Reports Summary

Anand Rampadarath (Ph.D),
email:a.rampadarath@auckland.ac.nz

N.B. This document lists the

MIT Model

10 Simple Rules for Credible practice of Modeling and Simulation	Conformance Level	Comments	Summary Comments and Overall conformance
Define context clearly	Extensive	- A critical tool for COVID-19 planning is charting out the progression of the pandemic across the United States and the world.	MIT's epidemiologically based DELPHI model is disseminated broadly and provides links to model descriptions and data sources from their project website. The codes utilized in the research are accessible to the public via a github repository and the model limitations are adequately described. Overall conformance level: Partial/Adequate **Overall conformance level: Adequate/Extensive** **Overall conformance level: Extensive (update)**
Use appropriate data	Extensive	- Country-level projections are modelled based on all historical data to increase the accuracy of future predictions. - Data is aggregated over 100 published clinical studies and preprints released between December 2019 and March 2020. - **Declaration of collaborators and partner institutions that provide data and insights to model development team**	
Evaluate within context	Unable to determine	- These require detailed knowledge of model needed for validation, verification, uncertainty quantification and sensitivity analysis, however for Code verification: The codes reflect the model equations found in the documentation	
List limitations explicitly	Adequate	- Differences between JHU map and MIT cases reported - Total counts only account for countries in which we have sufficient data and where the pandemic is currently active. - Limitation explicitly stated in the paper	
Use version control	**Extensive (update)**	- **Extensive documentation on differences between versions and updates.** - Model codes are available on Github:https://github.com/COVIDAnalytics/DELPHI	
Document adequately	**Extensive(update)**	- Code not well commented, but understandable. **update: Code documentation significantly improved, possible independent implementation possible** - Model documentation contains the system of equations and rates. -**Code is well documented and there are detailed instructions on how to reproduce the results**	
Disseminate broadly	Extensive	- Model results regularly published with interactive graphics. - Results, data, models and simulations are all available to the public and scientific community.	
Get independent reviews	Insufficient/**Partial**	- No scientific paper is reported to be submitted to an arXIv or journal for review. **Paper uploaded to medRxiv:** https://doi.org/10.1101/2020.06.23.20138693	
Test competing implementations	Unable to determine	- No information provided	
Conform to standards	Partial	- Codes are written in python and Mathematica. **update: data provided in csv format.**	

IHME Model

10 Simple Rules for Credible practice of Modeling and Simulation	Conformance Level	Comments	Summary Comments and Overall conformance
Define context clearly	Extensive	- IHME's COVID-19 projections were developed in response to requests from the University of Washington School of Medicine and other US hospital systems and state governments working to determine when COVID-19 would overwhelm their ability to care for patients	IHME uses a hybrid real-time data driven modeling approach which combines both a statistical and disease transmission approach. However this effort is without any assumptions about the spread of the disease. Regular reports are disseminated on their website and a scientific paper was submitted to medaRxiv for peer review. The source code for the curve fitting tool utilized in this work is available on a github repository. Overall conformance: Partial/Adequate **Overall conformance: Adequate** **Overall conformance level: Adequate/Extensive**
Use appropriate data	Extensive	- data from local and national governments, hospital networks and associations, the World Health Organization, third-party aggregators, and a range of other sources. - Johns Hopkins University (JHU), French governmental dashboard, Colorado's Department of Public Health and Environment website, Illinois's Department of Health COVID-19 website, the New York City Department of Health and Mental Hygiene website, and the New York Times GitHub repository. - The COVID 19 project:https://covidtracking.com/data	
Evaluate within context	Unable to determine	These require detailed knowledge of model needed for validation, verification, uncertainty quantification and sensitivity analysis	
List limitations explicitly	Partial	- The model and data analysis are described in the model FAQ's, however limitations of the model and data analysis are not explicitly stated.	
Use version control	Partial **Adequate/Extensive (update)**	- The codes for the curve fitting tool are available on Github:**(Depreciated)** https://github.com/ihmeuw-msca/CurveFit - **The codes being used have been moved to: https://github.com/ihmeuw/covid-model-seiir and https://github.com/ihmeuw/covid-model-seiir-pipeline**	
Document adequately	Adequate	- Their scientific paper describes the analysis of the curve fit procedure used in their model. They include descriptions of the functional forms of the death rate of COVID-19 as well as specifications of parameters, constraints and uncertainties used in the model. - **The code and FAQ suggest that they use disease transmission models as well, however no mathematical description of their hybrid model is presented**	
Disseminate broadly	Adequate/**Extensive**	- Model results regularly published with interactive graphics. - **Interactive graphs show different prediction scenarios and they are clearly described**	
Get independent reviews	Partial/**Adequate Extensive (update)**	- A scientific paper was published on https://www.nature.com/articles/s41591-020-1132-9 - A scientific paper was uploaded to medRxiv preprint: https://doi.org/10.1101/2020.04.21.20074732	
Test competing implementations	Unable to determine	- No information provided	
Conform to standards	Partial	- The curvefit tool is written in python (**Depreciated**) - **The SEIIR model is written in python however has not yet been configured for use outside the IHME infrastructure.**	

