The distribution of COVID-19 mortality

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ABSTRACT

We estimate the distribution of COVID-19 mortality (measured as daily deaths) from the start of the pandemic until July 31st, 2022, for six European countries and the USA. We use the Pareto, the stretched exponential, the log-normal and the log-logistic distributions as well as mixtures of the log-normal and log-logistic distributions. The main results are that the Pareto does not describe well the data and that mixture distributions tend to offer a very good fit to the data. We also compute Value-at-Risk measures as well as mortality probabilities with our estimates. We also discuss the implications of our results and findings from the point of view of public health planning and modelling.

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1. Introduction

The distribution of mortality due to infectious diseases has begun to gather more interest from researchers. Having a better understanding of the distribution of the mortality for infectious diseases is important because public health and government officials can better plan for epidemics and pandemics by making suitable preparations, such as stockpiling personal protective equipment or planning for case surges at hospitals (Campolieti, 2021). In addition, having a better understanding of the distribution mortality can also be informative to public health and government officials who are deciding whether to lift or maintain public health measures (Vasconcelos et al., 2020, 2021). Some of the studies examining mortality from infectious diseases have focused on the “tail risks” of mortality and have also emphasized that the distribution of mortality can be heavy- or fat-tailed. A heavy- or fat-tailed distribution would mean that the probability of extreme mortality events would be much larger than expected based on a thin-tailed distributions, such as the normal. For example, Cirillo and Taleb (2020) considered the distribution of mortality from epidemics and pandemics during history and found evidence for a generalized Pareto distribution. Corral (2021) re-examined Cirillo and Taleb’s data and found that there were other distributions that are plausible fits to their mortality data, such as a log-normal. Campolieti (2021) looked at influenza mortality for the U.S. from 1900 to 2018. Campolieti (2021) considered two measures of influenza mortality: 1) influenza mortality including

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death from pneumonia; and 2) influenza mortality excluding deaths from pneumonia. Campolieti (2021) found that the distribution of influenza mortality including pneumonia was heavy-tailed, but found that a Beta or exponential distribution could not be ruled out. However, when he considered influenza mortality excluding deaths from pneumonia, he could rule out the thinner tailed Beta and exponential distributions. Overall, while there is evidence of heavy- or fat-tailed distributions, such as the power-law (Pareto), in the distribution of mortality for infectious diseases there is also evidence for alternative distributions. Consequently, there is some debate about what distribution best fits the distribution of mortality for infectious diseases. This is not like what has been observed in other settings, e.g., in physics, economics and computer science, where a power-law as well as other distributions could be plausible fits to the data (Clauset et al., 2009; Laherrère & Sornette, 1998; Mitzenmacher, 2004). Consequently, it is also important to use an empirical framework where one can consider alternative distributions and determine which is the most suitable for the mortality data being studied.

Our interest is also on the distribution of mortality from infectious diseases, but we focus on COVID-19 (SARS-COV-2) mortality during the pandemic (up until the end of July 2022). There have been some papers studying the distribution of morbidity for COVID-19 during the early phases of the pandemic (Beare & Toda, 2020; Blasius, 2020; Chan et al., 2021; Komarova et al., 2020; Singer, 2020; Vazquez, 2020). Beare and Toda (2020); Blasius (2020); Komarova et al. (2020); Singer (2020); Vazquez (2020); Ahundjanov et al. (2022) and some have found evidence of a power-law distribution in the number of COVID-19 cases. Chan et al. (2021) found a negative binomial was the best fitting count regression model to COVID-19 case counts. There have been some papers that have studied COVID-19 mortality in Europe as well as other parts of the world. Xenikos and Asimakopoulos (2021) studied COVID-19 mortality for several European countries up until March 2020 and found that the power-law distribution fit these data well. Vasconcelos et al. (2020) studied COVID-19 fatalities with data from China, France, Germany, Iran, Italy, South Korea, Spain and Brazil. They described these countries as being at the middle or late stage of the epidemic, which they believed to be the case in the Fall of 2020. They used the Richards growth model, which allows for both exponential and sub-exponential regimes in mortality dynamics, to evaluate intervention strategies. In a related paper, Vasconcelos et al. (2021) also studied the distribution of COVID-19 mortality for the period up to July 2020 in Canada, Germany, Italy, the Netherlands and the United Kingdom. They found that the power-law distribution fit the distribution of COVID-19 mortality during what they considered the final phase of the pandemic. These papers have generally considered the fit of the distributions visually. However, the disadvantage of this visual approach is that it is difficult to rule out competing distributions that provide a plausible fit to the data as well. Consequently, as pointed out by Corral (2021) there could be alternative heavy- or fat-tailed distributions that offer a plausible fit to the data. This point was also made in Clauset et al. (2009) when considering the fit of the power-law distribution versus other alternative distributions.

