

# A Review of Time-to-Event Data Methods

---

Thomas Braun

Department of Biostatistics  
University of Michigan School of Public Health  
BIOSTAT 699: Design and Analysis of Biostatistical Investigations

---



# Introduction to Survival Data

- Commonly used names:
  - Survival data
  - Censored data
  - Time-to-event data
  - Failure time data
- Numerous applications in biomedicine as well as engineering
- Outcome of interest:  $T$ , which is the span of time from entry into a study until the occurrence of some event (death, disease recurrence, implant failure, stroke, etc.)

# Introduction to Survival Data

- $T$  is a continuous random variable, but is restricted to be positive
  - Assuming normality of  $T$  seems implausible
  - Inference about means seems less useful
- More often we are interested in (cumulative) probabilities, i.e.
  - what is the probability that a cancer patient relapses within one year of chemotherapy?
  - does this probability vary by the stage of cancer?

# Introduction to Survival Data

- In order to compute cumulative probabilities, we need to estimate the entire distribution of  $T$
- Parametric approaches:
  - Exponential
  - Weibull
  - Log-normal
- Non-parametric approaches:
  - No assumed form for distribution of  $T$
  - Most common approach

# Introduction to Survival Data

- There are five functions that characterize a survival distribution:

(1) Cumulative distribution function (CDF)

$$\begin{aligned} F(t) &= \Pr(T \leq t) \\ &= \text{probability that event occurs by time } t \end{aligned}$$

(2) Probability density function (PDF)

$$\begin{aligned} f(t) &= \lim_{\Delta \rightarrow 0} \frac{F(t + \Delta) - F(t)}{\Delta} \\ &= \text{instantaneous probability that event} \\ &\quad \text{occurs at time } t \end{aligned}$$

# Introduction to Survival Data

## (3) Survival function

$$\begin{aligned} S(t) &= \Pr(T > t) \\ &= 1 - \Pr(T \leq t) \\ &= 1 - F(t) \\ &= \text{probability of no event by time } t \end{aligned}$$

## (4) Hazard function (force of mortality)

$$\begin{aligned} \lambda(t) &= \lim_{\Delta \rightarrow 0} \frac{\Pr(t \leq T < t + \Delta \mid T \geq t)}{\Delta} \\ &= f(t)/S(t) \\ &= \text{instantaneous event rate at time } t \\ &\quad \text{given event-free up to time } t \end{aligned}$$

# Introduction to Survival Data

## (5) Cumulative hazard function

$$\Lambda(t) = \int_0^t \lambda(s) ds$$

- If we know any one of  $f(t)$ ,  $F(t)$ ,  $S(t)$ ,  $\lambda(t)$  or  $\Lambda(t)$ , we know the other four
- We are most interested in  $S(t)$ , which tells us the probability that a subject makes it to time  $t$  **without** the event

# Introduction to Survival Data

- An important relationship is

$$\begin{aligned}-\frac{d}{dt}\log\{S(t)\} &= \frac{dS(t)/dt}{S(t)} \\ &= \frac{f(t)}{S(t)} \\ &= \lambda(t)\end{aligned}$$

so that

$$\begin{aligned}\log\{S(t)\} &= -\int_0^t \lambda(u)du \\ S(t) &= \exp\{-\Lambda(u)du\}\end{aligned}$$

- Thus, regression methods for survival data focus upon modeling  $\lambda(t)$  as a function of covariates and then getting  $S(t)$  indirectly from  $\lambda(t)$



# Introduction to Survival Data

- The major challenge with time-to-event outcomes is that many subjects will be not be followed long enough to observe when the outcome occurred
  - We have missing data!
  - We refer to missing outcomes as being (right) **censored**
  - For these subjects, we do not have an event time, but have an amount of time followed without the event
- With censoring, we make a crucial assumption that censoring is independent of the times-to-event, conditional on covariates
  - In other words, censored individuals are representative of individuals still under observation at the same time
  - Non-independent censoring can lead to severe biases, but it is difficult in most situations to gauge the magnitude or direction of the biases
    - We need to model the censoring distribution - do we have the right model?

