issue, and thus require special attention.

On the other hand, Farzanegan et al. choose to use data from 2019 for the international tourism independent variable, which is a way to rule out the effects of COVID-19 on tourism after the crisis began. Similarly, Stojkoski et al. (2022, p.4) choose to use data for each of their correlate from 2019, stating that such a method "prevents the possible problem of endogenous independent variables in the specification of the regression". This leads to a situation in which the explained variable and the explanatory variables are respectively using data from the crisis, or from the pre-crisis period. When using development related predictors, it also makes sense to follow this approach to carefully examine which pre-crisis parameters predisposed a country to be more or less vulnerable to the COVID-19 outbreak.

Furthermore, authors write that they "stop the sample at the end of 2020 to ensure that our analyses are unaffected by the COVID-19 vaccination, which has been rolled out since January 2021 in many countries" (Chang et al., 2022, p.2). Otherwise, including vaccination as an additional variable in the model specification should already allow to disentangle any intermediary effects. However, it is possible that this variable is correlated with other predictors, such as the development variables, for example. One should therefore take these undesired effects into consideration to avoid introducing a bias that would inflate the estimates of any collinear variables.

On the other hand, Bayesian Model Averaging (BMA) can be implemented to better determine which variables should be included in a linear regression model, "to account for model uncertainty by estimating each possible specification, and thus evaluating the posterior distribution of each parameter value and probability that a particular model is the correct one" (Stojkoski et al., 2022, p.3). This method is a way to determine which variables are the most relevant when trying to find the determinants of the severity of COVID-19 at the country level, among a pool of many candidate variables. Such an approach follows the same statistical and methodological principles as the ones used in research papers that aim to find the determinants of long-term growth, such as in Sara D'Andrea (2022) and Sala-i-Martin et al. (2004). The BMA approach reduces model uncertainty by testing all combinations of the tested variables in the specification, and by assigning posterior inclusion probabilities (PIP) to them, which "summarises our uncertainty over the value of a parameter" (Lambert, 2018, p.53). Furthermore, this method additionally "creates a weighted average of the regression coefficients (and their respective variances) across all regressions" (Jones & Schneider, 2006, p.81). Such a method requires the specification of the prior distribution of the parameters, i.e., "a probability distribution which represents our pre-data beliefs across different values of the parameters in our model" (Lambert, 2018, p.52). However, it is possible to choose a prior that reflects the lack of initial knowledge of the researcher, as explained below in section 2. More specifically, the literature shows that it is possible to apply the BMA method to reduce model uncertainty when studying the determinants of COVID-19 severity at the country level. For example,

Stojkoski et al. (2022, p.5) “investigate the critical correlates of the log of the mortality rate due to the coronavirus”. In other words, the methodology employed in the determinants of growth literature can also be used to study the relationship between the severity of COVID-19 waves across countries and economic development. This is thus a way to depart from the classical framework in which conditioning on a model is essential (Sala-i-Martin et al., 2004, p.814). This methodological choice allows for the selection of the most relevant additional predictors from a set of many candidate variables, and the accurate computation of their weighted coefficients.

Although Bayesian Model Averaging (BMA) is a way to reduce model uncertainty, this approach leads to the testing of many variables, which might create a multicollinearity issue. Indeed, in their paper on study design and publication bias, Bajzik et al. (2020, p.23) note that “because we use 32 variables, collinearity is a potentially important problem in our analysis”. However, they use a *dilution* prior in their BMA approach to solve this issue. Still, they also note that this solution “alleviates but does not fully address collinearity” (Bajzik et al., 2020, p.23). As it is likely that the inclusion of a high number of candidate regressors leads to a collinearity issue, then this method is a way to partially correct this bias, and thus to increase the reliability of the estimates.

Different robustness checks can be implemented to test the results yielded by the BMA procedures. First, removing outliers and re-performing the Bayesian procedure with a different sample is a way to verify that each potential correlate is not highly dependent on the inclusion of one or a few specific countries (Stojkoski et al., 2022, p.6). Second, changing the sample period is a second strategy to test the robustness of the results (Stojkoski et al, 2022, p.7). Such a method could be used to solve the reporting delay differences problem at the beginning or at the end of a period, or to include or exclude additional COVID-19 waves to ensure that the results are robust and are not specific to a particular wave. However, other robustness checks can be designed and implemented, as described in the section below.

II - Final approach

Should a relationship exist between development and COVID-19 severity at the country level, this study then attempts to identify its parameters and to estimate the magnitude of their effects on the response variable. Thus, three hypotheses are tested in this paper. First, this work evaluates whether direct components of development are positively associated with an increase in COVID-19 severity. Second, the potential role of demographic differences, such as the age structure of a population, is explored. Indeed, such predictors could act as intermediary

variables between economic development and COVID-19 severity. Third, this paper also checks whether other additional factors can explain the variations of the response variable observed at the country level to disentangle any hidden effects. The following subsections explore the methods used to test these hypotheses.

1) Model and methodology

LOG-LINEAR REGRESSION MODEL

It was demonstrated in the literature that a linear regression can yield statistically significant results with a relatively small sample size when studying the relationship between economic development and COVID-19 severity at the country level (Drydakis & Pardhan, 2021). To this extent, it is consistent to conduct a cross-sectional study of the relationship between these two variables, taking COVID-19 severity metrics that cover the whole chosen period, and not necessarily measures per month as in a time series. However, as the relationship between the main economic development predictors and the response variable appears to follow an exponential trend instead of a linear one, the equation on which the Bayesian Model Averaging (BMA) procedures are based is modified into a log-linear model. To this extent, the data for the COVID-19 severity explained variable are logarithmically transformed using the natural logarithm, as detailed later in the data section. Thus, this study chooses to use a log-linear model specification for each linear regression performed as part of the BMA procedures

$$\ln(y_i) = \alpha + \sum_{i=1}^{n} \beta_i x_i + \sum_{i=1}^{k} \beta_i' x_i' + e_i$$

Where "y_i" is the severity of COVID-19 at the country level (dependent variable), "α" the intercept, "$\sum_{i=1}^{n} \beta_i x_i$" the development variable, or in other word the sum of the *n* development proxies associated with their respective coefficients (main independent variables), "$\sum_{i=1}^{k} \beta_i' x_i'$" the sum of the *k* other socio-economic, demographic, health, political-legal, and *government response* additional predictors associated with their respective coefficients (additional independent variables), and "e_i" the error term. All *additional* variables should be understood as a set of predictors that go beyond the direct economic development characteristics of countries, but that can be used to disentangle the effects potentially hidden behind the main independent variables.

On the other hand, COVID-19 severity cross-sectional data are likely to suffer from reporting delay differences, as previously mentioned. Nevertheless, the use of a large sample of multiple waves of COVID-19 over several years should make this bias weak enough that it does not consequently affect the final coefficient estimates. Furthermore, using a longer period is a way to make sure that the observations collected in one country in terms of COVID-19 severity are not unrepresentative of the relationship studied. Indeed, some countries may have *escaped* the first wave of COVID-19 for specific reasons, which do not stem from the different variables included in this paper. By using a longer period over multiple years, this potential bias should be ruled out, or at least alleviated. Thus, the data collection period for COVID-19 severity should therefore be as long as possible, starting from the beginning of the pandemic until the end of 2022. These period considerations are further explored in the variables an data subsection.

Many authors carefully state that they are studying a correlation relationship between their COVID-19 severity dependent variable and their predictors. As previously quoted, Stojkoski et al. (2022) designate their explanatory variables as "correlates", while Chang et al. (2022, p.2) write that the "relations between the predetermined factors and the COVID-19 outcomes reflect correlation rather than causation". However, multiple reasons support the idea that the approach followed in this paper moves away from correlation to causation. First, the development economics literature supports the existence of a clear relationship between development and a country's ability to reduce the impact of an epidemic on its population, as previously mentioned. This means that such a causal relationship is likely to be found, whether it is positive or negative. Second, this paper focuses on the impact of a set of specific development variables on COVID-19 severity at the country level, while considering the other additional predictors as tools to disentangle any hidden effects. To this extent, the main purpose of this study is not to assess any causal relationship that goes beyond the scope of economic development and the severity of COVID-19 waves. Third, the development proxies are based on data that were collected before the crisis. To this extent, it is not possible that the relationship is in fact inverse due to the temporal sequence of the variables. Thus, only the additional variables which are *government response* predictors can be affected by this problem, as their data come from the 2020-2022 period. Such variables are therefore included in the analysis in a second step. Furthermore, the *Gini coefficient* variable is also added in another phase to solve a sample size issue, as detailed in the variables and data subsection. Thus, this multi-step approach also works as a robustness check of the results.

BAYESIAN MODEL AVERAGING

Such an approach is consistent with the use of Bayesian statistical tools to deal with the model uncertainty problem. Indeed, as previously mentioned when looking at the methodology of the

determinants of growths literature, the study of the many potential parameters that can affect COVID-19 severity at the country level also suffers from a model specification problem. In order to select the most consistent predictors, a Bayesian approach is followed. Furthermore, this paper also relies on BMA to obtain the most accurate estimates as possible by computing weighted coefficients.

Indeed, the literature shows that many variables of interest could have an impact on COVID-19 severity. As the number of predictors grows, using a single linear regression model becomes less efficient. This issue is all the more important as the available sample size for a cross-sectional data analysis at the country level is fairly limited. BMA is therefore a way to test all possible combinations of independent variables and to select the most relevant covariates based on the posterior model probability (PMP) of each model. As explained in Feldkircher & Zeugner (2015, p.2), the latter is calculated using the following formula

$$p(M_\gamma|y,X) = \frac{p(y|M_\gamma,X)p(M_\gamma)}{p(y|X)}$$

where $p(y|M_\gamma,X)$ is the marginal likelihood of the model (i.e., the probability that the observed data match model M_γ), and $p(M_\gamma)$ a prior model probability which corresponds to the initial believes or insights of the researcher on model M_γ with respect to the probability that the data match it. Finally, Feldkircher & Zeugner (2015, p.2) state that $p(y|X)$ is "the *integrated* likelihood which is constant over all models and is simply a multiplicative term".

Beyond the choice of a prior model probability, Bayesian Model Averaging also usually relies on *Zellner's g prior*, which corresponds to the prior believes of the researcher on the mean and variance-covariance structure of the regression coefficients β_γ. In other words, the g prior represents the degree of certainty or uncertainty that the coefficients are zero. For more details, a more thorough explanation of the Bayesian Model Averaging theory is available in Feldkircher & Zeugner (2022c).

A posterior inclusion probability (PIP) for each covariate can then be computed by summing the PMPs of all models where a covariate is included (i.e., non-zero). A more intuitive way to understand the PIP of each independent variable is given by Havránek & Sokolova (2020, p.107) as they write that it could be considered as the "Bayesian analogy of statistical significance". The PIP can thus be used as a variable selection criterion to solve the model uncertainty issue by comparing it to the prior inclusion probability, which is equal to $\frac{\bar{k}}{K}$, with $\bar{k}$

the expected model size and K the number of candidate variables included in the BMA procedures.

Then, the coefficients are computed using the average of their values over all models, even those where the variable is not included, in which case it is equal to zero. Thus, as the PIP of a variable decreases, so does its coefficient value. A low coefficient with a high PIP will therefore inform that, although the models where this covariate is included do fit the data, they also suggest that this predictor is not an important parameter of the response variable.

Such as previously mentioned, Bajzik et al. (2020) use a *dilution* prior in their BMA procedures to overcome the collinearity between their candidate predictors. Indeed, as put forward in George (2010), the classic independence prior fails in case of high multicollinearity between the regressors. Let be the independence model space prior π_I

$$\pi_I(\gamma) = \prod_{i=1}^{p} w_i^{\delta_i} (1 - w_i)^{1-\delta_i}$$

where model $\gamma \in \Gamma$, with Γ a space of models, $\delta_i = I$ (X_i in γ) and $w_i = \pi$ (X_i in γ), with a set of p predictors $X_1, \dots, X_p$. Now, suppose X_1 uncorrelated with $X_2, \dots, X_p$, but $X_2, \dots, X_p$ almost fully multicollinear. In this situation, "any subset $X_2, \dots, X_p$ would then have an equivalent effect in the model […]. Effectively, adding $X_2, \dots, X_p$ to the mix is tantamount to adding an equivalent single new potential predictor" (George, 2010, p.160).

To solve this issue, the author proposes a collinearity adjusted *dilution* prior π_R. For each γ, R_γ is the correlation matrix such that $R_\gamma \propto {X'}_\gamma X_\gamma$, with $|R_\gamma|$ an overall measure of collinearity such that $|R_\gamma| = 1$ when the columns of X_γ are orthogonal, and $|R_\gamma|$decreases to 0 as the columns of X_γ become more redundant (George, 2010, p.163). Thus, prior π_R is defined as

$$\pi_R(\gamma) \propto h(|R_\gamma|) \prod_{i=1}^{p} w_i^{\delta_i} (1 - w_i)^{1-\delta_i}$$

with h a monotone function satisfying $h(1) = 1$ and $h(0) = 0$. Two intuitive choices for h would then be $h(r) = r$ and $h(r) = r^{1/2}$.

The *dilution* prior thus disqualifies models considered as redundant, i.e., downweighs the probability of model γ for the collinearity in a set of predictors X_γ, partially crowding out this undesired effect.

BMS PACKAGE AND PARAMETERISATION

The Bayesian Model Averaging Library (Feldkircher et al, 2022a) for R was used to conduct the analysis. As explained in Feldkircher et al. (2022b, pp.6-10), the *bms* function requires the choice of parameters, including in terms of prior model probability and *g* prior, as previously defined. A BMS add-on programmed by Hofmarcher & Moser, *dilutBMS2* (2014), was also used, as it introduces the *dilut* prior that was eventually employed in the analysis.

An intuitive choice of prior model probability $p(M_\gamma)$ is the *uniform* one, which means that the prior model probability for all models is proportional to 1, reflecting the absence of initial knowledge on which model is likely to be the *best* one. However, as previously mentioned, the *dilution* prior (*dilut*) is used in this paper in order to crowd out the effect of multicollinearity in the computation of the PIP, and thus also of the weighted coefficients. The BMA procedures were still carried out with the *uniform* prior in a first step to allow a comparison with the results obtained using the *dilution* prior, thus testing their robustness.

On the other hand, the *unit information prior* was selected as the *g* prior. To this extent, $g = N$ for all models, with N the number of observations. Different reasons explain the choice of this prior in this paper. First, as shown by Eicher et al. (2011, p.30), "the UIP with uniform model prior generally outperformed the other priors". Second, the *uniform* prior model probability best reflects the absence of initial believes of the researcher, or of previous posterior probability results from past studies. Thus, it is a fair starting point for a first analysis of this set of potential covariates to choose priors that are likely to perform better, and that correspond to the initial state of knowledge of the study.

The *mprior.size* parameter in the *bms* function corresponds to the prior expected value of the model size. Here, this prior is set by default on K/2, with K the number of covariates included in the BMA procedures, which reflects the absence of initial information on the optimal number of variables to be selected. As shown in Sala-i-Martin et al. (2004, p.823), the resulting expected model size is $\bar{k}$, which is therefore $\bar{k} = \frac{K}{2}$, and the prior inclusion probability is equal to $\frac{\bar{k}}{K}$.

The *bms* function uses a Markov chain Monte Carlo (MCMC) parameter to set up the model sampler, whose choice depends on both the type and number of independent variables. In this paper, up to 21 explanatory variables are included in the BMA procedures, which is a relatively high number of regressors. Still, the MCMC parameter is set on full enumeration, so that all

predictor combinations are iterated (thus up to 2^{21} possibilities) for the entire model space (Feldkircher et al., 2022b, p.7).

2) Variables and data

As previously mentioned, this paper studies the relationship between COVID-19 severity, as the dependent variable, and a set of economic development regressors, as well as additional predictors to disentangle any hidden effects. Beyond the HDI components, other covariates are less directly or not even linked to the development level of a country, such as the *population density* variable. Still, these variables are included as the literature suggests that they are likely to be important parameters of the severity of COVID-19 waves at the country level. These predictors are also referred to as *non-government response* additional variables. For all these covariates, a five-year average for each country is used to build the final sample, such as in Farzanegan et al. (2021). This approach alleviates the impact of any unrepresentative observation, which should lead to the computation of more accurate estimates. Finally, the last type of additional regressors is the *government response* variables group, which corresponds to different metrics on COVID-19-specific policy measures, whose absence could create an omitted variable bias.

It is important to mention that all variables do not use data that were collected during the same period. Indeed, three groups can be distinguished. First, the COVID-19 severity dependent variable is a cumulative metric from 01/01/2020 to 10/30/2022, when data collection for this paper ends. Second, the main economic development regressors as well as all *non-government response* additional variables are mostly pre-crisis data that stop in 2018. More generally, the variables for which an average is computed use a period that does not include any data collected from November 2019, when the virus was first detected in China. Indeed, any annual data that would include the end of 2019 would risk being impacted by the onset of the pandemic, including for countries like China where the outbreak started early. Finally, the *government response* variables use data that were by nature collected after the beginning of the outbreak. Depending on the type of *government response* variable, the data can be measured with a cumulative metric or an average on the whole post-outbreak period, up to the end of October 2022. A summary of all the variables used in this study as well as their corresponding source is available in Figure 1 below.

GROUP/Variable	Measure	Source
RESPONSE VARIABLE		
COVID-19 severity	Deaths per million inhabitants	JHU
SOCIO-ECONOMIC		
Life expectancy	Life expectancy at birth	UNDP
Education (expected)	Expected years of schooling at school-entry	UNDP
Education (actual)	Mean years of schooling (adult population)	UNDP
Income	GNI per capita, US$, PPP	UNDP
Income inequality	Gini index (0-1)	WB
DEMOGRAPHIC		
Population	In thousands of inhabitants	UN WPP
Population density	In people per square kilometre	UN WPP
Age structure	Median age (years)	UN WPP
POLITICAL-LEGAL		
Democracy	Democracy index (0-10)	EIU
Press Freedom	Press Freedom index (0-100)	RSF
Corruption	Corruption Perception Index (CPI, 0-100)	TI
PUBLIC HEALTH		
Health investment	Current health expenditure (CHE, $ per capita, PPP)	WHO GHED
Overweight	Overweight prevalence (per hundred people)	WHO GHO
Pollution	Concentrations of fine particulate matter (µg/m3)	WHO GHO
GOVERNMENT RESPONSE VARIABLES		
Stringency	Stringency index (0-100)	OxCGRT
Vaccination	Vaccination rate (percentage of population per month)	Owid
GOVERNMENT RESPONSE VARIABLES – EARLY TREATMENTS		
(Hydroxy)chloroquine	Official country-wide use (0-1, dummy variable)	C19early
Acetaminophen	Official country-wide use (0-1, dummy variable)	C19early
Remdesivir	Official country-wide use (0-1, dummy variable)	C19early
Ivermectin	Official country-wide use (0-1, dummy variable)	C19early
Favipiravir	Official country-wide use (0-1, dummy variable)	C19early

Figure 1. List of the response variable and all candidate variables.

The choice of the period is crucial for the analysis, as this paper uses cross-sectional data instead of time series or panel data. Therefore, the period considerations for each variable are explored in the following paragraphs, that are organised in groups of variables.

THE DEPENDENT VARIABLE

For the COVID-19 severity variable, this study relies on the *total COVID-19 deaths per million inhabitants* data from the Johns Hopkins University (JHU) database (Dong et al., 2020) [1]. Indeed, recorded deaths should be less dependent on country differences in terms of the availability of tests or of the compliance of the population to the various reporting systems than the reported cases data. Similarly, the number of hospitalisations is also dependent on the number of hospital beds available in each country's health infrastructure, and the use of such a proxy would be less meaningful than COVID-19 fatalities without further work on the total number of beds available during the pandemic. This would be all the more difficult to study since the total number of available hospital beds is likely to have evolved over the course of the pandemic from the beginning of year 2020 to the end of year 2022, which is harder to include in a cross-sectional dataset.

The data on the cumulative number of deaths per million inhabitants was collected between 01/01/2020 and 10/30/2022, where the sample period stops. The choice of this period has multiple advantages. First, the period starts as early as possible during the pandemic to include the first COVID-19 waves. At this early time, it is possible to capture differences between countries before too many government responses are put in place to mitigate the impact of COVID-19. For the following waves, a set of *government response* variables is included in this study to disentangle the effects of public emergency response to the virus, as described in a following subsection. On the other hand, extending the period beyond the early time of the pandemic reduces the likelihood that the results are affected by the fact that some countries or regions were initially *spared*, and were only hit later by the virus. Finally, ending the data collection on 30 October 2022 allows the analysis to focus on a period when the new deaths per million inhabitants still reveal differences between countries before they start to converge too much, as shown in the graphs below (Figures 2 and 3). This way, the effects of the regressors are not diluted by a prolonged period that blurs the country differences in total COVID-19 deaths over time.

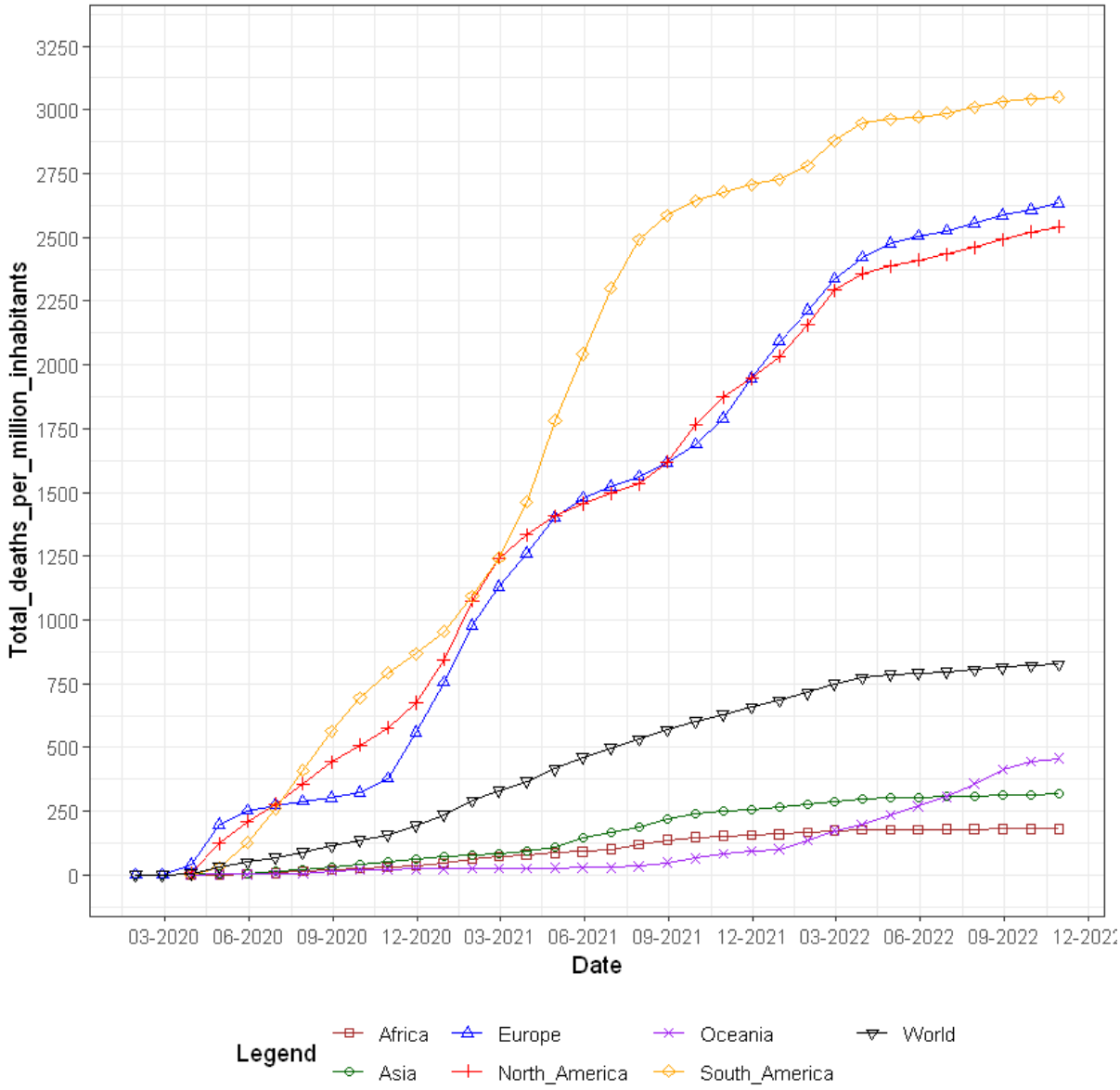

Figure 2. Total number of deaths per million inhabitants per month by region over time, 01/01/2020-10/30/2022.

