

Q4

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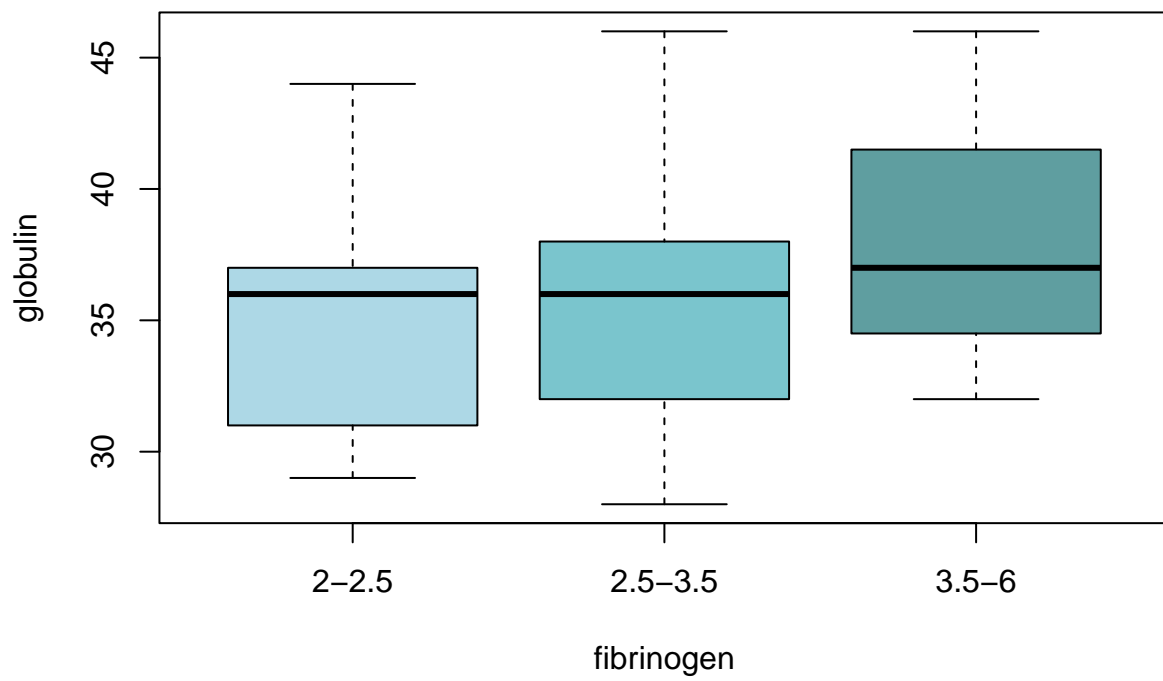
```
library(tools)
library(HSAUR)
library(car)

## Loading required package: carData

data(plasma)
fibrinogen <- cut(plasma$fibrinogen, breaks=c(0, 2.5, 3.5, 6), labels=c("2-2.5", "2.5-3.5", "3.5-6"), include.lowest=TRUE)
fibrinogen <- as.factor(fibrinogen)
globulin <- as.numeric(plasma$globulin)
anovafib <- aov(plasma$globulin ~ fibrinogen)
fib_res <- residuals(anovafib)
shapiro.test(fib_res) #normal

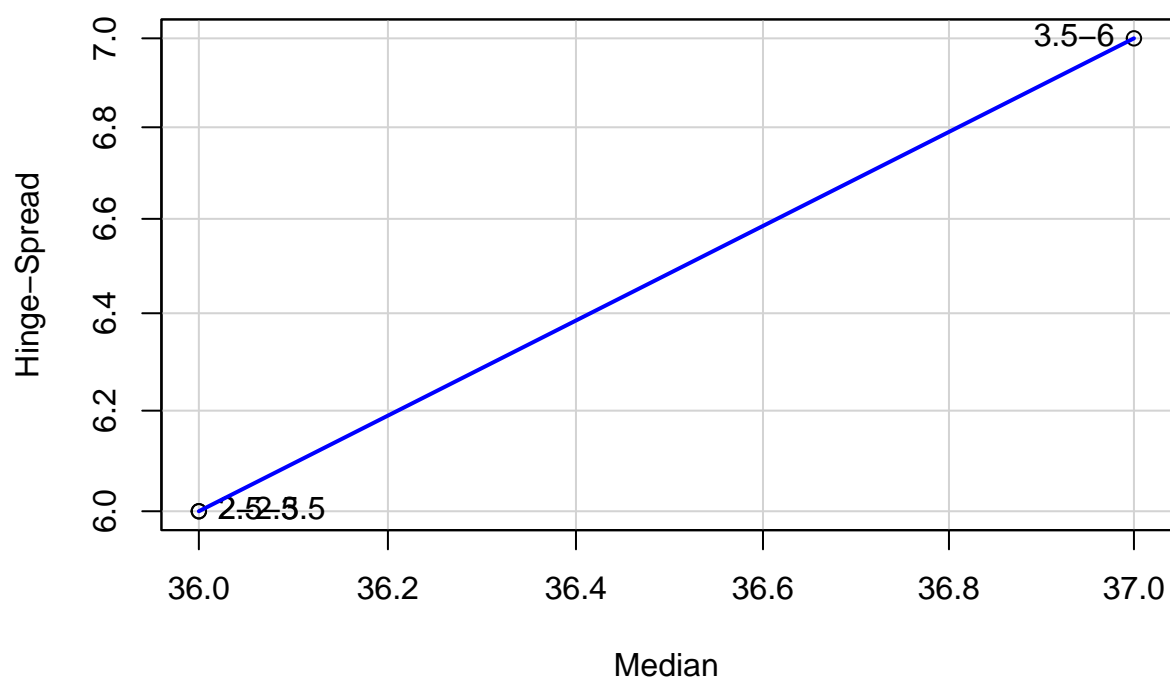
##
## Shapiro-Wilk normality test
##
## data: fib_res
## W = 0.95771, p-value = 0.2375

boxplot(globulin~fibrinogen, col = c('lightblue', 'cadetblue3', 'cadetblue'))
```



```
spreadLevelPlot(globulin, by = fibrinogen) #??
```

Spread–Level Plot for globulin by fibrinogen



```
##           LowerHinge Median UpperHinge Hinge-Spread
## 2.5-3.5      32.0      36      38.0           6
## 2-2.5       31.0      36      37.0           6
## 3.5-6       34.5      37      41.5           7
##
## Suggested power transformation:  -4.626148
leveneTest(globulin ~fibrinogen)

## Levene's Test for Homogeneity of Variance (center = median)
##      Df F value Pr(>F)
## group  2  0.3905 0.6802
##      29

summary(lm(anovafib))

##
## Call:
## lm(formula = anovafib)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -7.765 -3.833  0.701  2.235 10.235
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)    34.8333     1.3363  26.068  <2e-16 ***
## fibrinogen2.5-3.5  0.9314     1.7453   0.534   0.598
```

```
## fibrinogen3.5-6      3.5000      2.9880   1.171   0.251
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 4.629 on 29 degrees of freedom
## Multiple R-squared:  0.0458, Adjusted R-squared:  -0.02001
## F-statistic: 0.696 on 2 and 29 DF,  p-value: 0.5067
```