# Supplementary Materials

### **Contents**



#### <span id="page-1-0"></span>*Structuring electronic health record data*

Cleveland Clinic uses the Epic electronic health record (EHR) system. To generate our databases, statistical techniques including similarity calculations and fuzzy matching, are used to clean, parse, map and validate the raw EHR data. The raw data are extracted from both the EHR and other disparate data sources, mapped to discrete ontologies, cleaned and standardized, and finally deposited into a clinical research data repository. Approximately 185 tables from different data sources are condensed into 18 research-ready tables in the data repository. We utilize identifiers from the freely available Unified Medical Language System (UMLS) to map 6.8 million patient-related terms, as well as approximately half a million custom UMLS identifiers that include providers, locations, and their relationships. The Metathesaurus from the UMLS combines synonymous terms and codes from disparate medical vocabularies into concise terms and identifiers. Only 9% of columns in the data repository (approximately 1,000 data points per patient) do not utilize UMLS identifiers. These non-UMLS columns include patient identifiers, dates, and visit identifiers, which we manually queried for this project. Ultimately, there are approximately 32,000 discrete data elements per patient comprised of both UMLS and non-UMLS data. From this large collection, we selected variables to predict outcomes during hospitalization based on expert opinion and published literature, then extracted these into tables suitable for machine learning algorithms.<sup>1</sup> The total number of variables for each prediction task varied based on which features would be appropriate, ranging from 285 for prediction of 30-day readmission (including variables that would be available at the

2

beginning, during the duration, and at the end of the admission), to 171 for length of stay (including only variables that would be available during the first 24-hours of admission). See Supplementary Tables 1 and 2 for a list of the variables that were used overall (Supplementary Table 1) and for each predictive task (Supplementary Table 2).

#### <span id="page-2-0"></span>Inclusion Criteria and Outcome Definitions

#### <span id="page-2-1"></span>*Readmission*

Readmission was defined as any new Cleveland Clinic (CC) hospitalization starting 4 hours after any CCF discharge. For prediction of readmission, patients whose discharge disposition was "expired" were removed. Patients with an admission class of "observation" were retained, as it has been suggested that readmission reduction programs have resulted in an increased use of the observational setting.<sup>2,3</sup> The 4 hour cutoff removed patients who were simply transferring from one CCF department or hospital to another, and was selected based on histogram analysis of first-day readmissions.

#### <span id="page-2-2"></span>*Length of Stay*

Length of stay was defined as the time between a given discharge date and admission date for each hospitalization. Only variables available within 24 hours of admission were considered with the exception of primary diagnosis code, and patients with an admission class of "observation" were removed.

#### <span id="page-2-3"></span>*Death*

Death within 48–72 hours of admission was defined as a recorded EHR, Social Security, or Ohio Death Index death date, or a discharge disposition of "expired," within the given time frame. Only variables available within 24 hours of admission were considered with the exception of primary diagnosis code, and patients with an admission class of "observation" were removed.

#### <span id="page-3-0"></span>Machine Learning Models

We used Gradient Boosting Machines (GBMs) to predict binary and numeric outcomes of interest. Gradient boosting machines function by consecutively training decision trees to predict the outcome of interest. Each consecutive tree learns from the ensemble of predictions that came before it, and attempts to minimize the error of the current prediction.<sup>4</sup> The GBM implemented by LightGBM contains several optimizations that allow it to obtain robust models quickly. The chief optimization is onthe-fly binning of continuous variables into discrete buckets, in order to allow for more straightforward splitting of the decision tree.<sup>5</sup>

