Dissertation for the degree of Doctor of Philosophy

A study on performance improvement through machine learning method when analyzing survival data including censoring

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Department of Statistics
The Graduate School
Jeonbuk National University

August, 2024

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Under the direction of **Seong-Jun Yang**

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Seong-Yun Hwang

has been approved by the committee members.

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ABSTRACT

A study on performance improvement through machine learning method when analyzing survival data including censoring

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This paper contains the contents of a total of two studies, all of which are related to the analysis of survival data.

The first study relates to a method that can improve predictive power when regression analysis is performed on data with censoring. Censorship is usually caused by internal or external causes, such as the death of a patient due to a factor other than the disease being studied in the survival data related to the patient's survival time, which appears frequently in the medical field. will do The main purpose of analyzing survival data is to determine which factors have a significant effect on the patient's survival time and to predict the patient's survival time through this. In the case of survival data including such censoring, since the survival time, which is the subject of estimation, is only partially observed, a synthetic response can be created to analyze the data. However, these artificial variables have a characteristic that the conditional variance when an explanatory variable is given tends to be larger than the conditional variance of the original survival time, and the width increases as the survival time increases. Because of this, the stability of the estimator is poor, which can be a problem. To compensate for this problem, in this study, when constructing a regression model for artificial variables, the data in the explanatory variable space is moved to a high-dimensional characteristic space by using an appropriate mapping function for complex nonlinear data without specifying a transformation function. When there is a problem of the kernel trick method and multicollinearity, the applicable ridge regression method is applied. In addition, we would like to propose a method for improving the predictive power of survival time by reducing the variance of the estimator by applying ensemble methods such as bagging and random forest. Through computer simulation, various situations were assumed and the predictive power of explanatory variables was compared and analyzed in data including censoring. Through this, it was confirmed that the method proposed in this study showed overall superior predictive power compared to the general method.

The second study relates to a method that can improve the overall time-dependent AUC that can be calculated when analyzing survival data. Continue to explain...

keywords : survival data, synthetic response, ridge regression, machine learning, kernel trick method, ensemble method, time-dependent AUC, Cox proportional hazard model

1 Introduction

1.1 Background and purpose of the study

Survival data is data mainly used in the medical field to check and study the survival time of patients. Recently, in addition to the medical field, it is widely used in various research fields such as analyzing the survival rate of companies or the unemployment rate of workers in the economy and management fields, and its use is also increasing. In particular, one of the greatest characteristics of survival data is that censoring is included. Censoring is caused by various causes, such as when a patient dies due to a cause other than the disease being studied, when a hospitalized patient is transferred to another hospital, when the researcher arbitrarily adjusts the observation time, and when the ongoing research is stopped. Therefore, in the survival data, the actual patient's survival time to be estimated is only partially observed when censoring has not occurred. Based on these characteristics of survival data, various analysis methods such as Kaplan-Meier estimation, Nelson-Aalen estimation, Cox proportional hazard model, Parametric model, and Accelerated failure time model have been proposed. For details on the various survival analysis methods, see Kleinbaum, D.G. and Klein, M. (2010).

However, in the recent big-data era, the data we actually encounter has a nonlinear relationship between a response variable and explanatory variables, or in most cases, standardization is not done. Therefore, there are many cases in which the researcher has to process the data in advance so that the data has an appropriate form for analysis in consideration of various methods such as variable transformation. In addition, the problem of multicollinearity caused by the association between explanatory variables included in the data is one of the important issues to be overcome. This problem is no exception in survival data dealt with in the medical field. Therefore, in this paper, as the first research result, when analyzing survival data including censoring, we propose a method that can overcome these problems to some extent.

두 번째 연구결과 설명...

1.2 Research method and composition

In this paper, two major studies have been conducted, and all of them contain information on how to obtain more improved results by applying methods such as machine learning to the analysis of survival data.

First, the contents of the first study will be explained as a whole. If you want to predict the survival time from survival data with censorship, you can use a synthetic response defined to replace the actual patient's survival time, which is only partially observed, when building a model. For the data conversion method using this synthetic response, see Buckley, J. and James, I. (1979), Koul et al. (1981), Leurgans, S. (1987), et al. And when regression analysis is performed with this synthetic response as a response variable, kernel ridge censored regression method, which is combined the advantages of the kernel trick method and ridge regression method, is applied. Kernel trick method is widely mentioned in the field of machine learning, which is a hot topic recently, as a method that can automatically perform an appropriate transformation without applying an appropriate transformation function to the data to be analyzed in advance. In particular, this method is widely used in various algorithms such as support vector machine (SVM), which is frequently used in classification problems. And the ridge regression method is a kind of penalized regression method that can be used to supplement the multicollinearity problem. Plus, an ensemble method that can significantly reduce the variance of the estimator is additionally applied to build a more stable and reliable prediction model. In this study, bagging that can reduce variance and reduce the risk of overfitting by averaging the results from multiple bootstrap samples selected through iterative sampling with replacement using raw data and a random forest that enables more accurate estimation by reducing the association between explanatory variables through the process of selecting only some of the explanatory variables without including all explanatory variables during bootstrap sampling are applied. A method of increasing the predictive power for survival time through this process is proposed as the first research result.

Next, the contents of the second study will be introduced as a whole. An important key of the second study is the calibration of the time-dependent AUC (Area Under Curve). In other words, a method was studied to increase the overall value of time-dependent AUC, which can be calculated when analyzing time-dependent survival data and is an index to evaluate the accuracy of the analysis result. 두 번째 연구결과 요약 설명 계속...

This dissertation consists of a total of 13 chapters. Chapter 1 outlines the background of the research presented in this paper and the research method accordingly. Chapters 2 to 6 describe the case of applying the kernel trick method and ensemble method in regression analysis on survival data including censoring, which can improve predictive power to predict survival time. Chapter 2 briefly describes the characteristics of survival data and the commonly used survival analysis method when analyzing it, and then mentions how a synthetic response for censored data analysis can be defined. Chapter 3 describes kernel ridge censored regression analysis, which is the core of the first study, and chapter 4 introduces the ensemble method. Next, Chapter 5 explains how to apply the ensemble method to kernel ridge censored regression analysis. And in Chapter 6, we present and evaluate the results of simulation and real data analysis conducted to prove that the kernel ridge censored regression analysis using ensemble method has overall better predictive power than the normal method. Next, Chapters 7 to 12 describe the study of the calibration of time-dependent AUC with Cox regression model. 두번째 연구 종료 후 추가... Finally, Chapter 13 summarizes the research method presented in this paper as a whole and concludes the dissertation.

2 survival data

2.1 survival data

Survival data are often used in the medical field to analyze and study the survival time of patients. As mentioned in the introduction, the biggest characteristic of this data is censoring that it has been caused by internal or external factors, such as a patient's death due to a cause other than the disease being studied or the researcher's arbitrary observation time adjustment. These data include explanatory variables $(x_1, x_2, \ldots, x_p)$, observed survival time $t = \min(y, c)$, and $\delta = I(y \leq c)$, which is an indicator variable indicating whether censoring or not, is included by default. Here, y is the time until the event of interest occurs (usually the patient's actual survival time in the medical field), and c is the censoring time. That is, if the patient's actual survival time is observed by satisfying $y \leq c$, $t = y$ and $\delta = 1$. On the contrary, when censoring is performed by satisfying $y > c$, $t = c$ and $\delta = 0$. In other words, in the actual survival data, the actual survival time of all patients cannot be confirmed, and only in the case of $y \leq c$, the survival time of the actual patients can be partially observed. Therefore, a special method for analyzing survival data is required, and it is collectively called a survival analysis method.

2.2 survival analysis

In survival analysis, the following functions are basically defined based on the observed survival time t.

$$S(t) = P(T > t) = \int_t^\infty f(x)dx = 1 - P(T \leq t) = 1 - F(t) \tag{2.1}$$

$$h(t) = \lim_{\Delta t \to 0} \frac{P(t \leq T < t + \Delta t | T \geq t)}{\Delta t} = \frac{f(t)}{S(t)} = -\frac{d}{dt} \log[S(t)] \tag{2.2}$$

$$H(t) = \int_0^t h(u)du = \int_0^t \frac{\frac{d}{du}[1 - S(u)]}{S(u)} du = -\log[S(t)] \tag{2.3}$$

Here, $S(t)$ is a survival function, $h(t)$, $H(t)$ are hazard function and cumulative hazard function, respectively, and $f(t)$ and $F(t)$ are distribution function and cumulative distribution function for survival time, respectively. And Figure 2.1 shows the graph of estimated survival function $\hat{S}(t)$, which is according to explanatory variable sex by applying Kaplan-Meier estimation based on 'cancer' data, which is related to patients with lung cancer. This graph was drawn using the program R 4.1.1 version, and the 'cancer' data is embedded in 'survival', a package used for survival analysis. And the p-value $p = 0.0013$ displayed in this graph represents the results of the log-rank test whether there is a difference in the survival function according to gender. After all, since the p-value is much smaller than the general significance level $\alpha = 0.05$, it can be interpreted that the survival rate varies according to gender. In addition, the number below the survival function graph represents the number of surviving patients over time.

As can be seen from Figure 2.1, in general, the survival function $S(t)$ starts from 1 and gradually decreases to 0 as time passes. This means that the survival

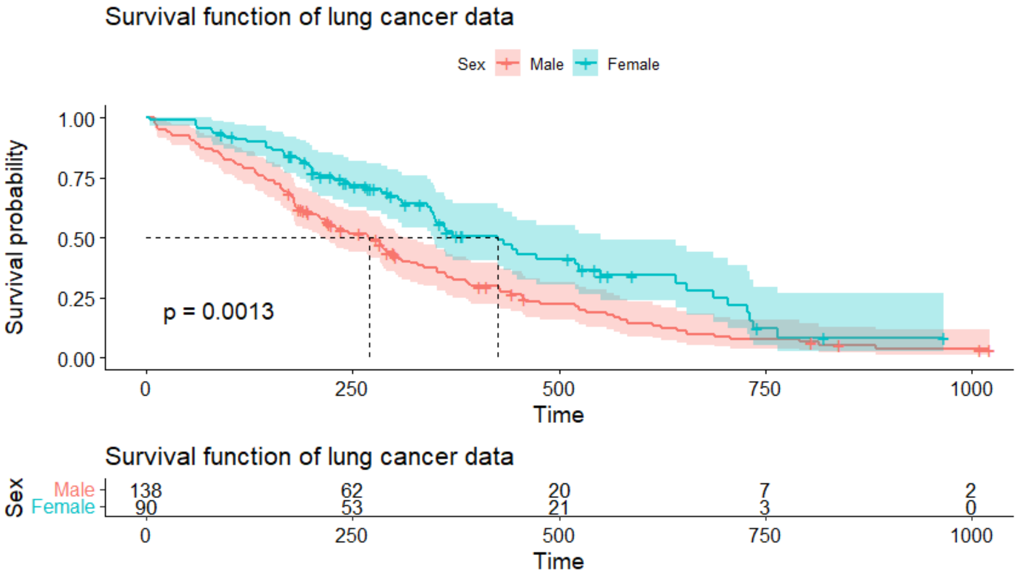


Figure 2.1: Survival function of lung cancer data

rate of patients decreases as time goes by. Of course, like the survival cure model that additionally considers a cure object, there is a case in which a situation in which there is an individual surviving over time due to a special cause is considered. However, as shown in Figure 2.1, a survival function $S(t)$ is usually used that starts at 1 and converges to 0. For details on the survival cure model, please refer to Sposto, R. (2002) et al. And as can be seen from the above equation, the survival function $S(t)$, the hazard function $h(t)$, and the distribution function of survival time $f(t)$ are related to each other. Therefore, if the survival function $S(t)$ is estimated from the survival data, the hazard function $h(t)$ and the distribution function of survival time $f(t)$ can be estimated naturally using this. In general, as shown in Table 2.1, in survival analysis, Kaplan-Meier estimation for estimating the survival function $S(t)$ with a non-parametric method, Nelson-Aalen estimation for estimating the cumulative hazard function $H(t)$ with a non-parametric method, Cox proportional hazard model that models the hazard function $h(t)$ with a semi-parametric method under the assumption that the hazard between groups to be compared is uniformly proportional during the follow-up period, and Parametric model that models the hazard function $h(t)$ as a parametric method assuming a specific distribution are mainly used. In addition, various survival analysis methods exist, and detailed descriptions of them are provided by Sabin, C. and Petrie, A. (2019) and Chen et al. (2017) et al.

Kaplan-Meier Estimation	$\hat{S}(t) = \begin{cases} 1, & \text{if } t < t_1 \\ \prod_{t_i \leq t}[1 - \frac{d_i}{Y_i}], & \text{if } t \geq t_1 \end{cases}, i = 1, 2, \ldots, D$	
Nelson-Aalen Estimation	$\tilde{H}(t) = \begin{cases} 0, & \text{if } t < t_1 \\ \Sigma_{t_i \leq t} \frac{d_i}{Y_i}, & \text{if } t \geq t_1 \end{cases}, i = 1, 2, \ldots, D$	
Cox Proportional Hazard Model	$h(t \mid X) = h_0(t)\exp(X\beta),\ S(t \mid X) = \{\exp[-H_0(t)]\}^{\exp(X\beta)}$	
Parametric Model	Exponential	$h(t) = \lambda_0 > 0,\ S(t) = \exp(-\lambda_0 t)$
	Weibull	$h(t) = \lambda_0 \lambda_1 t^{\lambda_1 - 1},\ S(t) = \exp(-\lambda_0 t^{\lambda_1}),\ (\lambda_0 > 0, \lambda_1 > 0)$
	Rayleigh	$h(t) = \lambda_0 + 2\lambda_1 t,\ S(t) = \exp[-(\lambda_0 t + \lambda_1 t^2)],\ (\lambda_0 > 0, \lambda_1 \geq 0)$
	Gompertz	$h(t) = \exp(\lambda_0 + \lambda_1 t),\ S(t) = \exp[\frac{1}{\lambda_1}\{\exp(\lambda_0) - \exp(\lambda_0 + \lambda_1 t)\}],\ (\lambda_1 > 0)$
	Lognormal	$f(t) = \frac{1}{\sqrt{2\pi}\sigma t}\exp[-\frac{\{\log(t) - \mu\}^2}{2\sigma^2}],\ S(t) = 1 - \Phi[\frac{\log(t) - \mu}{\sigma}]$

Table 2.1: Representative example of survival analysis method

In addition, among the parts for the Kaplan-Meier estimator and the Nelson-Aalen estimator in Table 2.1, d_i is the number of events that occurred at time t_i, and Y_i is the number of individuals at risk at time t_i . And $\Phi(\cdot)$ of the Lognormal distribution part means cumulative distribution function of standard normal distribution. Additionally, in the case of the parametric model, using the hazard function $h(t)$ and the distribution function of survival time $f(t)$ presented in Table 2.1, and Equation 2.1 $\sim$ 2.3, we can derive $h(t)$, $f(t)$, $S(t)$, and the cumulative hazard function $H(t)$. Detailed proof of this will be omitted.

2.3 Synthetic response for censored data analysis

As mentioned in Section 2.1, the only variable related to survival time included in the survival data is the observed survival time for patients, $t = \min(y, c)$. Therefore, it is not possible to know the exact survival time for all patients, that is, the time it takes for the event of interest to occur. Therefore, when constructing a regression model for predicting survival time, it is somewhat unreasonable to set the observed survival time t as a response variable. Therefore, in this study, we used the synthetic response from Koul et al. (1981) to transform the data, and the form is as follows. For details, see Kim, J. (2018) and Lee, S. (2018).

$$Y^S = \frac{\delta t}{1 - G(T)} \tag{3.4}$$

$$G(t) = P(C \leq t), \delta = I(Y \leq C), T = \min(Y, C) \tag{3.5}$$

Here, the function $1 - G(T)$ is estimated using the Kaplan-Meier estimator on the assumption that the censoring variable T does not depend on the explanatory variable X. If there is a dependency, the following type of estimator proposed by Beran, R. (1981) should be used. In this estimator, W_0 means Nadaraya-Watson weight, h_0 means bandwidth, and K_0 means kernel function.

$$1 - \hat{G}(t|x) = \prod_{i=1}^{n} [1 - \frac{(1-\delta_i) I_{\{\phi(T_i) \leq t\}} W_{0i}(x, h_0)}{\Sigma_{j=1}^{n} I_{\{\phi(T_i) \leq \phi(T_j)\}} W_{0j}(x, h_0)}] \tag{3.6}$$

$$W_{0i}(x, h_0) = \frac{K_0(\frac{X_i - x}{h_0})}{\Sigma_{j=1}^{n} K_0(\frac{X_j - x}{h_0})} \tag{3.7}$$

In this study, the Kaplan-Meier estimator of the following form was used based on the assumption that the censoring variable T does not depend on the explanatory variable X.

$$1 - \hat{G}(t) = \prod_{i=1}^{n}[1 - \frac{(1-\delta_i)I(T_i \leq t)}{\Sigma_{j=1}^{n} I(T_j \geq T_i)}] \tag{3.8}$$

One thing to note is that when generating this synthetic response Y^S, the value of the estimator $1 - \hat{G}(t)$ for the denominator almost approaches 0, that is, in the case of $1 - \hat{G}(t) \approx 0$, the value of Y^S is infinitely divergent or undefined. In this study, a method of determining the truncation point was used in case such a situation occurs. If the value of the observed survival time t is greater than the point at which the cumulative probability becomes 0.98, $Y^S = 0$ is set.

The synthetic response Y^S has the following properties assuming some suitable conditions. Here, some suitable conditions are that the patient's actual survival time Y and censoring time C are independent of each other ($Y \perp C$), and the probability that Y is less than or equal to C is not depend on the explanatory variable X ($P(Y \leq C|X, Y) = P(Y \leq C|Y)$).

$**$

If $Y \perp C$ and $P(Y \leq C|X, Y) = P(Y \leq C|Y)$, then $E(Y|X = x) = E(Y^S|X = x)$

proof)

$E(Y^S|X = x) = E(\frac{\delta T}{1-G(T)}|X = x) = E(\frac{\delta Y}{1-G(Y)}|X = x)$

$= E(\frac{Y \times I(Y \leq C)}{1-G(Y)}|X = x) \approx E(Y\frac{1-G(Y)}{1-G(Y)}|X = x) = E(Y|X = x)$

$\because$ If $Y \leq C$, then $\delta = 1, T = Y$. So $Y^S = \frac{1 \times Y}{1-G(Y)} = \frac{\delta Y}{1-G(Y)}$

And if $Y > C$, then $\delta = 0, T = C$. So $Y^S = \frac{0 \times C}{1-G(C)} = \frac{\delta Y}{1-G(Y)}$

And $E(I(Y \leq C)|X = x) = P(Y \leq C|X = x, Y = y) = P(Y \leq C|Y) = 1 - G(Y)$

$**$

That is, if the patient's actual survival time Y and censoring time C are independent of each other, and the probability that censoring does not occur does not depend on the explanatory variable X, the conditional mean of the synthetic response Y^S is coincides with the conditional mean of patient's actual survival time Y. Therefore, instead of putting the variable Y as a response variable, it can be said that it is reasonable to build a regression model with synthetic response Y^S as a new response variable. However, in the case of conditional variance, the case of synthetic response Y^S is larger than the case of variable Y as follows.

****

If $Y \perp C$ and $P(Y \leq C|X, Y) = P(Y \leq C|Y)$, then

$Var(Y^S|X = x) = Var(Y|X = x) + E(\frac{G(T)}{1-G(T)}Y^2|X = x)$

proof)

$Var(Y^S|X = x) = E((Y^S)^2|X = x) - \{E(Y^S|X = x)\}^2$

$= E[(\frac{\delta T}{1-G(T)})^2|X = x] - \{E(Y|X = x)\}^2$

$= E[(\frac{\delta T}{1-G(T)})^2|X = x] - E(Y^2|X = x) + Var(Y|X = x)$

$= E[\frac{\delta}{1-G(Y)}\frac{Y^2}{1-G(T)} - Y^2|X = x] + Var(Y|X = x)$ $(\because \delta^2 = \delta)$

$= E[\frac{I(Y \leq C)}{1-G(Y)}\frac{Y^2}{1-G(T)} - Y^2|X = x] + Var(Y|X = x)$

$\approx E[\frac{1-G(Y)}{1-G(Y)}\frac{Y^2}{1-G(T)} - Y^2|X = x] + Var(Y|X = x)$

$= Var(Y^S|X = x) = Var(Y|X = x) + E(\frac{G(T)}{1-G(T)}Y^2|X = x)$

****

Because of this property, when a regression model to predict the patient's actual survival time Y is constructed using the synthetic response Y^S, as the variance of the estimator increases, the volatility also increases, which reduces the stability and reliability of the model. There are disadvantages. To compensate for this problem, the ridge regression method and the ensemble method can be applied, and these will be introduced in Chapters 3 and 4, respectively.

3 Kernel ridge censored regression analysis

This chapter describes the Kernel ridge censored regression analysis method. The main purpose of this method is to predict the time it takes for an event of interest to occur in a patient through survival data, and a multiple regression model is fitted with the synthetic response described in Section 3 in Chapter 2 as a response variable. Here, in the case of estimating the regression coefficient, we can more apply the ridge regression method that can supplement the multicollinearity problem based on regulation through the penalty function, and the kernel trick method that complements non-linear relationship between the response variable and the explanatory variable using space transformation. The Kernel ridge censored regression analysis is a method to build a model with stronger predictive power through this. Through this, if the survival data is analyzed and predicted the time taken until the event of interest occurs by fitting a model, good prediction results can be obtained based on higher accuracy than the normal method. Before introducing the Kernel ridge censored regression analysis method in earnest, Section 3.1 will first explain the multiple regression analysis that is the basis of this method.

