Biostatistics (MATH11230)

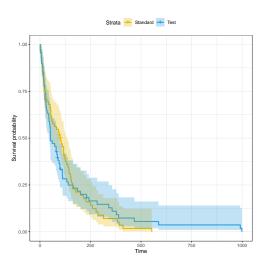
Vanda Inácio

University of Edinburgh



Semester 1, 2021/2022

- → Often, there is additional information about the patients/individuals, and we would like to add this to our analysis.
- → A very first step towards this end is to compare the survival curves from two groups.
- → Last week we have also looked at the veteran dataset, available in the survival package.
- This was a study conducted by the US Veterans Administration. Male patients with advanced inoperable lung cancer were given either a standard therapy or a test chemotherapy.



- \hookrightarrow We can see that the two estimated Kaplan–Meier curves slightly differ and that there is a good amount of overlap between the 95% pointwise confidence bands.
- Clearly, however, it would also be nice to formally test for a difference between the two groups survival curves.
- \hookrightarrow Specifically, we want to test the null hypothesis $H_0: S_1 = S_2$, where S_1 and S_2 are the survival functions for two different groups of patients. This is the topic of today's lecture.

- → Of course, one possibility would be to compute the survival curves for each group and compare the proportions surviving at any specific time.
- → The weakness of this approach is that it does not provide a comparison of the total survival experience of the two groups, but rather gives a comparison at some arbitrary time point(s).
- \hookrightarrow If we knew that S_1 and S_2 were in the same parametric family (e.g., $S_j(t) = e^{-\lambda_j t}$, j=1,2), then the null hypothesis would reduce to testing whether the parameters were the same (e.g, $\lambda_1 = \lambda_2$).
- → However, we instead want a nonparametric test, that is, a test whose validity does not depend on any parametric assumptions.
- The log rank test is the most widely used approach to compare survival curves. It adapts methods for analysing 2 × 2 contingency tables (Mantel, 1966) to accommodate censoring.
- The goal of this lecture is to introduce the log rank test from a heuristic perspective and to discuss popular extensions.

Log rank test

- \hookrightarrow Let $0 = t_0 < t_1 < t_2 < \ldots < t_J < t_{J+1} = \infty$ denote the pooled event times (times at which any subject in either group had an event).
- \hookrightarrow Let d_{1j} denote the number of events at time t_j in group 1, d_{2j} the number of events at time t_j in group 2 and d_j denote the total number of events at time t_j .
- \hookrightarrow Similarly, let n_{1j} be the number of individuals at risk in group 1 at time t_j , n_{2j} be the number of individuals at risk in group 2 at time t_j and n_j denote the total number of individuals at risk at time t_j .

Log rank test

 \hookrightarrow The information available at each event time t_j , $j=1,\ldots,J$, is usually represented in a 2 \times 2 contingency table

	$\#$ with an event at t_j	$\#$ without an event at t_j	Total
Group 1	d_{1j}	$n_{1j}-d_{1j}$	n _{1j}
Group 2	d_{2j}	$n_{2j}-d_{2j}$	n_{2j}
Total	d_j^{\cdot}	$n_j - d_j$	n_j

 \hookrightarrow Formally, we are testing

$$H_0: S_1(t) = S_2(t),$$
 for all $t \le t_J$,
 $H_1: S_1(t) \ne S_2(t),$ for some $t < t_J$.

The idea behind the log rank test is to compare, at each event time, the observed number of events with the expected number of events under the null hypothesis that the two survival curves are equal.

Log rank test

- \hookrightarrow One can show that, conditional on the marginal totals and under the null hypothesis that survival is independent of the group being true, d_{1j} follows an hypergeometric distribution with mean

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

which therefore represents, under H_0 , the expected number of events in group 1 at time t_j .

 \hookrightarrow This value is intuitively appealing since under the null hypothesis that the probability of an event occurring at time t_j does not depend on the group that an individual is in, the probability of an event at t_j is d_j/n_j . Multiplying this by n_{1j} gives e_{1j} as the expected number of events in group 1 at time t_j .

