10-Year Breast Cancer Survival Prediction Research based on Missing Value Imputation

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Abstract: The use of machine learning for medical data mining is one of most preferable research field in the healthcare field. In the medical health field, there is a large amount of data containing information, and these data will be continuously stored in the database. Using machine learning to mine valuable information from medical data can provide a certain scientific reference for decision-making about patient health. This paper used breast cancer data from SEER (Surveillance of Epidemiology and End Result) which is contributed by National Cancer Institute. The database is a large-scale and open database. The proposed research work first analyzes the breast cancer data set, and then applies data mining methods to evaluate the results. Data mining is used to obtain disease patterns that doctors can effectively use. In order to predict the survival ability of breast cancer patients, this paper proposes an hybrid missing values imputation method that is KNNI + kmeans-GMM to deal with missing values, and four classifiers (XGBoost, Random Forest, Decision tree, K-nearest neighbor) are used to established 10-year survival models. The experimental results show that the accuracy of breast cancer survival model can be improved through missing value imputation. KNNI + kmeans-GMM is an effective missing value imputation method, which combines the survival model established by the XGBoost classifier with the best accuracy(0.854) and AUC(0.835). Besides, the accuracy and AUC of the 10-year breast cancer survival model established based on this data and the XGBoost algorithm are 0.847 and 0.818, respectively.

1 INTRODUCTION

According to the World Health Organization (WHO), breast cancer is the most common cancer among women worldwide in 2020, it is estimated that about 30% of the newly added female patients are diagnosed as breast cancer patients, which not only seriously threatens the health of women but also affects countries at all levels of modernization. Thankfully, the mortality rate of breast cancer has been declining since about 1990, one of the main reasons for this is the continuous improvement of treatment. In recent years, machine learning algorithms to construct cancer survival data-driven model can help predict prognosis and management of cancer, to make informed decisions provide a reference for physicians to potential necessity to adjuvant therapy. Therefore, over the years, there have been many studies trying to use data mining or machine learning techniques to predict patient survival rates. The literature shows that it has made a certain contribution to the treatment of breast cancer patients by predicting the survival rate.

Survival model prediction is based on scientific data analysis of big data, and most of the medical data has missing values, that is, the effective information of the data is uncertain, which makes the data difficult to use. Besides, the data basis of machine learning algorithms is complete and categorizable. Therefore, how to deal with the data to obtain valid information to improve the accuracy of survival models become one of the new challenges.

In order to deal with the problem of missing data more effectively, it is necessary to understand the mechanism and form of missing data. Variables (attributes) in the data set that do not contain missing values are called complete variables, and variables in the data set that contain missing values are called incomplete variables, Little and Rubin define the following three different data missing mechanisms. (1) Missing completely at random (MCAR), the missing data is completely random, does not depend on any incomplete or complete variables, and does

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not affect the unbiasedness of the sample,

for example patients' race. (2) Missing at random (MAR), missing data is not completely random, that is, missing data of this type depends on other complete variables, eg. the extension of tumor is related to tumor size. (3) Not missing at random (NMAR), missing values depend on both the complete variable and the incomplete variable itself, such as tumor size depend on whether the patient's tumor is benign or malignant. Missing value processing is one of important parts of data preprocessing.

The purpose of this study is to establish a better breast cancer survival model from the data level. There are many strategies available for handling missing data. Delen et al. used a complete analysis method to impute SEER breast cancer data, and three machine learning algorithms (neural network, decision tree (DT), and logistic regression (LR)) were used to build survival models. Rathore et al. replaced missing value with mean value in their SEER breast cancer data preprocessing, and ensemble approach was used to classify. Lotfnezhad Afshar used the multiple imputation method for missing value based on SEER breast cancer data. Pedro J.et al. compared three missing value imputation methods, mode imputation, expectation maximization imputation (EMI), K-nearest neighbor imputation (KNNI) methods and combined four classification algorithms of K-nearest neighbor (KNN), decision tree (DT), logistic regression (LR), and support vector machine (SVM) to establish breast cancer survival model, respectively, the result showed that the combination of KNNI and KNN classifier was the best. Missing values are dealt differently in different studies. Although the most commonly reported dealing with missing value approaches in breast cancer survival are simple statistical analysis methods, it is worth noting that missing value processing is an area that is getting more and more attention, several techniques, derived from machine learning and improved methods, have been developed and applied for breast cancer datasets. Migdady used enhanced fuzzy kmeans clustering methods to impute missing values, the experiments showed a clear improvement in the imputation accuracy. Zhang. et al. predicted missing values in medical data via XGBoost regression, and the result showed that their model exhibits an imputation improvement by over 20% on average. Marco proposed EM-based finite mixed multivariate Gaussian (GMM) for missing data, Rahman applied fuzzy clustering methods and fuzzy expectation maximization algorithms (FEMI) to identify a group of similar records and estimate missing values based on the group of records, the result showed that it performs significantly better than EMI, GkNN, FKMI, SVR, and IBLLS.