We examine the distribution of COVID-19 mortality during the first two and a half years of the pandemic for France, Germany, Italy, Spain, Sweden, the United Kingdom and the United States. Our paper makes several contributions to the literature. First, we update the data to include much more of the pandemic, not just the first few months of the first year. This provides us with much longer window on the mortality that has occurred during the pandemic. Second, we consider a number of alternative fat- and heavy-tailed distributions, such as the power-law, stretched exponential, log-normal, mixtures of log-normals, log-logistic and mixtures of log-logistic. Third, we assess the fit of the distributions to the data using goodness-of-fit tests, such as the Kolmogorov-Smirnov, Cramér-von Mises and Anderson-Darling, as well as information criteria, unlike the existing literature which has primarily relied on visual checks. Using these tests and statistical information criteria means that we are better able to assess the fit of the distributions we consider to the data and determine the most plausible distribution. Fourth, we also consider the fit of distributions to the data below the upper tail, unlike some papers that have only considered the fit of power-law distributions to the upper tail of the distribution. Fifth, we also consider the distribution of mortality for specific years (and phases) of the pandemic, to assess whether the distribution of COVID-19 mortality changes over time.

In Section 2 we describe our data and the distributions we consider for mortality. Section 3 presents our findings. We end the paper with a summary of our main findings and discussion of their implications for public policy and future research.

2. Data and methods

We consider data on daily COVID-19 mortality (measured as the number of daily deaths) from the following countries: France; Germany; Italy; Spain; Sweden; the United Kingdom; and the United States of America. We obtained our data on daily deaths from https://ourworldindata.org/covid-cases and it includes data from the start of pandemic (February 1st, 2020) until July 31st, 2022. We consider the distribution for the whole period and also for the individual years (2020, 2021, 2022) in the pandemic as public health measures that are in place vary over time as does the dominant strain of the virus in circulation (Challen et al., 2021; Abdool Karim & de Oliveira, 2021; Several Authors, 2021; Abdool Karim & Abdool Karim, 2021; Callaway, 2022; Walker, J., Grubaugh, N. D., Gonsalves, G., Pitzer, V. and Rizvi, Z., 2022) and this might have an effect on mortality.

Many individuals who have influenza can also develop pneumonia and in the more serious cases death results from the pneumonia, which will be listed as the cause of death on the death certificate. While measuring influenza mortality including deaths from pneumonia is the convention in most of the literature, Doshi (2008) argued that measuring influenza mortality without the deaths from pneumonia was a more reliable measure of mortality.

Of course the pandemic is still continuing as new variants emerge and cases surge around the world.
We briefly describe next the distributions we fit to the daily mortality data. We let $x$ denote our measure of mortality, which is the number of daily deaths. The first distribution we will consider is the well-known power-law distribution (or Pareto distribution):

$$f_{\rho}(x; \alpha, x_{\min}) = \frac{\alpha - 1}{x_{\min}} \left( \frac{x}{x_{\min}} \right)^{-\alpha}$$

(1)

where $\alpha$ is the power-law exponent and $x_{\min}$, which is such that $x \geq x_{\min} > 0$, is the lower bound on power-law behavior.

The second distribution we consider for mortality, $x > 0$, is the Weibull or stretched exponential (STEXP) distribution

$$f_{STEXP}(x; \gamma, \eta) = \frac{\gamma}{\eta} \left( \frac{x}{\eta} \right)^{\gamma-1} \exp \left( - \left( \frac{x}{\eta} \right)^{\gamma} \right)$$

(2)

where $\gamma > 0$ is a shape parameter and $\eta > 0$ is a scale parameter. Weibull or stretched exponential distributions have often been found to fit skewed and heavy-tailed data (Jiang et al., 2013; Laherrère & Sornette, 1998).

The third distribution in our study is the well-known log-normal distribution

$$f_{LN}(x; \mu, \sigma) = \frac{1}{\sqrt{2\pi}\sigma x} \exp \left( - \frac{\ln(x) - \mu)^2}{2\sigma^2} \right)$$

(3)

where $\mu \in \mathbb{R}$ is the mean of $\ln(x)$ and $\sigma > 0$ is its standard deviation according to this distribution. Log-normal distributions have been found to fit many economic and physical phenomena with heavy tails (Mitzenmacher, 2004).

We will also consider 2-mixtures and 3-mixtures (McLachlan & Peel, 2003) of log-normal distributions, like in Kwong and Nadarajah (2019); Băncescu et al. (2019); Su (2020); Puente-Ajovín et al. (2020a,b); Campolieti and Ramos (2021):

$$f_{2LN}(x; \mu_1, \mu_2, \sigma_1, \sigma_2, p_1) = p_1 f_{1LN}(x; \mu_1, \sigma_1) + (1 - p_1) f_{1LN}(x; \mu_2, \sigma_2)$$

(4)

where $0 \leq p_1, 1 - p_1 \leq 1$, and

$$f_{3LN}(x; \mu_1, \mu_2, \mu_3, \sigma_1, \sigma_2, \sigma_3, p_1, p_2) = p_1 f_{1LN}(x; \mu_1, \sigma_1) + p_2 f_{1LN}(x; \mu_2, \sigma_2) + (1 - p_1 - p_2) f_{1LN}(x; \mu_3, \sigma_3)$$

(5)

where $0 \leq p_1, p_2, 1 - p_1 - p_2 \leq 1$.

