

Reporting Summary

Nature Portfolio 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 Portfolio 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 <i>Only common tests should be described solely by name; describe more complex techniques in the Methods section.</i>
☒	☐ 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 <i>Give P values as exact values whenever suitable.</i>
☒	☐ 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	No software was used for data collection.
Data analysis	No commercial and open-source codes are used. Our team develops the Python code for analyzing the volume of patient visits and measuring system resilience and adaptivity. The code is provided at https://github.com/lucinezhong/healthcare_resilience_quantification_framework .

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 Portfolio [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 description of any restrictions on data availability
- For clinical datasets or third party data, please ensure that the statement adheres to our [policy](#)

The electronic medical record dataset that supports the findings of this study is available from the Healthjump database, provided by the COVID-19 Research Database consortium (<https://covid19researchdatabase.org/>). However, restrictions apply to the availability of these data, which were used under license for the current study. The EMR dataset is not publicly available.

The data on COVID-19 infection cases in each state is collected from the Johns Hopkins Coronavirus Resource Center (<https://github.com/CSSEGISandData/COVID-19>).

The general physician abundance data regarding physician numbers in each state is collected from the 2019 State Physician Workforce Data (<https://www.aamc.org/data-reports/workforce/report/state-physician-workforce-data-report>).

The social factors include poverty levels, unemployment rates, uninsured levels, the proportion of the youth (less than 17), the proportion of the elderly (greater than 65), and the proportion of minority populations are collected from the CDC/ATSDR Social Vulnerability Index (<https://www.atsdr.cdc.gov/placeandhealth/svi/index.html>).

For validation, external summary datasets on patient visits to physicians, emergency departments, and the number of hospital discharges during the pandemic are supplied by the National Center for Health Statistics (<https://www.cdc.gov/nchs/index.htm>) and the US Census Bureau (<https://www.census.gov/>).

Research involving human participants, their data, or biological material

Policy information about studies with [human participants or human data](#). See also policy information about [sex, gender \(identity/presentation\), and sexual orientation](#) and [race, ethnicity and racism](#).

Reporting on sex and gender

Use the terms sex (biological attribute) and gender (shaped by social and cultural circumstances) carefully in order to avoid confusing both terms. Indicate if findings apply to only one sex or gender; describe whether sex and gender were considered in study design; whether sex and/or gender was determined based on self-reporting or assigned and methods used.

Provide in the source data disaggregated sex and gender data, where this information has been collected, and if consent has been obtained for sharing of individual-level data; provide overall numbers in this Reporting Summary. Please state if this information has not been collected.

Report sex- and gender-based analyses where performed, justify reasons for lack of sex- and gender-based analysis.

Reporting on race, ethnicity, or other socially relevant groupings

Please specify the socially constructed or socially relevant categorization variable(s) used in your manuscript and explain why they were used. Please note that such variables should not be used as proxies for other socially constructed/relevant variables (for example, race or ethnicity should not be used as a proxy for socioeconomic status).

Provide clear definitions of the relevant terms used, how they were provided (by the participants/respondents, the researchers, or third parties), and the method(s) used to classify people into the different categories (e.g. self-report, census or administrative data, social media data, etc.)

Please provide details about how you controlled for confounding variables in your analyses.

Population characteristics

Describe the covariate-relevant population characteristics of the human research participants (e.g. age, genotypic information, past and current diagnosis and treatment categories). If you filled out the behavioural & social sciences study design questions and have nothing to add here, write "See above."

Recruitment

Describe how participants were recruited. Outline any potential self-selection bias or other biases that may be present and how these are likely to impact results.

Ethics oversight

Identify the organization(s) that approved the study protocol.

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

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

This study is a quantitative analysis that harnesses billions of electronic health records to assess the resilience and adaptability of healthcare systems during the COVID-19 pandemic. This quantitative framework aims to identify disruption timelines and evaluate system performance in delivering essential services such as chronic disease treatment and maternal care across various racial and ethnic population groups.

Research sample

The dataset utilized in this study comprises over one billion electronic medical records spanning the period from 2017 to 2022 across 50 US states. Among these records, approximately 30 millions contain ICD codes related to services for chronic illness treatment and maternal care. The breakdown of records by racial and ethnic groups is as follows: one million (0.5%) for Asian, twenty million (10.4%) for Black, twenty million (10.4%) for Hispanic, and one hundred and fifty million (78%) for White patients. The dataset also encompasses additional demographic attributes, such as age. It comprises three age groups: youth (0-19 years, 9%), middle-aged (19-60 years, 53%), and elderly individuals (60-100 years, 38%).

To compare the resilience and adaptivity index across states, along with their respective social factors such as poverty levels, unemployment rates, uninsured levels, proportions of youth (under 17), elderly (over 65), and minority populations, we gathered data from the CDC/ATSDR Social Vulnerability Index (SVI) available at <https://www.atsdr.cdc.gov/placeandhealth/svi/index.html>.

Sampling strategy

No sampling strategy is used for analysis.

Data collection	We collect monthly number of patient visits , their demographic information (e.g., race and ethnicity) , and the ICD-10 code in their diagnosis at each state from the Healthjump database. The Healthjump database collection relies on comprehensive integration of facilities that join EMR technology. Concerning personal demographic information, the database is committed to complying with all pertinent federal and state laws and adheres strictly to the Privacy Policy. It establishes agreements with healthcare providers to ensure the transfer of patient information to the database is in accordance with HIPAA (Health Insurance Portability and Accountability Act of 1996) regulations.
Timing	The data we studies is monthly data from 2017/01 to 2022/12.
Data exclusions	NONE
Non-participation	NONE
Randomization	Not relevant in this study. This study measures outcomes without any manipulation or intervention by researchers. When exploring the correlation between resilience and adaptivity index with social factors in each state, randomization is irrelevant.

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
☒	☐ Clinical data
☒	☐ Dual use research of concern
☒	☐ Plants

Methods

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

Plants

Seed stocks	Report on the source of all seed stocks or other plant material used. If applicable, state the seed stock centre and catalogue number. If plant specimens were collected from the field, describe the collection location, date and sampling procedures.
Novel plant genotypes	Describe the methods by which all novel plant genotypes were produced. This includes those generated by transgenic approaches, gene editing, chemical/radiation-based mutagenesis and hybridization. For transgenic lines, describe the transformation method, the number of independent lines analyzed and the generation upon which experiments were performed. For gene-edited lines, describe the editor used, the endogenous sequence targeted for editing, the targeting guide RNA sequence (if applicable) and how the editor was applied.
Authentication	Describe any authentication procedures for each seed stock used or novel genotype generated. Describe any experiments used to assess the effect of a mutation and, where applicable, how potential secondary effects (e.g. second site T-DNA insertions, mosaicism, off-target gene editing) were examined.