

STA 5364, Report 3.4

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Problem

Use the `survminer` package with the `pairwise_survdiff` function to test the hypothesis that the survival curves corresponding to the BMT data in KM, p. 484ff, (AML low, AML high, and ALL) are coincident.

```
# Load necessary libraries
library("survival")
library("KMsurv")
library("survminer")

# Load the BMT data
data(bmt)

# Perform pairwise comparisons of survival curves
(pairwise_results <- pairwise_survdiff(
  formula = Surv(t1, d3) ~ group,
  data = bmt
))
```

```
##
## Pairwise comparisons using Log-Rank test
##
## data: bmt and group
##
## 1 2
## 2 0.03145 -
## 3 0.13807 0.00094
##
## P value adjustment method: BH
```