An Explainable Machine Learning Approach to Visual-Interactive Labeling: A Case Study on Non-communicable Disease Data

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Abstract

We introduce a new visual-interactive tool: Explainable Labeling Assistant (XLabel) that takes an explainable machine learning approach to data labeling. The main component of XLabel is the Explainable Boosting Machine (EBM), a predictive model that can calculate the contribution of each input feature towards the final prediction. As a case study, we use XLabel to predict the labels of four non-communicable diseases (NCDs): diabetes, hypertension, chronic kidney disease, and dyslipidemia. We demonstrate that EBM is an excellent choice of predictive model by comparing it against a rule-based and four other machine learning models. By performing 5-fold cross-validation on 427 medical records, EBM’s prediction accuracy, precision, and F1-score are greater than 0.95 in all four NCDs. It performed as well as two black-box models and outperformed the other models in these metrics. In an additional experiment, when 40% of the records were intentionally mislabeled, EBM could recall the correct labels of more than 90% of these records. The detailed code, documentation and installation instructions of XLabel have been made available at: https://github.com/donlapark/XLabel.

1 Introduction

In healthcare, there are many sources of every growing data, such as patients' records, electronic health records and laboratory results. If properly managed and analyzed, such data can provide useful information to patients, physicians and medical researchers, who then take advantage of the information to improve medical research and patient care. In spite of this, it will be difficult to conduct impactful research without a carefully labeled dataset. For example, an observational study of a particular disease will be difficult if each record in the dataset does not come with a clear disease label, which is common for records of follow-up visits. It then becomes a medical experts’ important task to label all medical records before releasing them to the public for future research use.

Labeling a large amount of data can be expensive and time consuming. Thus, there has been increasing interest in using an assistant tool to speed up the labeling process. One approach to build such a tool is to treat the data labeling problem as a classification problem, where each input

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consists of each record’s features, and the output is the record’s label. Though such a problem can be tackled by machine learning (ML) models, many of these are black-box models, which cannot explain the internal processes that lead to their prediction. Without explanations, the model has no grounds to convince the labeler that its predictions are the correct ones.

Our Contributions

We propose a visual-interactive tool, called Explainable Labeling Assistant (XLabel), which takes an explainable ML approach to data labeling. The main component of XLabel is a predictive ML model that not only accurately predicts the label of each record, but also provides a visual explanation that indicates which input features highly influence its label prediction; the model’s explanation is what allows the user to fully understand the prediction, and then promptly accept it as the true label, or make a correction as needed. We thus have an interactive human-machine system at hand: XLabel’s predictions and explanations reinforce the user’s labeling decisions, and new labels from the user allow XLabel to improve the predictive model. In addition, XLabel can also be used to detect mislabeled data by comparing its predictions with the existing labels.

In this study, we focus on the task of labeling medical records of patients with potential non-communicable diseases (NCDs), which is one of the most concerning health issues worldwide. We will focus on four common NCDs: diabetes mellitus (DM), hypertension (HTN), chronic kidney disease (CKD), and dyslipidemia (DLP). We will design a user interface that allows the user to interact with the model’s predictions. In addition, we will perform experiments which demonstrate that 1) our explainable model is as accurate as black-box ML models, and 2) it can recall most of the correct labels even when a sizable portion of the data has been mislabeled.

Related Work

There have been many studies that apply ML techniques for prediction of various NCDs; for example, hypertension [1, 2], diabetes mellitus [23, 14], stroke [27, 24] and asthma [11, 19]. Some of these works take the explainable ML approach. For example, Rashed-Al-Mahfuz et al. [25] use Shapley Additive Explanations (SHAP) [18] to interpret the decisions of various ML models for chronic kidney disease diagnosis. Shafi et al. [29] use DeepSHAP [6] to explain ML models’ predictions of Alzheimer’s disease. Davagdorj et al. [9] use DeepSHAP to explain predictions of multiple NCDs. Cheng et al. [8] use Partial Dependence Plot [12], SHAP, Anchors [26] and Accumulated Local Effects [3] to explain predictions of multiple NCDs. In contrast to these works, in which the ML models are trained on fully labeled datasets, our work is the first to employ an explainable ML model to assist with data labeling.

