1   **Title:** Inter-rater reliability of the Infectious Disease Modeling Reproducibility Checklist

2   (IDMRC) as applied to COVID-19 computational modeling research

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22

23 **Abstract**

24

25 **Background:** Infectious disease computational modeling studies have been widely published

26 during the coronavirus disease 2019 (COVID-19) pandemic, yet they have limited

27 reproducibility. Developed through an iterative testing process with multiple reviewers, the

28 Infectious Disease Modeling Reproducibility Checklist (IDMRC) enumerates the minimal

29 elements necessary to support reproducible infectious disease computational modeling

30 publications. The primary objective of this study was to assess the reliability of the IDMRC and

31 to identify which reproducibility elements were unreported in a sample of COVID-19

32 computational modeling publications. **Methods:** Four reviewers used the IDMRC to assess 46

33 preprint and peer reviewed COVID-19 modeling studies published between March 13th, 2020,

34 and July 31st, 2020. The inter-rater reliability was evaluated by mean percent agreement and

35 Fleiss' kappa coefficients (κ). Papers were ranked based on the average number of reported

36 reproducibility elements, and average proportion of papers that reported each checklist item were

37 tabulated. **Results:** Questions related to the computational environment (mean κ = 0.90, range =

38 0.90–0.90), analytical software (mean κ = 0.74, range = 0.68–0.82), model description (mean κ =

39 0.71, range = 0.58–0.84), model implementation (mean κ = 0.68, range = 0.39–0.86), and

40 experimental protocol (mean κ = 0.63, range = 0.58–0.69) had moderate or greater (κ > 0.41)

41 inter-rater reliability. Questions related to data had the lowest values (mean κ = 0.37, range =

42 0.23–0.59). Reviewers ranked similar papers in the upper and lower quartiles based on the

43 proportion of reproducibility elements each paper reported. While over 70% of the publications

44 provided data used in their models, less than 30% provided the model implementation.

45 **Conclusions:** The IDMRC is the first comprehensive, quality-assessed tool for guiding

46 researchers in reporting reproducible infectious disease computational modeling studies. The

47   inter-rater reliability assessment found that most scores were characterized by moderate or

48   greater agreement. These results suggests that the IDMRC might be used to provide reliable

49   assessments of the potential for reproducibility of published infectious disease modeling

50   publications. Results of this evaluation identified opportunities for improvement to the model

51   implementation and data questions that can further improve the reliability of the checklist.

52   **Keywords:** Reproducibility, infectious disease, epidemiology, modeling, COVID-19,

53   coronavirus disease 2019

54   **Background**
55
56   Throughout the coronavirus disease 2019 (COVID-19) pandemic, policy makers relied

57   extensively on epidemiological, biostatistical, and computational infectious disease models to

58   inform decisions regarding public health interventions (1). Although there was increased interest

59   in transparent research prior to the pandemic (2), increasingly complex modeling methods and

60   frequently insufficiently detailed descriptions of those methods have led to increasing

61   reproducibility concerns. We recently proposed the Infectious Disease Modeling Reproducibility

62   Checklist (IDMRC) a comprehensive set of guidelines that researchers can follow to publish

63   reproducible modeling results (3). Our goal in this paper is to assess the reliability of the IDMRC

64   to facilitate the reporting of elements impacting the reproducibility of COVID-19 research.

65   Reproducibility is a cornerstone of the scientific method, enabling the verification of

66   discoveries and protecting against scientific misconduct (4). However, the rapid pace of COVID-

67   19 research has raised concerns about the reproducibility of modeling results. For years

68   governing bodies have published advice to enhance reproducibility of scientific research and

69   proposed lists of elements that should be included in publications to ensure reproducibility have

70   been reported (5–9). Prior to our work, these initiatives have not been synthesized into reliable

71   guidelines for infectious disease computational modeling research. We filled this critical gap in

72   the literature by creating a framework for the implementation of reproducible computational

73   infectious disease models. We formatted the framework into the Infectious Disease Modeling

74   Reproducibility Checklist (IDMRC), a checklist that is applicable to varying types of infectious

75   disease models with ranging complexities (3).