# Estimating the Survival Function

$$S(t)$$

# Parametric Approach

- Each subject  $i = 1, 2, \dots, n$  has **two** data points:

$$\begin{aligned} t_i &= \text{amount of time followed} \\ \delta_i &= \begin{cases} 0 & \text{if no event at } t_i \text{ (censored)} \\ 1 & \text{if event at } t_i \text{ (not censored)} \end{cases} \end{aligned}$$

- Suppose we assume event times have a Weibull distribution:

$$\begin{aligned} \lambda(t; \theta, \alpha) &= \alpha \theta (\theta t)^{\alpha-1} \\ S(t; \theta, \alpha) &= \exp\{-(\theta t)^\alpha\} \end{aligned}$$

- We can estimate  $\theta$  and  $\alpha$  via maximum likelihood; our likelihood is:

$$L(\theta, \alpha | t_1, \dots, t_n; \delta_1, \dots, \delta_n) = \prod_i \{f(t_i; \theta, \alpha)^{\delta_i} \times S(t_i; \theta, \alpha)^{1-\delta_i}\}$$

# Non-Parametric Approach

- To motivate this approach, we start with a simple set of data:
  - We have four subjects whose cancer returned 10, 13, 14, and 23 weeks, respectively after treatment
  - We have one subject who was cancer-free at 14 weeks and then was lost to follow-up
- The first step is to identify and order the *unique* times among the subjects with an event
  - For our example, there are  $J = 4$  values:  $t_1 = 10$ ,  $t_2 = 13$ ,  $t_3 = 14$ , and  $t_4 = 23$
  - These times define  $J = 4$  non-overlapping intervals:
$$[10, 13), [13, 14), [14, 23), [23, \infty]$$
  - For each interval, we compute  $p_j$ , the probability of surviving through the entire interval, given being in the study (at risk) at the beginning at the interval

## Kaplan-Meier Estimate of $S(t)$

- For the  $j^{\text{th}}$  interval,  $j = 1, 2, \dots, J$ , we have:

$$\begin{aligned} p_j &= 1 - \frac{\text{\# of events at } t_j}{\text{\# of subjects at risk just prior to } t_j} \\ &= 1 - \frac{d_j}{n_j} \\ &= \frac{n_j - d_j}{n_j} \\ &= \frac{s_j}{n_j} \end{aligned}$$

- Note that if any subject is censored at the same time when an event occurs, we assume the censoring occurs *after* the event

## Kaplan-Meier Estimate of $S(t)$

- We assume that each of these intervals is independent of the others
- Thus, the probability of surviving to the end of interval  $j^*$  is simply the product of the probability of all intervals prior to and including interval  $j^*$
- For example:

$$\begin{aligned} \text{Prob}(\text{surviving to end of third interval}) &= \\ &\text{Prob}(\text{surviving first interval}) \times \\ &\text{Prob}(\text{surviving second interval}) \times \\ &\text{Prob}(\text{surviving third interval}) \end{aligned}$$

## Kaplan-Meier Estimate of $S(t)$

- This concept defines the (Kaplan-Meier) KM estimate of  $S(t)$ :

$$\hat{S}(t) = \prod_{j:t_j \leq t} \left(1 - \frac{d_j}{n_j}\right) = \prod_{j:t_j \leq t} \frac{n_j - d_j}{n_j} = \prod_{j:t_j \leq t} \frac{s_j}{n_j}$$

- In words, the Kaplan-Meier estimate of survival to time  $t$  is the product of surviving each interval that occurs before or includes  $t$
- For our example, the estimated survival to  $t = 20$  would be the product of surviving the intervals  $[10, 13)$ ,  $[13, 14)$ , and  $[14, 23)$

## Kaplan-Meier Estimate of $S(t)$

- For our example, we rewrite the data as:

Index	Event Time	Number at Risk	Number of Events	Number of Non-Events
$j$	$t_j$	$n_j$	$d_j$	$s_j$
1	10	5	1	4
2	13	4	1	3
3	14	3	1	2
4	23	1	1	0

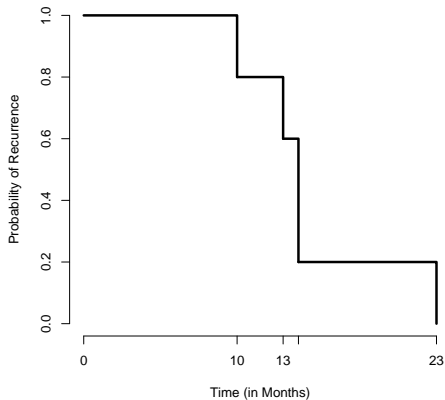
- Using this table, we can compute the KM estimate:

For $t$ in	$\hat{S}(t)$
$[0, 10)$	1
$[10, 13)$	$1 \times 4/5 = 0.8$
$[13, 14)$	$1 \times 4/5 \times 3/4 = 0.6$
$[14, 23)$	$1 \times 4/5 \times 3/4 \times 2/3 = 0.4$
$[23, \infty)$	$1 \times 4/5 \times 3/4 \times 2/3 \times 0/1 = 0.0$



# Kaplan-Meier Plot

- These estimates of survival are displayed in a Kaplan-Meier plot:



## Inference with KM Estimates

- The variance for  $\widehat{S}(t)$  was derived by Greenwood:

$$\widehat{Var}\{\widehat{S}(t)\} = \widehat{S}(t)^2 \left\{ \sum_{t_j: t_j \leq t} \frac{d_j}{n_j(n_j - d_j)} \right\}$$

- However, the standard 95% CI for  $S(t)$

$$\widehat{S}(t) \pm 1.96 \sqrt{\widehat{Var}\{\widehat{S}(t)\}}$$

is not restricted to have values inside  $[0, 1]$ .

# Inference with KM Estimates

- An alternative approach:
  - Transform  $S(t)$  to  $\log[-\log\{S(t)\}]$ , which ranges over  $(-\infty, \infty)$
  - Compute CI for  $\log[-\log\{S(t)\}]$
  - Transform back to find CI for  $S(t)$ 
    - This confidence interval will be guaranteed to lie in  $[0, 1]$
- This is similar to what we do when finding a confidence interval for an odds ratio or rate ratio:
  - We first found a CI for the log-odds and then transformed back

## Inference with KM Estimates

- The variance of  $\log[-\log\{\hat{S}(t)\}]$  is

$$\widehat{Var} \left( \log[-\log\{\hat{S}(t)\}] \right) = \frac{1}{\log \hat{S}(t)} \left\{ \sum_{t_j: t_j \leq t} \frac{d_j}{n_j(n_j - d_j)} \right\}$$

- A 95% CI for  $\log[-\log S(t)]$  is

$$\log[-\log\{\hat{S}(t)\}] \pm 1.96 \sqrt{\widehat{Var} \left( \log[-\log\{\hat{S}(t)\}] \right)}$$

- Thus, a 95% CI for  $S(t)$  is

$$\hat{S}(t) \times \exp \left\{ \pm 1.96 \sqrt{\widehat{Var} \left( \log[-\log\{\hat{S}(t)\}] \right)} \right\}$$

# Inference with KM Estimates

- For the example, we have:

Time	$\hat{S}(t)$	$SE\{\hat{S}(t)\}$	95% Conf Int	
			Lower Bound	Upper Bound
10	0.80	0.18	0.52	1.00
13	0.60	0.22	0.29	1.00
14	0.40	0.22	0.14	1.00
23	0.00	n/a	n/a	n/a

# Estimating the Hazard Function

- Recall our definition of the hazard:

$$\lambda(t) = \lim_{\Delta \rightarrow 0} \frac{1}{\Delta} \Pr(t \leq T \leq t + \Delta \mid T \geq t).$$

- For  $t$  in  $[t_j, t_{j+1})$ , we estimate  $\lambda(t)$  as

$$\hat{\lambda}(t) = \frac{d_j/n_j}{t_{j+1} - t_j},$$

which takes the probability of an event in the whole interval  $(d_j/n_j)$  and derives the probability of an event per unit time

# Estimating the Hazard Function

- Using our data:

Index	Event Time	Number at Risk	Number of Events	Number of Non-Events
$j$	$t_j$	$n_j$	$d_j$	$s_j$
1	10	5	1	4
2	13	4	1	3
3	14	3	1	2
4	23	1	1	0

we estimate the hazard to be:

For $t$ in	$\hat{\lambda}(t)$
$[0, 10)$	0
$[10, 13)$	$\frac{1/5}{13-10} = 1/15$
$[13, 14)$	$\frac{1/4}{14-13} = 1/4$
$[14, 23)$	$\frac{1/3}{23-14} = 1/27$
$[23, \infty)$	n/a

