

Predictive Probabilities for New Patients.

Daehyun Chung¹⁾

Abstract

Under the certain assumptions, we derive the recursive formula for the predictive probabilities that a new patient will survive up to the time, conditional on the data. The formula for a new patient is extended to obtain the computational algorithms for the predictive probabilities for several new patients. We correct Genest and Kalbfleisch's approach for several new patients, since we find that their approach is incorrect.

1. Introduction

This study extends the work of Berliner and Hill(BH)(1988) in which they consider the posterior predictive distribution of a new patient. For a group of N patients, (x_1, \dots, x_n) are the observed death times and (u_1, \dots, u_m) are the observed censoring times with $N = n + m$. A patient may die during the study due to the illness. Then we observe x_i , the death time of the patient. Some patients may withdraw from the study or die for non-related reasons. They may be alive at the end of the study. Then we observe the censoring time u_i of the censored patient. Let X_{N+1} be the death time of a new patient. They adapt three assumptions to obtain the posterior predictive distribution of X_{N+1} . These are the basic three assumptions which they assume.

A1. The new and the old patients are deemed to be exchangeable in term of death times.

A2. The posterior prediction rule assigns equal probability of $\frac{1}{n+1}$ to each interval determined by n death times in case of no censoring or ties among observed death times.

A3. The censoring mechanisms are "noninformative".

Lane and Sudderth(1978) describe quite well A2. They propose that the distribution of X_{N+1} should assign equal weight to each interval regardless of the observed values which

1) Department of Statistics, Chungbuk National University, Cheongju, Chungbuk, 320-763., KOREA

are sampled without replacement. More precisely

$$Pr\{(X_1, \dots, X_n) \in B \text{ and } X_{n+1} \in I_i\} = \frac{1}{n+1} Pr\{(X_1, \dots, X_n) \in B\}$$

for any Borel set B .

The assumption A2 was proposed by Hill(1968) to represent extremely vague subjective knowledge about the form of the true distribution. He pose a question about the existence of a prior distribution. Lane and Sudderth(1978) show that finitely additive distributions with the assumption A2 do exist for all n . Hill suggest the new version of the assumption A2,

$$Pr\{X_{n+1} \in I_i | x_1, \dots, x_n\} = \frac{1}{n+1}.$$

Hill's version is stronger than Lane and sudderth's version in sense that it gives the conditional probability, even when the conditioning event has probability 0.

In this study, we want to derive an efficient formula for predicting the death times of several new patients. We also point out that the sequential approach of Genest and Kalfleisch is incorrect and find the correct version of their formula.

2. Predictive probabilities of a new patient

Let X_i be the death time of the i th patient. From the data set $\{\underline{x}, \underline{u}\}$ given in Section 1 where $\underline{x} = (x_1, \dots, x_n)$ and $\underline{u} = (u_1, \dots, u_m)$, we can determine the time of death of an uncensored patient, $x_{(j)}$ and the time of a censored patient who could have died, $u_{(j)}$:

$$\text{Data} = \{(X_1 = x_{(1)}, \dots, X_n = x_{(n)}); (X_{n+1} \geq u_{(1)}, \dots, X_{n+m} \geq u_{(m)})\}.$$

Since the random variables are exchangeable, we can order them like Data.

Let the exact censoring information (ECI) be the event defined by

$$\text{ECI} = \{X_{n+j} \geq u_{(j)} \text{ for } j = 1, \dots, m\}$$

For each censored observation $u_{(j)}$, $j = 1, 2, \dots, m$, define $x_{(r_j)}$ to be $\max_i \{x_{(i)} : x_{(i)} \leq u_{(j)}\}$.