76   Previously developed guidelines, such as the Strengthening the Reporting of

77   Observational Studies in Epidemiology (STROBE) checklist and the EPIFORGE 2020

78   guidelines for epidemic forecasting have been instrumental in enhancing the quality of modeling

79   research (10,11). However, they focus on general recommendations for describing elements in a

80   publication without including specific items related to data, analytical software, operating

81   systems (including both names and version numbers), and other key computational components

82   used to conduct the analyses. The IDMRC overcomes these limitations through the inclusion of

83   specific items relevant to publishing reproducible infectious disease modeling studies. Here, we

84   assess the reliability of the IDMRC with multiple reviewers and a sample of COVID-19

85   computational modeling studies. To our knowledge, this is the first time the reliability of a

86   checklist used to assess the reproducibility of infectious disease modeling studies has been

87   evaluated.

88   The Models of Infectious Disease Agent Study (MIDAS) Coordination Center

89   (midasnetwork.us) is an NIGMS-funded center supporting the infectious disease research

90   community. Four researchers from the MIDAS Coordination Center evaluated the reliability of

91   the checklist by assessing a random selection of preprint and peer-reviewed COVID-19 modeling

92   papers published between March 13th, 2020, and July 31st, 2020. The purpose of this study was

93   to assess the inter-rater reliability of the IDMRC, characterize papers based on the reviewers'

94   qualitative rankings, and determine which reproducibility elements are frequently included or

95   overlooked in COVID-19 computational modeling studies.

96   **Methods**

97

98   The IDMRC was previously developed as a framework for the implementation of

99   reproducible computational infectious disease models (Additional File 1) (3). The IDMRC

100   consists of twenty-two questions grouped into six categories: computational environment,

101   analytical software, model description, model implementation, data, and experimental protocol

102   (Additional File 2). We evaluated the performance of the IDMRC in the COVID-19 modeling

103   literature by measuring the agreement among four reviewers for the overall instrument and for

104   individual questions. Based on the evaluations, we made suggested changes to the IDMRC

105   (Additional File 3).

106   We searched PubMed, medRxiv, arXiv, and bioRxiv using queries for COVID-19

107   modeling papers between March 13th, 2020, and July 31st, 2020 (Additional File 4). As preprint

108   servers were widely used to disseminate COVID-19 models at the beginning of the pandemic

109   (12), we included medRxiv, arXiv, and bioRxiv in our search. We dd not restrict to certain types

110   of computational modeling studies in our assessment given that our checklist should be

111   applicable to all computational infectious disease modeling studies ranging from regression

112   models to complex agent-based models. From the search results, we randomly selected 100

113   papers for title and abstract review (Figure 1).

114   Four researchers (DP, AAQ, KC, MM) used the IDMRC to independently review the 46

115   modeling papers to assess which IDMRC elements were included. All four reviewers had

116   experience in reading modeling papers, including training of at least a Master's in Public Health

117   Degree. DP and AAQ were involved with the development of the checklist and had more

118   experience using the IDMRC relative to KC and MM.

119   We performed an inter-rater reliability analysis to assess the concordance of the ratings of

120   the ordinal categorical items. Reliability was assessed based on the mean percent agreement with

121   Wald 95% confidence intervals and Fleiss' kappa (κ) estimates. Fleiss' kappa is the observed

122   agreement corrected for the agreement expected by chance and is appropriate when there are

123   more than two raters assessing ordinal or nominal data (13). We used the Power4Cats function in

124   the kappaSize package in R version 4.0.2, RStudio Version 1.3.107 to determine that 46

125   publications could reliably produce a lower limit for a kappa estimate of 0.293 (1). Fleiss' kappa

126   was computed with linear weights using the wlin.conc function in the R raters package 2.0.1

127   (14,15). Monte Carlo simulations were used to calculate percentile bootstrap confidence

128   intervals. Results were interpreted using previously published guidelines: $\kappa < 0.01$ indicates no

129   agreement; $\kappa = 0.01–0.20$, slight; $\kappa = 0.21–0.40$, fair; $\kappa = 0.41–0.60$, moderate; $\kappa = 0.61–0.80$

130   substantial; and $\kappa = 0.81–1$ almost perfect agreement (15). A kappa score below 0.41 falls into

131   the category of "slight" agreement and was deemed by the authors as indicative of questions that

132   needed to be reviewed and revised.