3.1 Multiple regression analysis

Multiple regression analysis is a statistical analysis method proposed to analyze data based on the assumption that when there is a specific linear relationship between one response variable and two or more explanatory variables. For details on this, refer to Han, S. (2016) and Hwang, S. (2017). Let's look at an example to help you understand. If there are data (y_i, x_i), $i = 1, 2, \ldots, n$ including n observations and k explanatory variables, in multiple regression analysis, the data is analyzed with the basic assumption of the following model formula. As can be seen from this model, the multiple regression analysis method basically assumes that a linear relationship exists between the response variable and the explanatory variables.

$$y_i = \beta_0 + \beta_1 x_{i1} + \beta_2 x_{i2} + \cdots + \beta_k x_{ik} + \epsilon_i, i = 1, 2, \ldots, n \tag{1.1}$$

Here, ϵ_i is the error assumed by the multiple regression model, and normally assumed ϵ_i follow a normal distribution with mean 0 and variance σ^2 and are independent (iid: identical and independently distributed). The above regression model is usually expressed in the form of the following matrix and vector, and I think that this type of expression is a better way of expression in terms of computational and readability for theoretical proof.

$$y = X\beta + \epsilon, \epsilon \sim N_n(0, \sigma^2 I_n) \tag{1.2}$$

Here, $y = (y_1, y_2, \ldots, y_n)^T$ is a response variable vector of length n, $\epsilon = (\epsilon_1, \epsilon_2, \ldots, \epsilon_n)^T$ is an error vector of length n. And $\beta = (\beta_0, \beta_1, \ldots, \beta_k)^T$ is a regression coefficient vector of length $p(= k + 1)$, and X in Equation 1.3 is a data matrix that $n \times p$ dimension.

$$X = \begin{bmatrix} 1 & x_{11} & x_{12} & \cdots & x_{1k} \\ 1 & x_{21} & x_{22} & \cdots & x_{2k} \\ \vdots & \vdots & \vdots & \ddots & \vdots \\ 1 & x_{n1} & x_{n2} & \cdots & x_{nk} \end{bmatrix} = \begin{bmatrix} x_1^T \\ x_2^T \\ \vdots \\ x_n^T \end{bmatrix} \tag{1.3}$$

Also, 0 is a zero vector with a length of n, and I_n is an identity matrix that $n \times n$ dimension. The estimator of the regression coefficient vector $\hat{\beta}$ is usually calculated using least squares estimation. Of course, the maximum likelihood estimation assuming the normality of the error can also be used. However, in the case of multiple regression analysis, the shape of the estimator calculated by these two methods is the same as a result. The calculation process to apply least squares estimation is as the following equation, and the equation obtained through this process is called the normal equation.

****

$Q = \Sigma_{i=1}^{n} \epsilon_i^2 = (y - X\beta)^T (y - X\beta)$

$\frac{\partial Q}{\partial \beta} = -2X^T (y - X\beta) = 0$

$(X^T X)\hat{\beta} = X^T y$

****

For the normal equation above, if the matrix $X^T X$ has an inverse matrix, that is, if the matrix X satisfies the full-rank property, then $\hat{beta}$, which is the estimator of β, is determined to be a unique solution of the form. And the expected value and variance of this estimator $\hat{\beta}$ can be proved as follows. In conclusion, it can be confirmed that the estimator $\hat{\beta}$ is an unbiased estimator of the regression coefficient vector β.

****

$\hat{\beta} = (X^T X)^{-1} X^T y$

$E(\hat{\beta}) = E[(X^T X)^{-1} X^T y] = (X^T X)^{-1} X^T X \beta = \beta$

$Var(\hat{\beta}) = Var[(X^T X)^{-1} X^T y]$

$= (X^T X)^{-1} X^T (\sigma^2 I_n)[(X^T X)^{-1}]^T$

$= (X^T X)^{-1} X^T X[(X^T X)^{-1}]^T \sigma^2$

$= (X^T X)^{-1} X^T X[(X^T X)^T]^{-1} \sigma^2$

$= (X^T X)^{-1} X^T X(X^T X)^{-1} \sigma^2$

$= (X^T X)^{-1} \sigma^2$

$\because y \sim N_n(X\beta, \sigma^2 I_n)$

****

For reference, calculating the $\hat{\beta}^{MLE}$, which is the estimator of regression coefficient vector β using maximum likelihood estimation is as follows.

****

If $x \sim N_r(\mu, \Sigma)$, then probability distribution function(pdf) of vector x is

$f(x|\mu, \Sigma) = (2\pi)^{-\frac{r}{2}} |\Sigma|^{-\frac{1}{2}} \exp\{-\frac{1}{2}(x-\mu)^T \Sigma^{-1} (x-\mu)\}, x \in R^r$

And $y = X\beta + \epsilon, \epsilon \sim N_n(0, \sigma^2 I_n)$.

Therefore, pdf of vector ϵ is

$f(\epsilon) = (2\pi)^{-\frac{n}{2}} |\sigma^2 I_n|^{-\frac{1}{2}} \exp\{-\frac{1}{2}\epsilon^T (\sigma^2 I_n)^{-1} \epsilon\}, \epsilon \in R^n$

Hence, likelihood function of β and σ^2 is

$L(\beta, \sigma^2) = (2\pi)^{-\frac{n}{2}} |\sigma^2 I_n|^{-\frac{1}{2}} exp\{-\frac{1}{2}(y - X\beta)^T (\sigma^2 I_n)^{-1} (y - X\beta)\}$

$\log L(\beta, \sigma^2) = -\frac{n}{2}\log(2\pi) - \frac{n}{2}\log(\sigma^2) - \frac{1}{2\sigma^2}(y - X\beta)^T (y - X\beta)$

$\frac{\partial}{\partial\beta}\log L(\beta,\sigma^2) = -\frac{1}{\sigma^2}X^T(y - X\beta) = 0$

$\frac{\partial}{\partial\sigma^2}\log L(\beta,\sigma^2) = -\frac{n}{\sigma^2} + \frac{1}{2(\sigma^2)^2}(y - X\beta)^T(y - X\beta) = 0$

So, if matrix X is full-rank, maximum likelihood estimator of β and σ^2 are

$\hat{\beta}^{MLE} = (X^TX)^{-1}X^Ty$ and

$\hat{\sigma^2}^{MLE} = \frac{1}{n}(y - X\hat{\beta}^{MLE})^T(y - X\hat{\beta}^{MLE})$

****

3.2 Ridge regression analysis

Ridge regression analysis is a type of penalized regression method represented together with Lasso regression (Least Absolute Shrinkage Selector Operator). This method is frequently used in various situations when applying the multiple regression analysis introduced in Section 3.1 when analyzing data, such as there is a multicollinearity problem that occurs because there is a correlation between explanatory variables, or when the estimator is not uniquely determined because the number of explanatory variables is greater than the number of observations. The essence of this method is that a certain amount of bias is allowed to obtain the estimator of the regression coefficient, and instead of giving up the advantage of the unbiased estimator, a more reliable estimator is obtained by appropriately regulating the variance to significantly reduce the variance. The estimator is calculated using a method similar to least squares estimation as follows. However, unlike general multiple regression analysis, to obtain an estimator using ridge regression analysis, penalty function with quadratic form $\lambda||\beta||^2 = \lambda\beta^T\beta$ multiplied by a positive real λ is added. This is a great feature of Ridge regression analysis compared with normal multiple regression analysis.

$$\hat{\beta} = \min_{\beta}\{||y - X\beta||^2 + \lambda||\beta||^2\} = \min_{\beta}\{(y - X\beta)^T(y - X\beta) + \lambda\beta^T\beta\}, (\lambda > 0) \quad (2.4)$$

Here, λ means the ridge parameter and plays an important role in properly setting the ratio of bias and variance of the estimator calculated by ridge regression analysis. If the value of λ approaches 0, the bias of the estimator approaches 0 and the variance increases. Conversely, if the value of λ increases, the bias increases but the variance decreases. Therefore, in order to calculate the estimator through ridge regression analysis, the appropriate parameter λ should be determined in advance. In general, using the method of cross validation, parameter λ, in which makes the most desirable condition that the estimated value of the test MSE (mean squared error) is calculated to the minimum, is selected. The $\hat{\beta}$, which is the estimator of β, obtained through this method as follows.

****

$Q^* = (y - X\beta)^T(y - X\beta) + \lambda\beta^T\beta$

$\frac{\partial Q^*}{\partial\beta} = -2X^T(y - X\beta) + 2\lambda\beta = 0$

$(X^TX + \lambda I_n)\hat{\beta} = X^Ty$

$\hat{\beta} = (X^TX + \lambda I_n)^{-1}X^Ty, (\lambda > 0)$

****

The expected value of this estimator $\hat{\beta}$ is different from the regression coefficient vector β. Therefore, this estimator does not satisfy unbiased for β. However, in the above expression, the matrix $X^TX + \lambda I_n$ must have an inverse matrix by λ. Therefore, the estimator $\hat{\beta}$ is determined as the only one value according to the value of λ. For reference, the form of the penalty function used in Lasso regression analysis is $\lambda||\beta||$, and there are some cases where the value of the regression coefficient estimated according to the value of λ becomes 0. Because of these characteristics, lasso regression analysis includes the function of variable selection, and to calculate the estimator $\hat{\beta}$, soft-thresholding method is used, which is in order to estimate the regression coefficient for a specific explanatory variable, assume that the regression coefficients for the remaining explanatory variables are given and estimates the regression coefficient. For this, please refer to Kim, J. (2018). Also, there is Elastic-net regression, a hybrid method created by combining Ridge regression analysis and Lasso regression analysis, which is extremely preferred when the number of variables p is greater than the number of observations n or strong multicollinearity problem is exist. For more details on penalized regression, see Friedman et al. (2007) and Hastie et al. (2011) and summarizes the core of each method as follows.

$***$

Ridge regression :

$\min_{\beta=(\beta_0,\ldots,\beta_k)^T}[\Sigma_{i=1}^n(y_i-\beta_0-\Sigma_{j=1}^k\beta_jx_{ij})^2+\lambda\Sigma_{j=1}^k\beta_j^2]$

Lasso regression :

$\min_{\beta=(\beta_0,\ldots,\beta_k)^T}[\Sigma_{i=1}^n(y_i-\beta_0-\Sigma_{j=1}^k\beta_jx_{ij})^2+\lambda\Sigma_{j=1}^k|\beta_j|]$

Elastic-net regression :

$\min_{\beta=(\beta_0,\ldots,\beta_k)^T}[\Sigma_{i=1}^n(y_i-\beta_0-\Sigma_{j=1}^k\beta_jx_{ij})^2+\lambda_1\Sigma_{j=1}^k\beta_j^2+\lambda_2\Sigma_{j=1}^k|\beta_j|]$

$***$

3.3 Kernel ridge regression analysis

The Ridge regression analysis method introduced in Section 3.2 proceeds with the analysis based on the assumption that there is a linear relationship between the response variable and the explanatory variables. However, since most of the data we actually collect and analyze is not organized for smooth processing, it is necessary for the researcher to organize it according to the purpose of the analysis in advance. Since it is common to show an almost nonlinear relationship structure, it is necessary to consider an appropriate transformation function, and in some cases, it is often necessary to consider the interaction effect between explanatory variables. The Kernel trick method is a method that can be applied when there are these problems. By applying this method, if an appropriate mapping function Φ, which is according to the characteristics of this data, is applied to the nonlinear data with complex structure, the data existing in the p dimension explanatory variable space can be transformed according to the characteristics. And the result is placed in a high-dimensional Hilbert space or feature space. If the data is transformed through this process, the same result as applying a transformation function suitable for the characteristics of the data can be obtained appropriately even without considering the transformation function in advance, and the analysis can be carried out by fitting a linear model to the transformed data. If the core of the Kernel trick method is expressed briefly, it can be represented as in Figure 3.1 below. In other words, since the original data shows a nonlinear relationship, even if it is a problem that it is difficult to fit an appropriate model when analyzing it as it is, but if it is appropriately transformed and moved to the feature space, the relationship changes to linear, so it turns into a problem that is easy to fit model. That is the core of the Kernel trick method.

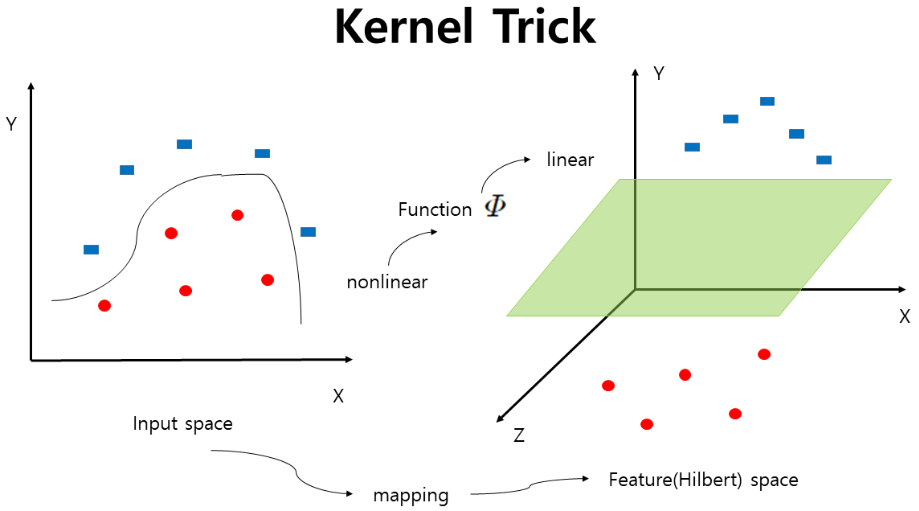


Figure 3.1: Kernel-trick method

From now on, how this Kernel trick method can be applied to ridge regression analysis is described. For more details, see Huh, M. (2015), Lee et al. (2016), Han, S. (2016), and Hwang, S. (2017). Suppose there are training data X with n observations and p dimension explanatory variable space, and n observations in this training data are $(y_i, x_i), i = 1, 2, \ldots, n$. In this regard, by using the mapping function Φ, it is possible to appropriately convert the n explanatory variable data in the training data X through the following method.

$$x_1, x_2, \ldots, x_n \to \Phi(x_1), \Phi(x_2), \ldots, \Phi(x_n) \tag{3.5}$$

Here, $x_i = (x_{i1}, x_{i2}, \ldots, x_{ip})^T, i = 1, 2, \ldots, n$. The explanatory variable data

$\Phi(x_1), \Phi(x_2), \ldots, \Phi(x_n)$, which is transformed using the mapping function Φ, is placed on the feature space with high dimension, and the following regression model can be fitted using this.

$$E(y|x_1, \ldots, x_n) = \Phi(x_1)d_1 + \Phi(x_2)d_2 + \cdots + \Phi(x_n)d_n \tag{3.6}$$

Through the process of fitting the above model, a regression coefficient vector $d = (d_1, d_2, \ldots, d_n)^T$ of length n can be set. Space transformation through this kernel trick method is actually performed through calculation by the kernel function $k(\cdot, \cdot)$. Through this process, the projection of $\Phi(X)$, which is related to the linear combination of $\Phi(x_1), \Phi(x_2), \ldots, \Phi(x_n)$, $v = d_1\Phi(x_1) + d_2\Phi(x_2) + \cdots + d_n\Phi(x_n)$, is calculated as follows.

$$\Sigma_{j=1}^{n} \langle \Phi(x_i), \Phi(x_j) \rangle \, d_j = \Sigma_{j=1}^{n} k_{i,j} d_j \tag{3.7}$$

Here, $k_{i,j} = \langle \Phi(x_i), \Phi(x_j) \rangle = \Phi(x_i)^T \Phi(x_j) = k(x_i, x_j)$ is the (i, j)th element of matrix $K = (K_{i,j})$, $i = 1, \ldots, n$, $j = 1, \ldots, n$. The response variable y is explained using the matrix K and the regression coefficient vector d obtained through this calculation process. For more details on this, see Schölkopf and Smola (2002). The kernel used to calculate the matrix K must satisfy the following Mercer's theorem, according to Minh et al. (2006) and Nguyen, V. (2015).

****

Mercer's theorem

A symmetric function $k_{i,j}$ can be expressed as an inner product

$$k_{i,j} = \langle \Phi(x_i), \Phi(x_j) \rangle = \Phi(x_i)^T \Phi(x_j)$$

for some Φ if and only if $k_{i,j}$ is positive semi-definite, is equal to,

$$\int k_{i,j} g(x_i) g(x_j) dx_i dx_j \geq 0, \forall g$$

or, equivalently $K = (K_{i,j})$, $i = 1, \ldots, n$, $j = 1, \ldots, n$ is positive semi-definite matrix for any collection $x_1, x_2, \ldots, x_n$.

****

In other words, when the kernel function $k_{i,j}$ is a continuous function in the form of an inner product, if the matrix K made from the value of the kernel function is a symmetric matrix and a positive semi-definite matrix, there exist Φ that satisfies $k_{i,j} = k_{j,i} = \langle \Phi(x_i), \Phi(x_j) \rangle$. This is the main core of Mercer's theorem. The form of the kernel that satisfies this Mercer's theorem exists in various ways as shown in Table 3.1. For details, see Karatzoglou et al. (2006) and Souza, C. R. (2010) et al.

In this study, Polynomial kernel and Gaussian kernel are applied among the kernels that satisfy Mercer's theorem presented in Table 3.1. These two kernels are as follows.

****

Polynomial kernel : $k_{i,j} = [\alpha(x_i^T x_j) + \beta]^\gamma, \alpha \neq 0, \gamma > 0$

Gaussian kernel : $k_{i,j} = \exp(\sigma||x_i - x_j||^2), \sigma > 0$

Here, $i = 1, 2, \ldots, n$, $j = 1, 2, \ldots, n$

****

In particular, compared to other kernels, Gaussian kernel has a strong characteristic that flexible application is possible even when prior information about the data to be analyzed is not known. The reason is that in the case of the Gaussian

Linear	$k(x,y) = x^T y + c$
Polynomial	$k(x,y) = [\alpha(x^T y) + \beta]^\gamma$
Gaussian (Radial Basis)	$k(x,y) = \exp(-\sigma \lvert\lvert x-y \rvert\rvert^2)$
Laplace	$k(x,y) = \exp(-\sigma \lvert\lvert x-y \rvert\rvert)$
ANOVA	$k(x,y) = [\Sigma_{k=1}^n \{-\sigma(x^k - y^k)^2\}]^d$
Sigmoid	$k(x,y) = \tanh[\alpha(x^T y) + \beta]$
Rational Quadratic	$k(x,y) = 1 - \frac{\lvert\lvert x-y \rvert\rvert^2}{\lvert\lvert x-y \rvert\rvert^2 + c}$
Multiquadratic	$k(x,y) = \sqrt{\lvert\lvert x-y \rvert\rvert^2 + c^2}$
Inverse Multiquadratic	$k(x,y) = \frac{1}{\sqrt{\lvert\lvert x-y \rvert\rvert^2 + c^2}}$
Bessel	$k(x,y) = \frac{(Bessel)^n_{(\nu+1)}(\sigma \lvert\lvert x-y \rvert\rvert)}{(\lvert\lvert x-y \rvert\rvert)^{-n(\nu+1)}}$
Cauchy	$k(x,y) = \frac{1}{1 + (\frac{\lvert\lvert x-y \rvert\rvert}{\sigma})^2}$
Generalized T-Student	$k(x,y) = \frac{1}{1 + \lvert\lvert x-y \rvert\rvert^d}$
Power(conditionally positive definite)	$k(x,y) = -\lvert\lvert x-y \rvert\rvert^d$
Log(conditionally positive definite)	$k(x,y) = -\log(\lvert\lvert x-y \rvert\rvert^d + 1)$
Triangular(positive definite in R)	$k(x,y) = 1 - \frac{\lvert\lvert x-y \rvert\rvert}{2\gamma}, \lvert\lvert x-y \rvert\rvert < 2\gamma$

Table 3.1: Various kernel types that satisfy Mercer's theorem

kernel, it can be expressed as the sum of infinite series by expanding and expressing the expression of the function through Taylor series expansion as shown in the following equation. This means that it can be expressed as the inner product of the transformed explanatory variables $\Phi(x_i)$ and $\Phi(x_j)$ in the form of vectors with infinite dimensions. That is, if the Gaussian kernel is applied, the data to be analyzed is appropriately transformed and moved to the feature space of infinite space.

$***$

$k_{i,j} = \exp(-\sigma||x_i - x_j||^2)$

$= \{\exp(-||x_i - x_j||^2)\}^\sigma$

$= [\exp(-||x_i||^2)\exp(-||x_j||^2)\Sigma_{r=1}^{\infty}\frac{(x_i^T x_j)^r}{r!}]^\sigma$

$= \Phi(x_i)^T\Phi(x_j) = \langle\Phi(x_i), \Phi(x_j)\rangle$

$***$

In this study, when a polynomial kernel is applied, the degree parameter γ that determines the flexibility of the boundary created by the kernel is fixed as $\gamma = 3$. The reason is that the larger the number of explanatory variables, the greater the complexity, so to compensate for this, the size of γ should be reduced. It was determined that fixing $\gamma = 3$ would be a sufficient solution. Based on the same logic, the scale parameter α was set to $\alpha = \frac{1}{p^2}$, and the offset parameter β was fixed to $\beta = 1$. And in the case of applying the Gaussian kernel, the tuning parameter σ that determines the flexibility of the boundary created by the kernel was set $\sigma = \frac{1}{p}$ in order to set the boundary in a simple form as the number of explanatory variables increases. Here, p means the dimension of the explanatory variable space where the original data in the state before conversion through the kernel function is placed. Using this kernel transformation, the following regression model can be obtained.

$$y = Kd + \epsilon \tag{3.8}$$

And it is worth noting that the inverse matrix for the matrix K obtained through transformation does not always exist. To compensate for this, the regression coefficient vector d is estimated by applying the penalty function $\lambda d^T Kd$ in the form of ridge regression analysis. The regression coefficient vector $\hat{d}$ estimated through this is calculated as follows.

****

$Q^* = (y - Kd)^T (y - Kd) + \lambda d^T Kd$

$\frac{\partial Q^*}{\partial d} = -2K(y - Kd) + 2\lambda Kd = 0$

$\hat{d} = \min_d[(y - Kd)^T (y - Kd) + \lambda d^T Kd]$

$= (K + \lambda I_n)^{-1} y, (\lambda > 0)$

****

Here, the optimal value of the ridge parameter λ is selected through k-fold cross validation. In this study, $k = 5$ was set, and the optimal λ value was determined and selected as the optimal situation when the mean value of RMSE (Root Mean Square Error) was the minimum. In this way, in order to proceed with the evaluation of the test data X^* through the training data X, several procedures are necessary. First, compute the projection of $\Phi(X^*)$, which is related to $v = d_1\Phi(x_1) + d_2\Phi(x_2) + \cdots + d_n\Phi(x_n)$ that the linear combination of transformed explanatory variable data $\Phi(x_1), \Phi(x_2), \ldots, \Phi(x_n)$, that is transformed using kernel function $k(\cdot, \cdot)$. Then, based on this, we need to calculate the matrix K^* to be used for test data evaluation. The calculation process for this is as follows. Here, n means the number of observations in the training data, and u means the number of observations in the test data.

****

$\Sigma_{j=1}^{n} \langle \Phi(x_i^*), \Phi(x_j) \rangle \, d_j = \Sigma_{j=1}^{n} k_{i,j}^* d_j$

$k_{i,j}^* = \langle \Phi(x_i^*), \Phi(x_j) \rangle = \Phi(x_i^*)^T \Phi(x_j) = k(x_i^*, x_j)$

****

And in this study, the following types of Polynomial kernel and Gaussian kernel are applied.