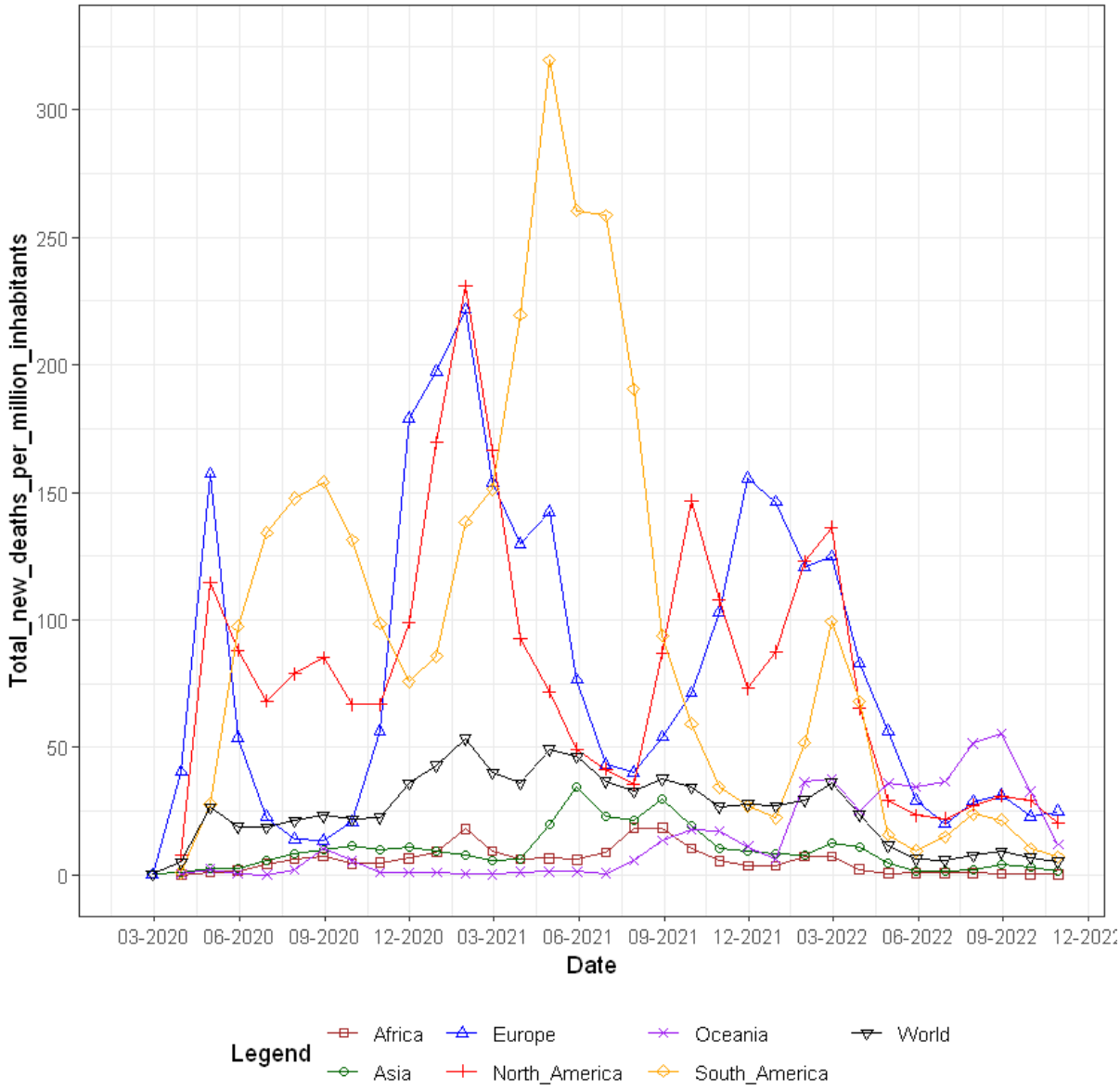

Figure 3. New deaths per million inhabitants per month by region over time, 01/01/2020-10/30/2022.

Indeed, Figure 2 reveals that the number of deaths per million inhabitants in the most affected regions starts to increase more slowly from the first months of 2022. Indeed, in Figure 3, the number of new deaths per million falls abruptly at the same period in most regions. As a result, this change is also observable for the world trend on both figures.

The next subsections detail which variables are included in the BMA approach, and which periods were used for each of them. As in Chang et al. (2022, p.2), the independent variables that are likely to affect COVID-19 severity at the country level are organised in groups. Indeed, out of the 21 covariates studied in this paper, most can be categorised as socio-economic, demographic, political-legal, and health variables. Finally, a *government-response* variables

group is used in the analysis, to separate the effects of the economic development and other pre-crisis country characteristics from those of emergency public health policies, which are specific to the pandemic.

SOCIO-ECONOMIC VARIABLES

HDI & components

Economic development is approximated using the three components of the Human Development Index (HDI): health, education, and standard of living. These three predictors have in turn their respective proxies: *life expectancy* at birth, *expected years of schooling* of children at school-entry and *mean years of schooling* of the adult population, as well as *Gross National Income* (GNI) in dollar per capita in purchasing parity power. The data for these proxy variables come from the Human Development Reports of the United Nations Development Programme (UNDP) [2].

As mentioned in the literature review, many studies show that age is an important factor of COVID-19 severity at the country level. To this extent, development variables such as *life expectancy* at birth are likely to have an effect on the response variable. Including predictors related to the age of a population therefore allows the results to show the separate effects of each component of development on the total number of deaths per million inhabitants. Here, the pre-crisis five-year average is computed using the UNDP data on the 2014-2018 period.

As the HDI is highly correlated with its components, it is not included in the analysis to avoid redundancy and the consequences of multicollinearity, and this despite the use of a *dilution* prior.

Gini index

The income inequality variable is included using the *Gini index*, from the World Bank (WB) database [3]. This index varies between 0 and 1, with 1 the highest level of economic inequality in a society. Low levels of inequality do not necessarily correspond to a high degree of development. For example, the sample in this paper shows that the correlation coefficients between the five-year averages of the Gini index and the HDI components range from -0.32 to -0.44 (see Figure A3 in Appendix A). It is therefore not redundant to include such a variable in the analysis, since the literature suggests that unequal access to health, education, and sanitation can lead to unequal vulnerability of the different socio-economic classes within a single territory. Thus, countries with a similar level of economic development could still have different magnitudes of total COVID-19 deaths per million inhabitants, based on their respective degrees of inequality.

The period used to compute the five-year average of the *Gini index* is 2014-2018. However, there are some missing data for some years depending on the country. In this case, the average is computed using only the available years. Some data are therefore less reliable for some countries. However, trying to compute an average on multiple years is still more accurate than using data for a single year only. Furthermore, this method allows to include countries that would have been excluded from the sample had the data for the single selected year not been reported.

DEMOGRAPHIC VARIABLES

Population, density, and median age

Data from the United Nations World Population Prospects 2022 (UN WPP) [4] are used for the *population* (thousands of inhabitants), *population density* (people per square kilometre), and population *median age* (years) additional variables.

The two first predictors are not directly linked to development, while *median age* does not exactly correspond to the *life expectancy* at birth HDI component. Indeed, the median age of a country's population provides direct information on its age structure. Thus, this type of data is likely to be informative on the vulnerability of a country to COVID-19 waves severity, as the literature highlights the importance of such a variable in explaining fatalities. Thus, and although there is a correlation between *median age* and *life expectancy*, both variables are kept in the analysis as they do not provide the same information. Such a choice is allowed by the use of a *dilution* prior, as the latter should alleviate the effects of collinearity.

To build a five-year average that respects the condition that the sample should not include any data collected from November 2019 onwards, this paper uses the UN available data whose period starts on 1st July 2015 and ends on 1st July 2019. Thus, and although most averages of the *non-government response* independent variables use the 2014-2018 period, this difference should not be a problem. Indeed, country characteristics should not vary too much in a few months, as long as the period does not include the COVID-19 crisis.

POLITICAL-LEGAL VARIABLES

Democracy

The *Democracy Index* from the Economist Intelligence Unit (EIU) [5] of the Economist Group is an index that varies between 0 and 10. The higher its value, the higher it reflects the democratic character of a country. The index is calculated using the ratings of 60 indicators grouped into five categories: "electoral process and pluralism; civil liberties; the functioning of government; political participation; and political culture" (EIU, 2022, p.66). As a result, the

final score on the 0 to 10 scale can either designate a country as an authoritarian regime (0-4), a hybrid regime (4-6), a flawed democracy (7-8), or a full democracy (8-10). As highlighted in the literature, the degree of democracy may play a role in explaining a country's vulnerability to the pandemic. Indeed, Chang et al. (2022, p.15) show that democracy is an aggravating factor of COVID-19 severity, as it can be more difficult for a liberal state to take quick and effective decisions, for example with respect to restrictions of freedom.

As for most of the additional *non-government response* variables, the period selected for this data is 2014-2018. In this way, using pre-crisis data to compute this five-year average index will not capture the fall in democratic score stemming from the pandemic-related restrictions that lasted until 2022 in many countries (EIU, 2022, p. 5). Thus, the BMA approach should reveal the relationship between the pre-crisis level of democracy of a state, and COVID-19 severity, i.e., how the democratic character of a country makes it more or less vulnerable to the pandemic.

Press Freedom

The *Press Freedom Index* from Reporters Without Borders (RSF) [6] measures the "degree of freedom available to journalists […] determined by pooling the responses of experts to a questionnaire" (RSF, 2022). To build the index, a set of seven criteria is evaluated based on scores that vary between 0 and 100. Press freedom aspects such as pluralism, media independence, censorship, or abuses against journalists are evaluated in order to build the *Press Freedom Index*, that also uses the 0-100 scale.

Such a variable can be used to detect the effects of the distribution of information in a country with respect to its ability to absorb the pandemic shock in terms of COVID-19 deaths per million inhabitants. Indeed, as for the *democracy index*, it could be possible that a high degree of press freedom impedes a government from quickly putting in place centralised decisions against the pandemic. On the other hand, it is also plausible to think that free information could also benefit a population and prevent COVID-19 deaths, in a situation where a government would be slow to react, for example.

However, careful interpretation is needed, as the correlation coefficient between the *press freedom* variable and the *democracy* variable is fairly high (0.77) (see Figure A3 in Appendix A), possibly making one of the two predictors a redundant variable. The use of a *dilution* prior should nevertheless alleviate the effects of multicollinearity and reveal the true impact of each of these two predictors on the response variable.

The *press freedom* five-year average is computed using annual data from the 2014-2018 period. Once again, this period allows to see whether the pre-crisis degree of media freedom of a state

has a role to play in explaining how much a country suffered from the COVID-19 pandemic, i.e., how the distribution of information affects total deaths per million inhabitants.

Corruption Perception Index

The *Corruption Perception Index* (CPI) [7] is an index from the Transparency International organisation (TI) that varies between 0 (highly corrupt), and 100 (very clean). It aggregates data from "different sources that provide perceptions of businesspeople and country experts of the level of corruption in the public sector" (TI, 2023, p.15). Finally, there must be at least three sources in a single country that provide data to consider that they can be included in the reports and datasets.

The underlying idea is that, as an indirect aspect of development, corruption might hinder the ability of a country to act in the interest of its population in a time of crisis, which may have consequences on the response variable. This is the case in Chang et al. (2022, p.8) where the authors find that "political corruption contributes to the inefficiencies of government interventions to control the pandemic", probably due to a weaker ability to quickly mobilise as many public resources as possible in the name of the public interest.

An average of all sources in a single territory is computed after the provided data are standardised to a 0-100 scale. Furthermore, for this paper, a 2014-2018 average of the *CPI* is calculated to provide a reliable overview of the degree of pre-crisis perceived corruption that characterises a country.

PUBLIC HEALTH

Current health expenditure

The *current health expenditure* (CHE) in constant (2020) US$ (Constant 2020) in Purchasing Parity Power per capita from the WHO Global Health Expenditure Database (WHO GHED) [8] is an indicator that calculates the average expenditure on health per capita in a country. It is expressed in purchasing parity power (PPP) to take into account economic frictions such as transaction costs or trade barriers for certain goods and services. In addition, the *CHE* indicator is calculated here on a per capita basis, which further contributes to making this measure suitable for international comparisons.

One could intuitively think that the more a country was investing in health before the crisis, the more it was capable of absorbing the pandemic shock, thus reducing its final number of deaths per million inhabitants. Such a predictor therefore captures this effect, and may be able to separate it from the other development variables.

This variable is included in the BMA procedures as it is possible that these expenditures per capita do not only depend on the level of economic development of countries, but also on public policy choices, or a country's culture, for example. Thus, it is possible that this predictor has effects of its own on COVID-19 fatalities per million inhabitants. Still, there is a fairly high correlation coefficient of 0.82 (see Figure A3 in Appendix A) between the *CHE* and the *GNI per capita* variables, which is also expressed in purchasing parity power. To this extent, the degree of correlation is high enough to suggest that the *CHE* predictor might be a redundant variable. Still, as a *dilution* prior was used for multiple BMA settings, the resulting multicollinearity effect should be taken into account and alleviated. The resulting PIPs of the *GNI per capita* and *CHE* regressors are therefore analysed taking these elements into consideration.

An average of the annual data for the *CHE* variable is computed for the period 2014-2018. This independent variable is expected to reflect the ability of a country characterised by high investment in health to be less vulnerable to COVID-19 waves, i.e., to reduce their severity.

Overweight prevalence

The *prevalence of overweight* among adults (Body Mass Index ≥ 25, age-standardised estimate, %) from the WHO Global Health Observatory (WHO GHO) [9] provides annual data that allows this country-specific health characteristic of the population to be taken into account in the analysis. Indeed, this factor is highlighted in the literature as essential in explaining COVID-19 deaths at the country level. Including this variable in the BMA approach is thus a way to solve the omitted variable bias, and to study the real effects of the main economic development predictors on the response variable.

However, it is also important to note that the correlation coefficients between the HDI components and the *overweight prevalence* variable range from 0.56 to 0.69 (see Figure A3 in Appendix A). To this extent, overweight cannot be totally detached from the degree of development of a country, and could even be one of its characteristics. Using the *dilution* prior is thus all the more important as it allows the PIPs and thus the coefficients of the collinear variables not to be overestimated, increasing the accuracy and reliability of the results without having to remove one or multiple variables that are highly but not fully collinear.

The period selected to compute the average for the *overweight prevalence* predictor is only 2014-2016 due to the limited availability of the data. While this shorter and older time period means that the data are less likely to be representative of the prevalence of overweight in the population of countries when the pandemic reached them, it should be noted that this is a more accurate measure than one that would only include 2016, i.e., the last available year. Country health characteristics such as this one should not evolve quickly over time, except during an

important shock, such as a pandemic. Thus, as this characteristic is part of the pre-crisis predictors for whom an average is computed, this lack of more recent data should not have important consequences on the final results.

Environmental pollution

As certain forms of pollution might have dramatic impacts on public health, including in terms of respiratory diseases, it is logical to think about adding pollution-related variables to the BMA procedures. As highlighted by Stojkoski et al. (2022, p.5), air pollution might be correlated with COVID-19 severity. To this extent, this paper uses the *concentrations of fine particulate matter* variable[1] from the WHO Global Health Observatory (WHO GHO) [10] to detect these effects.

As previously mentioned, the environmental economics EKC theory suggests that pollution and economic development are related. To this extent, pollution could be one intermediary variable between development and COVID-19 deaths. Indeed, the correlation coefficients between the *concentrations of fine particulate matter* and the HDI components range from -0.29 to -0.49 (see Figure A3 in Appendix A), which reveals a non-negligeable degree of collinearity between these predictors. However, the latter is not a high one, and should not inflate the BMA results in terms of PIPs and weighted coefficients, especially since a *dilution* prior is employed. Including an *environmental pollution* variable should therefore disentangle some effects that could be hidden behind economic development and increase the explanatory power of the analysis.

Such as for most of the *non-government response* independent variables, the selected period is 2014-2018. Including this variable should therefore reveal whether the degree of air pollution of a country is an important parameter in determining the vulnerability of a population to the COVID-19 pandemic.

GOVERNMENT RESPONSE VARIABLES

Government response variables are additional predictors included in the BMA procedures to crowd out any omitted variable effect. Unlike the other independent variables studied in this paper, they do not use pre-crisis data, but correspond to public policies put in place by governments in response to the pandemic. As the literature highlights the importance of these predictors in explaining COVID-19 severity, it is necessary to include them in the analysis in order to disentangle any effects that could be hidden behind the variables related to economic development.

[1] Measured as the annual mean concentration of particulate matter of less than 2.5 microns of diameter (PM2.5) in urban and rural areas, as well as cities and towns, and expressed in $\mu g/m^3$.

For example, using the UNDP and the Johns Hopkins University datasets, it appears that the number of people vaccinated per hundred on the 30th of December 2021 is highly correlated with the HDI components. To this extent, this intuitively suggests that the choice of a government response and its efficiency depend on the pre-crisis characteristics of a country. Once again, the effects of collinearity should be alleviated due to the use of a *dilution* prior, which means that the results should not be inflated. However, removing one of these variables would therefore prevent the analysis from revealing the separate effects of each variable. Overall, this paper includes as many predictors as possible, and chooses to correct the effects of multicollinearity by using a *dilution* prior. Only the most correlated variables are removed from the BMA procedures.

Vaccination rate

In the end, the number of people vaccinated per hundred inhabitants is not used as the vaccination variable. Instead, a *vaccination rate* is computed using the percentage of vaccinated people in a country for the last reported month divided by the number of consecutive reported months over the period 12/30/2020-10/30/2021. Indeed, vaccination campaigns have different durations depending on the country. This measure is thus expressed in percentage of the population by month, and corresponds to the average speed at which a country vaccinated its population against COVID-19. In the end, and compared to the number of people vaccinated per hundred inhabitants, the *vaccination rate* variable is less correlated with economic development variables such as the HDI components, which should therefore further reduce the consequences of multicollinearity.

Using the *vaccination rate* instead of the percentage of people vaccinated at the same date has an advantage. Indeed, an average rate takes into account the time a country took to vaccinate its population. This makes a difference between a state that vaccinated 60% of its population in 8 months, and a country that vaccinated the same percentage of its population in 12 months, for example. To this extent, the *vaccination rate* is a more relevant measure.

As this study does not use a time series but cross-sectional data, the choice of the end date for the vaccination data collection period is crucial. The aim is to choose an end date for the sample that allows the *vaccination* variable to capture differences between countries in terms of effect on the number of COVID-19 fatalities per million inhabitants. Two elements justify the choice of the period. First, as shown in Figures 2 and 3 above, COVID-19 deaths start to stabilise and increase more slowly from the end of 2021. Second, the vaccination rates tend to converge from the beginning of early 2022, blurring the observable differences between countries, as shown in Figure 4 and 5 below.

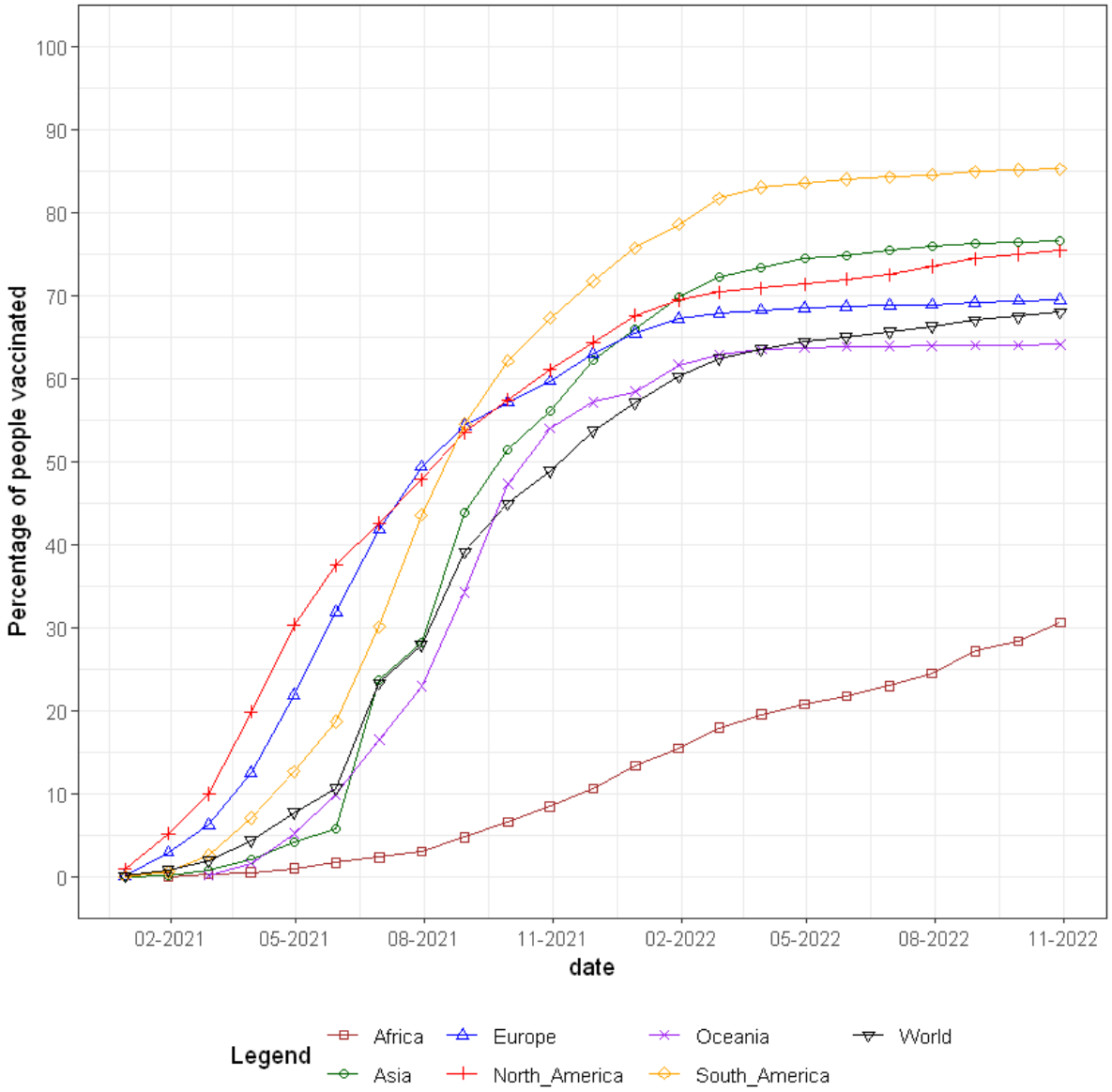

Figure 4. Cumulative percentage of inhabitants vaccinated per month by region over time, 12/2020-10/2022.

