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Research Article

Sensitivity Analysis to Select the Most Influential Risk Factors in a Logistic Regression Model

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Abstract

The traditional variable selection methods for survival data development process assumes tuning parameters that are problematic and time-consuming and have a large number of risk factors. In this paper, we propose a sensitivity analysis (GSA) to select the most influential risk factors. This can be done by excluding the irrelevant risk factors, thus eliminating the need for a large number of risk factors. Data from medical trials are suggested as a way to test the efficacy of the proposed method. This leads to construction of an appropriate model according to their importance.

1. Introduction

Sensitivity analysis (SA) plays a central role in a variety of statistical applications such as discrimination, calibration, comparison, and model selection [1]. The most important input factors (if any) accounts for most of the output variance (a certain percentage can be fixed to any value within their range [2]. In this paper, we will discuss the important variables to simplification of the model; the original model will be simplified to arrive at such a determination. Although SA has been widely used, it is not clear how to select the most important input variables from a complex model so as to arrive at

it has limited use for selection of risk factors despite the presence of survival regression models. The limited use of these methods to select risk factors illustrates the desirability of development of a new method of SA that extends beyond traditional methods and also simplifies survival regression models by

A considerable number of methods of variable selection have been developed, but these developments are squarely in the context of normal regression models and linear regression models [3]. A comprehensive review of many methods such as forward, backward, and stepwise selection and shrinkage methods (and Bayesian information criterion (BIC)) are available; however, none are available in either a logistic regression model or in other survival regression models. These methods use standard errors and P -values. They also can delete variables whose coefficients are not significant. They regard all the risk factors of a situation as equal, and they select variables sequentially; furthermore, most of these methods focus on the main effects of variables (interactions of variables).

New methods of variable selection, such as *least absolute shrinkage and selection operator* (LASSO) method in [6], are available for survival regression models. These methods use the penalized likelihood approach. These two approaches differ from traditional methods in that they select the model by estimating their effects as 0. A nice feature of these methods is that they select variables simultaneously, but, nevertheless, these methods have some problems that are dealt with in more detail in [7, 8].

This study aims to use SA to extend and develop an effective, efficient method for selecting the best subsets according to specified criteria for survival regression models in the field of survival regression models. The paper is organized as follows: Section 2 gives the background of building a logistic regression model. The results of implementing this method and logistic regression model are given in Section 3. Section 4 consists of the discussion and conclusions.

2. Background of Constructing a Logistic Regression Model

Often the response variable in clinical data is not a numerical value (e.g., not diseased). When the latter occurs, a binary logistic regression model is used to describe the relationship between the disease's measurements and its risk factors. The response variable (the disease measurement) is a dichotomy and the relationship between the response variable and the risk factors in a logistic regression model neither assumes the linearity in the relationship between the response variable and the risk factors, nor does it require normally distributed variables. It also has less stringent requirements than linear regression models. The response variable is independent and that the independent risk factors are linearly related to the response variable. However, models involving the association between risk factors and the response variable are used in disciplines such as medicine, engineering, and the natural sciences. How can we select the best risk factors and binary response variable? The answer to this question is given in this section.

2.1. Constructing a Logistic Regression Model

The first step in modeling binomial data is a transformation of the response variable. Instead of using the linear model for the response variable of the probability of success (π), the logit transformation or logit of the probability of success (π) is $\log \{ \pi / (1 - \pi) \}$, the log odds of success. It is easily seen that any value of π in the interval $(0, 1)$ corresponds to a unique value of $\log \{ \pi / (1 - \pi) \}$ in the interval $(-\infty, +\infty)$. Usually, binary data results from a nonlinear relationship

has less impact when $\{n(x)\}$ is near (0 or 1) than when $\{n(x)\}$ is n

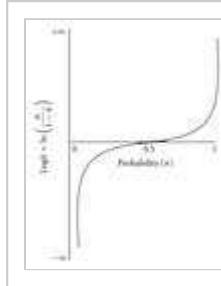


Figure 1: Logit = $\ln(n / (1 - n))$ as a function of n from $(-\infty)$ to $(+\infty)$ as probability ranges from (0) to (1)