133   For each reviewer, we qualitatively ranked the papers by the number of reported elements

134   in each publication. Publications with the most elements included (as rated by the reviewers)

135   were ranked the highest. We also averaged the reviewers' rankings to report the average

136   qualitative rankings of the 46 publications. To assess if the potential impact of the peer-review on

137   the number of reproducibility elements, DP independently reviewed the five highest-rated and 5

138   lowest-rated publications to determine 1) if any of the publications that were published in

139   preprint servers at the time of the review had since been published in peer-reviewed journals, and

140   2) if the papers that had been published in peer-reviewed journals had reported more

141   reproducibility elements in those publications. Finally, we tabulated the proportion of papers that

142   reported each checklist element as well as the proportion of checklist elements reported in all

143   publications (both averaged across all reviewers).

144   **Results**

145   Four MIDAS researchers used the IDMRC to review 46 COVID-19 computational

146   modeling papers published between March 13th, 2020, and July 31st, 2020. After title and

147   abstract review, 48 papers were excluded based on the following exclusion criteria:

148   observational, genomic, immunological, and molecular studies, commentaries, reviews,

149   retractions, letters to editor, response papers, papers not related to COVID-19, and descriptions

150   of software applications. Of the remaining 48 papers, two publications reviewing previously

151   developed COVID-19 models were excluded after full text review (Figure 1). The final 46 paper

152   sample consisted of 39 (85%) publications published in preprint servers (n = 34 from medRxiv; n

153   = 5 from arXiv) and 7 (15%) from peer-reviewed journals (Additional File 5).

154   **[Figure 1.** Publications included in the inter-rater reliability analysis of the Infectious Disease
155   Modeling Reproducibility Checklist. *Abbreviations:* COVID-19, coronavirus disease 2019]
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157
158   *Inter-rater reliability of the IDMRC*

159
160   The inter-rater reliability evaluation indicated that the IDMRC was a reliable tool with

161   most questions characterized by moderate or better ($\kappa > 0.41$) agreement between the four

162   reviewers. Overall, the mean percent agreement ranged from 54% (data question 5.3) to 94%

163   (computational environment 1.1, 1.2; model implementation 4.6). Fleiss' kappa estimates ranged

164   from 0.23 (95%CI 0.10, 0.40) for IDMRC data question 5.5 to 0.90 (95%CI 0.79, 0.98) for both

165   computational environment questions. Several Fleiss' kappa estimates in the model

166   implementation and data categories fell below moderate agreement (Table 1).

167   **[Table 1.** Infectious Disease Modeling Reproducibility Checklist elements reported in COVID-
168   19 modeling papers.]
169

170   *Characterization of papers based on reviewer qualitative rankings*

171   Reviewers identified similar publications as reporting the most reproducibility elements

172   (i.e., reviewers reported "yes" for more questions) or the least number of elements (i.e.,

173   reviewers reported "yes" less often). KC and MM, the two reviewers with the least experience

174   using the IDMRC, agreed upon eight publications in the top 25% (n = 13) and the eight

175   publications in the bottom 25% (n = 13) (Additional File 6). DP and AAQ, the two reviewers

176   with more experience using the checklist, agreed on nine publications in the top 25% and ten

177   publications in the bottom 25% (Additional File 6). All four reviewers agreed on six publications

178   in the top 25% and seven publications were reported in the bottom 25% (Additional File 7). The

179   publications with the most reproducibility elements based on average scores (publications 9, 15,

180   16, 19, and 27) and the least reported reproducibility elements (2, 12, 20, 23, and 37) were all

181   originally published as preprints. Four publications (2, 19, 20, and 27) have since been published

182   in peer-reviewed journals. An independent review of these four papers by DP determined that the

183   peer-reviewed versions did not have a significantly increased number of reported reproducibility

184   elements.

185   **[Figure 2.** Average quantitative paper ranking (n = 46) among four reviewers. Green bars
186   correspond to the average number of reported elements in each publication ("yes" responses);
187   yellow indicates partially reported elements; red indicates not reported elements, gray indicates
188   not applicable responses.]
189

190   *Average proportion of papers that reported each checklist item*

191   Rates of inclusion of the 22 checklist elements varied from 2% of papers reporting the

192   operating system version (question 1.2) to 92% providing the model description in the journal or

193   publication as opposed to referencing a previously developed model (question 3.2, Figure 3A).

194   Fifty percent (n = 23) of publications provided less than 40% of all checklist categories (Figure

195   3B). Over 94% of studies did not provide either the name or the version of the operating system

196   used in their analysis (questions 1.2, 1.3, respectively) (Figure 3A). The analytical software name

197   (e.g., R, STATA, SAS) was provided in 62% of publications (question 2.1), but only 41% of the

198   software tools were openly accessible without a licensing fee (question 2.2). Most studies

199   provided the input data (70%; question 5.4); however, only 25% provided the model

200   implementation, or code, used to generate the data (question 4.1). Averaged across the raters,

201   over 50% of the publications provided all five data elements (questions 5.1−5.5), but less than

202   50% of the publications provided all six model implementation elements (questions 4.1−4.6).