****

Polynomial kernel : $k_{i,j}^* = [\alpha(x_i^{*T} x_j) + \beta]^\gamma, \alpha = \frac{1}{p^2}, \beta = 1, \gamma = 3$

Gaussian kernel : $k_{i,j}^* = \exp(\sigma ||x_i^* - x_j||^2), \sigma = \frac{1}{p}$

Here, $i = 1, 2, \ldots, u$, $j = 1, 2, \ldots, n$

****

Here, $k_{i,j}^*$ is the (j, i)th element of matrix $K^* = (k_{i,j}^*)$, $i = 1, 2, \ldots, u$, $j = 1, 2, \ldots, n$ and x_i^* is the explanatory variable data for ith element in test data X^*. Through this process, we can do final evaluation of the test data X^* using the matrix K^* and the estimator $\hat{d}$, which is calculated through the training data X. In other words, using the matrix K^* and the estimator $\hat{d}$, we can calculate $\hat{y^*} = (\hat{y_1^*}, \hat{y_2^*}, \ldots, \hat{y_u^*})^T$, which is the estimator of response variable $y^* = (y_1^*, y_2^*, \ldots, y_u^*)^T$ from test data, using training data as follows.

$$\hat{y^*} = K^{*T} \hat{d} \tag{3.9}$$

Based on this estimator, the following RMSE value is calculated, and the smaller this value is, the higher the predictive power of the built model is judged.

$$\sqrt{MSE} = \sqrt{\frac{1}{u}\Sigma_{i=1}^{u}(y_i^* - \hat{y_i^*})^2} \tag{3.10}$$

3.4 Kernel ridge censored regression analysis

Kernel ridge censored regression can be expressed by changing the response variable y_i in the data in the kernel ridge regression analysis described in Section 3.3 to the synthetic response y_i^S introduced in Section 3 of Chapter 2. And the form can be expressed as follows. Here, $i = 1, 2, \dots, n$.

$$y_i^S = \frac{\delta_i t_i}{1 - G(t_i)} \tag{4.11}$$

$$G(t_i) = P(C \leq t_i), \delta_i = I(y_i \leq c_i), t_i = \min(y_i, c_i) \tag{4.12}$$

In other words, using the observed survival time t_i and censoring indicator variable δ_i in the survival data to be analyzed, calculate the synthetic response y_i^S that replaces patient's real survival time y_i and applied it to kernel ridge regression analysis. In this study, for estimating the function $1 - G(t_i)$, we use Kaplan-Meier estimator based on the assumption that censoring variable does not depend on explanatory variable $x_i = (x_{i1}, x_{i2}, \dots, x_{ip})^T$. Other than that, the details are the same as those of kernel ridge regression analysis, so a detailed description will be omitted. However, in Kernel ridge censored regression analysis, synthetic response $y^{S*} = (y_1^{S*}, y_2^{S*}, \dots, y_u^{S*})^T$ is additionally used. So when evaluating the built model, the evaluation criterion of predictive power should be divided into two cases, synthetic response variable $y^{S*} = (y_1^{S*}, y_2^{S*}, \dots, y_u^{S*})^T$ and the actual response variable $y^* = (y_1^*, y_2^*, \dots, y_u^*)^T$. In other words, if the evaluation criterion is synthetic response, the RMSE is calculated as $\sqrt{MSE1} = \sqrt{\frac{1}{u}\Sigma_{i=1}^{u}(y_i^{S*} - \hat{y}_i^{S*})^2}$, and when the evaluation criterion is the actual response variable, the RMSE is calculated as $\sqrt{MSE2} = \sqrt{\frac{1}{u}\Sigma_{i=1}^{u}(y_i^{*} - \hat{y}_i^{S*})^2}$. However, it is necessary to take into account that the actual survival time of all patients, that is, the time taken until the event of interest occurs, is not recorded in the actual survival data. In this study, in the simulation study that can generate data arbitrarily, both criteria described above will be used to evaluate the performance of the methodology. But in in real data analysis based on real data, only one criteria, which is related with synthetic response, will be used to evaluate the performance of the methodology.

4 Ensemble method

This chapter introduces the ensemble method, a method that can greatly reduce the variability of the estimator by applying the bootstrap method. The ensemble method is a method derived from the tree-model method, which is a type of machine learning, and is a technique to generate more accurate results by creating multiple predictors or classifiers and then combining them. In this study, among various ensemble methods, bagging and random forests are used. The key shared by these two methodologies is that the average of the results obtained using bootstrap samples extracted independently of each other is used as the estimator to significantly reduce the variance to promote the stability of the prediction. If this method is applied, more accurate and reliable predictions can be made. In addition to bagging and random forests, various boosting algorithms such as AdaBoost (Adaptive Boosting), GBM (Gradient Boosting Machine), XGBoost, and LightGBM also belong to the ensemble method. The key to these methods is to increase the performance of the model by sequentially combining several weak learners. For this, see Freund et al. (1999), Lee, J. (2020), Han, S. (2016), and Hwang, S. (2017).

Let's look at a simple example. If it is assumed that the random n samples $X_1, X_2, \ldots, X_n$ are independent and the variances are all equal to σ^2, the variance of their sample mean $\bar{X} = \frac{1}{n}\Sigma_{i=1}^{n} X_i$ will be greatly reduced, like $\frac{\sigma^2}{n}$. That is, the estimator obtained by extracting a large number of samples and averaging them has a very small variance compared to the estimator obtained through the general method without going through such a process, so the variability is greatly reduced. Therefore, the estimator obtained through averaging shows better performance than the general estimator in terms of reliability. And through the form of the formula, it is easy to understand that the number of samples n and the variance $\frac{\sigma^2}{n}$ are inversely proportional to each other. Therefore, if you want to obtain a more preferable estimator in terms of reliability compared to a general estimator, you can extract a large number of samples, obtain an estimator for each, and significantly reduce the variance value through the process of averaging them. However, it is practically impossible to increase the number of samples to the point of being near infinity. Therefore, it can be said that methods such as bagging or random forests that extract and analyze a sufficient number of bootstrap samples from the original data are analysis methods that overcome these limitations to some extent.

4.1 Bagging

Bagging (bootstrap aggregation) is a method of ensemble method that extracts and analyzes several bootstrap samples with the same number of observations compared to the training data by repeatedly sampling with replacement on one training data. All extracted bootstrap samples are analyzed using the same type of algorithm-based predictor or classifier, and it has the advantage of supplementing the problem of overfitting that may occur when the model is fitted. Here, overfitting means a phenomenon in which the training data is over-learned in machine learning, so that the error decreases for the training data, but the error increases for the test data. Conversely, a phenomenon in which an inappropriate model is fitted due to insufficient learning on the training data may occur, which is called underfitting. For details on this, see Hastie et al. (2011) and James et al. (2014). Figure 4.1 shows the bootstrap technique. As can be seen from this figure, the core of bootstrap is to extract a large number of bootstrap samples from the training data, obtain all the estimators based on each sample, and then properly combine them. The estimator obtained in this way has a better performance than the estimator obtained by using the training data once. And Figure 4.2 simply expresses the concepts of overfitting and underfitting. Through this figure, it can be confirmed that it is important to implement the algorithm to avoid overfitting and underfitting when fitting the model.

For example, suppose there are B estimators calculated for each sample obtained through bootstrap of B times as follows.

$$g^{1}_{bag}\hat{}(x), g^{2}_{bag}\hat{}(x), \ldots, g^{B}_{bag}\hat{}(x) \tag{1.1}$$

The bagging estimator can be obtained by averaging these B estimators. Through this process, the following type of bagging estimator with relatively small variance can be created.

$$g_{bag}\hat{}(x) = \frac{1}{B}\Sigma^{B}_{b=1} g^{b}_{bag}\hat{}(x) \tag{1.2}$$

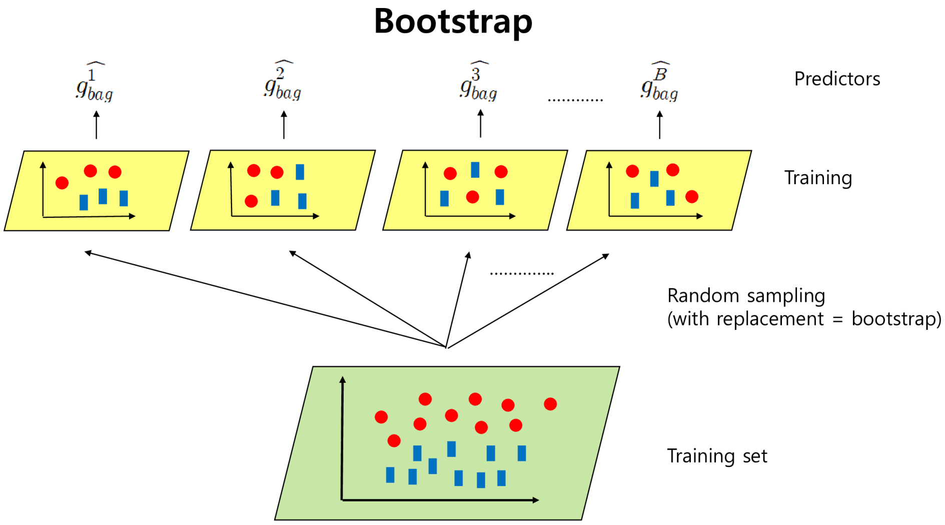


Figure 4.1: Bootstrap

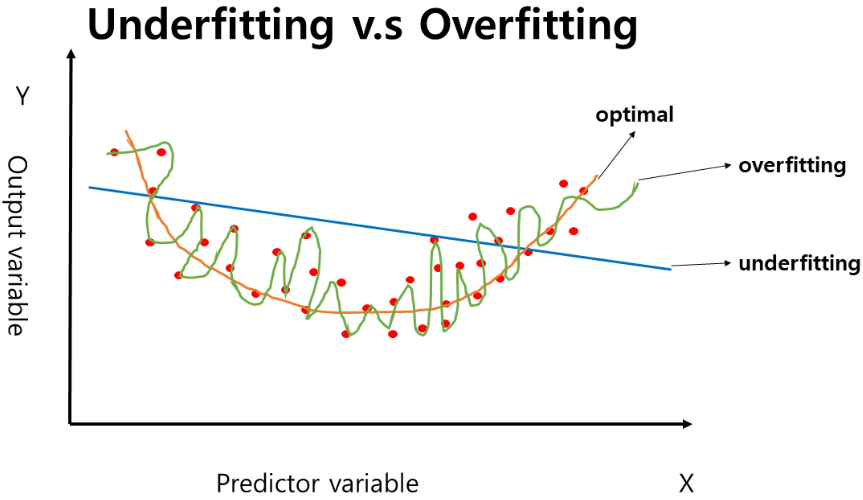


Figure 4.2: Overfitting and Underfitting

4.2 Random forests

Random forests is one of the ensemble methods proposed to compensate for the problem of bagging, and the overall process of obtaining the estimator is similar to the principle of bagging. In this method, similar to the case of bagging introduced in Section 4.1, a final estimator can be obtained by calculating the average of several estimators using the bootstrap method. However, the feature of selecting and using only some of these explanatory variables rather than using all of the explanatory variables for each sample gives a big difference in improving predictive power and reliability compared to bagging that uses all explanatory variables. If the bagging technique to obtain the estimator by including all explanatory variables for the bootstrap sample is used, the accuracy of estimation may be lowered because there may be a correlation between the submodels made by each bootstrap sample. In order to compensate for this shortcoming, the correlation can be greatly reduced by selecting only some of all explanatory variables and applying them to each bootstrap sample. Of course, if you go through this process, bias will inevitably occur. However, since the correlation is greatly reduced, the variance can be reduced to a larger extent, thereby canceling the effect on the bias and reducing it. In this way, more accurate predictions can be made.

Let's take a look at an example. Suppose that there is training data with the number of explanatory variables is p, and using this training data, B samples are extracted through the bootstrap of B times. Here, in the case of random forests, unlike the case of bagging, for each sample extraction, only m explanatory variables should be randomly selected from all p explanatory variables in the training data and included in the bootstrap sample. In general, in the case of m, $m \approx \frac{p}{3}$ or $m \approx \sqrt{p}$ is set. In this study, $m \approx \sqrt{p}$ is set. When the value of m is not expressed in the form of a natural number, rounding to the nearest decimal point was used to determine the number of explanatory variables to be included in the bootstrap sample. Also, it is necessary to pay attention to the fact that the m explanatory variables to be included in each bootstrap sample must be selected differently each time the bootstrap sample is extracted through random sampling. Through this process, the following B estimators are calculated.

$$g_{rf}^{1}\hat{}(x), g_{rf}^{2}\hat{}(x), \ldots, g_{rf}^{B}\hat{}(x) \tag{2.3}$$

The random forests estimator can be obtained by averaging these B estimators. Through this, it is possible to obtain an excellent random forests estimator of the following form, which is more accurate than the bagging estimator.

$$g_{rf}\hat{}(x) = \frac{1}{B}\Sigma_{b=1}^{B} g_{rf}^{b}\hat{}(x) \tag{2.4}$$

The random forests estimator obtained through this process shows more desirable performance in terms of accuracy and reliability when compared with the estimator calculated by bagging technique. Chapter 5, which follows, introduces how ensemble methods such as bagging and random forests can be applied to kernel ridge censored regression analysis.

5 Kernel ridge censored regression analysis using ensemble method

본 장에서는 4장에서 소개한 앙상블 기법을 어떻게 커널 능형 중도절단 회귀분석에 적용할 수 있는지 설명한다. 4장에서도 언급했듯이 앙상블 기법은 다수의 독립적인 부트스트랩 표본을 사용하여 추정량의 분산과 설명변수들 사이의 연관성을 큰 폭으로 줄임으로써 추정의 정확도와 신뢰도를 크게 높일 수 있는 방법론이다. 이를 커널 능형 중도절단 회귀분석에 적용한다면 보다 더 환자의 생존시간, 다시 말해서 관심사건이 일어날 때까지 걸리는 시간을 정확하게 예측하는 모형을 구축할 수 있게 된다.

5.1 배깅 기법을 이용한 커널 능형 중도절단 회귀분석

관측치의 개수가 n이고 설명변수 공간이 p차원인 중도절단이 포함된 훈련자료 (training data with censoring) X가 있다고 하고 이 자료에 다음과 같은 n개의 관측치가 포함되어 있다고 가정해보자. 본 연구에서는 함수 $1 - G(t_i)$를 절단변수 t_i가 설명변수 $x_i = (x_{i1}, x_{i2}, \ldots, x_{ip})^T$에 의존하지 않는다는 가정을 바탕으로 카플란-마이어 추정량(Kaplan-Meier estimator)을 사용하여 추정한다.

$$(y_i, c_i, x_i, \delta_i, t_i, y_i^S), i = 1, 2, \ldots, n \tag{1.1}$$

$$y_i^S = \frac{\delta_i t_i}{1 - \hat{G}(t_i)} \tag{1.2}$$

$$G(t_i) = P(C \le t_i), \delta_i = I(y_i \le c_i), t_i = \min(y_i, c_i) \tag{1.3}$$

이 자료에 대하여 부트스트랩을 통해 b번째 표본 X^b를 추출하였다고 할 때 이 표본 안에 다음과 같은 인조변수(synthetic response) $y_i^{Sb} = \frac{\delta_i^b t_i^b}{1-\hat{G}(t_i^b)}$와 설명변수 $x_i^b = (x_{i1}^b, x_{i2}^b, \ldots, x_{ip}^b)^T$가 있다고 가정해보자. 단, $i = 1, 2, \ldots, n$, $b = 1, 2, \ldots, B$이다.

$$(y_i^{Sb}, x_i^b) \tag{1.4}$$

이에 대하여 사상함수 Φ를 이용하여 다음과 같이 부트스트랩 훈련자료 X^b에 대한 n개의 설명변수 데이터들을 변환할 수 있다.

$$x_1^b, x_2^b, \ldots, x_n^b \to \Phi(x_1^b), \Phi(x_2^b), \ldots, \Phi(x_n^b) \tag{1.5}$$

사상함수 Φ를 이용하여 변환된 설명변수 데이터 $\Phi(x_1^b), \Phi(x_2^b), \ldots, \Phi(x_n^b)$은 고차원의 특성공간(feature space with high dimension)에 위치하게 되며, 이를 이용하여 다음과 같은 회귀모형을 적합할 수 있다.

$$E(y^{Sb}|x_1^b, \ldots, x_n^b) = \Phi(x_1^b)d_1^b + \Phi(x_2^b)d_2^b + \cdots + \Phi(x_n^b)d_n^b \tag{1.6}$$

위와 같은 모형을 적합하는 과정을 통해 길이가 n인 회귀계수벡터 $d^b = (d_1^b, d_2^b, \ldots, d_n^b)^T$를 설정하게 된다. 이러한 커널트릭을 통한 공간변환은 실제적으로 커널함수 $k(\cdot,\cdot)$에 의한 계산을 통하여 이루어진다. 다시 말해서 $\Phi(x_1^b), \Phi(x_2^b), \ldots, \Phi(x_n^b)$의 선형결합(linear combination) $v^b = d_1^b\Phi(x_1^b) + \cdots + d_n^b\Phi(x_n^b)$에 대한 의 사영(projection)은 다음과 같은 계산을 통하여 얻어지게 된다.

$$\Sigma_{j=1}^n \left\langle \Phi(x_i^b)\Phi(x_j^b) \right\rangle d_j^b = \Sigma_{j=1}^n k_{i,j}^b d_j^b \tag{1.7}$$

여기에서 $k_{i,j}^b = \left\langle \Phi(x_i^b)\Phi(x_j^b) \right\rangle = \Phi(x_i^b)^T\Phi(x_j^b) = k(x_i^b, x_j^b)$는 행렬 $K^b = (k_{i,j}^b)$, $i = 1, \ldots, n$, $j = 1, \ldots, n$의 (i, j)번째 원소이다. 이러한 과정을 통해서 얻어지게 되는 행렬 K^b와 회귀계수벡터 d^b를 이용해서 인조변수 y^S를 설명하게 된다. 본 연구에서는 다항커널(Polynomial kernel)과 가우시안 커널(Gaussian kernel)을 적용한다. 이 2가지 커널은 다음과 같다.

****

Polynomial kernel : $k_{i,j}^b = [\alpha(x_i^{bT}x_j^b) + \beta]^\gamma, \alpha = \frac{1}{p^2}, \beta = 1, \gamma = 3$

Gaussian kernel : $k_{i,j}^b = \exp(\sigma||x_i^b - x_j^b||^2), \sigma = \frac{1}{p}$

단, $i = 1, 2, \ldots, n$, $j = 1, 2, \ldots, n$

****

이와 같은 커널 변환을 통하여 다음과 같은 형태의 회귀모형을 얻을 수 있다.

$$y^{Sb} = K^b d^b + \epsilon^b \tag{1.8}$$

그리고 변환을 통해서 계산된 행렬 K^b에 대한 역행렬이 항상 존재하지 않는다는 점을 보완하기 위해 능형 회귀분석 형태의 벌점함수 $\lambda^b d^{bT} K^b d^b$를 적용하여 회귀계수벡터 d^b를 추정한다. 이를 통해 추정된 회귀계수벡터 $\hat{d^b}$는 다음과 같이 계산된다. 여기에서 최적의 능형모수 λ^b의 값은 훈련자료에서 임의의 B^*개의 부트스트랩 표본을 추출하여 실시하게 되는 out-of-bag(OOB)의 방법을 통하여 결정한다. 즉, 추출한 표본을

새로운 훈련자료로 두고 이 표본을 추출할 때 뽑히지 않은 나머지 관측치를 해당 표본에 대한 평가자료(validation data)로 이용하여 최적의 조건을 찾는 과정을 거치게 된다. 여기에서 최적의 조건이란 각 λ^b의 값에 대하여 얻어지는 B^*개의 RMSE(root mean squared error)에 대한 평균값이 가장 작게 나오는 경우를 의미한다.

****

$Q^{b*} = (y^{Sb} - K^b d^b)^T (y^{Sb} - K^b d^b) + \lambda^b d^{bT} K^b d^b$

$\frac{\partial Q^{b*}}{\partial d^b} = -2K^b(y^{Sb} - K^b d^b) + 2\lambda^b K^b d^b = 0$

$\hat{d^b} = \min_{d^b}[(y^{Sb} - K^b d^b)^T (y^{Sb} - K^b d^b) + \lambda^b d^{bT} K^b d^b]$

$= (K^b + \lambda^b I_n)^{-1} y^{Sb}, (\lambda^b > 0)$

****

이러한 방법을 통하여 훈련자료(training data) X에서 추출한 b번째 부트스트랩 훈련자료 X^b를 바탕으로 검증자료(test data) X^*에 대한 평가를 진행하기 위해서는 커널함수 $k(\cdot,\cdot)$를 사용해서 변환된 설명변수 데이터 $\Phi(x_1^b), \Phi(x_2^b), \ldots, \Phi(x_n^b)$의 선형결합인 $v^b = d_1^b \Phi(x_1^b) + \cdots + d_n^b \Phi(x_n^b)$에 대한 $\Phi(X^*)$의 사영(projection)을 계산한 뒤 이를 이용하여 검증자료 평가에 사용할 행렬 K^{b*}를 계산해야 하며, 이에 대한 계산과정은 다음과 같다. 단, n은 훈련자료의 관측치 개수, u는 검증자료의 관측치 개수이다.

****

$\Sigma_{j=1}^n \left\langle \Phi(x_i^*), \Phi(x_j^b) \right\rangle d_j^b = \Sigma_{j=1}^n k_{i,j}^{b*} d_j^b$

$k_{i,j}^{b*} = \left\langle \Phi(x_i^*), \Phi(x_j^b) \right\rangle = \Phi(x_i^*)^T \Phi(x_j^b) = k(x_i^*, x_j^b)$

****

그리고 본 연구에서는 다음과 같은 형태의 다항커널(Polynomial kernel)과 가우시안 커널(Gaussian kernel)을 적용한다.