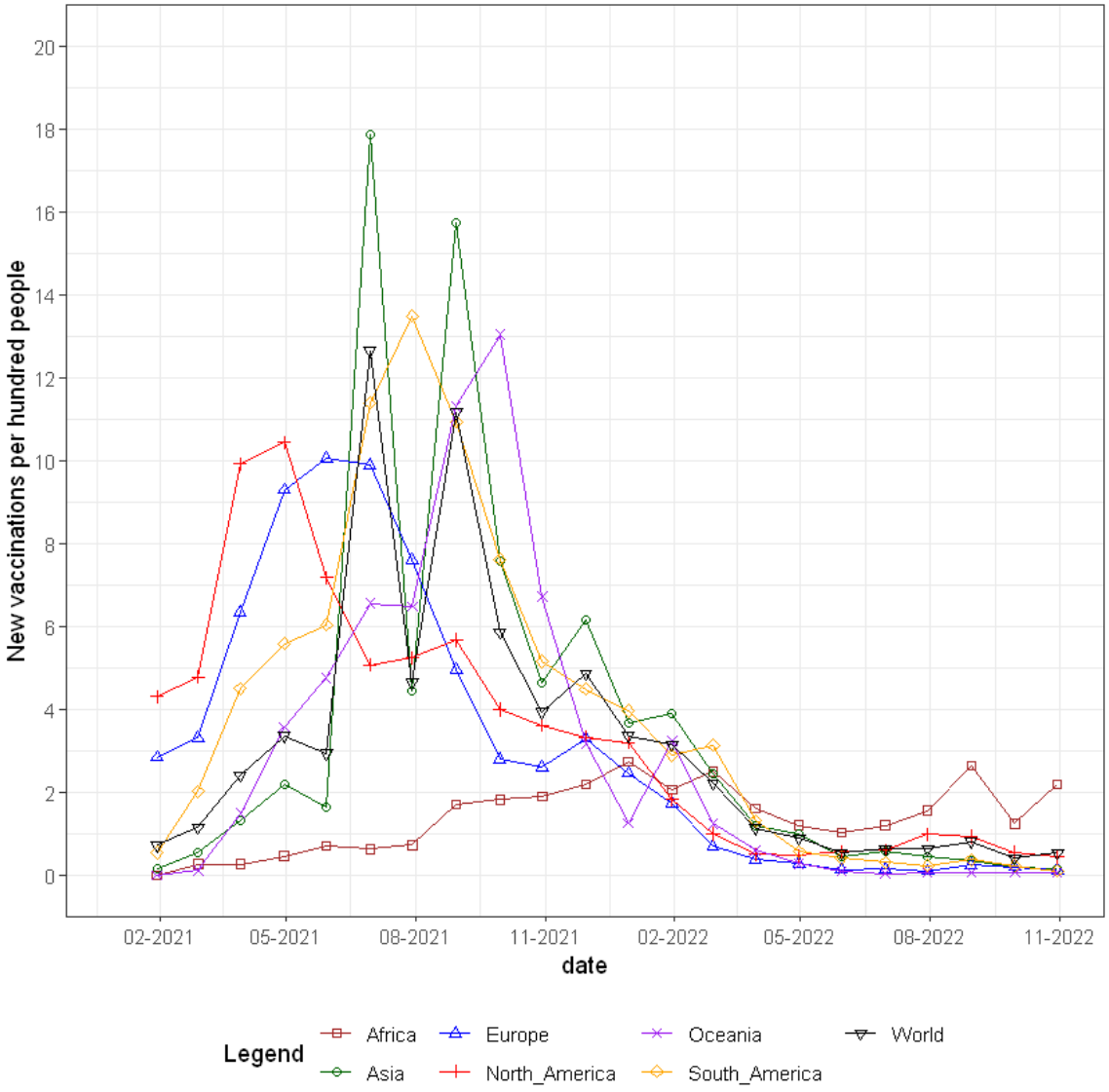

Figure 5. New vaccinations (% population) per month by region over time, 12/2020-10/2022.

Choosing the end of 2021 as the end of the period for the *vaccination* data collection first ensures that vaccination rate differences are captured by the variable before the different rate trends slowly converge towards lower values. Second, not stopping the data collection earlier allows the *vaccination* variable to produce an observable effect on the number of COVID-19 deaths per million inhabitants, which should reveal differences between countries.

Finally, the selected period used to compute the average vaccination rate per month for each country is 12/2020-12/2021, and the data on vaccination by country comes from the Our World in Data (Owid) database [11].

Stringency

The Oxford COVID-19 Government Response Tracker (OxCGRT) is a project that aims at collecting data on the policy measures taken by governments against the pandemic. This paper uses the *stringency index* variable [12], which "records the strictness of 'lockdown style' policies that primarily restrict people's behaviour. It is calculated using all ordinal containment and closure policy indicators, plus an indicator recording public information campaigns" (Hale et al., 2021). The index varies between 0 and 100, the highest value corresponding to the strictest responses. It is computed using data on 8 different indicators, such as school, workplace, and public transport closing, the prohibitions of public events and gatherings, or different movement restrictions such as stay at home requirements.

There are only low levels of correlation between the *stringency index* variable and the other predictors. To this extent, adding this regressor should disentangle any hidden effects of the omitted variable bias, without causing important multicollinearity consequences. Furthermore, and although this paper focuses mainly on explaining the role of economic development in parametrising the vulnerability of countries to the COVID-19 pandemic, the literature highlights the importance of the stringency of government responses with respect to COVID-19 deaths. Thus, including this independent variable should also increase the explanatory power of the model.

The data were recorded and computed on a daily basis, which gives more weight to a degree of stringency that has lasted over a long period of time when this paper calculates an average. Unlike the *vaccination rate* variable, the *stringency index* data do not follow a slower trend at the beginning of 2022. On the contrary, they increase and decrease over time, reaching peaks of different values depending on the date. This could probably be explained by the fact that governments were implementing stricter policies during active waves of COVID-19. It is therefore possible that the degree of *stringency* decreases when there are less new deaths per million inhabitants, which is dependent on many factors, and which varies over time. Moreover, it appears that *stringency* peaks are observable in countries even at the end of the period studied. Thus, it is more logical to include data on the *stringency index* from the beginning of the pandemic to the end of the collection period of COVID-19 deaths, as no trend in the data suggests that any other choice is more relevant.

A *stringency index* average for the whole period is computed using the daily data for each country, and is used to build a cross-sectional dataset. This measure thus reflects the global strictness of the public responses of a government during the pandemic.

Early treatments

Before the vaccination campaigns start, countries all around the world were already using early treatments to fight against the pandemic. Such as in Skidmore & Toya (2021), data on the early

adoption of treatments against COVID-19 from the C19early project [13] is included in the BMA procedures. These data are less informative than for the *vaccination* data, for example, as they only provide two types of information. First, the project collected evidence on the *official* or *unofficial* use of a treatment against COVID-19 in a country. Second, the data specify whether the use of an early treatment was characterised by the researchers as corresponding to an *isolated use, some regions use*, *mixed usage*, or *country-wide adoption*.

This paper uses this information to build a dataset for a dummy variable on the adoption of an early treatment. When an early treatment is adopted, the dummy takes the value 1, and 0 when it is not. Following a conservative approach, the early treatment is considered as adopted in a country when the data from the C19early project attribute to a country both the *official* and *country-wide* adoption characteristics. Once again, the analysis conducted in this paper uses cross-sectional data. To this extent, there is no difference between two countries whose dates of adoption are different. However, the dummy variable for any country that was officially using an early treatment at a country-wide scale but that then stopped using it is set to 0, still according to a conservative approach. However, most countries continued to use early treatments until the end of the period. Thus, as opposed to the *vaccination* variable, and as for the *stringency index* data, no information suggests that it is more relevant to use the collected data for a shorter period than the one used for the total number of COVID-19 fatalities per million inhabitants (01/2020-10/2022). In any case, the few latest reported early treatment adoptions happened in January 2021, which should let enough time for the *early treatment* variable to produce observable effects on COVID-19 deaths at the country level.

Five early treatments appear to be the most frequently used by countries worldwide: (*hydroxy)chloroquine*, *acetaminophen*, *remdesivir*, *ivermectin*, and *favipiravir*. However, the data suggest that the nature of the treatment varies depending on the region. Thus, to avoid mixing these effects and to capture differences between countries, the *early treatment* dummy variable is splitted into five dummy variables, one for each of the five early treatments included in this paper. Including them in the analysis could therefore help capture their impact on the response variable, which further reduces the probability of an omitted variable bias.

3) Final methodological considerations

CAUSALITY

Parameterising a linear model for a regression is already assuming a causation between a set of explanatory variables and the response variable. However, it could be the case here that the

relationship is the reverse. Indeed, the economic development indicators could deteriorate due to the COVID-19 pandemic consequences, and the total number of deaths per million inhabitants could therefore simply be a proxy for the duration of the shock. Moreover, there could be a double causality relationship between one or multiple independent variables and the response variable. To this extent, strong theoretical arguments must support the direction of causation.

In this paper, causation directly stems from the temporal sequence of the data. Indeed, as the aim of this analysis is to reveal and estimate any relationship between the degree of economic development of a country and the severity of the COVID-19 waves, pre-crisis development indicators and additional variables are used as predictors. Thus, when the five-year average of a variable is calculated over the 2014-2018 period, it is not possible to argue that the variations of the response variable could be responsible for a change in the predictor's value. Still, any observed relationship could just be a correlation at this stage. However, the use of many candidate variables as part of a BMA approach that solves the uncertainty issue in modelling supports a causal interpretation of the results. Indeed, as many important variables highlighted by the literature are included in the analysis, the probability that the hidden effects of intermediary variables still create a consequent omitted variable bias is low. Furthermore, the development economics literature already provides strong evidence that development and public health are closely related. Thus, the results and interpretation of this paper depart from simple correlation measures, and attempt to highlight a causal relationship between characteristics of economic development and the severity of the COVID-19 pandemic at the country level.

LOGARITHMIC TRANSFORMATION

When plotting the COVID-19 deaths per million inhabitants' data against the data of each predictor, multiple variables display data plots that suggest a relationship. However, the latter seems to be exponential rather than linear. Thus, applying the natural logarithm to the response variable data allows the linear model to be used for each regression run in the BMA procedures, while effectively analysing a non-linear relationship. The comparison between the initial plots and the ones that use the logarithmically transformed COVID-19 deaths per million inhabitants' data reveals that the log-linear model better fits the relationship between the variables. These plots are available in Appendix A for three of the HDI components (Figures A4 – A9). However, this data transformation does not necessarily allow the model to yield a well-fitted linear relationship for the predictors that did not initially display any apparent relationship with the response variable.

ROBUSTNESS CHECKS AND SAMPLE SIZE

This analysis follows a multiple-step approach, as several BMA procedures were successively run due to different reasons, as previously explained. First, the "BMS" package that was used in the program does not use data that includes *not available values* (NA). To this extent, the variable for which the smallest number of countries is reported determines the sample size. Using a high number of predictors in the analysis therefore increases the probability that the data for one country are not available for at least one variable, excluding the country from the BMA procedures. For example, only 133 of the 214 countries initially available for the response variable also have available data for the *Gini* variable, which is the predictor with the smallest amount of available data. The sample size is then further reduced as the data for some countries that are available for the *Gini* predictor are not reported for other explanatory variables. This issue motivated a multiple-step approach that consists in first running BMA procedures with all the independent variables whose sample size was approximately the same, before including the *Gini* variable in a second step. In the end, for the BMA settings that exclude the *Gini coefficient* data and the *government response* variables, the sample size is 159, against 124 for the ones that additionally includes the *Gini* variable. When the *government response* variables are also added, the number of countries in the analysis without the *Gini* variable falls to 152, against 119 when it is included. Furthermore, the countries that are excluded from the sample when using the *Gini coefficient* data are not randomly selected. Indeed, they are essentially developing and less developed countries whose development characteristics are therefore different from those of developed countries. To this extent, the final results obtained by carrying out the BMA procedures using such a sample are less representative of the whole population of large continental countries, and should be carefully interpreted.

When the sample size is reduced due to the addition of other variables than the *Gini* one, countries that are excluded from the final sample but that were initially available in the COVID-19 deaths per million inhabitants dataset are islands whose population is far below one million inhabitants. To this extent, losing them should prevent the results from being unrepresentative of large continental countries. Indeed, as this study focuses on generalising results related to the spread of a virus through populations worldwide, then these small and isolated countries can be considered as potential outliers. Thus, removing them from the sample does not weaken the conclusions of this study, on the contrary.

Second, as the causality of the relationship stems from the temporality of the sequence of the variables, it is therefore logical not to include the post-outbreak additional variables, i.e., the *government response* variables, since the first BMA procedures. Indeed, these predictors use data that is not anterior to the pandemic and are therefore subject to more careful interpretation with respect to the direction of causality. If it is intuitive to think that the more vaccinated a population is the less deaths per million inhabitants will be observed, this relationship can as well hold in the other direction, as part of a reverse causality phenomenon. Indeed, one could

argue that the more severe the COVID-19 waves are in a country, the more motivations its government have to massively and efficiently roll out a vaccination campaign. Moreover, it is possible that both relationships hold at the same time. Thus, the *government response* variables are included in a later phase to check whether the PIPs and weighted coefficients of the economic development variables and additional predictors still hold, as part of a robustness check. Furthermore, and although the *Gini* variable is added in a second step for other reasons, its inclusion also allows the robustness of the results to be tested.

Finally, the use of a *dilution* prior instead of a *uniform* one also constitutes another possibility for robustness checks to be conducted. Indeed, as in Bajzik et al. (2020, p.27), this paper uses different priors to compare the PIPs and weighted coefficients of the predictors included in the BMA procedures. Overall, the variety of the BMA procedures, with or without the *Gini* variable and the *government response* variables, as well as with two possible priors allows the robustness of the results to be tested in multiple ways, ensuring the reliability of the results.

III - Results and interpretation

The different steps in the approach imply that there are results for multiple BMA procedures which differ in terms of their sample size, model prior, and candidate variables, as previously mentioned. Their comparison allows robustness checks to be conducted. The results yield various elements, such as the PIP of a predictor, its estimated weighted coefficient, and its corresponding standard deviation. As most independent variables have different units, standardised coefficients are additionally computed to allow the comparison of their relative effect on the response variable.

In total, 8 types of BMA procedures are run, depending on whether the *Gini* variable is included, the *government response* variables are added or not, and finally on whether the *uniform* or the *dilution* prior is used.

1) Model selection

Each time BMA procedures are run, a PIP is computed for each candidate variable included in the analysis. To this extent, these probabilities can be used for model selection to solve the uncertainty issue of modelling in linear regressions. However, although Havránek & Sokolova (2020, p.107) consider the PIP as the "Bayesian analogy of statistical significance", the same

rule as in linear regressions cannot be directly employed to determine whether a variable should be selected or not in order to build the best model specification. To this extent, a variable selection criterion must be defined. As Havránek & Sokolova (2020, p.115) and Stojkoski et al (2022, p.5), this paper uses the PIP of each predictor as an indicator of statistical significance and defines a posterior probability threshold of 0.50 at which an independent variable can be included in a hypothetic linear regression model. Such a criterion corresponds to the median probability model rule, as described in Barbieri & Berger (2004) for another Bayesian modelling setting. Here, it stems from the lack of prior knowledge on the expected model size $\bar{k}$, which is therefore equal to $\frac{K}{2}$, with K the number of candidate variables. As a result, the prior inclusion probability of a predictor is $\frac{\bar{k}}{K}$, which in the most relevant BMA setting of this paper is equal to $\frac{21/2}{21} = 0.5$, as further explained below. One should note that, in the absence of prior knowledge on $\bar{k}$, the prior inclusion probability will always be 0.5, as $\frac{\bar{k}}{K} = \frac{K/2}{K} = 0.5$.

This first step in the interpretation solves the uncertainty issue, and only selects a set made of the most meaningful variables, in the sense that they are statistically significant enough so that it is reasonable to believe that their coefficient is non-zero. However, a second criterion must be validated by a candidate variable in this study, based on its standard deviation. As in Havránek et al. (2017, p.52), two standard deviations σ are added and subtracted from the weighted coefficients to build intervals that allow the reliable estimation of the magnitude of a predictor's effect on the response variable. To this extent, a variable whose coefficient would be too close to zero to be economically relevant for the interpretation does not pass the model selection process. In any case, the results of each set of BMA procedures in this paper show that the covariates whose PIPs are the lowest also have a standard deviation value that is high enough to blur any consistent and accurate interpretation of the scale of their coefficients. This supports the idea that only the highest PIPs (here ≥ 0.93) allow reliable and informative results to be calculated. However, this could be due to the limited sample size used in this study. Thus, it is consistent to use both the PIP and standard deviation criteria altogether to evaluate the quality of the results for each predictor.

In the end, 6 variables validate the two previously mentioned conditions of PIP threshold and of low enough standard deviation value. In the demographic variables group, both the *median age* (years) and the *population mean* (thousands) are selected following the median probability model selection method, and standard deviation magnitude considerations. In the political-legal group, only the *democracy* variable (0-10 index) can be considered as selected, while in the public health category the only selected variable is the *overweight prevalence* (%) one. Finally, both the *stringency* (0-100 index) and the *(hydroxy)chloroquine* (0-1 dummy) *government response* variables validate the two selection criteria used in this paper. However, considerations of temporal sequence complicate the accurate estimation of the results and their

interpretation, as it is likely that a phenomenon of double causality affects these two predictors. On the other hand, careful analysis of the *population* variable is made, as the interpretation of its estimated weighted coefficient can be inconsistent. The results for this set of selected variables are discussed in more detail in the paragraphs below.

2) Selected variables

All 8 different BMA settings employed for estimation in this paper use the natural logarithm of the total number of deaths per million inhabitants. However, the BMA approach that should yield the most relevant, accurate and reliable results is the one that includes the *government response* variables, but which excludes the *Gini* variable, while using a *dilution* prior instead of the *uniform* one. This BMA parameterisation is referred to as the *Best Bayesian Setting* (BBS) thereafter.

Indeed, adding the *government response* variables is a way to disentangle any potential effects hidden behind the other explanatory variables, as previously mentioned. Furthermore, the use of a *dilution* prior improves the quality of the results, as the *uniform* prior does not allow the undesired effects of multicollinearity to be alleviated. Nevertheless, the *Gini* variable is not included in the BBS procedures as its data come from a smaller sample where many developing and less developed countries are missing, harming the representativeness of the final results. Still, the other types of BMA procedures are used as robustness checks.

The following subpart explains in detail how the raw results of each type of BMA procedures are processed to get more interpretable coefficients for both the *overweight prevalence* and *median age* selected variables. Then, Figure 6 and 7 on the results and intervals by type of BMA procedures for the selected variables are provided, while the raw version is available in Figure A10 in Appendix A. Raw results and standardised coefficients for the BBS for all variables are also available in Figure A11 and A12 in Appendix A. Finally, the raw results and standardised coefficients for all other BMA settings are available in Appendix B.

OVERWEIGHT PREVALENCE, AND MEDIAN AGE

By PIP order, the most statistically significant predictor is the *overweight prevalence*, followed in third position by the *median age* variable. Both covariates have a very high PIP of almost 100%, and 99% respectively. It is important to note that whether additional predictors are added or not, these variables remain among the three first ones in terms of statistical significance. This does mean that it is highly relevant to include them in a linear regression model to explain the observed changes in COVID-19 fatalities per million inhabitants at the country level.

Beyond this result, one should note that the magnitude of their coefficients is not negligeable. Although the linear models used in the BMA procedures are log-linear model specifications, it is possible to express the computed weighted coefficients as a variation of the response variable in percentage by using $e^{\hat{\beta}} - 1$ (with $\hat{\beta}$ the estimated weighted coefficient of a predictor). Thus, using the output of the BBS procedures $\hat{\beta}_{overweight} = 3.70 \times 10^{-2}$. This means that a one-unit (1%) increase in *overweight prevalence* results in a 3.77% increase in the number of COVID-19 deaths per million inhabitants. Similarly, a one-year increase in the *median age* covariate is associated with an 8.47% increase in the response variable. The meaning of these weighted coefficients is explored in detail in the paragraph below.

On the whole 01/01/2020-10/30/2022 period for data collection on COVID-19 fatalities used in this study, the number of deaths per million inhabitants in France is approximately 2314, for a pre-crisis five-year average of *overweight prevalence* of 59%. All things being equal, should the overweight structure in the French population have been the same as in the United States (67%), these results suggest that the number of COVID-19 fatalities per million should have increased by $e^{8*\hat{\beta}} - 1 = e^{8*3.70\times10^{-2}} - 1$.This corresponds to a 34.45% increase, i.e., a new total number of deaths per million of 3111, now very close to the 3163 fatalities per million inhabitants of the United States. Using the same unit increase but this time for the *median age* variable, the additional number of deaths would have been even greater due to the size of the estimated coefficient of this predictor. However, these two independent variables use different units. To compare their relative effect with respect to the response variable, it is possible to use standardised coefficients, as advised in Feldkircher & Zeugner (2022, p.4-5).

To continue with the detailed interpretation of the results for these two predictors, their standardised coefficients can be used to study the magnitude of their effects on the explained variable as if they were unitless. Indeed, these coefficients use standardised data for each predictor, as if the variances of both the dependent and independent variables were the same, and equal to 1. In other words, this measures the number of standard deviations by which the response variable will change when an explanatory variable increases by one standard deviation. Using the BBS parameterisation, the standardised coefficients for the *overweight prevalence* and the *median age* variables are respectively 0.33 and 0.42. This confirms the previous intuition that, despite the differences between the predictors in terms of the units employed, the age structure of the population has a more important effect on the number of COVID-19 deaths per million inhabitants over the period. Moreover, the standardised coefficients for these covariates are the highest of all the candidate variables included in this study.

As these results suggest a very important role for these two predictors, one may wonder whether they are not overestimated. Once again, the potential overinflation of the results as a

consequence of multicollinearity should be alleviated by the use of a *dilution* prior, as it is the case in the BBS. Other elements in this analysis do support the idea that both the PIPs and weighted coefficients magnitudes of these variables are robust.

Indeed, these results do not solely hold for the BBS procedures. On the contrary, all BMA configurations not only support the selection of the two covariates due to their high and stable PIPs, but they also provide evidence that the magnitude of their weighted coefficients is also correct. For example, the *overweight prevalence* coefficients vary between 3.77% and 4.62%, depending on the inclusion of additional variables and on the type of prior. In the case of the *median age* predictor, the estimated coefficients are between 8.39% and 9.41%, showing that they are fairly robust to various changes in the set of initial parameters in the analysis. Another element that allows for the robustness of the results to be tested is the magnitude of the posterior standard deviations yielded by the BMA procedures. For example, the BBS parameters lead to a standard deviation of 0.61%, which is also the smallest of the posterior standard deviations calculated using the different sets of BMA parameters. In the BBS case, an interval can be computed to get a reliable measure of the weighted coefficient, such as in Havránek et al. (2017, 152). To this extent, the lower and upper limits are computed by adding or subtracting two standard deviations (σ) from the coefficient, to reveal whether it is reliable to state that the covariate's effect on the response variable is not too close to zero to be meaningful. For the *overweight prevalence* variable, the interval ranges from 2.51% to 5.04%, while for the *median age* variable it ranges from 1.39% to 11.43%. Thus, it appears that the effect of the age structure of a population on its number of COVID-19 fatalities per million is not as accurate as for the overweight measure. Overall, across all BMA settings, the intervals for these two variables have non-negligeable values that could not approach zero, which suggests that these predictors do play a significant role in explaining the variations in COVID-19 deaths between countries.

The previous paragraphs explain in detail how the final results of this paper are computed for all predictors. The weighted coefficients expressed as a variation (%) of the response variable and their corresponding standard deviations and intervals, as well as the standardised results for all selected candidate variables are available in Figures 6 and 7 below[2]. On the other hand, the corresponding raw version including the PIP are in Appendix A (Figure A10), while the raw results and standardised coefficients of the BBS for all candidate variables are also available in Figures A11 and A12 of Appendix A. Finally, the raw results and standardised coefficients for all other types of BMA procedures are provided in Appendix B.

[2] In these figures, coefficients for the *population* variable were also computed for a million and ten million inhabitants.

	Post SD	Lower limit	Post Mean	Upper limit
results_log				
overweight (%)	0.73%	2.66%	4.17%	5.71%
democracy (0-10)	8.54%	16.78%	37.57%	62.07%
median age (years)	1.97%	4.65%	8.82%	13.15%
results_log_dilut				
overweight (%)	0.70%	2.87%	4.32%	5.79%
democracy (0-10)	7.93%	15.98%	35.11%	57.40%
median age (years)	1.79%	5.41%	9.20%	13.14%
results_log_gini				
overweight (%)	1.03%	2.04%	4.15%	6.30%
median age (years)	3.40%	1.86%	8.91%	16.44%
results_log_gini_dilut				
overweight (%)	1.03%	2.28%	4.39%	6.54%
median age (years)	3.82%	1.51%	9.41%	17.93%
results_resp_log				
overweight (%)	0.63%	2.49%	3.78%	5.09%
stringency (0-100)	0.78%	2.70%	4.30%	5.93%
median age (years)	1.52%	5.25%	8.47%	11.79%
democracy (0-10)	7.17%	12.45%	29.15%	48.34%
population (k)	0.00%	0.00%	0.00%	0.00%
- population (m)	*0.05%*	*-0.29%*	*-0.19%*	*-0.09%*
- population (10m)	*0.52%*	*-2.93%*	*-1.90%*	*-0.86%*
hcq_cq (dummy)	21.94%	-65.20%	-48.25%	-23.05%
results_resp_log_dilut				
overweight (%)	0.61%	2.51%	3.77%	5.04%
stringency (0-100)	0.77%	2.74%	4.32%	5.93%
median age (years)	1.39%	5.44%	8.39%	11.43%
democracy (0-10)	6.14%	12.87%	27.15%	43.23%
population (k)	0.00%	0.00%	0.00%	0.00%
- population (m)	0.05%	-0.29%	-0.19%	-0.09%
- population (10m)	0.51%	-2.85%	-1.85%	-0.85%
hcq_cq (dummy)	21.78%	-65.54%	-48.89%	-24.20%

Figure 6 (1/2). Results and intervals by type of BMA procedures for the selected variables, expressed in percentage variation in COVID-19 deaths per million inhabitants.

