THE LANCET Digital Health

Supplementary appendix 2

This appendix formed part of the original submission and has been peer reviewed. We post it as supplied by the authors.

Supplement to: Rasmy L, Nigo M, Kannadath BS, et al. Recurrent neural network models (CovRNN) for predicting outcomes of patients with COVID-19 on admission to hospital: model development and validation using electronic health record data. *Lancet Digit Health* 2022; published online April 21. https://doi.org/10.1016/ S2589-7500(22)00049-8**.**

PROBAST

(Prediction model study Risk Of Bias Assessment Tool)

Published in Annals of Internal Medicine (freely available):

- 1. PROBAST: A Tool to Assess the Risk of Bias and [Applicability](https://annals.org/aim/fullarticle/2719961/probast-tool-assess-risk-bias-applicability-prediction-model-studies) of Prediction Model [Studies](https://annals.org/aim/fullarticle/2719961/probast-tool-assess-risk-bias-applicability-prediction-model-studies)
- 2. PROBAST: A [Tool to Assess Risk of Bias and Applicability](https://annals.org/aim/fullarticle/2719962/probast-tool-assess-risk-bias-applicability-prediction-model-studies-explanation) of Prediction Model Studies: Explanatio[n](https://annals.org/aim/fullarticle/2719962/probast-tool-assess-risk-bias-applicability-prediction-model-studies-explanation) and [Elaboration](https://annals.org/aim/fullarticle/2719962/probast-tool-assess-risk-bias-applicability-prediction-model-studies-explanation)

What does PROBAST assess?

PROBAST assesses both the *risk of bias* and *concerns regarding applicability* of a study that evaluates (develops, validates or updates) a multivariable diagnostic or prognostic prediction model. It is designed to assess primary studies included in a systematic review.

Bias occurs if systematic flaws or limitations in the design, conduct or analysis of a primary study distort the results. For the purpose of prediction modelling studies, we have defined *risk of bias* to occur when shortcomings in the study design, conduct or analysis lead to systematically distorted estimates of a model's predictive performance or to an inadequate model to address the research question. Model predictive performance is typically evaluated using calibration, discrimination and sometimes classification measures, and these are likely inaccurately estimated in studies with high risk of bias. *Applicability* refers to the extent to which the prediction model from the primary study matches your systematic review question, for example in terms of the participants, predictors or outcome of interest.

A primary study may include the development and/or validation or update of more than one prediction model. A PROBAST assessment should be completed for each distinct model that is developed, validated or updated (extended) for making individualised predictions. Where a publication assesses multiple prediction models, only complete a PROBAST assessment for those models that meet the inclusion criteria for your systematic review. Please note that subsequent use of the term "model" includes derivatives of models, such as simplified risk scores, nomograms, or recalibrations of models.

PROBAST is not designed for all multivariable diagnostic or prognostic studies. For example, studies using multivariable models to identify predictors associated with an outcome but not attempting to develop a model for making individualised predictions are not covered by PROBAST.

PROBAST includes four steps.

If this is your first time using PROBAST, we strongly recommend reading the detailed explanation and elaboration (E&E, see link above) paper and to check the examples on www.probast.org

Step 1: Specify your systematic review question

State your systematic review question to facilitate the assessment of the applicability of the evaluated models to your question. *The following table should be completed once persystematic review.*

Step 2: Classify the type of prediction model evaluation

Use the following table to classify the evaluation as model development, model validation or model update, or combination. Different signalling questions apply for different types of prediction model evaluation. If the evaluation does not fit one of these classifications then PROBAST should not be used.

This table should be completed once for each publication being assessed and for each relevant outcome in vour review.

Step 3: Assessrisk of bias and applicability

PROBAST is structured as four key domains. Each domain is judged for risk of bias (low, high or unclear) and includes signalling questions to help make judgements. Signalling questions are rated as yes (Y), probably yes (PY), probably no (PN), no (N) or no information (NI). All signalling questions are phrased so that "yes" indicates absence of bias. Any signalling question rated as "no" or "probably no" flags the potential for bias; you will need to use your judgement to determine whether the domain should be rated as "high", "low" or "unclear" risk of bias. The guidance document contains further instructions and examples on rating signalling questions and risk of bias for each domain.

The first three domains are also rated for concerns regarding applicability (low/ high/ unclear) to your review question defined above.

Complete all domains separately for each evaluation of a distinct model. Shaded boxes indicate where signalling questions do not apply and should not be answered.