****

Polynomial kernel : $k_{i,j}^{b*} = [\alpha(x_i^{*T} x_j^b) + \beta]^\gamma, \alpha = \frac{1}{p^2}, \beta = 1, \gamma = 3$

Gaussian kernel : $k_{i,j}^{b*} = \exp(\sigma||x_i^* - x_j^b||^2), \sigma = \frac{1}{p}$

단, $i = 1, 2, \ldots, u$, $j = 1, 2, \ldots, n$

****

여기에서 $k_{i,j}^{b*}$는 행렬 $K^{b*} = (k_{i,j}^{b*})$, $i = 1, \ldots, u$, $j = 1, \ldots, n$의 (j, i)번째 원소이며 x_i^*는 검증자료 X^*안에 있는 i번째 관측치에 대한 설명변수 데이터를 의미한다. 이러한 과정을 통해서 얻어지게 되는 행렬 K^{b*}, 그리고 부트스트랩 훈련자료 X^b를 통하여 계산된 추정량 $\hat{d^b}$을 이용해서 검증자료 X^*에 대한 최종적인 평가를 진행한다. 결과적으로 행렬 K^{b*}와 추정량 $\hat{d^b}$을 이용하여 다음과 같은 형태의 부트스트랩 훈련자료를 이용하여 계산된 검증자료에 대한 인조변수 $y^{Sb*} = (y_1^{Sb*}, y_2^{Sb*}, \ldots, y_u^{Sb*})^T$의 추정량 $y^{\hat{S}b*} = (y_1^{\hat{S}b*}, y_2^{\hat{S}b*}, \ldots, y_u^{\hat{S}b*})^T$을 구할 수 있다.

$$y^{\hat{S}b*} = K^{b*T} \hat{d^b} \tag{1.9}$$

이러한 과정을 B개의 부트스트랩 훈련자료 X^b, $b = 1, 2, \ldots, B$에 대해 각각 실시하여 총 B개의 추정량 $y^{\hat{S}b*} = K^{b*T} \hat{d^b}$, $b = 1, 2, \ldots, B$를 얻은 뒤 이를 평균하여 검증자료 X^*에 대한 배깅 기법을 이용한 인조변수의 추정량을 구할 수 있으며 그 형태는 다음과 같다.

$$y_{bag}^{\hat{S*}} = \frac{1}{B} \Sigma_{b=1}^{B} y^{\hat{S}b*} = (y_{bag,1}^{\hat{S*}}, y_{bag,2}^{\hat{S*}}, \ldots, y_{bag,u}^{\hat{S*}})^T \tag{1.10}$$

커널 능형 중도절단 회귀분석에서는 인조변수 $y^{S*} = (y_1^{S*}, y_2^{S*}, \ldots, y_u^{S*})^T$를 모형구축 시 사용하기 때문에 구축된 모형을 평가 시 예측력의 평가기준을 인조변수 $y^{S*} = (y_1^{S*}, y_2^{S*}, \ldots, y_u^{S*})^T$로 하는 경우와 실제 반응변수 $y^* = (y_1^*, y_2^*, \ldots, y_u^*)^T$로 하는 경우로 나누어서 살펴봐야 한다. 이에 따라 본 연구에서는 평가기준을 인조변

수로 하는 경우에는 RMSE를 $\sqrt{MSE1} = \sqrt{\frac{1}{u}\Sigma_{i=1}^{u}(y_i^{S*} - y_{bag,i}^{\hat{S*}})^2}$로 계산하고, 평가 기준을 실제 반응변수로 하는 경우에는 RMSE를 $\sqrt{MSE2} = \sqrt{\frac{1}{u}\Sigma_{i=1}^{u}(y_i^{*} - y_{bag,i}^{\hat{S*}})^2}$로 계산하여 성능을 평가한다.

5.2 랜덤포레스트 기법을 이용한 커널 능형 중도절단 회귀분석

배깅 기법을 적용하는 경우와 동일하게 관측치의 개수가 n이고 설명변수 공간이 p차원인 중도절단이 포함된 훈련자료 X가 있다고 하고 이 자료에 다음과 같은 n개의 관측치가 포함되어 있다고 가정해보자. 물론 여기에서도 함수 $1-G(t_i)$는 배깅의 경우와 마찬가지로 절단변수 t_i가 설명변수 $x_i = (x_{i1}, x_{i2}, \ldots, x_{ip})^T$에 의존하지 않는다는 가정을 바탕으로 카플란-마이어 추정량(Kaplan-Meier estimator)을 사용하여 추정한다.

$$(y_i, c_i, x_i, \delta_i, t_i, y_i^S), i = 1, 2, \ldots, n \tag{2.11}$$

$$y_i^S = \frac{\delta_i t_i}{1 - \hat{G}(t_i)} \tag{2.12}$$

$$G(t_i) = P(C \le t_i), \delta_i = I(y_i \le c_i), t_i = \min(y_i, c_i) \tag{2.13}$$

이 자료에 대하여 부트스트랩을 통해 b번째 표본 X^b를 추출하였다고 할 때 이 표본 안에 다음과 같은 인조변수(synthetic response) $y_i^{Sb} = \frac{\delta_i^b t_i^b}{1-\hat{G}(t_i^b)}$와 설명변수 $x_i^b = (x_{i1}^b, x_{i2}^b, \ldots, x_{ip}^b)^T$가 있다고 가정해보자. 단, $i = 1, 2, \ldots, n$, $b = 1, 2, \ldots, B$이다.

$$(y_i^{Sb}, x_i^b) \tag{2.14}$$

여기에서 랜덤포레스트 기법을 적용하는 경우에는 배깅 기법의 경우와는 다르게 B개의 부트스트랩 훈련자료 X^b, $b = 1, 2, \ldots, B$에 대하여 p개의 모든 설명변수를 포함시키지 않고 이들 중 m개만 선택해서 X^b에 포함시키게 된다. 본 연구에서는 $m \approx \sqrt{p}$로 정하였으며 m의 값이 자연수로 나오지 않을 시 소수점 이하 반올림을 사용하였다. 한가지 주의할 점은 각각의 부트스트랩 훈련자료에 포함되는 설명변수는 모두 다르게 선택해야 한다는 것이다. 이러한 과정을 통해 설명변수 사이의 연관성을 큰 폭으로 줄일 수 있으며 이를 통해 보다 더 정확한 예측값을 얻을 수 있다.

결과적으로 랜덤포레스트 기법을 이용하여 검증자료 X^*에 대한 인조변수의 추정량을 구하는 과정은 부트스트랩 훈련자료 X^b, $b = 1, 2, \ldots, B$를 추출 시 일부의 설명변수만을 선택해서 포함시킨다는 것만 차이가 있고 나머지 계산과정과 모형을 평가하는 과정은 배깅 기법의 내용과 동일하다. 따라서 이에 대한 자세한 설명은 생략하도록 한다. 다만, 랜덤포레스트 기법을 통해서 얻어지는 추정량과 성능 평가를 위한 RMSE를 배깅 기법을 통해서 얻어지는 추정량과 성능 평가를 위한 RMSE와 구별하기 위해 이들을 아래와 같이 표기하도록 한다.

$$y_{rf}^{\hat{S}*} = (y_{rf,1}^{\hat{S}*}, y_{rf,2}^{\hat{S}*}, \ldots, y_{rf,u}^{\hat{S}*})^T \tag{2.15}$$

$$\sqrt{MSE1} = \sqrt{\frac{1}{u}\Sigma_{i=1}^{u}(y_i^{S*} - y_{rf,i}^{\hat{S}*})^2} \tag{2.16}$$

$$\sqrt{MSE2} = \sqrt{\frac{1}{u}\Sigma_{i=1}^{u}(y_i^{*} - y_{rf,i}^{\hat{S}*})^2} \tag{2.17}$$

본 연구에서 제안하는 앙상블 기법을 이용한 커널 능형 중도절단 회귀분석이 실제 관심사건이 일어날 때까지 걸리는 시간에 대한 예측력의 측면에서 Huh, M. (2015)에서 제안한 sub-sampling 등의 다른 방법론과 비교했을 때 전체적으로 우수한 성능을 보임을 입증하기 위해 실시한 모의실험 및 실증분석의 결과 제시, 그리고 이에 대한 해석과 평가는 6장에서 진행하도록 하겠다.

6 모의실험 및 실증분석 (앙상블 기법을 이용한 커널 능형 중도절단 회귀분석)

본 장에서는 2 5장에서 제안하는 앙상블 기법을 이용한 커널 능형 중도절단 회귀분석 방법이 다른 방법론과 비교했을 때 전체적으로 예측력이 우수하다는 사실을 입증하기 위해 실시한 모의실험과 실증분석에 관한 내용을 설명한다. 우선 모의실험의 경우는 훈련자료(training data)과 검증자료(test data)를 각각 연구의 목적에 맞게 생성하여 실시하였으며, 실증분석의 경우는 실제 연구에 의하여 작성된 생존자료를 임의로 train:test=7:3 의 비율로 나누어서 진행하였다. 그리고 모든 모의실험과 실증분석은 프로그램 R 4.1.1 version을 이용하여 실시하였다.

6.1 모의실험

모의실험에서는 평가하고자 하는 방법론의 목적에 맞게 임의로 생성한 훈련자료(training data)와 검증자료(test data)에 대해서 다음과 같은 방법론들을 비교, 분석하였다.

1) **PKR1** : Polynomial Kernel Ridge Regression with Synthetic Response Y^S

2) **PKRS1** : Polynomial Kernel Ridge Regression with Sub-sampling and Synthetic Response Y^S

3) **PKRB1** : Polynomial Kernel Ridge Regression with Bagging and Synthetic Response Y^S

4) **PKRR1** : Polynomial Kernel Ridge Regression with Random Forest and Synthetic Response Y^S

5) **GKR1** : Gaussian Kernel Ridge Regression with Synthetic Response Y^S

6) **GKRS1** : Gaussian Kernel Ridge Regression with Sub-sampling and Synthetic Response Y^S

7) **GKRB1** : Gaussian Kernel Ridge Regression with Bagging and Synthetic Response Y^S

8) **GKRR1** : Gaussian Kernel Ridge Regression with Random Forest and Synthetic Response Y^S

9) **PKR2** : Polynomial Kernel Ridge Regression with Generated(Original) Response Y

10) **PKRS2** : Polynomial Kernel Ridge Regression with Sub-sampling and Gen-

erated(Original) Response Y

11) **PKRB2** : Polynomial Kernel Ridge Regression with Bagging and Generated(Original) Response Y

12) **PKRR2** : Polynomial Kernel Ridge Regression with Random Forest and Generated(Original) Response Y

13) **GKR2** : Gaussian Kernel Ridge Regression with Generated(Original) Response Y

14) **GKRS2** : Gaussian Kernel Ridge Regression with Sub-sampling and Generated(Original) Response Y

15) **GKRB2** : Gaussian Kernel Ridge Regression with Bagging and Generated(Original) Response Y

16) **GKRR2** : Gaussian Kernel Ridge Regression with Random Forest and Generated(Original) Response Y

위에 제시된 16가지 방법론들 중 PKRS1, GKRS1, PKRS2, 그리고 GKRS2 에서 사용되는 sub-sampling은 Huh, M. (2015) 에 의하여 제안된 방법론이다. 이 방법론의 원리에 대해서는 모의실험 step을 설명하면서 간단하게 언급하도록 하겠다. 본 모의실험에서는 다음과 같은 방법을 통해 임의의 모의실험 데이터를 생성하였다.

****

$y_i \sim N(\mu_i, 1^2)$

$\mu_i = 1 + \Sigma_{j=1}^{p}(\frac{x_{ij}}{10})^j$, $x_{ij} \sim U(-10, 10)$

$c_i \sim N(a, 1^2)$, $t_i = \min(y_i, c_i)$

$y_i^S = \frac{\delta_i t_i}{1-\hat{G}(t_i)}$, $\delta_i = I(y_i \leq c_i)$

****

여기에서 $1-\hat{G}(t_i)$는 2장에서 소개한 카플란-마이어 추정량(Kaplan-Meier estimator)을 사용하여 계산하였다. 그리고 반응변수 y_i는 평균이 $\mu_i = 1+\Sigma_{j=1}^{p}(\frac{x_{ij}}{10})^j$이고 표준편차가 1인 정규분포를 따르도록 생성하여 강한 비선형성(non-linearity)을 만족하도록 하였다. 추가로 중도절단변수 c_i의 경우는 평균 a를 모의실험 상황에 따라 적절하게 설정하여 원하는 중도절단의 비율을 나타내도록 설계하였으며, Synthetic Response와 관련된 방법론(PKR1, PKRS1, PKRB1, PKRR1, GKR1, GKRS1, GKRB1, GKRR1)에 대해서는 RMSE(Root Mean Squared Error)를 $\sqrt{MSE1} = \sqrt{\frac{1}{u}\Sigma_{i=1}^{u}(y_i^{S*} - y_i^{\hat{S}*})^2}$를 통해 계산하였고, Original Response와 관련된 방법론(PKR2, PKRS2, PKRB2, PKRR2, GKR2, GKRS2, GKRB2, GKRR2)에 대해서는 RMSE를 $\sqrt{MSE2} = \sqrt{\frac{1}{u}\Sigma_{i=1}^{u}(y_i^{*} - y_i^{\hat{S}*})^2}$을 통해 계산하였다. 모의실험을 위해 생성한 임의의 훈련자료(training data)와 검증자료(test data)에 대한 설명변수의 개수는 $p = 3, 5, 7, 9$로 설정하고 중도절단의 비율은 $0\%, 10\%, 30\%, 50\%$로 설정하였다. 그리고 훈련자료에 대한 관측치의 개수는 $n = 50, 100, 200$으로 설정하였고 커널트릭 기법 적용 시 2가지의 커널함수(Polynomial, Gaussian)를 적용하여 총 192가지의 상황을 가정하였다. 그리고 검증자료의 경우는 관측치의 개수를 $u = 1000$으로 고정하였다. 본 연구에서 진행한 모의실험 step은 다음과 같으며 각 방법론마다 100번의 반복을 실시하였다.

1) PKR1, GKR1, PKR2, GKR2

Step1) 모의실험을 하기 위한 훈련자료와 검증자료를 각각 생성한다.

Step2) 5-fold CV(cross-validation)를 통해서 최적의 능형모수(ridge parameter) λ의 값을 선정한다.

Step3) Step2)에서 선정한 최적의 λ의 값과 훈련자료를 이용하여 회귀계수벡터의 추정량인 $\hat{d}$의 값을 구하고 이를 바탕으로 검증자료에 대한 최종적인 인조변수 추정량 $y^{\hat{S}*}$을 결정한 뒤 test RMSE $\sqrt{MSE1} = \sqrt{\frac{1}{u}\Sigma_{i=1}^{u}(y_i^{S*} - y_i^{\hat{S}*})^2}$ 또는 $\sqrt{MSE2} = \sqrt{\frac{1}{u}\Sigma_{i=1}^{u}(y_i^{*} - y_i^{\hat{S}*})^2}$를 계산한다.

2) PKRS1, GKRS1, PKRS2, GKRS2 (Sub-sampling)

Step1) 모의실험을 하기 위한 훈련자료와 검증자료를 각각 생성한다.

Step2) 훈련자료에 있는 관측치들 중 70%를 임의로 선택하여 새로운 훈련자료를 설정하고 나머지 30%를 이에 대한 평가자료로 사용하여 5-fold CV를 통해 최적의 λ의 값을 구한 뒤 test RMSE를 계산한다. 이 과정을 50번 반복하여 test RMSE의 값을 가장 작게 만들어주는 새로운 훈련자료와 이 훈련자료를 통해서 얻은 최적의 λ의 값을 최종적인 평가기준으로 선택한다.

Step3) Step2)에서 선정한 최적의 λ의 값과 새로운 훈련자료를 이용하여 회귀계수벡터의 추정량 $\hat{d}$의 값을 구하고 이를 바탕으로 검증자료에 대한 최종적인 인조변수에 대한 sub-sampling 추정량 $y_{ss}^{\hat{S}*}$을 결정한 뒤 test RMSE $\sqrt{MSE1} = \sqrt{\frac{1}{u}\Sigma_{i=1}^{u}(y_i^{S*} - y_{ss,i}^{\hat{S}*})^2}$ 또는 $\sqrt{MSE2} = \sqrt{\frac{1}{u}\Sigma_{i=1}^{u}(y_i^{*} - y_{ss,i}^{\hat{S}*})^2}$를 계산한다.

3) PKRB1, GKRB1, PKRB2, GKRB2 (Bagging)

Step1) 모의실험을 하기 위한 훈련자료와 검증자료를 각각 생성한다.

Step2) 훈련자료를 이용하여 훈련자료와 관측치의 개수가 동일한 50개의 부트스트랩 표본들을 복원추출을 통해서 생성하고 이들을 새로운 훈련자료로 설정한다. 각각의 부트스트랩 표본에 대한 평가자료의 경우는 복원추출 시 제외된 번호에 해당하는 관측치를 모아서 설정한다.

Step3) Step2)에서 생성한 각각의 부트스트랩 표본들에 대하여 각각의 λ의 값에 대한 회귀계수벡터의 추정량 $\hat{d}$의 값을 구하고 이를 이용하여 test RMSE를 계산한다.

Step4) Step3)에서 계산한 test RMSE의 결과를 각 λ의 값에 따라 정리하고 평균하여 그 결과가 가장 작은 경우의 λ의 값을 최종적으로 결정한다. 만약 이에 해당하는 λ의 값이 여러 가지로 나타나는 경우에는 그 중 최대인 값을 선택하도록 한다.

Step5) Step4)에서 결정한 λ의 값을 바탕으로 서로 다른 100개의 부트스트랩 훈련자료들과 이에 대한 평가대상인 검증자료를 이용하여 최종적인 인조변수에 대한 배깅 추정량(bagging estimator) $y_{bag}^{\hat{S}*}$을 결정한다. 이러한 과정을 통하여 검증자료에 대한 test RMSE $\sqrt{MSE1} = \sqrt{\frac{1}{u}\Sigma_{i=1}^{u}(y_i^{S*} - y_{bag,i}^{\hat{S*}})^2}$ 또는 $\sqrt{MSE2} = \sqrt{\frac{1}{u}\Sigma_{i=1}^{u}(y_i^{*} - y_{bag,i}^{\hat{S*}})^2}$를 계산한다.

4) PKRR1, GKRR1, PKRR2, GKRR2 (Random forests)

Step1) 모의실험을 하기 위한 훈련자료와 검증자료를 각각 생성한다.

Step2) 훈련자료를 이용하여 훈련자료와 관측치의 개수가 동일한 50개의 부트스트랩 표본들을 복원추출을 통해서 생성하고 이들을 새로운 훈련자료로 설정한다. 이때 각각의 표본에 대하여 $m \approx \sqrt{p}$개의 설명변수들을 임의로 추출하여 포함시키도록 한다. 설명변수들의 종류는 표본마다 다르게 정한다. 각각의 부트스트랩 표본에 대한 평가자료의 경우는 복원추출 시 제외된 번호에 해당하는 관측치를 모아서 설정한다. 이러한 평가자료에 포함시킬 설명변수들의 종류는 대응되는 부트스트랩 훈련자료의 경우와 동일하도록 설정한다.

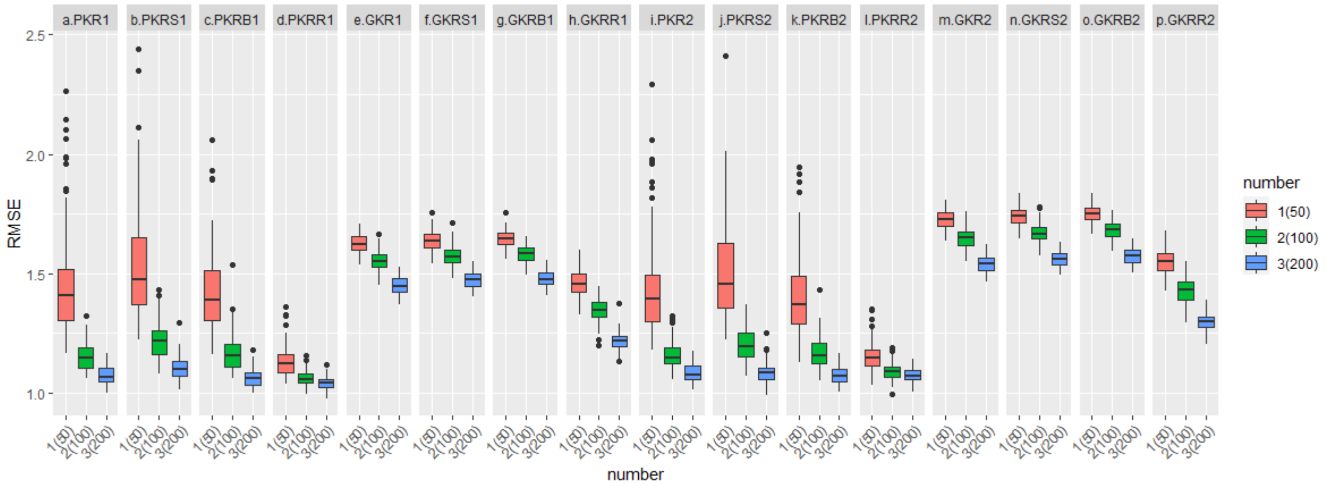
Step3) Step2)에서 생성한 각각의 부트스트랩 표본들에 대하여 각각의 λ의 값에 대한 회귀계수벡터의 추정량 $\hat{d}$의 값을 구하고 test RMSE를 계산한다.

Step4) Step3)에서 계산한 test RMSE의 결과를 각 λ의 값에 따라 정리하고 평균하

여 그 결과가 가장 작은 경우의 λ의 값을 최종적으로 결정한다. 만약 이에 해당하는 λ의 값이 여러 가지로 나타나는 경우에는 그 중 최대인 값을 선택하도록 한다.

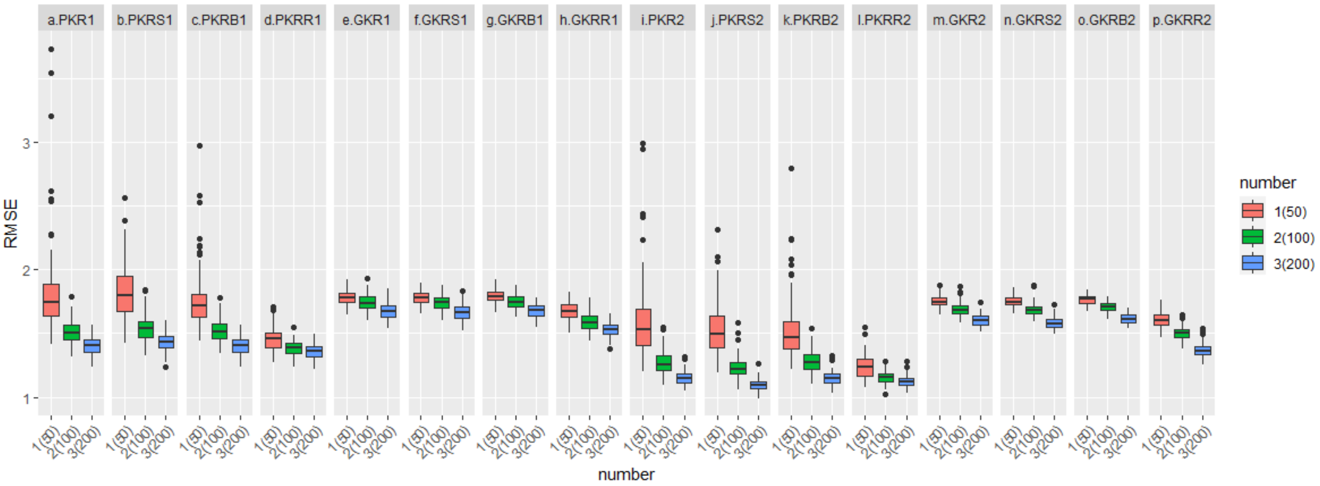
Step5) Step4)에서 결정한 λ의 값을 토대로 서로 다른 100개의 부트스트랩 훈련자료들과 이에 대한 평가대상인 검증자료를 이용하여 최종적인 인조변수에 대한 랜덤 포레스트 추정량(random forests estimator) $y_{rf}^{\hat{S}*}$을 결정한다. 이 때 각각의 부트스트랩 훈련자료에 대하여 $m \approx \sqrt{p}$개의 설명변수들을 임의로 추출해서 포함시키도록 한다. 설명변수들의 종류는 부트스트랩 훈련자료마다 다르게 설정한다. 그리고 평가대상인 검증자료에 포함될 설명변수의 종류는 해당하는 부트스트랩 훈련자료들의 기준을 따라서 설정하도록 한다. 이러한 과정을 통하여 검증자료에 대한 test RMSE $\sqrt{MSE1} = \sqrt{\frac{1}{u}\Sigma_{i=1}^{u}(y_i^{S*} - y_{rf,i}^{\hat{S}*})^2}$ 또는 $\sqrt{MSE2} = \sqrt{\frac{1}{u}\Sigma_{i=1}^{u}(y_i^{*} - y_{rf,i}^{\hat{S}*})^2}$를 계산한다.

