Chapter 2

Descriptive Methods for Survival Data

Describing Survival Data

- The first step of any statistical analysis should be describing and visualizing the data
 - Measures of location and spread
 - Graphs
- In survival analysis, start by estimating the cumulative distribution function (CDF)
 - Let T be the survival time
 - The CDF is $F(t) = P(T \le t)$
 - It's more common to work with the survival function, S, where S(t) = P(T > t)

Notation

- □ Have a sample of n independent observations $(t_1, c_1), (t_2, c_2), ..., (t_n, c_n)$, where
 - t is the survival time
 - c is an indicator variable for whether the observation was censored
- □ Observations are ordered so that t₁ < t₂ < ... t_n
- \neg n_i is the number of subjects at risk of dying at time t_i
- \Box d_i is the number of deaths that occur at time t_i

- The Kaplan-Meier estimator is the most common method of estimating the survival function
 - KM uses conditional probability
- □ Recall: $P(A \cap B) = P(B|A)P(A)$
 - Let A be the event $T \ge t_i$ (survival to at least time t_i)
 - Let B be the event $T > t_i$ (survival past time t_i)
- $P(A \cap B) = P(B) = P(T > t_i) = S(t_i)$
- \square Since there are no events between t_{i-1} and t_i ,

$$P(A) = P(T \ge t_i) = P(T > t_{i-1}) = S(t_{i-1})$$

The K-M estimate of the survival function is

$$\hat{S}(t_i) = P(B) = P(B|A)P(A)$$

$$= P(T > t_i|T \ge t_i)S(t_{i-1})$$

$$= \prod_{k=1}^{i} P(T > t_k|T \ge t_k)$$

□ How do we estimate $P(T > t_i | T \ge t_i)$?

At time t_i , there are n_i subjects at risk. d_i of these subjects died and n_i - d_i survived, so we can estimate this conditional probability as

$$\hat{p}_i = \frac{n_i - d_i}{n_i}$$

So the K-M estimate of the survival function is

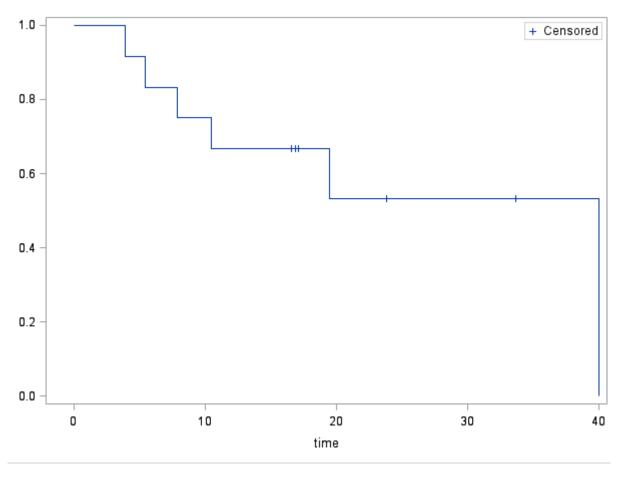
$$\hat{S}(t_i) = \prod_{k=1}^{i} P(T > t_k | T \ge t_k)$$

$$= \prod_{k=1}^{i} \frac{n_k - d_k}{n_k}$$

The K-M estimates the survival function with a step function, with the steps at the non-censored survival times.

- □ For $0 \le t < t_1$, $\hat{S}(t) = 1$
- For $t > t_n$, $\hat{S}(t)$ is undefined

□ A typical K-M plot



- Once we've estimated the survival function, S, we can use it to estimate the percentiles of the survival time distribution
- The median survival time is a common measure of location
 - The time at which the probability of surviving past that time is exactly 50%
 - Estimate the median survival time as

