responses is likely to be 'tweakable' through judicious choice of vaccines. In general, extensive molecular studies of SARS-CoV-2 and neutralizing antibody responses will be of value should rational design strategies be needed to generate optimal vaccines[12].

Overall, we are optimistic, given the number of platforms being investigated and the huge ongoing efforts, that a vaccine (or vaccines) against COVID-19 with immune responses and protection superior to that achieved through natural infection is an achievable goal. ❐

Dennis R. Burton[1,2]✉ and Eric J. Topol[1,3]✉

[1]*The Scripps Research Institute, La Jolla, CA, USA.* [2]*Ragon Institute of MGH, Harvard and MIT, Cambridge, MA, USA.* [3]*Scripps Translational Research Institute, La Jolla, CA, USA.*
✉*e-mail: burton@scripps.edu; etopol@scripps.edu*

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Author contributions

D.R.B. and E.J.T. conceived of the idea and wrote the piece together.

Competing interests

The authors declare no competing interests.

Check for updates

Automated screening of COVID-19 preprints: can we help authors to improve transparency and reproducibility?

To the Editor—The COVID-19 pandemic has thrust preprints into the spotlight, attracting attention from the media and the public, as well as from scientists. Preprints are articles not yet published in a peer-reviewed journal, and as such they offer a unique opportunity to improve reporting. The Automated Screening Working Group (https://scicrunch.org/ASWG/about/COVIDPreprint) aims to provide rapid feedback that may help authors of COVID-19 preprints to improve their transparency and reproducibility.

One quarter of COVID-19 papers published have been preprints. Most of these appear on medRxiv; others appear on bioRxiv or other servers[1]. Although publishing results in preprints allows them to be posted rapidly, the absence of traditional peer review has raised concerns about preprint quality. Unfortunately, it has been impossible for scientists to keep pace with the thousands of COVID-19 preprints published since February. Preprints are vetted before posting to confirm that they describe scientific studies and to prevent posting on topics that could damage public health; however, routine assessment of manuscript quality or flagging of common reporting problems is not feasible at this scale.

Although automated screening is not a replacement for peer review, automated tools can identify common problems. Examples include failure to state whether experiments were blinded or randomized[2], failure to report the sex of participants[2] and misuse of bar graphs to display continuous data[3]. We have been using six tools[4–8] to screen all new medRxiv and bioRxiv COVID-19 preprints (Table 1). New preprints are screened daily[9]. By this means, reports on more than 8,000 COVID preprints have been shared using the web annotation tool hypothes.is (RRID:SCR_000430) and have been tweeted out via @SciScoreReports (https://hypothes.is/users/sciscore). Readers can access these reports in two ways. The first option is to find the link to the report in the @SciScoreReports tweet in the preprint's Twitter feed, located in the metrics tab. The second option is to download the hypothes.is bookmarklet. In addition, readers and authors can reply to the reports, which also contain information on solutions.

Screening of 6,570 medRxiv and bioRxiv COVID-19 preprints posted before 19 July revealed several interesting results. 13.6% of preprints shared open data and 14.3% shared open code, making it easier for others to reuse data or reproduce results. Approximately one third (34.4%) of COVID-19 preprints acknowledged at least one study limitation. 7.3% of preprints included bar graphs of continuous data. This is problematic because many different datasets can lead to the same bar graph, and the actual data may suggest different conclusions from those implied by the summary statistics alone[3]. Therefore, authors should use dot plots, box plots or violin plots instead[3]. Among papers with color maps, 7.6% used rainbow colormaps, which are not colorblind safe and also create visual artifacts for viewers with normal vision[7]. Rainbow color maps should be replaced with more-informative color maps that are perceptually uniform and colorblind accessible, such as viridis[7]. 1,775 preprints (27%) contained an ethics approval statement for human or animal research. This suggests that nearly three quarters of COVID-19 preprints are secondary or tertiary analyses, modeling studies or cell line studies that do not require approval. Although there are known sex differences in COVID-19[10], only 20% of all COVID-19 preprints, and 38% of preprints with an ethics approval statement, address sex as a biological variable. Statements regarding sample size calculations (1.4%), blinding (2.7%) and randomization (11.4%) were uncommon, even among studies that contained a human ethics statement (present in 2.4%, 5.4% and 12.6%, respectively). Many COVID-19 preprints are modeling studies, however, and hence these criteria