	Post SD	Lower limit	Post Mean	Upper limit
results_gini_resp_log				
overweight (%)	0.84%	2.88%	4.62%	6.40%
stringency (0-100)	0.94%	2.66%	4.59%	6.57%
democracy (0-10)	10.45%	7.76%	31.47%	60.40%
median age (years)	2.43%	3.70%	8.80%	14.16%
population (k)	0.00%	0.00%	0.00%	0.00%
- population (m)	*0.06%*	-0.31%	-0.18%	-0.05%
- population (10m)	*0.64%*	-3.01%	-1.76%	-0.49%
results_gini_resp_log_dilut				
overweight (%)	0.83%	2.89%	4.59%	6.33%
stringency (0-100)	0.94%	2.66%	4.60%	6.58%
median age (years)	2.53%	3.48%	8.77%	14.34%
democracy (0-10)	9.98%	3.91%	25.68%	52.00%
population (k)	0.00%	0.00%	0.00%	0.00%
- population (m)	*0.07%*	-0.30%	-0.17%	-0.04%
- population (10m)	*0.66%*	-3.00%	-1.72%	-0.42%

Figure 6 (2/2). Results and intervals by type of BMA procedures for the selected variables, expressed in percentage variation in COVID-19 deaths per million inhabitants.

	Std SD	Lower limit	Std coeffs	Upper limit
results_log				
overweight (%)	0.07	0.24	0.37	0.50
democracy (0-10)	0.10	0.18	0.38	0.58
median age (years)	0.10	0.24	0.44	0.64
results_log_dilut				
overweight (%)	0.06	0.25	0.38	0.51
democracy (0-10)	0.09	0.18	0.36	0.54
median age (years)	0.09	0.27	0.46	0.64
results_log_gini				
overweight (%)	0.09	0.17	0.35	0.52
median age (years)	0.18	0.10	0.45	0.80
results_log_gini_dilut				
overweight (%)	0.09	0.19	0.37	0.54
median age (years)	0.20	0.08	0.47	0.87

Figure 7 (1/2). Results and intervals of standardised coefficients by type of BMA procedures for the selected variables.

	Std SD	Lower limit	Std coeffs	Upper limit
results_resp_log				
overweight (%)	0.06	0.22	0.33	0.45
stringency (0-100)	0.04	0.15	0.24	0.33
median age (years)	0.08	0.27	0.42	0.58
democracy (0-10)	0.08	0.14	0.30	0.47
population (k)	0.05	-0.27	-0.17	-0.08
hcq_cq (dummy)	0.05	-0.26	-0.16	-0.06
results_resp_log_dilut				
overweight (%)	0.05	0.22	0.33	0.44
stringency (0-100)	0.04	0.15	0.24	0.33
median age (years)	0.07	0.28	0.42	0.56
democracy (0-10)	0.07	0.14	0.28	0.43
population (k)	0.05	-0.26	-0.17	-0.08
hcq_cq (dummy)	0.05	-0.26	-0.16	-0.07
results_gini_resp_log				
overweight (%)	0.07	0.24	0.39	0.53
stringency (0-100)	0.05	0.14	0.25	0.35
democracy (0-10)	0.11	0.08	0.31	0.53
median age (years)	0.13	0.19	0.45	0.70
population (k)	0.06	-0.31	-0.18	-0.05
results_gini_resp_log_dilut				
overweight (%)	0.07	0.24	0.39	0.53
stringency (0-100)	0.05	0.14	0.25	0.35
median age (years)	0.13	0.18	0.45	0.71
democracy (0-10)	0.11	0.04	0.26	0.47
population (k)	0.07	-0.31	-0.18	-0.04

Figure 7 (2/2). Results and intervals of standardised coefficients by type of BMA procedures for the selected variables.

DEMOCRACY INDEX

The BBS results for the *democracy index* predictor show that its coefficient is highly significant, with a PIP of almost 100%. Furthermore, its posterior standard deviation is low enough for the estimate to be considered non-negligeable. The *democracy* variable coefficient is 27.15%, once expressed as a variation of the response variable. As the predictor can take values between 0 and 10, this means that the magnitude of this effect is consistent with the ones observed for the previous selected variables. The standardised coefficient of the *democracy index* allows for a better comparison. The latter is equal to 0.28, not too far below the standardised coefficient of

the *overweight prevalence* predictor (0.33). This implies that the *democracy* variable is the third most important predictor to play a role in explaining changes in COVID-19 fatalities per million inhabitants in terms of relative effect size.

The robustness of these results is high, as 6 out of the 8 BMA configurations yield very high PIPs (≥ 0.95) with low enough standard deviations for the variable to be selected. Overall, the weighted coefficients of the *democracy* predictor in all these settings vary between 25.68% and 37.57%, which does not question the magnitude of its effect. Furthermore, the two types of BMA procedures for which the predictor is not selected are the ones that include the *Gini* variable but not the *government response* predictors. This could be explained by the fact that the sample used for these BMA configurations mainly exclude developing and less developed countries from the study. Indeed, there are non-negligeable correlation coefficients between the *democracy index* and the HDI components variables, that range from 0.52 to 0.64 (see Figure A3 in Appendix A). Thus, it is likely that these samples are less representative of the whole population of large continental countries, and are therefore less capable of capturing differences based on their degree of development, which is related to democracy. On the other hand, the BMA settings that do not include the *democracy* variable still yield high PIPs (72% and 86%), and the predictor only fails the selection process due to its high standard deviation values. Beyond this, the posterior probability of the positivity of the estimated coefficients[3] is still close to 100% in both types of BMA procedures.

Overall, the results captured by the BBS on the role played by the *democracy* variable in explaining changes in the number of COVID-19 deaths per million inhabitants are fairly robust. This suggests that the more democratic a country is before the outbreak, the more it is vulnerable to the pandemic shock, as its total number of COVID-19 fatalities per million increases with the index. This result is explored in more details in the discussion subsection.

POPULATION MEAN

The BBS output shows that the *population* variable from the demographic group of covariates has a very high PIP (99%) as well as non-negligeable weighted coefficients when expressed in a more relevant unit. Indeed, as the initial unit of the *population* data is in thousands, it needs to be converted into at least 10 million people to show an interpretable effect. Thus, it first appears that a 10-million people population increase is associated with a 1.85% fall in COVID-19 fatalities per million inhabitants. The robustness of these results is evaluated before exploring any interpretative considerations. In the BBS, this predictor has a standard deviation of 0.51%, which leads to the construction of an interval that includes the estimated weighted coefficients between -2.85% and -0.85%. It is therefore reasonable to think that the impact of

[3] Expressed in the output of the "BMS" package as *Cond.Pos.Sign*.

the *population* predictor on the response variable is not negligeable, especially since the population size differences between countries can easily reach tens of millions of inhabitants. Additionally, the standardised coefficient of the *population* variable is -0.17, and belongs to the [-0.26, -0.08] interval. As a unitless measure, it thus shows that the role of the *population* predictor is indeed non-negligeable in explaining COVID-19 fatalities per million inhabitants, especially since it accounts for about half of the standardised coefficient of the *overweight prevalence* variable.

Nevertheless, only 4 out of the 8 types of BMA procedures yield results that lead to the selection of the *population* variable. Indeed, in the four settings where the *government response* variables are not included, this predictor has weaker PIPs and higher standard deviation values. For example, although the *population*'s posterior inclusion probabilities are above the 0.50 threshold in these cases (51%-66%), they are significantly lower than the ones obtained using the BMA procedures that include the *government response* variables (94%-99%). However, the most important issue is that the standard deviations are so high that they question the fact that the weighted coefficients of this predictor are not too close to zero. Still, it is not possible to state that these coefficients may be zero, due to their relatively high PIPs that therefore suggest they are non-zero in many linear regression model specifications. Furthermore, the posterior probabilities of the positivity of the weighted coefficients show in all types of BMA procedures that it is almost 100% sure that they are negative, i.e., 0% likely that they are positive. Still, the spread of their interval is so wide in the BMA configurations that do not include the *government response* variables that it is not possible to reliably state that these coefficients are not very close to zero, which would make them meaningless. However, as previously discussed, the best BMA settings are the ones that include the *government response variables*, especially since the BBS is among them. Furthermore, Stojkoski et al. (2022, p.6) also find in their BMA estimation that their *population* variable has a negative coefficient, although its PIP is lower than its initial prior inclusion probability, and its standard deviation is too high to accurately measure the magnitude of the estimate. To this extent, it is still relevant to try to find an interpretation to the non-negligeable and negative coefficients of the *population* independent variable.

Intuitively, it is logical to think that should a country reach a critical population size and not be an outlier such as a small and isolated island, then the number of inhabitants should not matter. After all, the unit used for the response variable is the number of fatalities per million inhabitants, which should make different countries comparable. Furthermore, a larger population should also mean that more inhabitants can spread the virus, become infected, and then risk dying, compensating for any change in the coefficient. What could then explain these rather robust estimates? First, the sample composition could bias the results by introducing too many outliers such as small islands, whose presence in the study would give the *population* variable its effect on COVID-19 deaths per million inhabitants. Indeed, these outliers are

countries whose population is quite limited, and that could possibly easily slow down the spread of the virus by controlling all international inflows and outflows. On the opposite, any outbreak on this type of territory would easily result in very high scores of COVID-19 severity. However, this explanation does not hold for multiple reasons. First, many outliers were naturally excluded from the final sample by the BMA procedures, as the latter cannot include countries whose data is missing for at least one variable, as previously explained. Second, only 10 countries whose population size is below one million inhabitants remain in the sample. The use of a one-million threshold to qualify countries as potential outliers directly stems from the use of the deaths per million inhabitants measure for the response variable. Additionally, half of these countries is not made of islands, and four of them have COVID-19 fatalities per million that are above the sample median, which is 719. To this extent, it is not plausible to think that a non-negligeable and negative coefficient is observed due to the impact of possible outliers. Second, it is not likely that any multicollinearity effect causes this result, as the *population* variable is one of the predictors whose correlation coefficients are the lowest. Furthermore, half of the BMA settings uses a *dilution* prior, which should alleviate any undesired collinearity consequence in the results.

Some reasons may however explain why the weighted coefficient of the *population* variable is not close to zero, and negative. Indeed, as the coefficient of the *population* variable only becomes highly significant and resilient to the standard deviation selection criterion when the *government response* variables are added, it may be that this predictor suffers from negative confounding. It is possible that the inclusion of these variables in the BMA procedures better allows for the study of the impact of *population size* alone. In this case, this would mean that adding these variables to disentangle any potential effects was a relevant way to increase the quality of the results. Indeed, the highest correlation coefficients of the *population* variables are associated with the *government response* variables. Still, they remain quite low (< 0.30) compared to other covariates, which limits the potential impact of negative confounding. Overall, this does not fully explain the observed result, as no obvious mechanism describes how such an effect could apply anyway.

An answer to this question could be that countries with a sizeable population have regions that are as large as certain countries included in the sample. For example, the virus could spread across the different regions of a single country as it spreads across entire countries. Thus, it could be that a very large country is more likely to have *spared* areas while other regions are going through a COVID-19 wave. This could also mean that such a country could channel national and centralised resources towards specific territories that are being hit by the pandemic. Overall, a high population could be a factor of lower fatalities per million inhabitants. After all, a nation's borders may not be the most relevant scope to measure of the spread and lethality of a virus. In this case, *more millions* would then mean *less deaths per million*. Nevertheless, such

effects should be evaluated by conducting studies that focus on the specific role played by the size of a country in controlling a pandemic to verify whether this reasoning explains or not the value of the *population* variable coefficient. Finally, as mentioned in Chang et al. (2022, p.3), "Dietz and Heerstbeek also show that the growth of infectious viruses is relatively independent of the total population size". Thus, there is no certainty that this type of mechanism does explain the characteristics of the *population* coefficient.

To this extent, the statistical significance, as well as the moderately robust, non-negligeable and negative characters of the *population*'s coefficient after the addition of the *government response* predictors need to be further investigated. Future work could provide a clear explanation of any underlying mechanism or element that would explain this result.

STRINGENCY AND (HYDROXY)CHLOROQUINE

The BBS results show that the *stringency* and the *(hydroxy)chloroquine* explanatory variables are statistically significant in the sense that they have very high PIPs far above the 0.50 threshold, around 100% and 98% respectively. Furthermore, their weighted coefficients are high enough to be considered as having a non-negligeable impact on COVID-19 deaths per million inhabitants. Indeed, once expressed in variation (%) of the response variable, a one-unit change in the *stringency index* is associated with a 4.32% increase in the explained variable. Considering that this predictor uses a 0-100 scale, this means that the impact of *stringency* variations on the number of fatalities per million inhabitants can be consequent. Moreover, the posterior standard deviations of this variable reveal that its coefficient ranges from 2.74% to 5.93%, which excludes the possibility that it is close to zero.

For the *(hydroxy)chloroquine* variable, the estimated coefficient is -48.89%. However, as it is a dummy variable, such a high value should be evaluated with respect to a radical change in the use of this early treatment at the country level. Moreover, compared to the *vaccination* variable, the results on this covariate are less likely to be informative. Indeed, the *(hydroxy)chloroquine* variable is defined as a dummy. In this sense, it is as if the data on *vaccination* could only reveal whether a country had a *high vaccination coverage* or not. Thus, this type of insight is not very informative on the relationship between the use of this early treatment at the country-level and the response variable.

As these two predictors are *government response* variables, their robustness can only be evaluated using the BMA settings that do include them as candidate variables. In the end, out of the 4 types of Bayesian procedures in which they are present, the *stringency* predictor is always highly significant with PIPs of almost 100%, while it also validates the standard deviation selection criterion. On the other hand, the *(hydroxy)chloroquine* is only selected in the two BMA settings that include the *government response* variables, but in which the *Gini*

variable is excluded. Indeed, when the *Gini* sample is used, the posterior standard deviations of this early treatment variable are too high to reliably state that its weighted coefficients are meaningful. However, as previously mentioned, the addition of the *Gini* predictor as a candidate variable leads to a non-random restriction of the sample size. Indeed, developing and less developed countries are overrepresented among the countries for which data on inequality is missing. Thus, and as the most important and negative correlation coefficients of the *(hydroxy)chloroquine* are with the HDI components variables, it is likely that the non-random reduction of the sample size decreases the importance of the relationship between this early treatment predictor and the response variable. Moreover, the PIPs of this covariate are still fairly high ($> 73\%$) in the two other BMA configurations, and the posterior probabilities that its weighted coefficients are negative are almost 100%. Therefore, these results still suggest that this predictor does play a non-negligeable role in explaining the observed cross-country differences in COVID-19 severity.

Overall, the BBS standardised coefficients for the *stringency* and the *(hydroxy)chloroquine* variables are 0.24 and -0.16 respectively, which supports the idea that they matter as parameters of the response variable. However, one could think that these results lead to odd interpretations with respect to the *stringency* predictor. Indeed, its weighted coefficients suggest that the strictest policy responses, i.e., the highest values for the index, are associated with more COVID-19 fatalities per million inhabitants. In addition to being counterintuitive, these results are in contradiction with Stojkoski et al. (2022, p.8). Indeed, these authors build a government response index, and conclude that this variable has a negative coefficient and plays the most important role in explaining COVID-19 severity at the country level. How to explain such opposed results? First, Stojkoski et al. (2022, p.2) use a sample of 105 countries and state that it was "the largest set of countries for which all data were available" at the time. By comparing their sample with the one used in this paper, it appears that the countries with the lowest numbers of fatalities per million over the 01/01/2020-10/30/2022 period are overrepresented among the countries for which data was not available at the time. To this extent, a stringency-related variable may have had very different effects if their sample is in fact not representative of the same population of countries. Furthermore, the authors write that their data were collected on the 13th of November 2020 (Stojkoski et al. 2022, SI p.2), which further supports the idea that differences in the data can be the cause of differences in the results.

However, it remains that the positive coefficient of the *stringency* predictor is still a counterintuitive result. According to Lewis (2022), although the effects of restriction measures on reducing infections and deaths across countries can be considered as less effective than initially thought, they are still given a mitigating effect on COVID-19 severity in the literature. The most probable explanation stems from a causality issue. Indeed, as previously discussed, most of the explanatory variables in this study use pre-crisis data. The *government response*

predictors, on the other hand, are by nature covariates that use data collected after the beginning of the outbreak. To this extent, it very likely that a variable such as the *stringency* one suffers from a double causality issue with respect to the response variable. Indeed, the severity of a COVID-19 wave could be an important factor in government response decision-making. In other words, it does seem logical to think that a government has high incentives to implement very strict measures when its country is being hit hard by the pandemic. Here, the temporal sequence of the variables does not allow for a one-way causation to be easily established. As a result, the *government response* variables should be driven toward more positive values. Thus, it is possible that although a set of strict policies does reduce the degree of COVID-19 severity, the reverse causality effect weighs so much on government decision-making that the overall observable impact of the *stringency* predictor yields a positive coefficient. Therefore, it cannot be reliably concluded that its coefficient is truly positive.

The other *government response* variables such as the *(hydroxy)chloroquine* or the *vaccination* ones could also suffer from this issue. However, two elements nuance both the effect and existence of such a phenomenon. First, if a double causality phenomenon also occurs for these predictors, the resulting impact should be less important than for the *stringency* variable, due to the way these government responses are implemented over time. Indeed, the initial OxCGRT dataset for the *stringency index* provides daily data by country. Thus, it can be observed that the values of the index vary considerably over time, widely increasing and decreasing depending on the context, and this even in a single country. A vaccination campaign or any early treatment-based national strategy cannot be quickly adjusted depending on the severity of a COVID-19 wave. Such nuances could be better observed and captured over time in a study that would use panel data or times series instead of cross-sectional data. However, even if it was the case for the *government response* variables other than *stringency* to be significantly affected by a reverse causality effect, this would mean that the estimated weighted coefficients for the *(hydroxy)chloroquine* predictor would already be more positive than they should be had the double causality phenomenon not existed. To this extent, such an interpretation would mean that the coefficient of this predictor should be more negative, which would suggest that this variable has an even more important role to play in explaining COVID-19 fatalities at the country level.

Thus, although multiple elements support the robustness of these results, causality considerations question the quality of the estimates for the *government response* variables, especially for the *stringency* one. In the case of the early treatment variables and the *vaccination* variable, it is however less likely that such undesirable effects introduce an important bias. This is especially true for the *(hydroxy)chloroquine* predictor, as its weighted coefficient is negative, whereas any potential double causality phenomenon should increase the estimated coefficients toward positive values.

3) Non-selected variables

Beyond the 6 previously mentioned variables, the other 15 ones were not selected in any BMA setting. Only the *Gini* and the *CHE* predictors exceed the 0.50 PIP threshold in most cases, but eventually fail to validate the standard deviation criterion used in this paper. For the other development and additional predictors, the results do not suggest that their inclusion in a linear regression model increases its probability to match the observed data, and neither do they provide any accurate and reliable information on their coefficients.

CHE AND GINI

The *Current Health Expenditure* (*CHE*) variable and the *Gini* variable show some statistical significance across the different BMA configurations. Indeed, the PIPs for the *CHE* predictor vary between 60% and 73% in most settings. Only the two BMA procedures in which the *Gini coefficient* is included while the *government response* variables are not prevent the *CHE* variable from validating the PIP selection criterion. Even in these cases, the predictor is not far from the 0.50 threshold, with PIPs of 42% and 44%. For the *Gini index*, in all cases where the variable is included, its PIPs oscillate between 59% and 68%. Thus, both predictors mainly fail because of their inability to validate the standard deviation selection criterion for all possible BMA configurations.

It is likely that the limited size of the sample prevents the coefficients of theses variables from having low enough standard deviations to be accurately interpreted. This is especially true for the *Gini* predictor as its inclusion as a candidate variable in a BMA setting significantly decreases the size of the sample, as previously mentioned.

However, and although the magnitude of the estimated coefficients cannot be interpretated with certainty, the results still yield reliable information on the sign of these two variables. Indeed, the posterior probability of positivity of the *CHE* and the *Gini* predictors are respectively close to 0% and 100% for all BMA configurations. This means that it can reliably said that, should the weighted coefficients of these variables be far enough from zero to have a meaningful impact, then an increase in the *CHE* variable would be associated with a decrease in COVID-19 fatalities per million, while an increase in the *Gini coefficient* would result in an increase in the number of deaths. Thus, and despite fairly robust results in terms of PIPs, a question remains as to whether these negative and positive coefficients are different enough from zero to produce an observable impact.

OTHER ADDITIONAL VARIABLES

The rest of the additional covariates is never selected, as they have very low PIPs and high standard deviations overall. For many of them, no conclusion can be reliably drawn on their sign, and most standardised coefficients are too low to suggest that any meaningful relationship may exist between them and the response variable.

Only the *CPI*, and the *vaccination* predictors can have a PIP that exceeds the 0.50 threshold. However, these occurrences are rare among the 8 configurations, as the *CPI* covariate appears with a high enough PIP in only two BMA settings, while the coefficient of the *vaccination* variable only exceeds the threshold in one configuration. Moreover, the latter is a type of BMA procedures where the *Gini* variable is included, which means that the sample size is reduced, and thus less representative of the population studied. However, as it was previously mentioned that this smaller sample mainly excludes developing and less developed countries, this could mean that the *vaccination* predictor may better explain variations in COVID-19 deaths per million inhabitants in a subset of more developed countries. On the other hand, it is important to note that the use of the *dilution* prior leads to a decrease in the PIP of the *vaccination* variable in the only model where it is selected, whose value falls from 55% to 35%. As a result, the weighted coefficient also significantly decreases, and it is likely that a non-negligeable part of the initial results of this predictor was in fact inflated due to multicollinearity.

Another weakness in the results is that the PIPs for these two variables are not robust and are not above the 0.50 threshold in the BBS. Furthermore, their standard deviation values are never low enough for their coefficients to be reliably interpreted. Finally, their standardised coefficients are low in the BBS, as they are below 0.02 in absolute value.

HDI COMPONENTS

As the initial reason that motivates this study stems from a correlation relationship between development and COVID-19 severity, it is interesting to look at the results for the four HDI component variables. Indeed, the latter have fairly high correlation coefficients between 0.46 and 0.71 with the natural logarithm of COVID-19 deaths per million (see Figure A3 in Appendix A). However, by introducing many additional covariates and by weighting the estimated coefficients across all possible linear regression models, it appears that these variables are never selected, neither for their PIP nor for their standard deviation, with one exception for the *mean years of schooling* variable.

Indeed, this predictor exceeds the 0.50 threshold when its PIP reaches 57% in the BMA setting where the *Gini* variable is included, and the *government response* variables are not. However, the use of a *dilution* prior once again triggers a decrease in the posterior inclusion probability of this predictor to 26%. An interpretation similar to the one of the *vaccination* variable can explain these results. Indeed, it is likely that the *mean years of schooling* predictor has an

inflated PIP and weighted coefficient due to a multicollinearity phenomenon. This argument is further supported by the fact that the use of the *dilution* prior instead of the *uniform* one for each BMA setting always leads to a significant fall of the PIP and estimated coefficient values of the *mean years of schooling* variable.

Overall, it appears that the PIPs, weighted coefficients, and standardised coefficients of all the HDI component variables are very low across all BMA settings, including in the BBS. As furtherly explored in the discussion subsection, these results suggest that the set of initial candidate variables included in each type of BMA procedures allowed the effects of these development variables to be disentangled and attributed to other predictors, whose absence would have created a sizeable omitted variable bias. It is interesting to note that the most important explanatory variable is the *median age* one, while the HDI component *life expectancy* predictor is never selected in any BMA setting. As there is a high correlation coefficient of 0.86 between these two independent variables (see Figure A3 in Appendix A), it is likely that *median* age is an intermediary variable in the relationship between *life expectancy* and the total number of COVID-19 deaths per million at the country level. In the end, these results do not suggest that there is a clear and direct relationship between any of the HDI component explanatory variables and COVID-19 severity, once other relevant predictors have been added. However, several of the selected variables are still related to development to some extent. This therefore reflects its impact on a country's vulnerability to a pandemic such as the COVID-19 one, as explained in the subsection below.