There has been a surge of interest in human-machine interactive labeling. In Nadj et al.’s review [20] interactive labeling systems are categorized into five design principles. Viana et al. [30] extend this work by also analyzing their user interfaces. Yakimovich et al. [31] provide an extensive review over many automatic data annotation strategies, with different levels of human involvement. For specific methods, Desmond et al. [10] design a labeling assistant that uses a semi-supervised learning algorithm for label suggestions. Ashktorab et al. [4] design a labeling interface that presents the labeler with a batch consisting of nearest neighbors of a random example; these neighbors are likely to share a label. All in all, one must be careful when designing an interactive labeling system, as an experiment by Bondi et al. [5] shows that human judgement is biased towards the model’s
Figure 1: A high-level picture of XLabel. It sends pseudo-labels and their explanations to the user. The user then turns the pseudo-labels into true labels by keeping the correct pseudo-labels or flipping the wrong ones. The labels are then sent back to XLabel and the data warehouse.

predictions. To this end, our method introduces one way of reducing the bias—by providing the labeler with explanations of the predictions.

2 Materials and Methods

2.1 The Data Labeling Task

We start with a raw database of check-up records of NCD patients; note that one patient can have more than one record (in the case of revisits). Each record contains the following information:

- Personal features that are age, sex, height, and weight.
- Laboratory results such as blood sugar level and blood pressures.
- International Classification of Diseases (ICD-10) codes of diagnosed diseases.
- Doctor’s notes.
- A list of prescribed drugs.

In the case of minor visits (e.g., to refill the prescription), the record might not have some laboratory results and ICD-10 codes.

To make the database useful for future NCD analysis, we ask a medical expert to label each record with four NCD labels: diabetes mellitus (DM), hypertension (HTN), chronic kidney disease (CKD), and dyslipidemia (DLP). In other words, the database will have four additional columns, each of which contains the labels of each NCD.

In this work, we introduce a new visual-interactive tool that helps with data labeling, which will be described in the next section.

2.2 Visual-Interactive Labeling

Labeling massive medical data can be very time-consuming. To reduce medical experts’ workload, we design a visual-interactive tool called Explainable Labeling Assistant (XLabel). The most im-
portant part of **XLabel** is a prediction model that takes a patient’s record as an input, and suggests a label \( y \in \{0, 1\} \) of that record to the user; here, \( y \) is 1 if the disease is present, and 0 otherwise.

To ensure that the model’s suggestions are trustworthy, we take an explainable approach; the model must be able to explain the reasons behind its suggestions. A high-level picture of the labeling process with **XLabel** is as follows (also shown in Figure 1:

- **XLabel** reads the data of all unlabeled records, then creates a pseudo-label for each record.
- **XLabel** shows a subset of records, their pseudo-labels, and their explanations to the user.
- The user reads the explanations, then turns the pseudo-labels into true labels by keeping the correct pseudo-labels and flipping the wrong ones (i.e., from 0 to 1 or 1 to 0).
- **XLabel** accepts the labels from the user and retrains its prediction model. Now the model can provide more accurate pseudo-labels to the next unlabeled sample.

The user’s labeling workload will be vastly reduced if most of the pseudo-labels are already correct. Thus, in addition to being explainable, the prediction model inside **XLabel** must be accurate. Recently, there have been a series of works showing that, contrary to widespread belief that there is a trade-off between explainability and accuracy, it is possible for a ML model to be both explainable and accurate [16, 28].

### 2.3 Explainable Boosting Machine (EBM)

The prediction model that we use in **XLabel** is Explainable Boosting Machine (EBM) [17, 21], an explainable version of gradient boosting machine [12, 13], which is known for its predictive performance.

Let \( x = \{x_1, \ldots, x_n\} \) be a patient’s record with true label \( y \in \{0, 1\} \). The EBM is an additive model, that is, its prediction on \( x \) is given by

\[
f(x) = \beta_0 + \sum_i f_i(x_i) + \sum_{i,j} f_{ij}(x_i, x_j),
\]

where \( \beta_0 \) is the intercept, and each \( f_i \) is a sum of regression trees, that is,

\[
f_i(x_i) = \sum_k f_{ik}(x_i)
\]

\[
f_{ij}(x_i, x_j) = \sum_k f_{ijk}(x_i, x_j).
\]

Here, \( f_{ik} \) and \( f_{ijk} \) are regression trees for all \( i, j \) and \( k \).