위에서 설명한 step을 바탕으로 하여 각 방법론에 대해 총 192가지의 상황을 가정하고 모의실험을 진행하였으며 이를 통해 산출된 test RMSE에 대한 결과를 상자그림(boxplot)과 표로 정리하였으며 이는 그림 6.1 $\sim$ 그림 6.16을 통해 확인할 수 있다. 여기에서 상자그림의 높이와 길이는 각각 test RMSE의 평균값과 분산과 관련이 있다. 그러므로 상자그림의 높이가 낮을수록 해당하는 방법론의 예측력이 정확하다는 것을 의미하고, 상자그림의 길이가 짧을수록 해당하는 방법론의 안정성이 우수하다는 것을 의미한다. 이러한 사실을 바탕으로 하여 상자그림의 높이와 길이가 각각 낮고 짧게 나타나는 방법론을 예측력이 우수한 것으로 판단하면 된다. 추가로 test RMSE 관련 표의 경우 각 모의실험 상황마다 가장 우수한 성능을 보인 방법론에 대하여 그 결과를 진한 글씨로 표시하여 눈에 띄도록 하였다.



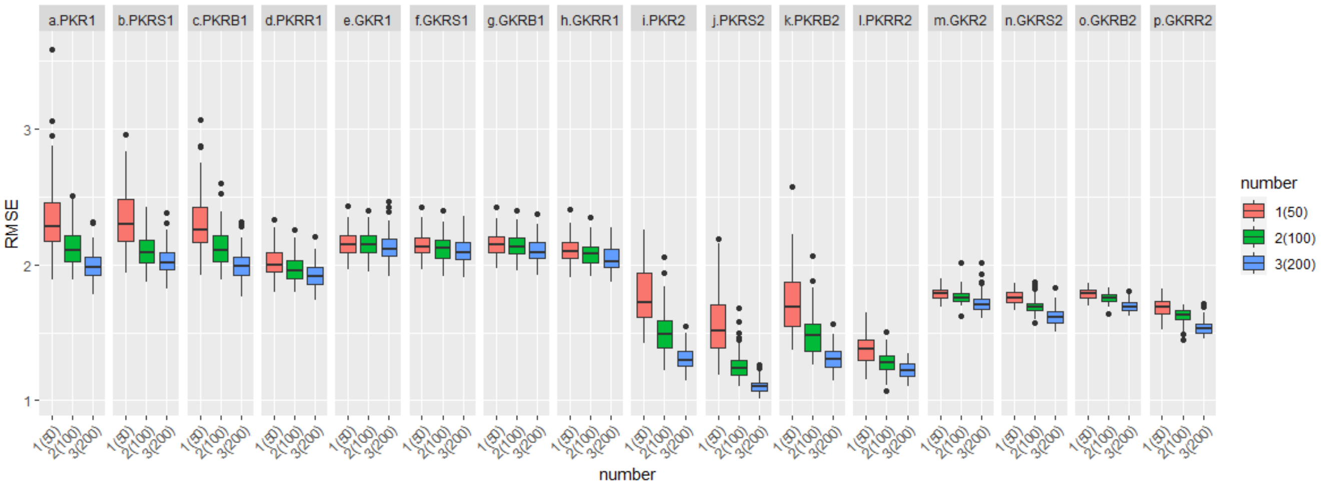
		PKR 1	PKRS 1	PKRB 1	PKRR 1	GKR 1	GKRS 1	GKRB 1	GKRR 1	PKR 2	PKRS 2	PKRB 2	PKRR 2	GKR 2	GKRS 2	GKRB 2	GKRR 2
n=50	**mean**	1.453	1.542	1.432	**1.131**	1.627	1.637	1.648	**1.459**	1.442	1.507	1.404	**1.151**	1.727	1.739	1.752	**1.549**
	sd	0.229	0.240	0.170	**0.063**	0.040	0.039	0.035	**0.053**	0.216	0.211	0.162	**0.061**	0.040	0.041	0.036	**0.054**
n=100	**mean**	1.154	1.223	1.165	**1.060**	1.553	1.573	1.581	**1.346**	1.161	1.204	1.169	**1.090**	1.650	1.667	1.682	**1.429**
	sd	0.058	0.077	0.071	**0.030**	0.042	0.039	0.034	**0.049**	0.058	0.069	0.064	**0.036**	0.043	0.038	0.035	**0.056**
n=200	**mean**	1.073	1.104	1.062	**1.040**	1.449	1.474	1.477	**1.217**	1.082	1.085	1.073	**1.072**	1.537	1.561	1.573	**1.297**
	sd	0.040	0.046	0.037	**0.027**	0.037	0.033	0.034	**0.037**	0.038	0.042	0.037	**0.030**	0.038	0.034	0.035	**0.036**

Figure 6.1: $p = 3$, 중도절단 0%



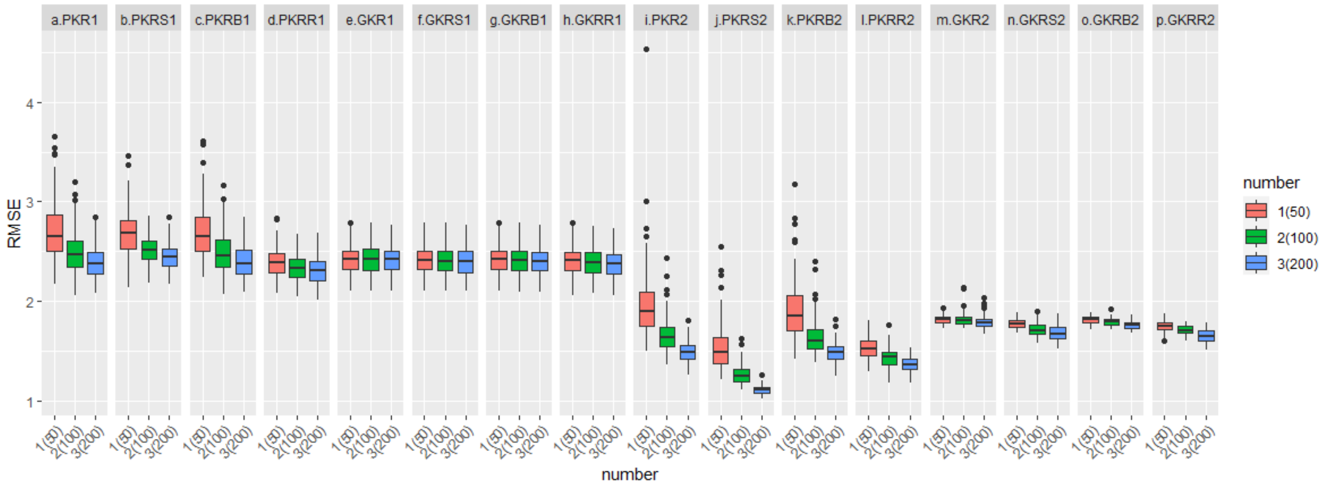
		PKR 1	PKRS 1	PKRB 1	PKRR 1	GKR 1	GKRS 1	GKRB 1	GKRR 1	PKR 2	PKRS 2	PKRB 2	PKRR 2	GKR 2	GKRS 2	GKRB 2	GKRR 2
n=50	**mean**	1.832	1.820	1.759	**1.455**	1.782	1.781	1.793	**1.674**	1.610	1.542	1.524	**1.235**	1.749	1.748	1.766	**1.599**
	sd	0.372	0.213	0.236	**0.084**	0.059	0.054	0.056	**0.070**	0.328	0.207	0.237	**0.088**	0.044	0.041	0.038	**0.057**
n=100	**mean**	1.506	1.547	1.518	**1.381**	1.740	1.736	1.746	**1.593**	1.270	1.224	1.278	**1.155**	1.692	1.685	1.706	**1.497**
	sd	0.088	0.105	0.089	**0.059**	0.064	0.060	0.056	**0.072**	0.095	0.083	0.089	**0.051**	0.051	0.050	0.037	**0.049**
n=200	**mean**	1.402	1.432	1.399	**1.353**	1.677	1.666	1.679	**1.530**	1.151	**1.094**	1.144	1.119	1.602	1.579	1.615	**1.371**
	sd	0.069	0.065	0.071	**0.057**	0.061	0.064	0.056	**0.059**	0.055	**0.045**	0.055	0.042	0.045	0.044	0.037	**0.056**

Figure 6.2: $p = 3$, 중도절단 10%



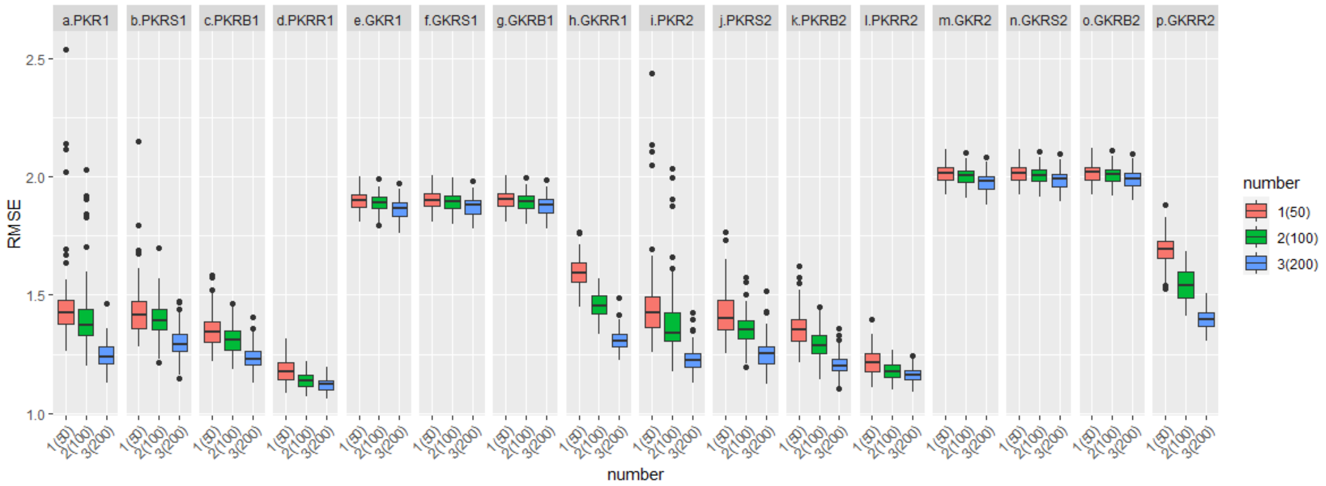
		PKR 1	PKRS 1	PKRB 1	PKRR 1	GKR 1	GKRS 1	GKRB 1	GKRR 1	PKR 2	PKRS 2	PKRB 2	PKRR 2	GKR 2	GKRS 2	GKRB 2	GKRR 2
n=50	mean	2.345	2.332	2.306	**2.015**	2.156	2.146	2.155	**2.116**	1.770	1.564	1.723	**1.379**	1.784	1.757	1.788	**1.685**
	sd	0.263	0.207	0.206	**0.101**	0.091	0.092	0.090	**0.098**	0.213	0.231	0.226	**0.110**	0.043	0.044	0.039	**0.060**
n=100	mean	2.129	2.112	2.132	**1.962**	2.156	2.120	2.142	**2.082**	1.500	**1.253**	1.483	1.278	1.763	1.697	1.753	**1.621**
	sd	0.139	0.114	0.136	**0.092**	0.093	0.095	0.088	**0.090**	0.151	**0.096**	0.140	0.077	0.051	0.056	0.035	**0.053**
n=200	mean	1.996	2.032	1.999	**1.925**	2.137	2.100	2.112	**2.044**	1.307	**1.107**	1.310	1.227	1.717	1.619	1.695	**1.532**
	sd	0.109	0.101	0.111	**0.093**	0.108	0.100	0.090	**0.094**	0.078	**0.053**	0.077	0.057	0.069	0.061	0.040	**0.049**

Figure 6.3: $p = 3$, 중도절단 30%



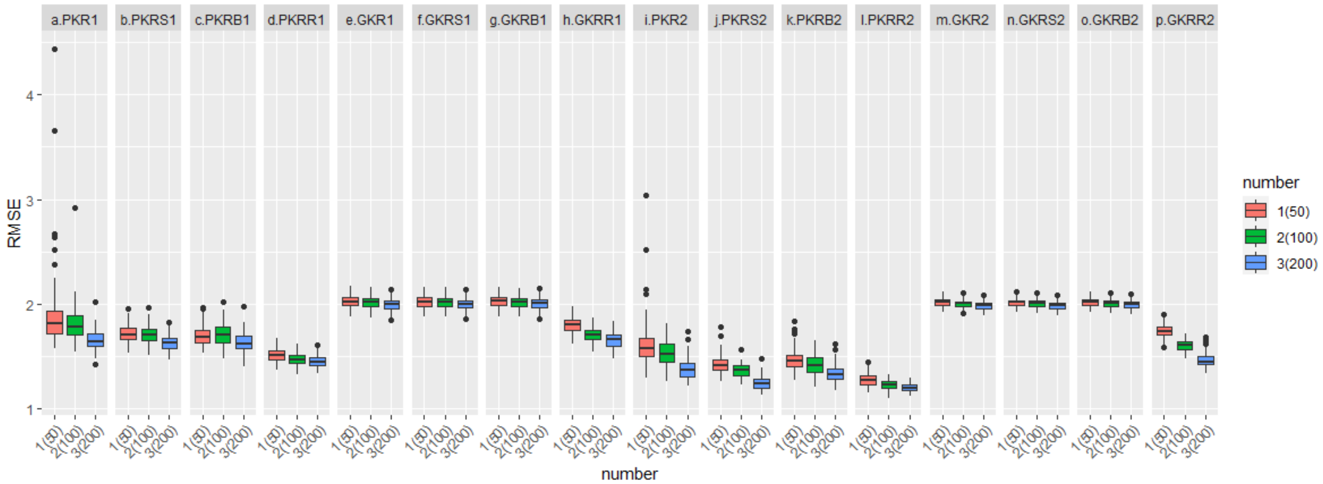
		PKR 1	PKRS 1	PKRB 1	PKRR 1	GKR 1	GKRS 1	GKRB 1	GKRR 1	PKR 2	PKRS 2	PKRB 2	PKRR 2	GKR 2	GKRS 2	GKRB 2	GKRR 2
n=50	**mean**	2.710	2.701	2.690	**2.384**	2.422	2.415	2.418	**2.408**	1.987	1.543	1.922	**1.524**	1.816	1.776	1.810	**1.748**
	sd	0.295	0.242	0.279	**0.156**	0.150	0.149	0.151	**0.151**	0.391	0.238	0.307	**0.112**	0.040	0.048	0.037	**0.049**
n=100	**mean**	2.491	2.521	2.488	**2.336**	2.426	2.405	2.415	**2.396**	1.667	**1.260**	1.646	1.430	1.815	1.716	1.794	**1.708**
	sd	0.218	0.147	0.209	**0.149**	0.155	0.153	0.153	**0.151**	0.189	**0.098**	0.182	0.096	0.064	0.063	0.038	**0.046**
n=200	**mean**	2.393	2.451	2.395	**2.312**	2.422	2.399	2.406	**2.379**	1.492	**1.110**	1.493	1.366	1.791	1.680	1.760	**1.649**
	sd	0.168	0.139	0.170	**0.152**	0.151	0.148	0.150	**0.149**	0.098	**0.045**	0.097	0.074	0.062	0.080	0.040	**0.064**

Figure 6.4: $p = 3$, 중도절단 50%



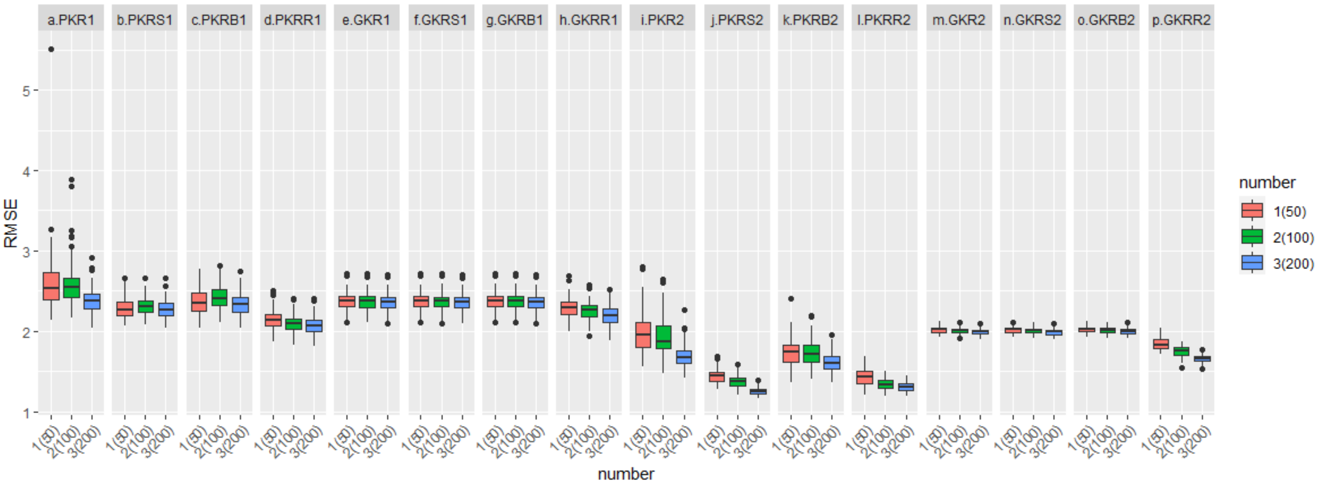
		PKR 1	PKRS 1	PKRB 1	PKRR 1	GKR 1	GKRS 1	GKRB 1	GKRR 1	PKR 2	PKRS 2	PKRB 2	PKRR 2	GKR 2	GKRS 2	GKRB 2	GKRR 2
n=50	**mean**	1.460	1.438	1.350	**1.178**	1.897	1.899	1.901	**1.595**	1.458	1.419	1.359	**1.216**	2.011	2.013	2.015	**1.690**
	sd	0.176	0.113	0.067	**0.050**	0.038	0.038	0.038	**0.068**	0.173	0.096	0.075	**0.055**	0.037	0.038	0.037	**0.068**
n=100	**mean**	1.403	1.398	1.312	**1.138**	1.887	1.891	1.893	**1.457**	1.381	1.357	1.290	**1.178**	2.001	2.005	2.007	**1.543**
	sd	0.145	0.071	0.059	**0.033**	0.037	0.038	0.037	**0.057**	0.150	0.070	0.061	**0.038**	0.037	0.038	0.037	**0.068**
n=200	**mean**	1.245	1.302	1.234	**1.123**	1.863	1.872	1.877	**1.309**	1.232	1.252	1.207	**1.165**	1.976	1.986	1.991	**1.398**
	sd	0.055	0.062	0.048	**0.028**	0.039	0.038	0.038	**0.044**	0.056	0.067	0.047	**0.030**	0.038	0.038	0.038	**0.043**

Figure 6.5: $p = 5$, 중도절단 0%



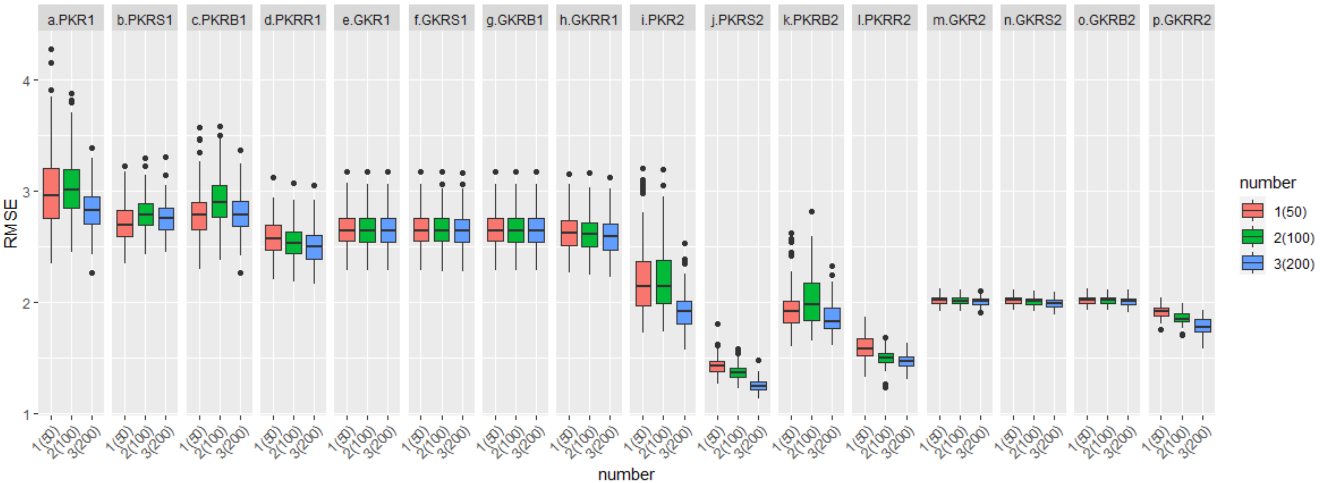
		PKR	PKRS	PKRB	PKRR	GKR	GKRS	GKRB	GKRR	PKR	PKRS	PKRB	PKRR	GKR	GKRS	GKRB	GKRR
		1	1	1	1	1	1	1	1	2	2	2	2	2	2	2	2
n=50	**mean**	1.897	1.717	1.700	**1.518**	2.022	2.023	2.024	**1.808**	1.629	1.423	1.466	**1.280**	2.013	2.013	2.015	**1.738**
	sd	0.371	0.088	0.096	**0.065**	0.056	0.055	0.056	**0.071**	0.229	0.088	0.103	**0.063**	0.038	0.037	0.037	**0.063**
n=100	**mean**	1.802	1.711	1.704	**1.471**	2.014	2.015	2.018	**1.706**	1.530	1.365	1.421	**1.229**	2.003	2.005	2.008	**1.611**
	sd	0.167	0.085	0.105	**0.057**	0.056	0.056	0.056	**0.070**	0.125	0.064	0.097	**0.048**	0.038	0.037	0.037	**0.050**
n=200	**mean**	1.659	1.634	1.633	**1.454**	1.996	2.000	2.006	**1.654**	1.385	1.250	1.337	**1.209**	1.983	1.986	1.994	**1.470**
	sd	0.093	0.070	0.088	**0.056**	0.057	0.056	0.056	**0.076**	0.097	0.063	0.079	**0.037**	0.038	0.038	0.038	**0.074**