The log-logistic distribution has been used to model mortality data (Muse et al., 2021), so we also consider it:

$$f_{LL}(x; \mu, \sigma) = \frac{\exp \left( - \frac{\ln(x) - \mu}{\sigma} \right)}{x\sigma \left( 1 + \exp \left( - \frac{\ln(x) - \mu}{\sigma} \right) \right)}$$

(6)

where $\mu \in \mathbb{R}$ is a location parameter and $\sigma > 0$ is a shape parameter. Like the log-normal distribution, we also use 2- and 3-mixtures of log-logistic distributions (Puente-Ajovín et al., 2020a):

$$f_{2LL}(x; \mu_1, \mu_2, \sigma_1, \sigma_2; p_1) = p_1 f_{1LL}(x; \mu_1, \sigma_1) + (1 - p_1) f_{1LL}(x; \mu_2, \sigma_2)$$

(7)

where $0 \leq p_1, 1 - p_1 \leq 1$, and

$$f_{3LL}(x; \mu_1, \mu_2, \mu_3, \sigma_1, \sigma_2, \sigma_3, p_1, p_2) = p_1 f_{1LL}(x; \mu_1, \sigma_1) + p_2 f_{1LL}(x; \mu_2, \sigma_2) + (1 - p_1 - p_2) f_{1LL}(x; \mu_3, \sigma_3)$$

(8)

where $0 \leq p_1, p_2, 1 - p_1 - p_2 \leq 1$.

We estimate all these distributions with maximum likelihood (ML) estimation, and compute the standard errors (SE) of the estimates according to Efron and Hinkley (1978); McCullough and Vinod (2003).\footnote{We obtain our estimates using the command mle in MATLAB®, with usage shown in a file of supplementary material.}

We assess the fit of the estimated distributions to the data with goodness-of-fit test statistics. In particular, we use the Kolmogorov–Smirnov (KS), Cramér–von Mises (CM) and Anderson–Darling (AD) tests. We bootstrap the $p$-values for the test statistics because we estimate the parameters of the distributions, so our $p$-values are more conservative because they incorporate the uncertainty about the parameters than the analytical $p$-values, which assume the parameters are fixed (not estimated).

We also use three well-known information criteria to perform model selection. As we increase the number of parameters we can improve the maximum of the log-likelihood function. The information criteria recognize this and incorporate a penalty term, which penalizes over-parameterized models. We consider the following information criteria:

\begin{align*}
\text{AIC} &= \ln(L) + \frac{2k}{n} \\
\text{BIC} &= \ln(L) + \frac{k\ln(n)}{n} \\
\text{HQIC} &= \ln(L) + \frac{2k\ln\ln(n)}{n} \\
\end{align*}
The Akaike Information Criterion (AIC) Akaike (1974); Burnham and Anderson (2002, 2004), defined as

\[ AIC = 2k - 2\ln L^* \]

where \( k \) is the number of parameters of the distribution and \( \ln L^* \) is the corresponding (maximum) log-likelihood. The minimum value of AIC corresponds (asymptotically) to the minimum value of the Kullback–Leibler divergence, so a model with the lowest AIC is selected from among the competitors.

The Bayesian or Schwarz Information Criterion (BIC) Burnham and Anderson (2002, 2004); Schwarz (1978), defined as

\[ BIC = k\ln(n) - 2\ln L^* \]

where \( k \) is the number of parameters of the distribution, \( n \) the sample size and \( \ln L^* \) is as before. The BIC penalizes more heavily the number of parameters used than does the AIC. The model with the lowest BIC is selected according to this criterion.

The Hannan–Quinn Information Criterion (HQC) Burnham and Anderson (2002, 2004); Hannan and Quinn (1979), defined as

\[ HQC = 2k\ln(\ln(n)) - 2\ln L^* \]

where \( k \) is the number of parameters of the distribution, \( n \) the sample size and \( \ln L^* \) is as before. The HQC implements an intermediate penalization of the number of parameters when compared to the AIC and BIC. The model with the lowest HQC is selected according to this criterion.

Likewise, for the samples that take into account the data for individual years, we will consider two information criteria more adapted to reduced sample sizes (they take into account corrections for small sample sizes). They are:

The corrected Akaike Information Criterion like in Akhundjanov et al. (2017):

\[ AIC_c = 2k - 2\ln L^* + \frac{2(k + 1)(k + 2)}{n - k - 2} \]

where \( k \) is the number of estimated parameters, \( n \) is the sample size and \( \ln L^* \) is the maximum log-likelihood of the corresponding model (Hurvich & Tsai, 1989).

The adjusted Bayesian or Schwarz Information Criterion:

\[ BIC_a = k\ln\left(\frac{n + 2}{24}\right) - 2\ln L^* \]

where \( k, n \) and \( \ln L^* \) are as before, see Sclove (1987) for details. Also, the minimum values of each of these criteria point out to the selected model according to it.

Finally, we describe two measures of risk that we will use in Subsection 3.3 to provide some assessment about the probability of extreme mortality. They are:

The Value-at-Risk (VaR) measure for the upper tail, to the level of significance \( \alpha \) is the number \( \text{VaR}_\alpha \) satisfying...
cdf(VaR_\alpha) = 1 - \alpha

where cdf is the cumulative distribution function the VaR_\alpha is computed respect to it, see, e.g., Jorion (2006) and references therein.

- The Tail-Value-at-Risk (TVaR) measure for the upper tail, is defined for a given VaR_\alpha as

$$TVaR_\alpha = \frac{1}{\alpha} \int_{VaR_\alpha}^{\infty} xf(x) dx$$

where f is the probability density function the TVaR_\alpha is computed respect to it, see, e.g., Rachev et al. (2007) and references therein.