$$\hat{t}_{50} = \min\{t : \, \hat{S}(t) \le 0.50\}$$

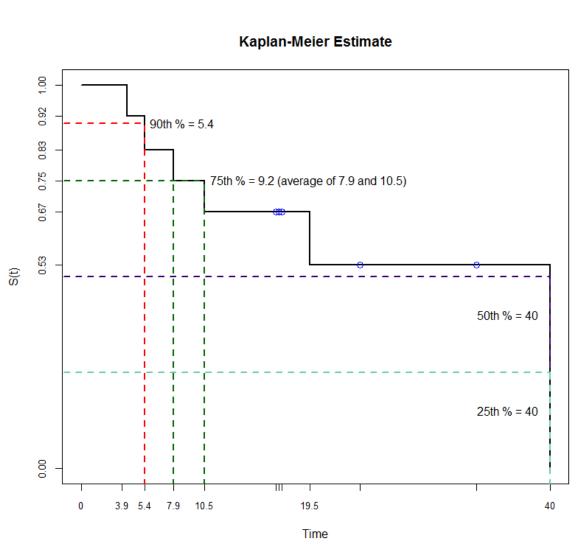
 \Box In general, the p^{th} percentile is estimated as either

$$\hat{t}_p = \min\left\{t: \, \hat{S}(t) \le \frac{p}{100}\right\} \qquad \text{(Book)}$$

or

$$\hat{t}_p = \min \left\{ t : \, \hat{S}(t) \le \frac{100 - p}{100} \right\}$$
 (SAS)

- Another way to think of estimating \hat{t}_p is to draw a horizontal line at $y = \frac{p}{100}$ and find the first place that line crosses the KM curve.
- In this example, t = 7.9 is the first time the line y = 0.75 crosses the curve.
 - Note that the KM estimate is exactly 0.75 for all times within the interval [7.9, 10.5).
 - SAS reports 9.2 (the midpoint of this interval) as the estimate for this percentile.
 - Either 7.9 or 9.2 is an acceptable estimate.



□ For a non-negative, continuous random variable

$$\mu = \int_{0}^{\infty} S(u) \ du$$

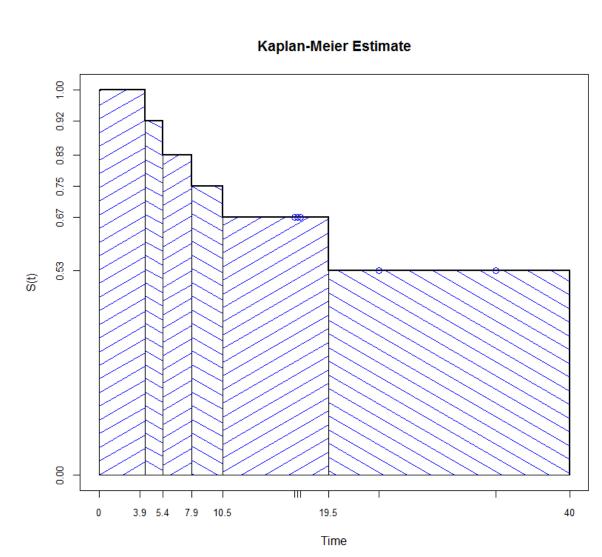
□ Since $\hat{S}(t)$ is undefined after the largest survival time, use $\mu(t^*)$ to estimate the mean survival time, where

$$\mu(t^*) = \int_0^{t^*} S(u) du,$$

and t* can either be the largest survival time or the largest *non-censored* survival time.

SAS uses the largest non-censored survival time

- To estimate the mean survival time using the KM estimate, calculate the area under the curve between 0 and t*.
 - Usually the median, and not the mean, survival time is reported



Standard Error

- There is uncertainty in any estimate, need to calculate the standard error to quantify this uncertainty.
- \Box For a given time t, what is $Var(\hat{S}(t))$?
 - Variance of a sum is easier to calculate than the variance of a product, so take the natural log

$$log(\hat{S}(t)) = \sum_{t_i \le t} log\left(\frac{n_i - d_i}{n_i}\right) = \sum_{t_i \le t} log(\hat{p}_i)$$

$$Var\left(log\left(\hat{S}(t)\right)\right) = \sum_{t_i \le t} Var(log(\hat{p}_i))$$

□ Using the Delta method several times, we can derive an estimate of the variance of $\hat{S}(t)$

Standard Error

 \Box Greenwood's estimator of the variance of $\hat{S}(t)$:

$$\widehat{V}(\widehat{S}(t)) = (\widehat{S}(t))^2 \sum_{t_i < t} \frac{d_i}{n_i(n_i - d_i)}$$

 Using this estimate of the variance to form confidence intervals could lead to endpoints less than zero or greater than one.