We may call r_j the rank of $u_{(j)}$ relative to $x_{(1)}, \dots, x_{(n)}$. Define the partial censoring

information (PCI) as

$$\text{PCI} = \{X_{n+j} \geq x_{(r_j)} \text{ for } j=1, \dots, m\}$$

Our goal is to compute

$$P(i) = \Pr\{X_{N+1} \in I_i | \underline{x}, \text{PCI}\} \text{ for } i=0, 1, \dots, n,$$

since ECI can be approximated by PCI as follows;

$$\begin{aligned} \Pr\{X_{N+1} \in I_i | \text{Data}\} &= \Pr\{X_{N+1} \in I_i | \underline{x}, \text{ECI}\} \\ &\approx \Pr\{X_{N+1} \in I_i | \underline{x}, \text{PCI}\} \\ &= \Pr\{X_{N+1} \in I_i, \text{PCI} | \underline{x}\} / \Pr\{\text{PCI} | \underline{x}\} \end{aligned} \quad (1)$$

BH argue that such an approximation is reasonable; it is also implicit in other nonparametric approaches to censored data (e.g., Kaplan and Meier (1958)). We compute $\Pr\{X_{N+1} \in I_i, \text{PCI} | \underline{x}\}$ and $\Pr\{\text{PCI} | \underline{x}\}$. For simplicity, when $m=1$,

$$\begin{aligned} \Pr\{\text{PCI} | \underline{x}\} &= \Pr\{X_{N+1} \geq x_{r_1} | \underline{x}\} \\ &= 1 - \frac{r_1}{n+1}, \end{aligned}$$

where r_1 is the number of $x_{(i)}$'s, $i=1, 2, \dots, n$, which are not greater than $u_{(1)}$. Generalizing this approach, we obtain the following lemma.

Lemma 1. Let n and m be positive integers and r_1, \dots, r_m be the integers such that $0 \leq r_1 \leq \dots \leq r_m \leq n$. If A2 holds, then it follows that

$$\begin{aligned} \Pr\{\text{PCI} | \underline{x}\} &= \Pr\{X_{n+1} \geq x_{(r_1)}, \dots, X_{n+m} \geq x_{(r_m)} | \underline{x}\} \\ &= \left(1 - \frac{r_m}{n+1}\right) \left(1 - \frac{r_{m-1}}{n+2}\right) \dots \left(1 - \frac{r_1}{n+m}\right). \end{aligned} \quad (2)$$

Now let us consider the simple method to compute $\Pr\{X_{N+1} \in I_i, \text{PCI} | \underline{x}\}$ which can be

expressed by the product of

$$Pr\{X_{N+1} \in I_i | \underline{x}\} \text{ and } Pr\{\text{PCI} | \underline{x}, X_{N+1} \in I_i\}.$$

While $Pr\{X_{N+1} \in I_i | \underline{x}\} = \frac{1}{n+1}$ by the assumption of A2,

$$Pr\{\text{PCI} | \underline{x}, X_{N+1} \in I_i\} = \left(1 - \frac{r_m^*}{n+2}\right) \left(1 - \frac{r_{m-1}^*}{n+3}\right) \cdots \left(1 - \frac{r_1^*}{n+1+m}\right) \quad (3)$$

by Lemma 1 when r_j^* is the rank of $x_{(r)}$ relative to $x_{(1)}, \dots, x_{(n)}$ and the survival time specified by $X_{N+1} \in I_i$. The survival time is assumed to be known in the interval, say $X_{N+1} = w_1$. Note that r_j^* does not depend upon the value of w_1 in I_i .

Now we are at a moment that we find the computational form of r_j^* for $j=1, \dots, m$. Let us define g_j by the rank of $x_{(r)}$ relative to the multiple survival times specified by $X_{N+1} \in I_{j_1}, \dots, X_{N+k} \in I_{j_k}$, which is also useful to develop a computational formula for predictive probabilities of several new patients. It follows that

$$\begin{aligned} g_j &= \sum_{i=1}^k I_{(x_{(i)}, \infty)}(x_{(r)}) \\ &= \sum_{i=1}^k \{1 - I_{(0, x_{(i)})}(x_{(r)})\} \\ &= k - \sum_{i=1}^k I_{(0, x_{(i)})}(r_j) \end{aligned}$$

where $I(\cdot)$ is an indicator function.

