

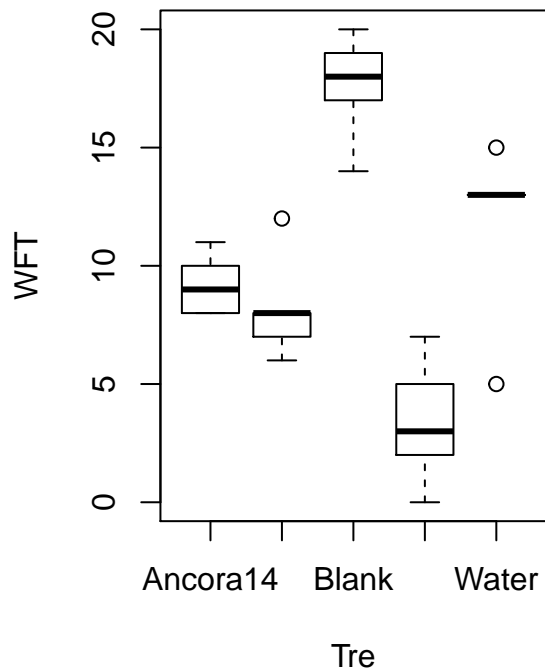
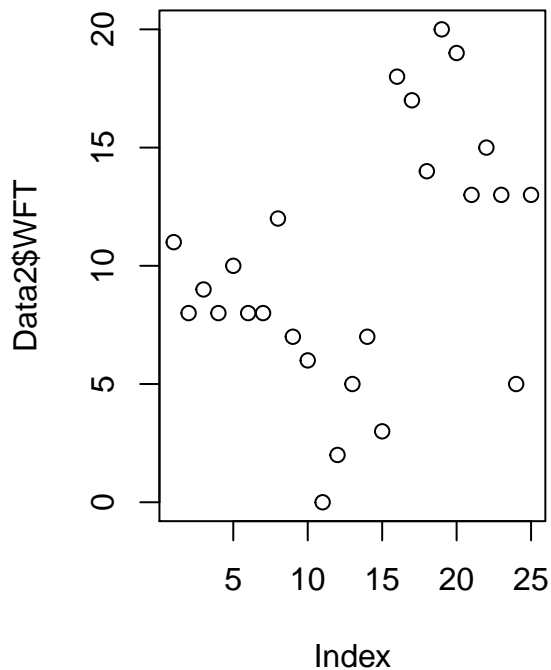
Project2

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```
Tre <- rep(c("Ancora14", "Ancora28", "Fulcrum2", "Blank", "Water"), each = 5)
Rep <- rep(1:5, length = 25)
Num <- rep(20, length = 25)
WFT <- c(11, 8, 9, 8, 10, 8, 8, 12, 7, 6, 0, 2, 5, 7, 3, 18, 17, 14, 20, 19,
         13, 15, 13, 5, 13)
Data2 <- data.frame(Tre = as.factor(Tre), Rep, Num, WFT)
```