Columbia University model:

10 Simple Rules for Credible practice of Modeling and Simulation	Conformance Level	Comments	Summary Comments and Overall conformance
Define context clearly	**Extensive**	- county-level demand for severe COVID-19 cases and supply estimates of hospital critical care beds, including ICU beds and other hospital beds that could be made available for critical care. - **clear description of different models** **- improved descripton of purpose of the interactive tool**	Columbia University uses an epidemiologically based metapopulation model with data extracted from publicly accessible US data sources for its parameter estimations. The results are regularly updated on the website and past projections are available for download in csv format from the project's github repository. A scientific paper has been published in Science detailing the model initialization and analysis, and further model description and methodology can be obtained from links on the website. Overall conformance: Adequate **Overall conformance: Adequate/Extensive** **Overall conformance: Extensive**
Use appropriate data	Extensive	- Several datasets, including four primary sources of data were used: (1)the 2020 Centers for Medicare & Medicaid Services (CMS), Health Care Information System (HCRIS) Data File, Sub-System Hospital Cost Report (CMS-2552-96 and CMS-2552-10), Section S-3, Part 1, Column 2; (2)the 2018 American Hospital Association (AHA) Annual Survey;(3)the 2020 US DHHS Health Resources and Services Administration,Area Health Resources Files (AHRF); and (4)the 2017-2019CMS Medicare Provider of Services file, Medicare Cost Report, Hospital Compare Files.	
Evaluate within context	Unable to determine	- These require detailed knowledge of model needed for validation, verification, uncertainty quantification and sensitivity analysis	
List limitations explicitly	Adequate	- Interpretation considerations are reported in the Methodology live document: https://behcolumbia.files.wordpress.com/2020/05/yamana_etal_reopening_projections.pdf	
Use version control	Adequate	- Projection results are available on the github page:https://github.com/shaman-lab/COVID-19Projection	
Document adequately	Adequate	- Methodolgy and model description can be found at : https://behcolumbia.files.wordpress.com/2020/05/yamana_etal_reopening_projections.pdf - Initial methods for website maps after detailed in https://behcolumbia.files.wordpress.com/2020/04/flattening-the-curve-before-it-flattens-us-20200405b.pdf	
Disseminate broadly	Adequate/**Extensive**	- Model results regularly published with interactive graphics. - **state-based projections can be viewed at** https://cuepi.shinyapps.io/COVID-19/	
Get independent reviews	Extensive	- A scientific paper has been published in Science detailing the model initialization and analysis: https://science.sciencemag.org/content/sci/368/6490/489.full.pdf	
Test competing implementations	Unable to determine	- No information provided	
Conform to standards	Partial	- Data is stored as csv files on github	