Let $k=1, j_i=i$, in the expression of g_j to derive a computational formula for $Pr\{X_{N+1} \in I_i | \underline{x}, \text{PCI}\}$. The g_j is just the rank of $x_{(r)}$ relative to the survival time specified by $X_{N+1} \in I_i$. It follows that

$$g_j = 1 - I_{(0, i]}(r_j) = \begin{cases} 0 & \text{if } r_j \leq i \\ 1 & \text{otherwise.} \end{cases} \quad (4)$$

Noting that the rank of $x_{(r_j)}$ relative to $x_{(1)}, \dots, x_{(n)}$ is r_j , we observe $r_j^* = r_j + g_j$ for $j = 1, \dots, m$. Using $r_j^* = r_j + g_j$ and the equation,

$$Pr\{X_{N+1} \in I_i, \text{PCI} \mid \underline{x}\} = Pr\{X_{N+1} \in I_i \mid \underline{x}\} \cdot \{\text{PCI} \mid \underline{x}, X_{N+1} \in I_i\},$$

we can find a recursive formula in the following theorem.

Theorem 1. Let $P(i)$ denote $Pr\{X_{N+1} \in I_i \mid \underline{x}, \text{PCI}\}$. Under the three assumptions in Section 1, it follows that

$$P(0) = \frac{1}{n+m+1} \prod_{j:r_j=0} \left(1 + \frac{1}{n+m+1-j-r_j}\right)$$

and

$$P(i) = P(i-1) \prod_{j:r_j=i} \left(1 + \frac{1}{n+m+1-j-r_j}\right), \quad i = 1, \dots, n$$

where r_j is the rank of $u_{(j)}$ relative to $x_{(1)}, \dots, x_{(n)}$ for $j = 1, \dots, m$.

Proof. Using (1), (2), (3), and (4), we can prove that

$$\begin{aligned} P(i) &= Pr\{X_{N+1} \in I_i \mid \underline{x}, \text{PCI}\} \\ &= \frac{1}{n+1} \prod_{j=1}^m \left\{ \left(\frac{n+m+2-j-r_j^*}{n+m+2-j} \right) \middle/ \left(\frac{n+m+1-j-r_j}{n+m+1-j} \right) \right\} \\ &= \frac{1}{n+m+1} \prod_{j=1}^m \left(\frac{n+m+2-j-r_j-g_j}{n+m+1-j-r_j} \right) \\ &= \frac{1}{n+m+1} \prod_{j:r_j \leq i} \left(1 + \frac{1}{n+m+1-j-r_j} \right). \quad \blacksquare \end{aligned}$$

3. Predictive probabilities for several new patients

In some clinical trials, a group of new patients will be given common treatments. In this situation we are interested in computing the predictive probabilities for a number of new patients given the treatment. Suppose we have a_i new patients in the interval I_{j_i} for

$i = 1, \dots, l$. Without loss of generality we can assume $0 \leq j_1 \leq \dots \leq j_l \leq n$. Then the following constraints hold :

$$1 \leq l \leq n+1, \quad 1 \leq a_i \text{ for } i = 1, \dots, l \text{ and } \sum_{i=1}^l a_i = k.$$

Let A_i denote $\sum_{j=1}^i a_j$ for $i = 1, \dots, l$ and $A_0 = 0$. Define the event $j_i^{(a)}$ as

$$\{ X_{N+A_{i-1}+1} \in I_{j_i}, \dots, X_{N+A_{i-1}+a_i} \in I_{j_i} \}$$

for $i = 1, \dots, l$. Then the even $j_i^{(a)}$ implies that the a_i new patients belong to the interval I_{j_i} . For l intervals, let $\underline{j}^{(a)}$ denote $(j_1^{(a)}, \dots, j_l^{(a)})$.

Our goal is to evaluate $Pr\{ \underline{j}^{(a)} | \text{PCI}, \underline{x} \}$ which is the predictive probabilities that the i th interval has a_i new patients respectively for $i = 1, \dots, l$. Extending Theorem 1 into the case for several new patients, we obtain the following theorem to compute $Pr\{ \underline{j}^{(a)} | \text{PCI}, \underline{x} \}$.