The Value-at-Risk measures are often used in financial modelling for risk management and they provide the extreme quantiles of the distribution. The expression for the Value-at-Risk measure will depend on the distribution being considered. We consider the VaR measures at \alpha = 0.01, 0.05, 0.10, which correspond with the 99th, 95th and 90th percentiles of the distribution.

3. Results

3.1. Pooled analysis

The first part of our analysis focuses on the pooled data sets, i.e., the data covering the period from February 1st, 2020 to July 31st, 2022 for the previously mentioned seven countries. We offer the descriptive statistics for these data in Table 1. As the support for several of the different distributions we consider require positive values, the zeros have been removed from the data.

The descriptive statistics indicate that there is a great deal of dispersion in the mortality data, although the extent of this dispersion does differ across countries we consider. The daily deaths data we consider also exhibit a great of skewness, which suggests that the distribution of mortality is a skewed one. In addition, all of the kurtosis measures exceed 3, so the mortality distribution is not thin-tailed.

We provide maximum likelihood estimates for all the distributions we estimate in a supplemental file (an Excel spreadsheet), to keep the number of tables in the text of the paper to a manageable number.\footnote{This file is available at \url{https://doi.org/10.7910/DVN/HWHKSG}.} We are able to obtain estimates for all of the distributions we consider, except for the 3LL distribution for Sweden.\footnote{Please recall that we are considering the full data sets and not only the upper tails.}

The goodness-of-fit tests are presented in Table 2 and we provide a summary of the results of those tests in Table 3. We say that a distribution is “Non-rejected” if all of the three tests yield non-rejection; “Mixed” if one test or two yield(s) rejection, and “Rejected” if all of the three tests yield rejection or if the distribution cannot be estimated. For the Pareto distribution, the tests always reject it.\footnote{For the stretched exponential, we have non-rejected in 5 occasions and rejected in the other countries. For the log-normal distribution, we soundly reject it in all 7 countries. Using a mixture of two log-normals dramatically improves the fit to the data, as we do not reject this distribution for all of the 7 countries we consider. We observe similar findings, namely that we cannot reject the distribution when we take 3-mixtures of log-normals (3LN). For the log-logistic distribution, like the log-normal we reject it in all 7 countries. Taking the 2LL (a mixture of two log-logistics) improves the fit to the data notably as well by the corresponding numbers, as we obtain full 7 non-rejections. When we use a mixture of 3 log-logistic distributions, the fit is not as good as the 2LL distribution, as we obtain 4 non-rejections, 2 mixed instance and 1 non-rejection.}

\begin{table}[h]
\centering
\caption{Descriptive statistics of the pooled samples.}
\begin{tabular}{llllllll}
\hline
\textbf{} & \textbf{Number of Observations} & \textbf{Mean} & \textbf{SD} & \textbf{Skewness} & \textbf{Kurtosis} & \textbf{Min} & \textbf{Max} \\
\hline
France & 836 & 182.343301 & 215.734102 & 2.49969992 & 10.9769701 & 1 & 1438 \\
Germany & 844 & 170.616114 & 212.359863 & 2.27145146 & 9.02510462 & 1 & 1244 \\
Italy & 891 & 193.17284 & 202.771747 & 1.30693711 & 4.01375786 & 1 & 993 \\
Spain & 563 & 198.293073 & 207.947094 & 1.80859547 & 7.8383609 & 1 & 1623 \\
Sweden & 423 & 46.3687943 & 62.0282092 & 3.18970358 & 17.1423396 & 1 & 474 \\
UK & 808 & 222.861386 & 295.517366 & 2.33697674 & 8.99371869 & 1 & 1820 \\
USA & 882 & 1168.03175 & 966.110268 & 1.12954673 & 3.69423338 & 1 & 4411 \\
\hline
\end{tabular}
\end{table}
One result that we observe is that the mixture distributions (both log-normal and log-logistic) tend to fit the data much better than the non-mixture distributions' counterparts. Consequently, the 2LN, 3LN and 2LL (and 3LL to a lesser extent) are excellent distributions in terms of goodness-of-fit. We present the detailed information criteria in Table 4, where the selected model according to each criterion is marked in bold. The AIC and HQC information criteria tend to favour the mixture of log-normal distributions, but the results for the BIC are a little more varied. While the BIC does select the

Table 2
Outcomes of the KS, CM and AD tests in the format p-value (statistic). Non-rejections at the 5% level are marked in bold.

