Predicting 30-Day All-Cause Readmissions from Hospital Inpatient Discharge Data

Chengliang Yang1, Chris Delcher2, Elizabeth Shenkman2, and Sanjay Ranka1

1Dept. of Computer & Information Science & Engineering
University of Florida, Gainesville, FL 32611, USA
ximen14@ufl.edu, ranka@cise.ufl.edu

2Dept. of Health Outcomes & Policy
University of Florida, Gainesville, FL 32611, USA
cdelcher@ufl.edu, eshenkman@ufl.edu

Abstract—Inpatient hospital readmissions for potentially avoidable conditions are problematic and costly. In this paper, we build machine learning models using variables widely available in health claims data to predict patients’ 30-day readmission risks at the time of discharge. These models show high predictive power on a U.S. nationwide readmission database. They are also capable of providing interpretable risk factors globally at the population level and locally associated with each single discharge. In addition, we propose a model-agnostic approach to provide confidence for each prediction. Altogether, using models with high predictive power, interpretable risk factors and prediction confidence may enable health care systems to accurately target high-risk patients and prevent recurrent readmissions by accurately anticipating the probability of readmission at the point of care.

I. INTRODUCTION

Potentially avoidable hospital inpatient readmissions have received worldwide attention in recent years due to negative financial impacts and increased mortality and morbidity for patients. In the United States, the Centers for Medicare and Medicaid Services (CMS) reported [1] that 76% of readmissions are potentially avoidable. The Affordable Care Act of 2010 required the US Department of Health and Human Services to establish a program to reduce 30-day readmissions for targeted clinical conditions that meet this criteria. These conditions are estimated to account for more than $17 billion in Medicare expenditures annually [2]. Outside of the United States, various countries have conducted controlled intervention trials to prevent hospital readmissions [3]. In the age of "big data", clinicians, statisticians, and computer scientists are challenged to predict hospital readmissions from heterogeneous medical datasets.

The body of literature in predictive analytics, as applied to inpatient readmissions, leverages multiple data sources and predictive models. In terms of data sources, most studies [4], [5], [6], [7], [8] are developed from administrative claims datasets and [9], [10], [11], [12], [13] integrate components of electronic health records (EHR) including vital signs and lab tests. In terms of the predictive methods, standard logistic regression is the primary method for many studies [9], [10], [11]. Other methods [6], [7], [8] include a range of statistical and machine learning models such as decision trees, random forest, support vector machines (SVM) and neural networks. Most studies focus on disease-specific models. However, it is possible to build general models across disease cohorts [14], [6], [15] is a recent review on predicting readmissions.

Despite the growing use of predictive models, they are not widely used in clinical practice. First, most developed models are designed for specific diseases and rely on domain knowledge of clinicians [9], [10], [11]. This could be problematic in applying predictions to large health information systems because of the availability of multiple, complex data sources and the heterogeneous mixture of patients and diagnoses. Second, computer scientists and statistician-developed models tend to focus on prediction accuracy [6], [8] but rarely explain their predictions in clinical terms. This is especially true with "black box" models such as support vector machines (SVM) and neural networks. A readmission study on HIV [16] points out that these methods "lack the ability to examine the detailed clinical and social reasons for readmission or to determine if and how readmissions may have been prevented.” Predictive models should help inform interventions and therefore need to be both statistically robust and clinically relevant. Finally, though various models have been applied to predict readmissions, the framework for establishing confidence intervals for these predictions is lacking. Addressing this limitation is critical if clinicians are expected to adopt the results of predictive models in clinical practice.

The goal of this paper is to: 1) develop accurate and state-of-the-art, generalizable machine learning models that are applicable to predicting 30-day all cause readmissions due to a range of diseases; 2) interpret model results in a manner accessible for clinicians; and 3) estimate the confidence for readmission predictions at the patient-level. The paper proceeds as follows: Section 2 introduces the dataset we use, the models deployed and the methods. Section 3 reports the prediction results, interprets the models and estimates prediction confidence. Section 4 concludes the paper and discusses limitations and future scope of this work.

II. DATA AND METHODS

We aim to optimally predict 30-day, all-cause hospital readmissions, which occur when a patient is readmitted to an inpatient hospital for any reason within 30 days of a prior inpatient discharge.