Theorem 2. Under the three assumptions in Section 1,

$$Pr\{ \underline{j}^{(a)} | \text{PCI}, \underline{x} \} = \frac{\prod_{i=1}^l a_i!}{\prod_{i=1}^k (N+i)} \prod_{i=1}^m \left(1 + \frac{k - g_i}{N+1 - i - r_i} \right)$$

where g_i is the rank of $x_{(r_i)}$ relative to the survival times specified by $\underline{j}^{(a)}$, i.e.,

$$g_i = \sum_{t: j_t \leq r_i} a_t.$$

Proof. Since $Pr\{ \underline{j}^{(a)} | \text{PCI}, \underline{x} \} = \frac{Pr\{ \underline{j}^{(a)} | \underline{x} \} \cdot Pr\{ \text{PCI} | \underline{j}^{(a)}, \underline{x} \}}{Pr\{ \text{PCI} | \underline{x} \}}$, it suffices to find the

three probabilities on the right hand side.

It is not difficult to show

$$Pr\{j^{(a)} | \underline{x}\} = \frac{a_1! \cdots a_l!}{\prod_{i=1}^k (N+i)}$$

by using Hill(1968, p.686).

By Lemma 1,

$$Pr\{PCI | \underline{x}\} = \left(1 - \frac{r_m}{n+1}\right) \cdots \left(1 - \frac{r_1}{n+m}\right)$$

and

$$Pr\{j^{(a)} | PCI, \underline{x}\} = \left(1 - \frac{r'_m}{n+k+1}\right) \cdots \left(1 - \frac{r'_1}{n+k+m}\right)$$

where r_i is the rank of $u_{(i)}$ relative to $x_{(1)}, \dots, x_{(n)}$, and r'_i is the rank of $x_{(r_i)}$ relative to $x_{(1)}, \dots, x_{(n)}$ and the survival times specified by $j^{(a)}$. It is obvious that r_i is the rank of $x_{(r_i)}$ relative $x_{(1)}, \dots, x_{(n)}$. Let us define g_i as the rank of $x_{(r_i)}$ relative to the survival times specified by $j^{(a)}$. Then $r'_i = r_i + g_i$.

Hence we get

$$\begin{aligned} Pr\{j^{(a)} | PCI, \underline{x}\} &= \frac{Pr\{j^{(a)} | \underline{x}\} \cdot Pr\{PCI | j^{(a)}, \underline{x}\}}{Pr\{PCI | \underline{x}\}} \\ &= \frac{a_1! \cdots a_l!}{\prod_{i=1}^k (N+i)} \frac{\left(\frac{n+k+1-r_m-g_m}{n+k+1}\right) \cdots \left(\frac{n+k+m-r_1-g_1}{n+k+m}\right)}{\left(\frac{n+1-r_m}{n+1} \cdots \frac{n+m-r_1}{n+m}\right)} \\ &= \frac{a_1! \cdots a_l!}{\prod_{i=1}^k (N+i)} \cdot \prod_{i=1}^m \left(1 + \frac{k-g_i}{N+1-i-r_i}\right) \end{aligned}$$

This proves the theorem. ■

It is not difficult to show that Theorem 1 is a special case of Theorem 2 when $k=1$, $l=1$, and $a_1=1$.

In Genest and Kalbfleisch's (GK) comment on BH method, they prepare a sequential approach that leads to the predictive probability for G new patients. They derive a formula for

predictive probability for two new patients such that

$$\begin{aligned} &Pr\{Z_1 \in I_i, Z_2 \in I_j \mid \underline{x}, \text{PCI}\} \\ &= \left[\prod_{l=0}^{i-1} \left(1 - \frac{2}{n_{l+2}}\right) \prod_{l=i}^{j-1} \left(1 - \frac{1}{n_{l+1}}\right) \right] \left(\frac{1 + \delta_{ij}}{(n_i + 2)(N_j + 1)} \right) \end{aligned}$$

for $i \leq j$, where δ_{ij} is the Kronecker delta, and n_l is the number of patients at risk at t_{l+1} . In other words, n_l is defined as the number of patients known to be alive at t_{l+1} . Continuing in this way, they give a formula for G new patients, which turns out to be wrong. So we want to find a correct version of the predictive probability for G new patients.