# Estimating the Cumulative Hazard Function

- Recall our definition of the CHF:

$$\Lambda(t) = \int_0^t \lambda(s) ds$$

- Thus, we define our estimate of  $\Lambda(t)$  to be

$$\begin{aligned}\hat{\Lambda}(t) &= \sum_{t_j: t_j \leq t} \hat{\lambda}(t_j)(t_{j+1} - t_j) \\ &= \sum_{t_j: t_j \leq t} \frac{d_j}{n_j(t_{j+1} - t_j)}(t_{j+1} - t_j) \\ &= \sum_{t_j: t_j \leq t} \frac{d_j}{n_j}\end{aligned}$$

This is known as the **Nelson-Aalen** cumulative hazard estimator



## Using Nelson-Aalen to Estimate $S(t)$

- Recall that  $S(t) = e^{-\Lambda(t)}$
- Using the Nelson-Aalen estimate of  $\Lambda(t)$ , we have another estimate (Breslow) of survival:

$$\hat{S}(t) = \exp \left\{ - \sum_{t_j: t_j \leq t} \frac{d_j}{n_j} \right\}$$

- Compare this to the Kaplan-Meier estimate:

$$\hat{S}(t) = \prod_{j: t_j \leq t} \frac{s_j}{n_j} = \prod_{j: t_j \leq t} \left( 1 - \frac{d_j}{n_j} \right)$$

## Using Nelson-Aalen to Estimate $S(t)$

- Both of these estimates are quite similar because

$$\exp(-x) \approx (1 - x)$$

for “small” values of  $x$

- Thus we have

$$\begin{aligned}\widehat{S}(t) &= \exp \left\{ - \sum_{t_j: t_j \leq t} \frac{d_j}{n_j} \right\} = \prod_{j: t_j \leq t} \exp \left\{ - \frac{d_j}{n_j} \right\} \\ &\approx \prod_{j: t_j \leq t} \left( 1 - \frac{d_j}{n_j} \right) = \prod_{j: t_j \leq t} \frac{s_j}{n_j}\end{aligned}$$

# Comparing Survival Functions

# Comparing Two Survival Functions

- Suppose we have follow-up data from two groups
- Group 1 consists of  $n_1$  subjects; Group 2 consists of  $n_2$  subjects
- For subject  $i = 1, \dots, n_1$  in Group 1, we have:

$Y_i$  = length of follow-up for subject  $i$

$$\delta_i = \begin{cases} 1 & \text{if had event at } Y_i \\ 0 & \text{if censored at } Y_i \end{cases}$$

# Comparing Two Survival Functions

- For subject  $j = 1, \dots, n_2$  in Group 2, we have:

$$Y_j = \text{length of follow-up for subject } j$$

$$\delta_j = \begin{cases} 1 & \text{if had event at } Y_j \\ 0 & \text{if censored at } Y_j \end{cases}$$

- Our goal is to compare  $S_1(t)$  to  $S_2(t)$  and to formally test

$$H_0 : S_1(t) = S_2(t)$$

versus

$$H_a : S_1(t) \neq S_2(t)$$

## $S_1(t)$ and $S_2(t)$ at a Specific $t$

- We are only interested in comparing survival probabilities at a single time (e.g.  $t = 5$  years)
- We look at  $\hat{S}_1(t) - \hat{S}_2(t)$  at that single time, divide by a standard error estimate and compare to 1.96
- This approach does not allow us to compare whether the two *entire* survival curves are the same

## Comparing $S_1(t)$ and $S_2(t)$ at Every $t$

- Recall that if  $S_1(t) \neq S_2(t)$ , then  $\Lambda_1(t) \neq \Lambda_2(t)$ , which implies  $\lambda_1(t) \neq \lambda_2(t)$ 
  - Comparing survival functions is the same as comparing hazard functions
- Thus, our hypotheses are equivalently

$$H_0 : \lambda_1(t) = \lambda_2(t)$$

versus

$$H_a : \lambda_1(t) \neq \lambda_2(t)$$

- This alternative hypothesis is too vague to be tested

# Proportional Hazards Model

- We choose to use the specific alternative hypothesis:

$$H_a : \lambda_1(t) = c\lambda_2(t),$$

which is known as the assumption of **proportional hazards**

- The alternative hypothesis states that the two hazard functions are not equal and that

$$\frac{\lambda_1(t)}{\lambda_2(t)} \equiv c$$

at every time  $t$ , i.e. the hazard functions of the two groups are proportional to each other