As mentioned in the main text, Gradient Boosting Machines, and LightGBM in particular, allow for heterogeneous data input, including variables with a large number of categories, missing values, and zero values. They do therefore not require imputation, which is advantageous when the lack of a variable for a particular case is important (as in a patient who has never been admitted before and therefore has a "Length of stay of last admission" of "missing," rather than "zero," which may indicate something entirely different). Additionally, not every patient has the same set of labs drawn, and it would be inappropriate to impute values for these, especially if the imputation was based on the average or median value across the cohort, considering that many patients are likely to have abnormal values if the lab warranted being drawn. GBMs also do not require scaling, rendering the output of the explanations more human-readable. Lastly, because of the nonlinear combinations of variables probable

in a large healthcare dataset, a tree-based method such as GBM may be more interpretable than a linear model. This is primarily due to the likelihood of the latter to exhibit greater sensitivity to "model mismatch," wherein the high-bias nature of the linear model cannot adequately represent the underlying nature of the data, and so may be more likely to report spurious associations even at a comparable accuracy.<sup>6</sup>

We used Bayesian hyperparameter optimization, as available in the Python package hyperopt, to select hyperparameters for the main predictive targets.

We also used several comparator models, including a deep neural network within the Pytorch framework as implemented by fast.ai and several standard ML models from sklearn. Standard data imputation and scaling techniques were applied to the data to allow ingestion by the models.

#### <span id="page-4-0"></span>Interpretation of the final model

The SHAP packages provides utilities for calculating Shapley values for a variety of machine learning algorithms, and is optimized for tree-based algorithms such as GBM. Shapley values come from classical game theory, and are the only additive feature attribution method that yield the combination of local accuracy, consistency, and allowance for missingness.<sup>6,7</sup>

SHAP values may be used to explain a model globally, by examining the average contribution of a given feature to the model output, or locally, by examining the most important variables for a given prediction.<sup>7</sup> They may also be used to examine interactions between variables. SHAP values were generated using the Python package shap v0.28.5. Visualizations were created using the Python package matplotlib v3.0.311, as well as the LaTeX typesetting language, as appropriate.

5

#### <span id="page-5-0"></span>Statistical analysis

ROC curves, precision-recall curves, and calibration plots were generated for visual assessments of model performance. Additionally, summary values for these were calculated, including Brier scores for calibration plots, average precision for the precision-recall curves, and ROC AUC for ROC curves.

Calibration curves are used to assess the trustworthiness of a model's predicted probability. They provide a visual representation of the model's predicted probability vs. the fraction of samples at that probability with the actual outcome. The curve of perfectly calibrated model would exhibit a straight 45° line. Lower Brier scores are better, with a score  $< 0.25$  generally considered indicative of a useful model.<sup>8</sup> They are calculated as the mean squared difference between the probability assigned to each sample and the actual outcome (1 or 0). <sup>8</sup>

ROC curves, the corresponding ROC AUC, and precision-recall curves, with the average precision metric, show classification performance at all possible classification thresholds.<sup>9</sup> Higher numbers are better. ROC AUC and average precision of 0.5 indicate a model that performs no better than chance. An AUC of 1.0 indicates 100% true positive and 0% false positive rates, while an average precision of 1.0 indicates a positive predictive value of 100%. Confusion matrices show the number of samples correctly and incorrectly classified.

RMSE is calculated as the square root of the average of squared errors, or difference between observed and expected values, and yields a metric in the same units as the predictive target (here, days or years).<sup>10</sup> Median absolute error is the median absolute difference between the predicted target and the actual value, and

6

mean absolute error is the mean of the same. R2 scores are the percentage of the target variable variation captured by the model, where 100% indicates a model that explains all of the variability and 0% indicates a model that explains none.

#### <span id="page-7-0"></span>Supplementary Figures

#### <span id="page-7-1"></span>Supplementary Figure 1. ROC-AUC and calibration curves for readmission and

#### extended length of stay

a Receiver operator characteristic curve for 30-day b Calibration curve for 30-day readmission. readmission.





 $1.0$ 

c Receiver operator characteristic curve for length d Calibration curve for length of stay over 5 days. of stay over 5 days.