The result given by GK for G new patients is

$$\begin{aligned} &P\{G_0, \dots, G_n \mid \underline{x}, \text{PCI}\} \\ &= G! \prod_{l=0}^{n-1} \left\{ 1 - \frac{G_{(l+1)}}{n_l + G_{(l+1)}} \right\} \Bigg| (n_l + G_{(l)})_{(G)} \end{aligned} \tag{5}$$

where G_i is the number of new patients in i th interval, $G_{(i)} = G_i + \dots + G_n$, $G_{(0)} = G$, and $n_{(k)} = n(n-1)\dots(n-k+1)$ for $k \geq 1$ with $n_{(0)} = 1$. GK mention that if there is no censoring, (5) reduces to $\frac{G! n!}{(n+G)!}$. But we can verify that it reduces to $\frac{G! n! G_n!}{(n+G)!}$ when there is no censoring. Therefore we suppose the correct formula of (5)

$$Pr\{G_0, \dots, G_n \mid \underline{x}, \text{PCI}\} = \frac{G!}{G_n!} \prod_{l=0}^{n-1} \left\{ 1 - \frac{G_{(l+1)}}{n_l + G_{(l+1)}} \right\} \Bigg| (n_l + G_{(l)})_{(G)} \tag{6}$$

To prove (6), let us define Z_j to be the death time of the j th new patient. For simplicity, let us assume a specified order $Z_G < \dots < Z_1$. Then we can denote the predictive probability with the special order by $Pr\{(G_0, \dots, G_n) \mid \underline{x}, \text{PCI}\}$ where $(G_0, \dots, G_n) = \{Z_1 \in I_n, \dots, Z_{G_n} \in I_0, \dots, Z_{G-G_0+1} \in I_0, \dots, Z_G \in I_0, Z_G < \dots < Z_1\}$. It follows that

$$\begin{aligned}
 &Pr\{G_0, \dots, G_n | \underline{x}, PCI\} \\
 &= \binom{G}{G_0 \dots G_n} Pr\{Z_1 \in I_n, \dots, Z_{G_n} \in I_n, \dots, Z_{G-G_0+1} \in I_0, \dots, Z_G \in I_0 | \underline{x}, PCI\} \\
 &= \binom{G}{G_0 \dots G_n} (G_0! \dots G_n!) Pr\{(G_0, \dots, G_n) | \underline{x}, PCI\}
 \end{aligned}$$

If $G_n > 0$, then

$$\begin{aligned}
 &Pr\{(G_0, \dots, G_n) | \underline{x}, PCI\} \\
 &= \prod_{i=0}^n Pr\{(G_{n-i}, \dots, G_n) | \underline{x}, PCI, (G_{n-i+1}, G_n)\} \tag{7}
 \end{aligned}$$

where $(G_{n+1}, G_n) = \phi$.

We will derive a computational formula for (7). It suffices to show how to find the first and the second components of the product of (7). Then we can continue in the same way to find the predictive probability of (7). The first component can be decomposed as follows:

$$\begin{aligned}
 &Pr\{(G_n) | \underline{x}, PCI\} \\
 &= Pr\{Z_1 \in I_n, \dots, Z_{G_n} \in I_n, Z_G < \dots < Z_1 | \underline{x}, PCI\} \\
 &= Pr\{x_{(n)} < Z_1 < x_{(n+1)} | \underline{x}, PCI\} \\
 &\quad Pr\{x_{(n)} < Z_2 < Z_1 | x_{(n)} < Z_1 < x_{(n+1)}, \underline{x}, PCI\} \\
 &\quad \vdots \\
 &Pr\{x_{(n)} < Z_{G_n} < Z_{G_n-1} | x_{(n)} < Z_{G_n-1} < \dots < Z_1 < x_{(n+1)}, \underline{x}, PCI\}
 \end{aligned}$$

where $x_{(n+1)} = \infty$.