Each strategy for handling missing data has an underlying assumption regarding the missing data mechanism, that is, the missing value processing method conforms to the missing mechanism of missing data, if not satisfied, it may lead to deviations in parameter estimates. For example, the commonly used complete case analysis assumes that the missingness in the covariates is not associated with the outcome. Most single imputation and multiple imputation approaches assume that the missingness is related to the observed data but does not depend on the unobserved value itself. Therefore, in this research, we propose an improved missing value imputation method KNN imputation (KNNI) + kmeans-GMM to fill in missing values and compared with six commonly use missing value methods(KNNI, EMI, LRI, mean& mode, missforest, deleting). Finally, an effective 10-year breast cancer survival prediction model based on complete dataset was established.

2 SEER BREAST CANCER DATASET

Surveillance, Epidemiology, and End Results (SEER) database is the authoritative cancer statistical database in US, which collects cancer diagnosis, treatment and survival data for approximately 30% of the American population. Among these data, SEER contains information about over 1.6 million incidences of BC between the years 1973 and 2015. Due to the database has huge and comprehensive data, it not only provides a good data foundation for machine learning, but also supplies data support for the establishment of breast cancer survival model. By referring to literatures, in this experiment, more than 1.3 million cases with 22 features from 1973 to 2015 are used to establish breast cancer survival model after data type conversion, features merging and data cleaning. It is similar to literature, that after simple data processing, many features in the data still have a lot of data missing. The data information is shown in the Figure 1 below.

And not all features of each sample are missing, but a single or a certain feature in the sample is missing.

For the prediction of the overall survival rate of patients, we use the final state of the patient that is ‘vital status’(‘vst’) as the classification label, when ‘vst’ is ‘alive’, patient is alive, otherwise the patient is dead. According to the relative survival framework, for different survival prediction (for example, 10 years), patient survival information is used to define classification categories. Patients who survive beyond the prognosis period are marked as positive, while patients who die before reaching this stage are considered as negative. Therefore, when predicting the 10-year survival probability of breast cancer patients, the label of ‘survival month’&(‘SM’) is more than 10 years that the patient is survival, otherwise, non-survival. As a result, the problem of predicting breast cancer survival can be correctly defined as a binary classification problem, and the prediction model of machine learning can be used.

3 METHODS

In this section, common missing data imputation methods applied in our breast cancer dataset and the machine learning methods used to predict survival models will be described. We first introduce the commonly used missing value imputation methods, which are mean imputation, K-Nearest neighbors imputation(KNNI), MissForest imputation(MI), Linear regres- sion imputation(LRI), Expectation maximization imputation(EMI) and the hybrid imputation KNNI + kmeans-GMM. Then, the four classification algorithms XGBoost classifier(XGBoost), Random Forest classifier(RF), K Nearest Neighbor classifier (KNN) and Decision Tree classifier (DT) are introduced.

3.1 Mean or Mode Imputation

The mean imputation method is to fill in the missing value with the corresponding attribute mean of the existing data, but it should be noted that the data variable needs to obey or approximately obey the near-state distribution, otherwise the mode or median under the attribute is used to fill in the missing value. In other words, it is to first determine the data type of the missing value, and then adopt different filling methods according to the data type, fill the average value of other objects under the same attribute to the numerical missing value; or use the principle of majority to take the same attribute down The value with the most number of values is filled with non-numeric missing values. Mean filling method is currently the most used in filling methods.

