

How do I perform a Log Rank Test in R?

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The Log Rank Test is a statistical test used to compare the survival rates of two or more groups. In order to perform this test in R, you will need to first import your data into R using a data frame. Next, you will need to load the "survival" package, which contains the necessary functions for conducting the Log Rank Test. Then, you can use the "survdiff" function to perform the test and obtain the p-value and test statistic. The results can be interpreted to determine if there is a significant difference in survival rates between the groups being compared. Overall, the Log Rank Test in R is a simple and efficient way to compare survival rates and can provide valuable insights in various research and analysis contexts.

Perform a Log Rank Test in R

A log rank test is the most common way to compare survival curves between two groups.

This test uses the following :

H0: There is no difference in survival between the two groups.

HA: There *is* a difference in survival between the two groups.

If the p-value of the test is less than some significance level (e.g. $\alpha = .05$), then we can reject the null hypothesis and conclude that there is sufficient evidence to say there is a difference in survival between the two groups.

To perform a log rank test in R, we can use the `survdiff()` function from the survival package, which

uses the following syntax:

```
survdif(Surv(time, status) ~ predictors, data)
```

This function returns a Chi-Squared test statistic and a corresponding p-value.

The following example shows how to use this function to perform a log rank test in R.

Example: Log Rank Test in R

For this example, we'll use the ovarian dataset from the survival package. This dataset contains the following information about 26 patients:

Survival time (in months) after being diagnosed with ovarian cancer
Whether or not survival time was censored
Type of treatment received (rx =1 or rx = 2)

The following code shows how to view the first six rows of this dataset:

```
library(survival)
```

```
#view first six rows of dataset
```

```
head(ovarian)
```

```
futime fustat age resid.ds rx ecog.ps
```

```
1 59 1 72.3315 2 1 1
```

```
2 115 1 74.4932 2 1 1
```

```
3 156 1 66.4658 2 1 2
```

```
4 421 0 53.3644 2 2 1
```

```
5 431 1 50.3397 2 1 1
```

```
6 448 0 56.4301 1 1 2
```

The following code shows how to perform a log rank test to determine if there is a difference in survival between patients who received different treatments:

```
#perform log rank test
```

```
survdif(Surv(futime, fustat) ~ rx, data=ovarian)
```

Call:

```
survdif(formula = Surv(futime, fustat) ~ rx, data =  
ovarian)
```

```
N Observed Expected (O-E)^2/E (O-E)^2/V
```

```
rx=1 13 7 5.23 0.596 1.06
```

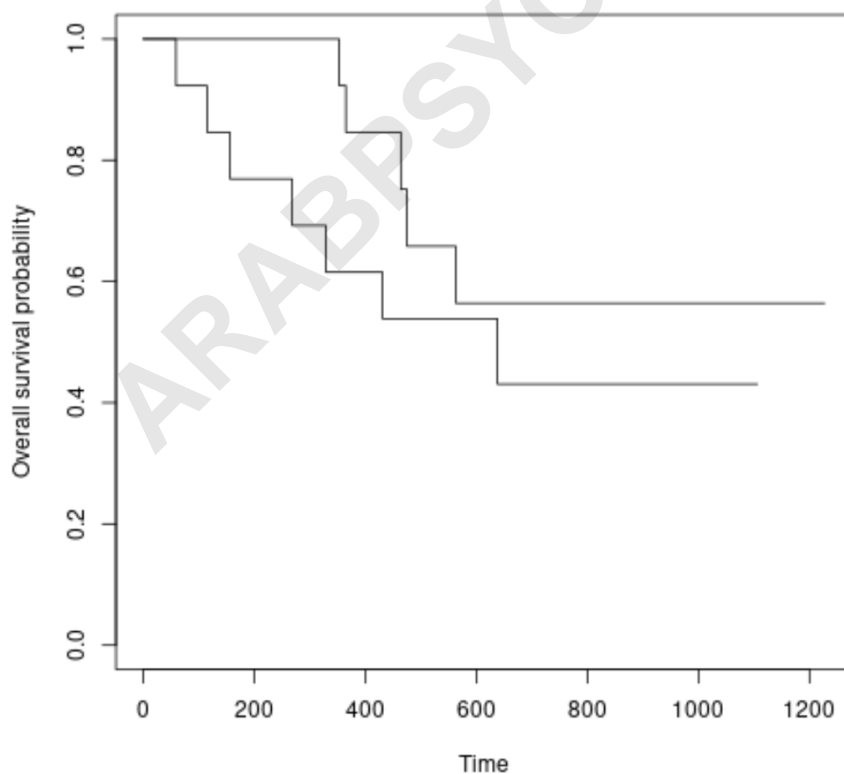
```
rx=2 13 5 6.77 0.461 1.06
```

```
Chisq= 1.1 on 1 degrees of freedom, p= 0.3
```

The Chi-Squared test statistic is 1.1 with 1 degree of freedom and the corresponding p-value is 0.3. Since this p-value is not less than .05, we fail to reject the null hypothesis.

We can also plot the survival curves for each group using the following syntax:

```
#plot survival curves for each treatment group  
plot(survfit(Surv(futime, fustat) ~ rx, data = ovarian),  
xlab = "Time",  
ylab = "Overall survival probability")
```



We can see that the survival curves are slightly different, but the log rank test told us that the difference is not statistically significant.

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