<table>
<thead>
<tr>
<th>Distribution eq.</th>
<th>Non-rejected</th>
<th>Mixed</th>
<th>Rejected</th>
<th>Total</th>
</tr>
</thead>
<tbody>
<tr>
<td>Pareto</td>
<td>0 (0.369)</td>
<td>0.505</td>
<td>0.378</td>
<td>0.000881 (0.0683)</td>
</tr>
<tr>
<td>STEXP</td>
<td>0 (0.29)</td>
<td>0.118</td>
<td>0.061</td>
<td>0.0000216 (2.35)</td>
</tr>
<tr>
<td>LN</td>
<td>0 (0.107)</td>
<td>0.014</td>
<td>0.0114</td>
<td>0.00000743 (13.4)</td>
</tr>
<tr>
<td>France</td>
<td>0 (0.39)</td>
<td>0.117</td>
<td>0.0085</td>
<td>0.00156 (0.636)</td>
</tr>
<tr>
<td>Germany</td>
<td>0 (0.277)</td>
<td>0.0255</td>
<td>0.77</td>
<td>0.00000179 (0.366)</td>
</tr>
<tr>
<td>Italy</td>
<td>0 (0.344)</td>
<td>0.017</td>
<td>0.0059 (3.76)</td>
<td>0.00000216 (2.35)</td>
</tr>
<tr>
<td>Spain</td>
<td>0 (0.35)</td>
<td>0.257</td>
<td>0.103</td>
<td>0.00000179 (0.366)</td>
</tr>
<tr>
<td>Sweden</td>
<td>0 (0.251)</td>
<td>0.017</td>
<td>0.0059</td>
<td>0.00000216 (2.35)</td>
</tr>
<tr>
<td>UK</td>
<td>0 (0.321)</td>
<td>0.114</td>
<td>0.0029</td>
<td>0.00000216 (2.35)</td>
</tr>
<tr>
<td>USA</td>
<td>0 (0.451)</td>
<td>0.00156</td>
<td>0.000123 (7.93)</td>
<td>0.00000000113 (0.00156)</td>
</tr>
</tbody>
</table>

Table 3
Summary of the results of the goodness-of-fit tests KS, CM and AD for the pooled samples.

<table>
<thead>
<tr>
<th>Distribution eq.</th>
<th>Non-rejected</th>
<th>Mixed</th>
<th>Rejected</th>
<th>Total</th>
</tr>
</thead>
<tbody>
<tr>
<td>Pareto</td>
<td>0 (191.)</td>
<td>0.487</td>
<td>0.378</td>
<td>0.000881 (0.0683)</td>
</tr>
<tr>
<td>STEXP</td>
<td>0 (137.)</td>
<td>0.107</td>
<td>0.0059 (3.76)</td>
<td>0.00000216 (2.35)</td>
</tr>
<tr>
<td>LN</td>
<td>0 (193.)</td>
<td>0.0069</td>
<td>0.0059 (3.76)</td>
<td>0.00000216 (2.35)</td>
</tr>
<tr>
<td>France</td>
<td>0 (272.)</td>
<td>0.017</td>
<td>0.0059 (3.76)</td>
<td>0.00000216 (2.35)</td>
</tr>
<tr>
<td>Germany</td>
<td>0 (27.2)</td>
<td>0.017</td>
<td>0.0059 (3.76)</td>
<td>0.00000216 (2.35)</td>
</tr>
<tr>
<td>Italy</td>
<td>0 (39.3)</td>
<td>0.017</td>
<td>0.0059 (3.76)</td>
<td>0.00000216 (2.35)</td>
</tr>
<tr>
<td>Spain</td>
<td>0 (23.2)</td>
<td>0.017</td>
<td>0.0059 (3.76)</td>
<td>0.00000216 (2.35)</td>
</tr>
<tr>
<td>Sweden</td>
<td>0 (9.55)</td>
<td>0.017</td>
<td>0.0059 (3.76)</td>
<td>0.00000216 (2.35)</td>
</tr>
<tr>
<td>UK</td>
<td>0 (31.9)</td>
<td>0.017</td>
<td>0.0059 (3.76)</td>
<td>0.00000216 (2.35)</td>
</tr>
<tr>
<td>USA</td>
<td>0 (57.6)</td>
<td>0.017</td>
<td>0.0059 (3.76)</td>
<td>0.00000216 (2.35)</td>
</tr>
</tbody>
</table>

rejection (estimation non-obtained). One result that we observe is that the mixture distributions (both log-normal and log-logistic) tend to fit the data much better than the non-mixture distributions' counterparts. Consequently, the 2LN, 3LN and 2LL (and 3LL to a lesser extent) are excellent distributions in terms of goodness-of-fit. We present the detailed information criteria in Table 4, where the selected model according to each criterion is marked in bold. We summarize the results from the information criteria in Table 5. The information criteria do not offer much support to the Pareto, log-normal, log-logistic and mixture of two log-logistic distributions. The AIC and HQC information criteria tend to favour the mixture of log-normal distributions, but the results for the BIC are a little more varied. While the BIC does select the
Table 4
Maximum log-likelihoods, AIC, BIC and HQC information criteria. Selected models according to each criterion are marked in bold.

<table>
<thead>
<tr>
<th>Country</th>
<th>Pareto log-likelihood</th>
<th>Pareto AIC</th>
<th>Pareto BIC</th>
<th>Pareto HQC</th>
<th>STEXP log-likelihood</th>
<th>STEXP AIC</th>
<th>STEXP BIC</th>
<th>STEXP HQC</th>
<th>LN log-likelihood</th>
<th>LN AIC</th>
<th>LN BIC</th>
<th>LN HQC</th>
</tr>
</thead>
<tbody>
<tr>
<td>France</td>
<td>5875.5617</td>
<td>11753.1234</td>
<td>11757.8521</td>
<td>11754.9362</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td>-5178.129</td>
<td>10360.2579</td>
<td>10363.8834</td>
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M. Campolieti, A. Ramos Infectious Disease Modelling 7 (2022) 856–873
mixture of log-normal distributions, the stretched exponential distribution is also selected in 3 countries. Overall, it seems that a mixture of log-normal distributions tends to fit the mortality data for this pandemic from its start quite well.