4) Discussion

Overall, 6 candidate variables out of the initial 21 are selected based on their respective PIP, weighted coefficient, and standardised coefficient. The robustness of these results is tested across all 8 BMA settings. However, it has been previously shown that any interpretation of the results for 3 of these variables is questionable. Indeed, considerations of double causality for all *government response* variables were highlighted, as they could inflate the PIPs of these predictors and bias their coefficients toward higher and positive values. This is especially the case for the *stringency* variable as it is likely that public policy decision-making is affected by the COVID-19 severity context. Nevertheless, other *government response* variables should be less sensitive to such a phenomenon, which makes a careful interpretation of the *(hydroxy)chloroquine* variable possible, as it is one of the selected predictors. On the other hand, the *population* variable exhibits inconsistent results with respect to the literature, and to any intuitive reasoning. To this extent, it remains a weakness of this study, as no clear

mechanism that explains the characteristics of its weighted coefficients has been found. As a result, further work on this question is required to shed light on this grey area.

THE CHARACTERISTICS OF DEVELOPMENT

If the results did not show any obvious relationship between the HDI component variables and the number of COVID-19 deaths per million inhabitants, they nevertheless reveal that other predictors play an important role in explaining variations of the response variable. In the end, these covariates act as intermediary variables in this relationship as they are related to development.

Overweight prevalence

For example, the *overweight prevalence* data used in this paper have correlation coefficients of 0.56 to 0.69 with the logarithmically transformed response variable data. On the other hand, authors such as Ng. et al. (2014) show that there are country level differences in terms of overweight and obesity based on the degree of development of countries, as shown in Figure 8 below. This means that overweight can be considered as characteristic of development. As a result, the importance of *overweight prevalence* in explaining COVID-19 severity suggests that the populations of developed countries are more vulnerable to this type of pandemic. Furthermore, worldwide direct consequences of overweight are so important, including in terms of deaths, that the authors even describe it as a "global pandemic" (Ng et al., 2014, p.767). The results of this paper add to this finding by showing that the consequences of overweight with respect to the COVID-19 shock further worsen its impact on public health, especially in developed countries. This conclusion is supported by the fact that the *overweight prevalence* variable also shows a significant and positive effect on COVID-19 severity at the country level in Stojkoski et al. (2022, p.6), as the authors state that it is even the only predictor for which there is strong evidence of its impact on the response variable.

Regarding the consistency of the weighted coefficient, the BBS output yields a 3.77% value, which is highly statistically significant. Furthermore, this estimate only varies by less than 1% across the different BMA settings. This robust result is not far from the one of Arulanandam et al. (2023, p.6) who find that "a rise in the obese adult population by 1 percentage point explains 1.5 percentage point rise in mortality due to COVID-19 for high income countries". Although the coefficient found in this study is higher than in the authors' paper, differences in the choice of the population studied and the data collection period can explain these disparities. Overall, the magnitudes of the coefficients are the same, which supports the accuracy and reliability of these estimates.

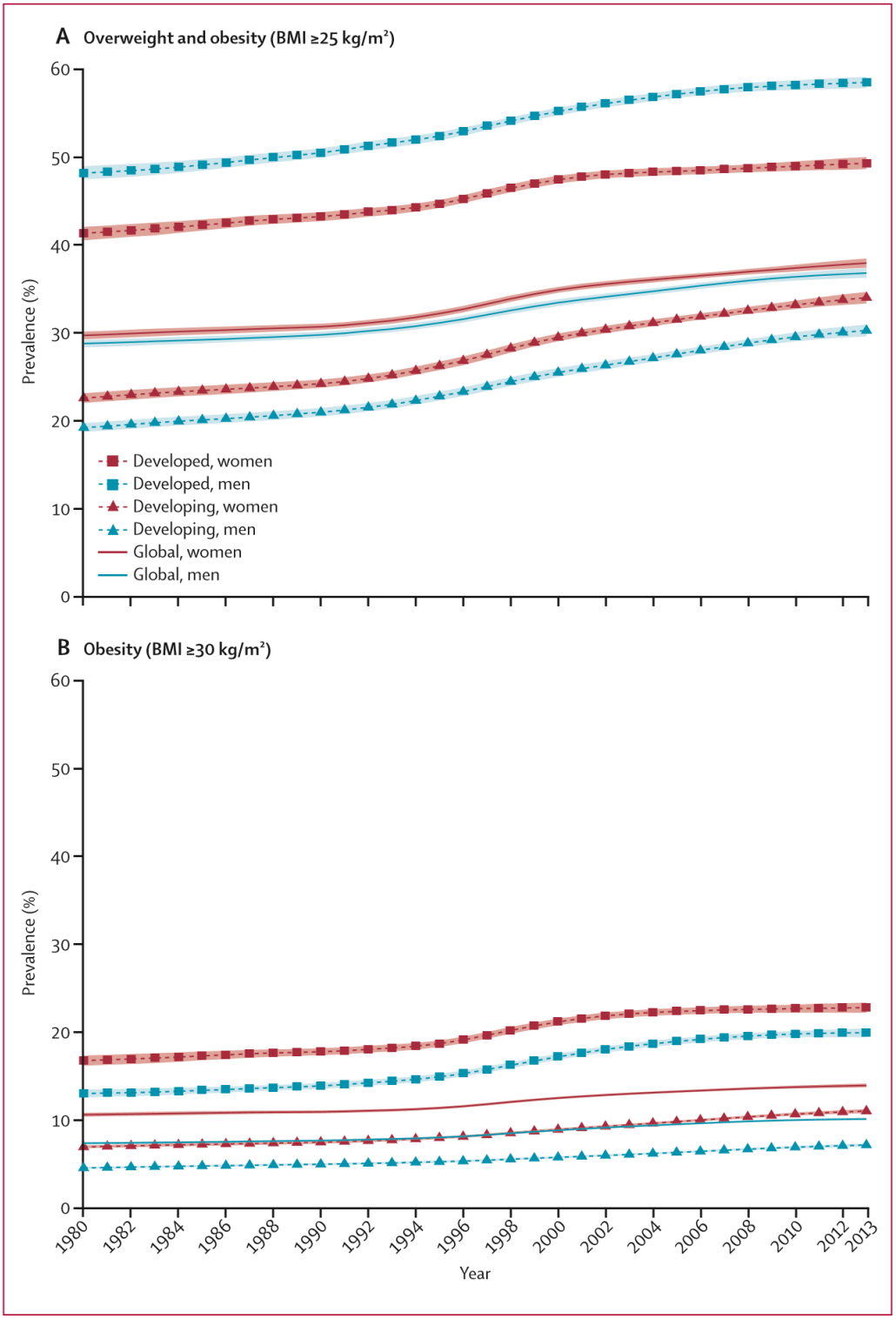

Figure 8. "Age-standardised prevalence of overweight and obesity and obesity alone, ages ≥ 20 years, by sex, 1980-2013" (Ng et al., 2014, pp.767).

These results stress out that a high degree of *overweight prevalence* has indirect negative consequences on public health with respect to the vulnerability of a country to a pandemic

shock, as illustrated here for the COVID-19 outbreak. These conclusions therefore suggest that public health policies that aim at fighting against overweight would make a sizeable difference in terms of COVID-19 deaths per million, which would be observable at the country level. Furthermore, this highlights overweight segments of a population as more vulnerable to such a pandemic. These results could therefore also mean that targeted healthcare would be an appropriate way to increase the efficiency of *government response* variables, although the results in this paper show that there is moderate evidence on the interpretability of their coefficients.

As countries develop over time, overweight prevalence should also increase. Indeed, Ng et al. (2014, pp.779) write that "unlike other major global risks such as tobacco and childhood malnutrition, obesity is not decreasing worldwide". To this extent, the results in this paper stress out the importance of addressing overweight as a major public health issue, as it is likely to be a determinant factor of the vulnerability of countries to future pandemics similar to COVID-19.

Median age

The *median age* predictor is also highly correlated with the HDI component variables in the sample, with correlation coefficients ranging from 0.71 to 0.86 (see Figure A3 in Appendix A). To this extent, development is associated with older population structures. Moreover, as the *median age* standardised coefficient (0.42) is the highest one of all candidate variables, then this means that the most developed countries should also be the most vulnerable to the pandemic in terms of deaths per million inhabitants. This would also explain the initially observed correlation between the response variable and the HDI components.

Thus, the results related to the role played by the age structure of a population in explaining the COVID-19 deaths toll in a country are consistent with Chang et al. (2022, p.6), who find that their *age* variable has positive and significant coefficients. According to them, these results are supported in the rest of the literature, such as in Dowd et al. (2020) and Boehmer et al. (2020), as well as in public reports as from the U.S. Centres for Disease Control and Prevention (CDC). This result is also supported by Kang & Jung (2020, p.160) as they conclude in their study that elderly people are more vulnerable to COVID-19 as they are more likely to develop symptoms.

The interpretation of the *median age* results is closely linked to the *overweight prevalence* one. Indeed, they suggest that as a country develops, it will face new challenges in terms of the ageing of its population. This phenomenon is already a stake in itself, as a growing proportion of elderly people as well as a rise in the maximum life expectancy both increase the healthcare needs of a country. Beyond this, the results of this paper show that an older population is also more vulnerable to a pandemic like the COVID-19 one. Furthermore, this effect is far from being negligeable as *median age* is the most important variable to explain variations in COVID-

19 fatalities per million inhabitants out of the 21 candidate predictors. To this extent, the use of targeted healthcare, this time focusing on the older part of the population, could once again be a way to efficiently channel public resources toward the most vulnerable segments. As a result, the number of COVID-19 deaths per million should be significantly reduced, enough to create observable differences at the country level.

Thus, both the *overweight prevalence* and *median age* variables results suggest that a country's vulnerability to a pandemic such as COVID-19 is largely explained by the weight and age structures of its population. This paper therefore identifies two population characteristics that shape a country's ability to absorb a pandemic shock with respect to its number of deaths per million. To this extent, the scope of these results includes elements that could be used in the future, with respect to the vulnerability of populations to pandemics at the country level, and to the design of public health policies.

Democracy

The *democracy index* variable has the third most important role to play in explaining COVID-19 fatalities per million inhabitants. Indeed, the results show that the weighted coefficient of this predictor is positive, with a BBS standardised value of 0.28. This means that more democratic states were more vulnerable to the COVID-19 outbreak, i.e., that democracy is an aggravating factor of the virus impact.

At first, this result could seem contradictory, as some authors as Bollyky et al. (2019 p.1638) have already studied the relationship between democracy and public health and concluded that "democratic governance and its promotion, along with other government accountability measures, might further enhance efforts to improve population health". To this extent, their result is not consistent with the one found in this paper. However, Chang et al. (2022, p.8) highlight that democratic countries could be slower to implement lockdown measures, and that individualism was a stronger phenomenon for more liberal countries, which could impact the spread of the virus. Indeed, the deliberative decision-making processes of democracy imply that government responses are likely to take more time to be decided and implemented.

Chang et al. (2022, p.6) use a similar *democracy* variable and find that it has a statistically significant positive coefficient whose magnitude is non-negligeable in explaining COVID-19 cases and deaths. To this extent, the findings of these authors are consistent with the ones of this paper. In terms of magnitude, they find that a one-unit increase in the *democracy* variable is associated with a 17.7% increase in confirmed deaths per week. In this study, the BBS weighted coefficient has a fairly robust value which shows that a one-unit increase in the *democracy* variable corresponds to a 27.15% increase in the response variable. Thus, and although the studied periods are not the same, the two coefficients are not far from each other,

which supports the consistency of their magnitude beyond their positive sign. This paper therefore concludes that there is some reliable evidence that the more democratic a country is, the more vulnerable it is to an outbreak such as the COVID-19 one.

On the other hand, there is a correlation between this predictor and development, as its coefficients with the four HDI components range between 0.52 and 0.64 (see Figure A3 in Appendix A). This relationship is also described in Olson (1993, pp.572-573), where the author argues that the conditions for economic development are the same as the ones that are needed for a lasting democracy. To this extent, he writes that "it is no accident that the countries that have reached the highest level of economic development and have enjoyed good economic performance across generations are all stable democracies". This also supports the idea that democracy is a supportive characteristic of development. Thus, a country whose development is allowed by democratic improvements will however become more vulnerable to a pandemic shock similar to COVID-19.

Furthermore, this conclusion also interacts with the results on the *overweight prevalence* and *median age* variables. On the one hand, development is associated with weight and age population characteristics that aggravate the potential severity of a pandemic. On the other hand, a more developed country will be less capable of making quick and efficient decisions to respond to emergency health shocks such as the COVID-19 outbreak. In conclusion, these results suggest that development should be accompanied by long-term investments in public health to compensate for the increase in overweight and the ageing of the population, as well as for the loss of government responsiveness which comes from the acquisition of democratic characteristics. These elements also highlight the possibility to design targeted health policies for the most vulnerable segments of the population in order to reduce the vulnerability of a country to a pandemic such as the COVID-19 one. The previously discussed weak evidence on the potential role of the *Current Health Expenditure* (*CHE*) predictor could therefore suggest that such long-planned investments, as opposed to emergency investment, have a role to play in improving a country's capacity to absorb pandemic shocks as it develops.

GOVERNMENT RESPONSE

The results of this study provide information on the impact of different emergency measures on COVID-19 severity at the country level. Indeed, two of the selected predictors are *government response* variables, whose inclusion allows the effects of the pre-crisis country characteristics to be disentangled. Beyond this purpose, these explanatory variables nevertheless suffer from a temporal sequence issue, which leads to a double causality phenomenon. As a result, the PIPs and weighted coefficients of the *government response* predictors are inflated, as a high number of COVID-19 fatalities per million inhabitants is likely to be a decision-making incentive for government to implement a response. As previously explained, this type of bias should affect

the *stringency* variable more, which makes any interpretation unreliable for this covariate, while this should not be the case for the *(hydroxy)chloroquine* predictor. This independent variable is therefore the only *government response* covariate for which this study provides evidence of a relationship with the response variable.

(Hydroxy)chloroquine

The results of this study show that the PIPs and weighted coefficients of the *(hydroxy)chloroquine* variable are robust to the use of a *dilution* prior instead of a *uniform* one, as previously detailed. Furthermore, this predictor also validates the standard deviation selection criterion, and its standardised coefficient is -0.16 in the BBS. To this extent, it appears that the nation-wide official use of this early treatment variable can be associated with a non-negligeable decrease in the total number of COVID-19 deaths per million at the country level.

However, some elements should be discussed before these results can be interpreted and conclusions drawn. Indeed, the mitigating effect of this predictor on the response variable is contradictory to multiple health studies on the efficiency of (hydroxy)chloroquine, which is the case of the two following meta-analyses. For example, Fiolet et al. (2020, p.24) find that this early treatment is not effective against COVID-19 and can even increase the risk of mortality, while this result is later confirmed by Axfors et al. (2021). To this extent, the results of this study are contradictory to those found by these authors as part of the health literature. However, Toya & Skidmore (2021, p.6) also find a significant and important effect for *(hydroxy)chloroquine* in mitigating the number of COVID-19 deaths at the country level, expressed in fatalities per hundred thousand inhabitants. Their study focuses on the role of public policies and other factors in "determining a county's vulnerability" to COVID-19 (Toya & Skidmore, 2021, p.2). Thus, and although their methodology is not the same, their results confirm the ones found in this paper. Finally, another element that further supports the fact that a consensus on the role played by this early treatment with respect to COVID-19 severity in the literature is not clear is that a sizeable number of countries did choose to use this treatment on a national-scale. Indeed, the *(hydroxy)chloroquine* dataset reveals that 40 out of 166 countries have chosen to use this treatment to fight against COVID-19 as part of their government response measures. Moreover, as described in the data section, a conservative approach was followed to ensure the best possible quality for this data, so that the inclusion of this predictor in the set of candidate variables can reliably capture country differences. To this extent, a less conservative approach would have further increased the number of countries for which this dummy variable is equal to one. The Ministry of Health (MoHFW) in India, for example, has published successive advisory documents on the use of hydroxychloroquine as a country-wide official way to fight against COVID-19 in March and May 2020. Moreover, these instructions have not been subsequently revised. To this extent, they write that several studies motivate their

decision (MoHFW, 2020a; MoHFW, 2020b), which further highlights the lack of unanimous result on this topic.

Overall, the potential but unlikely effects of reverse causality as well as the diversity of results with respect to the role of the *(hydroxy)chloroquine* predictor in mitigating COVID-19 deaths hinders a reliable and meaningful interpretation of the results. This conclusion is also supported by the nature of the data of this predictor, as it only provides information in the form of a dummy variable, which does not capture nuances in the use of the treatment. Any further interpretation or conclusion on the *(hydroxy)chloroquine* variable would therefore require the use of a higher quality dataset, so that the final results can be more informative on the relationship of this early treatment predictor with the response variable.

In the end, the true effect of *(hydroxy)chloroquine* at the country level cannot be reliably assessed despite highly significant, accurate and fairly robust results that correspond to the findings of a part of the literature. Still, these actual results provide moderate evidence that this predictor plays a role in explaining COVID-19 deaths. Thus, this conclusion could be associated with the previous interpretations on *overweight prevalence, median age*, and *democracy*. Indeed, these selected predictors suggest that there is a segment of the population whose characteristics make it significantly more vulnerable to the pandemic. Therefore, it appears that government responses such as the use of early treatments could increase in efficiency through the use of targeted public policies.

These combined conclusions therefore provide evidence on the factors that explain country differences in terms of COVID-19 severity. The latter suggest that improvement can be found in the design and implementation of health policies and emergency responses that focus on country level weaknesses that are related to their level of development. To this extent, these stakes are likely to become increasingly important in the future as nations develop, and therefore as their vulnerability to potential new pandemics increases.

Conclusion

This paper follows an original perspective by reversing the direction of the relationship that is usually studied between economic development and the COVID-19 outbreak. Indeed, this work does not focus on how economic growth was affected by the pandemic, for example. On the contrary, it rather analyses how the pre-crisis characteristics of countries did act as parameters of COVID-19 severity. In other words, this work studies the country level factors

that can be considered as weaknesses that predetermined the resilience of a population to the virus.

By choosing a Bayesian Model Averaging (BMA) approach, this paper overcomes the uncertainty issue with respect to model specification. Indeed, the predictors that are highlighted in the literature as the most important ones in explaining COVID-19 deaths per million inhabitants are selected to build a set of 21 candidate variables. It is important to note that this paper transforms the data on COVID-19 fatalities per million using the natural logarithm to better fit a linear setting. This is necessary as BMA procedures are then run to test all combinations of the candidate covariates in all possible linear regression models. Posterior inclusion probabilities (PIPs) for each variable are then calculated to provide information on their statistical significance, while their weighted coefficients are also computed. A median probability model threshold of 0.50 is chosen as a PIP-based selection criterion, as it is suitable for a situation where no initial knowledge is available to assess the inclusion probability of a variable. The BMA procedures also compute posterior standard deviations that are used in this paper to determine whether each coefficient can be confidently estimated as sufficiently different from zero. Indeed, they could not be considered as having a meaningful impact on the response variable otherwise. Furthermore, 8 different BMA settings are used based on the additional inclusion of the *Gini* variable, of the *government response* variables, and on the choice of the *uniform* or the *dilution* prior as a prior model probability. Thus, a step-by-step approach is followed, which allows the robustness of the results to be tested across all types of BMA procedures. In this paper, the *Best Bayesian Setting* (BBS) is defined as the configuration in which the *government response* variables are included as candidate predictors, which uses the *dilution* prior, but which excludes the *Gini* variable. It is therefore used as the starting point for the analysis of the results. In the end, 6 out of the initial 21 candidate predictors are selected using the PIP and standard deviation selection criteria. However, 2 of them are eventually discarded due to reverse causality and inconsistence limitations, leaving only 4 of them open to reliable interpretation.

Indeed, the estimated coefficient for the *stringency* (0-100) predictor, which measures the strictness of restriction policies, cannot be interpreted due to the probable impact of a double causality phenomenon. As part of the *government response* variables category, its data are collected after the beginning of the crisis, which prevents causality from being inferred from the temporal sequence of the variables. Indeed, the fact that all *non-government response* predictors use pre-crisis data is one of the arguments that support the existence of a causal relationship between development and the severity of COVID-19. Still, the inclusion of the *government response* predictors is a way to crowd out any intermediary effects that would result from an omitted bias phenomenon. On the other hand, the BMA procedures yield inconsistent estimates for the *population* (thousands) variable which contrast with the literature, and which

this paper is unable to adequately explain. This limitation remains a point of interest for future work. In the end, the *median age* (years), *overweight prevalence* (%), *democracy* (0-10), and *(hydroxy)chloroquine* (0-1) variables are found to have a robust non-negligeable effect on COVID-19 fatalities per million inhabitants that can be accurately and reliably estimated.

As most predictors have different units, the comparison of their respective effects is allowed by the conversion of the raw BMA results in estimates expressed in percentage of variation of the explained variable, and by the use of standardised coefficients. In the end, out of these four selected predictors, the *median age* and the *overweight* covariates are the most important ones in explaining a change in the response variable. Indeed, their coefficients are highly statistically significant in all types of BMA procedures, with PIPs almost always close to 100%. Furthermore, in the BBS, a one-year increase in *median age* is associated with an 8.39% increase in COVID-19 fatalities per million, while a one-percent rise in *overweight* leads to a 3.77% increase in the response variable. Using standardised estimates, their respective coefficients are 0.42 and 0.33, which further shows that the *median age* variable has a greater impact despite their different units. Furthermore, these results are robust across all BMA settings and consistent with the literature on this topic. Given that an older age structure and a higher prevalence of overweight are characteristics of developed countries, these results therefore suggest that development is indirectly linked to the vulnerability of a country to outbreaks such as COVID-19. To this extent, health policies targeted at the most vulnerable segments of a population should be more efficient in mitigating the impact of future similar pandemics.

On the other hand, the *democracy* variable is statistically significant with a PIP above the 0.50 threshold in 6 out of 8 types of BMA procedures. In these settings, its estimates only vary slightly, which supports the robustness of these results. Furthermore, its standardised coefficient is 0.28 in the BBS, which means that this predictor is the third most important selected covariate to explain changes in the response variable, not far below *overweight*. As its weighted coefficient is positive, an increase in the *democracy* predictor is associated with more COVID-19 fatalities per million. In other words, these results suggest that more democratic states are more vulnerable to the pandemic. This conclusion is in line with a part of the literature, although certain authors argue that more democratic countries are better at creating efficient health systems. Still, studies that focus more specifically on the parameters of COVID-19 severity at the country level do find that democratic characteristics are associated with more deaths per million inhabitants. This could be due to slower deliberative decision-making processes with respect to emergency responses in a context of crisis. Moreover, as the conditions for the emergence of democracy are the same as those for development, these results further support the idea that developed countries are more vulnerable to this type of pandemic. Overall, this conclusion is consistent with the previous reasoning on the *median age* and

overweight predictors. Indeed, it also suggests that public health stakes will become increasingly important as country develop in the future, and therefore as they become more vulnerable to pandemics such as COVID-19.

Finally, the *(hydroxy)chloroquine* variable is the only selected *government response* variable for which double causality considerations do not question the interpretability of its results. Indeed, the reverse causality that might affect these predictors should push their coefficients towards positive values, while the one of the *(hydroxy)chloroquine* covariate always has a negative sign. The PIP of this variable is considered statistically significant in all settings where it is included, while its standard deviations are low enough in only half of them. Thus, these elements support that these results are still fairly robust, as the variable is selected in the BBS. Indeed, this BMA setting shows that its coefficient is -0.16, which indicates that it is non-negligeable in explaining differences in COVID-19 severity at the country level. As the sign of this coefficient is negative, this means that it is associated with a decrease in deaths per million inhabitants. However, this result is not unanimous in the literature, as different studies find opposite effects. Furthermore, this covariate does not provide an accurate measure of the effects of the use of (hydroxy)chloroquine at the national level, as it is only a dummy variable. Thus, these results are not very informative as they cannot capture the nuances that a more detailed dataset would have. Therefore, the only interpretable aspects of the estimate are its sign and non-negligeable character. Overall, the potential effect of double causality, the partial robustness of the results, and the limited informativeness of this predictor as a dummy variable are weaknesses that prevent any further assessment of the role of the *(hydroxy)chloroquine* covariate in explaining COVID-19 fatalities per million at the country level.