DOMAIN 2: Predictors

A. Risk of Bias

List and describe predictors included in the final model, e.g. definition and timing of assessment: we propose a time-aware deep learning model to predict COVID-19 patients outcomes that require minimal data preprocessing. We used patient data available within the EHR on and before the day of admission and trained recurrent neural network (RNN) models to predict the future risk of three outcomes: in-hospital mortality, need for mechanical ventilation, and long length of stay (LOS >7 days). Our models were developed and validated using a 247,960 patients cohort from 87 health systems from Cerner Real World Dataset (CRWD). The transferability of our model was validated using 36,140 patients from OPTUM.

Rationale of biasrating:

Used a valid approach utilizing retrospective data, and means to prevent bias, measure outcomes, and analyze and report results.

*O*ur proposed model was based on a gated type of recurrent neural networks (RNN), a sequential deep learning architecture, namely gated recurrent unit (GRU). Our model was designed to consume all diagnoses, medications, laboratory results, and other clinical events information readily available in the EHR before or on the index date to predict the patient outcomes, without any need for specific feature selection or missing values imputation, for convenience and practicality. Our proposed model considered the temporal nature of patient history and gave more weight for most recent events compared to distant events that happened years ago. Furthermore, for iMort and mVent prediction tasks, we trained both survival and **B. Applicability**

Rationale of applicability rating:

Predicting patient outcomes in patients with COVID-19 in an early stage is a critical need.

DOMAIN 3: Outcome

A. Risk of Bias

Describe the outcome, how it was defined and determined, and the time interval between predictor assessment and outcome determination:

Our experiments showed that our GRU based models trained on large heterogeneous dataset of around 200,000 COVID-19 patients required minimum data curation to achieve high prediction accuracy (AUC: 97- 86%) for different patient clinical outcomes, namely iMort, mVent and pLOS. Our models were not only showing high prediction accuracy but it demonstrated good transferability between two large deidentified EHR databases with different structures, good external validity, proper model calibration, and the utility of fine-tuning for continuous improvement. Our model was trained and evaluated on larger multicenter cohorts from two large well-known de-identified EHR databases in the U.S. (A total of more than 300,000 patients) . The study was able to transfer the model between two completely different datasets that have some differences especially in clinical codes distributions. With a simple model fine-tuning step on a sample data from the destination dataset the model consistently achieved high prediction accuracy $\frac{1}{2}$

3.6 Was the time interval between predictor assessment and outcome determi Nation Yes appropriate?

Risk of biasintroduced by the outcome or its determination RISK: Low

(low/ high/ unclear)

Rationale of biasrating:

Efforts to reduce Bias include separating train, validation, and test datasets as well as external validation on a different data source.

B. Applicability

At what time point wasthe outcome determined:

Our experiments showed that our GRU based models trained on large heterogeneous dataset of around 200,000 COVID-19 patients required minimum data curation to adhieve high prediction accuracy (AUC: 97-86%) for different patient clinical outcomes, namely iMort, mVent and pLOS. Our models were not only showing high prediction accuracy but it demonstrated good transferability between two large deidentified EHR databases with different structures, good external validity, proper model calibration, and the utility of finetuning for continuous improvement. Additionally, We used integrated gradients to provide clinicians with a utility to understand the model predicted scores. Timing?

Concern that the outcome, its definition, timing or CONCERN: Low -

determination do not match the review question *(low/ high/ unclear)*

Rationale of applicability rating: The Determination matches the research question.

DOMAIN 4: Analysis

Risk of Bias

Describe numbers of participants, number of candidate predictors, outcome events and events per candidate predictor:

We extracted our main training cohort from Cerner Real-world (CRWD) COVID-19 Q3 cohort which included information for COVID-19 patients from 87 health systems until the end of September 2020. Eligible patients had a minimum of one emergency or inpatient encounter with a diagnosis code that could be associated with COVID-19 exposure or infection, or a positive result for a COVID-19 laboratory test. For our study, we excluded all patients who have less than one day of information after their first COVID-19 admission as well as patients who had confusing dates like discharge dates before the hospitalization start date. Our cohort included 247,960 patients, from which we excluded two hospitals data to use for external validation and the remaining subjects were split into training, validation, and test sets with the ratio of 7:1:2. Therefore, all our reported prediction accuracy metrics on CRWD was the results on a held out test set of 48,781 patients from around 85 health systems. For external validation, we evaluated the model on two randomly selected held out hospitals from CRWD, Hospital 1 from the south region with 3,469 patients and Hospital 2 from the west region with 706 patients. For further external validation we extracted a cohort of 36,140 patients from the OPTUM (COVID-19 v.1015) dataset. Further description of CRWD and OPTUM cohorts, along with differences and commonalities are available in supplementary material A. Table 1 shows the descriptive analysis of both CRWD and OPTUM cohorts.