Thus we obtain the global conclusion that the best fitting distributions for daily COVID-19 deaths in all of the 7 countries we consider are the 2LN and the 3LN, i.e., the mixtures of 2- or 3- log-normal distributions. Also the stretched exponential (STEXP) distribution seems to be a good model if one wants to deal with a model with only two parameters. This conclusion is similar to one in Campolieti and Ramos (2021) for the distribution of strike size: the 2LN and 3LN perform extremely well. And there is also one difference with the conclusion of Campolieti and Ramos (2021): there, the Weibull or stretched exponential performed very poorly; meanwhile for daily deaths’ data sets, the STEXP does offer a reasonable fit with as few as two parameters.

We also provide a graphical assessment of the fit for, our most preferred and plausible, models, i.e., the STEXP, 2LN and 3LN in Fig. 1 (for the log-coranks as a function of the log-daily deaths) and in Fig. 2 (for the log-ranks as a function of the log-daily deaths). In them, we see that the best graphical fit is obtained by far by the 3LN (black), although sometimes almost indistinguishable from the 2LN (green), while for the STEXP (red) there are some deviations, above all at the lower tail.

We have also computed the tail probabilities for the distributions we consider and present them in Table 6. We evaluate the distributions at a few different points to illustrate how the distributions differ both below and in the upper tail. We evaluate the distributions for each country at their respective mean, the mean plus one standard deviation, the mean plus two standard deviations and the mean plus three standard deviations.\footnote{We use the mean and standard deviation for each country to evaluate these probabilities as there are some differences in both the level of deaths and their dispersion. Recall that we measure mortality as the number of daily deaths in each country.} The quantities we present are the probability that the value exceeds the levels we consider. Having estimates of probabilities means that government and public health planners could compute the probability of mortality or the expected mortality and use this information to determine the benefits of various public health interventions.

Table 6 shows that as the level of mortality increases the probability of observing that level decreases. It also illustrates the differences between distributions. In particular, the mixtures of log-normal distributions tend to place much less probability on a given level of mortality than the log-normal distribution. The smallest probability tends to be in the mixture of 3 log-normal distributions (3LN), which was also the best fitting distribution. We see a similar pattern when we compare the mixture of log-logistic distributions (2LL and 3LL) with the log-logistic distribution. We also find that the probabilities from the 3LN mixture also tend to smaller than the probability from the 3LL mixture. Also the 3LN can be estimated for all the countries we consider but the 3LL is not numerically feasible for Sweden. The information criteria also favour the mixtures of log-normal distributions.

Another striking result is the comparison with the stretched exponential or Weibull and power-law distributions. The power-law distribution tends to place a much larger probability on all the mortality levels we evaluate across all countries. As our analysis shows, the power-law is rejected as a fit to the data and using it would tend to overestimate the probability of the tail risks of mortality from COVID-19. Even more striking, is how similar the probabilities for the stretched exponential distribution are to the mixture of 3 log-normal distributions for some of the countries we consider. This confirms our findings based on the goodness-of-fit and information criteria that the stretched exponential could be a plausible fit to the mortality data in many countries if one desired a more parsimonious distribution.

The best fitting distributions for the countries we consider are often mixtures distributions. These distributions have been shown to arise if a suitable stochastic process is specified and the Fokker-Planck equations are solved (Peña et al., 2022).\footnote{The same is also true for the stretched exponential as well as the other distributions we consider. In other words, these distributions can also be obtained as solutions to the Fokker–Planck equations.} The Fokker–Planck (or forward Kolmogorov) equations also arise in stochastic models of epidemics (Allen, 2008). While these stochastic models are generally applied to study an initial outbreak of an epidemic in a small population (Brauer, 2017), our findings suggest that there could be a greater role for them when studying mortality during a pandemic and epidemic (and not only during the opening phase of a pandemic or epidemic).
3.2. Analysis by year

As we indicated earlier, the COVID-19 pandemic has gone through different phases as public health interventions have changed and the dominant strain of the virus of has evolved. So we also estimate the distribution of COVID-19 mortality for each individual year in the pandemic, i.e., 2020, 2021 and 2022. We present the descriptive statistics for each country by year in Table 7. We can see in Table 7 that the number of observations varies by year, as mortality has declined during 2022 and some of the distributions we estimate require positive support, i.e., mortality greater than 0. As in the pooled data for 2020 to 2022, we observe a great deal of dispersion, skewness and kurtosis, indicating again skewed and heavy-tailed data.