Thus, the appropriate link is the log odds transformation (the logit form $n_i = y_i / n_i$ for $i = 1, 2, \dots, n_i$, where the expected value of the response is $E(Y_i) = n_i p_i$. The logistic regression model for association of X_1, X_2, \dots, X_k is such that [10]

$$\begin{aligned} \text{Logit}(n_i) &= \text{Log}\left\{\frac{n_i}{1 - n_i}\right\} \\ &= \beta_0 + \beta_1 x_{1i} + \beta_2 x_{2i} \end{aligned}$$

and the equation of success probability is

$$n_i = \frac{\exp(\beta_0 + \beta_1 x_{1i} + \dots)}{1 + \exp(\beta_0 + \beta_1 x_{1i} + \dots)}$$

The linear logistic model is a member of a family of generalized linear models. This model fitting process.

2.2. Fitting Logistic Regression Models

The mechanics of maximum likelihood (ML) estimation and model fitting in the case of GLM fitting, and then fitting the model requires estimation of this model using the Bernoulli ML as in the following [12]:

$$L(\beta) = \prod_{i=1}^n \binom{n_i}{y_i} n_i^{y_i} (1 - n_i)^{n - y_i}$$

The problem now is to obtain those values $(\tilde{\beta}_0, \tilde{\beta}_1, \dots, \tilde{\beta}_k)$ that maximize $L(\beta)$ as follows:

$$\begin{aligned} \text{Log} L(\beta) &= \sum_{i=1}^n \left\{ \text{Log} \binom{n_i}{y_i} + y_i \text{Log} n_i + (n_i - y_i) \text{Log} (1 - n_i) \right\} \\ &= \sum_{i=1}^n \left\{ \text{Log} \binom{n_i}{y_i} + y_i \text{Log} \left(\frac{n_i}{1 - n_i} \right) + (n_i - y_i) \text{Log} (1 - n_i) \right\} \\ &= \sum_{i=1}^n \left\{ \text{Log} \binom{n_i}{y_i} + y_i \text{Log} \left(\frac{n_i}{1 - n_i} \right) - (n_i - y_i) \text{Log} (1 - n_i) \right\} \end{aligned}$$

where $\{n_i = \sum_{j=0}^k \beta_j x_{ji}\}$ and $(x_{0i} = 1)$ represent all values of (i) . The maximum likelihood estimates of the $(k + 1)$ unknown β -parameters is given by

$$\frac{\partial \text{Log}L(\beta)}{\partial \beta_j} = \sum_{i=1}^n y_i x_{ji} - \sum_{i=1}^n n_i \pi_i x_{ji}, \quad j = 0, 1, 2, \dots, l$$

Then the likelihood equations are

$$\sum_i y_i x_{ji} - \sum_i n_i \tilde{\pi}_i x_{ji} = 0, \quad j =$$

where $\tilde{\pi}_i = e^{\eta_i} / (1 + e^{\eta_i})^{-1}$ is the ML estimate of $\{\pi_i\}$. There are two likelihood estimation of $(\tilde{\beta})$. The one most often used is known as with determination of the score matrix $\{U(\beta)\}$ and the information

$$\begin{aligned} U_j^{(t)}(\tilde{\beta}) &= \left. \frac{\partial L(\beta)}{\partial \beta_j} \right|_{\beta^{(t)}} \\ &= \sum_i (y_i - n_i \pi_i^{(t)}) x_{ij} \\ I_{jk}^{(t)}(\tilde{\beta}) &= \left. \frac{\partial^2 L(\beta)}{\partial \beta_j \partial \beta_k} \right|_{\beta^{(t)}} \\ &= - \sum_i x_{ij} x_{ik} n_i \pi_i^{(t)} \end{aligned}$$

Here $(\pi^{(t)})$ is obtained from $\{\beta^{(t)}\}$ through (2), then we use $\{\beta^{(t+1)} = \beta^{(t)} - (I^{(t)})^{-1} U^{(t)}\}$ to obtain the next value $(\beta^{(t+1)})$ as

$$\beta^{(t+1)} = \beta^{(t)} + \{X' \text{diag}[n_i \pi_i^{(t)}] (1 - \pi_i^{(t)})\}^{-1} U^{(t)}$$

where $\{\mu_i^{(t)} = n_i \pi_i^{(t)}\}$, this is to obtain $(\pi^{(t+1)})$, and so on.