203   Thirty-nine percent of publications provided the parameters used in their models (questions 6.1)

204   while 19% provided a clear explanation for how categories 1−5 were used together to create the

205   model results (question 6.2).

206   **[Figure 3.** Proportion of coronavirus disease 2019 (COVID-19) modeling publications (n = 46)
207   that reported each infectious disease modeling reproducibility checklist (IDMRC) component
208   elements. A, average percentage of papers that reported each checklist element; B, average
209   proportion of checklist elements that were reported in all publications. Dashed line in B indicates
210   the mean.]
211

212   **Discussion**
213
214   Improved reproducibility of infectious disease computational models will help

215   researchers efficiently build upon previous studies and accelerate the pace of scientific

216   advancements. We previously developed the Infectious Disease Modeling Reproducibility

217   Checklist (IDMRC) to enumerate the elements necessary to support reproducible infectious

218   disease computational modeling studies (3). Our evaluation indicated that the IDMRC is a

219   reliable tool with the majority of the inter-rater reliability estimates reporting moderate or greater

220   agreement between the four reviewers. Participating reviewers placed similar publications in the

221   top and bottom reproducibility score quantiles based on the number of elements missing in each

222   publication. The two experienced and the two novice checklist users had more similar rankings,

223   suggesting that formally training researchers to use the IDMRC prior to evaluating a study may

224   produce more consistent results. Furthermore, revisions to the checklist questions, primarily in

225   the model implementation and data sections, may increase reliability of future evaluations.

226   Our experience with the application of the checklist suggests that the question ordering

227   may have impacted reliability. The question regarding whether the model implementation

228   computer language was documented (question 4.4) may have received a lower score due to its

229   positioning after the analytical software name question (question 2.1). In most instances if a

230   publication reported the analytical software name (e.g., R, STATA), the model implementation

231   computer language would be evident (e.g., R uses R coding language, STATA uses STATA

232   coding language). However, occasionally the two may differ, such as when researchers use their

233   own developed software or utilize packages to develop scripts in languages that are not original

234   to the analytical software (e.g., writing Python scripts in R with the use of the *reticulate*

235   package). Additionally, if a reviewer had already selected "no" or "not applicable" for prior a

236   model implementation question (questions 4.1–4.3), the reviewer may have automatically

237   selected the same response for question 4.4 without independent thought to the question. Moving

238   the question from the model implementation section to the analytical software section (after

239   question 2.1) could improve the checklist reliability. We propose a revised version of the

240   checklist which includes question 4.4 directly after question 2.1 (Additional File 3).

241   Reliability assessments can also help highlight ambiguities in definitions commonly used

242   in infectious disease computational modeling literature. Lower κ estimates in the data section

243   may have been due to uncertainty regarding the definition of input data (question 5.1). For

244   example, some of the publications described susceptible-infected-recovered (SIR)

245   compartmental models which can be parametrized using input data, simulated data, or by

246   referencing previously reported parameters. In these situations, reviewers may have not

247   considered parameters as input data. To improve the reliability of the checklist, we defined input

248   data as "any data, including parameters, used to generate a model or initial conditions" in the

249   updated version of the checklist (Additional File 3). Furthermore, we originally included a "not

250   applicable" answer choice in question 5.1; however, after the reliability assessment, we deemed

251   that this answer choice was not warranted because a response of "yes" or "no" should capture all

252   possible answer choices. Thus, we removed the "not applicable" answer choice from question

253   5.1 in the newest version of the checklist (Additional File 3). Given that conditional nature of the

254   checklist questions (i.e., subsequent checklist questions are affected by prior responses),

255   including a definition of the input data as well as correcting the answer choices in question 5.1

256   could improve the reliability of the following data questions.

257   The computational environment, which comprises the operating system name and

258   version, was least reported. Failure to reproduce modeling studies, even if the data and code have

259   been made available, can be due to incompatibilities or specific requirements in the

260   computational environment (16). For example, SAS software is not compatible with the macOS

261   operating system unless it is run in a virtual machine. Software developed by the authors of a

262   given paper or analyses that require high-performance computing may also require specific types

263   of operating systems to be functional. We recommend including a short statement specifying the

264   name and version of the operating system in future infectious disease computational modeling

265   studies .