3.2 K-Nearest Neighbors Imputation (KNNI)

KNNI is a classical method for missing value imputation. KNN commonly uses Euclidean distance as the sample similarity measurement distance. Given two n-dimensional vectors $\{x_1, x_2, ..., x_n\}$, $\{y_1, y_2, ..., y_n\}$, then Euclidean distance $Dist= \sqrt{\sum_{k=1}^{n}(x_{ik}-y_{ik})^2}$. Through distance measurement, k neighboring samples of the missing data sample can be found, and then the approximate value of the missing sample can be determined. For example, Given data $X =$

[[3, *np.nan,* 5], [1, 0, 0], [3, 3, 3]], $d_{12} = \sqrt{(3-1)^2+(5-0)^2} > d_{13} = \sqrt{(3-3)^2+(5-3)^2}$ then the first sample is closer to the third sample so the approximate value of the null value is 3.

3.3 MissForest Imputation (MI)

MissForest is a highly flexible model that uses the random forest method to predict missing values, it can impute multivariate data consisting of continuous variables and categorical variables with missing values, and it outperforms KNNI, MICE and mean on multiple biological and medical data sets.

3.4 Linear Regression Imputation (LRI)

LRI is basically to establish a regression equation through a complete data set, and then use the predicted value of the regression equation to fill in the missing data. Assuming Y is the missing variable, existing complete features $X_i (i = 1, 2, ...m)$ having a linear regression relationship with Y , the regression equation is established as follows: $Y_i = \alpha_0 + \sum_{i=1}^{m}\alpha_i X_{ij}$, α_0 is intercept, α_i represents the relationship between variable X_i and dependent variable Y .

Table 1: Experimental data used to evaluate missing value imputation methods and establish survival prediction models.

Name	Type	SEER field	Description	Missing rate	
				80%train	20%test
nodesexamined	Continuous	Regional nodes examined (1988+)	Total number of regional lymph nodes detected	14.1%	14.1%
nodespositive	Continuous	Regional nodes positive (1988+)	Total number of regional lymph nodes metastasized	34.5%	34.5%
tumorsize	Continuous	CS tumor size (2004+)	Information on tumor size	22.8%	22.9%
extension	Continuous	CS extension (2004+)	Information on extension of the tumor	13.9%	14.0%
lymphnodes	Continuous	CS lymph nodes (2004+)	Information on involvement of lymph nodes	13%	13%
mets	Continuous	CS mets at dx (2004+)	Information of tumor on metastasis	47.8%	47%
grade	Discrete	Category based tumor stage	Category based on the appearance of tumor, tumor stage	23.3%	23.4%
reasonsurgery	Discrete	Reason no cancerdirected surgery	Reasons for not performing surgery at the primary site	0.8%	0.8%
ER	Discrete	ER Status Recode Breast Cancer (1990+)	Estrogen receptor	15.2%	15.3%
PR	Discrete	PR Status Recode Breast Cancer (1990+)	Progesterone receptor	16.6%	16.6%
race	Discrete	Race recode (W, B, AI, API)	Race information	0.6%	0.5%
surgery	Discrete	Surgery	Surgical site information	0.5%	0.5%
BCstage	Discrete	Breast Adjusted AJCC 6th Stage (1988+)	Breast tumor information	0.5%	0.5%
maritalstatus	Discrete	Marital status at diagnosis	Patient's marital status	16.9%	16.9%
historicstage	Discrete	SEER historic stage A	Extent of tumor spread based on histological type	4.3%	4.3%
behavior	Discrete	Behavior code ICD-O-3	Tumor classification(malignant or benign)	0	0
laterality	Discrete	Laterality	One side of the matched organ	0	0
histology	Discrete	Histology ICD-O-3	Tumor histological type	0	0
primsrysite	Discrete	The origin of the primary tumor	The origin of the primary tumor	0	0
Year	Discrete	Year of diagnosis	Year when the tumor was first diagnosed	0	0
raceethnicity	Discrete	Race/ethnicity	Patient's nationality	0	0
age	Continuous	Age at diagnosis	Age of the patient at diagnosis	0	0
SM	Continuous	survival month	Survival time after diagnosis (months)	0.4%	0.5%
vst	Discrete	vital status record	Survival status of patients on follow-up deadline	0	0

3.5 Expectation Maximization Imputation (EMI)

The Expectation Maximization (EM) algorithm is an iterative method to find maximum likelihood or maximum a posteriori (MAP) estimates of parameters in statistical models, where the model depends on unobserved latent variables. The EM iteration alternates between performing an expectation (E) step, which creates a function for the expectation of the log-likelihood evaluated using the current estimate for the parameters, and a maximization (M) step, which computes parameters maximizing the expected log-likelihood found on the E step. These parameter estimates are then used to determine the distribution of the latent variables in the next E step, and missing values are imputed.

