nature research

Corresponding author(s): Ilaria Dorigatti and Andrea Crisanti

Last updated by author(s): Jun 6, 2020

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	Data were collated using Microsoft Excel (version 16.16.6).
Data analysis	We developed code in the R programming language (version 3.6.0) using packages tidyr, dplyr, readr, janitor, lubridate, magrittr, ggplot2, plotly, htmlwidgets, epicontacts, igraph, GGally, epitrix, ggpubr, flextable, network, sna, scales, intergraph, cowplot, readxl, odin, stringr, ggrepel, gridExtra, sf, ggspatial and in Python (version 3.7.3) using modules scipy 1.4.1, numpy 1.18.1, and matplotlib 3.2.1. The code is available at https://github.com/ncov-ic/SEIR_Covid_Vo.

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

The dataset is available at https://github.com/ncov-ic/SEIR_Covid_Vo.

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

Life sciences study design

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

Sample size	Vo' has a resident population of 3,275 inhabitants. We collected nasopharyngeal swabs from 2,812 and 2,343 subjects in the first and second screening respectively, corresponding to 85.9% and 71.5% of the eligible population. No sample size calculation was performed, we aimed to recruit as many residents as possible.
Data exclusions	We excluded from the analysis the data collected on a small number of subjects, including 11 confirmed COVID-19 infections, who did not reside in Vo'.
Replication	Detection of SARS-CoV-2 RNA was performed by an in-house real-time RT-PCR method performed at the Clinical Microbiology and Virology Unit of Padova University Hospital, which is the Regional Reference Laboratory for emerging viral infections. The samples collected in the initial phase of the survey were validated by the National Reference Laboratory at the Italian Institute of Health (Istituto Superiore di Sanità) and demonstrated 100% agreement with the in-house assay. Given the 100% agreement on the samples collected in the initial phase and due to the large number of samples analyzed by the laboratory during the epidemic, we did not validate all samples collected in Vo' across the two surveys.
Randomization	Randomization is not relevant in our study, we aimed to enroll as many study participants as possible.
Blinding	Blinding is not relevant in our study, it was an observational study.

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	Involved 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	Involved in the study
☒	☐ ChIP-seq
☒	☐ Flow cytometry
☒	☐ MRI-based neuroimaging

Human research participants

Policy information about studies involving human research participants

Population characteristics	We collected information on sampling dates, results of SARS-CoV-2 testing, age, sex, symptoms, underlying health conditions, pharmacological therapy, hospitalization, household composition and contact network. The recruited subjects were between 1 month and 100 years of age and 49.9% were male and 50.1% were female. The underlying health conditions and pharmacological therapies of the recruited population at the time of the study are described in Supplementary Tables S3 and S4.
Recruitment	Study participation was by consent. For subjects under the age of 18 years, consent was provided by a parent or legal guardian. Participation in the study was publicized through local authorities. The age distribution of the recruited versus not recruited population was statistically different, as described in the main text and in Extended Data Figure 1.
Ethics oversight	The Ethics Committee for Clinical Research of the province of Padova approved the study.

Note that full information on the approval of the study protocol must also be provided in the manuscript.