We have re-estimated the same statistical distributions using data for the individual years in the pandemic. The maximum likelihood estimates, along their standard errors, are presented in the supplemental Excel file. Unfortunately, we encounter more numerical problems with the data for individual years and we cannot obtain estimates for all the distributions we consider. We can obtain estimates for Pareto, log-normal and log-logistic distributions as well as mixtures of two log-logistic distributions for all countries and all years. We cannot obtain estimates for the following distributions: the stretched exponential for Sweden in 2021; mixture of two log-normals for Sweden in 2021 and the UK in 2022; the mixture of three

![Log-corank plots for the whole samples of log-new-deaths, using the STEXP (red), 2LN (green) and 3LN (black) distributions and the empirical data (blue).](image)

**Fig. 1.** Log-corank plots for the whole samples of log-new-deaths, using the STEXP (red), 2LN (green) and 3LN (black) distributions and the empirical data (blue).
log-normals for Spain and Sweden in 2021 and the UK in 2022; and the mixture of three log-logistic distributions for Sweden and UK in 2022.

As they are quite numerous, the goodness-of-fit tests, i.e., the KS, CM and AD tests, are presented in the supplementary Excel file. However, we do provide a summary of the results from these tests in Table 8 (with the same terminology as that used for the pooled samples we discussed earlier).

The Pareto distribution is always strongly rejected (21 out of 21 times). For 2020, the STEXP, the LN and the LL are rejected 5 times out of 7, and non-rejected and mixed once. The 2LN, 3LN, 2LL and 3LL are non-rejected 7 times. For 2021, the STEXP is non-rejected 3 times and rejected 4, the LN and LL are non-rejected and mixed 3 times each and rejected once. The 2LN is non-rejected 6 times and rejected (non-estimated) once. The 3LN is similar to the 2LN, but 5 non-rejections and 2 rejected (non-estimated). The 2LL and 3LL achieve both 7 non-rejections. For 2022 the STEXP fits the data better, with 5 non-rejections, one mixed and rejected once. The 2LN and 3LN behave exactly as in 2021. Finally, the 2LL gets 6 non-rejections and one mixed, and the 3LL gets 5 non-rejections and 2 rejections (non-estimations). Overall, the mixture distributions tend to offer a good fit data.

We next present the results of the information criteria adapted to the fact that the sample sizes have been reduced by roughly a factor of 1/3 with respect to the pooled samples. This means that it is advisable to take into account small sample

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**Fig. 2.** Log-rank plots for the whole samples of log-new-deaths, using the STEXP (red), 2LN (green) and 3LN (black) distributions and the empirical data (blue).
sizes in the information criteria, and therefore we will use the previously defined corrected AIC (AICc) and adjusted BIC (BICa). To the best of our knowledge, there exist no version of the HQC adapted or adjusted to small sample sizes, so we will use only the first two in what follows. The complete set of information criteria statistics are available in the supplementary Excel file, but we provide a summary of the results in Table 9.

For 2020, the 2LN and 3LN are clearly selected 3 times each, and the 3LL once. For the 2021, information criteria the LN and the STEXP appear with corrected AIC and adjusted BIC twice, and once in 2021. The results for 2022 are much more varied than those for 2021. The results for 2022 are much more varied as the information criteria suggest that the distribution of COVID-19 mortality does vary somewhat over time. For 2020, our findings are much like those for the pooled sample, in that we find a great deal of support for the mixture of log-normal distributions, the 2LN and 3LN. While the 3LN distribution is selected twice in the 2021 data, the information criteria favour the 3LL distribution, i.e., the mixture of 3 log-logistic distributions. The findings for 2021 are thus not as clear as those for 2020, which had strong support for the mixture of log-normal distributions. The information criteria for 2022 are much more varied as they select candidates such as the stretched exponential, the 2LN, 3LN, 2LL and 3LL. The clearest result based on the information criteria is that the Pareto distribution is not selected in any country we study during any phase of the pandemic. This finding is quite striking as the Pareto distribution has been the focus of earlier research studying the distribution of COVID-19 mortality. In summary, our findings suggest that the distribution of COVID-19 mortality does appear to vary over time. This finding is perhaps not too surprising because, as we have noted earlier, new variants of the disease have emerged and public health measures used to control the spread of the disease have changed over time, e.g., mass vaccination programs. Moreover, it also appears that mixture distributions are quite useful for modelling COVID-19 mortality, although whether they are log-normal or log-logistic does vary across time. Overall, it seems a mixture of log-normal distributions fits best in 2020, but a mixture of log-logistic distributions may offer a better fit in 2021. The results for 2022 are much more varied across time. Overall, it seems a mixture of log-normal distributions fits best in 2020, but a mixture of log-logistic distributions may offer a better fit in 2021.

### Table 6

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To provide a summary of the results in Table 9.
indeterminate, but this also reflects that there is less complete data than in the other years we consider, which makes it more difficult to distinguish between alternative distributions (Clauset et al., 2009).

### 3.3. An assessment on prediction

The distribution of mortality can also be used to undertake some predictive exercises. As we are estimating the distribution of COVID-19 mortality, we do not forecast the level of mortality as we would with a regression or time series model, but present the VaR and TVaR measures we discussed earlier. Recall that the VaR and TVaR present the level of mortality in the upper tails of the distribution, i.e., 99th, 95th and 90th percentiles.

We compute the VaR measures using the most recent data from 2022. For each country and sample, we successively remove the last 30, 29, 28, ..., 2, 1 observations. This splits the data into “in-sample”, which is used for estimation, and “out-of-
sample” portions, with the out-of-sample portion corresponding (more or less) to the month of data, i.e., July 2022, which we use to compute the VaR measures based on the rolling in-sample data.

