

Reporting Summary

Nature Research wishes to improve the reproducibility of the work that we publish. This form provides structure for consistency and transparency in reporting. For further information on Nature Research policies, see [Authors & Referees](#) and the [Editorial Policy Checklist](#).

Statistics

For all statistical analyses, confirm that the following items are present in the figure legend, table legend, main text, or Methods section.

n/a Confirmed

- The exact sample size (n) for each experimental group/condition, given as a discrete number and unit of measurement
- A statement on whether measurements were taken from distinct samples or whether the same sample was measured repeatedly
- The statistical test(s) used AND whether they are one- or two-sided
Only common tests should be described solely by name; describe more complex techniques in the Methods section.
- A description of all covariates tested
- A description of any assumptions or corrections, such as tests of normality and adjustment for multiple comparisons
- A full description of the statistical parameters including central tendency (e.g. means) or other basic estimates (e.g. regression coefficient) AND variation (e.g. standard deviation) or associated estimates of uncertainty (e.g. confidence intervals)
- For null hypothesis testing, the test statistic (e.g. F , t , r) with confidence intervals, effect sizes, degrees of freedom and P value noted
Give P values as exact values whenever suitable.
- For Bayesian analysis, information on the choice of priors and Markov chain Monte Carlo settings
- For hierarchical and complex designs, identification of the appropriate level for tests and full reporting of outcomes
- Estimates of effect sizes (e.g. Cohen's d , Pearson's r), indicating how they were calculated

Our web collection on [statistics for biologists](#) contains articles on many of the points above.

Software and code

Policy information about [availability of computer code](#)

Data collection

Data processing was conducted using the statistical software R (version 3.6.3)

Data analysis

All analyses were conducted using R (version 3.6.3) and INLA (version 20.03, available from www.r-inla.org). The code is available at <http://globalenvhealth.org/code-data-download>.

For manuscripts utilizing custom algorithms or software that are central to the research but not yet described in published literature, software must be made available to editors/reviewers. We strongly encourage code deposition in a community repository (e.g. GitHub). See the Nature Research [guidelines for submitting code & software](#) for further information.

Data

Policy information about [availability of data](#)

All manuscripts must include a [data availability statement](#). This statement should provide the following information, where applicable:

- Accession codes, unique identifiers, or web links for publicly available datasets
- A list of figures that have associated raw data
- A description of any restrictions on data availability

Estimates of weekly excess deaths by country are available at <http://globalenvhealth.org/code-data-download/>. Input data on deaths, population and temperature are available from <http://globalenvhealth.org/code-data-download/>.

The datasets used in the study are publicly available from the following locations:

Deaths and population:

<https://www.abs.gov.au/AUSSTATS/abs@.nsf/DetailsPage/3303.0.55.004Jan%20-%20May%202020>

<https://population.un.org/wpp>

<https://ec.europa.eu/eurostat/data/database> (tables demo_r_mwk_05 and demo_pjangroup)

<https://www.ons.gov.uk/peoplepopulationandcommunity/birthsdeathsandmarriages/deaths/datasets/weeklyprovisionalfiguresondeathsregisteredinenglandandwales>
<https://www.ons.gov.uk/peoplepopulationandcommunity/populationandmigration/populationestimates/datasets/populationestimatesforukenglandandwalesscotlandandnorthernireland>
<https://www.istat.it/it/archivio/240401>
<https://www.stats.govt.nz/experimental/covid-19-data-portal>
<https://www.nrscotland.gov.uk/statistics-and-data/statistics/statistics-by-theme/vital-events/general-publications/weekly-and-monthly-data-on-births-and-deaths/deaths-involving-coronavirus-covid-19-in-scotland/related-statistics>

Gridded temperature and population estimates:
<https://www.ecmwf.int/en/forecasts/datasets/reanalysis-datasets/era5>
<https://sedac.ciesin.columbia.edu/data/collection/gpw-v4>

Field-specific reporting

Please select the one below that is the best fit for your research. If you are not sure, read the appropriate sections before making your selection.

Life sciences Behavioural & social sciences Ecological, evolutionary & environmental sciences

For a reference copy of the document with all sections, see nature.com/documents/nr-reporting-summary-flat.pdf

Behavioural & social sciences study design

All studies must disclose on these points even when the disclosure is negative.

Study description	We applied an ensemble of 16 Bayesian probabilistic models to vital statistics data on all-cause mortality, by age group and sex, to consistently and comparably estimate the total mortality impacts of the first wave of the Covid-19 pandemic, from mid-February to the end of May for 21 industrialised countries.
Research sample	<p>We included industrialised countries from Europe and the Pacific in the analysis if</p> <ul style="list-style-type: none"> • Their total population in 2020 was > 4 million. • They had up-to-date weekly data on all-cause mortality divided by age group and sex that extended through May 2020. • The time series of data went back at least to 2015. <p>We used data on deaths and population from Eurostat, Office for National Statistics, National Records of Scotland, UN, Australian Bureau of Statistics, Stats New Zealand, Istat. We used data on temperature from ERA5. Links to the publicly available datasets are listed in the Data Availability section.</p>
Sampling strategy	N/A (count of all deaths were used)
Data collection	We obtained data on deaths and population from Eurostat, UN, Office for National Statistics, National Records of Scotland and the Italian National Institute of Statistics. We obtained data on temperature from ERA5. Vasilis Kontis, Robbie M Parks, Theo Rashid and James E Bennett accessed, harmonised and analysed data.
Timing	We used data from 2010 to 2020.
Data exclusions	We excluded countries which did not meet our criteria described in the "Research sample" section, because they did not have sufficient data to reliably estimate model parameters. These countries were Estonia, Iceland, Latvia, Liechtenstein, Lithuania, Luxembourg and Montenegro.
Non-participation	N/A (we used population-level data on death counts and population numbers)
Randomization	Our study did not include individual participants and we did not carry out experiments. We used the entire available data on population and deaths.

Reporting for specific materials, systems and methods

We require information from authors about some types of materials, experimental systems and methods used in many studies. Here, indicate whether each material, system or method listed is relevant to your study. If you are not sure if a list item applies to your research, read the appropriate section before selecting a response.

Materials & experimental systems

- | | |
|-------------------------------------|------------------------------------------------------|
| n/a | Involvement in the study |
| <input checked="" type="checkbox"/> | <input type="checkbox"/> Antibodies |
| <input checked="" type="checkbox"/> | <input type="checkbox"/> Eukaryotic cell lines |
| <input checked="" type="checkbox"/> | <input type="checkbox"/> Palaeontology |
| <input checked="" type="checkbox"/> | <input type="checkbox"/> Animals and other organisms |
| <input checked="" type="checkbox"/> | <input type="checkbox"/> Human research participants |
| <input checked="" type="checkbox"/> | <input type="checkbox"/> Clinical data |

Methods

- | | |
|-------------------------------------|-------------------------------------------------|
| n/a | Involvement in the study |
| <input checked="" type="checkbox"/> | <input type="checkbox"/> ChIP-seq |
| <input checked="" type="checkbox"/> | <input type="checkbox"/> Flow cytometry |
| <input checked="" type="checkbox"/> | <input type="checkbox"/> MRI-based neuroimaging |