2.3. Evaluating the Fitted Model

A simple model that fits adequately has the advantage of model describes reality well, it tends to provide more accurate estimates. "we are mistaken if we think that we have found the true model. In light of this assertion, what then is the logic of testing the fit of the model? The answer lies in the evaluation of the specific properties of this model. The Wald Score test, the Pearson chi-square, and the Hosmer-Lemeshow test. Usually the first stage of construction of any model presents a large number of risk factors. This may lead to an unattractive model from a statistical viewpoint. In a model, a decision should be made early about the proper method of selecting risk factors. Because traditional methods of selecting variables have been used in regression models, a new method of variables selection will be developed. This is the subject of the following section.

3. Sensitivity Analysis to Select the Most Influential Risk Factors

There are two key problems in variable selection procedure: (i) how to select the most influential risk factors from the set of risk factors, and (ii) how to improve final model performance. These questions are the objective of our proposed method by applying the logistic regression model.

3.1. General Concept of GSA

GSA was defined in [14] as “the study of how the uncertainty in the model output can be apportioned to different sources of uncertainty in the model input factors with respect to the model response”. The importance of the input factors with respect to the model response given risk factor X_i can be measured via the so-called sensitivity index to the model output variance because of the uncertainty in X_i . It is computed using the following decomposition formula for the total variance

$$V(Y) = \sum_i V(X_i) + \sum_i \sum_{j>i} V(X_i, X_j) +$$

where

$$\begin{aligned} V(X_i) &= V_{X_i}(E_{X_{-i}}(Y|X_i)), \\ V(X_i, X_j) &= V_{X_i, X_j}(E_{X_{-ij}}(Y|X_i, X_j)) \\ &\quad - V_{X_j}(E_{X_{-j}}(Y|X_j)), \end{aligned}$$

where $V(Y)$ is the unconditional variance of output of the model (in terms of risk factor X_i), and $V(X_i, X_j)$ is the variance of interaction between risk factors X_i and X_j . The fraction of the unconditional output variance $V(Y)$ that is accounted for by the first order sensitivity index (S_i) for the factor X_i is given as

$$S_i = \frac{V(X_i)}{V(Y)}.$$

The second terms in (9) are known as the effect of interactions. Interaction terms usually grow (i) with the number of risk factors and (ii) with the number of risk factors [16]. This means that if all of the $V(X_i)$ terms are computed, then the total $V(Y)$, because the difference $V(Y) - \sum_{i=1}^k V(X_i)$ is nonadditive. Consequently, when $\sum_{i=1}^k S_i = 1$, then the model is additive (i.e., the first order of conditional variances of (10) are all we need). In a nonadditive model, higher-order sensitivity indices account for the interactions between risk factors. However, higher-order sensitivity indices are usually not estimated. If the model is nonadditive, then the total number of indices (including the S_i 's) that are needed to account for the total variance is $2^k - 1$. For this reason, a more compact sensitivity measurement is used; this measurement is the total sensitivity index (S_{Ti}), which concentrates in one single term on all the interactions involving risk factor X_i . For $k = 3$ risk factors, the three total sensitivity indices would be [2]

$$\begin{aligned} S_{T1} &= \frac{V(Y) - V_{X_2, X_3}(E_{X_1}(Y|X_2, X_3))}{V(Y)} \\ &= S_1 + S_{12} + S_{13} + S_{123} \end{aligned}$$

and analogously

$$\begin{aligned} S_{T2} &= S_2 + S_{12} + S_{23} \\ S_{T3} &= S_3 + S_{13} + S_{23} \end{aligned}$$

where the conditional variance in (12) expresses the total contribution of the risk factor X_i (including the interactions with the $k - 1$ remaining factors), so that $V(Y) - V_{X_{-i}}(E_{X_i}(Y|X_{-i}))$ include

in (9)) that involve risk factor X_i . For a given risk factor X_i , the coefficients S_{T_i} and S_i that reflects an important role of interactions for that risk factor.