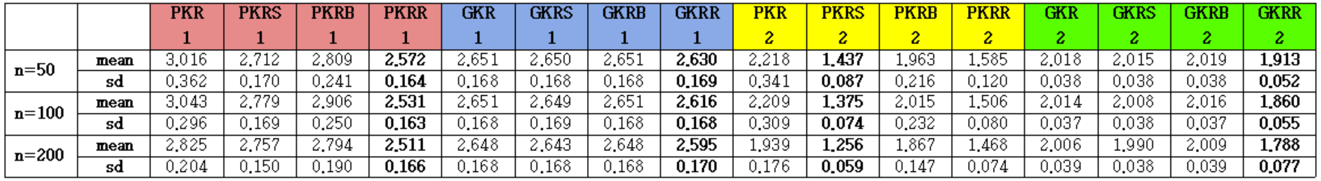
Figure 6.6: $p = 5$, 중도절단 10%



		PKR 1	PKRS 1	PKRB 1	PKRR 1	GKR 1	GKRS 1	GKRB 1	GKRR 1	PKR 2	PKRS 2	PKRB 2	PKRR 2	GKR 2	GKRS 2	GKRB 2	GKRR 2
n=50	**mean**	2.592	2.278	2.366	**2.148**	2.373	2.372	2.374	**2.296**	1.974	1.436	1.734	**1.427**	2.016	2.014	2.018	**1.838**
	sd	0.379	0.119	0.161	**0.125**	0.107	0.107	0.107	**0.117**	0.254	0.086	0.174	**0.109**	0.038	0.038	0.038	**0.066**
n=100	**mean**	2.599	2.316	2.429	**2.093**	2.369	2.368	2.371	**2.253**	1.932	1.372	1.738	**1.341**	2.009	2.006	2.012	**1.747**
	sd	0.282	0.117	0.152	**0.110**	0.107	0.107	0.107	**0.115**	0.228	0.075	0.162	**0.068**	0.038	0.038	0.037	**0.066**
n=200	**mean**	2.379	2.269	2.342	**2.071**	2.362	2.360	2.364	**2.193**	1.687	**1.254**	1.616	1.311	1.993	1.988	2.001	**1.654**
	sd	0.150	0.118	0.135	**0.112**	0.108	0.108	0.107	**0.121**	0.139	**0.048**	0.118	0.054	0.038	0.038	0.038	**0.047**

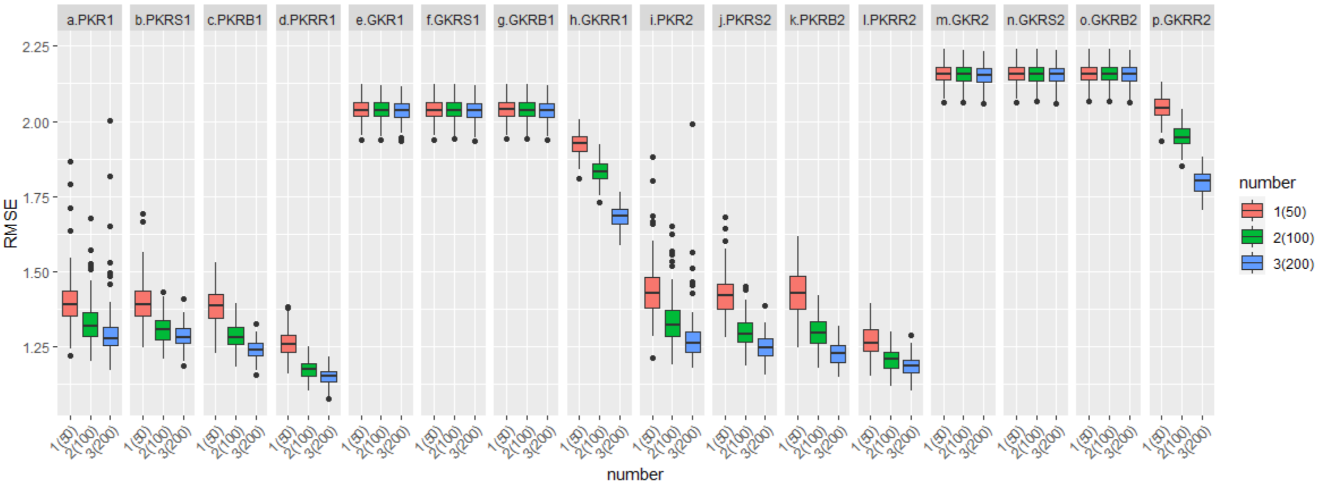
Figure 6.7: $p = 5$, 중도절단 30%





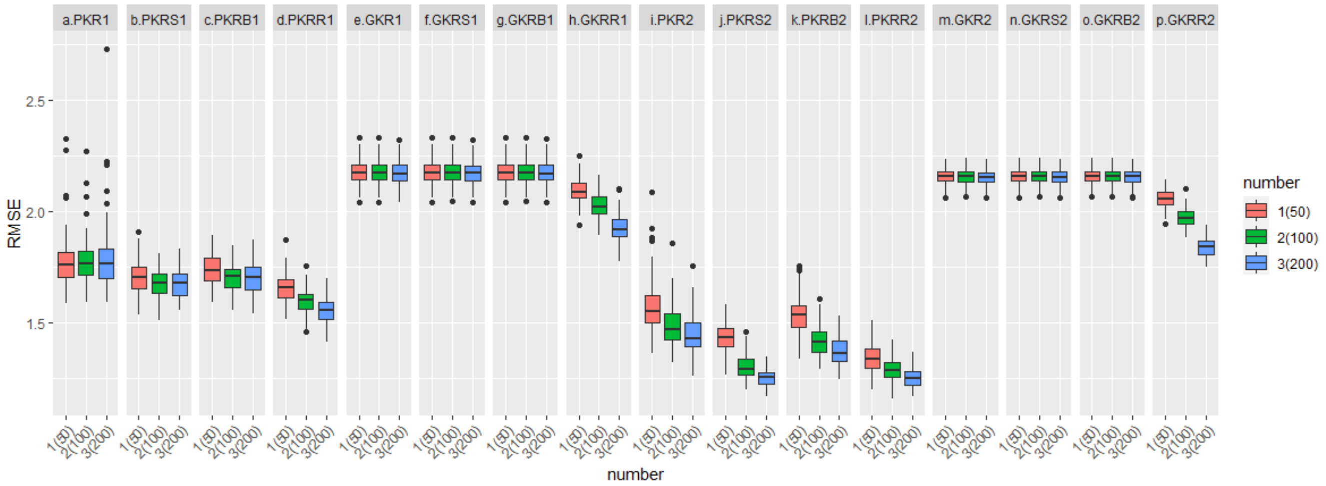
		PKR	PKRS	PKRB	PKRR	GKR	GKRS	GKRB	GKRR	PKR	PKRS	PKRB	PKRR	GKR	GKRS	GKRB	GKRR
		1	1	1	1	1	1	1	1	2	2	2	2	2	2	2	2
n=50	mean	3.016	2.712	2.809	**2.572**	2.651	2.650	2.651	**2.630**	2.218	**1.437**	1.963	1.585	2.018	2.015	2.019	**1.913**
	sd	0.362	0.170	0.241	**0.164**	0.168	0.168	0.168	**0.169**	0.341	**0.087**	0.216	0.120	0.038	0.038	0.038	**0.052**
n=100	mean	3.043	2.779	2.906	**2.531**	2.651	2.649	2.651	**2.616**	2.209	**1.375**	2.015	1.506	2.014	2.008	2.016	**1.860**
	sd	0.296	0.169	0.250	**0.163**	0.168	0.169	0.168	**0.168**	0.309	**0.074**	0.232	0.080	0.037	0.038	0.037	**0.055**
n=200	mean	2.825	2.757	2.794	**2.511**	2.648	2.643	2.648	**2.595**	1.939	**1.256**	1.867	1.468	2.006	1.990	2.009	**1.788**
	sd	0.204	0.150	0.190	**0.166**	0.168	0.168	0.168	**0.170**	0.176	**0.059**	0.147	0.074	0.039	0.038	0.039	**0.077**

Figure 6.8: $p = 5$, 중도절단 50%



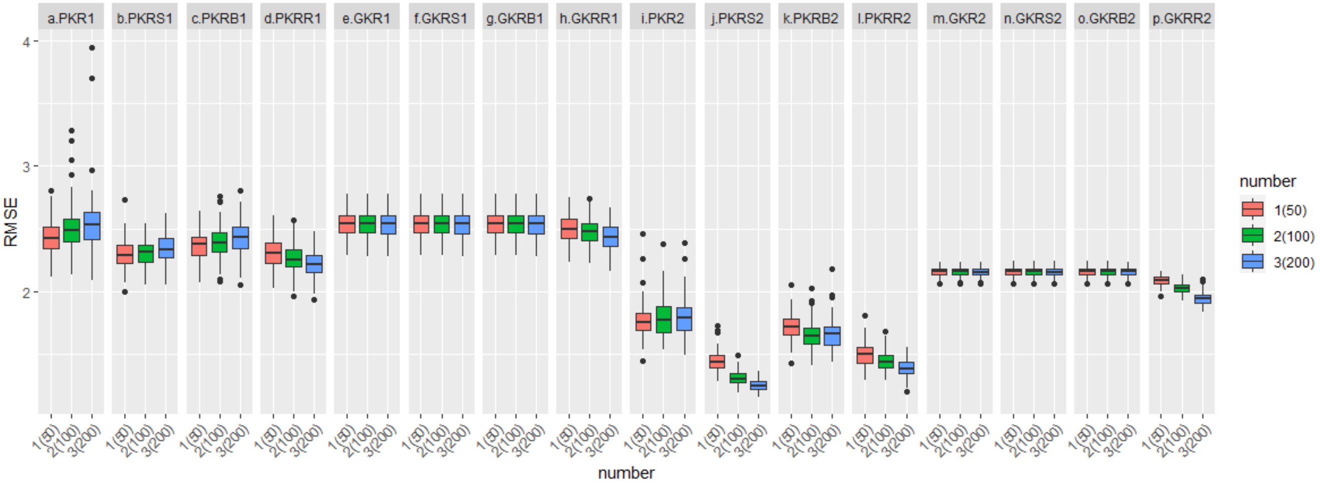
		PKR 1	PKRS 1	PKRB 1	PKRR 1	GKR 1	GKRS 1	GKRB 1	GKRR 1	PKR 2	PKRS 2	PKRB 2	PKRR 2	GKR 2	GKRS 2	GKRB 2	GKRR 2
n=50	**mean**	1.404	1.401	1.387	**1.263**	2.039	2.039	2.039	**1.926**	1.443	1.426	1.430	**1.268**	2.159	2.159	2.159	**2.045**
	sd	0.096	0.074	0.059	**0.047**	0.036	0.036	0.036	**0.037**	0.100	0.074	0.079	**0.051**	0.036	0.036	0.036	**0.038**
n=100	**mean**	1.332	1.308	1.285	**1.176**	2.037	2.038	2.038	**1.831**	1.342	1.300	1.299	**1.207**	2.157	2.158	2.158	**1.949**
	sd	0.077	0.044	0.045	**0.033**	0.036	0.036	0.036	**0.038**	0.088	0.051	0.050	**0.038**	0.036	0.036	0.036	**0.039**
n=200	**mean**	1.304	1.285	1.242	**1.152**	2.034	2.036	2.036	**1.683**	1.280	1.248	1.227	**1.187**	2.154	2.155	2.156	**1.796**
	sd	0.113	0.040	0.033	**0.027**	0.036	0.036	0.036	**0.037**	0.098	0.040	0.036	**0.034**	0.036	0.037	0.036	**0.038**

Figure 6.9: $p = 7$, 중도절단 0%



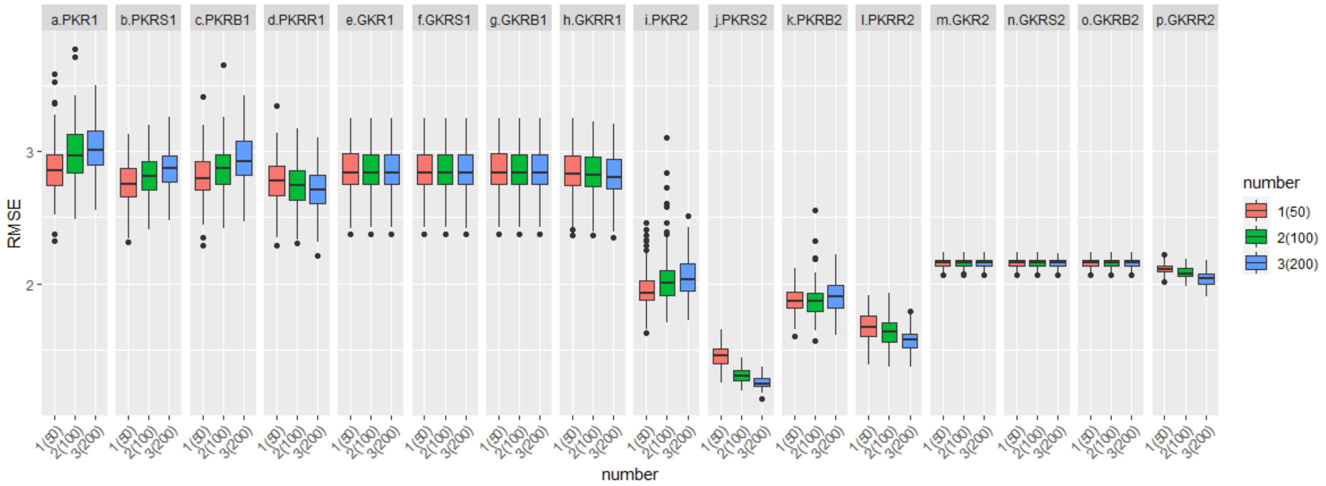
		PKR	**PKRS**	**PKRB**	**PKRR**	**GKR**	**GKRS**	**GKRB**	**GKRR**	**PKR**	**PKRS**	**PKRB**	**PKRR**	**GKR**	**GKRS**	**GKRB**	**GKRR**
		1	**1**	**1**	**1**	**1**	**1**	**1**	**1**	**2**	**2**	**2**	**2**	**2**	**2**	**2**	**2**
n=50	**mean**	1.783	1.707	1.747	**1.657**	2.178	2.178	2.178	**2.094**	1.568	1.436	1.534	**1.342**	2.159	2.159	2.159	**2.058**
	sd	0.113	0.071	0.072	**0.069**	0.055	0.055	0.055	**0.056**	0.123	0.067	0.085	**0.072**	0.036	0.036	0.036	**0.039**
n=100	**mean**	1.776	1.674	1.700	**1.594**	2.177	2.177	2.178	**2.025**	1.487	1.302	1.416	**1.287**	2.158	2.158	2.158	**1.973**
	sd	0.104	0.061	0.064	**0.059**	0.055	0.055	0.055	**0.057**	0.089	0.054	0.065	**0.053**	0.036	0.036	0.036	**0.040**
n=200	**mean**	1.785	1.676	1.700	**1.555**	2.175	2.175	2.176	**1.927**	1.451	**1.252**	1.374	1.253	2.155	2.156	2.157	**1.842**
	sd	0.148	0.064	0.073	**0.055**	0.055	0.054	0.055	**0.060**	0.086	**0.039**	0.063	0.045	0.036	0.036	0.036	**0.042**

Figure 6.10: $p = 7$, 중도절단 10%



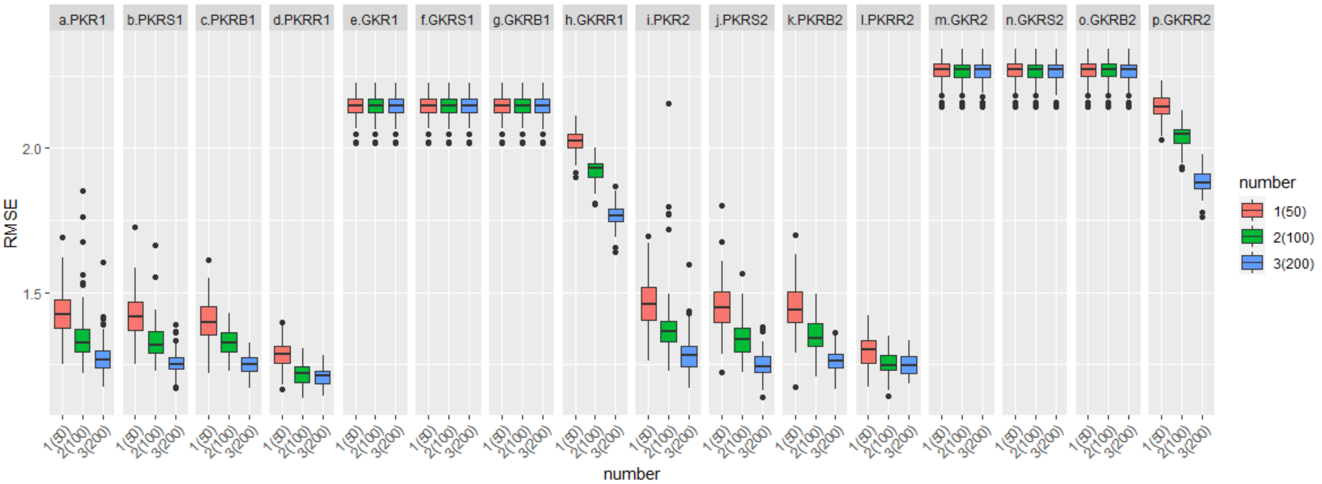
		PKR 1	**PKRS 1**	**PKRB 1**	**PKRR 1**	**GKR 1**	**GKRS 1**	**GKRB 1**	**GKRR 1**	**PKR 2**	**PKRS 2**	**PKRB 2**	**PKRR 2**	**GKR 2**	**GKRS 2**	**GKRB 2**	**GKRR 2**
n=50	**mean**	2.429	**2.296**	2.371	2.313	2.536	2.536	2.536	**2.500**	1.771	**1.446**	1.716	1.502	2.159	2.159	2.159	**2.086**
	sd	0.134	**0.119**	0.116	0.115	0.103	0.103	0.103	**0.105**	0.139	**0.082**	0.103	0.106	0.036	0.036	0.036	**0.041**
n=100	**mean**	2.506	2.310	2.393	**2.259**	2.535	2.535	2.535	**2.474**	1.787	**1.312**	1.656	1.446	2.158	2.158	2.159	**2.027**
	sd	0.188	0.108	0.130	**0.114**	0.103	0.103	0.103	**0.106**	0.150	**0.056**	0.110	0.081	0.036	0.036	0.036	**0.043**
n=200	**mean**	2.546	2.342	2.431	**2.216**	2.534	2.534	2.535	**2.435**	1.792	**1.253**	1.664	1.391	2.156	2.156	2.157	**1.945**
	sd	0.246	0.116	0.142	**0.112**	0.104	0.104	0.103	**0.106**	0.155	**0.043**	0.123	0.066	0.037	0.036	0.036	**0.050**

Figure 6.11: $p = 7$, 중도절단 30%



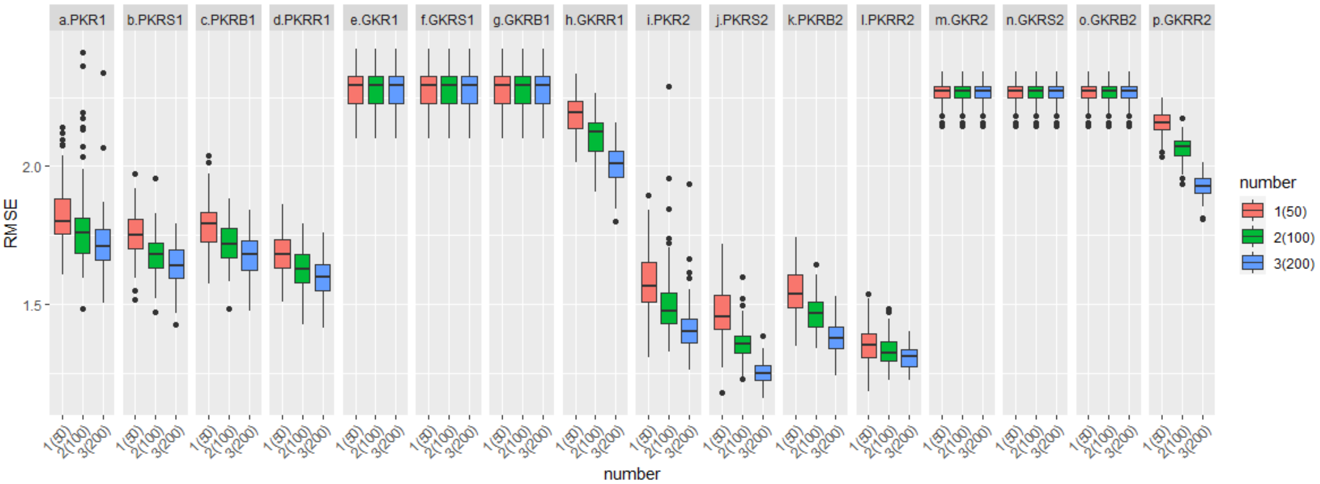
		PKR 1	PKRS 1	PKRB 1	PKRR 1	GKR 1	GKRS 1	GKRB 1	GKRR 1	PKR 2	PKRS 2	PKRB 2	PKRR 2	GKR 2	GKRS 2	GKRB 2	GKRR 2
n=50	mean	2.884	**2.757**	2.819	2.788	2.851	2.851	2.851	**2.840**	1.959	**1.454**	1.873	1.679	2.159	2.159	2.159	**2.112**
	sd	0.217	**0.172**	0.193	0.179	0.179	0.179	0.179	**0.180**	0.156	**0.074**	0.098	0.117	0.036	0.036	0.036	**0.039**
n=100	mean	2.992	2.814	2.880	**2.747**	2.851	2.851	2.851	**2.833**	2.040	**1.306**	1.876	1.636	2.159	2.158	2.159	**2.084**
	sd	0.226	0.165	0.195	**0.174**	0.179	0.179	0.179	**0.178**	0.228	**0.055**	0.141	0.106	0.036	0.036	0.036	**0.040**
n=200	mean	3.033	2.868	2.941	**2.710**	2.850	2.850	2.850	**2.819**	2.050	**1.251**	1.906	1.576	2.157	2.156	2.158	**2.036**
	sd	0.201	0.168	0.185	**0.177**	0.180	0.179	0.179	**0.179**	0.155	**0.042**	0.127	0.086	0.036	0.036	0.036	**0.052**

