

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 our [Editorial Policies](#) 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

Visualization code: The code to visualize county- and state-level risk was written in R and used the R Shiny Package for map deployment. The input data was a county shapefile from the U.S. Census that included all 50 states, the District of Columbia, and Puerto Rico whose boundaries were generalized using the 'rmapshaper' package. This file was converted to a geojson file for faster drawing. The projection was relegated to a web Mercator standard instead of a traditional conic projection due to the constraints of the R package. New York City was agglomerated as a set of five counties in order to accommodate the New York Times' county level case data (New York Times, 2020a), which reported New York City as a single region. The risk value shown on the county-level map takes into account the county's new cases for the past 10 days, the user's chosen ascertainment bias (5 or 10) from a radio button, and the user's chosen case size from a slider with eight discrete increments (10, 25, 50, 100, 500, 1,000, 5,000, and 10,000). The map symbology was chosen as a univariate color ramp showing intensity in red, and allows for interactive zooming and panning. Upon hover, a pop up shows the county name and the likelihood (in terms of a percentage) that an individual at that event is infected with SARS-CoV-2.

Web application: The web application is built using the R-Shiny web development framework and deployed as a self-contained Docker container using the open-source shiny-server. Application containers are deployed to a fleet of servers hosted at Georgia Institute of Technology, with multiple application instances running on each. Users are load-balanced across instances using Nginx. All static data used in the application (e.g. map HTML files, data used for interactive plots) are automatically updated and distributed to each application instance.

Data Availability: Population demographics for US states and counties were obtained from the publicly available United States Census Bureau American Community Survey for 2018 (U.S. Census Bureau, 2019). State-level cases were obtained from CovidTracking.com – a project developed by Alexis Madrigal and colleagues at The Atlantic (The Atlantic Monthly Group, 2020). County-level cases were obtained from the New York Times github site (New York Times, 2020a).

Code availability: The website code is open source and available on Github: <https://github.com/appliedbinf/covid19-event-risk-planner>.

Data analysis

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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 and 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

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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](https://www.nature.com/documents/nr-reporting-summary-flat.pdf)

Life sciences study design

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

Sample size

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Data exclusions

N/A

Replication

N/A

Randomization

N/A

Blinding

N/A

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 | Included in the study |
| ☒ | ☐ Antibodies |
| ☒ | ☐ Eukaryotic cell lines |
| ☒ | ☐ Palaeontology and archaeology |
| ☒ | ☐ Animals and other organisms |
| ☒ | ☐ Human research participants |
| ☒ | ☐ Clinical data |
| ☒ | ☐ Dual use research of concern |

Methods

- | | |
|-------------------------------------|---|
| n/a | Included in the study |
| ☒ | ☐ ChIP-seq |
| ☒ | ☐ Flow cytometry |
| ☒ | ☐ MRI-based neuroimaging |