$$IC_i = S_{T_i} - S_i.$$

Explaining the interactions among risk factors helps us to improve the Estimators for both (S_i, S_{T_i}) are provided by a variety of methods such as (FAST), and others; for more details, see [17].

3.2. GSA in a Logistic Regression Model

In this study, partitioning the total variance of the objective function to perform a GSA. How can this model be extended to deal with a continuous response variable? The extension of this partitioning to models with binary responses is a variance partitioning method to our binary response variable (incidence of the disease). The data is consisting of y_i , the number of people who have CHD. For the i th observation n_i will have a Bernoulli distribution with probability p_i . This response probability is therefore p_i must be equal to zero when p_i is zero or unity, and then a relationship between risk factors can be fitted. Typically a logistic regression model with n people who have a binomial distribution (i.e., $\{Y_i \sim B(n, p_i)\}$ with probability of the incidence of the disease is $p_i = y_i / n$ for i th observation and (5). This model assumes independence between the n observations. The estimates of the probabilities will be binomial with equal variance:

$$V(Y_i) = np_i(1 - p_i)$$

The binomial is not the only possible distribution for fitting proportion variation (known as overdispersion) or less variation (known as underdispersion) conditional on the values of p_i 's. The simplest function for the multiplicative scale factor to determine the variance of the response is

$$\text{var}(n_i) = r p_i(1 - p_i)$$

where r is a scale factor that is equal to 1. If we have a binomial distribution with overdispersion and less than 1 if there is underdispersion, and the advantages of the multiplicative approach are that it will allow both Y_i is associated with the observed number of incidences of the disease, and then the mean of Y_i , conditional on n_i , is

$$E(Y_i | n_i) = n p_i$$

and the conditional variance of Y_i is

$$V(Y_i | n_i) = n p_i(1 - p_i)$$

Since p_i cannot be calculated, then the observed proportion of the

$$p_i = \frac{y_i}{n}$$

According to a standard result from the conditional probability the variance of Y can be obtained from the conditional expectation of Y given X

$$E(Y) = E\{E(Y|X)\}$$

and the unconditional variance of Y is given by [20]

$$V(Y) = E\{V(Y|X)\} + V\{E\}$$

Applying these two results on our response variable gives

$$E(Y_i) = E\{E(Y_i|n_i)\} = E(n_i)$$

$$V(Y_i) = E\{V(Y_i|n_i)\} + V\{E\}$$

now

$$\begin{aligned} E\{V(Y_i|n_i)\} &= E\{nn_i(1-n_i)\} \\ &= n\{E(n_i) - E(n_i)^2\} \\ &= n\{E(n_i) - V(n_i)\} \\ &= n\{p_i - rp_i(1-p_i)\} \\ &= np_i(1-p_i)(1-r) \end{aligned}$$

also

$$\text{var}\{E(Y_i|n_i)\} = \text{var}(nn_i) = nrp_i(1-p_i)$$

and so

$$V(Y_i) = nrp_i(1-p_i)$$

in the absence of random variation in the response probability, Y_i will be constant. In this case when $r = 1$ as required, then

$$V(Y_i) = np_i(1-p_i)$$

If, on the other hand, r is greater than 1, then a variation in the response probability will exceed $np_i(1-p_i)$, the variance under binomial sampling that leads to overdispersion. If $r < 1$, then a variation in the response probability will be less than $np_i(1-p_i)$, the variance under binomial sampling that leads to underdispersion. To use GSA to select the most influential risk factors, we will use the following steps to construct an appropriate logistic regression model, as illustrated in Figure 2.