Confidence Intervals

- Kalbfleisch and Prentice suggested estimating the variance of a function of $\hat{S}(t)$, and then transforming to calculate a confidence interval
 - Use $\log(-\log(\hat{S}(t)))$, the log-log survival function

$$\widehat{V}\left(\log\left(-\log(\widehat{S}(t))\right)\right) = \frac{1}{\left(\log(\widehat{S}(t))\right)^{2}} \sum \frac{d_{i}}{n_{i}(n_{i}-d_{i})}$$

 \Box A 100(1- α)% confidence interval for the log-log survival function is

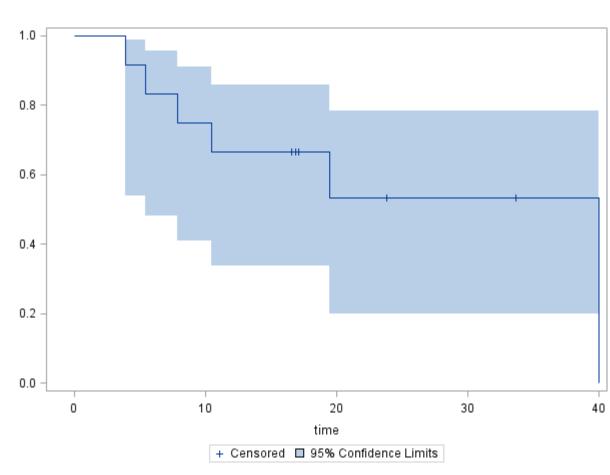
$$\log(-\log(\hat{S}(t))) \pm z_{1-\alpha/2} \sqrt{\hat{V}(\log(-\log(\hat{S}(t))))}$$

□ The CI for $\hat{S}(t)$ is then found using the transformation

$$f(x) = e^{-e^x}$$

Confidence Intervals

Can construct
 point-wise
 confidence
 intervals at each
 point on the
 survival curve



Confidence Intervals

□ To calculate a confidence interval for the p^{th} percentile, estimate variance of \hat{t}_p :

$$\hat{V}(\hat{t}_p) \approx \frac{\hat{V}(\hat{S}(\hat{t}_p))}{(\hat{f}(\hat{t}_p))^2}$$

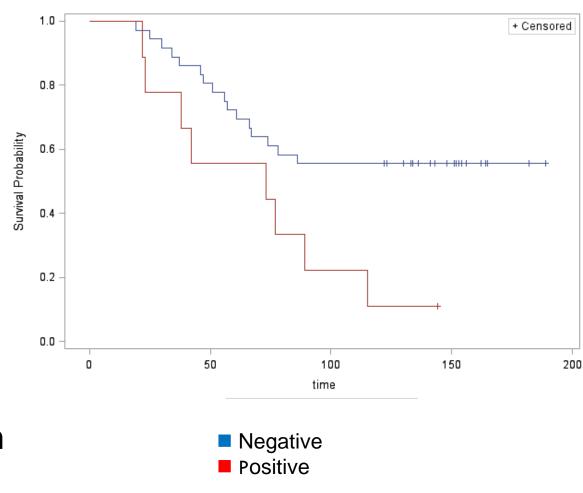
where $\hat{V}(\cdot)$ is Greenwood's estimator and $\hat{f}(\cdot)$ is an estimate of the density function of the survival time. (See p.37 of textbook for more details).

 \square A 100(1- α)% CI for \hat{t}_p is

$$\hat{t}_p \pm z_{1-\alpha/2} \sqrt{\hat{V}(\hat{t}_p)}$$

- How can we test for differences in the survival functions?
 - Example:

 Comparing survival for breast cancer patients who were either positive or negative for metastasis in lymph nodes



- □ Want to test H_0 : $S_1(t) = S_2(t)$ vs H_1 : $S_1(t) \neq S_2(t)$
- Motivation:
 - At a given survival time, t_i, can create a contingency table:

	Group 1	Group 2	
Died	d _{1i}	d _{2i}	d_{i}
Survived	n _{1i} - d _{1i}	n _{2i} - d _{2i}	n _i -d _i
Number at Risk	n _{1i}	n _{2i}	n _i