The model then outputs the probability prediction through the logistic function:

\[
p_x = \Pr(y = 1 \mid x) = \frac{1}{1 + e^{-f(x)}}.
\]

The predicted label is then \( \hat{y} = 1 \) if \( \Pr(y = 1 \mid x) \geq 0.5 \) and \( \hat{y} = 0 \) if \( \Pr(y = 1 \mid x) < 0.5 \).
2.4 XLabel’s Explanations

The fact that EBM is an additive model allows XLabel to measure the contribution from each input feature towards the prediction. More precisely, from (1), we can treat \( f_i(x_i) \) as the contribution from \( x_i \) (we shall ignore the interactive terms \( f_{ij}(x_i, x_j) \) as they are used to model the residual [17]). In particular, \( f(x_i) > 0 \) implies that \( x_i \) contributes to a positive label, while \( f(x_i) < 0 \) implies that \( x_i \) contributes to a negative label.

To visualize these features’ contributions, we chose the heatmap, as its compact representation allows the user to scroll through the records very quickly. In each heatmap, a rectangle is drawn for each feature, and the color is determined by its contribution. Since the contribution of each variable can be an arbitrarily large positive or negative number, we have to scale it to a range of \((0, 1)\) using the logistic function:

\[
\text{HEAT}(x_i) = \frac{1}{1 + e^{-f_i(x_i)}}.
\]

The rectangle is then colored red if \( \text{HEAT}(x_i) \) is close to 1 and blue if it is close to 0. This heatmap allows the user to quickly notice the features that contribute the most to the label, and then promptly decide to keep or flip the label.

In addition to the heatmap, XLabel displays the doctor’s notes and highlights keywords that are associated with the labels. The keywords are provided by the NCD experts.

2.5 Sampling Method

Now, our goal is to make EBM as accurate as possible with only a few labeled records sent from the user to XLabel. To accomplish this, XLabel sends the “least confident” records to the user. After the user submits the true labels, EBM then learns from these labels and becomes more confident in predicting labels of similar records.

To compute the EBM’s confidence score of a record \( x \), i.e., how confident it is in its prediction \( \hat{y} \) of \( x \), we use the misclassification rate:

\[
C_x = \min\{p_x, 1 - p_x\}. \tag{2}
\]

Note that \( C_x \in [0.5, 1] \), \( C_x = 1 \) when EBM is most confident in \( x \)’s prediction (i.e., \( p_x = 1 \) or \( p_x = 0 \)) and \( C_x = 0.5 \) when it is least confident (i.e., \( p_x = 0.5 \)).

At the beginning, XLabel lets the user choose between two sampling methods:

- **Confidence threshold**: XLabel will select all records whose confidence scores are less than a threshold specified by the user.
- **\( n \)-least confident**: XLabel will select \( n \) records with the smallest confidence scores. Here, the sample size \( n \) is specified by the user.

Starting from the probability predictions of all records, XLabel computes the confidence scores according to (2) and samples a subset of records according to the chosen sampling method.
2.6 Correcting Mislabeled Data

Sometimes the expert might mislabel the data due to missing an important keyword or fatigue. For example, the expert might miss the “DM” tag (which indicates that the record has diabetes mellitus) in the clinical note and label the record as “non-DM”.

XLabel can also be used to detect mislabeled records. To illustrate this, let us denote the whole dataset by $\mathcal{X} = \mathcal{X}_L \cup \mathcal{X}_U$, where $\mathcal{X}_L$ is the set of labeled records and $\mathcal{X}_U$ is the set of unlabeled records. Suppose that the EBM has been trained on $\mathcal{X}_L$, which contains sufficiently many correctly labeled records. Instead of asking EBM to predict only on $\mathcal{X}_U$, XLabel can ask EBM to give predictions to the whole dataset $\mathcal{X}$. Sometimes, there is a record whose EBM ’s prediction is different from the current label, indicating that the record might be mislabeled; XLabel will show such records (together with the sampled records from $\mathcal{X}_U$ as described above) and ask the user to confirm or change the label.

3 Results

3.1 Experiment Data

To demonstrate the effectiveness of XLabel, we will perform several experiments on sample data consisting of 427 medical records of clinical visits to Sriphat Medical Center, Chiang Mai, Thailand, which have been carefully labeled by medical experts. Specifically, the data consists of 53 DM, 51 HTN, 26 CKD, and 44 DLP records.

It is inefficient to train EBM on all features since most of the features are unrelated to each NCD type. Therefore, for each NCD type, we train EBM only on a subset of features. The features suggested by the medical experts are listed in Table 1. The full list of keywords, ICD-10 codes, and drugs for each NCD type can be found in Tables 2 to 4.