# Proportional Hazards Model

- Thus, we can rewrite our hypotheses again as

$$H_0 : c = 1$$

versus

$$H_a : c \neq 1,$$

where  $c$  is the ratio of the two hazards (**hazard ratio**)

- Notice the similarity between these hypotheses and those used with binary outcomes

$$H_0 : OR = 1$$

versus

$$H_a : OR \neq 1,$$

where OR is a ratio of odds rather than hazards

# Proportional Hazards Model

- Note that the assumption of proportional hazards does not mean the survival functions are proportional to each other, i.e.

$$\lambda_1(t) = c\lambda_2(t) \Rightarrow S_1(t) = \{S_2(t)\}^c$$

- For example, if one hazard is 50% of the other hazard, one survival function is the square root of the other survival function
- The important property of proportional hazards is that the resulting survival functions *never* intersect each other, i.e. one survival curve is *always* higher than the other.

# Two-sample Log-rank Test

- To test a difference in hazard (survival) functions, we use a **log-rank** test
- The construction of the test statistic is based upon a series of  $2 \times 2$  tables like those used in a chi-squared test of association
- We first pool both groups together, then identify and order the unique event times (those of non-censored subjects)
  - We label these times  $t_1 < t_2 < \dots < t_J$

# Two-sample Log-rank Test

- At each time  $t_j$  ( $j = 1, \dots, J$ ), we create a  $2 \times 2$  table

	Group		
	1	2	
# events at $t_j$	$d_{1j}$	$d_{2j}$	$d_j$
# at risk beyond $t_j$	$s_{1j}$	$s_{2j}$	$s_j$
Total	$n_{1j}$	$n_{2j}$	$n_j$

- If the event rate (hazard) is the same in the two groups:
  - The total number of events at  $t_j$  ( $d_j$ ) should be divided equally among the two groups in relation to the number at risk at  $t_j$  in each group ( $n_{1j}$  and  $n_{2j}$ )
    - Allocate  $d_j(n_{1j}/n_j)$  events to Group 1
    - Allocate  $d_j(n_{2j}/n_j)$  events to Group 2

# Two-sample Log-rank Test

- We then focus upon one of the groups (we'll use Group 1) and express the values in terms we used with the chi-squared test of association:

- Observed events in Group 1 at  $t_j$ :

$$O_j = d_{1j}$$

- Expected events in Group 1 if  $H_0$  is true:

$$E_j = \frac{n_{1j}d_j}{n_j}$$

- The squared difference  $(O_j - E_j)^2$  tells us how valid the null hypothesis is at  $t_j$ 
  - The bigger the difference, the more likely  $H_0$  is false

## Two-sample Log-rank Test

- Forming the typical Pearson statistic for  $t_j$ :

$$\frac{(O_j - E_j)^2}{E_j},$$

we combine the results for all event times  $t_1 < t_2 < \dots < t_J$  into a single statistic:

$$\chi_L^2 = \sum_{j=1}^J \frac{(O_j - E_j)^2}{E_j}$$

- However, we have one problem:
  - This formula assumes the number of events at each  $t_j$  are independent of each other (i.e. the  $2 \times 2$  tables are independent)

## Two-sample Log-rank Test

- Although slight, there is some dependence between the  $2 \times 2$  tables, as the number of events at one time point restricts how many events can happen later
  - Thus, the statistic just shown is only an *approximation* for the actual statistic
- The log-rank statistic used by all statistical packages is

$$\chi_L^2 = \frac{[\sum_{j=1}^J (O_j - E_j)]^2}{\sum_{j=1}^J V_j},$$

where

$$V_j = \frac{n_{1j}n_{2j}d_js_j}{n_j^2(n_j - 1)}$$

## Two-sample Log-rank Test

- Under  $H_0$  (no difference in survival functions),  $\chi_L$  has approximately a chi-squared distribution with 1 df
  - Thus a value of  $\chi_L \geq 4$  is evidence to reject  $H_0$  (gives  $p$ -value less than 0.05)
- These concepts can be extended to comparisons of  $G$  groups ( $G > 2$ )
  - In general,  $\chi_L$  has a chi-squared distribution with  $(G - 1)$  df