A. Dataset

To test the inpatient readmission predictive models, we use the Healthcare Utilization Project (HCUP) U.S. Nationwide Readmissions Database (NRD) from the Agency for Healthcare Research and Quality (AHRQ) [17]. This dataset was
Refined Diagnosis-Related Group (APR-DRG) is a clinical classification system that categorizes inpatient stays into groups for hospital stay provided in the NRD. APR-DRG is a clinical classification system that categorizes inpatient stays into groups for hospital stay provided in the NRD.

**B. Methods**

Due to space limitations, please track readmissions. Table I provides a summary of predictors that are used in all models. Given the same set of training instances in II-B1, it generates an ensemble of different APR-DRGs. For each APR-DRG, we first randomly divide the dataset into a 70%/30% partition. The models are trained on the 70% portion and tested on the 30% one. This process is repeated for 10 times and averaged to calculate the area under the Receiver Operator Curve (AUC). As done by [6], the Deep Neural Networks (DNN) model requires extensive computing resources, we only apply it to five diseases for which CMS will reduce payments for excess readmissions [19]. They are chronic obstructive pulmonary disorder (COPD, APR-DRG 140), heart failure (HF, APR-DRG 194), pneumonia (PN, APR-DRG 139), acute myocardial infarction (AMI, APR-DRG 190) and total hip arthroplasty/total knee arthroplasty (TA, APR-DRG 301/302). In the following section, we will introduce the machine learning models chosen to be trained on the data.

1) **Regularized Logistic Regression (LASSO)**: Regularized regression, also known as the least absolute shrinkage and selection operator (LASSO) [20], is usually the default approach in many supervised machine learning tasks. This is because it is robust enough to deal with high dimensional data, helps avoid overfitting the data and provides high accuracy. $L_1$ regularized logistic regression is considered the state-of-the-art in readmission prediction tasks [6], [21]. Given $M$ training instances $\{(x_i, y_i), i = 1, 2, ..., M\}$, where $x_i \in \mathbb{R}^N$ is a N-dimensional predictor vector, $y_i \in \{0, 1\}$ is the class label, logistic regression estimates the probability of $y$ given $x$ as:

$$p(y = 1|x) = \frac{1}{1 + \exp(-\theta^Tx)}$$

where $\theta \in \mathbb{R}^N$ are the linear coefficients. $L_1$ regularized logistic regression tries to minimized the objective function below when solving for $\theta$:

$$\min_{\theta} \sum_{i=1}^{M} -\log p(y = 1|x) + \beta||\theta||_1$$

The regularizing term $||\theta||_1$ drives most entries of $\theta$ to zero. This is preferable because it makes the model robust to overfitting and automatically generates a short list of influential predictors to help identify potential factors associated with readmissions. In our study, we use the implementation of LASSO provided by the authors [20]. A 10-fold cross validation is used to select the hyper-parameter $\beta$.

2) **Gradient Boosting Machine (GBM)**: Gradient boosting [22] is another set of successful machine learning techniques to handle high dimensional datasets. Given the same set of training instances in II-B1, it generates an ensemble of decision trees $f_t$ as the predictive model. It learns these trees by examine variation in model performance for each condition. To prepare the data, first we remove the diagnoses and procedures occurring less than 10 times. After this step each APR-DRG dataset usually contains approximately 2,000 predictors. Then, in order to have sufficient data to train and test a model and avoid overfitting, we only keep the APR-DRGs that have more than 20,000 records. With this criteria, we end up with 74 different APR-DRGs.

The NRD dataset contains summary information from inpatient hospital discharges similar to data found in most health insurance claims databases. Each row represents selected information recorded during the inpatient hospital stay including patients’ demographics, the International Classification of Diseases, Ninth Revision, Clinical Modification (ICD-9-CM) diagnoses and procedure codes, hospital information, etc. For this study, we use all data fields provided in the NRD to predict 30-day readmissions. Given that previous admissions are expected to be strong predictors of readmissions [10], [6], we create a series of features to incorporate prior admissions information. We limit the training and test data to July through November 2013 so that we have 6 months time to collect prior admissions information and 30 days post discharge time to track readmissions. Table I provides a summary of predictors that are used in all models. Due to space limitations, please refer to [17] for the specifications of all data elements. We use dummy coding for categorical variables.