```
par(mfrow = c(1, 2))
plot(Data2$WFT)
plot(WFT ~ Tre, data = Data2)
```



```
tapply(WFT, Tre, mean, data = Data2)
```

```
## Ancora14 Ancora28 Blank Fulcrum2 Water
##      9.2      8.2    17.6      3.4    11.8
```

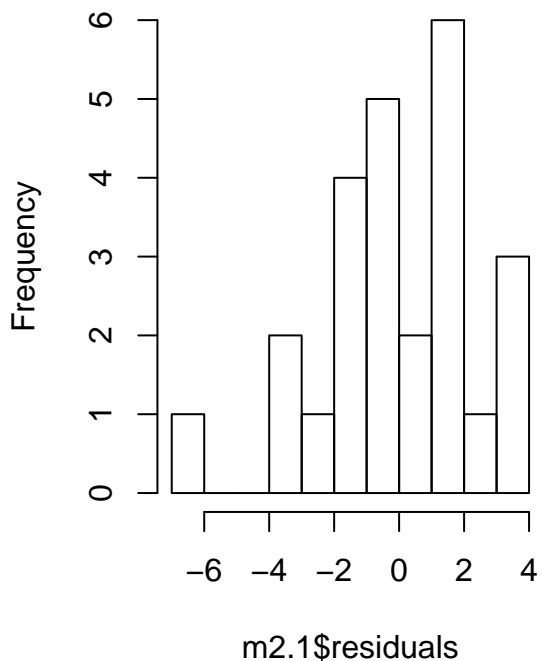
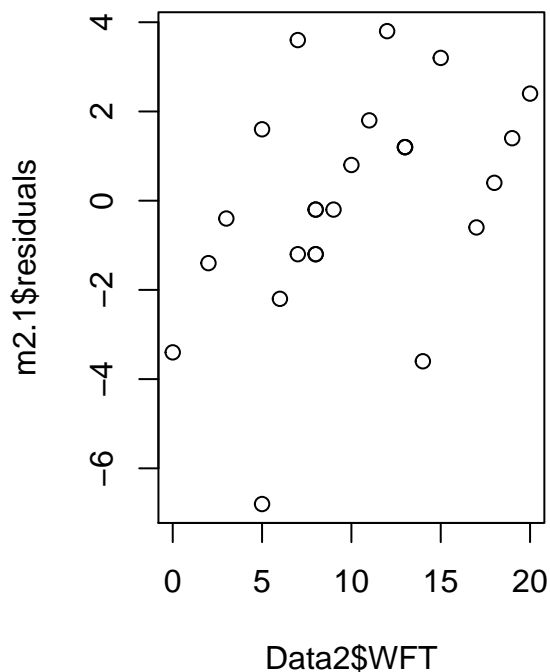
```
m2.1 <- lm(WFT ~ Tre - 1, data = Data2)
summary(m2.1)
```

```
##
## Call:
```

```
## lm(formula = WFT ~ Tre - 1, data = Data2)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
##     -6.8     -1.2     -0.2      1.4      3.8
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## TreAncora14      9.200      1.178   7.809 1.69e-07 ***
## TreAncora28      8.200      1.178   6.960 9.34e-07 ***
## TreBlank        17.600      1.178  14.939 2.59e-12 ***
## TreFulcrum2       3.400      1.178   2.886 0.00914 **
## TreWater        11.800      1.178  10.016 3.08e-09 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 2.634 on 20 degrees of freedom
## Multiple R-squared:  0.9566, Adjusted R-squared:  0.9458
## F-statistic: 88.25 on 5 and 20 DF,  p-value: 6.276e-13
```

```
par(mfrow = c(1, 2))
plot(Data2$WFT, m2.1$residuals) #Checking the assumption of normality(*Nonnormal*).
hist(m2.1$residuals, breaks = 15)
```

Histogram of m2.1\$residuals

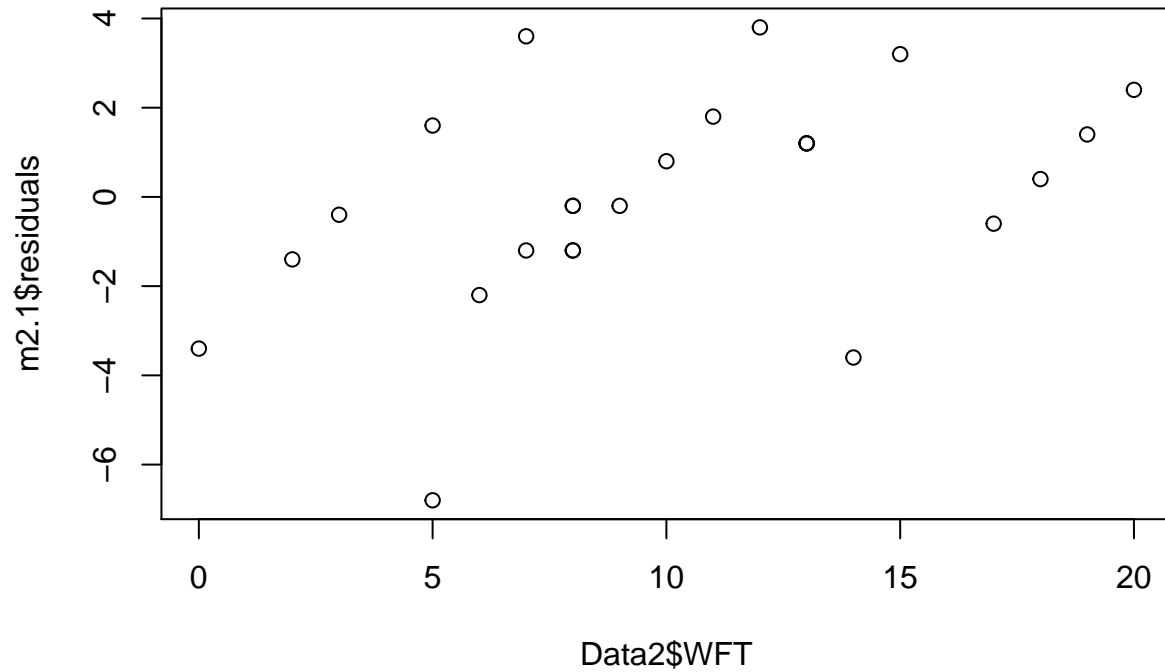