Since CKD’s prediction can only be made when DM and HTN’s predictions are available, and DLP’s prediction requires all the other three NCDs’ predictions. Thus, the predictions have to be made in the following order: DM → HTN → CKD → DLP.

3.2 XLabel’s User Interface

We have implemented XLabel in Streamlit (https://streamlit.io), which is an open-source application framework in Python. Inside XLabel, we employ the InterpretML’s implementation of EBM [21]. A screenshot of the interface is shown in Figure 2. After the user uploads a file of unlabeled records, they will be asked to select 1) whether to identify pre-labeled records, whose labels do not match with EBM ’s predictions and 2) one of the two sampling methods.

After the user clicks the Sample button, EBM makes predictions on all unlabeled records and suggests them as pseudo-labels. XLabel then shows the pseudo-labels and the heatmaps (the explanations) in the main window. Regardless of the sampling method, records with low confidence scores will show up early during the labeling process. In each heatmap, red features are the main contributors of positive labels, while the blue features are those of negative labels. As we can see in Figure 2, the main contributor of the positive labels of both records is the “DM” tags, which indicate that both patients have been diagnosed with diabetes mellitus during prior visits.

Moreover, XLabel is able to detect mislabeled records; in Figure 2, we notice that Record #105 and #121 were mislabeled as negatives, even though the medical notes indicate that the labels are
3.3 Performance of EBM

In the first experiment, we demonstrate that, in addition to being explainable, EBM performs well compared to a baseline and several top-performing ML models for tabular data. Here, the baseline is a simple rule-based model (RuleBased) that classifies a medical record based on a well-known guideline for each disease; see Figure 5 and 6 for the full descriptions of RuleBased. The ML models that are used to compare against EBM are random forest (RF), support vector machine (SVM) (implemented in Scikit-learn [22]), extreme gradient boosting machine (XGB) [7] and light gradient boosting machine (LGBM) [15]. The hyperparameter settings of these models can be found in Table 5.

To evaluate these models, we apply 5-fold cross-validation to assess their out-of-sample performances. The metrics that we use to evaluate the models are F1-score, Accuracy, Precision, and Recall. Among these, F1-score is our main performance metric, as it is robust to imbalanced data (e.g., a trivial model that classifies all records as 0 will receive a high accuracy but low F1-score).

For each NCD, we perform 5-fold cross-validation, resulting in models’ predictions over five different test sets. For each test set, we calculate the F1-score, accuracy, precision, and recall of the predictions against the true labels. As a result, we obtain five values for each metric, whose mean and standard deviation (SD) are reported as a bar chart with ±1SD error bars. The performances of
Figure 3: The results of 5-fold cross-validations of EBM, SVM, LGBM, XGB, RF and RuleBased. Here, four classification metrics across all NCDs are reported. The error bars represent the one standard deviations.

EBM and the other models for classifications of four NCDs are displayed by the metrics (rows) and the NCDs (columns) in Figure 3. Note that some of the RuleBased's scores are below the charts' lower bound (0.8) and hence missing from the plots. For the results in table form, see Tables 6 to 9.
3.4 Robustness of EBM to Label Noise

One purpose of XLabel is to identify mislabeled records and correct them. We herein perform an experiment to demonstrate that EBM is robust to label noise, compared to the other models introduced in the previous experiment.

This experiment starts with the dataset of medical records, which has been carefully labeled by medical experts. We flip the labels of a random sample consisting of 5%, 10%, ..., 50% of the records. We then train EBM on the dataset with the noisy labels and use it to make predictions on the mislabeled records. The model’s robustness to label noise will be measured by how many of these predictions match with the true labels. In other words, we will measure the accuracy of the predictions on the mislabeled records.

We compare EBM against RuleBased and several ML models. For each model and each percentage level $p$, we sample and train the models ten times and average the resulting accuracies. The plots of the models’ average accuracies against the proportion of mislabeled records for each NCD are shown in Figure 4.