### TABLE I: Summary of Predictors

<table>
<thead>
<tr>
<th>Predictor</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td><strong>Demographics</strong></td>
<td>Age, Sex, Payer(Medicare, Medicaid, private insurance, self-pay, no charge, other), Patient location (urban/rural classification), Household income quartiles</td>
</tr>
<tr>
<td><strong>Admission &amp; discharge information</strong></td>
<td>Admission on weekend, Disposition of patient, Elective admission, Emergency Department (ED) services, Transferring to rehabilitation, Length of stay</td>
</tr>
<tr>
<td><strong>Clinical information</strong></td>
<td>Type and number of Diagnoses (ICD-9-CM), External causes of injury codes (ICD-9-CM), Procedures (ICD-9-CM), Number of chronic conditions, Major operating room procedure indicator</td>
</tr>
<tr>
<td><strong>Severity information</strong></td>
<td>Risk of mortality of 3M All Patient Refined Diagnosis-Related Group (APR-DRG), Severity of illness of APR-DRG, AHRQ comorbidity measures, Chronic condition body system indicators, Procedure class for all ICD-9-CM procedures</td>
</tr>
<tr>
<td><strong>Hospital information</strong></td>
<td>Control/ownership of hospital, Size of hospital based on the number of beds, Teaching status of hospital, Hospital urban-rural location</td>
</tr>
<tr>
<td><strong>Previous Admissions information</strong></td>
<td>Number of days from the most recent previous admission of any kind and the same APR-DRG in CY2013, Number of previous admissions of any kind and the same APR-DRG in CY2013, Frequency of previous admissions of any kind and the same APR-DRG in CY2013, Average number of days between admissions</td>
</tr>
</tbody>
</table>

released in November 2015 and is the first publicly available, nationally representative database for inpatient readmissions in the United States. The NRD contains unique, non-informative patient identifiers to follow all hospital admissions for the same patient. The NRD is a sample of 2,006 acute care hospitals and contains approximately 14 million inpatient discharges in calendar year 2013. Single admission patients are also included.

To model specific health conditions, we use 3M All Patient Refined Diagnosis-Related Group (APR-DRG) for each hospital stay provided in the NRD. APR-DRG is a clinical classification system that categorizes inpatient stays into groups for the purposes of payment. As with most readmission prediction studies [18], [8], [7], we model each of these APR-DRGs to
in an additive manner. In each round, it learns a new tree \( f_t \) by optimizing the objective function of:

\[
\min_{f_t} \sum_{i=1}^{M} (g_i f_t(x_i) + \frac{1}{2} h_i f_t^2(x_i)) + \gamma T + \lambda \sum_{j=1}^{T} w_j^2
\]

(3)

where \( g_i \) and \( h_i \) are the first and second order derivatives of some loss function, which is AUC in our case. \( T \) is the number of leaves in decision tree \( f_t \) and \( w_j \) are the leaf weights. The last two terms are regularizers to control mode complexity.

One advantageous property of GBM is that the information gain of the trees can be aggregated as a measure of predictor importance, which is similar to the coefficients in LASSO. This makes tree methods interpretable in applications. In practice, we use the implementation of GBM provided by [23]. We train 1,000 decision trees for each GBM. We do a grid search and 5-fold cross validation to decide other hyper-parameters such as learning rate and tree structure.

3) Deep Neural Networks (DNN): Deep learning has made great progress in machine learning tasks like object image classification, voice recognition and natural language processing. However, use of deep learning [24], [6] is limited in healthcare. The NRD does not have a topological or sequential structure that can take advantage of the popular convolutional neural networks (CNN) or recurrent neural networks (RNN), therefore we applied a regular multilayer perceptron (MLP) approach. In our analysis, we perform a grid search over network depth (maximum 3 hidden layers) and number of nodes in each layer (maximum 2,000 nodes) and choose the optimum using cross validation. Network initialization is sampled from a standard normal distribution. We use momentum in stochastic gradient descent for optimization to avoid local minima. Also, we apply batch normalization [25] to accelerate convergence. We use the implementation of DNN in [26].

III. RESULTS

In this section we will present the readmission prediction results. We will first examine the prediction accuracy in terms of AUC. Then, we will interpret the models at the population and discharge level. Finally, we will examine the confidence of the predictions.