```
shapiro.test(m2.1$residuals)
```

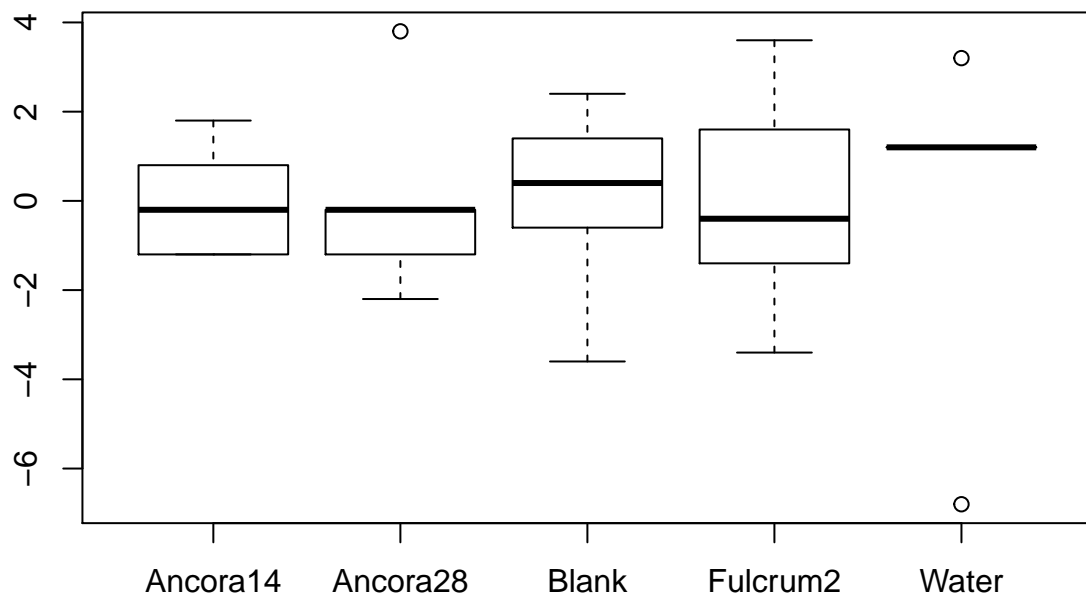
```
##
```

```
## Shapiro-Wilk normality test
##
## data: m2.1$residuals
## W = 0.95121, p-value = 0.2669
```

```
plot(Data2$WFT, m2.1$residuals) #Checking the assumption of constant variance
```



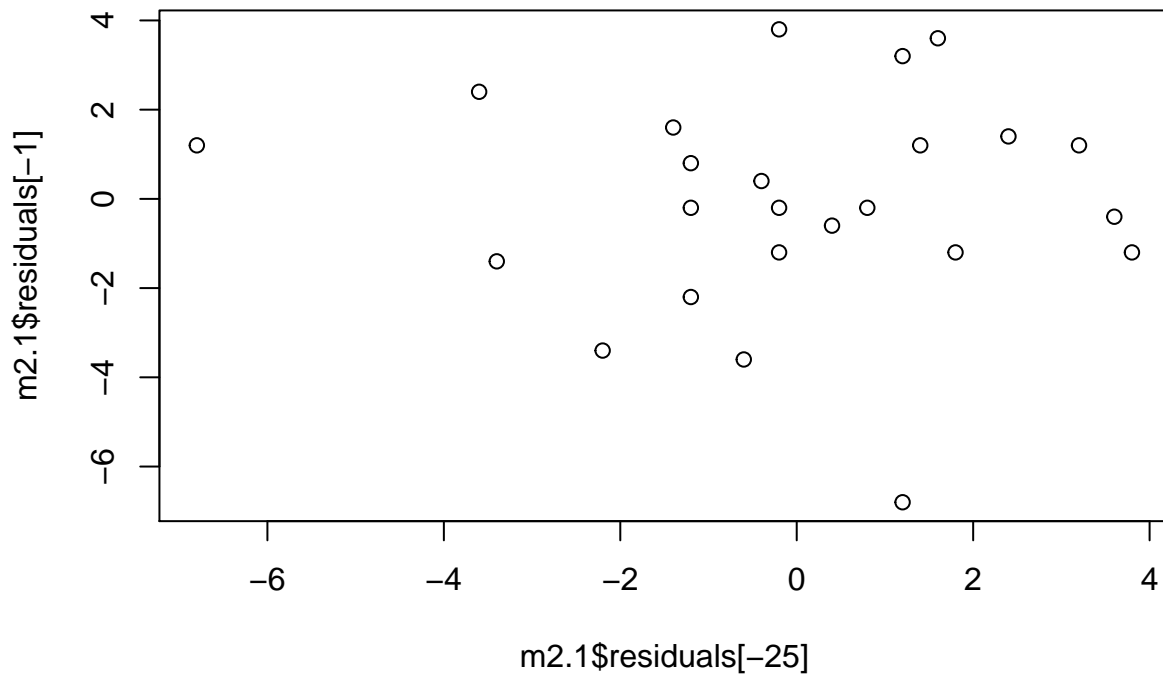
```
plot(Data2$Tre, m2.1$residuals)
```