- Treat the margins of each contingency table as fixed
 - d_{1i} follows a hypergeometric distribution

$$P(d_{1i} = k) = \frac{\binom{d_i}{k} \binom{n_i - d_i}{n_{1i} - k}}{\binom{n_i}{n_{1i}}}$$

The test statistic is

$$Q = \frac{\left[\sum_{i} w_{i}(d_{1i} - \hat{e}_{1i})\right]^{2}}{\sum_{i} w_{i}^{2} \hat{v}_{1i}}$$

where \hat{e}_{1i} and \hat{v}_{1i} are the expected value and variance of d_{1i} , respectively

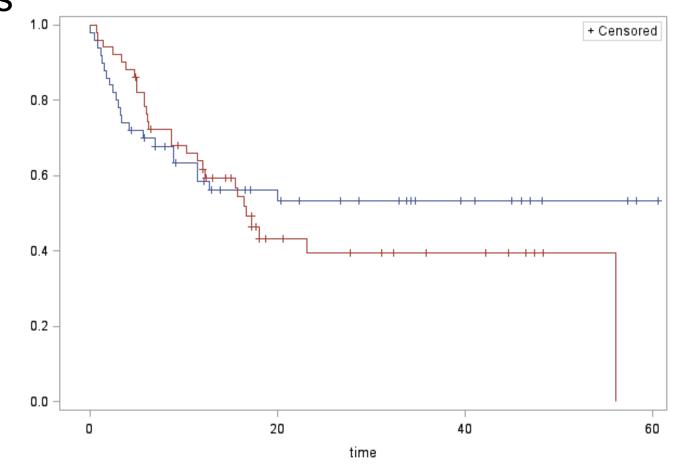
$$\hat{e}_{1i} = \frac{n_{1i}d_i}{n_i}$$
 , $\hat{v}_{1i} = \frac{n_{1i}n_{2i}d_i(n_i - d_i)}{n_i^2(n_i - 1)}$

and $w_i = w(t_i)$ is a weighting function

- If H_0 is true, Q follows a χ^2 distribution with 1 degree of freedom
- The (two-sided) p-value is $P(\chi_1^2 > Q)$

- Different choices of the weighting function lead to different tests
 - Log-rank test: $w(t_i) = 1$
 - Gehan test or Wilcoxon test: w(t_i) = n_i
 - Tarone and Ware: $w(t_i) = f(n_i)$ for some function f
- Log-rank and Wilcoxon tests are the most common choices
 - Log-rank test weights all survival times equally
 - The Wilcoxon test gives more weight to the earlier part of the survival curve where more subjects are at risk

 These tests should not be used when the survival curves cross



 Can generalize these tests to comparing the survival distributions of K groups

$$\blacksquare$$
 H₀: S₁(t) = S₂(t) = ... = S_K(t) vs H₁: Not H₀

	Group 1	Group 2		Group k		Group K	
Died	d _{1i}	d _{2i}		d _{ki}	•••	d _{Ki}	d _i
Survived	n _{1i} - d _{1i}	n _{2i} - d _{2i}		n _{ki} - d _{ki}		n _{Ki} – d _{Ki}	n _i -d _i
Number at Risk	n _{1i}	n _{2i}	•••	n _{ki}		n _{Ki}	n _i

□ At each time t_i , calculate the expected number of deaths in Group k under H₀:

$$\hat{e}_{ki} = \frac{d_i n_{ki}}{n_i}$$
, $k = 1, ..., K - 1$

Use vector notation to extend the test to K groups

$$d_i^T = (d_{1i}, d_{2i}, \dots d_{K-1,i})$$

$$\hat{e}_i^T = (\hat{e}_{1i}, \hat{e}_{2i}, \dots \hat{e}_{K-1,i})$$

- Let \hat{V}_i be the (K-1) x (K-1) covariance matrix of d_i^T :
 - The diagonal elements of \hat{V}_i are

$$\hat{v}_{kk,i} = \frac{n_{ki}(n_i - n_{ki})d_i(n_i - d_i)}{n_i^2(n_i - 1)}, k = 1, \dots K - 1$$

■ The off-diagonal elements of \hat{V}_i are

$$\hat{v}_{jk,i} = \frac{n_{ji}n_{ki}d_i(n_i - d_i)}{n_i^2(n_i - 1)}, \text{ for } j \neq k$$

The test statistic is

$$Q = \left[\sum_{i} W_i(d_i - \hat{e}_i)\right]^T \left[\sum_{i} W_i \hat{V}_i W_i\right]^{-1} \left[\sum_{i} W_i(d_i - \hat{e}_i)\right]$$

where W_i is a diagonal matrix of weights.