A. Prediction Accuracy

We use AUC as the measure of prediction performance. AUC is robust to imbalanced readmitted and non-readmitted proportions. So that even if the readmission rates vary substantially across different APR-DRGs, we still have a stable measure. Table II provides AUC comparisons between LASSO, GBM and DNN on CMS targeted diseases. Table III presents AUC comparisons between LASSO and GBM over all 74 APR-DRGs.

From Table II, we can see the performance of LASSO, GBM and DNN are similar. However, DNN shows larger standard errors and larger differences between the training and test AUCs. The latter result is not surprising given that DNN is more complex and thus more likely to overfit. The results suggest that simple models like linear models (LASSO) and tree models (GBM) are sufficient in this context. Table III, both LASSO and GBM show acceptable predictive power (AUC around 0.7). In comparison, GBM is slightly better than LASSO. GBM has a better AUC in 70 APR-DRGs out of all 74 though in most cases the difference in AUC is negligible (less than 0.001). GBM, however, is substantially more predictive in two specific APR-DRGs: vaginal delivery (APR-DRG 560) and chemotherapy (APR-DRG 693). The AUCs improve from 0.5222 to 0.633 (11%) and from 0.635 to 0.705 (7%), respectively.

From this part of the analysis, we can conclude that LASSO, GBM and DNN models perform similarly in predicting readmissions. GBM is preferable, however, because it is simpler, robust, and accounts for some non-linear variation in the NRD.

B. Interpret Models and Predictions

Machine learning models have achieved high accuracy in many prediction tasks. In some cases, such as voice recognition, it may be irrelevant to understand how important factors operate to effect the likelihood of an outcome. In healthcare studies, it is often desirable to elucidate modifiable risk (or protective) factors, in part, because results provide the basis for preventative action. In the methods section, we mentioned that LASSO and GBM are interpretable methods that can produce human understandable explanations of the trained model and predictions. In this section, we interpret readmissions using these models at the population and discharge level. DNN is not directly interpretable but [27] provides an approach that approximates LASSO.

1) Global Interpretation: Understand Trained Model: LASSO and GBM are capable of generating a list of predictors that it finds most correlated to readmissions.

LASSO is a general linear model so that the linear coefficients of predictors can be roughly regarded as the degree of correlation to readmission risks. Note that this is a rough approximation because of the different scales of the predictors. The left panel of Table IV shows the 10 predictors with largest coefficients in a LASSO model to predict readmissions. GBM also provides a way to show predictor importance. A tree model (GBM) is sufficient in this context. Table III, both LASSO and GBM show acceptable predictive power (AUC around 0.7). In comparison, GBM is slightly better than LASSO. GBM has a better AUC in 70 APR-DRGs out of all 74 though in most cases the difference in AUC is negligible (less than 0.001). GBM, however, is substantially more predictive in two specific APR-DRGs: vaginal delivery (APR-DRG 560) and chemotherapy (APR-DRG 693). The AUCs improve from 0.5222 to 0.633 (11%) and from 0.635 to 0.705 (7%), respectively.

From this part of the analysis, we can conclude that LASSO, GBM and DNN models perform similarly in predicting readmissions. GBM is preferable, however, because it is simpler, robust, and accounts for some non-linear variation in the NRD.
also assigned weights, which are assigned back to the nodes on the tree that follows a decision path. The decision path consists of splitting nodes that are described by predictors. The leaves are also assigned weights, which are assigned back to the nodes on the decision path and are weighed by the gain in each node. As a result, the predictors in the splitting nodes receive a portion of the weights. The portions are then summed by the predictors across all trees. As the sum of these quantities equals to the score the instance will receive (the sum of leaves’ weights across all trees. As the sum of these quantities equals to the score the instance will receive (the sum of leaves’ weights

Readmissions for an Example Discharge with Asthma

Table V: Top 5 Most Significant Predictors for Risk of Readmissions after Discharged with Asthma