To assess whether the two partitions of the data come from the same distribution, we have performed two-sample Kolmogorov–Smirnov (KS), Cramér–von Mises (CM) and Anderson–Darling (AD) tests. In general, the null hypothesis that the data come from the same distribution is non-rejected for France, Germany, Italy, Spain, Sweden, but we reject this null for the UK and the USA. This suggests that the COVID-19 mortality distribution for the UK and the USA for our out-of-sample data differs from the in-sample data, meanwhile for the other countries it is more stable. Another observation that emerges from these computations is that the COVID-19 mortality distribution is somewhat sensitive to the addition or removal of observations. This will be reflected in the VaR and TVaR we present.

We compute the VaR and TVaR for the mixture of three log-normal distributions (3LN) as we can always obtain estimates for this distribution in the period we consider for the VaR computations and the fit of the distribution to the data is good. Using the estimates for the 3LN, we have computed the VaR and TVaR for the levels of significance $\alpha = 0.01$, $\alpha = 0.05$ and $\alpha = 0.10$ for all the rolling samples. The results are plotted in Figs. 3–5, respectively.

The main result out of these figures is that the VaR and TVaR remain quite stable for all the studied countries except the UK and the USA, but with the qualification that even one more or less observation can cause these measures to jump somewhat. Another result is that for the UK, both the VaR and TVaR increase during the out-of-sample period. This pattern might reflect our observation that the distribution for mortality in the in-sample and out-of-sample periods is likely different. For the USA we observe that the VaR and TVaR are decreasing during the out-of-sample period. As with the UK, this could reflect that distribution of mortality for the in-sample and out-of-sample periods is different for the USA.

In short, there is variability in the values of the extremes of COVID-19 mortality; for some countries this value remains more or less stable, but for other countries it is much more variable. It is not inconceivable that these patterns could interchange among themselves for a given country as the pandemic evolves. An important implication of the VaR and TVaR measures is that they could be used to obtain worst case scenarios for mortality, i.e., the tails of the distribution or, equivalently, providing the tail risks of mortality, and be used for risk management during a pandemic by public health and government officials.

4. Concluding remarks and discussion

We studied the distribution of daily COVID-19 deaths for six European countries and the United States. While some earlier papers have found evidence for a power-law distribution in COVID-19 mortality, we soundly reject this distribution based on

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8 The results are available in the supplemental Excel file. There are missing results but are so because one of the samples is too small to perform the tests.
the goodness of fit tests and the information criteria. Our analysis shows the potential problems of using visual methods of assessing the fit of a distribution. Our results also point to a mixture of 2- or 3- log-normal distributions as a better fitting alternative to the data from the start of the pandemic to the end of July 2022. This confirms the observation in Corral (2021) about the potential for alternative distributions to fit the distribution of mortality from infectious diseases. Our analysis also includes the data below the upper tail and from three years of the pandemic, so the preferred mixture distributions can be used to assess the probability of differing levels of mortality. When we conduct our analysis by year, we find that distribution of COVID-19 mortality does change over time. This should not be too surprising as new variants have emerged and public health measures have changed. In particular, we find a mixture of log-normal distributions is best for 2020, but a mixture of log-logistic distributions for 2021. For 2022, our results are much more varied, but this could also reflect that the sample size for our data is much smaller and this can make it much more difficult to distinguish between alternative distributions.

We used Value-at-Risk measures to estimate the levels of mortality in the tails of the distribution for an out-of-sample period, i.e., July 2022. While there is some instability in the estimates for the USA and the UK, the estimates for the other countries are amenable to these sorts of computations and provide some indication of the tail risks of mortality during this phase of the pandemic.

Our findings and results are of great interest to government and public health officials as they can use these distributions to assess the probability of elevated mortality as part of their pandemic planning. Our results show that the probabilities from
the most plausible distribution can differ substantially from some of the other distributions we consider, which are not a plausible fit to the data, such as the Pareto (power-law) distribution (which has been a focus of earlier research). Consequently, government and public health officials would have better estimates of the consequences of the initiatives that they are considering by using the distribution that best fits the data. In addition, our paper also presents Value-at-Risk measures as a tool for pandemic planning and risk management. While Value-at-Risk measures are often used in financial and insurance markets, our results show that these measures could also be used to assess the tail risks for mortality from infectious diseases. Value-at-Risk measures are thus an interesting area for future research on modelling mortality from infectious diseases and pandemic management to consider.

Fig. 4. Graphs of the VaR and TVaR for the value of $\alpha = 0.05$ and the samples contained in 2022 where we remove the last 30, 29, 28, …1 days of observations.
Author contributions

Michele Campolieti: Conceptualization, data curation, formal analysis, investigation, methodology, software, supervision, validation, visualization, writing-original draft, writing-review & editing. Arturo Ramos: Conceptualization, data curation, formal analysis, funding acquisition, investigation, methodology, resources, software, validation, visualization, writing-original draft, writing-review & editing.

Data availability statement

Data are fully and freely available at https://ourworldindata.org/covid-cases. Code files are available at https://doi.org/10.7910/DVN/HWHKSG.
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Appendix A. Supplementary data

Supplementary data to this article can be found online at https://doi.org/10.1016/j.idm.2022.11.003.

References