## Two-sample Log-rank Test

- Suppose we have the following data:

Group 1	$Y$	4	10	15	16
	$\delta$	1	0	1	0
Group 2	$Y$	7	11	19	22
	$\delta$	1	0	0	1

- For this data, we have:

$$\begin{aligned}\sum_{j=1}^J (O_j - E_j) &= \left(1 - \frac{4 \times 1}{8}\right) + \left(0 - \frac{3 \times 1}{7}\right) \\ &\quad + \left(1 - \frac{2 \times 1}{4}\right) + \left(0 - \frac{0 \times 1}{1}\right) \\ &= 0.5 - 0.429 + 0.5 \\ &= 0.571\end{aligned}$$

## Two-sample Log-rank Test

- The denominator is computed as:

$$\begin{aligned}\sum_{j=1}^J V_j &= \frac{4 \times 4 \times 1 \times 7}{8 \times 8 \times 7} + \frac{3 \times 4 \times 1 \times 6}{7 \times 7 \times 6} + \frac{2 \times 2 \times 1 \times 3}{4 \times 4 \times 3} \\ &= 0.25 + 0.2449 + 0.25 \\ &= 0.7449\end{aligned}$$

- Therefore, we find:

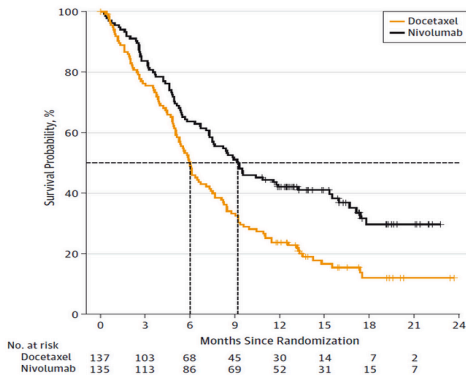
$$\chi_L^2 = \frac{[\sum_{j=1}^J (O_j - E_j)]^2}{\sum_{j=1}^J V_j} = \frac{0.571^2}{0.7449} = 0.438,$$

yielding a p-value of 0.51 based on a  $\chi_{(1)}^2$  distribution

# Visually Displaying Results

- This is an example of an excellent Kaplan-Meier plot:

Figure. Kaplan-Meier Curves of Overall Survival Found in Study CM017



The CM017 study is well described by Brahmer and colleagues.<sup>18</sup> Per the O'Brien-Fleming boundary,<sup>19</sup> the significance level for the interim overall survival analysis with 199 deaths was 2-sided  $P = .03$ .

# Assessing Proportional Hazards

- We can visually assess whether proportional hazards is a reasonable assumption
- If we plot  $\log\{-\log \hat{S}_1(t)\}$  and  $\log\{-\log \hat{S}_2(t)\}$  against  $\log(t)$  for each group and proportional hazards holds, the two lines should be roughly parallel to each other
- Why?

$$\begin{aligned}\lambda_1(t) = c\lambda_0(t) &\Rightarrow \Lambda_1(t) = c\Lambda_0(t) \\ &\Rightarrow -\log S_1(t) = c[-\log S_0(t)] \\ &\Rightarrow \log\{-\log S_1(t)\} \\ &\quad = \log c + \log\{-\log S_0(t)\}\end{aligned}$$

# Non-proportional Hazards

- If the hazards are not proportional, we use a weighted log-rank statistic:

(1) Wilcoxon Test

$$\chi^2_W = \frac{[\sum_{j=1}^J n_j(O_j - E_j)]^2}{\sum_{j=1}^J n_j^2 V_j}$$

- This test gives more weight to early event times (when  $n_j$  is big) and less weight to late event times (when  $n_j$  is small)

(2) Generalized Wilcoxon (GW) Test

$$\chi^2_{GW} = \frac{[\sum_{j=1}^J w_j(O_j - E_j)]^2}{\sum_{j=1}^J w_j^2 V_j}$$

- The weights can be chosen to emphasize a particular time or range of times and is most powerful under certain situations
- Note that if  $w_j = 1$  for all  $j$ , GW test reduces to the log-rank test