Table 1 | Tools used to screen COVID-19 preprints

Tool	Screens for	Link and RRID
SciScore[4]	Blinding, randomization, sample-size calculations, sex/gender, ethics and consent statements, resources, RRIDs	http://sciscore.com; RRID:SCR_016251
ODDPub[5]	Open data, open code	https://github.com/quest-bih/oddpub; RRID:SCR_018385
Limitation- Recognizer[6]	Author-acknowledged limitations	https://github.com/kilicogluh/limitation-recognizer; RRID:SCR_018748
Barzooka	Bar graphs of continuous data	https://quest-barzooka.bihealth.org; RRID:SCR_018508
JetFighter[7]	Rainbow color maps	https://jetfighter.ecrlife.org; RRID:SCR_018498
Seek and Blastn[8]	Correct identification of nucleotide sequences[a]	http://scigendetection.imag.fr/TPD52/; RRID:SCR_016625

[a]Semiautomated tool—requires human confirmation of results. RRID, research resource identifier.

are not always relevant. 6.1% of preprints used nonhuman organisms, mainly mice. Among the 552 preprints that included cell lines, 7% described how the cell lines were authenticated (e.g., short tandem repeat profiling) or were kept free of contamination (e.g., mycoplasma detection tests).

Our work shows that it is feasible to conduct large-scale automated screening of preprints and provide rapid feedback to authors and readers. Automated tools are not perfect—they make mistakes, and they cannot always determine whether a problem is relevant to a given paper. Moreover, some problems are too complex for automated tools to detect. Despite these limitations, automated tools can quickly flag potential problems and may complement peer reviews. We hope that these reports will raise awareness about factors that affect transparency and reproducibility, while helping authors to improve their manuscripts. Further research is needed to determine whether automated tools improve reporting. ❐

Tracey Weissgerber[1,2]✉, Nico Riedel[1], Halil Kilicoglu[3], Cyril Labbé[4], Peter Eckmann[5,6], Gerben ter Riet[7,8], Jennifer Byrne[9,10], Guillaume Cabanac[11], Amanda Capes-Davis[12], Bertrand Favier[13], Shyam Saladi[14], Peter Grabitz[1,2], Alexandra Bannach-Brown[1], Robert Schulz[1,2], Sarah McCann[1,2], Rene Bernard[15] and Anita Bandrowski[5,6]

[1]Quality | Ethics | Open Science | Translation (QUEST), Berlin Institute of Health, Berlin, Germany. [2]Charité–Universitätsmedizin Berlin, Berlin, Germany. [3]School of Information Sciences, University of Illinois at Urbana–Champaign, Champaign, IL, USA. [4]University Grenoble Alpes, CNRS, Grenoble INP, LIG, Grenoble, France. [5]Department of Neuroscience, University of California, San Diego, La Jolla, CA, USA. [6]SciCrunch Inc., San Diego, CA, USA. [7]Department of Cardiology, Amsterdam UMC, University of Amsterdam, Amsterdam, the Netherlands. [8]Urban Vitality Center of Expertise, Amsterdam University of Applied Sciences, Amsterdam, the Netherlands. [9]New South Wales Health Statewide Biobank, New South Wales Health Pathology, Sydney, New South Wales, Australia. [10]Faculty of Medicine and Health, University of Sydney, Sydney, New South Wales, Australia. [11]UMR 5505 IRIT, Université de Toulouse, UPS, Toulouse, France. [12]CellBank Australia, Children's Medical Research Institute and The University of Sydney, Westmead, NSW, Australia. [13]University Grenoble Alpes, TIMC UMR5525, La Tronche, France. [14]California Institute of Technology, Pasadena, CA, USA. [15]NeuroCure Cluster of Excellence, Charité–Universitätsmedizin Berlin, corporate member of the Freie Universität Berlin, Humboldt-Universität zu Berlin and Berlin Institute of Health, Berlin, Germany.
✉*e-mail: tracey.weissgerber@charite.de*

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