Figure 4: The results of an experiment for label noise robustness of EBM, SVM, LGBM, XGB, RF and RuleBased. In this experiment, we intentionally mislabeled a portion of the records, and then measured the accuracies of the models on the mislabeled data. Each of the four plots shows the accuracy (y-axis) against the proportion of mislabeled data (x-axis) for each NCD.
4 Discussion

4.1 Performance of EBM

From Figure 3, we notice that all ML models perform well in all NCDs, having more than 0.9 in all classification metrics; EBM in particular has more than 0.99 accuracy and 0.96 F1-score. Moreover, all ML models have perfect predictions on chronic kidney disease and dyslipidemia. We also notice that, while being outperformed by the other models in F1-score, accuracy, and precision, RuleBased has 100% recall rate in all NCDs, meaning that the model is exceptional at identifying NCD patients, although with high false positive rates. Since our goal is to reduce medical experts’ workload by making our label suggestions as accurate as possible, the ML models, which have higher F1-scores and accuracies, should be preferred over RuleBased.

Comparing against the other ML models, we see that EBM performs equally well as the other gradient boosting models, namely XGB and LGBM, and outperforms SVM and RF. EBM also has an additional benefit of being an additive model, which allows us to quantify and visualize the contribution of each variable towards the final prediction. This experiment demonstrates that an ML model can be both accurate and explainable.

Looking at the error bars of the recalls, we notice that the recalls of all ML models vary a lot across different test sets; this is caused by the fact that the records are heavily skewed towards negative labels. For example, there are 52 records with DM-positive labels. During the cross-validations, the models are evaluated on five test sets, each of which consists of one-fifth of the dataset, resulting in a small number of 9–12 DM-positive records per test set; this causes large swings in recalls across different test sets, as they are the proportions of DM-positive records that are correctly classified by the models.

We also inspect the records that EBM misclassifies, which turn out to be one of the following cases:

- Records with blood sugar more than 250 mg/dL but are not identified with Diabetes mellitus. In this case, EBM will most likely give us a false positive.
- Records with typographical errors on important keywords in the doctor’s notes. Specifically, there is a medical note with “DM” mistyped as “DN”. If the record contains no other indication of diabetes mellitus, then EBM will give us a false negative.
- Hypertension records with no relevant keywords (such as “HT” or “HTN”) in the medical notes, and the systolic or diastolic blood pressure is just in the hypertension range. There are two patients whose medical notes contain no indicator of hypertension, while their blood pressures are 153/72 mmHg and 145/93 mmHg, indicating that they have hypertension.

The mistyping issue can be fixed by Edit Distance-based spelling correction. In the other two cases, XLabel will give the record with a low confidence score—such a record will be presented earlier to the user in either of the two sampling methods.

4.2 Robustness of EBM to Label Noise

We see from Figure 4 that EBM, SVM, LGBM, and RuleBased are the most robust to label noises. We note that the accuracy of RuleBased does not go down with the label noise, because RuleBased is a set of rules based solely on the features, and not the label. However, when only 5%–20% of the
records are mislabeled (or 5%–45% in the cases of HTN and CKD), it is less accurate than EBM, SVM, and LGBM.

Even when 40%–45% of the records are mislabeled, EBM, SVM, and LGBM still retain their high accuracies; in the cases of diabetes mellitus, hypertension, and dyslipidemia, EBM is more accurate than the other ML models. Although the accuracies of these models drop quickly after the 45% mark, we do not expect this many records to be mislabeled in a real-life scenario.

5 Conclusions

We developed a new visual-interactive tool for NCD data labeling called Explainable Labeling Assistant (XLabel). The main feature of XLabel is its ability to provide explanations of the label suggestions in the form of heatmaps. Under the hood, XLabel employs Explainable Boosting Machine (EBM) which is an explainable machine learning model inspired by the top-performing gradient boosting machine. Our experiments show that, not only does EBM outperform RuleBased and several machine learning models, but it is also very robust to label noise; even when 40% of the data are mislabeled, EBM can recall almost all of the true labels. Even though XLabel was employed specifically to label NCD data, we hope that XLabel will be of use in other labeling tasks as well.

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## A Input Features for NCD classifications