Future work could focus on designing a study that uses time series or panel data rather than cross-sectional data, as well as a better-quality dataset to assess the relationship between the *(hydroxy)chloroquine* variable, the other *government response* predictors, and the response variable. However, in this cross-sectional study, these independent variables are primarily used as additional covariates whose purpose is to disentangle effects so that the estimates of the pre-crisis variables can be more accurate and reliable.

Overall, the results of this study do suggest that the classic relationship between economic development and public health is questioned in the case of the COVID-19 outbreak. Indeed, it appears that pre-crisis development characteristics acted as parameters that aggravated the toll of the pandemic. However, the direct components of the Human Development Index (HDI) do not appear to be important direct factors of the number of COVID-19 deaths per million inhabitants. Indeed, more indirect characteristics of development such as the age structure of a population, overweight prevalence, and the level of democracy determine a country's vulnerability to this type of outbreak. This paper therefore concludes by stressing that public

health stakes are likely to be even more important in the future, as countries develop and become increasingly vulnerable to pandemics such as COVID-19. To this extent, targeted health policies should be an efficient means of improving the resilience of countries and their populations to such threats.

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Appendix A[5]

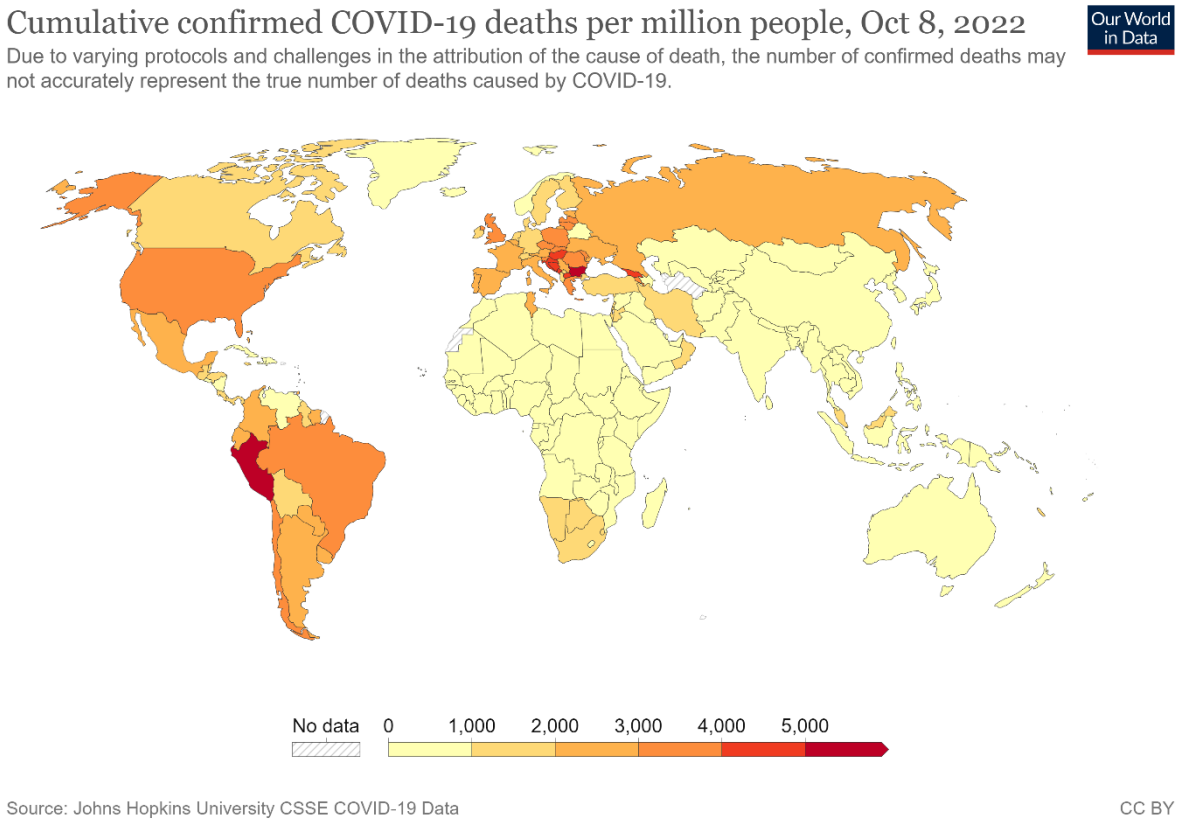

Figure A1. World map of the cumulative number of confirmed COVID-19 deaths per million people on October 8th, 2022 (Mathieu et al., 2020/2022).

[5] Appendix A includes all the figures directly mentioned in the thesis, while all other useful results can be found in Appendix B.

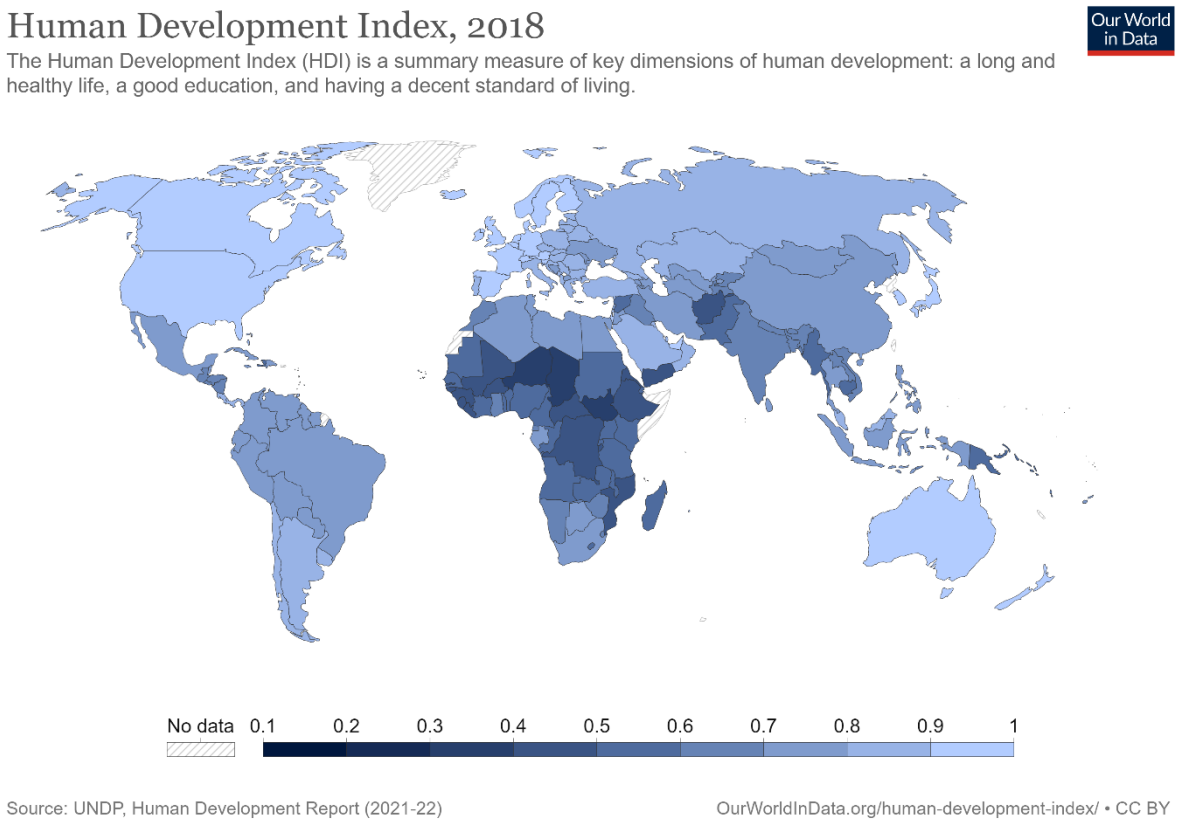

Figure A2. World map of the Human Development Index in the world, 2018 (Roser, 2014/2022).

	tdpm_log	le	eys	mys	gnipc	pop	density	median_age	democracy	CPI	Gini
tdpm_log	1.00	0.68	0.68	0.71	0.46	-0.16	-0.01	0.72	0.58	0.45	-0.11
le	0.68	1.00	0.81	0.79	0.76	0.01	0.17	0.86	0.59	0.68	-0.41
eys	0.68	0.81	1.00	0.81	0.69	-0.03	0.09	0.82	0.64	0.70	-0.32
mys	0.71	0.79	0.81	1.00	0.70	-0.06	0.08	0.84	0.56	0.65	-0.39
gnipc	0.46	0.76	0.69	0.70	1.00	-0.07	0.31	0.71	0.52	0.82	-0.44
pop	-0.16	0.01	-0.03	-0.06	-0.07	1.00	0.01	0.03	-0.03	-0.05	0.01
density	-0.01	0.17	0.09	0.08	0.31	0.01	1.00	0.13	0.04	0.18	-0.19
median_age	0.72	0.86	0.82	0.84	0.71	0.03	0.13	1.00	0.61	0.69	-0.49
democracy	0.58	0.59	0.64	0.56	0.52	-0.03	0.04	0.61	1.00	0.73	-0.17
CPI	0.45	0.68	0.70	0.65	0.82	-0.05	0.18	0.69	0.73	1.00	-0.35
Gini	-0.11	-0.41	-0.32	-0.39	-0.44	0.01	-0.19	-0.49	-0.17	-0.35	1.00
CHE	0.36	0.62	0.63	0.60	0.82	-0.02	0.07	0.60	0.63	0.81	-0.35
Overweight	0.68	0.69	0.63	0.68	0.56	-0.18	-0.07	0.60	0.35	0.42	-0.19
Media_Freedom	0.34	0.29	0.40	0.34	0.39	-0.26	-0.11	0.35	0.77	0.58	-0.19
concentration_fpm	-0.51	-0.39	-0.49	-0.45	-0.29	0.22	-0.01	-0.49	-0.62	-0.44	-0.03
stringency	0.27	0.16	0.12	0.09	0.00	0.28	0.01	0.08	-0.01	-0.09	0.12
vacc_rate	0.51	0.78	0.68	0.60	0.58	0.08	0.14	0.67	0.43	0.55	-0.21
hcq_cq	-0.46	-0.31	-0.34	-0.38	-0.21	0.06	-0.04	-0.34	-0.40	-0.23	0.01
iver	0.06	0.03	-0.09	-0.05	-0.14	-0.04	0.01	-0.06	-0.03	-0.24	0.14
remd	0.38	0.39	0.48	0.46	0.43	-0.07	-0.04	0.54	0.45	0.46	-0.36
Favipiravir	0.08	0.10	0.09	0.11	0.06	0.02	-0.03	0.11	-0.13	-0.05	-0.10
Acetaminophen	0.39	0.50	0.56	0.53	0.55	0.19	0.14	0.63	0.53	0.60	-0.34

Figure A3 (1/2). Correlation coefficients matrix for all response and independent variables.

	CHE	Overweight	Media_Freedom	concentration_fpm	stringency	vacc_rate	hcq_cq	iver	remd	Favipiravir	Acetaminophen
tdpm_log	0.36	0.68	0.34	-0.51	0.27	0.51	-0.46	0.06	0.38	0.08	0.39
le	0.62	0.69	0.29	-0.39	0.16	0.78	-0.31	0.03	0.39	0.10	0.50
eys	0.63	0.63	0.40	-0.49	0.12	0.68	-0.34	-0.09	0.48	0.09	0.56
mys	0.60	0.68	0.34	-0.45	0.09	0.60	-0.38	-0.05	0.46	0.11	0.53
gnipc	0.82	0.56	0.39	-0.29	0.00	0.58	-0.21	-0.14	0.43	0.06	0.55
pop	-0.02	-0.18	-0.26	0.22	0.28	0.08	0.06	-0.04	-0.07	0.02	0.19
density	0.07	-0.07	-0.11	-0.01	0.01	0.14	-0.04	0.01	-0.04	-0.03	0.14
median_age	0.60	0.60	0.35	-0.49	0.08	0.67	-0.34	-0.06	0.54	0.11	0.63
democracy	0.63	0.35	0.77	-0.62	-0.01	0.43	-0.40	-0.03	0.45	-0.13	0.53
CPI	0.81	0.42	0.58	-0.44	-0.09	0.55	-0.23	-0.24	0.46	-0.05	0.60
Gini	-0.35	-0.19	-0.19	-0.03	0.12	-0.21	0.01	0.14	-0.36	-0.10	-0.34
CHE	1.00	0.41	0.51	-0.43	-0.07	0.44	-0.23	-0.14	0.44	-0.09	0.51
Overweight	0.41	1.00	0.26	-0.31	0.11	0.48	-0.23	0.14	0.34	0.10	0.33
Media_Freedom	0.51	0.26	1.00	-0.45	-0.24	0.08	-0.25	-0.08	0.45	-0.21	0.36
concentration_fpm	-0.43	-0.31	-0.45	1.00	-0.02	-0.31	0.38	0.01	-0.31	0.02	-0.32
stringency	-0.07	0.11	-0.24	-0.02	1.00	0.28	-0.02	0.06	-0.08	0.07	0.02
vacc_rate	0.44	0.48	0.08	-0.31	0.28	1.00	-0.27	0.06	0.19	0.14	0.33
hcq_cq	-0.23	-0.23	-0.25	0.38	-0.02	-0.27	1.00	-0.03	-0.09	0.03	-0.23
iver	-0.14	0.14	-0.08	0.01	0.06	0.06	-0.03	1.00	-0.01	0.10	-0.14
remd	0.44	0.34	0.45	-0.31	-0.08	0.19	-0.09	-0.01	1.00	0.11	0.73
Favipiravir	-0.09	0.10	-0.21	0.02	0.07	0.14	0.03	0.10	0.11	1.00	0.03
Acetaminophen	0.51	0.33	0.36	-0.32	0.02	0.33	-0.23	-0.14	0.73	0.03	1.00

Figure A3 (2/2). Correlation coefficients matrix for all response and independent variables.

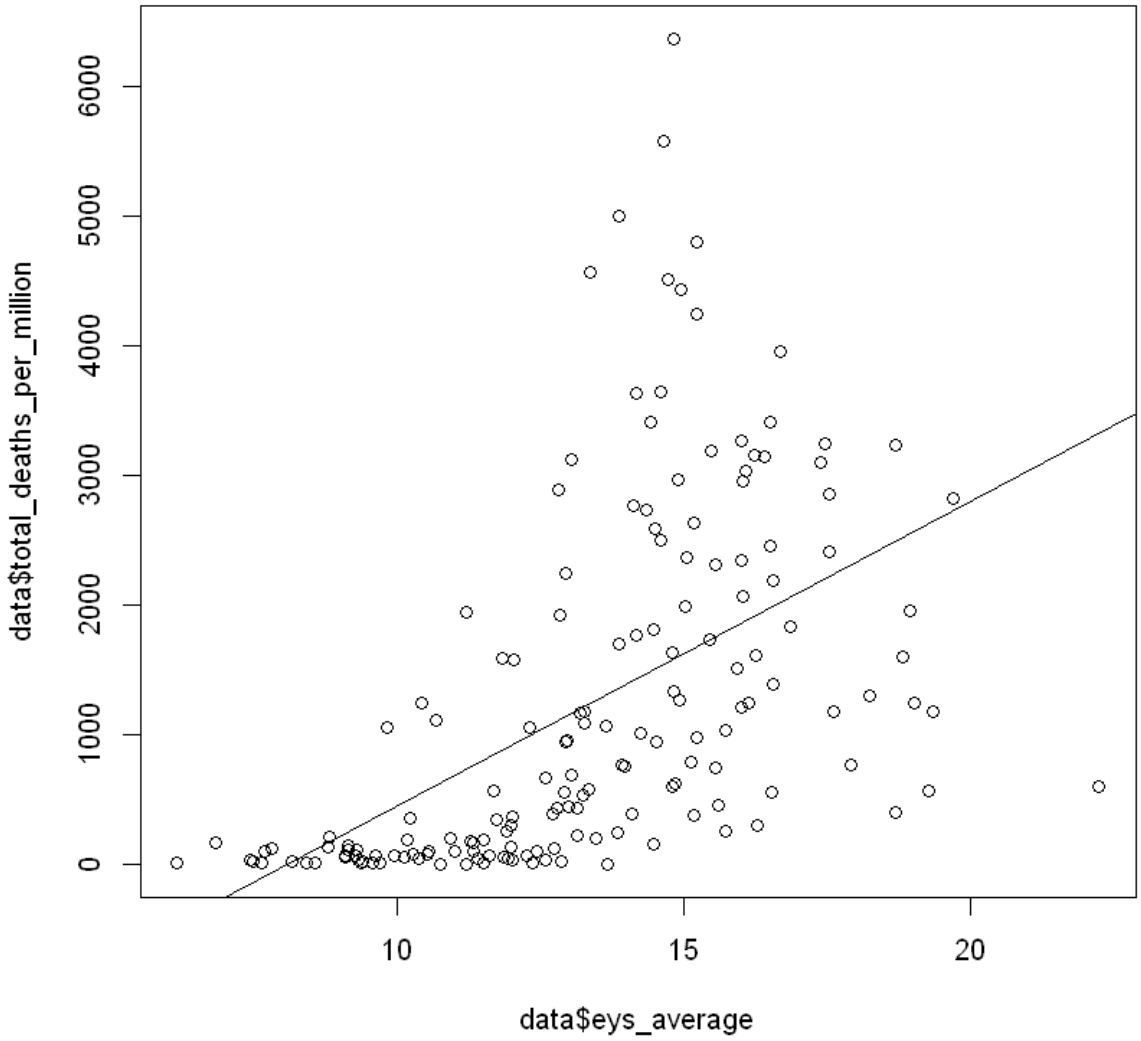

Figure A4. Plot of total COVID-19 deaths per million inhabitants against the five-year averages of expected years of schooling, with a linear regression line.

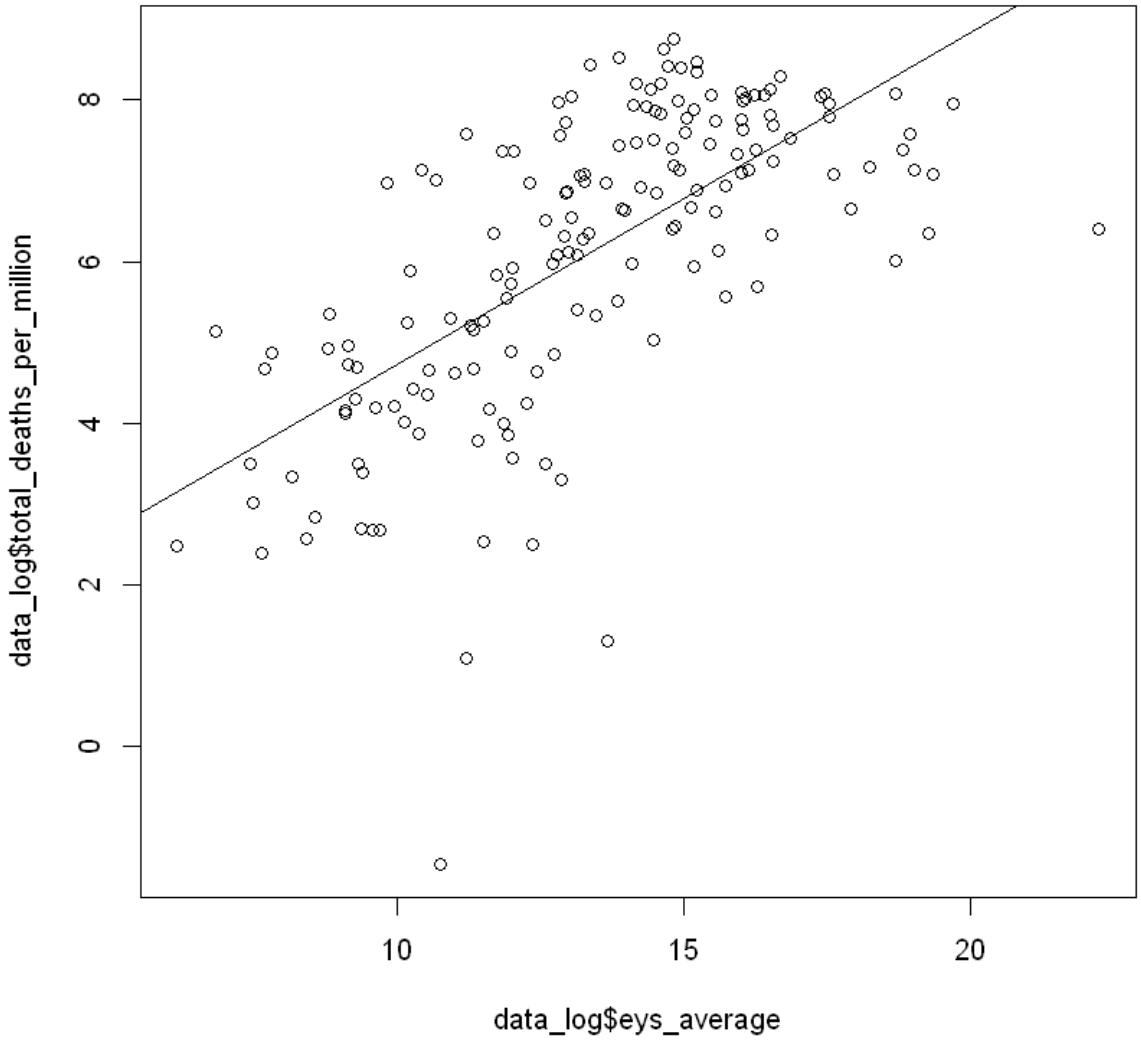

Figure A5. Plot of the natural logarithm of total COVID-19 deaths per million inhabitants against the five-year averages of expected years of schooling, with a linear regression line.

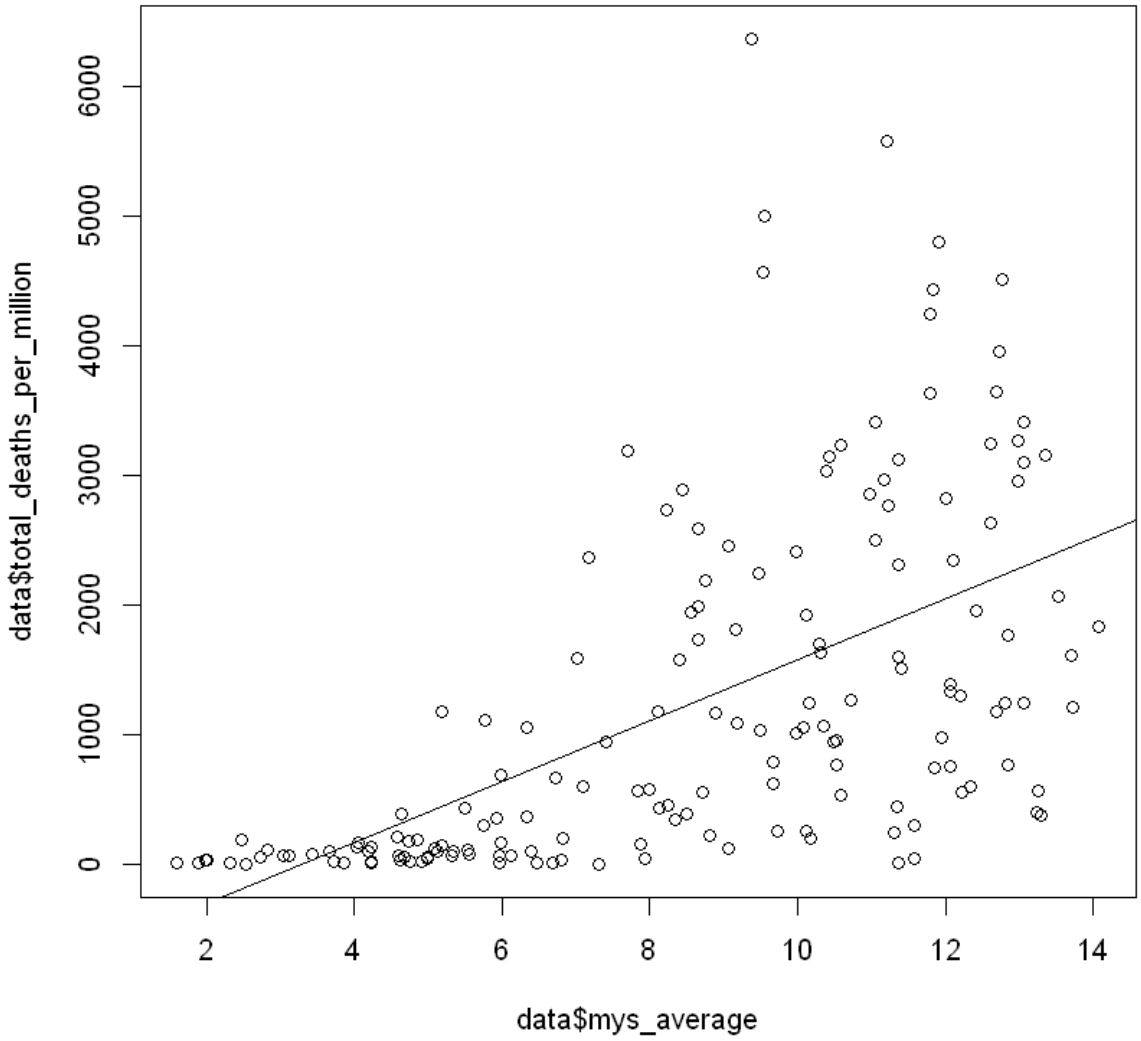

Figure A6. Plot of total COVID-19 deaths per million inhabitants against the five-year averages of mean years of schooling, with a linear regression line.