Figure 6.12: $p = 7$, 중도절단 50%



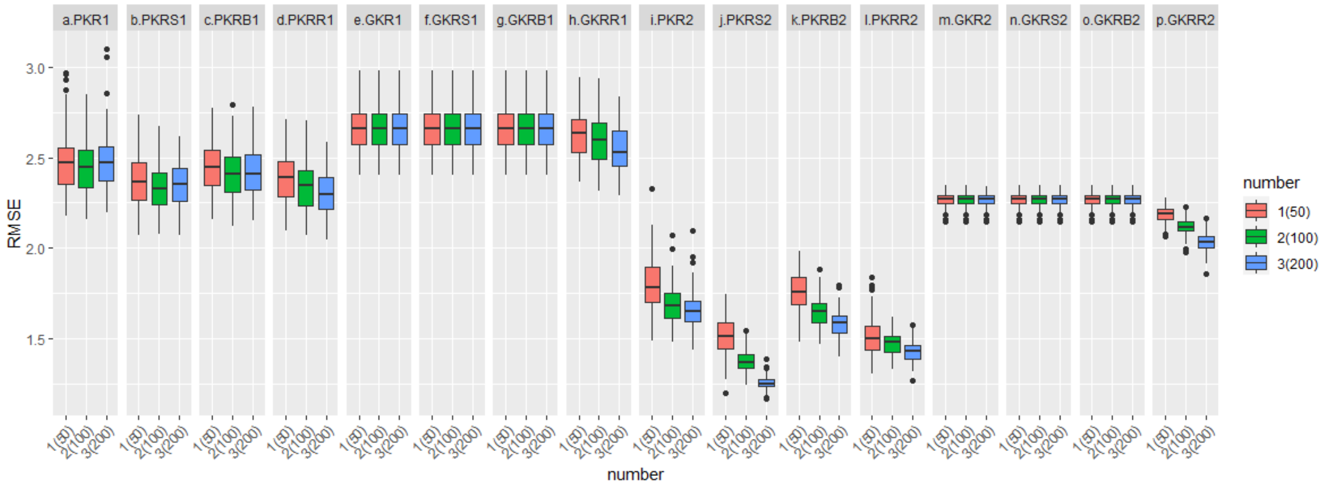
		PKR 1	PKRS 1	PKRB 1	PKRR 1	GKR 1	GKRS 1	GKRB 1	GKRR 1	PKR 2	PKRS 2	PKRB 2	PKRR 2	GKR 2	GKRS 2	GKRB 2	GKRR 2
n=50	**mean**	1.428	1.419	1.403	**1.285**	2.145	2.145	2.146	**2.022**	1.460	1.450	1.448	**1.294**	2.267	2.267	2.267	**2.144**
	sd	0.079	0.075	0.070	**0.051**	0.040	0.040	0.040	**0.041**	0.085	0.089	0.086	**0.054**	0.040	0.040	0.040	**0.041**
n=100	**mean**	1.348	1.331	1.326	**1.217**	2.145	2.145	2.145	**1.923**	1.384	1.339	1.352	**1.254**	2.267	2.267	2.267	**2.042**
	sd	0.097	0.064	0.046	**0.038**	0.040	0.040	0.040	**0.039**	0.125	0.059	0.061	**0.043**	0.040	0.040	0.040	**0.039**
n=200	**mean**	1.275	1.255	1.249	**1.206**	2.145	2.145	2.145	**1.768**	1.287	1.251	1.263	**1.248**	2.267	2.267	2.267	**1.883**
	sd	0.060	0.038	0.035	**0.032**	0.040	0.040	0.040	**0.039**	0.063	0.045	0.040	**0.035**	0.040	0.040	0.040	**0.039**

Figure 6.13: $p = 9$, 중도절단 0%



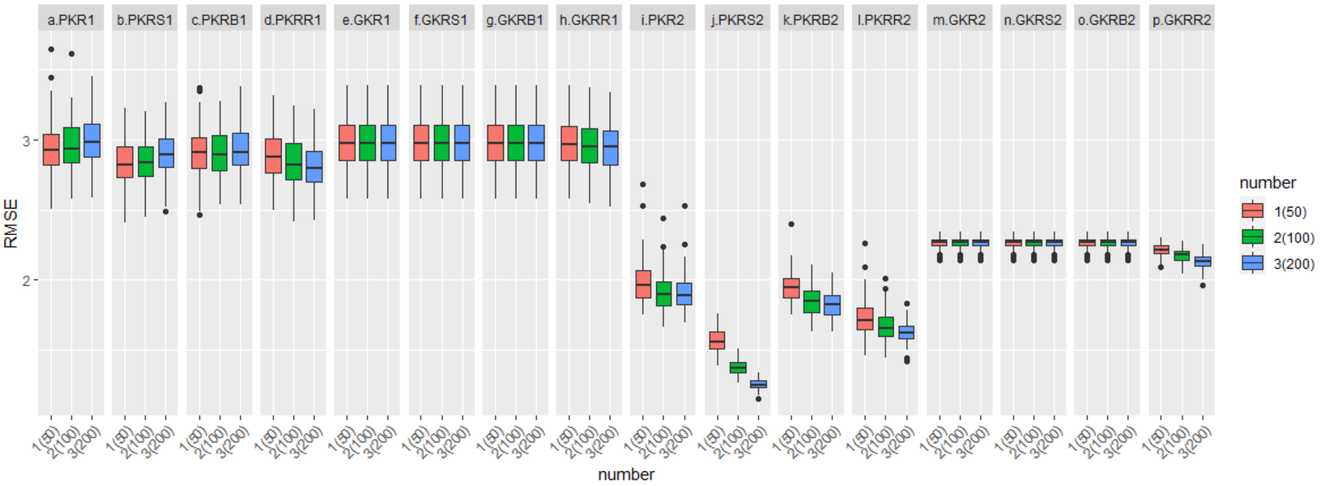
		PKR	PKRS	PKRB	PKRR	GKR	GKRS	GKRB	GKRR	PKR	PKRS	PKRB	PKRR	GKR	GKRS	GKRB	GKRR
		1	1	1	1	1	1	1	1	2	2	2	2	2	2	2	2
n=50	mean	1.821	1.751	1.783	**1.681**	2.278	2.278	2.278	**2.185**	1.582	1.469	1.542	**1.355**	2.267	2.267	2.267	**2.156**
	sd	0.108	0.088	0.090	**0.077**	0.065	0.065	0.065	**0.068**	0.112	0.106	0.089	**0.072**	0.040	0.040	0.040	**0.041**
n=100	mean	1.782	1.677	1.718	**1.625**	2.278	2.278	2.278	**2.112**	1.505	1.360	1.470	**1.330**	2.267	2.267	2.267	**2.066**
	sd	0.153	0.074	0.076	**0.075**	0.065	0.065	0.065	**0.069**	0.127	0.058	0.064	**0.052**	0.040	0.040	0.040	**0.040**
n=200	mean	1.717	1.643	1.678	**1.598**	2.278	2.278	2.278	**2.005**	1.415	**1.253**	1.375	1.307	2.267	2.267	2.267	**1.929**
	sd	0.103	0.073	0.073	**0.069**	0.065	0.065	0.065	**0.070**	0.087	**0.041**	0.054	0.039	0.040	0.040	0.040	**0.040**

Figure 6.14: $p = 9$, 중도절단 10%



		PKR 1	PKRS 1	PKRB 1	PKRR 1	GKR 1	GKRS 1	GKRB 1	GKRR 1	PKR 2	PKRS 2	PKRB 2	PKRR 2	GKR 2	GKRS 2	GKRB 2	GKRR 2
n=50	**mean**	2.469	**2.362**	2.437	2.379	2.663	2.663	2.663	**2.623**	1.809	**1.513**	1.760	1.517	2.267	2.267	2.267	**2.185**
	sd	0.168	**0.132**	0.130	0.130	0.123	0.123	0.123	**0.124**	0.142	**0.111**	0.106	0.106	0.040	0.040	0.040	**0.043**
n=100	**mean**	2.439	2.335	2.405	**2.332**	2.663	2.663	2.663	**2.590**	1.686	**1.375**	1.650	1.474	2.267	2.267	2.267	**2.117**
	sd	0.142	0.128	0.135	**0.131**	0.123	0.122	0.123	**0.129**	0.105	**0.063**	0.081	0.067	0.040	0.040	0.040	**0.047**
n=200	**mean**	2.476	2.351	2.410	**2.301**	2.663	2.663	2.663	**2.548**	1.659	**1.253**	1.581	1.430	2.267	2.267	2.267	**2.031**
	sd	0.158	0.120	0.126	**0.123**	0.123	0.123	0.123	**0.126**	0.098	**0.038**	0.070	0.057	0.040	0.040	0.040	**0.049**

Figure 6.15: $p = 9$, 중도절단 30%



		PKR	PKRS	PKRB	PKRR	GKR	GKRS	GKRB	GKRR	PKR	PKRS	PKRB	PKRR	GKR	GKRS	GKRB	GKRR
		1	1	1	1	1	1	1	1	2	2	2	2	2	2	2	2
n=50	mean	2.936	**2.835**	2.907	2.890	2.980	2.980	2.980	**2.970**	1.985	**1.571**	1.948	1.729	2.267	2.267	2.267	**2.216**
	sd	0.202	**0.180**	0.191	0.188	0.178	0.179	0.179	**0.178**	0.147	**0.083**	0.103	0.129	0.040	0.040	0.040	**0.042**
n=100	mean	2.956	2.852	2.906	**2.842**	2.980	2.980	2.980	**2.959**	1.907	**1.377**	1.850	1.664	2.267	2.267	2.267	**2.175**
	sd	0.180	0.171	0.172	**0.177**	0.179	0.178	0.178	**0.179**	0.133	**0.054**	0.107	0.106	0.040	0.040	0.040	**0.049**
n=200	mean	2.996	2.902	2.939	**2.816**	2.980	2.980	2.980	**2.946**	1.910	**1.254**	1.821	1.628	2.267	2.267	2.267	**2.131**
	sd	0.185	0.172	0.177	**0.177**	0.179	0.179	0.179	**0.177**	0.125	**0.039**	0.088	0.072	0.040	0.040	0.040	**0.051**

Figure 6.16: $p = 9$, 중도절단 50%

그림 6.1 ∼ 그림 6.16, 그리고 이에 해당하는 test RMSE에 대한 표를 통해 알 수 있듯이 총 192가지 상황을 가정하고 모의실험을 진행한 결과 전체적으로 커널 능형 중도절단 회귀분석 방법에 랜덤포레스트 기법을 적용한 경우 예측력이 좋아진다는 것을 확인할 수 있다. 물론 설명변수의 개수가 많고 중도절단의 비율이 큰 상황에서는 분포의 변동성이 커지기 때문에 랜덤포레스트 기법에 의한 성능의 향상이 일어나지 않는 경우도 존재할 수 있다. 하지만 전체적으로 살펴본다면 다양한 모의실험 상황을 가정했음에도 불구하고 배깅이나 랜덤포레스트 등의 앙상블 기법을 적용했을 때 확실히 예측력이 좋아진다는 사실을 알 수 있다. 이에 따라 본 모의실험을 통해 앙상블 기법을 적용한 커널 능형 중도절단 회귀분석 방법이 다른 방법론과 비교했을 때 예측력이 우수하다는 사실을 입증할 수 있었다.

6.2 실증분석

실증분석에서는 총 5가지의 실제 중도절단이 포함된 데이터를 임의로 train:test=7:3의 비율로 분할한 뒤 1절에서 소개한 step을 통하여 방법론들의 예측력을 비교하기 위한 분석을 진행하였다. 다만 3장의 4절에서도 언급했듯이 실제 중도절단이 포함된 데이터에서는 모든 관측치에 대하여 실제 관심사건이 일어나기까지 걸린 시간을 알 수 없다는 점을 고려하여 평가기준을 인조변수로 두는 방법론에 대해서만 분석을 진행하였다. 그리고 1절의 모의실험 결과를 통해서도 알 수 있듯이 커널트릭 기법 적용 시 다항커널(Polynomial kernel)을 사용하는 경우에는 변동성이 매우 크고 이상치도 자주 발생하게 되어 분석에 대한 안정성이 떨어지는 단점이 있다. 그렇기 때문에 다항커널을 이용하여 실제 데이터를 분석하는 경우에는 역행렬(inverse matrix)을 계산 시 나오게 되는 행렬식(determinant)의 값이 0은 아니지만 0에 매우 가까운 양의 실수인 경우가 빈번하게 발생하기 때문에 알고리즘이 중단되는 경우가 종종 나타난다. 이에 따라 실증분석에서는 모든 데이터에 대해 비교적 좋은 유연성(flexibility)과 안정성(stability)을 보이는 가우시안 커널(Gaussian kernel)에 한하여 분석을 진행하였다. 이러한 원인에 따라 실증분석에서는 16가지 방법론들 중 GKR1, GKRS1, GKRB1, 그리고 GKRR1 이렇게 4가지 방법론들에 대하여 비교, 분석을 실시하였다. 그리고 각 방법론에 대해서는 100번의 반복을 실시하였다. 본 실증분석에서 사용된 모든 데이터는 프로그램 R 4.1.1 version의 생존분석 관련 package인 survival, KMsurv, survMisc, 그리고 survMiner에 내장되어 있다.

1) UIS Data

본 데이터는 미국의 University of Massachusetts에서 1989년부터 1994년까지 약 5

년간 협동연구로 진행한 AIDS Research Unit (UMARU) IMPACT Study (UIS)에 대한 결과물이다. 주된 목적은 환자의 약물 남용(drug abuse)을 조사하는 것이며 예측변수는 환자가 유혹을 참지 못하고 다시 약물에 손을 대기까지 걸린 시간(days)이다. 본 연구에서는 2가지의 다른 치료 프로그램을 각각 A site와 B site에서 실시하였으며, 이 중 A site에 해당하는 경우에 한하여 실증분석을 실시하였다. 관측치의 개수는 결측치와 이상치를 제외하여 총 398개이며 사용한 설명변수는 총 8개이다. 그리고 중도절단의 비율은 약 20%이다. 본 데이터에 대한 자세한 설명은 Hosmer et al. (2008)을 참고하기 바란다. 실증분석 결과 다른 방법론들에 비해 랜덤포레스트를 적용하였을 때 test RMSE의 평균값이 작게 산출됨을 확인할 수 있었다. 이를 토대로 앙상블 기법을 적용한 커널 능형 중도절단 회귀분석 방법이 다른 방법론들과 비교했을 때 예측력이 좋다고 판단할 수 있겠다.

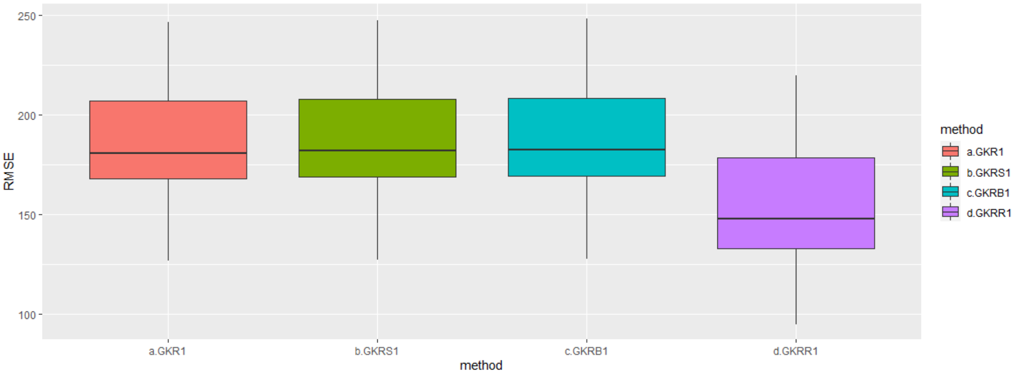


Figure 6.17: UIS data 실증분석

2) PBC Data

본 데이터는 미국의 Mayo Clinic에서 1974년부터 1984년까지 약 10년간 수행된 원발성 담즙성 간경화증(primary biliary cholangitis) 환자에 대한 연구를 통해서 나온

결과물이다. 주된 목적은 위약(placebo)과 D-penicillamine의 효능을 비교하는 것이다. 예측변수는 환자의 생존시간이며 관측치의 개수는 결측치를 제외하여 총 276개이다. 그리고 사용한 설명변수는 총 17개이며 중도절단된 비율은 약 50%이다. 본 데이터에 대한 자세한 설명은 Therneau, T. and Grambsch, P. (2000)을 참조하기 바란다. 실증분석 결과 랜덤포레스트를 적용한 경우에 대해 성능의 향상이 크게 일어나지는 않았다. 이는 설명변수의 개수가 17개로 많으며 중도절단의 비율도 약 50%로서 매우 큰 편이기 때문에 복잡성이 커짐에 따른 결과라고 판단된다. 하지만 이러한 조건에도 불구하고 랜덤포레스트를 적용한 커널 능형 중도절단 회귀분석을 적용시 다른 방법론들보다 test RMSE의 평균값이 작게 산출되었기 때문에 본 연구에서 주장하고자 하는 바를 입증하는 데는 무리가 없다고 생각한다.

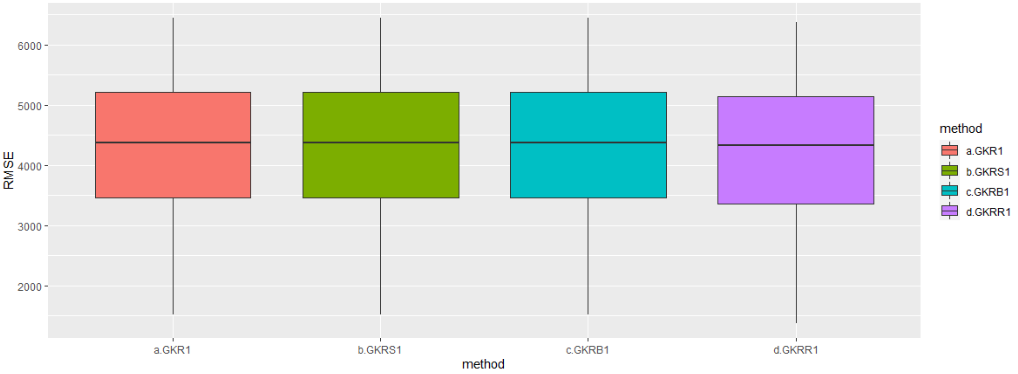


Figure 6.18: PBC data 실증분석

3) Cancer Data

본 데이터는 북아메리카 지역의 암(cancer) 전문가 네트워크로 구성된 North Central Cancer Treatment Group에서 실시한 폐암(lung cancer) 환자에 대한 연구를 통해서 나온 결과물이다. 폐암 환자의 생존시간을 예측하는 것이 주된 목적이며 관

측치의 개수는 결측치를 제외하여 총 167개이다. 그리고 사용한 설명변수는 총 7개이며 중도절단된 비율은 약 30%이다. 실증분석 결과 UIS data의 경우와 마찬가지로 다른 방법론들에 비해 랜덤포레스트를 적용하였을 때 test RMSE의 평균값이 작게 산출됨을 확인할 수 있었다. 이를 토대로 앙상블 기법을 적용한 커널 능형 중도절단 회귀분석 방법이 다른 방법론들과 비교했을 때 예측력이 좋다고 판단할 수 있겠다.

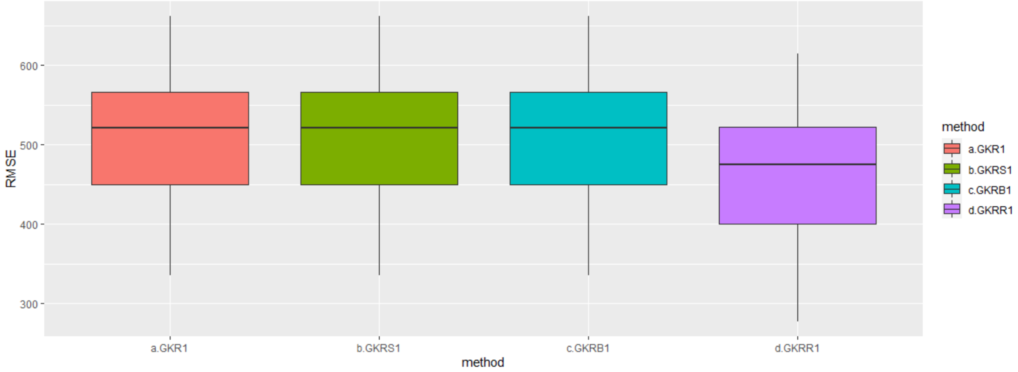


Figure 6.19: Cancer data 실증분석

4) Retinopathy Data

본 데이터는 당뇨병성 망막병증(diabetic retinopathy)을 지연시키는 치료방법으로 레이저 응고법(laser coagulation)의 효과를 검증하는 연구를 통해서 나온 결과물이다. 시력을 잃을 때까지 걸리는 시간을 예측하는 것이 주된 목적이며 관측치의 개수는 총 394개이다. 그리고 사용한 설명변수는 총 6개이며 중도절단의 비율은 약 60%이다. 실증분석 결과 PBC data의 경우와 마찬가지로 랜덤포레스트를 적용한 경우에 대해 성능의 향상이 크게 일어나지는 않았다. 이는 중도절단의 비율이 약 60%로서 매우 큰 편이기 때문에 복잡성이 커짐에 따른 결과라고 판단된다. 하지만 이러한 조건에도

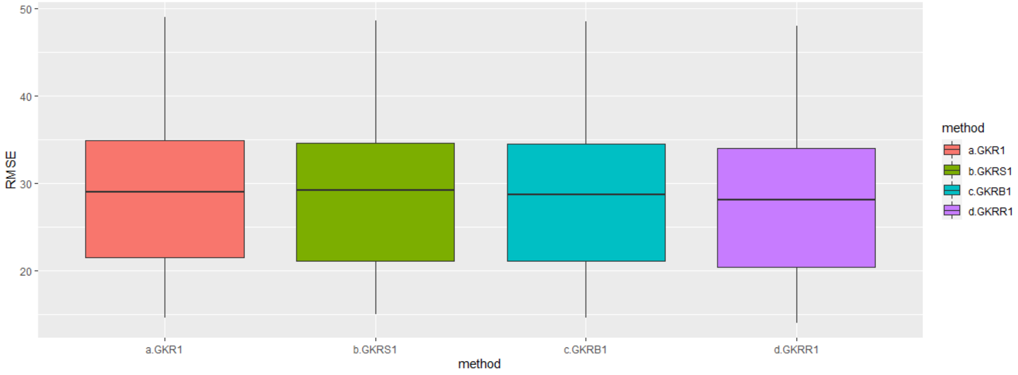


Figure 6.20: Cancer data 실증분석

불구하고 랜덤포레스트를 적용한 커널 능형 중도절단 회귀분석을 적용 시 다른 방법론들보다 test RMSE의 평균값이 작게 산출되었기 때문에 본 연구에서 주장하고자 하는 바를 입증하는 데는 무리가 없다고 생각한다.