| Target label | Feature name | Description |
|--------------|--------------|-------------|
| DM           | DM_key       | 1 if the medical note has DM-related keywords, 0 otherwise |
|              | DM_ICD10     | 1 if at least one of the ICD-10 codes is DM-related, 0 otherwise |
|              | DM_drugs     | 1 if the prescribed drugs are DM-related, 0 otherwise |
|              | Glucose      | Blood sugar level (mg/dL) |
|              | HbA1c        | Hemoglobin A1c (%) |
|              | eGFR         | Estimated glomerular filtration rate (mL/min/1.73m²) |
| HTN          | HTN_key      | 1 if the medical note has HTN-related keywords, 0 otherwise |
|              | HTN_ICD10    | 1 if at least one of the ICD-10 codes is HTN-related, 0 otherwise |
|              | HTN_drugs    | 1 if the prescribed drugs are HTN-related, 0 otherwise |
|              | sbp1         | Systolic blood pressure (mmHg) |
|              | dbp1         | Diastolic blood pressure (mmHg) |
| CKD          | CKD_key      | 1 if the medical note has CKD-related keywords, 0 otherwise |
|              | CKD_ICD10    | 1 if at least one of the ICD-10 codes is CKD-related, 0 otherwise |
|              | CKD_drugs    | 1 if the prescribed drugs are CKD-related, 0 otherwise |
|              | DM_pred      | EBM’s predicted label of DM (0 or 1) |
|              | HTN_pred     | EBM’s predicted label of HTN (0 or 1) |
|              | eGFR         | Estimated glomerular filtration rate (mL/min/1.73m²) |
| DLP          | DLP_key      | 1 if the medical note has DLP-related keywords, 0 otherwise |
|              | DLP_ICD10    | 1 if at least one of the ICD-10 codes is DLP-related, 0 otherwise |
|              | DLP_drugs    | 1 if the prescribed drugs are DLP-related, 0 otherwise |
|              | Glucose      | Blood sugar level (mg/dL) |
|              | DM_pred      | EBM’s predicted label of DM (0 or 1) |
|              | HTN_pred     | EBM’s predicted label of HTN (0 or 1) |
|              | CKD_pred     | EBM’s predicted label of CKD (0 or 1) |
|              | LDL-c        | Low-density lipoprotein cholesterol (mg/dL) |
## List of keywords, ICD-10 codes and drugs associated with each NCD

### Table 2: Keywords associated with each NCD

| NCD                          | Feature name | Keywords                      |
|------------------------------|--------------|-------------------------------|
| Diabetes mellitus            | DM_key       | DM, diabetes, T1D, T2D        |
| Hypertension                 | HTN_key      | HT, hypertension, bisoprolol   |
| Chronic kidney disease       | CKD_key      | CKD                           |
| Dyslipidemia                 | DLP_key      | DLP, dyslipid, statin         |

### Table 3: ICD-10 codes associated with each NCD

| NCD                          | Feature name | Related ICD-10                |
|------------------------------|--------------|-------------------------------|
| Diabetes mellitus            | DM_ICD10     | E109, E112, E118, E119, E132 |
| Hypertension                 | HTN_ICD10    | I10, I482, I158, I159         |
| Chronic kidney disease       | CKD_ICD10    | N179, N182, N183, N184, N185, N189 |
| Dyslipidemia                 | DLP_ICD10    | E782, E785, E789             |

### Table 4: Drugs associated with each NCD

| NCD                          | Feature name | Related drugs                                      |
|------------------------------|--------------|---------------------------------------------------|
| Diabetes mellitus            | DM_drugs     | Alogliptin, Empagliflozin, Gliclazide, Glimepiride, Glipizide, Loranta, Teneligliptin, Desmopressin, Insulin, Metformin, Pioglitazone, Semaglutide, Sitagliptin |
| Hypertension                 | HTN_drugs    | Amlodipine, Bisoprolol, Carvedilol, Doxazosin, Hydrochlorothiazide, Lercanidipine, Losartan, Mande Dipine, Valsartan |
| Chronic kidney disease       | CKD_drugs    | Allopurinol, Epoetin alfa, Folic acid, Furosemide, Hydrochlorothiazide, Sodium bicarbonate, |
| Dyslipidemia                 | DLP_drugs    | Atorvastatin, Simvastatin                        |
C Rule-based Classification Models

The details of RuleBased for classification of diabetes mellitus (DM), hypertension (HTN), chronic kidney disease (CKD) and dyslipidemia (DLP) are shown in Figure 5 and Figure 6.