<table>
<thead>
<tr>
<th>Predictor</th>
<th>Coefficient</th>
<th>GBM Gain</th>
</tr>
</thead>
<tbody>
<tr>
<td>Diagnostic, ICD9 78459, Other speech disturbance</td>
<td>1.457</td>
<td>224,453</td>
</tr>
<tr>
<td>Comorbidity present</td>
<td>0.998</td>
<td>Most recent admission of any kind 109,598</td>
</tr>
<tr>
<td>Diagnosis, ICD9 7821, Rash and other non-specific skin eruption</td>
<td>0.922</td>
<td>Number of chronic conditions 100,600</td>
</tr>
<tr>
<td>Diagnosis, ICD9 E8798, Other specified procedures as the cause of abnormal reaction of patient</td>
<td>0.921</td>
<td>Age 72,032</td>
</tr>
<tr>
<td>Diagnosis, ICD9 72400, Spinal stenosis, unspecified region</td>
<td>0.866</td>
<td>Number of previous admissions of same APR-DRG 23,932</td>
</tr>
<tr>
<td>Procedure, ICD9 9462, Alcohol Detoxification</td>
<td>0.789</td>
<td>Number of diagnoses 21,773</td>
</tr>
<tr>
<td>Diagnosis, ICD9 0045, Intestinal infection due to Clostridium difficile</td>
<td>0.770</td>
<td>Discharged against medical advice 19,811</td>
</tr>
<tr>
<td>Diagnosis, ICD9 V862, Long-term (current) use of antibiotics</td>
<td>0.725</td>
<td>Length of stay 17,274</td>
</tr>
<tr>
<td>Diagnosis, ICD9 28261, Hb-SS disease without crisis</td>
<td>0.709</td>
<td>Payer is private insurance 13,975</td>
</tr>
</tbody>
</table>

Table III: LASSO vs. GBM, All 74 APR-DRGs

Comparing GBM and LASSO’s results in Table IV, we can see GBM identifies many likely, highly correlated predictors such as the prior history variables that we included. In contrast, predictors with the largest coefficients in LASSO seem independent from each other. Among a set of highly correlated predictors, LASSO usually selects one to have a non-zero coefficient and the rest are assigned zero coefficients. This feature reduces information redundancy in presenting predictor importance. This selection, however, is performed automatically and is not informed by clinical logic. In contrast, GBM relies on the approximate global loss function gain in each split. If a set of predictors is informative at the population level, they will appear more frequently when assembling the decision trees, causing redundancies in the predictor importance table. As such, LASSO appears to find useful information more efficiently.

2) Local Interpretation: Understand Each Prediction: For doctors and patients, instead of knowing the most important predictor for the entire population, they are more interested in important predictors at the patient-level. Thus, it is helpful to understand the predictive contribution (i.e., importance) for each single prediction. In the prediction phase of our problem, both LASSO and GBM generate a score for each discharge, then apply a logistic transform to that score and interpret the outcome as the probability of readmission. By the property of logistic transform, we have:

$$\text{odds of readmitted} = \frac{p(\text{readmitted})}{p(\text{not readmitted})} = \exp(\text{score})$$

If we can decompose the score into a sum of the contribution from each predictor, the total odds becomes a product of the terms $\exp(\text{contribution from each predictor})$. These terms are the odds ratios that many clinicians and healthcare practitioners are familiar with. Next, we will describe how we decompose the total score as a sum of the contribution from each predictor.

Compared to GBM, the LASSO case is more straightforward. Since LASSO is a form of logistic regression, the coefficients are readily converted to odds ratios and are ranked. Rank ordering odds ratios are directly interpretable. For GBM, however, each data instance is assigned to a leaf in a decision tree that follows a decision path. The decision path consists of splitting nodes that are described by predictors. The leaves are assigned weights, which are assigned back to the nodes on the decision path and are weighed by the gain in each node. As a result, the predictors in the splitting nodes receive a portion of the weights. The portions are then summed by the predictors across all trees. As the sum of these quantities equals to the score the instance will receive (the sum of leaves’ weights

Table IV: Top 10 Most Significant Predictors of Readmissions after Discharged with Asthma

<table>
<thead>
<tr>
<th>Predictor</th>
<th>Odds contribution</th>
<th>GBM Gain</th>
</tr>
</thead>
<tbody>
<tr>
<td>Number of previous admissions of any kind</td>
<td>2.86</td>
<td>Number of previous admissions of any kind 1.83</td>
</tr>
<tr>
<td>Transferred to short term hospital</td>
<td>1.39</td>
<td>Age 1.17</td>
</tr>
<tr>
<td>Age</td>
<td>1.31</td>
<td>Previous admission frequency 1.16</td>
</tr>
<tr>
<td>Number of diagnoses</td>
<td>1.15</td>
<td>Number of previous admissions of same APR-DRG 1.06</td>
</tr>
<tr>
<td>Length of stay</td>
<td>1.04</td>
<td>Number of chronic conditions 1.04</td>
</tr>
</tbody>
</table>

Table V: Top 5 Most Significant Predictors for Risk of Readmissions for an Example Discharge with Asthma
that the instance is assigned to), we successfully decompose the score into contributions from each predictor. Finally, we apply an exponential transform to the contributions to get the contribution odds. In Table V, we present the predictors in rank order from the LASSO and GBM models.