Log rank test

- \hookrightarrow The idea is then to compare the number of observed, d_{1j} , and expected, e_{1j} , events and to combine the information from all event times.
- \hookrightarrow The most straightforward way of doing this is to sum the differences $d_{1j} e_{1j}$ over the total number of event times, J, in the two groups.

$$U_L = \sum_{j=1}^{J} (d_{1j} - e_{1j}) = \sum_{j=1}^{J} \left(d_{1j} - n_{1j} \frac{d_j}{n_j} \right).$$

 \hookrightarrow Obviously, this is equivalent to $\sum_{j=1}^J d_{1j} - \sum_{j=1}^J e_{1j}$, which is the difference between the observed and expected number of events in group 1, sometimes abbreviated as O-E (for observed minus expected).

Log rank test

- \hookrightarrow This U_L statistic has zero mean since $E(d_{1j} \mid H_0) = e_{1j}$.
- \hookrightarrow Moreover, since the event times are independent of one another, the variance of U_L is simply the sums of the variances of the $d_{1/S}$

$$var(U_L) = var\left(\sum_{j=1}^{J} d_{1j} - e_{1j}\right) = \sum_{j=1}^{J} var(d_{1j}).$$

 \hookrightarrow Because d_{1j} follows a hypergeometric distribution, under H_0 , the variance of d_{1j} is given by

$$var(d_{1j}) = v_{1j} = \frac{n_{1j}n_{2j}d_j(n_j - d_j)}{n_j^2(n_j - 1)}.$$

Log rank test

- \hookrightarrow It then follows that

$$\frac{U_L}{\sqrt{\text{var}(U_L)}} \sim N(0,1).$$

$$\frac{U_L^2}{\operatorname{var}(U_L)} \sim \chi_1^2.$$

- \hookrightarrow The statistic $U_L^2/\text{var}(U_L)$ summarises the extent to which the observed event times in the two groups deviate from those expected under the null hypothesis of no group differences.

Log rank test

- → The log rank test is particularly powerful when the ratio between the two hazard functions being compared is constant across time, i.e.,

$$\frac{h_2(t)}{h_1(t)} = \text{constant}.$$

Log rank test

Group 1:
$$3.1$$
, 6.8^+ , 9 , 9 , 11.3^+ , 16.2
Group 2: 8.7 , 9 , 10.1^+ , 12.1^+ , 18.7 , 23.1^+

- \hookrightarrow We have that J=5 and the distinct event times are: 3.1, 8.7, 9, 16.2, and 18.7.
- \hookrightarrow We have that for $t_1 = 3.1$

	$\#$ with an event at t_1	$\#$ without an event at t_1	Total
Group 1	1	5	6
Group 2	0	6	6

 \hookrightarrow We have that for $t_2 = 8.7$

	$\#$ with an event at t_2	$\#$ without an event at t_2	Total
Group 1	0	4	4
Group 2	1	5	6

Log rank test

 \hookrightarrow We have that for $t_3=9$

	$\#$ with an event at t_3	$\#$ without an event at t_3	Total
Group 1	2	2	4
Group 2	1	4	5

 \hookrightarrow We have that for $t_4 = 16.2$

	$\#$ with an event at t_4	$\#$ without an event at t_4	Total
Group 1	1	0	1
Group 2	0	2	2

 \hookrightarrow We have that for $t_5 = 18.7$

	$\#$ with an event at t_5	$\#$ without an event at t_5	Total
Group 1	0	0	0
Group 2	1	1	2

Log rank test

- \hookrightarrow We have that $\sum_{j=1}^{5} d_{1j} = 1 + 0 + 2 + 1 + 0 = 4$.

$$\sum_{j=1}^{5} e_{1j} = 6 \times \frac{1}{12} + 4 \times \frac{1}{10} + 4 \times \frac{3}{9} + 1 \times \frac{1}{3} + 0 = 2.566667.$$

- \hookrightarrow After doing the calculation, one has that $\text{var}(U_L) = \sum_{j=1}^5 \textit{v}_{1j} = 1.267778$.
- \hookrightarrow Finally, we have that the value of the test statistic is $(4-2.566667)^2/1.267778 = 1.620508$.
- The resulting p-value is 0.2 and so there is no evidence to reject the null hypothesis that the survival curves of the two groups are the same.