![DM classification flow chart]

![HTN classification flow chart]

Figure 5: Left: a flow chart of RuleBased for DM classification. Right: a flow chart of RuleBased for HTN classification.
Figure 6: Left: a flow chart of RuleBased for CKD classification. Right: a flow chart of RuleBased for DLP classification.
### D Models’ hyperparameters

Most of the hyperparameters are set at the corresponding package’s default values. All hyperparameters with non-default values are shown in Table 5.

| Model | Hyperparameter | Value |
|-------|----------------|-------|
| RF    | Number of trees | 200 (DM), 100 (HTN, DLP), 50 (CKD) |
|       | Minimum number of records per leaf | 1 |
| XGB   | Number of trees | 2 |
|       | Minimum sum of record weight in a leaf | 1 (DM), 0 (HTN, CKD, DLP) |
| LGBM  | Number of trees | 6 (DM, DLP), 5 (HTN, CKD) |
|       | Minimum number of records per leaf | 1 |
|       | Maximum number of leaves | 2 |
| SVM   | C | 0.1 (DM, DLP), 0.05 (HTN, CKD) |
|       | Kernel | Linear |
|       | Optimization | Primal |
| EBM   | Number of pairwise interactions | 0 |
|       | Maximum number of bins in feature binning | 2 |
### E Additional Results

#### Table 6: Average diabetes mellitus (DM) classification scores with one standard deviation

| Model   | F1-score   | Accuracy   | Precision | Recall    |
|---------|------------|------------|-----------|-----------|
| RuleBased | 0.833±0.065 | 0.951±0.020 | 0.719±0.096 | 1.000±0.000 |
| RF      | 0.940±0.097 | 0.988±0.018 | 0.950±0.100 | 0.932±0.097 |
| SVM     | 0.951±0.052 | 0.991±0.009 | 0.980±0.040 | 0.932±0.097 |
| LGBM    | **0.962±0.056** | **0.993±0.009** | **1.000±0.000** | 0.932±0.097 |
| XGB     | **0.962±0.056** | **0.993±0.009** | **1.000±0.000** | 0.932±0.097 |
| EBM (ours) | **0.962±0.056** | **0.993±0.009** | **1.000±0.000** | 0.932±0.097 |

#### Table 7: Average hypertension (HTN) classification scores with one standard deviation

| Model   | F1-score   | Accuracy   | Precision | Recall    |
|---------|------------|------------|-----------|-----------|
| RuleBased | 0.462±0.078 | 0.724±0.053 | 0.304±0.070 | 1.000±0.000 |
| RF      | **0.980±0.025** | **0.995±0.006** | **1.000±0.000** | 0.962±0.047 |
| SVM     | **0.980±0.025** | **0.995±0.006** | **1.000±0.000** | 0.962±0.047 |
| LGBM    | **0.980±0.025** | **0.995±0.006** | **1.000±0.000** | 0.962±0.047 |
| XGB     | **0.980±0.025** | **0.995±0.006** | **1.000±0.000** | 0.962±0.047 |
| EBM (ours) | **0.980±0.025** | **0.995±0.006** | **1.000±0.000** | 0.962±0.047 |

#### Table 8: Average chronic kidney disease (CKD) classification scores with one standard deviation

| Model   | F1-score   | Accuracy   | Precision | Recall    |
|---------|------------|------------|-----------|-----------|
| RuleBased | 0.438±0.188 | 0.845±0.054 | 0.297±0.139 | 1.000±0.000 |
| RF      | **1.000±0.000** | **1.000±0.000** | **1.000±0.000** | **1.000±0.000** |
| SVM     | **1.000±0.000** | **1.000±0.000** | **1.000±0.000** | **1.000±0.000** |
| LGBM    | **1.000±0.000** | **1.000±0.000** | **1.000±0.000** | **1.000±0.000** |
| XGB     | **1.000±0.000** | **1.000±0.000** | **1.000±0.000** | **1.000±0.000** |
| EBM (ours) | **1.000±0.000** | **1.000±0.000** | **1.000±0.000** | **1.000±0.000** |

#### Table 9: Average dyslipidemia (DLP) classification scores with one standard deviation

| Model   | F1-score   | Accuracy   | Precision | Recall    |
|---------|------------|------------|-----------|-----------|
| RuleBased | 0.671±0.073 | 0.902±0.016 | 0.509±0.080 | 1.000±0.000 |
| RF      | **1.000±0.000** | **1.000±0.000** | **1.000±0.000** | **1.000±0.000** |
| SVM     | **1.000±0.000** | **1.000±0.000** | **1.000±0.000** | **1.000±0.000** |
| LGBM    | **1.000±0.000** | **1.000±0.000** | **1.000±0.000** | **1.000±0.000** |
| XGB     | **1.000±0.000** | **1.000±0.000** | **1.000±0.000** | **1.000±0.000** |
| EBM (ours) | **1.000±0.000** | **1.000±0.000** | **1.000±0.000** | **1.000±0.000** |