- Under H_0 , Q follows a χ^2 distribution with K-1 degrees of freedom
- The two-sided p-value is $P(\chi_{K-1}^2 > Q)$
- Note, that for the simple case (K=2), this test statistic is the same as before.

So far we have focused on the survival function,S:

$$S(t) = P(T > t) = 1 - F(t)$$

where F(t) is the cdf of the survival time, T.

□ Let the pdf of T be f(t)

$$f(t) = \lim_{\Delta t \to 0} \frac{P(t \le T \le t + \Delta t)}{\Delta t}$$

f(t) is also called the unconditional failure rate

- Subjects who have died before time t are no longer at risk during (t, t+Δt), so it makes sense to think instead of a conditional failure rate
 - □ Conditional failure rate: instantaneous risk of an event occurring at time *t*, given subject has survived to time *t*.
 - Also called the hazard function:

$$h(t) = \lim_{\Delta t \to 0} \frac{P(t \le T \le t + \Delta t \mid T \ge t)}{\Delta t}$$

- h(t) > 0
- Note: h(t) is not a probability

Can also define the cumulative hazard function, H

$$H(t) = \int_{0}^{t} h(u) \ du$$

H(t) is the total amount of risk accumulated up to time

- Note S(t), f(t), and h(t) are equivalent ways of describing any continuous probability distribution.
- □ If we know one of them, we can get the others:

$$f(t) = -\frac{d}{dt}S(t)$$

$$h(t) = \frac{f(t)}{S(t)} = -\frac{d}{dt}\log(S(t))$$

$$S(t) = e^{-H(t)}$$

Estimating the Cumulative Hazard Function

- □ Instead of using the Kaplan-Meier estimator $\hat{S}(t)$ to estimate the survival function, can instead estimate H(t)
- The Nelson-Aalen estimate:

$$\widetilde{H}(t) = \sum_{t_i < t} \frac{d_i}{n_i}$$

$$Var(\widetilde{H}(t)) = \sum_{t_i < t} \frac{d_i}{n_i^2}$$

Estimating the Cumulative Hazard Function

 The Nelson-Aalen estimator of the survival function is therefore

$$\tilde{S}(t) = e^{-\tilde{H}(t)}$$

■ A $100(1-\alpha)$ % CI for H(t) is

$$\widetilde{H}(t) \pm z_{1-\alpha/2} \sqrt{Var(\widetilde{H}(t))}$$

■ A confidence interval for $\tilde{S}(t)$ can be found by exponentiating the CI for $\tilde{H}(t)$

Nelson-Aalen Kaplan-Meier

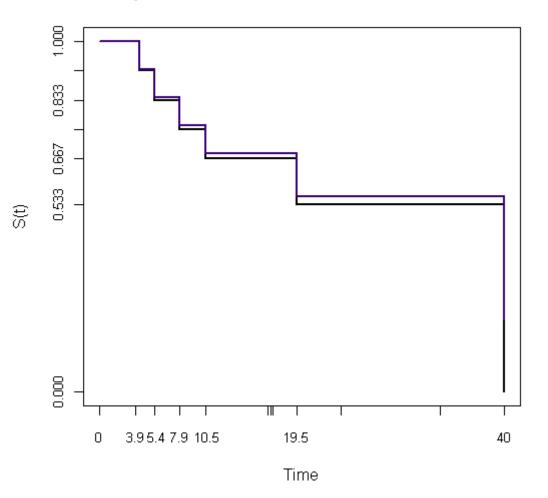
 \Box $\tilde{S}(t) \ge \hat{S}(t)$ for all t, but the two estimates are often very close

Estimating the Cumulative Hazard Function

Previous example:

Survival times: 3.9,
5.4, 7.9, 10.5,
16.6+, 16.9+,
17.1+, 19.5, 23.8+,
33.7+, 33.7+, 40

Kaplan-Meier and Nelson-Aalen Estimates



- The hazard function is useful for describing the way that the risk of an event changes with time.
- □ In contrast to S(t), the graph of h(t) can start anywhere and can increase, decrease, remain constant, or change constantly over time.