Log rank test

- → The function survdiff in the survival package implements the log rank test.
- → For instance, for the 'motivating' veteran dataset, there are 101 distinct event times across the two treatment groups!
- In this case, the p-value is 0.9, and not surprisingly, we do not reject the null hypothesis of no difference in the survival of the two treatment groups.

Weighted log rank test

 \hookrightarrow The U_l statistic of the log rank test

$$U_L = \sum_{j=1}^{J} (d_{1j} - e_{1j})$$

gives the same weight to the difference between the observed and expected number of events at all timepoints.

→ One natural extension is the family of weighted log rank tests, whose test statistic is

$$U = \sum_{j=1}^{J} w_j (d_{1j} - e_{1j}),$$

and where the weights $\{w_j\}_{j=1}^J$ are chosen to emphasise or deemphasise various time points.

 \hookrightarrow The variance of this weighted sum is obtained as before, $var(U) = \sum_{j=1}^{J} w_j^2 v_{1j}$, and we still have that $U^2/var(U) \sim \chi_1^2$.

Weighted log rank test

→ For example, one reasonable weighting scheme would be to weight time points by the number of individuals at risk at time t_i, that is,

$$w_j = n_j, \quad j = 1, \ldots, J.$$

- The idea is to give less weight to the difference between observed and expected number of events for the event times where there are less information, i.e, when the risk set becomes small.
- → This is known as the Gehan, Gehan–Breslow, or Gehan–Wilcoxon test.

Weighted log rank test

- \hookrightarrow A somewhat similar idea is to consider $w_j = \widehat{S}(t_j)$, with $\widehat{S}(\cdot)$ an estimate of the common survival function of both groups.
- This is known as the Peto-Prentice or Peto-Peto test and also gives more weight to early differences compared to late differences, but independently of the number individuals still at risk.
- → The survdiff function has an option, rho, that can be set to 1 in order to perform the Peto-Prentice test.
- → The package survminer also allows to perform both weighted tests.

Extension to multiple groups

- \rightarrow The log rank test can be extended to compare three or more groups of event times data.
- Suppose that the survival distributions of G groups of event times data are to be compared, for G ≥ 2.
- \hookrightarrow We then define the analogous of the U-statistics for comparing the observed and expected number of events in groups 1, 2, . . . , G-1.
- \hookrightarrow Let

$$U_{Lg} = \sum_{j=1}^{J} \left(d_{gj} - n_{gj} \frac{d_j}{n_j} \right) = \sum_{j=1}^{J} (d_{gj} - e_{gj}), \qquad g = 1, \dots, G - 1.$$

 \hookrightarrow These quantities are then expressed in the form of a vector with G-1 components

$$\boldsymbol{U}_L = (U_{L1}, \dots, U_{L,G-1})'.$$



Extension to multiple groups

- \hookrightarrow We also need the expressions for the variances of the U_{Lg} and for the covariances between pairs of values.
- \hookrightarrow In particular, the covariance between U_{Lg} and $U_{Lg'}$ is given by

$$V_{Lgg'} = \sum_{j=1}^{J} \frac{n_{gj} d_j (n_j - d_j)}{n_j (n_j - 1)} \left(\delta_{gg'} - \frac{n_{g'j}}{n_j} \right),$$

for g, g' = 1, 2, ..., G - 1 and where $\delta_{qq'} = 1$ if g = g' and 0 otherwise.

- \hookrightarrow These terms are then assembled in the form of a variance-covariance matrix, V_L .
- → For example, in the comparison of three groups of event times data, this matrix is

$$\mathbf{V}_{L} = \begin{pmatrix} V_{L11} & V_{L12} \\ V_{L12} & V_{L22} \end{pmatrix}.$$



Extension to multiple groups

 Finally, in order to test the null hypothesis of no group differences, we make use of the following result

$$\mathbf{U}_L'\mathbf{V}_L^{-1}\mathbf{U}_L\sim\chi_{G-1}^2.$$

- \hookrightarrow Note that in this setup, we have G groups but only G-1 independent counts in the contingency table because we are conditioning on the margins, and therefore only G-1 degrees of freedom.
- \hookrightarrow The function survdiff also implements this case.