Now we need the following theorem and corollary given by Hill(1968) to find the computational formula of (6).

Theorem 3. Suppose that $c(i)$ observations are censored in the interval I_i , and let $C(i) = \sum_{k=0}^i c(k)$ for $i=0, 1, \dots, n$. Then $C(i)$ is the total number of censored observations which are smaller than $x_{(i+1)}$. Let $\lambda(i) = 1/\{N - (i-1) - C(i)\}$ for $i=0, 1, \dots, n$. Then con-

ditional on PCI, $P(0) = \lambda(0)$ and for $i = 0, 1, \dots, n$

$$P(i+1) = \{1 - \lambda(0)\} \cdots \{1 - \lambda(i)\} \lambda(i+1)$$

Proof. See Hill (1988).

From the above theorem, a simple computational formula is obtained in the corollary.

Corollary. Let $n_i = N - i - C(i)$ for $i = 0, 1, \dots, n$. Then it follows that

$$P(i) = \frac{1}{n_1 + 1} \prod_{j=0}^{i-1} \left(1 - \frac{1}{n_j + 1} \right)$$

where an empty product is interpreted as an unity.

By the above corollary, for example the second probability of (8) is just $P(n)$ with $(n+1)$ death times instead of n death times which is

$$P(n) = \frac{1}{(n_n + 1) + 1} \prod_{j=0}^{n-1} \left(1 - \frac{1}{(n_j + 1) + 1} \right).$$

Similarly, it is straightforward to compute the remaining probabilities of (8). Thus

$$Pr\{(G_n) | \underline{x}, \text{PCI}\} = \frac{1}{(n_n + G_{(n)})_{(G_n)}} \prod_{j=0}^{n-1} \left(1 - \frac{G_n}{n_j + G_{(n)}} \right).$$

In similar way, the second probability of (7)

$$Pr\{(G_{n-1}, G_n) | \underline{x}, \text{PCI}, (G_n)\} = \frac{1}{(n_{n-1} + G_{(n-1)})_{(G_{n-1})}} \prod_{j=0}^{n-2} \left(1 - \frac{G_{n-1}}{n_j + G_{(n-1)}} \right).$$

Continuing this process, we are at the position that we obtain the result:

$$\begin{aligned} Pr\{(G_0, \dots, G_n) | \underline{x}, \text{PCI}\} &= \prod_{l=0}^n \left\{ \frac{1}{(n_l + G_{(l)})_{(G_l)}} \cdot \prod_{j=0}^{l-1} \left(1 - \frac{G_l}{n_j + G_{(l)}} \right) \right\} \\ &= \frac{1}{G_n!} \prod_{l=0}^{n-1} \left\{ \left(1 - \frac{G_{(l+1)}}{n_l + G_{(l+1)}} \right) \right\} (n_l + G_{(l)})_{(G_l)}. \end{aligned}$$

Finally we find the correct result for G new patients

$$\begin{aligned} & Pr\{G_0, \dots, G_n | \underline{x}, PCI\} \\ &= \frac{G!}{G_n!} \prod_{l=0}^{n-1} \left\{ \left(1 - \frac{G_{(l+1)}}{n_l + G_{(l+1)}} \right) \binom{n_l + G_{(l)}}{G_{(l)}} \right\}. \end{aligned}$$

We conclude this section to have an example of the cases in which we can use the predictive probabilities to compare the expected effects of treatments.

Example. (E.T. Lee, (1980)).

In an experiment comparing two treatments for solid tumor, six mice are assigned to treatment A and six to treatment B . The experiment is terminated after 30 days. The following survival times in days are recorded.