# Regression Models for Comparing Survival Functions

# Proportional Hazards Regression (Non-parametric)

- **Outcome variable:**  $(T_i, \delta_i)$  ( $i = 1, \dots, n$ ), where  $T_i$  is the observed survival time for the  $i$ th individual, and

$$\delta_i = \begin{cases} 1 & \text{event observed} \\ 0 & \text{event censored} \end{cases}$$

- **Covariates:**  $X_{1i}, X_{2i}, \dots, X_{pi}$  for the  $i$ th subject ( $i = 1, \dots, n$ )
- **Idea:** Model the hazard function of the event at a particular time  $t$  as a function of covariates

# Proportional Hazards Regression

- We use the typical regression model

$$\begin{aligned}\log \lambda(t) &= \log \lambda_0(t) + \beta_1 X_1 + \beta_2 X_2 + \cdots + \beta_p X_p \\ &= \log \lambda_0(t) + \sum_{j=1}^p \beta_j X_j\end{aligned}$$

- However, the model is more commonly written as

$$\begin{aligned}\lambda(t) &= \lambda_0(t) e^{\beta_1 X_1 + \beta_2 X_2 + \cdots + \beta_p X_p} \\ &= \lambda_0(t) e^{\sum_{j=1}^p \beta_j X_j}\end{aligned}$$

and is called a **Cox regression model**



# Proportional Hazards Regression

- In the Cox regression model  $\lambda(t) = \lambda_0(t)e^{\sum_{j=1}^p \beta_j X_j}$ :
  - $\lambda_0(t)$  is known as the **baseline hazard**, which measures the risk of an event for the reference group, i.e. subjects with all covariates equal to zero
  - We do not make any assumption on the actual functional form of  $\lambda_0(t)$
  - There is no intercept term  $\beta_0$  in the exponent
    - Our baseline hazard serves as our intercept (on the log scale)
  - The hazard ratio is  $\lambda(t)/\lambda_0(t) = \exp \left\{ \sum_{j=1}^p \beta_j X_j \right\}$ 
    - A covariate works to proportionally increase the hazard in reference to the baseline hazard
    - This proportion is constant over time, meaning the hazard ratio is constant over time

# Proportional Hazards Regression

- Deriving the interpretation of  $\beta_k$ :
  - We compare two randomly chosen individuals
    - One subject has covariate values  $(X_1, \dots, X_k, \dots, X_p)$
    - One subject has covariate values  $(X'_1, \dots, X'_k + 1, \dots, X'_p)$
  - Then we have:

$$\frac{\lambda(t \mid X_1, \dots, X_k + 1, \dots, X_p)}{\lambda(t \mid X_1, \dots, X_k, \dots, X_p)} =$$
$$\frac{\lambda_0(t) \exp^{\beta_1 X_1 + \beta_2 X_2 + \dots + \beta_k (X_k + 1) + \dots + \beta_p X_p}}{\lambda_0(t) e^{\beta_1 X_1 + \beta_2 X_2 + \dots + \beta_k (X_k) + \dots + \beta_p X_p}} = e^{\beta_k}$$

- Again, the association for  $X_k$  with the time-to-event is assumed to be constant over time

# Proportional Hazards Regression: Example

- We have data from a 10-year double-blinded trial in 312 patients with primary cirrhosis of the liver (PBC) who were randomized to either the drug D-penicillamine (DPCA) or placebo
- Available covariates: age, albumin, bilirubin, edema, prothrombin time
- Our current example focuses on a model with variables age, edema and drug (1: DPCA, 0: placebo), in which

$$\text{edema} = \begin{cases} 0 & \text{no edema and no diuretic therapy} \\ 1/2 & \text{edema present w/o or resolved by diuretics} \\ 1 & \text{edema despite diuretic therapy} \end{cases}$$

# Partial Likelihood

- Recall that Kaplan-Meier first divided the data by the unique event times
  - Used product of interval probabilities to estimate the distribution of event times
- Estimation of regression parameters  $\beta$  in Cox regression is done in a similar way
- Cox referred to his approach as “partial likelihood” in 1975; the rigorous theory came in 1981 (Tsiatis) and 1982 (Anderson & Gill)
  - Because the baseline hazard is not specified and is nuisance, we would like to remove it when estimating  $\beta$
  - We condition the risk of each subject with an event (based on their covariate) on the total risk all subjects

