

cancer

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reference:

- Cannon, et al., Stat2, chapter 07, example 7.2

Import the data.

```
data <- read.csv("CancerSurvival.CSV", header=TRUE)
head(data)
```

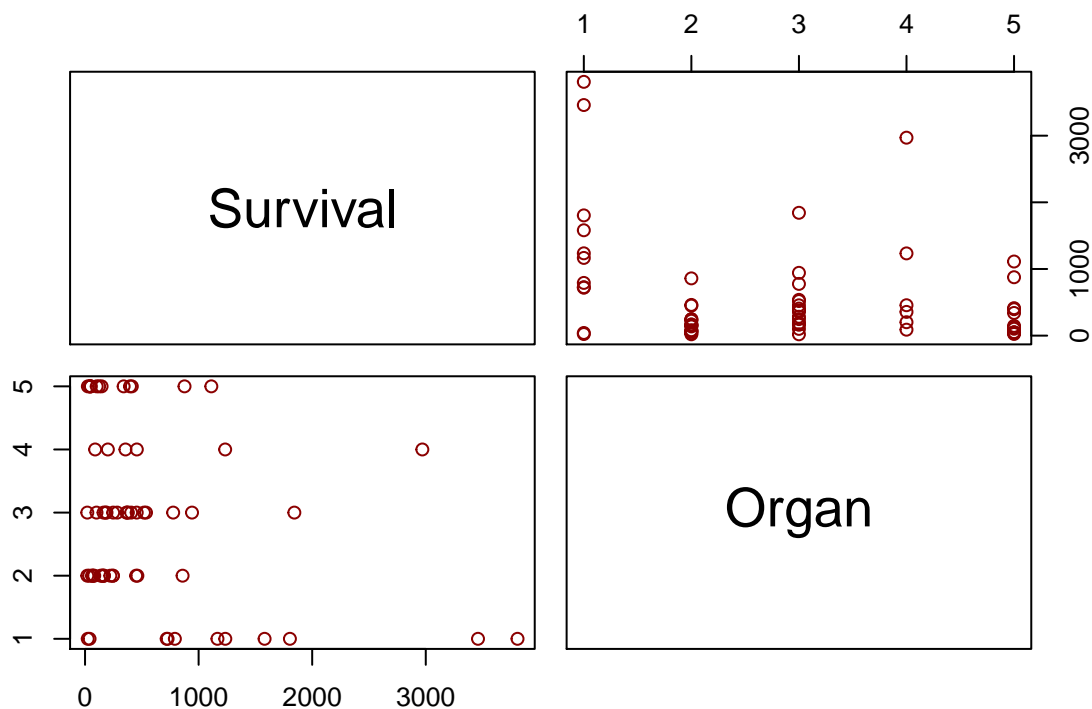
```
##   Survival  Organ
## 1     124 Stomach
## 2      42 Stomach
## 3      25 Stomach
## 4      45 Stomach
## 5     412 Stomach
## 6      51 Stomach
```

```
dim(data)
```

```
## [1] 64  2
```

Scatterplot matrix.

```
pairs(~ Survival + Organ, data=data, col="darkred")
```



Levene's test.

```
library(car)
leveneTest(Survival ~ Organ, data=data)
```

```
## Levene's Test for Homogeneity of Variance (center = median)
##      Df F value  Pr(>F)
## group 4  4.4524 0.003271 **
##      59
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
leveneTest(log(Survival) ~ Organ, data=data)
```

```
## Levene's Test for Homogeneity of Variance (center = median)
##      Df F value Pr(>F)
## group 4  0.6685 0.6164
##      59
```