We extracted all patient information on or before the date of their first hospital admission with COVID-19, including demographics, diagnosis, medication, procedures, laboratory results, and observations. We utilized standard terminologies in common use like ICD 9, ICD10, SNOMED CT, LOINC, Multum codes for medications, CPT-4, HCPCS, ICD-9 PCs, and ICD-10 PCs for procedures. Such standard terminologies are readily available in the majority of EHR systems for interoperability facilitation. In cases where a coding system is not used such as Multum codes for medication, pre-existing mapping tools are available13. The majority of our features were categorical such as diagnosis, medications, and procedures. For numeric variables like laboratory results and age we convert those to categorical variables as well. For example, for Laboratory results we used the "below normal low, normal, or above normal high" classification using the interpretation value provided in the CRWD rather than using the actual numerical value, while for OPTUM, we defined the result categories, based on the assigned normal result ranges. By doing so we can further convert our input either to multi-hot or embedding matrices to feed to our models. Based on our previous study14, we decided to use the clinical information in the coding standards it was recorded with, as the normalization of those codes provides minimal gain14. Further details of our data curation is available in en ji bi b Supplementary Material B. Our data curation pipeline will be available in our github repository

Describe how the model was developed (for example in regards to modelling technique (e.g. survival or logistic modelling), predictorselection, and risk group definition):

Our proposed model was based on a gated type of recurrent neural networks (RNN), a sequential deep learning architecture, namely gated recurrent unit (GRU). Our model was designed to consume all diagnoses, medications, laboratory results, and other clinical events information readily available in the EHR before or on the index date to predict the patient outcomes, without any need for specific feature selection or missing values imputation, for convenience and practicality.Our proposed model considered the temporal nature of patient history and gave more weight for most recent events compared to distant events that happened years ago. Furthermore, for iMort and mVent prediction tasks, we trained both survival and binary classification models, as our framework allows that to fit different clinical needs for healthcare workers confronting COVID-19.

Describe whether and how the model was validated, either internally (e.g. bootstrapping, cross validation, random split sample) or externally (e.g. temporal validation, geographical validation, different setting, different type of participants):

For Binary classification tasks we compared our proposed GRU based model, against machine learning algorithms like Logistic regression (LR)15 and light gradient boost machine (LGBM)16.

For survival prediction, we utilized the DeepSurv17 architecture, while replacing the multiple layer perceptrons (MLP) with GRU for better sequential information modeling. We were unable to adequately compare against machine learning survival models like random survival forest (RSF) for computational resource issues especially with the increased number of covariates and large training set size.

Describe the performance measures of the model, e.g. (re)calibration, discrimination, (re)classification, net benefit, and whether they were adjusted for optimism:

Describe missing data on predictors and outcomes as well as methods used for missing data:

Describe any participants who were excluded from the analysis:

The above questions we considered in the study We focused more on the evaluation and calibration of the binary classification models.

Our prediction tasks include the prediction of COVID-19 patients' in-hospital mortality (iMort), need for mechanical ventilation (mVent), and prolonged length of stay (pLOS), on admission. For iMort event definition, we relied on the preassigned flags on CRWD along with the encounter discharge disposition. The iMort event definition was slightly different on the OPTUM data and there were no clear discharge disposition indicating patient in-hospital death, rather we used the date of death and compare against the hospitalization discharge date to assign the proper label. For mVent, we mainly used all relevant mechanical ventilation procedure codes to define the outcome. Additionally on CRWD, we used other relevant observations or laboratory results not only to identify the instant of the event, but also to identify the earliest time of the event. For both iMort and mVent prediction tasks, we trained both survival and binary classification based prediction models. We defined pLOS as a binary indicator for hospitalizations longer than 7 days, as the median length of stay (LOS) in both CRWD and OPTUM cohorts were 3 and 5 respectively, and we only trained a binary classification model for the pLOS task.

Step 4: Overall assessment

Use the following tables to reach overall judgements about risk of bias and concerns regarding applicability of the prediction model evaluation (development and/or validation) across all assessed domains. *Complete for each evaluation of a distinct model.*