# Partial Likelihood

- Thus, instead of the exact likelihood, we attempt to maximize the partial likelihood:

$$PL(\beta; X) = \prod_{t_k=t_1}^{t_d} \frac{\exp\{X(t_k)\beta\}}{\sum_{i \in R_k} \exp(X_i\beta)}$$

in which

$t_1, \dots, t_d$  = unique event times

$X(t_k)$  = covariate vector for subject with event at  $t_k$

$R_k$  = group of subjects at risk for event from  $(t_{k-1}, t_k]$

# Proportional Hazards Regression: Example

- The resulting fitted model from SAS (code not shown) is:

$$\lambda(t) = \lambda_0(t) \exp\{0.035\text{age} + 2.23\text{edema} - 0.11\text{drug}\}$$

- $e^{-0.11} = 0.89$  is the HR comparing DPCA to placebo adjusted for age and edema status
- The estimated HR comparing a patient with age = 50, edema = 0.5, drug = 1 to a patient with age = 40, edema = 0 and drug = 1

$$\begin{aligned} &= e^{0.035(50-40)+2.23(0.5-0)-0.11(1-1)} \\ &= 4.33 \end{aligned}$$

# Assessing Proportional Hazards for One Covariate

- We have assumed that a one-unit change in a covariate  $X$  leads to a shift in the log-hazard, i.e. hazards are proportional
- If  $X$  is categorical, then we plot  $\log\{-\log \hat{S}(t)\}$  against  $\log(t)$  for each value of  $X$ 
  - Proportional hazards holds if the curves are roughly parallel to each other
- If  $X$  is continuous, then divide subjects into (four, five?) equally sized groups and fit model using categorical  $X$ 
  - Use same process as above to assess proportional hazards for  $X$
- Assessing PH gets harder with multiple covariates

# Estimating the Baseline Survival Function

- Recall that our model is

$$\begin{aligned}\lambda(t) &= \lambda_0(t)e^{\beta_1X_1+\beta_2X_2+\cdots+\beta_pX_p} \\ &= \lambda_0(t)e^{\sum_{j=1}^p \beta_jX_j}\end{aligned}$$

and we have made no attempt to estimate  $\lambda_0(t)$

- Thus, we can compare the risk of two subjects relative to each other (hazard ratio)
- We cannot estimate the individual risks (hazard) of each subject
- There are methods for estimating  $\lambda_0(t)$ ; most statistical packages are programmed with these methods



# Time-Varying Covariates

- Cox regression allows using covariates that change over time:

$$\lambda(t) = \lambda_0(t) \exp \left\{ \sum_{j=1}^p \beta_j \mathbf{X}_j(t) \right\}$$

- But, this impacts our estimation:

$$PL(\beta; X) = \prod_{t_k=t_1}^{t_d} \frac{\exp\{X(t_k)\beta\}}{\sum_{i \in R_k} \exp(\mathbf{X}_i(t_k)\beta)}$$

- At each event time  $t_k$ , we need covariate values for every subject in the risk set  $R_k$ , not just the subject with the event
- If missing, some suggest using  $X_i(t_k)$  as the covariate value measured closest in time to  $t_k$  (if reasonably close in time to  $t_k$ )

# Accelerated Failure Time Model

- A contemporary alternative to Cox regression is a parametric regression model known as the Accelerated Failure Time (AFT) model
  - We assume a baseline distribution  $\mathcal{F}_0$  for event times
  - For a subject with covariates  $X$ , their observed event time is  $T = e^{\beta X} T_0$ , where  $T_0 \sim \mathcal{F}_0$
  - This is a simple parametric regression model

$$\log(T) = \beta X + \epsilon,$$

with  $\epsilon \sim \mathcal{F}_0$

- $\mathcal{F}_0$  is often parametric, i.e. Normal or Logistic, with mean=0 and variance= $\sigma^2$
- $\mathcal{F}_0$  can be non-parametric - much harder problem to solve

# Residual Diagnostics with Cox Regression

- See supplementary slides based on lecture by P. Breheny