3.6 Hybrid Method of KNNI and Kmeans-Gaussian Mixture Model (GMM) Imputation (KNNI + kmeans-GMM)

In order to improve the accuracy of breast cancer survival model form the data level, Hybrid missing value imputation method of combining KNNI and kmeans-Gaussian Mixture Model(GMM) is used. In our experiment, KNNI is used for discrete feature missing value. For missing values of continuous features, kmeans-GMM is used to impute.

Considering large data scale and long running time, kmeans is firstly used to cluster data. k of kmeans is determined by the minimum error square sum(SSE). Given a data matrix $X = \{x_1, x_2, ...x_n\}$, formulated of SSE as

$$SSE = \sum_{i=1}^{k} \sum_{x_i \in C_i} \left| x_j - \mu_i \right|^2 \quad ,$$

j=1,2,…n.(1) 。where C_i is the *ith* cluster, μ_i is the centroid of C_i, and SSE is the clustering error of all samples, representing the quality of the clustering effect.

Within each cluster, Gaussian Mixture Model(GMM) is used to estimate model parameters for cluster data with missing values. The Maximum Likelihood Estimation (MLE) of the EM algorithm is the most commonly used method for parameter estimation. Each clustering data consists of observed data Y_{obs} and missing data Y_{mis}, $Y = \{Y_{obs}, Y_{mis}\}$, it is generated

by a Gaussian Mixture Model, Y distributed as a mixture of K Gaussian distributions $P\ (Y\ |\theta) = \sum_{k=1}^{k} \pi_k N_K(x_{j;}\theta_k)$,

where $\Sigma_k \pi_k = 1$, $\pi_k \geq 0$ for $k = 1, ..., K$, and $\theta_k = (\mu_k, \Sigma_k)$. Note that θ denotes the full set of parameters of the mixture model: $\theta = (\pi_1, ..., \pi_K; \theta_1, ..., \theta_K)$. We also introduce hidden variables $\gamma_i = \gamma_{i1}, ..., \gamma_{iK}$, where γ_{ik} is 1 if the *ith* sample belongs to group k, and 0 otherwise.

In each cluster, we first use the mean of observed data features to fill in the missing values of the corresponding features. And initialize the parameters to start iteration. At this time, the likelihood function of complete data can be written as the following formula,

$$\mathrm{P}(\mathrm{Y}, \gamma | \theta)$$
$$= \Pi_{k=1}^{k} \pi_k^{n_k} \Pi_{i=1}^{n} \left[\frac{1}{\sqrt{2\pi}\sigma_k} \exp\left(-\frac{(y_i - \mu_k)^2}{2\sigma^2} \right) \right] \hat{}(\gamma_k)$$

where, $n_k = \sum_{i=1}^{n} \gamma_{ik}$, $\sum_{k=1}^{K} n_k = n$. Then the log-likelihood function of the complete data is as follows:

$$logP(Y, \gamma | \theta) = \sum_{k=1}^{k} n_k \, log\pi_k + \sum_{i=1}^{n} \gamma_{ik} [\log\left(\frac{1}{\sqrt{2\pi}}\right) - log\sigma_k - \frac{1}{2\sigma_k^2}(y_i - \mu_k)\hat{}2]$$

E-step of EM algorithm: Determine the Q function.

$$\mathrm{Q}(\theta, \theta^{(t)}) = E\left[logP(Y, \gamma | \theta) \middle| Y, \theta^{(t)} \right]$$

$$= \sum_{k=1}^{K} \{ \sum_{i=1}^{n} (E_{\gamma_{ik}}) log\, \pi_k + \sum_{i=1}^{n} (E_{\gamma_{ik}}) [\log\, (\tfrac{1}{\sqrt{2\pi}}) - log\sigma_k - \tfrac{1}{2\sigma_k^2}(y_i - \mu_k)\hat{}2] \}$$

According to the current model parameters, calculate the responsiveness of sub-model k to observation data y_i,

$$\gamma_{ik}{}' = E(\gamma_{ik} | y_i, \theta' \ ) = \frac{\pi_k' N_k(y_i; \theta_k')}{\sum_{k=1}^{K} \pi_k' N_k(y_i; \theta_k')}$$