266   Two of the top qualitatively ranked publications (19 and 27) as well as two of the lower

267   ranked publications (2 and 20) were initially published in medRxiv, during the time of review,

268   but have since been published in peer reviewed journals. An independent review by DP indicated

269   that the peer reviewed versions of these paper did not include significant improvement in the

270   number of reported reproducibility elements. This suggests that the peer review process does not

271   necessarily improve the reproducibility of papers in our sample. Despite an increase in the

272   adoption of data and code sharing policies by journals, stricter application of the IDMRC or

273   similar guidelines may be needed to further improve reproducibility during the peer review

274   process (17). Some suggestions include the complementary submission of checklists, such as the

275   IDMRC, or dynamic computational notebooks (17,18).

276   Over 70% of the publications provided the data used for their analysis. Our estimate was

277   similar to the 60% (n = 29) of CDC-compiled COVID-19 modeling studies analyzed by Jalali et

278   al. and much higher than the 24.8% (n = 332) reviewed by Ioannidis et al. that reported to share

279   their data. However, Ioannidis et al., used a text mining algorithm which may not have picked up

280   publications that shared their data (19,20). Many journals now require researchers to provide a

281   data availability statement when submitting a publication but allow researchers to

282   circumnavigate the provision by stating "the datasets and code are available from the

283   corresponding author on reasonable request." Some publishers require authors to make their

284   publication data publicly available (21). As of January 25, 2023, National Institute of Health-

285   supported research requires researchers to include a plan for data sharing within their funding

286   applications. While our review included publications published on preprint servers, which have

287   less strict reporting guidelines, we reason that preprint COVID-19 computational models should

288   have been just as transparent with their data as peer-reviewed publications given their

289   widespread use by policymakers and news outlets during the start of the pandemic (12).

290   Although providing data access is becoming a common practice in infectious disease

291   computational studies, progress in sharing model implementations is lagging. In our sample,

292   most papers provided the model description; however, the code used to implement the model and

293   create the results was reported in less than 25% of the studies. In the previous review of COVID-

294   19 computational modeling studies, researchers found that a similar 21.5% of publications

295   reported the code (n = 288) (20). With increasingly complex computational methodologies in

296   infectious disease modeling literature, withholding the exact data manipulation and analysis steps

297   can impede the consistent regeneration of modeling results. Researchers should aim to provide

298   open-source access to appropriately versioned model implementations accompanied by

299   comprehensible annotations in online repositories.

300   Sharing a reproducible model consists of more than just sharing the data or code. Each

301   component in the checklist works together to produce the final modeling result. With each

302   additional missing component, the time and effort that it takes for future reproduction attempts

303   increases (22). Amid a pandemic, timely, reproducible research is critical in informing policies

304   and life-saving interventions.

305   The present study has several limitations. First, we sampled COVID-19 computational

306   modeling studies published early in the pandemic when authors may have reported fewer

307   reproducibility elements compared to publications published in later periods. In future work,

308   assessing the reproducibility of publications reported during various stages of the pandemic may

309   lead to insights regarding timing of publications and reproducibility of modeling literature.

310   Second, given that two of the reviewers had limited experience using the IDMRC prior to the

311   assessment, we may have underestimated the true reliability of the IDMRC. Furthermore,

312   differences in reviewer experience may have led to an under- or over-estimation of the average

313   number of reported reproducibility elements in our sample of publications. Finally, while the

314   reliability assessment of the IDMRC goes a step beyond most checklists, we did not assess the

315   reliability of the proposed changes to the IDMRC.

316   **Conclusions**

317   Our review focused on evaluating the performance of the IDMRC in COVID-19

318   computational modeling publications. Additional rounds of review with more reviewers and

319   modeling studies outside of COVID-19 might generalize reliability. Furthermore, lower inter-

320   rater reliability scores on some of the elements may have impacted the reported frequencies of

321   missing reproducibility elements. To address these issues, we proposed a revised version of the

322   IDMRC. Tools such as the IDMRC can encourage the documentation and sharing of all elements

323   necessary to reproduce a computational modeling study, thus supporting reproducible

324   computational infectious disease studies and accelerating scientific discoveries by allowing

325   others to validate results as well as by providing resources that might be reused in future studies.