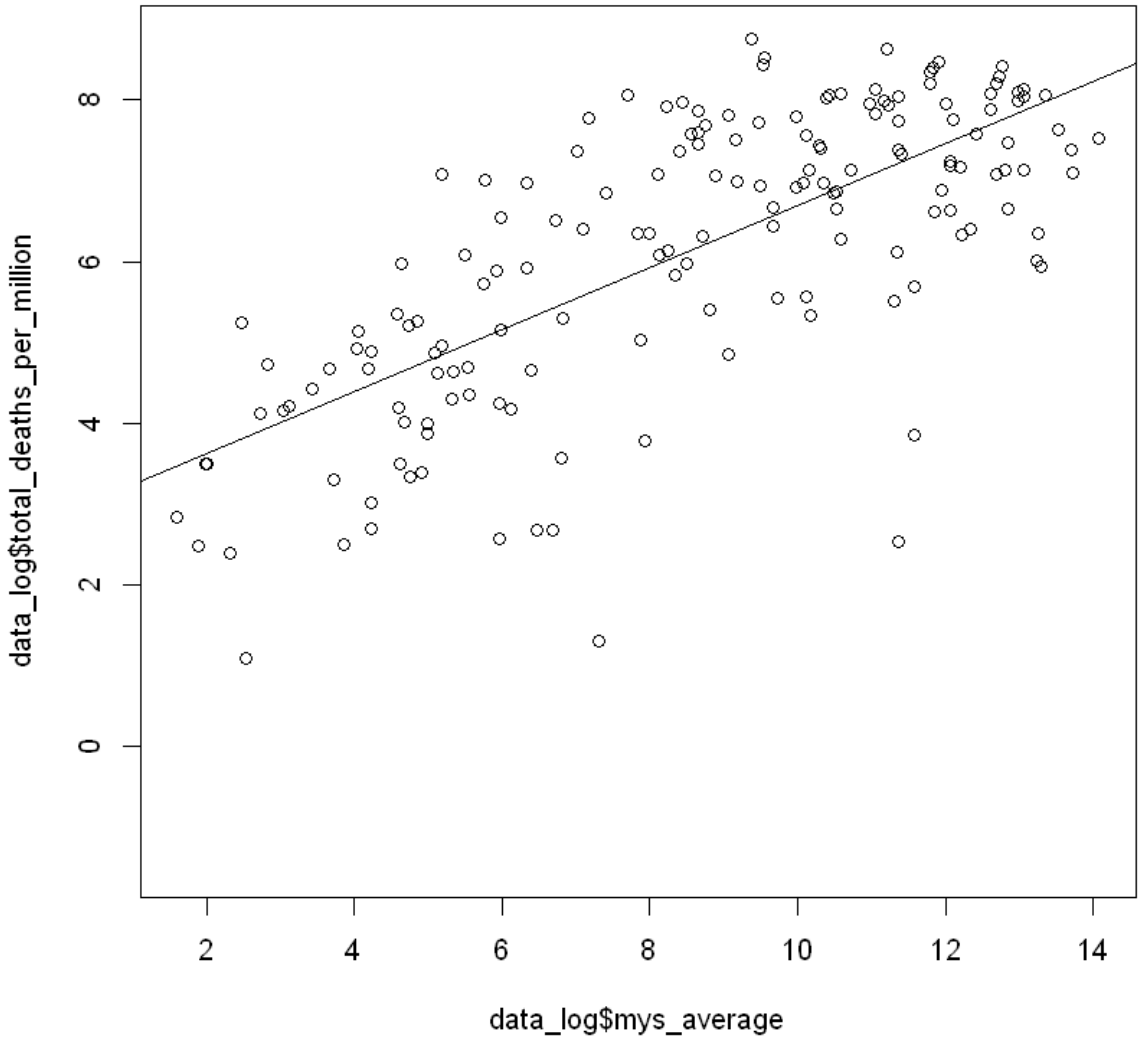

Figure A7. Plot of the natural logarithm of total COVID-19 deaths per million inhabitants against the five-year averages of mean years of schooling, with a linear regression line.

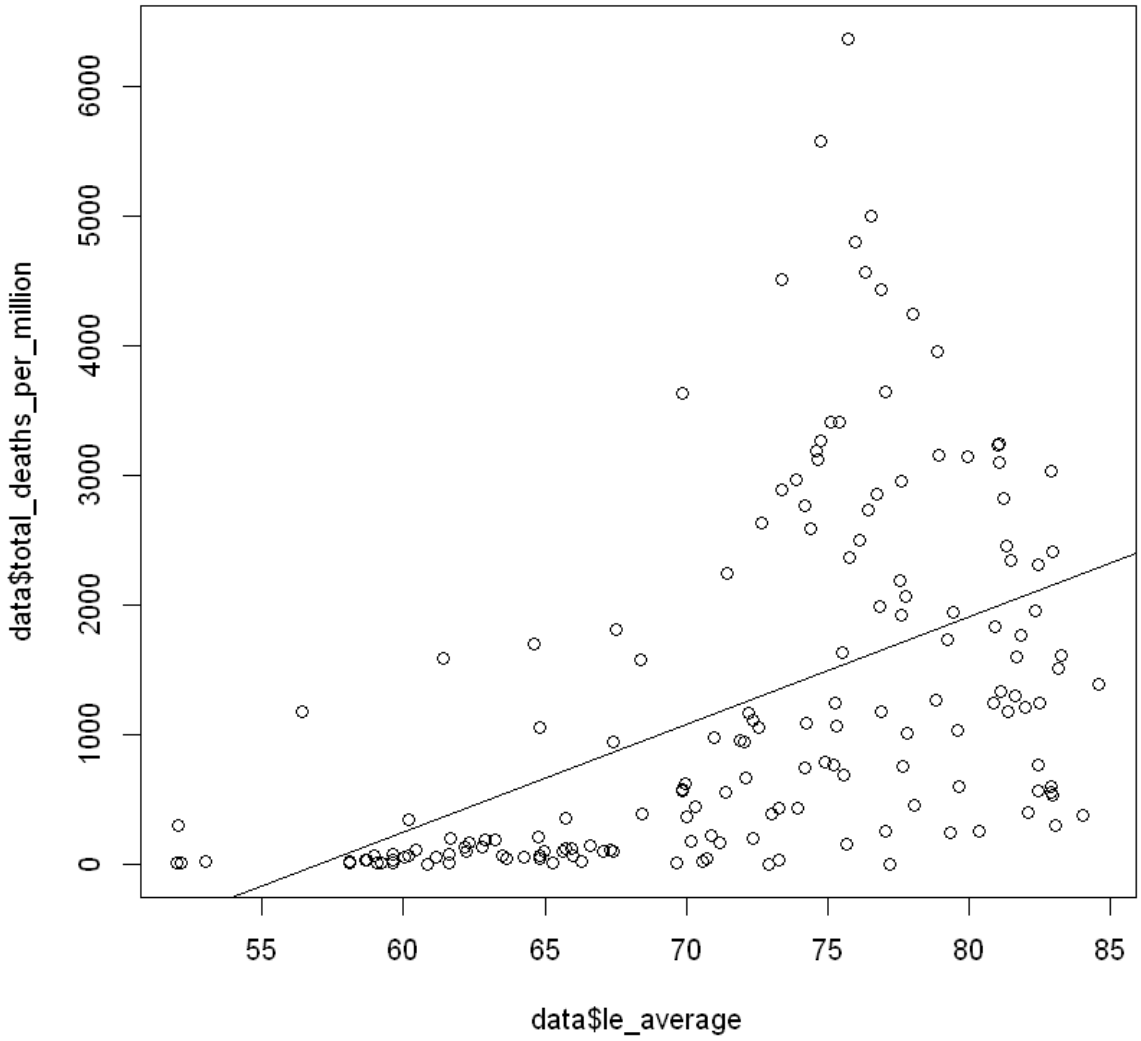

Figure A8. Plot of total COVID-19 deaths per million inhabitants against the five-year averages of life expectancy (years), with a linear regression line.

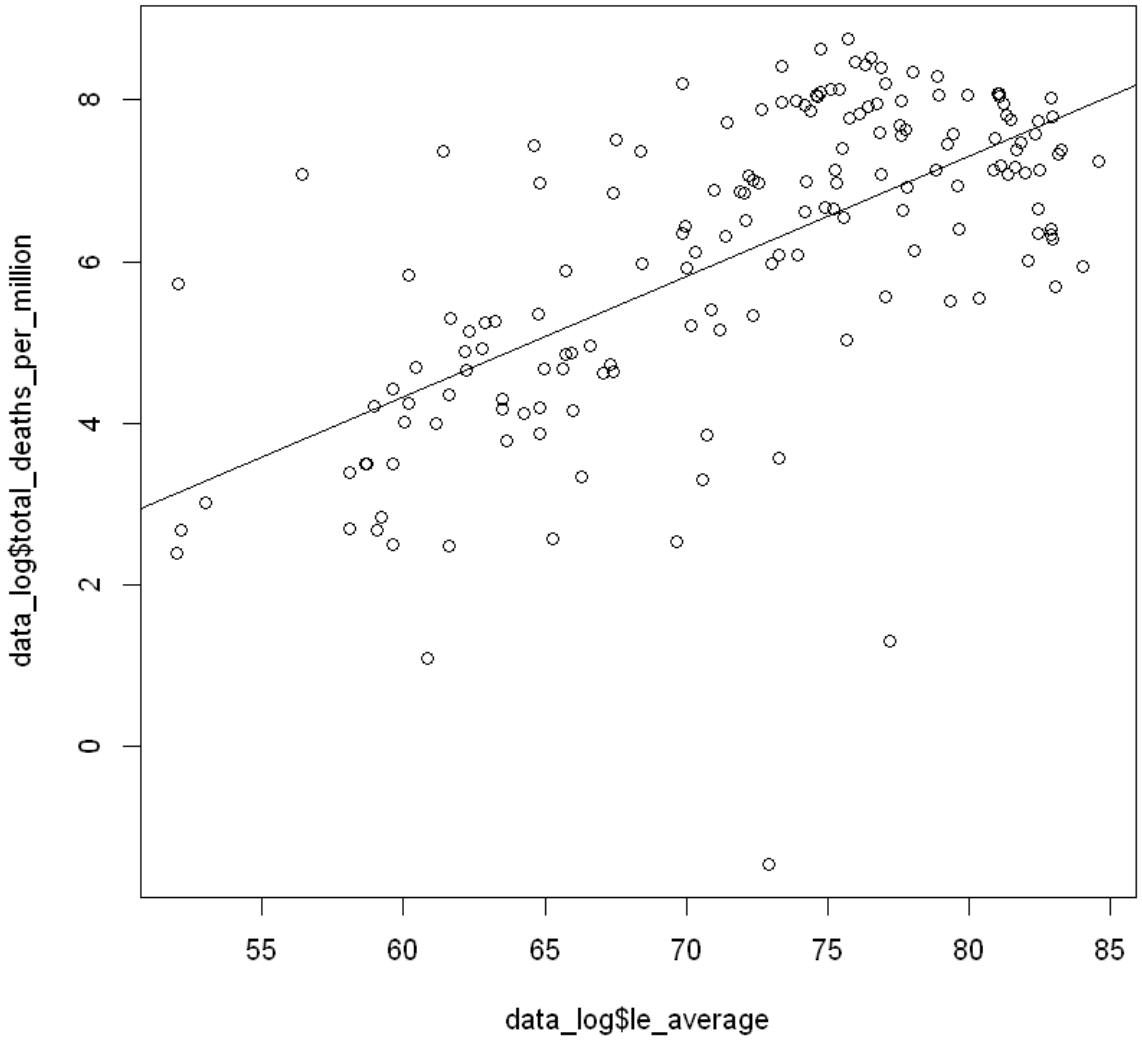

Figure A9. Plot of the natural logarithm of total COVID-19 deaths per million inhabitants against the five-year averages of life expectancy (years), with a linear regression line.

	PIP	Post mean	Post SD
results_log			
overweight (%)	100%	4.09E-02	7.30E-03
democracy (0-10)	100%	3.19E-01	8.19E-02
median age (years)	100%	8.45E-02	1.95E-02
results_log_dilut			
overweight (%)	100%	4.23E-02	7.00E-03
democracy (0-10)	100%	3.01E-01	7.63E-02
median age (years)	100%	8.80E-02	1.77E-02
results_log_gini			
overweight (%)	100%	4.07E-02	1.02E-02
median age (years)	96%	8.53E-02	3.34E-02
results_log_gini_dilut			
overweight (%)	100%	4.29E-02	1.02E-02
median age (years)	93%	9.00E-02	3.75E-02
results_resp_log			
overweight (%)	100%	3.71E-02	6.26E-03
stringency (0-100)	100%	4.21E-02	7.74E-03
median age (years)	100%	8.13E-02	1.51E-02
democracy (0-10)	100%	2.56E-01	6.93E-02
population (k)	99%	-1.90E-06	5.17E-07
- population (m)		*-1.90E-03*	*5.17E-04*
- population (10m)		*-1.90E-02*	*5.17E-03*
hcq_cq (dummy)	98%	-6.59E-01	1.98E-01
results_resp_log_dilut			
overweight (%)	100%	3.70E-02	6.09E-03
stringency (0-100)	100%	4.23E-02	7.65E-03
median age (years)	100%	8.06E-02	1.38E-02
democracy (0-10)	100%	2.40E-01	5.95E-02
population (k)	99%	-1.87E-06	5.11E-07
- population (m)		*-1.87E-03*	*5.11E-04*
- population (10m)		*-1.87E-02*	*5.11E-03*
hcq_cq (dummy)	98%	-6.71E-01	1.97E-01

Figure A10 (1/2). Raw results by type of BMA procedures for the selected variables.

	PIP	Post mean	Post SD
results_gini_resp_log			
overweight (%)	100%	4.52E-02	8.40E-03
stringency (0-100, +)	100%	4.49E-02	9.34E-03
democracy (0-10, +)	99%	2.74E-01	9.94E-02
median age (years)	99%	8.44E-02	2.40E-02
population (k)	96%	-1.78E-06	6.41E-07
- population (m)		*-1.78E-03*	*6.41E-04*
- population (10m)		*-1.78E-02*	*6.41E-03*
results_gini_resp_log_dilut			
overweight (%)	100%	4.49E-02	8.23E-03
stringency (0-100, +)	100%	4.50E-02	9.36E-03
median age (years)	98%	8.41E-02	2.50E-02
democracy (0-10, +)	95%	2.29E-01	9.51E-02
population (k)	94%	-1.74E-06	6.57E-07
- population (m)		*-1.74E-03*	*6.57E-04*
- population (10m)		*-1.74E-02*	*6.57E-03*

Figure A10 (2/2). Raw results by type of BMA procedures for the selected variables.

```
                                    PIP     Post Mean      Post SD
overweight_prevalence_average 0.99999805  3.699891e-02 6.088057e-03
stringency_period             0.99998207  4.232435e-02 7.646716e-03
median_age_average            0.99986850  8.060352e-02 1.380759e-02
democracy_average             0.99792362  2.401609e-01 5.954535e-02
pop_average                   0.99121614 -1.871502e-06 5.105246e-07
hcq_cq                        0.98485859 -6.712134e-01 1.970704e-01
CHE_average                   0.71276890 -1.463209e-04 1.043728e-04
gnipc_average                 0.25312076 -4.837993e-06 8.974056e-06
vacc_rate_p1                  0.10235668 -6.508905e-03 2.387235e-02
CPI_average                   0.09908539 -1.773225e-03 6.071470e-03
density_average               0.09642475 -7.309195e-06 4.231529e-05
Favipiravir                   0.08471341  1.636796e-02 1.022969e-01
iver                          0.07657679 -9.417408e-03 7.881045e-02
media_freedom_average         0.06066176 -7.529177e-04 3.824025e-03
Acetaminophen                 0.05349948 -9.594778e-03 6.757836e-02
concentration_fpm_average     0.05144845 -2.042681e-04 1.834676e-03
remd                          0.05107744  2.818162e-03 5.184222e-02
mys_average                   0.03837247  2.060483e-03 1.348507e-02
le_average                    0.02133139 -3.685740e-04 3.947746e-03
eys_average                   0.02026184  1.566812e-04 6.864638e-03
                             Cond.Pos.Sign Idx
overweight_prevalence_average    1.00000000  11
stringency_period                1.00000000  14
median_age_average               1.00000000   7
democracy_average                1.00000000   8
pop_average                      0.00000000   5
hcq_cq                           0.00000000  16
CHE_average                      0.00001530  10
gnipc_average                    0.00000217   4
vacc_rate_p1                     0.00003593  15
CPI_average                      0.00053594   9
density_average                  0.14746836   6
Favipiravir                      0.99919703  19
iver                             0.00603730  17
media_freedom_average            0.01489559  12
Acetaminophen                    0.00070817  20
concentration_fpm_average        0.16855542  13
remd                             0.87646524  18
mys_average                      1.00000000   3
le_average                       0.01156015   1
eys_average                      0.79662177   2

Mean no. regressors              Draws             Burnins                Time
           "7.6955"           "1048576"                 "0"     "2.460601 mins"
 No. models visited      Modelspace 2^K           % visited         % Topmodels
          "1048576"             "1e+06"               "100"             "0.048"
           Corr PMP            No. Obs.         Model Prior             g-Prior
               "NA"               "152"        "dilut / 10"               "UIP"
    Shrinkage-Stats
        "Av=0.9935"
```

Figure A11. Raw results of the *Best Bayesian Setting* (BBS) procedures – without the *Gini* variable, with the *government response* variables, and using the *dilution* prior.

	PIP	Post Mean	Post SD	Cond.Pos.Sign	Idx
overweight_prevalence_average	0.99999805	0.3328535886	0.05477003	1.00000000	11
stringency_period	0.99998207	0.2403811752	0.04342954	1.00000000	14
median_age_average	0.99986850	0.4204744602	0.07202836	1.00000000	7
democracy_average	0.99792362	0.2848253538	0.07061943	1.00000000	8
pop_average	0.99121614	-0.1707099976	0.04656777	0.00000000	5
hcq_cq	0.98485859	-0.1638349084	0.04810246	0.00000000	16
CHE_average	0.71276890	-0.1560427538	0.11130751	0.00001530	10
gnipc_average	0.25312076	-0.0541683259	0.10047754	0.00000217	4
vacc_rate_p1	0.10235668	-0.0087184951	0.03197634	0.00003593	15
CPI_average	0.09908539	-0.0189648116	0.06493497	0.00053594	9
density_average	0.09642475	-0.0029318956	0.01697369	0.14746836	6
Favipiravir	0.08471341	0.0022873912	0.01429579	0.99919703	19
iver	0.07657679	-0.0015350996	0.01284662	0.00603730	17
media_freedom_average	0.06066176	-0.0062222178	0.03160228	0.01489559	12
Acetaminophen	0.05349948	-0.0023621531	0.01663722	0.00070817	20
concentration_fpm_average	0.05144845	-0.0016891760	0.01517168	0.16855542	13
remd	0.05107744	0.0006619848	0.01217771	0.87646524	18
mys_average	0.03837247	0.0038429009	0.02515032	1.00000000	3
le_average	0.02133139	-0.0016877644	0.01807742	0.01156015	1
eys_average	0.02026184	0.0002643504	0.01158192	0.79662177	2
(Intercept)	1.00000000	-0.2888574337	NA	NA	0

Figure A12. Standardised coefficients of the *Best Bayesian Setting* (BBS) procedures – without the *Gini* variable, with the *government response* variables, and using the *dilution* prior.

Appendix B[6]

```
                                    PIP     Post Mean      Post SD
overweight_prevalence_average 0.99999071  4.089223e-02 7.299625e-03
democracy_average             0.99907922  3.189874e-01 8.192958e-02
median_age_average            0.99741019  8.450809e-02 1.950977e-02
CPI_average                   0.68436523 -1.735752e-02 1.441372e-02
CHE_average                   0.67384954 -1.433783e-04 1.216122e-04
pop_average                   0.66375665 -9.098095e-07 7.861474e-07
mys_average                   0.34597604  3.266759e-02 5.336564e-02
media_freedom_average         0.25367995 -3.828924e-03 8.026425e-03
concentration_fpm_average     0.23600980 -2.885674e-03 6.397070e-03
gnipc_average                 0.15800072 -1.912667e-06 6.145948e-06
eys_average                   0.10365334  4.587437e-03 2.190039e-02
density_average               0.08303353 -3.031994e-06 3.856093e-05
le_average                    0.07826287 -1.022574e-05 6.641710e-03
                             Cond.Pos.Sign Idx
overweight_prevalence_average    1.00000000  11
democracy_average                1.00000000   8
median_age_average               1.00000000   7
CPI_average                      0.00001014   9
CHE_average                      0.00000000  10
pop_average                      0.00000001   5
mys_average                      1.00000000   3
media_freedom_average            0.00098845  12
concentration_fpm_average        0.00000000  13
gnipc_average                    0.02278606   4
eys_average                      0.99995096   2
density_average                  0.24410851   6
le_average                       0.55693857   1

Mean no. regressors               Draws             Burnins                Time
          "6.2771"               "8192"                 "0"    "0.5585389 secs"
 No. models visited      Modelspace 2^K          % visited         % Topmodels
            "8192"               "8192"               "100"               "6.1"
          Corr PMP            No. Obs.         Model Prior             g-Prior
              "NA"               "159"     "uniform / 6.5"               "UIP"
    Shrinkage-Stats
        "Av=0.9938"
```

Figure B1. Raw results of the BMA setting without the *Gini* variable, without the *government response* variables, and using the *uniform* prior.

[6] Appendix B includes all useful results that are not directly mentioned in the thesis.

	PIP	Post Mean	Post SD	Cond.Pos.Sign	Idx
overweight_prevalence_average	0.99999071	3.671310e-01	0.06553612	1.00000000	11
democracy_average	0.99907922	3.802234e-01	0.09765760	1.00000000	8
median_age_average	0.99741019	4.377392e-01	0.10105767	1.00000000	7
CPI_average	0.68436523	-1.844715e-01	0.15318559	0.00001014	9
CHE_average	0.67384954	-1.494644e-01	0.12677438	0.00000000	10
pop_average	0.66375665	-8.083751e-02	0.06985001	0.00000001	5
mys_average	0.34597604	6.072029e-02	0.09919242	1.00000000	3
media_freedom_average	0.25367995	-3.254588e-02	0.06822467	0.00098845	12
concentration_fpm_average	0.23600980	-2.337155e-02	0.05181092	0.00000000	13
gnipc_average	0.15800072	-2.100040e-02	0.06748033	0.02278606	4
eys_average	0.10365334	7.692664e-03	0.03672472	0.99995096	2
density_average	0.08303353	-1.183731e-03	0.01505471	0.24410851	6
le_average	0.07826287	-4.652531e-05	0.03021860	0.55693857	1
(Intercept)	1.00000000	5.612335e-01	NA	NA	0

Figure B2. Standardised coefficients of the BMA setting without the *Gini* variable, without the *government response* variables, and using the *uniform* prior.

```
                                    PIP     Post Mean      Post SD
overweight_prevalence_average 0.99999520  4.226129e-02 7.004459e-03
democracy_average             0.99777499  3.009318e-01 7.634558e-02
median_age_average            0.99672693  8.804052e-02 1.769767e-02
pop_average                   0.60768767 -8.048772e-07 7.710597e-07
CHE_average                   0.60065925 -1.477545e-04 1.345648e-04
CPI_average                   0.50180314 -1.464626e-02 1.604252e-02
concentration_fpm_average     0.19516460 -2.646751e-03 6.345252e-03
media_freedom_average         0.12078432 -1.882518e-03 6.013589e-03
mys_average                   0.11073152  1.072025e-02 3.489467e-02
gnipc_average                 0.07976041 -1.467428e-06 5.793881e-06
density_average               0.07732162 -3.192225e-06 3.752208e-05
eys_average                   0.02849253  1.317311e-03 1.180548e-02
le_average                    0.01593488  1.719034e-05 2.990204e-03
                             Cond.Pos.Sign Idx
overweight_prevalence_average    1.00000000  11
democracy_average                1.00000000   8
median_age_average               1.00000000   7
pop_average                      0.00000004   5
CHE_average                      0.00000000  10
CPI_average                      0.00000828   9
concentration_fpm_average        0.00000000  13
media_freedom_average            0.00366866  12
mys_average                      1.00000000   3
gnipc_average                    0.00267828   4
density_average                  0.31663045   6
eys_average                      0.99980568   2
le_average                       0.63504629   1

Mean no. regressors               Draws             Burnins                Time
          "5.3328"               "8192"                 "0"     "1.199748 secs"
 No. models visited      Modelspace 2^K           % visited         % Topmodels
             "8192"              "8192"               "100"               "6.1"
          Corr PMP           No. Obs.         Model Prior             g-Prior
             "NA"              "159"       "dilut / 6.5"               "UIP"
    Shrinkage-Stats
        "Av=0.9938"
```

Figure B3. Raw results of the BMA setting without the *Gini* variable, without the *government response* variables, and using the *dilution* prior.