M-step of EM algorithm: Calculate the model parameters for the new iteration.

$$\mu_k' = \frac{\sum_{i=1}^{n} (\gamma_{ik}{}' * y_i)}{\sum_{i=1}^{n} \gamma_{ik}{}'}$$

$$\sigma_k'^2 = \frac{\sum_{i=1}^{n} \gamma_{ik}{}' (y_i - \mu_k)\hat{}2}{\sum_{i=1}^{n} \gamma_{ik}{}'}$$

$$\pi_{\mathrm{k}}^{'} = \frac{\sum_{i=1}^{n} \gamma_{ik}{}^{'}}{n}, k = 1,2,3, \ldots, K$$

Imputation: Conditional mean imputation is the most commonly used methods in imputation methods. Because the distribution of the complete data and the observation data is known, the missing data distribution P ($y_{mis}|y_{obs}$) under the observation data can be obtained by Bayes, so that the conditional expectation can be obtained and the corresponding missing data can be filled. EMI believes that the deviation between missing value $y_{ij} \in y_{mis}$ and the mean value of the *j-th* feature is proportional to the deviation between $y_{il} \in y_{mis}$ and the mean value of the *lth* feature, so that the missing value y_{mis} can be imputed using formula $y_{mis} = \mu_m + (y_a - \mu_a)B + e$, where, $_{m}$ is the mean vector of the features having missing values for a record $y_{.j} \in y_{mis}$, $_{a}$ is the mean vector of the features without missing values for a record $y_i \in y_{mis}$, B is a regression coefficient matrix. e is a residual error. Here, we believe that in the Gaussian Mixture distribution, the missing values $y_m \in y_{mis}$ can be imputed by the formula:

$$y_m = \sum_{k=1}^{k} \pi_{\mathrm{k}}^{\prime}(\mu_k^{\prime} + \frac{1\sigma_{m,l}^{\prime}{}^{k}}{\sigma_{l,l}^{k}}(y_l^k - \mu_l^k))$$

the *k-th* model of the *t-th* iteration, represents the covariance between the *mth* attribute and the *lth* attribute in the *k-th* model of the *t-th* iteration, σ^k is the covariance matrix of observed features in the *k-th* model, μ_l^k is the mean value of the *l-th* attribute in the *k-th* model.

3.7 Machine Learning Methods

In this section, we briefly introduce several classification algorithms applied in this research.

3.7.1 XGBoost

XGBoost is a reliable distributed machine learning system that can be used to expand tree boosting algorithms. XGBoost optimizes the construction of fast parallel trees to have good running speed and satisfactory accuracy. In addition, XGBoost can process tens of millions of samples on a single node so that it can handle large scale data, and when the a eigenvalue of the sample is missing, XGBoost can treat missing data as a sparse matrix so that it can effectively perform data modeling and analysis.

3.7.2 Random Forest (RF)

Random forest trains by selecting a data set with the same size of *N* that may have repetitions from all training samples *N* when training each tree (ie bootstrap sampling), and at each node, randomly select a subset of all features, the classifier built to calculate the best segmentation method. The final output category of the random forest is determined by the mode of the category output by each tree. RF has been widely used in data classification applications because of its good classification performance.

3.7.3 K-Nearst Neighbors (KNN)

The main idea of KNN is that if most of the k most similar samples in the feature space (that is, the closest neighbors in the feature space) of a sample belong to a certain category, the sample also belongs to this category. KNN commonly uses Euclidean distance as the sample similarity measurement distance. Through distance measurement, k neighboring samples of the missing data sample can be found, and then the approximate value of the missing sample can be determined.

3.7.4 Decision Tree (DT)

DT is a common type of machine learning method. The purpose is to produce a decision tree with strong generalization ability, that is, strong ability to deal with unseen examples. There are three algorithms for generating decision trees: ID3, C4.5 and CART. In this research, we use CART algorithm. The generation of CART decision tree is a process of recursively constructing a binary decision tree. The square error minimization criterion is used for the regression tree, and the Gini index minimization criterion is used to performed feature selection in the classification tree, and the binary tree is finally generated.