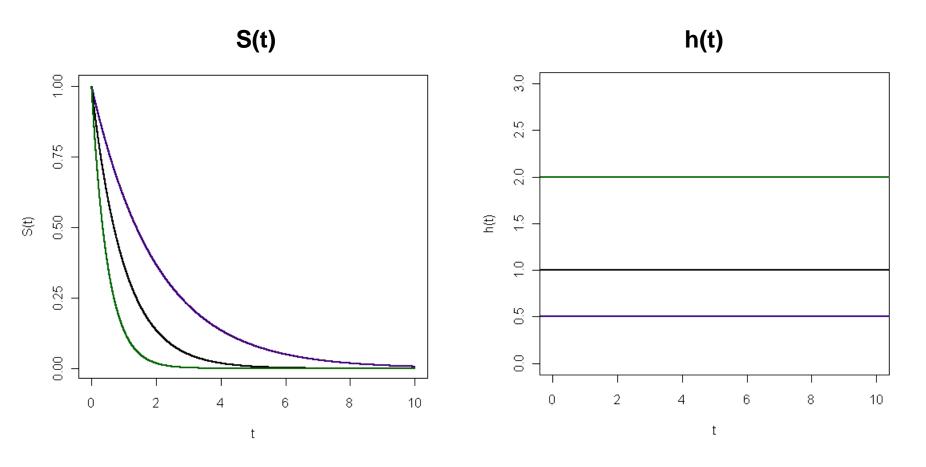
The simplest hazard function is one that says that the hazard is constant over time

$$h(t) = \lambda$$

which implies

- \Box S(t) = $e^{-\lambda t}$



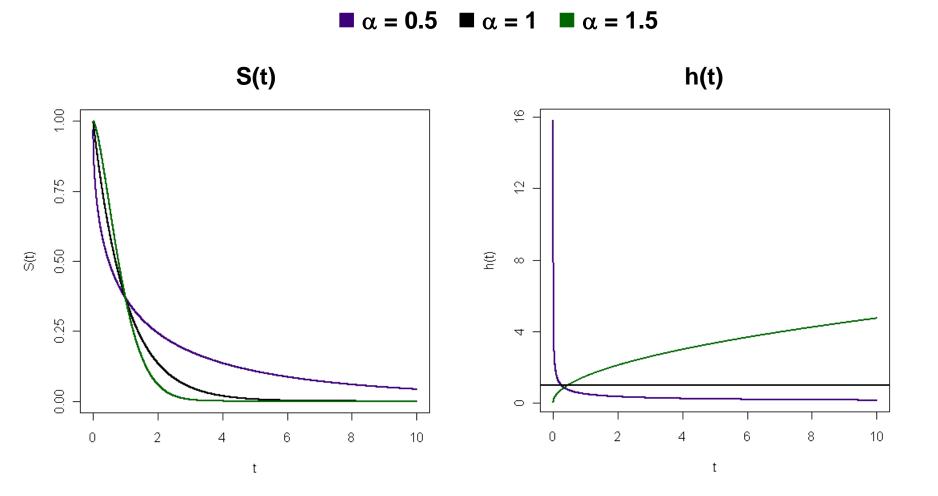


- The next step up in complexity is to let the hazard be some function of t.
- □ For example, one can use:

$$h(t) = \lambda \alpha t^{\alpha - 1}$$
$$\lambda > 0, \alpha > 0$$

which implies

- □ $f(t) = \lambda \alpha t^{\alpha-1} e^{-\lambda t^{\alpha}}$, i.e. T follows a Weibull distribution
- - If α = 1, the hazard is constant.
 - If α > 1, the hazard increases with time.
 - If α < 1, the hazard decreases with time.



- Note that the survival functions have the same basic shape, but the hazard functions are very different.
- The hazard function usually gives more information regarding the underlying mechanism of failure than the survival function.
- For this reason, it is usually preferred to use the hazard function to summarize survival data.