### <span id="page-8-0"></span>Supplementary Figure 2. Comparisons of model performances



a. Comparison of model calibration for 30 day readmission



### b. Comparison of model calibration for length of stay > 5 days

c. Precision-Recall Curve for 30 day readmission







# e. Extended model comparison figures for 30 day readmission (10x 10-fold cross validation)



### 30d readmission



### 30d readmission





Receiver operating characteristic for Complement Naive Bayes

### 30d readmission





Receiver operating characteristic for Support Vector Machine

f. Extended model comparison for length of stay > 5 days (10x 10-fold cross validation)



 $LOS > 5d$ 







18

### $LOS >5d$





### <span id="page-19-0"></span>Supplementary Figure 3. GBM Feature Importances

a. GBM feature importance (not SHAP), 30 Day Readmission



b. GBM feature importance (not SHAP), Length of Stay > 5d



#### <span id="page-21-0"></span>Supplementary Figure 4. Examples of Personalized Predictions, extended

#### a. Readmitted within 30 days



Pt with high probability of readmission within 30 days, largely due to significant history of admission and readmission, in addition to BlockGroup GeoID and other factors. Interestingly, the primary diagnosis (Bipolar disorder) decreased the likelihood of readmission.



Another pt with high probability of readmission within 30 days, primarily due to a diagnosis of hepatic failure, in addition to their BlockGroup GeoID, recent admission, and cancer diagnosis. Number of past admissions played a role, but a less extreme one compared to the example above.



Pt with very low probability of readmission within 30 days, largely due to a diagnosis of

osteoarthritis, a single prior admission that was over a year before the current

admission, a short length of stay, and other variables as shown.



Another pt with very low probability of readmission within 30 days, largely due to a very short length of stay for angioneurotic edema, no prior admissions or listed comorbidities, and low number of listed medications on the day of discharge (all prescribed treatments are counted in this number).

# b. Length of stay  $>$  5 days



Young pt with MRSA-related sepsis transferred to our facility, with a nearly

100% probability of LOS >5d.



Pt with alcoholic liver cirrhosis (K7031) transferred to our hospital with a pressure ulcer and a lengthy prior admission, with a non-recorded BMI and low systolic blood pressure, but no ICU admission. Assigned ~90% probability of long LOS.



Relatively young pt with Type 2 Diabetes admitted for ketoacidosis, who had

never been admitted before. Assigned a probability of LOS >5d ~15%.



24 year old pt with primary diagnosis of acute kidney failure unspecified, admitted on a Sunday outside of normal working hours, with a probability of long LOS just under 20%.



41 year old pt admitted on Wednesday during the working day for acute appendicitis, who had never had any recorded prior admissions and did not have BMI recorded at this admission.

#### <span id="page-30-0"></span>Supplementary Figure 5. Top SHAP Features.

#### a. 3-day readmission



#### b. 7-day readmission



#### c. Length of stay over 3 days



### d. Length of stay over 7 days



#### <span id="page-32-0"></span>Supplementary Figure 6. SHAP Variable Interactions for 30 day readmission

a Age vs. number of past hospitalizations.







**b** Length of stay of current vs. past hospitalization.



d Discharge disposition vs. number of past hospitalizations.



#### Supplementary Figure 7. SHAP Variable Interactions for length of stay > 5 days

a Number of medications administered in first 24 hours vs. age.

**b** Length of stay of last hospitalization vs. days since last hospitalization.



C Heart rate vs. age.





d ICU admission vs. number of medications administered in last 24 hours.



### <span id="page-35-1"></span>Tables

### <span id="page-35-2"></span>Supplementary Table 1. Model Performance Comparisons

### a. 30 day readmission



### b. Length of Stay > 5 days

<span id="page-35-0"></span>

# c. Model comparisons, extended





### d. Length of Stay predictions without primary diagnosis code, gradient boosting

machine



<span id="page-38-0"></span>Supplementary Table 2. Categorized variables







#### <span id="page-43-0"></span>**References**

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