4 PERFORMANCE EVALUATION

In this section, five common measures that are accuracy, precision, sensitivity, specificity and AUC are employed to evaluate the survival prediction models. The first four measures are given by follows: accuracy=(tp+tn)/(tp+tn+fp+fn), precision=tp/(tp+fn), sensitivity=tp/(tp+fp), specificity=tn/(tn+fp), where tp, tn, fp, fn represent true positive, true negatives, false positives and false negatives, respectively.

Table 2: Confusion matrix.

	Prediction	class
Actual	tp	fn
class	fp	tn

5 EXPERIMENTAL RESULTS

The experimental purpose of this research is to evaluate the impact of different missing value imputation methods on the performance of survival prediction in SEER breast cancer dataset, and we compare improved hybrid imputation method

KNNI + kmeans-GMMI with six common existing techniques namely mean& mode, KNNI, LRI, MI, EMI and deleting. In order to prove the effectiveness of the data imputation method for data modeling, we first used the classification algorithm of the XGBoost framework to establish a breast cancer survival prediction model for the data without preprocessing of missing values. Then, the missing value imputation methods are applied to the data to make the processed data without missing values, finally, to design survival prediction models using the resulting dataset.

Because XGBoost can treat missing values as a sparse matrix during the model building process, and it is more efficient when processing large-scale data. Therefore, in the first experiment, we build an overall survival model through XGBoost base on data with missing values, the evaluation result of this model is similar to the evaluation result of MI as shown in no preprocessing of Figure 1(a), and its AUC of this model is 0.826 as is showed in Figure 2(a).

In the second experiment, we used an improved hybrid imputation method KNNI + kmeans-GMM to preprocess the missing values and compare it with other six common imputation methods(deleting, mean&mode, KNNI, LRI, EMI, MI).

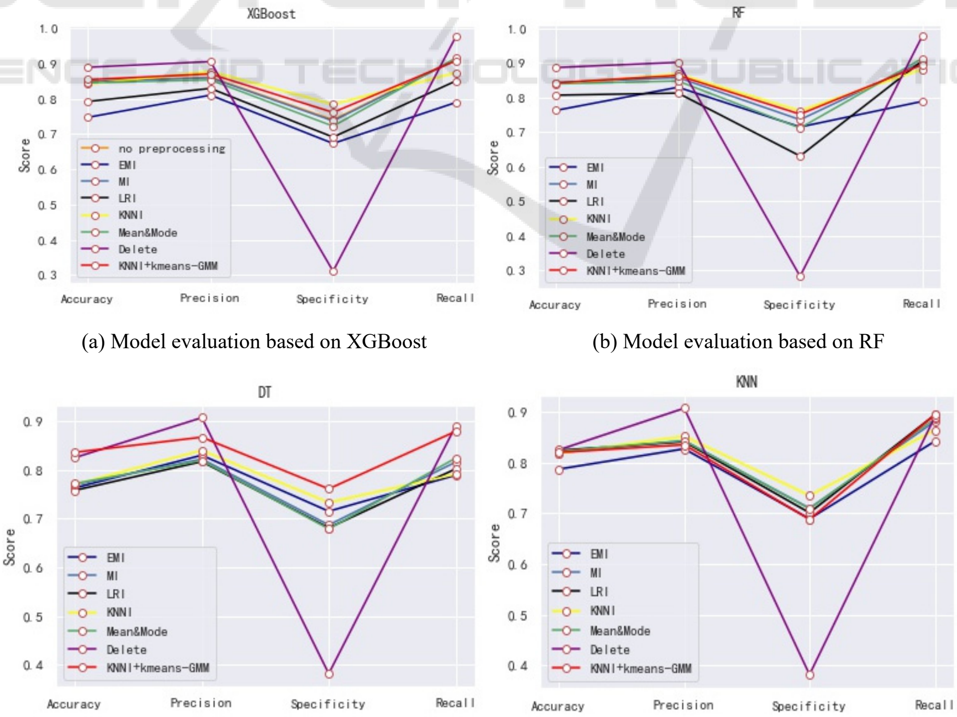
For KNNI + kmeans-GMM, we mainly consider the difference between discrete value and continuous imputation, and the long running time caused by the large scale of experimental data, so we use KNNI to fill discrete feature missing values, kmeans-GMM to impute continuous feature missing values. The resulting complete data set is divided into 80% training set and 20% test set. The training set is used to train the best survival prediction model, and the corresponding test set is used for testing. Four classification algorithms XGBoost classifier, KNN classifier, RF classifier, and DT classifier are used for overall survival prediction modeling. For each combination of imputation and classifiers, the corresponding set of model parameters are determined by the best AUC through small parameter adjustments. Figure 1 shows the obtained test results in terms of four measures of survival prediction: accuracy, precision, sensitivity and specificity. And Figure 2 shows AUC of each combination of imputation and classifiers. Next, we measure the impact of different missing value imputation techniques on survival prediction performance through accuracy, precision, specificity, sensitivity, and AUC five indicators. For the second experiment, the overall survival model is to predict the survival of the group as a whole, and whether a patient can survive for 10 years, a 10-year survival prediction model needs to be established. In this experiment, we use the complete data set imputed by KNNI + kmeans-GMM to predict the 10-year breast cancer survival model. The evaluation results of the model are shown in the Figure 3(a) and Figure 3(b).