Northeastern University

10 Simple Rules for Credible practice of Modeling and Simulation	Conformance Level	Comments	Summary Comments and Overall conformance
Define context clearly	Extensive	- use real-world data to perform in-silico simulations of the spatial spread of infectious diseases at the global level. - analyze the spatiotemporal spread and magnitude of the COVID-19 epidemic in the continental US.	Northeastern University's GLEAM model of COVID 19 is an individual-based, stochastic and spatial epidemic model which utilizes real-world data obtained from the Offices of Statistics of 30 countries in its simulations. Model limitations are clearly presented in the supporting documents submitted to the journal Science as well as in the model definition link on the website. Model results are regularly published with interactive graphics however there are no links to public repositories where source codes or results can be obtained. Overall conformance: Partial/Adequate **Overall conformance: Adequate.** **No change in conformance.**
Use appropriate data	Adequate/**Extensive**	- databases collected from the Offices of Statistics of 30 countries on five continents. The full dataset includes more than 80,000 administrative regions and over five million commuting flow connections between them - **Regularly updated with new publicly available data**	
Evaluate within context	Unable to determine	- These require detailed knowledge of model needed for validation, verification, uncertainty quantification and sensitivity analysis	
List limitations explicitly	Adequate	- Limitations are clearly presented in the supporting documents and disclaimers are cearly stated on the live webpage	
Use version control	Insufficient	- No links to any repository presented	
Document adequately	Extensive	- The calibration, analysis and dynamics of the model are all documented https://science.sciencemag.org/content/368/6489/395,	
Disseminate broadly	Adequate/**Extensive**	- Model results regularly published with interactive graphics. - **General GLEAM model is available at http://www.gleamviz.org/** **- US calibrated model is describes here:Modeling of COVID-19 in the United States1Modeling of COVID-19 epidemic in the United States**	
Get independent reviews	Adequate	- The calibration of the global model for COVID-19 is reported in Science. - The model description is also published: https://science.sciencemag.org/content/368/6489/395	
Test competing implementations	Unable to determine	- No information provided	
Conform to standards	Insufficient	- No information provided	

Imperial College US model

10 Simple Rules for Credible practice of Modeling and Simulation	Conformance Level	Comments	Summary Comments and Overall Conformance
Define context clearly	Adequate/**Extensive**	- Estimates the effective number of infections individuals, the current rate of transmission, total number of people who have been infected and the impact of changes in mobility on the rate of transmission in the absence of additional interventions	Imperial College's US-state-level tracking utilizes a bayesian model to estimate the past and present transmission rates. Effects are shared across all states, but individual effects are also included for state- and region-specific effects. Daily real-time state-level aggregated data is used and key assumptions and model properties are discussed in the Report 23. The model source code is available on the Github repository
Use appropriate data	Partial/**Extensive**	- Our model uses daily real-time state-level aggregated data published by New York Times (NYT) for New York State and John Hopkins University (JHU) for the remaining states.	
Evaluate within context	Unable to determine	- These require detailed knowledge of model needed for validation, verification, uncertainty quantification and sensitivity analysis	
List limitations explicitly	Adequate	- Key assumptions and model properties are defined on the webpage and limitations associated with the data acquisition and model behaviour is discussed in Report 23 https://www.imperial.ac.uk/mrc-global-infectious-disease-analysis/covid-19/report-23-united-states/	
Use version control	Extensive	- Model source code is available on github at: https://github.com/ImperialCollegeLondon/covid19model	

Document adequately	Adequate/**Extensive** **Extensive**	- A detailed report on the US state-level tracking of COVID-19 has been published. - Codes with documentations and instructions are available on github	and is written in R and python. Overall Conformance: Partial/Adequate **Data up to 20/07/2020 has been used in their US predictions. No indication if this will be updated in the future.** **Overall Conformance: Adequate/Extensive** **Overall Conformance: Extensive**
Disseminate broadly	Adequate/**Extensive**	- There are links to the technical published report at the end of the webpage where model results are published. - Detailed report is available on Imperial college's website: https://www.imperial.ac.uk/mrc-global-infectious-disease-analysis/covid-19/report-23-united-states/	
Get independent reviews	Adequate/Extensive **Extensive**	- Although the report has been produced, there is no information on whether this was peer reviewed. However the model is used for a Europe-based publication which has been independedly reviewved and published in Nature: https://doi.org/10.1038/s41586-020-2405-7 - US based model has been published in Science: https://science.sciencemag.org/content/early/2021/02/01/science.abe8372	
Test competing implementations	Unable to determine	- No information provided	
Conform to standards	Partial	- Model is written in R and python	

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