C. Prediction Confidence

One limitation to using machine learning in healthcare research is that many predictive modeling approaches do not have established methods for estimating confidence intervals. This is because the assumed distributions for these models are diverse and the prediction paths are usually non-linear. Some progress has been made in estimating confidence. [29] attempts to find an ambiguity region for classification and the remaining regions have certain classification accuracy at some confidence level. Their method, however, partitions the predictor space and does not provide the full confidence spectrum. In this section, we present alternative ways to estimate prediction confidence using bootstrapping [30].

Using the idea of bootstrapping, we resampled the training data with replacement for \( K \) times and built \( K \) different LASSO and GBM models. The \( K \) models were ensembled to make predictions and to estimate confidence by using voting or confidence intervals. In practice, we set \( K = 1000 \).

1) Voting and Consensus Rate: \( K \) models can be regarded as \( K \) experts. Each model sees a different aspect of the training data due to re-sampling. Thus, each model has a different knowledge about prediction. To combine them together, one strategy is to vote and make prediction using the majority rule. It is intuitive to think that the more the models agree about one prediction, the more confident that prediction is. We call the majority proportion the consensus rate. In the test data, predictions were grouped according to the consensus rate for every 5% level and were plotted against the classification accuracy. Figure 1 shows the consensus rate versus the classification accuracy for both LASSO and GBM.

As expected, the classification accuracy increased as the consensus rate increased. Therefore, the consensus rate is a good approximation of prediction confidence.

2) Providing Confidence Intervals: Another strategy to extract confidence from the \( K \) models is to build confidence intervals for readmission probabilities. As stated above, both LASSO and GBM generate a probability for the risk of readmission. We have \( K \) models which gives us \( K \) probabilities, which can be used to construct a 95% confidence interval. Intuitively, a wide confidence interval for a prediction suggests that confidence is low and that the models disagree on the readmission risks. If the interval confidence is narrow, then vice versa. We made predictions based on average probabilities over \( K \) models and present the width of the confidence intervals versus the classification accuracy in Figure 2.

We can see the classification accuracy decreased substantially as the width of the confidence intervals increased, which validates our method of estimating confidence intervals.

Table VI shows how the consensus rate and the estimated 95% confidence interval can be presented to the clinicians in practice. We used the same example of an asthma discharge in Table V. The consensus rate and the estimated 95% confidence interval are calculated from 1,000 rounds of resampling.

IV. Conclusion

In this paper, we built and compared three predictive machine learning models to predict 30-day hospital readmissions using a U.S. nationwide database. We achieved consistent performance with current readmission models using these state-of-the-art approaches. Interestingly, we found a significant improvement in performance using the GBM model for readmissions related to vaginal delivery and chemotherapy. In addition, we showed that our models are capable of providing important risk factors at the population and patient levels.
that can be translated into familiar clinical metrics. We also provided a methodological approach to creating confidence measures for the predictions that end users can employ to estimate accuracy. High predictive power, interpretable results and prediction confidence constitutes a comprehensive framework to predict and understand hospital readmissions using hospital discharge data. This framework can be integrated into modern health claim systems to help healthcare providers target high-risk populations, prevent recurrent admissions and deliver better care.

While state-of-the-art computer science models offer high predictive validity, we note that one limitation here is that key variable selection is not optimally informed by clinical logic. [31] recommends a team-based approach to model selection field by using an iterative process between clinicians and computer scientists to develop the most clinically relevant models. Our future work will include enhanced feedback from clinicians who work at a large integrated healthcare system.

Furthermore, to achieve better prediction accuracy, we plan to test similar models in environments with access to electronic health records (EHR). We hope to bridge heterogeneous medical datasets to build better predictive machine learning models for hospital readmissions.

ACKNOWLEDGMENTS

The authors would like to acknowledge the University of Florida Informatics Institute (UFII) for providing institutional funding for this work.

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