5) Bfeed Data

본 데이터는 태아를 출산한 산모의 모유 수유 기간(duration of breast feeding)에 대한 연구를 통해서 나온 결과물이다. 모유 수유 기간을 예측하는 것이 주된 목적이며 관측치의 개수는 총 927개이다. 사용한 설명변수는 총 8개이며 중도절단의 비율은 약 4%이다. 본 데이터에 대한 자세한 사항은 Klein and Moeschberger (1997)를 참조하기 바란다. 데이터에 포함된 변수는 다음과 같다. 실증분석 결과 확실히 배깅이나 랜덤포레스트 등의 앙상블 기법을 적용했을 때 test RMSE에 대한 평균값과 분산이 작아진다는 것을 확인할 수 있었다. 물론 중도절단의 비율이 약 4%이고 이는 그렇게 크지 않은 비율이기 때문에 중도절단의 비율이 큰 데이터에 비해 앙상블 기법을 적용한 방법론에 대한 성능의 향상이 많이 일어났다고 볼 수도 있다. 하지만 결과적으로는 앙상블 기법을 적용한 커널 능형 중도절단 회귀분석 방법이 다른 방법론들에

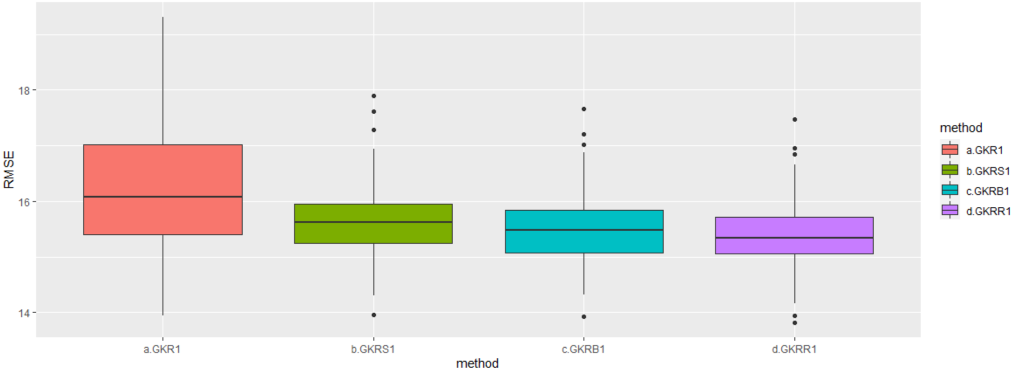


Figure 6.21: Bfeed data 실증분석

비해 예측력이 우수하다는 사실을 입증하기에는 충분하다고 판단된다.

6) 실증분석 결과 정리

지금까지 실시한 실증분석에서 산출된 test RMSE에 대한 결과를 종합하면 표 6.1과 같이 정리할 수 있다.

data		GKR1	GKRS1	GKRB1	GKRR1	Censoring rate	Number of explanatory variables	Number of observations
UIS	**mean**	186.132	187.691	187.857	**154.319**	0.2	8	398
	sd	26.033	25.899	25.836	**28.474**			
PBC	**mean**	4300.305	4300.305	4300.305	**4236.192**	0.5	17	276
	sd	1135.303	1135.303	1135.303	**1145.583**			
Cancer	**mean**	509.320	509.327	509.331	**465.783**	0.3	7	167
	sd	72.125	72.137	72.138	**74.089**			
Retinopathy	**mean**	29.230	29.117	28.859	**28.145**	0.6	6	394
	sd	8.663	8.757	8.704	**8.788**			
Bfeed	**mean**	16.192	15.639	15.502	**15.366**	0.04	8	927
	sd	1.069	0.696	0.677	**0.664**			

Table 6.1: 실증분석 결과 정리

결과적으로 실증분석에서 사용된 데이터마다 중도절단의 비율과 사용한 설명변수의 개수가 다르기 때문에 성능의 향상이 일어나는 정도에 차이가 있는 것은 분명한 사실이다. 하지만 그럼에도 불구하고 전체적으로 살펴봤을 경우에는 랜덤포레스트 기법을 적용했을 때 관심사건이 일어나기까지 걸리는 시간에 대한 예측력이 더 좋아진다는 것을 확인할 수 있었다. 이에 따라 본 실증분석을 통해서 앙상블 기법을 적용한 커널 능형 중도절단 회귀분석 방법이 다른 방법론들과 비교했을 때 전체적으로 예측력이 우수하다는 사실을 입증할 수 있었다.

이상으로 커널 능형 중도절단 회귀분석과 관련하여 진행한 연구에 대한 설명을 마치도록 하겠다. 이어지는 7장에서부터는 생존자료(Survival data)에 대한 분석을 통해서 얻을 수 있는 시간에 의존하는 AUC(Area Under Curve)를 향상시킬 수 있는 방안에 대하여 진행한 연구에 대하여 설명하도록 하겠다.

7 Time-dependent AUC

7.1 ROC curve

ROC (Receiver operating characteristic) curve is a graph drawn by measuring the performance of the model for various thresholds, and is mainly used when evaluating the performance of a classification model. In order to understand the ROC curve, it is first to understand the confusion matrix, which summarizes the results of classification and shows it in the form of a table, which is shown in Table 7.1. Through this confusion matrix, various indicators to evaluate the performance of the classification model can be calculated, and representatively, sensitivity:

		Predicted values	
	Total population $= P + N$	Positive(PP)	Negative(PN)
Actual values	Positive(P)	True positive (TP)	False negative (FN)
	Negative(N)	False positive (FP)	True negative (TN)

Table 7.1: Confusion matrix

true positive rate (TPR), specificity: true negative rate (TNR), accuracy(ACC), precision(PRE), and misclassification rate(MCR). For more details on these, see Fawcett, T. (2006). In here, sensitivity and specificity show an inversely proportional relationship with each other. That is, when sensitivity increases, specificity decreases, and when sensitivity decreases, specificity increases. Therefore, it is virtually impossible to increase the sensitivity and specificity at the same time, and it can be said that the higher the sensitivity and specificity value, the better the performance of the classification model used.

$$TPR = \frac{TP}{TP + FN} \tag{1.1}$$

$$TNR = \frac{TN}{TN + FP} \tag{1.2}$$

$$ACC = \frac{TP + TN}{TP + TN + FP + FN} \tag{1.3}$$

$$PRE = \frac{TP}{TP + FP} \tag{1.4}$$

$$MCE = \frac{FP + FN}{TP + TN + FP + FN} \tag{1.5}$$

The ROC curve sets the x axis to the false positive rate, that is, $1 - TNR$, and the y axis to the true positive rate. It can be completed by calculating the false positive rate and true positive rate for all thresholds, making a point on the coordinates and connecting it with a smooth curve. Here, the thresholds are reference points set for classifying the predicted values of the response variables in the classification model. If binary classification is to be performed, the thresholds will be random probabilities that serve as criteria for classification, and their values range from 0 to 1. The area under the ROC curve is called AUC (Area Under Curve), and it can be said that the larger the area of this AUC, the better the performance of the classification model used. AUC has a value between 0 and 1, but the minimum value of AUC is usually observed around 0.5. In other words, the closer the AUC value is to 1, the better the classification model's performance is. The ROC curve can be drawn as shown in Figure 7.1, and it can be judged that a classification model with better performance is used as the area of the yellow area, is equal to, AUC, is closer to 1.

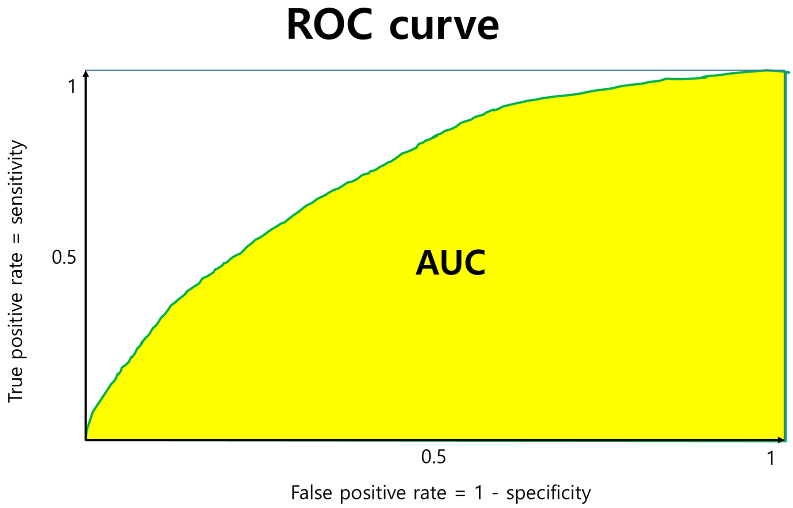


Figure 7.1: ROC curve

7.2 Time-dependent AUC

The ROC curve introduced in Section 7.1 and the AUC calculated through it are usually calculated with only one value for one model used to fit the data. However, in the case of the survival data introduced in Section 2.1, survival time is included, and the models used to analyze these data depend on the survival time. Therefore, the AUC calculated through a model that fits these survival data is various values depending on the survival time, which is called time-dependent AUC. For further details on this, see Kamarudin et al. (2017) and Cho, J. (2022).

Refer to Kamarudin et al. (2017), the time-dependent AUC for the survival model is defined as follows. First, let's define some variables to understand the time-dependent AUC. First, let T_i be the time of disease onset for individual values for each $i(= 1, \ldots, n)$, and X_i be the marker value. Here, the marker value is a value usually used to measure the risk status of a specific patient in medical research. If a research on diabetes is conducted, the patient's blood glucose level can be used as the marker value. In general, it is common to use the risk score calculated through the regression model or classification model as a marker value. In this study, the risk score calculated through the Cox regression model was used as the marker value. And let C_i be the censoring time, $Z_i = \min(T_i, C_i)$ be the observed event time, and $\delta_i = I(T_i \leq C_i)$ be defined as a censoring indicator. Finally, if $D_i(t)$ is disease status at time t, which has a value of 1 if disease occurs, and 0 otherwise, time-dependent sensitivity $Sen(c, t)$ and time-dependent specificity $Spe(c, t)$, which are calculated using threshold c and time t, and time-dependent AUC $AUC(t)$ which is calculated through the time-dependent ROC curve $ROC(t)$ from time-dependent sensitivity and specificity can be defined as follows.

$$Sen(c,t) = P(X_i > c|D_i(t) = 1) \tag{2.6}$$

$$Spe(c,t) = P(X_i \leq c|D_i(t) = 0) \tag{2.7}$$

$$AUC(t) = \int_{-\infty}^{\infty} Sen(c,t)d[1 - Spe(c,t)] \tag{2.8}$$

In above equation, $1 - Spe(c,t) = \frac{\partial[1-Spe(c,t)]}{\partial c}dc.$

Heatherty, P.J. and Zheng, Y. (2005) proposed three methods for defining time-dependent sensitivity and specificity and the time-dependent AUC calculated through them. Two of these definition methods are introduced as follows.

1) Cumulative sensitivity and dynamic specificity (C/D)

$Sen^C(c,t) = P(X_i > c|T_i \leq t)$

$Spe^D(c,t) = P(X_i \leq c|T_i > t)$

$AUC^{C,D}(c,t) = P(X_i > X_j|T_i \leq t, T_j > t), i \neq j$

2) Incident sensitivity and dynamic specificity (I/D)

$Sen^I(c,t) = P(X_i > c|T_i = t)$

$Spe^D(c,t) = P(X_i \leq c|T_i > t)$

$AUC^{I,D}(c,t) = P(X_i > X_j|T_i = t, T_j > t), i \neq j$

Here, definition C/D is appropriate to use when you are interested in finding a specific time to divide an individual patient into diseased and non-diseased cases, and definition I/D is appropriate to use when you want to divide an individual into those who have disease and those who do not using predetermined specific time. In this study, time-dependent AUC based on definition C/D was applied, and the following Conditional Inverse Probability of Censoring Weighting (IPCW) estimation method was used to estimate time-dependent sensitivity and specificity.

$$\hat{Sen}(c,t) = \frac{\Sigma_{i=1}^{n} I(X_i > c, Z_i \leq t)\{\delta_i / n\hat{S}_c(Z_i|X_i)\}}{\Sigma_{i=1}^{n} I(Z_i \leq t)\{\delta_i / n\hat{S}_c(Z_i|X_i)\}} \tag{2.9}$$

$$\hat{Spe}(c,t) = \frac{\Sigma_{i=1}^{n} I(X_i \leq c, Z_i > t)\{1 / n\hat{S}_c(t|X_i)\}}{\Sigma_{i=1}^{n} I(Z_i > t)\{1 / n\hat{S}_c(t|X_i)\}} \tag{2.10}$$

Here, $S_c(t|X_i) = P(C_i > t|X_i)$ is the censoring survival probability estimated through the Cox regression model.

8 Cox regression model

8.1 Cox proportional hazard model

The Cox proportional hazard model is a semi-parametric method frequently used to modeling the hazard function in survival analysis using survival data. As explained in Section 2.2, in order to use this model, the assumption that the hazard between the groups to be compared is uniformly proportional during the follow-up period must be satisfied. For more information on this, see Kleinbaum, D.G. and Klein, M. (2010) and Kim, J. (2016).

First, for the survival data (t_i, δ_i, x_i) for each $i(= 1, \ldots, n)$, assume that $t_i = \min(y_i, c_i)$ is the observed survival time, and $\delta_i = I(y_i \le c_i)$ is the censoring indicator (In here, y_i is the real survival time, c_i is the censoring time). If $x_i = (x_{i1}, \ldots, x_{ip})^T$ is a covariate vector and $\beta = (\beta_1, \ldots, \beta_p)^T$ is a regression coefficient vector, the Cox proportional hazard model results in the following form.

$$h(t|x_i) = h_0(t)\exp(x_i^T\beta) = h_0(t)\exp(x_{i1}\beta_1 + \cdots + x_{ip}\beta_p) \tag{1.1}$$

Calculating the hazard ratio for the above model is as follows.

$$HR = \frac{h(t|x_i)}{h(t|x_j)} = \exp[\Sigma_{b=1}^{p}\beta_b(x_{ib} - x_{jb})] \tag{1.2}$$

In other words, the hazard ratio for the Cox proportion hazard model does not depend on the survival time t. Therefore, this model is used only when the proportional hazard assumption is satisfied. In the above model equation, the regression coefficient vector β is estimated by maximizing the partial likelihood function using the Newton-Raphson algorithm. If we assume that there are no ties in the survival data, the partial likelihood function can be written as follows.

$$PL(\beta) = \prod_{i=1}^{n}[\frac{h_0(t_i)\exp(x_i^T\beta)}{\Sigma_{l\in R(t_i)}h_0(t_i)\exp(x_l^T\beta)}]^{\delta_i} = \prod_{i=1}^{n}[\frac{Z_i\exp(x_i^T\beta)}{\Sigma_{l\in R_i}Z_l\exp(x_l^T\beta)}]^{\delta_i} \qquad (1.3)$$

Here, $Z_i = Z_i(t)$ has a value of 1 if the ith object belongs to the risk set at the time t, otherwise 0. And $R_j = R(t_j)$ is a risk group, assuming that there are no ties, means a group of living individuals who have not experienced an event until just before time t_j.

The estimator $\hat{\beta}$ for the regression coefficient vector is obtained through the process of maximizing the log partial likelihood function $l(\beta) = \log[PL(\beta)]$. In this process, score function $U(\beta_k)$ and information matrix $I(\beta)$ are used as follows.

$$U(\beta_k) = \frac{\partial l(\beta)}{\partial \beta_k} = \Sigma_{i=1}^{n}\delta_i[x_{ik} - \frac{\Sigma_{l\in R_i}x_{lk}\exp(x_l^T\beta)}{\Sigma_{l\in R_i}\exp(x_i^T\beta)}] \qquad (1.4)$$

$$I(\beta) = [I_{gh}(\beta)]_{p\times p} = -\begin{bmatrix} \frac{\partial^2 l(\beta)}{\partial \beta_1^2} & \frac{\partial^2 l(\beta)}{\partial \beta_1 \partial \beta_2} & \cdots & \frac{\partial^2 l(\beta)}{\partial \beta_1 \partial \beta_p} \\ \vdots & \frac{\partial^2 l(\beta)}{\partial \beta_2^2} & \cdots & \frac{\partial^2 l(\beta)}{\partial \beta_2 \partial \beta_p} \\ \vdots & \vdots & \ddots & \vdots \\ \frac{\partial^2 l(\beta)}{\partial \beta_p \partial \beta_1} & \frac{\partial^2 l(\beta)}{\partial \beta_p \partial \beta_2} & \cdots & \frac{\partial^2 l(\beta)}{\partial \beta_p^2} \end{bmatrix}, g, h = 1, \ldots, p \qquad (1.5)$$

Using score function and information matrix in equation 1.3 and 1.4, and the appropriate pre-determined initial value $\hat{\beta}^{(0)}$ for the estimator $\hat{\beta}$ of the regression coefficient vector, Newton-Raphson algorithm $\hat{\beta}^{(k+1)} = \hat{\beta}^{(k)} + I^{-1}(\hat{\beta}^{(k)})U(\hat{\beta}^{(k)})$ is repeated to estimate β until the log partial likelihood derivative converges

$(l(\hat{\beta}^{(k+1)}) \approx l(\hat{\beta}^{(k)}))$. This allows us to obtain a Breslow estimator for the cumulative hazard function as follows.

$$\hat{H}(t|x) = \Sigma_{t(i)\leq t} \frac{\Sigma_{l=1}^{n} \delta_i I(t_l = t_i)}{\Sigma_{l\in R_i} \exp(x_l^T \hat{\beta})} \tag{1.6}$$

In here, $t_{(1)} < \cdots < t_{(n)}$ are order statistics of time t. And using the estimator $\hat{\beta}$ for the regression coefficient vector β, $x_i^T \hat{\beta}$, $i = 1, \ldots, n$ can be calculated. This is the estimator of the risk score obtained through the Cox proportional hazard model. This value can be used as a necessary marker value when calculating the time-dependent AUC introduced in Section 7.2.

8.2 Extended Cox regression model

The Cox proportional hazard model described in Section 8.1 can be used when it is assumed that the hazard between the groups to be compared is uniformly proportional during the follow-up period. However, when looking at various survival data, the explanatory variables in the covariate vector will not always be independent of the survival time. In some cases, it is possible that there may be a time varying covariate that is associated with a change in survival time. A model that can be considered in this case is the Extended Cox regression model. For details on the Extended Cox regression model, see Zhang et al. (2018) and Therneau, T. and Grambsch, P. (2000). For example, suppose we have the following Cox regression model.

$$h(t, x_i(t)) = h_0(t) \exp[\Sigma_{b=1}^{p_1} \beta_b x_{ib} + \Sigma_{b=1}^{p_2} \gamma_b x_{ib}(t)] \tag{2.7}$$

The regression coefficient vector for the above model is $\beta^* = (\beta_1, \beta_2, \ldots, \beta_{p_1}, \gamma_1, \gamma_2, \ldots, \gamma_{p_2})^T$ and the covariate vector is $x_i(t) = (x_{i1}, x_{i2}, \ldots, x_{ip_1}, x_{i1}(t), x_{i2}(t), \ldots, x_{ip_2}(t))^T$. That is, some explanatory variables depend on the change in survival time t. The hazard ratio for this model is calculated as follows.

$$HR = \frac{h(t, x_i(t))}{h(t, x_j(t))} = \exp[\Sigma_{b=1}^{p_1} \beta_b (x_{ib} - x_{jb}) + \Sigma_{b=1}^{p_2} \gamma_b (x_{ib}(t) - x_{jb}(t))] \tag{2.8}$$

In other words, the Extended Cox regression model including time varying covariates does not satisfy the proportional hazard assumption because the hazard ratio changes with the survival time t. Therefore, this model can be applied when the assumption that the risk between groups is proportionally proportional to the survival time during the follow-up period is not satisfied.

9 Calibration

9.1

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국문초록

중도절단이 포함된 생존자료 분석 시 기계학습 방법을 통한 성능향상에 관한 연구

황성윤

전북대학교 대학원 통계학과

본 논문은 총 2가지의 연구에 대한 내용을 담고 있으며 모두 생존자료를 분석하는 것과 관련이 있다.

첫 번째 연구는 중도절단(censoring)이 포함된 데이터에 대하여 회귀분석을 실시하는 경우 예측력(predictive power)을 향상시킬 수 있는 방법에 관한 것이다. 중도절단은 보통 의학 분야에서 자주 등장하는 환자의 생존시간(survival time)과 관련한 생존자료(survival data)에서 환자가 연구대상인 질병 이외의 요인에 의해 사망하게 되는 등의 내부적 또는 외부적인 원인에 의하여 발생하게 된다. 생존자료를 분석하는 가장 큰 목적은 어떠한 요인이 환자의 생존시간에 유의미한 영향력을 미치게 되는지 확인하고 이를 통해 환자의 생존시간을 예측하는 것이다. 이러한 중도절단이 포함된 생존자료의 경우는 추정의 대상이 되는 생존시간이 부분적으로만 관측되기 때문에 이를 대체하기 위한 인조변수(synthetic response)를 만들어서 자료를 분석할 수 있다. 하지만, 이러한 인조변수는 설명변수(explanatory variable)가 주어졌을 경우의 조건부분산(conditional variance)이 원래 생존시간의 조건부분산보다 커지는 경향이

있고 생존시간이 증가할수록 증가하는 폭도 커지는 특성이 있다. 이 때문에 추정량에 대한 안정성이 떨어져서 문제가 될 수 있다. 이러한 문제점을 보완하기 위해 본 연구에서는 인조변수에 대한 회귀모형을 구축할 경우 변환함수를 따로 지정할 필요 없이 복잡한 비선형 데이터에 대해 적절한 사상함수를 사용해 설명변수 공간에 있는 데이터를 고차원의 특성 공간으로 이동시키는 커널트릭 기법(kernel trick method)과 다중공선성(multicollinearity)의 문제가 있을 때 적용 가능한 능형 회귀분석(ridge regression) 방법을 적용한다. 여기에 추가로 배깅(bagging) 및 랜덤포레스트(random forest)와 같은 앙상블 기법(ensemble method)을 적용하여 추정량의 분산을 줄임으로써 생존시간에 대한 예측력을 향상시키는 방법에 관하여 제안하고자 한다. 컴퓨터 모의실험을 통하여 다양한 상황을 가정하고 중도절단이 포함된 데이터에서 설명변수에 대한 예측력을 비교, 분석하였다. 이를 통해 본 연구에서 제안하고자 하는 방법이 일반적인 방법과 비교했을 때 전체적으로 우수한 예측력을 보임을 확인할 수 있었다.

두 번째 연구는 생존자료를 분석 시 산출할 수 있는 time-dependent AUC를 전체적으로 향상시킬 수 있는 방법에 관한 것이다. 계속 설명...

주요용어 : 생존자료, 인조변수, 능형 회귀분석, 기계학습, 커널트릭 기법, 앙상블 기법, time-dependent AUC, Cox 비례위험모형

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