(1) The first step is identification of the probability distribution $f(x)$. The analysis starts from probability distribution functions (pdfs) given the best information available of the statistical properties of the input variables. This step starts with visualizing the observed data by examining its histogram and probability density function, as illustrated in Figure 2.



Figure 2: Common shapes of three types of probability density functions (PDFs).

A visual approach is not always easy, accurate, or valid, especially when the data is complex. To have a more formal procedure for deciding which distribution is most appropriate for the data, statistical tests such as the Kolmogorov-Smirnov and chi-square tests are used.

(2) In the second step, the logistic regression model as in (1) and the results from step one are used to create a Monte Carlo simulation to generate random samples and to estimate the unconditional variance of response probability Y_i using equations (23) to (26).

(3) These results from step two will be used in performing GSA in the next step.

in the result of decomposing as in (24) and (26), where the main e

$$S_i = \frac{np_i(1-p_i)(1}{nrp_i(1-p_i)}$$

and the total effect indices are

$$\begin{aligned} S_{T_i} &= \frac{V(Y_j) - V(E(Y_j))}{V(Y_j)} \\ &= \frac{E\{V(Y_j | X_{-i})\}}{V(Y_j)} \end{aligned}$$

where X_{-i} are all X 's but X_i , and the coefficients of importance are

$$IC_i = S_{T_i} - S_i.$$

These results and the two datasets are used to test and compare variable selection method to identify the important risk factors obtained from other existing methods of selecting variables.

4. Numerical Comparisons

The purpose of this section is to compare the performance of the proposed method on real data example to illustrate our SA approach as a variable selection method. We used the dataset and the results of the penalized likelihood SCAD, and LASSO that were computed by [7] as a way to compare these methods.

4.1. The First Example

In this example, Fan and Li [7] applied the proposed penalized likelihood method to a binary response variable Y is 1 for those victims who survived the hospital stay. The risk factors are age, $X_2 = \text{sex}$, $X_3 = \log(\text{burn area} + 1)$, and $X_4 = \text{abnormal}$ was considered. Quadratic terms of X_1 and X_3 , and all interactions were added, and the logistic regression model was fitted. The best subset selection method was applied to this dataset. The unknown parameter λ was chosen as 0.0015, respectively, for the penalized likelihood estimates with t was taken as 3.7. With the selected λ , the penalized likelihood estimates and standard errors for the transformed data, based on the penalized likelihood estimates, sensitivity indices obtained by using SimLab software to compare the proposed method with other methods. The first five columns were calculated

Table 1: Estimated coefficients and standard errors

In addition to GSA indices, Table 1 consists of the results of two traditional methods (BIC) and two new methods (LASSO and SCAD). The traditional method chooses five of 13 risk factors, whereas the SCAD chooses that the best subset keeps X_4 . Neither SCAD nor the best subset selection method selected subset, but both LASSO and the best subset variable s

quadratic terms of X_1 and X_3 rather than their linear terms. It also statistically significant. LASSO shrinks noticeably large coefficient selected the variables X_1 , X_3 , and X_1X_3 , in addition to the intercept from the other methods. According to the results in the last column according to sensitivity indices S_i and S_{T_i} . Age (X_1) is the first and contribution of 0.487, and the second most important risk factor percentage of contribution of 0.362. The third influential risk factor percentage of contribution of 0.143 as shown in Table 1. Consequently, the selection method resembles SCAD in choosing the same risk factor

4.2. The Second Example

A new dataset emerges from the original dataset prepared in [22] (backward elimination) as variable selection methods. Original prevalence of CHD risk factors among a population-based survey. Community-based screening evaluations included the determinants: height, weight, total and high-density lipoprotein (HDL) cholesterol. The results of this study were presented as percentages of prevalence (men, 15.6% of women), hypertension (30.9% of men, 43.1% of women), without building any models to study the relationship between risk factors and CHD [8]. A new dataset was generated based on the first one as a set of risk factors for CHD from among these new factors, and then in performance of the proposed method as follows.