The five commonly used evaluation indicators of accuracy, precision, specificity, recall and AUC are used to measure the impact of different missing value processing methods on survival prediction performance. As Figure1 and Figure2, an effective model can be built through XGBoost with missing data, and its accuracy, specificity and AUC are 0.849, 0.740, 0.826 respectively. For a given classifiers, in terms of AUC, the results obtained using KNNI + kmeans-GMM are statistically significantly better than using others imputation methods, except for KNN classifier, where the AUC values of KNNI + kmeans-GMM is 0.792 which is lower than KNNI (0.8), MI (0.796), LRI (0.798) and mean& mode (0.798). In terms of combination methods, we found that the difference between the AUC provided by RF classifier and KNN classifier is not statistically significant. On the contrary, the difference in DT classifier is the relatively significant, but the result gives the worst. In addition, based on specificity results, DT classifier and KNN classifier tend to favor the majority class (in the best case, the specificity is less than 0.761). Although the impact is small, this bad behavior also occurs in XGBoost classifier and RF classifier. The most robust and accurate method is the XGBoost method: For the same missing value imputation technique, it provides better AUC than the other three classifiers (using KNNI + kmeans-GMM up to 0.835), and its specificity is 0.761, precision is

0.870, which can reduce the number of FP, and then increase the number of TN.

6 DISCUSSIONS AND CONCLUSIONS

Breast cancer survival prediction models have been extensively studied and have provided great help in improving cancer treatment. These models are built using historical patient information stored in clinical data sets, and they can be used to predict breast cancer outcomes in new patient data. However, it should be noted that most of the historical information is incomplete or there are missing values, such as the breast cancer data set in the SEER database. Therefore, in order to carry out such research, some pre-processing measures need to be taken. Different from previous studies, we propose a hybrid imputation method to impute missing breast cancer data. Considering the messiness of data types, we use KNNI to perform numerical imputation on discrete data, and use an improved GMM algorithm to interpolate continuous missing data. Since using different imputation methods for the same incomplete data set may produce different imputation results, the better the quality of the imputation of the training data set, the higher the classification accuracy. Therefore, a better imputation method can be determined. For the phenomenon of missing values in the test set, in order to maintain the original data distribution, we use linear regression algorithms to train the corresponding model to impute the missing values in the test set. After the imputation process is completed, use different classifiers to train the imputed data set without missing values, and use the test set to test the model performance.