```
plot(m2.1$residuals[-25], m2.1$residuals[-1])  
cor(m2.1$residuals[-25], m2.1$residuals[-1])
```

```
## [1] -0.01239373
```

```
library(lmtest)
```



```
dwtest(m2.1)
```

```
##
## Durbin-Watson test
##
## data: m2.1
## DW = 1.9893, p-value = 0.1844
## alternative hypothesis: true autocorrelation is greater than 0
```

```
anova(m2.1)
```

```
## Analysis of Variance Table
##
## Response: WFT
##      Df Sum Sq Mean Sq F value    Pr(>F)
## Tre      5 3062.2   612.44  88.248 6.276e-13 ***
## Residuals 20  138.8     6.94
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
Differ <- TukeyHSD(x = aov(Data2$WFT ~ Data2$Tre), "Data2$Tre", conf.level = 0.95)
Differ
```

```
## Tukey multiple comparisons of means
## 95% family-wise confidence level
##
## Fit: aov(formula = Data2$WFT ~ Data2$Tre)
##
```

```
## $`Data2$Tre`
##           diff      lwr      upr      p adj
## Ancora28-Ancora14 -1.0 -5.985695  3.9856947 0.9734348
## Blank-Ancora14      8.4  3.414305 13.3856947 0.0005369
## Fulcrum2-Ancora14 -5.8 -10.785695 -0.8143053 0.0177738
## Water-Ancora14      2.6 -2.385695  7.5856947 0.5377667
## Blank-Ancora28      9.4  4.414305 14.3856947 0.0001410
## Fulcrum2-Ancora28 -4.8 -9.785695  0.1856947 0.0626669
## Water-Ancora28      3.6 -1.385695  8.5856947 0.2346048
## Fulcrum2-Blank     -14.2 -19.185695 -9.2143053 0.0000004
## Water-Blank         -5.8 -10.785695 -0.8143053 0.0177738
## Water-Fulcrum2      8.4  3.414305 13.3856947 0.0005369
```

```
library(multcomp)
cld(summary(glht(m2.1, linfct = mcp(Tre = "Tukey"))), decreasing = T)
```

```
## Ancora14 Ancora28      Blank Fulcrum2      Water
##          "b"      "bc"      "a"      "c"      "b"
```

```
library(agricolae)
model <- aov(Data2$WFT ~ Data2$Tre, data = Data2)
df <- df.residual(model)
MSerror <- deviance(model)/df
with(Data2, HSD.test(WFT, Tre, df, MSerror, group = TRUE, console = TRUE, main = "Difference between th
```

```
##
## Study: Difference between the treatments
##
## HSD Test for WFT
##
## Mean Square Error: 6.94
##
## Tre, means
##
##           WFT      std r Min Max
## Ancora14  9.2 1.303840 5   8 11
## Ancora28  8.2 2.280351 5   6 12
## Blank     17.6 2.302173 5  14 20
## Fulcrum2  3.4 2.701851 5   0  7
## Water     11.8 3.898718 5   5 15
##
## Alpha: 0.05 ; DF Error: 20
## Critical Value of Studentized Range: 4.231857
##
## Minimum Significant Difference: 4.985695
##
## Treatments with the same letter are not significantly different.
##
##           WFT groups
## Blank     17.6      a
## Water     11.8      b
## Ancora14  9.2      b
## Ancora28  8.2     bc
## Fulcrum2  3.4      c
```