- (1) CHD (Y) 10-year percentage risk is generated according as 1 if the percentage of the risk is $\geq 20\%$ and 0 otherwise [23]
- (2) Diabetes (diab, X_1): According to the criteria published by the American Association of Clinical Endocrinologists (AACE) [24] Glucose >140 mg/dL or Glycosylated Hemoglobin $>7\%$ or both diabetes 0 otherwise.
- (3) Total cholesterol (Chol, X_2): if a participant has total cholesterol >200 mg/dL, then the participant gets 1, otherwise [25].
- (4) High density lipoprotein (HDL, X_3): a participant with HDL >40 mg/dL (men) or >50 mg/dL (women) gets 1, otherwise [25].
- (5) Age (X_4): standardized values are used $(X - \mu) / \sigma$.
- (6) Gender (Gen, X_5): 1 is for a male and 2 for a female.
- (7) Body mass index (BMI, X_6): values for this standard are $\text{height}/(\text{weight})^2$, and the participant gets 1 if BMI is >30 and a
- (8) Blood pressure (hypertension, Hyp, X_7): a participant has hypertension if diastolic blood pressure is >90 or if both of them exceed these
- (9) Waist/hip ratio (X_8), in addition to BMI, is a second factor

This dataset was used to perform SA through the use of SimLab as discussed in Section 3. An evaluation of the efficiency of the proposed logistic regression models so as to obtain comparisons of factors chosen by traditional variable selection method (backward elimination). SF from fitting logistic regression models.

4.2.1. The Important Risk Factors

Implementation of the GSA method for this dataset gave the results in order of importance and the contribution of each one to the variable.

Risk Factor	Sensitivity Index	Contribution
Diab	0.266	0.365
Age	0.161	0.480
Ge	0.147	0.624
Hypt	0.024	0.935
W	1.874	0.36

Table 2: Sensitivity indices and risk factors ranked by importance.

According to the first order of sensitivity indices S_{i_1} , the BMI is the most influential risk factor, followed by the hip ratio ranks second. Both are components of the obesity factor. The other factors as listed in Table 2. The total sensitivity index shows the overall contribution of that risk factor to the output variance, taking into account the other risk factors. The difference between the total sensitivity index and the first order sensitivity index is a measure of the contribution to the output variance due to the interaction between risk factors (13). The second column in Table 2 shows the values of S_{T_i} . These indices point to the simple interaction between these risk factors. Figure 3 shows the compression between the first order S_{i_1} and the total S_{T_i} between risk factors.

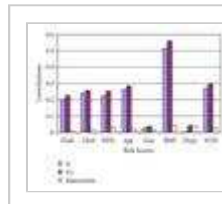


Figure 3: Sensitivity indices: the main effect IC_i for each risk factor.

4.2.2. Implementing the Logistic Regression Model

Does the proposed method yield a reliable model? To investigate this, we analyze the results of the fitted models. Basically, when the full logistic regression model is fitted, the results are as follows:

$$\begin{aligned} \text{Logit CHD} &= 0.365 - 0.266 \text{Diab} + 0.161 \text{Age} - 0.147 \text{Ge} \\ &\quad + 0.024 \text{Hypt} - 1.874 \text{W} \\ \text{Sig}(P) &\quad (0.862) \quad (0.480) \\ &\quad (0.304) \quad (0.624) \\ &\quad (0.935) \quad (0.36) \end{aligned}$$

$$\begin{aligned} -2\log L_0 &= 365.081, \quad -2\log L_1 \\ \text{Nag. } R^2 &= 0.39, \quad \chi^2_{\beta} = 9.394, \\ \chi^2_{HL} &= 12.509, \quad \text{Sig.}(P) \end{aligned}$$