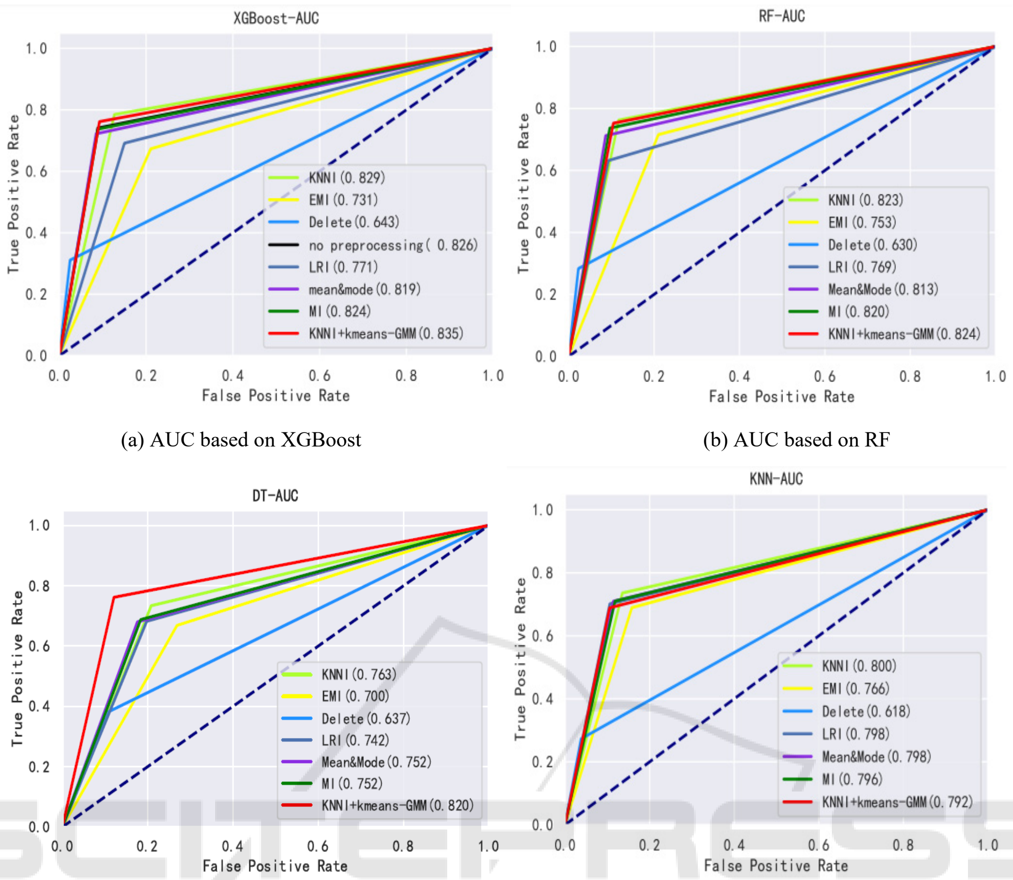
(a) Model evaluation based on XGBoost

(b) Model evaluation based on RF

(c) Model evaluation based on DT

(d) Model evaluation based on KNN

Figure 1: Overall Survival Model Evaluation.



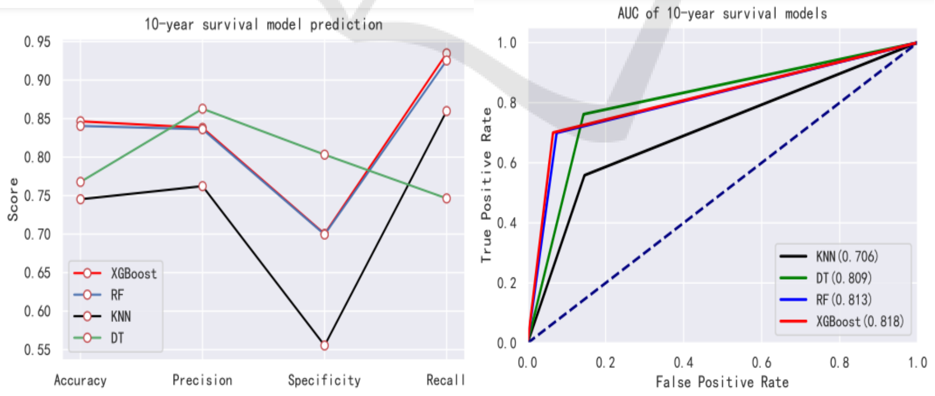
(a) AUC based on XGBoost

(b) AUC based on RF

(c) AUC based on DT

(d) AUC based on KNN

Figure 2: AUC of Overall Survival Model Evaluation.



(a) AUC of 10-year survival model

(b) The evaluation of 10-year survival models

Figure 3: AUC and evaluation based on 10 year-survival model.

From the Figure1 and Figure 2, it is obvious that the method of deleting will cause data imbalance and ultimately affect the accuracy of the model. In the combination of different imputation methods and classification algorithms, except for the KNN classification algorithm, the KNNI+kmeans-GMM is better than other imputation algorithms in terms of AUC evaluation indicators. Compared with models without missing value imputation, the model of kNNI+kmean+GMM + XGBoost is an effective combination whose AUC is 0.835 greater than other combinations.

This study considers the use of all data information as much as possible for survival modeling, and does not consider whether certain features are related to label. If a column of features and labels are not very relevant, then data imputation for this miss data will increase data noise. Therefore, in the following research, we will explore the importance of features in more depth in the future.

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