	PIP	Post Mean	Post SD	Cond.Pos.Sign	Idx
overweight_prevalence_average	0.99999520	0.379422404	0.06288612	1.00000000	11
democracy_average	0.99777499	0.358701630	0.09100164	1.00000000	8
median_age_average	0.99672693	0.456036699	0.09167127	1.00000000	7
pop_average	0.60768767	-0.071514170	0.06850945	0.00000004	5
CHE_average	0.60065925	-0.154026377	0.14027680	0.00000000	10
CPI_average	0.50180314	-0.155656948	0.17049603	0.00000828	9
concentration_fpm_average	0.19516460	-0.021436471	0.05139125	0.00000000	13
media_freedom_average	0.12078432	-0.016001413	0.05111555	0.00366866	12
mys_average	0.11073152	0.019926074	0.06485984	1.00000000	3
gnipc_average	0.07976041	-0.016111843	0.06361476	0.00267828	4
density_average	0.07732162	-0.001246287	0.01464913	0.31663045	6
eys_average	0.02849253	0.002208997	0.01979659	0.99980568	2
le_average	0.01593488	0.000078213	0.01360489	0.63504629	1
(Intercept)	1.00000000	0.508283244	NA	NA	0

Figure B4. Standardised coefficients of the BMA setting without the *Gini* variable, without the *government response* variables, and using the *dilution* prior.

```
                                PIP      Post Mean      Post SD Cond.Pos.Sign
%Overweight_average       0.99763414  4.066055e-02 1.021104e-02    1.00000000
medianage_mean            0.96056724  8.533905e-02 3.343762e-02    1.00000000
democracy_average         0.85871659  2.051302e-01 1.216808e-01    1.00000000
Gini_average              0.68204638  2.778928e-02 2.306646e-02    0.99998633
concentration_fpm_average 0.60117142 -1.604529e-02 1.563287e-02    0.00000000
pop_mean                  0.58348660 -8.375634e-07 8.484703e-07    0.00013750
mys_mean                  0.56716376  7.043346e-02 7.437956e-02    1.00000000
CPI_average               0.48135223 -1.147198e-02 1.404554e-02    0.00106868
CHE_average               0.42039328 -7.969050e-05 1.107189e-04    0.00000010
gnipc_mean                0.36875513 -9.514058e-06 1.479153e-05    0.00044096
MediaFreedom_average      0.33503523 -6.281852e-03 1.093194e-02    0.03353922
density_mean              0.10405116  2.858159e-05 1.722024e-04    0.92444036
le_mean                   0.10179513  9.139263e-04 9.079904e-03    0.70832045
eys_mean                  0.08954349 -7.684294e-04 1.826608e-02    0.36099753
                         Idx
%Overweight_average       12
medianage_mean             7
democracy_average          8
Gini_average              10
concentration_fpm_average 14
pop_mean                   5
mys_mean                   3
CPI_average                9
CHE_average               11
gnipc_mean                 4
MediaFreedom_average      13
density_mean               6
le_mean                    1
eys_mean                   2

Mean no. regressors              Draws             Burnins                Time
          "7.1517"            "16384"                "0"  "0.9624588 secs"
 No. models visited     Modelspace 2^K          % visited         % Topmodels
          "16384"            "16384"               "100"               "3.1"
          Corr PMP           No. Obs.         Model Prior             g-Prior
             "NA"              "124"      "uniform / 7"               "UIP"
    Shrinkage-Stats
         "Av=0.992"
```

Figure B5. Raw results of the BMA setting with the *Gini* variable, without the *government response* variables, and using the *uniform* prior.

	PIP	Post Mean	Post SD	Cond.Pos.Sign	Idx
%Overweight_average	0.99763414	0.348113773	0.08742142	1.00000000	12
medianage_mean	0.96056724	0.449891180	0.17627672	1.00000000	7
democracy_average	0.85871659	0.230897130	0.13696545	1.00000000	8
Gini_average	0.68204638	0.120367088	0.09991058	0.99998633	10
concentration_fpm_average	0.60117142	-0.121610732	0.11848492	0.00000000	14
pop_mean	0.58348660	-0.083000563	0.08408141	0.00013750	5
mys_mean	0.56716376	0.133192231	0.14065446	1.00000000	3
CPI_average	0.48135223	-0.118242802	0.14476874	0.00106868	9
CHE_average	0.42039328	-0.089314068	0.12408955	0.00000010	11
gnipc_mean	0.36875513	-0.097059494	0.15089864	0.00044096	4
MediaFreedom_average	0.33503523	-0.049546591	0.08622300	0.03353922	13
density_mean	0.10405116	0.003203117	0.01929860	0.92444036	6
le_mean	0.10179513	0.004187438	0.04160241	0.70832045	1
eys_mean	0.08954349	-0.001317461	0.03131693	0.36099753	2
(Intercept)	1.00000000	0.352002176	NA	NA	0

Figure B6. Standardised coefficients of the BMA setting with the *Gini* variable, without the *government response* variables, and using the *uniform* prior.

```
                                PIP     Post Mean      Post SD Cond.Pos.Sign
%Overweight_average       0.99728582  4.292888e-02 1.020413e-02    1.00000000
medianage_mean            0.93041922  8.995492e-02 3.747549e-02    1.00000000
democracy_average         0.71754434  1.612765e-01 1.258517e-01    1.00000000
Gini_average              0.62468632  2.779328e-02 2.511105e-02    0.99995972
concentration_fpm_average 0.55819773 -1.684599e-02 1.700820e-02    0.00000000
pop_mean                  0.51276304 -7.200469e-07 8.221019e-07    0.00095474
CHE_average               0.44342511 -9.519681e-05 1.184800e-04    0.00000001
CPI_average               0.36425032 -9.820065e-03 1.422656e-02    0.00091562
mys_mean                  0.26326762  3.688703e-02 6.919256e-02    1.00000000
gnipc_mean                0.20397106 -5.671346e-06 1.221328e-05    0.00009169
MediaFreedom_average      0.15603960 -2.754911e-03 8.029182e-03    0.09003310
density_mean              0.09977148  3.372228e-05 1.800541e-04    0.96214533
le_mean                   0.02706818  5.219799e-04 5.566824e-03    0.89620182
eys_mean                  0.02142073  1.929841e-04 8.890744e-03    0.64556898
                          Idx
%Overweight_average        12
medianage_mean              7
democracy_average           8
Gini_average               10
concentration_fpm_average  14
pop_mean                    5
CHE_average                11
CPI_average                 9
mys_mean                    3
gnipc_mean                  4
MediaFreedom_average       13
density_mean                6
le_mean                     1
eys_mean                    2

Mean no. regressors               Draws             Burnins                Time
           "5.9201"             "16384"                 "0"     "2.045546 secs"
 No. models visited      Modelspace 2^K           % visited         % Topmodels
            "16384"             "16384"               "100"               "3.1"
           Corr PMP            No. Obs.         Model Prior             g-Prior
               "NA"               "124"         "dilut / 7"               "UIP"
    Shrinkage-Stats
         "Av=0.992"
```

Figure B7. Raw results of the BMA setting with the *Gini* variable, without the *government response* variables, and using the *dilution* prior.

	PIP	Post Mean	Post SD	Cond.Pos.Sign	Idx
%Overweight_average	0.99728582	0.3675340076	0.08736229	1.00000000	12
medianage_mean	0.93041922	0.4742251530	0.19756363	1.00000000	7
democracy_average	0.71754434	0.1815348168	0.14166027	1.00000000	8
Gini_average	0.62468632	0.1203844373	0.10876653	0.99995972	10
concentration_fpm_average	0.55819773	-0.1276794286	0.12890880	0.00000000	14
pop_mean	0.51276304	-0.0713549560	0.08146837	0.00095474	5
CHE_average	0.44342511	-0.1066929534	0.13278790	0.00000001	11
CPI_average	0.36425032	-0.1012163897	0.14663456	0.00091562	9
mys_mean	0.26326762	0.0697547219	0.13084564	1.00000000	3
gnipc_mean	0.20397106	-0.0578573308	0.12459615	0.00009169	4
MediaFreedom_average	0.15603960	-0.0217286978	0.06332824	0.09003310	13
density_mean	0.09977148	0.0037792315	0.02017853	0.96214533	6
le_mean	0.02706818	0.0023916136	0.02550614	0.89620182	1
eys_mean	0.02142073	0.0003308685	0.01524306	0.64556898	2
(Intercept)	1.00000000	0.3358309712	NA	NA	0

Figure B8. Standardised coefficients of the BMA setting with the *Gini* variable, without the *government response* variables, and using the *dilution* prior.

```
                                    PIP     Post Mean      Post SD
overweight_prevalence_average 0.99999748  3.711770e-02 6.261863e-03
stringency_period             0.99997983  4.213231e-02 7.744195e-03
median_age_average            0.99987498  8.132488e-02 1.508318e-02
democracy_average             0.99895002  2.558398e-01 6.926465e-02
pop_average                   0.99225895 -1.895488e-06 5.167306e-07
hcq_cq                        0.98371772 -6.587272e-01 1.983675e-01
CHE_average                   0.72772370 -1.390218e-04 1.010513e-04
gnipc_average                 0.32039866 -5.112796e-06 8.792777e-06
CPI_average                   0.21102047 -2.933024e-03 7.136902e-03
vacc_rate_p1                  0.20346990 -1.384413e-02 3.446185e-02
media_freedom_average         0.19888211 -2.722847e-03 6.938711e-03
mys_average                   0.14829874  7.983385e-03 2.554826e-02
le_average                    0.10557357 -1.779599e-03 8.819423e-03
density_average               0.10400791 -7.484783e-06 4.400735e-05
Acetaminophen                 0.10252176 -1.950069e-02 9.707497e-02
Favipiravir                   0.09171555  1.742738e-02 1.057613e-01
concentration_fpm_average     0.08869714 -2.912606e-04 2.296217e-03
iver                          0.08729745 -1.222480e-02 8.711275e-02
remd                          0.08166879  5.828561e-03 7.099898e-02
eys_average                   0.07828301  7.631802e-04 1.378714e-02
                             Cond.Pos.Sign Idx
overweight_prevalence_average    1.00000000  11
stringency_period                1.00000000  14
median_age_average               1.00000000   7
democracy_average                1.00000000   8
pop_average                      0.00000000   5
hcq_cq                           0.00000000  16
CHE_average                      0.00001416  10
gnipc_average                    0.00002306   4
CPI_average                      0.00046750   9
vacc_rate_p1                     0.00002070  15
media_freedom_average            0.00324860  12
mys_average                      1.00000000   3
le_average                       0.02539096   1
density_average                  0.15117649   6
Acetaminophen                    0.00037205  20
Favipiravir                      0.99968626  19
concentration_fpm_average        0.17581797  13
iver                             0.00313975  17
remd                             0.84143168  18
eys_average                      0.79644351   2

Mean no. regressors              Draws             Burnins                Time
          "8.5243"           "1048576"                "0"     "1.009265 mins"
 No. models visited      Modelspace 2^K          % visited         % Topmodels
          "1048576"            "1e+06"             "100"               "0.048"
           Corr PMP          No. Obs.         Model Prior              g-Prior
               "NA"             "152"      "uniform / 10"                "UIP"
    Shrinkage-Stats
        "Av=0.9935"
```

Figure B9. Raw results of the BMA setting without the *Gini* variable, with the *government response* variables, and using the *uniform* prior.

	PIP	Post Mean	Post SD	Cond.Pos.Sign	Idx
overweight_prevalence_average	0.99999748	0.333922236	0.05633365	1.00000000	11
stringency_period	0.99997983	0.239290507	0.04398317	1.00000000	14
median_age_average	0.99987498	0.424237520	0.07868255	1.00000000	7
democracy_average	0.99895002	0.303420207	0.08214631	1.00000000	8
pop_average	0.99225895	-0.172897910	0.04713385	0.00000000	5
hcq_cq	0.98371772	-0.160787184	0.04841905	0.00000000	16
CHE_average	0.72772370	-0.148258647	0.10776535	0.00001416	10
gnipc_average	0.32039866	-0.057245145	0.09844786	0.00002306	4
CPI_average	0.21102047	-0.031368972	0.07632986	0.00046750	9
vacc_rate_p1	0.20346990	-0.018543826	0.04616068	0.00002070	15
media_freedom_average	0.19888211	-0.022501987	0.05734248	0.00324860	12
mys_average	0.14829874	0.014889405	0.04764875	1.00000000	3
le_average	0.10557357	-0.008149093	0.04038567	0.02539096	1
density_average	0.10400791	-0.003002328	0.01765242	0.15117649	6
Acetaminophen	0.10252176	-0.004800905	0.02389904	0.00037205	20
Favipiravir	0.09171555	0.002435442	0.01477994	0.99968626	19
concentration_fpm_average	0.08869714	-0.002408553	0.01898835	0.17581797	13
iver	0.08729745	-0.001992723	0.01419995	0.00313975	17
remd	0.08166879	0.001369126	0.01667762	0.84143168	18
eys_average	0.07828301	0.001287627	0.02326148	0.79644351	2
(Intercept)	1.00000000	-0.205245695	NA	NA	0

Figure B10. Standardised coefficients of the BMA setting without the *Gini* variable, with the *government response* variables, and using the *uniform* prior.

```
                              PIP     Post Mean      Post SD Cond.Pos.Sign
%Overweight_average       0.99996747  4.518817e-02 8.402732e-03    1.00000000
stringency_period         0.99983488  4.491340e-02 9.341850e-03    1.00000000
democracy_average         0.98821235  2.736322e-01 9.943493e-02    1.00000000
medianage_mean            0.98820620  8.438653e-02 2.401366e-02    1.00000000
pop_mean                  0.95796480 -1.776211e-06 6.413571e-07    0.00000001
hcq_cq                    0.73803203 -4.082698e-01 3.019397e-01    0.00000000
CHE_average               0.70892043 -1.274034e-04 9.798380e-05    0.00000132
Gini_average              0.62584646  1.917344e-02 1.787591e-02    0.99950205
vacc_rate_p1              0.55136140 -6.661994e-02 7.192912e-02    0.00000656
MediaFreedom_average      0.39390036 -7.915363e-03 1.184196e-02    0.00518624
concentration_fpm_average 0.35212341 -6.560590e-03 1.086008e-02    0.00000003
mys_mean                  0.28125120  2.411152e-02 4.769546e-02    1.00000000
gnipc_mean                0.26166212 -4.950664e-06 1.091126e-05    0.07826466
CPI_average               0.21226525 -3.106349e-03 7.843469e-03    0.00669501
Favipiravir               0.16394568  6.138981e-02 1.890557e-01    0.99817339
Acetaminophen             0.14889071 -4.113024e-02 1.411919e-01    0.00364092
iver                      0.14175635 -4.171495e-02 1.468326e-01    0.00014886
eys_mean                  0.11984434 -5.208571e-03 2.460155e-02    0.02258918
le_mean                   0.11829203 -1.201285e-03 1.085052e-02    0.34526197
remd                      0.09669867 -3.893170e-03 8.739424e-02    0.30363323
density_mean              0.08897310  1.448318e-06 1.233499e-04    0.53294518
                          Idx
%Overweight_average        12
stringency_period          15
democracy_average           8
medianage_mean              7
pop_mean                    5
hcq_cq                     17
CHE_average                11
Gini_average               10
vacc_rate_p1               16
MediaFreedom_average       13
concentration_fpm_average  14
mys_mean                    3
gnipc_mean                  4
CPI_average                 9
Favipiravir                20
Acetaminophen              21
iver                       18
eys_mean                    2
le_mean                     1
remd                       19
density_mean                6

Mean no. regressors              Draws             Burnins                Time
          "9.9379"          "2097152"                "0"    "2.102703 mins"
 No. models visited      Modelspace 2^K          % visited         % Topmodels
          "2097152"         "2097152"              "100"              "0.024"
           Corr PMP           No. Obs.        Model Prior             g-Prior
              "NA"              "119"   "uniform / 10.5"               "UIP"
    Shrinkage-Stats
        "Av=0.9917"
```

Figure B11. Raw results of the BMA setting with the *Gini* variable, with the *government response* variables, and using the *uniform* prior.

	PIP	Post Mean	Post SD	Cond.Pos.Sign	Idx
%Overweight_average	0.99996747	0.3882822715	0.07220101	1.00000000	12
stringency_period	0.99983488	0.2471052013	0.05139712	1.00000000	15
democracy_average	0.98821235	0.3066010789	0.11141547	1.00000000	8
medianage_mean	0.98820620	0.4468075057	0.12714689	1.00000000	7
pop_mean	0.95796480	-0.1794755233	0.06480531	0.00000001	5
hcq_cq	0.73803203	-0.0951545620	0.07037244	0.00000000	17
CHE_average	0.70892043	-0.1451673136	0.11164575	0.00000132	11
Gini_average	0.62584646	0.0842708233	0.07856797	0.99950205	10
vacc_rate_p1	0.55136140	-0.0827766924	0.08937346	0.00000656	16
MediaFreedom_average	0.39390036	-0.0636821358	0.09527314	0.00518624	13
concentration_fpm_average	0.35212341	-0.0502281469	0.08314519	0.00000003	14
mys_mean	0.28125120	0.0455856731	0.09017388	1.00000000	3
gnipc_mean	0.26166212	-0.0511732416	0.11278575	0.07826466	4
CPI_average	0.21226525	-0.0321902346	0.08127970	0.00669501	9
Favipiravir	0.16394568	0.0090327598	0.02781724	0.99817339	20
Acetaminophen	0.14889071	-0.0105137609	0.03609165	0.00364092	21
iver	0.14175635	-0.0067236713	0.02366667	0.00014886	18
eys_mean	0.11984434	-0.0090500722	0.04274605	0.02258918	2
le_mean	0.11829203	-0.0055285986	0.04993665	0.34526197	1
remd	0.09669867	-0.0009606044	0.02156373	0.30363323	19
density_mean	0.08897310	0.0001642975	0.01399284	0.53294518	6
(Intercept)	1.00000000	-0.6433674067	NA	NA	0

Figure B12. Standardised coefficients of the BMA setting with the *Gini* variable, with the *government response* variables, and using the *uniform* prior.

```
                              PIP     Post Mean      Post SD Cond.Pos.Sign
%Overweight_average       0.99994928  4.492238e-02 8.229093e-03    1.00000000
stringency_period         0.99982769  4.496905e-02 9.361415e-03    1.00000000
medianage_mean            0.97609173  8.410361e-02 2.496105e-02    1.00000000
democracy_average         0.94676067  2.285318e-01 9.510293e-02    1.00000000
pop_mean                  0.94296858 -1.735823e-06 6.570824e-07    0.00000010
hcq_cq                    0.76601156 -4.483276e-01 3.071897e-01    0.00000000
CHE_average               0.69517179 -1.315669e-04 1.001064e-04    0.00000023
Gini_average              0.59066114  1.937190e-02 1.888948e-02    0.99937785
vacc_rate_p1              0.34951588 -4.050080e-02 6.296720e-02    0.00001124
concentration_fpm_average 0.24343643 -5.299829e-03 1.077192e-02    0.00000010
gnipc_mean                0.15034415 -3.562184e-06 9.280568e-06    0.00865589
CPI_average               0.14013584 -2.863965e-03 7.960735e-03    0.00403919
MediaFreedom_average      0.13642575 -2.596959e-03 7.822349e-03    0.03667035
Favipiravir               0.13008706  4.514734e-02 1.651072e-01    0.98998793
iver                      0.11189926 -3.017938e-02 1.271842e-01    0.00048679
mys_mean                  0.08978758  9.115579e-03 3.414340e-02    1.00000000
density_mean              0.07688745  1.272205e-06 1.158503e-04    0.49655185
Acetaminophen             0.07053479 -1.857280e-02 9.632805e-02    0.00714327
remd                      0.05277682 -3.567022e-03 6.199391e-02    0.17069318
eys_mean                  0.02656839 -1.124125e-03 1.134290e-02    0.01834634
le_mean                   0.02269577 -3.151018e-04 4.714025e-03    0.21870116
                          Idx
%Overweight_average        12
stringency_period          15
medianage_mean              7
democracy_average           8
pop_mean                    5
hcq_cq                     17
CHE_average                11
Gini_average               10
vacc_rate_p1               16
concentration_fpm_average  14
gnipc_mean                  4
CPI_average                 9
MediaFreedom_average       13
Favipiravir                20
iver                       18
mys_mean                    3
density_mean                6
Acetaminophen              21
remd                       19
eys_mean                    2
le_mean                     1

Mean no. regressors              Draws             Burnins                Time
          "8.5185"          "2097152"                "0"     "4.842395 mins"
 No. models visited      Modelspace 2^K          % visited         % Topmodels
          "2097152"          "2097152"              "100"              "0.024"
           Corr PMP           No. Obs.        Model Prior             g-Prior
               "NA"              "119"     "dilut / 10.5"               "UIP"
    Shrinkage-Stats
        "Av=0.9917"
```

Figure B13. Raw results of the BMA setting with the *Gini* variable, with the *government response* variables, and using the *dilution* prior.

	PIP	Post Mean	Post SD	Cond.Pos.Sign	Idx
%Overweight_average	0.99994928	0.3859983977	0.07070900	1.00000000	12
stringency_period	0.99982769	0.2474113405	0.05150477	1.00000000	15
medianage_mean	0.97609173	0.4453094846	0.13216307	1.00000000	7
democracy_average	0.94676067	0.2560667719	0.10656152	1.00000000	8
pop_mean	0.94296858	-0.1753945149	0.06639425	0.00000010	5
hcq_cq	0.76601156	-0.1044907367	0.07159603	0.00000000	17
CHE_average	0.69517179	-0.1499113752	0.11406426	0.00000023	11
Gini_average	0.59066114	0.0851430961	0.08302276	0.99937785	10
vacc_rate_p1	0.34951588	-0.0503230991	0.07823808	0.00001124	16
concentration_fpm_average	0.24343643	-0.0405757089	0.08247027	0.00000010	14
gnipc_mean	0.15034415	-0.0368210239	0.09592991	0.00865589	4
CPI_average	0.14013584	-0.0296784760	0.08249490	0.00403919	9
MediaFreedom_average	0.13642575	-0.0208935291	0.06293380	0.03667035	13
Favipiravir	0.13008706	0.0066428778	0.02429351	0.98998793	20
iver	0.11189926	-0.0048643523	0.02049971	0.00048679	18
mys_mean	0.08978758	0.0172340748	0.06455211	1.00000000	3
density_mean	0.07688745	0.0001443192	0.01314208	0.49655185	6
Acetaminophen	0.07053479	-0.0047476001	0.02462349	0.00714327	21
remd	0.05277682	-0.0008801304	0.01529643	0.17069318	19
eys_mean	0.02656839	-0.0019532064	0.01970868	0.01834634	2
le_mean	0.02269577	-0.0014501731	0.02169506	0.21870116	1
(Intercept)	1.00000000	-0.7784835929	NA	NA	0

Figure B14. Standardised coefficients of the BMA setting with the *Gini* variable, with the *government response* variables, and using the *dilution* prior.