These results showed the significance of the overall fit of the model. The low value of Nag. R^2 ; also showed that the individual effect for H_0 cannot be rejected from the following null hypothesis:

$$H_0: \tilde{\beta} = 0 \text{ versus } H_1:$$

Second, application of the logistic regression model by using those ranked by the proposed method also shows that this method ranks ea

incidence of the CHD response variable. The question also become apply the logistic regression model. The possibility exists that the the model by selecting too few or too many variables. In the face the model that uses the least number of variables while simul variance in the dependent variable relative to the percentage expla models may be fitted from Table 2 to compare the results. The fir: factors (BMI, and W/H ratio), age, and total cholesterol factors th response variable according to the individual effect (S_i) as in Table and applying SPSS software were

$$\begin{aligned} \text{Logit CHD} &= -0.866 + 0.537 C \\ &\quad -0.352 \text{BMI} - 0.9 \\ \text{Sig. (P)} &\quad (0.026) \quad (0.0 \\ &\quad (0.021) \end{aligned}$$

$$\begin{aligned} -2\log L_0 &= 365.081, & -2\log \\ \text{Nag. } R^2 &= 0.71, & \chi^2_{\beta} = 7.497, \\ \chi^2_{H_L} &= 16.791, & \text{Sig. (P)} \end{aligned}$$

The results in (34) showed that using these criteria for the overa collectively and individually as risk factors that influence the inci comparison with the full model in (31) The second logistic regres HDL, to increase the percentage of explanation to 87%. The result:

$$\begin{aligned} \text{Logit CHD} &= -0.331 + 0.552 \text{Chol} - (\\ &\quad -0.306 \text{BMI} - 1.351 W, \\ \text{Sig. (P)} &\quad (0.085) \quad (0.056) \\ &\quad (0.028) \quad (0.05), \end{aligned}$$

$$\begin{aligned} -2\log L_{1st} &= 357.584, & -2\log \\ \text{Nag. } R^2 &= 0.698, & \chi^2_{\beta} = 8.648, \\ \chi^2_{H_L} &= 4.850, & \text{Sig. (P)} \end{aligned}$$

These results showed that adding the HDL risk factor does not model, but the parameter of this risk factor is not significant when

$$H_0: \beta_{HDL} = 0 \text{ versus } H_1:$$

Note that the difference between the deviances of the two model improve. Thus, according to the principle of parsimony, the first n risk factors used to construct this model are those that are the n the different results obtained from these two models demonstrate: all risk factors and fitting it with only selected risk factors.

The efficiency of the proposed method of variable selection (GSA (34) with the results gained from fitting the logistic regression (BEM). These results are shown in Tables 3 and 4.

Model	Nag. R ²	-2log L	χ ² _β	χ ² _{H_L}	Sig. (P)
Model 1	0.71	365.081	7.497	16.791	0.021
Model 2	0.698	357.584	8.648	4.850	0.056

Table 3: The overall fitting criteria for the BEM

Table 4: The estimated parameters and their BEM.

Table 3 shows the overall fitting criteria required for the last three use of the BEM.

Also Table 4 shows the last three steps of iteration to choose the sequential elimination of the factors, which requires eight step importance; however, the proposed method does not need these it

5. Conclusions

The results in Tables 1 to 4 and (31) to (36) for the two examples distinguishing between important and unimportant risk factors according to their decreasing importance as shown in Tables 1 and 2. Compared the proposed method with those methods that are typically used, we find that the SCAD method in which the same risk factors are selected. From the results, the most influential risk factors are age, the area of the burns, and the interaction between obesity factors (BMI and W/H) are the most influential risk factor, age, and the third risk factor is the total cholesterol. These play the most important role in the incidence of CHD. Thus, they are considered the most important risk factors. The percentages of contribution in the incidence of CHD as shown in Tables 3 and 4. The results of fitting of the full logistic regression model as in (31) and the choice of the proposed method in its selection of the most important risk factors according to the model evaluation criteria, because it consists of the most important risk factors. The care plan and medical interventions should comply with this order of results, one of the traditional variable selection methods was used, but it gave different results after eight steps, but the proposed method order of results need to fit multiple regression models. Finally, these results together with the proposed method as a variable selection method.

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