```
m2.2 <- glm(cbind(WFT, Num - WFT) ~ Tre - 1, family = quasibinomial(link = "logit"),
  data = Data2)
summary(m2.2)
```

```
##
## Call:
## glm(formula = cbind(WFT, Num - WFT) ~ Tre - 1, family = quasibinomial(link = "logit"),
##     data = Data2)
##
## Deviance Residuals:
##      Min       1Q   Median       3Q      Max
## -3.08721  -0.54080  -0.08978   0.80587   2.26127
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## TreAncora14  -0.1603     0.2788  -0.575 0.571648
## TreAncora28  -0.3640     0.2825  -1.288 0.212380
## TreBlank      1.9924     0.4276   4.659 0.000151 ***
## TreFulcrum2  -1.5856     0.3699  -4.286 0.000360 ***
## TreWater      0.3640     0.2825   1.288 0.212380
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for quasibinomial family taken to be 1.931019)
##
##      Null deviance: 162.165  on 25  degrees of freedom
## Residual deviance:  42.312  on 20  degrees of freedom
## AIC: NA
##
## Number of Fisher Scoring iterations: 5
```

```
library(multcomp)
Differ2.2 <- summary(glht(m2.2, linfct = mcp(Tre = "Tukey")))
Differ2.2
```

```
##
##      Simultaneous Tests for General Linear Hypotheses
##
## Multiple Comparisons of Means: Tukey Contrasts
##
##
## Fit: glm(formula = cbind(WFT, Num - WFT) ~ Tre - 1, family = quasibinomial(link = "logit"),
##     data = Data2)
##
## Linear Hypotheses:
##              Estimate Std. Error z value Pr(>|z|)
## Ancora28 - Ancora14 == 0  -0.2036     0.3969  -0.513  0.9858
## Blank - Ancora14 == 0     2.1528     0.5105   4.217 <0.001 ***
## Fulcrum2 - Ancora14 == 0  -1.4253     0.4632  -3.077  0.0176 *
## Water - Ancora14 == 0     0.5243     0.3969   1.321  0.6742
## Blank - Ancora28 == 0     2.3564     0.5125   4.598 <0.001 ***
## Fulcrum2 - Ancora28 == 0  -1.2217     0.4655  -2.624  0.0645 .
## Water - Ancora28 == 0     0.7279     0.3996   1.822  0.3564
## Fulcrum2 - Blank == 0    -3.5781     0.5654  -6.328 <0.001 ***
## Water - Blank == 0       -1.6285     0.5125  -3.177  0.0124 *
```

```

## Water - Fulcrum2 == 0      1.9496      0.4655      4.188      <0.001 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
## (Adjusted p values reported -- single-step method)

cld(Differ2.2, decreasing = T)

## Ancora14 Ancora28      Blank Fulcrum2      Water
##      "b"      "bc"      "a"      "c"      "b"

library(gamlss)
m2.3 <- gamlss(cbind(WFT, Num - WFT) ~ Tre - 1, data = Data2, family = BB)

## GAMLSS-RS iteration 1: Global Deviance = 123.995
## GAMLSS-RS iteration 2: Global Deviance = 112.6841
## GAMLSS-RS iteration 3: Global Deviance = 112.6369
## GAMLSS-RS iteration 4: Global Deviance = 112.6369

summary(m2.3)

## *****
## Family:  c("BB", "Beta Binomial")
##
## Call:  gamlss(formula = cbind(WFT, Num - WFT) ~ Tre - 1, family = BB,
##      data = Data2)
##
## Fitting method: RS()
##
## -----
## Mu link function:  logit
## Mu Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## TreAncora14  -0.1563      0.2485  -0.629 0.536921
## TreAncora28  -0.3580      0.2525  -1.417 0.172528
## TreBlank      2.0262      0.3890   5.209 5e-05 ***
## TreFulcrum2  -1.6186      0.3384  -4.783 0.000129 ***
## TreWater      0.3650      0.2552   1.430 0.168938
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## -----
## Sigma link function:  log
## Sigma Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)  -3.4942      0.7895  -4.426 0.00029 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## -----
## No. of observations in the fit:  25
## Degrees of Freedom for the fit:  6
##      Residual Deg. of Freedom:  19
##              at cycle:  4
##
## Global Deviance:      112.6369
##      AIC:      124.6369

```



```
##          SBC:      131.9502
## *****
```