Treatment A : 8, 8, 10, 12, 12, 13

Treatment B : 9, 12, 15, 20, 30+, 30+

We compute the predictive probabilities for each group so that we are able to compare the expected behavior of a new mouse given treatment A against that of a mouse given treatment B . For treatment A , the estimate of the posterior predictive distribution of the death time of a new mouse is

$$\hat{P}(0) = \dots = \hat{P}(7) = \frac{1}{7}$$

For treatment B ,

$$\hat{P}(0) = \dots = \hat{P}(7) = \frac{1}{7}$$

Figure 1 presents a graph of the expected survival function for the future death time of a new mouse based on the above predictive probabilities. For treatment A , the expected survival function is

$$\hat{S}(8) = \frac{6}{7} \quad \hat{S}(8.1) = \frac{5}{7} \quad \hat{S}(10) = \frac{4}{7} \quad \hat{S}(12) = \frac{3}{7} \quad \hat{S}(12.1) = \frac{2}{7} \quad \hat{S}(13) = \frac{1}{7}.$$

For treatment B , the expected survival function is

$$\hat{S}(9) = \frac{6}{7} \quad \hat{S}(12) = \frac{5}{7} \quad \hat{S}(15) = \frac{4}{7} \quad \hat{S}(20) = \frac{3}{7} .$$

Note that ties have been broken by adding $\epsilon = .10$. In this study, we assume continuity of the death time process. However we cannot avoid to collect tied observations because we cannot observe the exact time of a death, but count only the number of deaths in certain period. To apply our results for tied observations, we break them arbitrarily until ties are broken. If ties are not to prevalent, the predictive probabilities assigned to intervals which are formed by breaking ties are known not to be fatal.

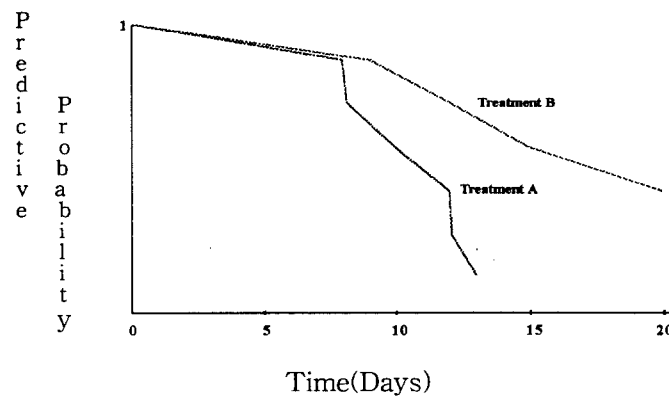


Figure 1. Example from Lee(1980)

We can find the difference in Figure 1 to be striking. The most crucial difference is to be seen after 12 days. That is, $Pr(X_7 \geq 12.1) = \frac{2}{7}$ for treatment *A* and $Pr(X_7 \geq 12) = \frac{5}{7}$ for treatment *B*. The predictive probability that a new mice given treatment *A* will survive more than 12 days is more than two times larger than the predictive probability that a new mice given treatment *B* will survive more than 12 days. Figure 1 shows that a new mice is unlikely to survive more than 15 days, being given Treatment *A*.

4. Conclusion

BH's procedure originates from the posterior distribution of percentiles suggested by Hill(1968). It requires a tremendous amount of computation to use their procedure. The referees of their paper suggest the simple method which enables us to avoid the huge work required to use their procedure.

We have derived the new method, which is eventually equivalent to the method suggested by the referees of BH's paper. The principle of the new method is then extended to derive the computational formula for the predictive probabilities for several new patients.

Genest and Kalbfleisch(1988) introduce the sequential approach to predict the death times of several new patients. But we find it to be incorrect after we check it when there is no censoring. We derive the correct formula in this paper.

What we discuss here about future patients is about the interval probabilities not the distributions of the death times of new patients. Geisser(1984) gives the entire predictive distribution in each interval for the exponential case.

The development of computable algorithms to obtain the expectations and the variances of the fractions of new patients that fall into some intervals is one of the unsolved problems. The regression analysis might be applied to predict the death times of a few future patients. The efficiency of the method presented here against the method in parametric cases is also an open problem.

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