

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 (<i>n</i>) 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. <i>F</i> , <i>t</i> , <i>r</i>) with confidence intervals, effect sizes, degrees of freedom and <i>P</i> 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 <i>d</i> , Pearson's <i>r</i>), 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	We used the (then) Twitter API for data collection.
Data analysis	All of the analyses of the manuscript and SI (Figures, Tables, SRD, and DiD) used R version 4.3.1. I The data for analysis (merging subgroups and demographics with the user URL sharing activity) and the files with daily summaries (pct, average, and total) were prepared using Python 3.11.6. The code repository is publicly available at https://osf.io/ku8z4/

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 analyses presented in this paper were performed on user-level aggregates, with user IDs anonymized to preserve privacy. We make this data available as part of the replication package on OSF: <https://osf.io/ku8z4/>. The tweet-level data, and specific user demographics, cannot be publicly shared due to privacy concerns

arising from matching data to administrative records, data use agreements, and platforms' terms of service. Our replication materials include the code used to produce the aggregate data from the tweet-level data, and the tweet-level data can be accessed after signing a data-use agreement; contact author D.L. with access requests.

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	We use administrative data from voting records for reporting on sex in the Extended Data.
Reporting on race, ethnicity, or other socially relevant groupings	We use inferred race from the voter data vendor (TargetSmart) in the Extended Data.
Population characteristics	The population is US registered voters that have active accounts on Twitter (now X) whose accounts tweeted between 2014 and 2016, who are registered voters, and whose self-reported names and locations could be linked to a fall 2017 snapshot of a commercial voter file. Because of these inclusion characteristics, the sample of users in this paper is not representative of the US registered voting population.
Recruitment	We developed the sample by matching voter data to Twitter handles. The sample size is based on the number of matches we were able to make successfully. This sample has been used in various prior papers, with a careful examination of the biases that might exist in the sample as a result. We include references in the paper. There are 599,697 active users in our panel under this definition, who tweeted over 8 million URLs during the study period. The sample size was not determined by a prospective power analysis. However, the sample size is sufficient to make appropriate conclusions because the study is about the effects of deplatforming on misinformation on twitter, and generally for social science applications such as this the typical sample sizes for making inferences are on the order of 1,000 participants while we have over a half million.
Ethics oversight	Northeastern University IRB protocol #17-12-13.

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 is a quantitative study, involving times series analysis of posting on Twitter, with an evaluation of whether patterns changed after January 6, 2021.
Research sample	The population is US registered voters that have active accounts on Twitter (now X) whose accounts tweeted between 2014 and 2016, who are registered voters, and whose self-reported names and locations could be linked to a fall 2017 snapshot of a commercial voter file. Because of these inclusion characteristics, the sample of users in this paper is not representative of the US registered voting population.
Sampling strategy	We developed the sample by matching voter data to Twitter handles. The sample size is based on the number of matches we were able to make successfully. This sample has been used in various prior papers, with a careful examination of the biases that might exist in the sample as a result. We include references in the paper. There are 599,697 active users in our panel under this definition, who tweeted over 8 million URLs during the study period. The sample size was not determined by a prospective power analysis. However, the sample size is sufficient to make appropriate conclusions because the study is about the effects of deplatforming on misinformation on twitter, and generally for social science applications such as this the typical sample sizes for making inferences are on the order of 1,000 participants while we have over a half million.
Data collection	We used the Twitter API for data collection of the Twitter data; and used the voter administrative data for demographic information (mostly contained in analyses in the SM).
Timing	This was a rolling data collection that started in 2017, and ceased when Twitter shut down their APIs in the summer of 2023.
Data exclusions	We exclude 11 users that were deplatformed during the January 2021 terms of use intervention but had their accounts restored. Beyond that, we do not exclude data.
Non-participation	NA

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.