326   **Declarations**

327   **Availability of data and materials**

328   All data generated or analyzed during this study are included in this published article and its

329   supplementary information files.

Authors' contributions

Conceptualization: DP, BC, WVP; Methodology: DP, BC, WVP; Software: DP; Validation: DP;

Formal analysis: DP; Investigation: DP, BC, WVP, AAQ, MM, KC; Data curation: DP; Writing

– original draft: DP, BC, WVP; Writing – review & editing: DP, BC, WVP, HH, MH, AAQ,

MM, KC, MR; Visualization: DP, BC, WVP, HH; Supervision: BC, WVP, HH; Project

administration: WVP, HH; Funding acquisition: WVP

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403

404   **Table 1.** Infectious Disease Modeling Reproducibility Checklist elements reported in COVID-19
405   modeling papers.

Question	Mean Percent Agreement (95% CI)	Fleiss Kappa (95% CI)
Computational Environment		
1.1) Is the operating system documented?	0.94 (0.87, 1.00)	0.90 (0.81, 0.97)
1.2) Is the operating system version documented?	0.94 (0.87, 1.00)	0.90 (0.79, 0.98)
Analytical Software		
2.1) Is the name of the analytical software documented (e.g., the programming language name)?	0.88 (0.79, 0.97)	0.82 (0.71, 0.92)
2.2) Is the analytical software accessible for free?	0.82 (0.71, 0.93)	0.68 (0.54, 0.81)
2.3) Is the version of the analytical software documented?	0.79 (0.67, 0.90)	0.75 (0.64, 0.85)
2.4) Do the authors include a specific identifier (DOI, URL, citation) that points to the analytical software that was used?	0.76 (0.64, 0.89)	0.72 (0.61, 0.81)
2.5) Is the analytical software installation guide accessible online?	0.89 (0.80, 0.98)	0.75 (0.60, 0.89)
Model Description		
3.1) Is the complete, structured model description provided in the publication, supplement, or referenced publication?	0.53 (0.38, 0.67)	0.58 (0.51, 0.66)
3.2) Is the model specified in the publication or supplement (contrary to being referenced in other papers)?	0.91 (0.83, 0.99)	0.84 (0.70, 0.94)
Model Implementation ("Code")		
4.1) Is the model implementation (e.g., code, workflow) openly accessible online?	0.86 (0.75, 0.96)	0.86 (0.77, 0.94)
4.2) Does the model implementation (e.g., code, workflow) have a version or modification date?	0.84 (0.73, 0.94)	0.69 (0.55, 0.84)
4.3) Does the model implementation (e.g., code, workflow) have an identifier?	0.79 (0.67, 0.90)	0.74 (0.62, 0.85)
4.4) Is the computer language of the model implementation (e.g., code, workflow) documented?	0.62 (0.48, 0.76)	0.39 (0.22, 0.54)
4.5) Are all model implementation (e.g., code, workflow) dependencies clearly specified in either the publication or supplemental files?	0.69 (0.56, 0.83)	0.63 (0.50, 0.75)
4.6) Are the model implementations (e.g., code, workflow) annotated with comments?	0.94 (0.87, 1.00)	0.80 (0.66, 0.92)
Data		
5.1) Does the model in the publication use input data?	0.75 (0.62, 0.87)	0.59 (0.47, 0.70)
5.2) Has the source and content of the input data been described in the publication or supplement?	0.59 (0.45, 0.74)	0.36 (0.20, 0.52)
5.3) Does the paper cite a specific, unique, and persistent identifier to refer to	0.54 (0.39, 0.68)	0.36 (0.20, 0.52)

each input dataset?

5.4) Is the input data openly accessible?	0.66 (0.52, 0.80)	0.34 (0.16, 0.52)
5.5) Is the data in a format that can be easily re-formatted (or "parsable") to meet the input specifications of the model implementation?	0.55 (0.41, 0.69)	0.23 (0.10, 0.40)

Experimental Protocol

6.1) Are all the mentioned parameter values for the model implementation (e.g., code, workflow) documented in a single location (e.g., table or list in the publication or supplement)?	0.65 (0.51, 0.79)	0.69 (0.60, 0.77)
6.2) Is there an explanation of how the described/mentioned categories (computational environment, analytical software, model implementation, and data) were used together to create the results (e.g., figures and/ or tables)?	0.50 (0.36, 0.64)	0.58 (0.52, 0.64)

406   *Abbreviations:* CI, confidence intervals