Normality_residuals_models

Fay

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Testing the residuals of the model predicting weight loss. Grouping with the variable "Sex"

```r
Field$Sex <- as.factor(Field$Sex)

fitWL_Sex <- parasiteLoad::analyse(data = Field,
                                   response = "predicted_WL",
                                   model = "normal",
                                   group = "Sex")
```

```
## [1] "Analysing data for response: predicted_WL"
## [1] "Fit for the response: predicted_WL"
## [1] "Fitting for all"
## [1] "Fitting model basic without alpha"
## [1] "Did converge"
## [1] "Fitting model basic with alpha"
## [1] "Did converge"
## [1] "Fitting model advanced without alpha"
## [1] "Did converge"
## [1] "Fitting model advanced with alpha"
## [1] "Did converge"
## [1] "Fitting for groupA : F"
## [1] "Fitting model basic without alpha"
## [1] "Did converge"
## [1] "Fitting model basic with alpha"
## [1] "Did converge"
## [1] "Fitting model advanced without alpha"
## [1] "Did converge"
## [1] "Fitting model advanced with alpha"
## [1] "Did converge"
## [1] "Fitting for groupB : M"
## [1] "Fitting model basic without alpha"
## [1] "Did converge"
## [1] "Fitting model basic with alpha"
## [1] "Did converge"
## [1] "Fitting model advanced without alpha"
## [1] "Did converge"
## [1] "Fitting model advanced with alpha"
## [1] "Did converge"
## [1] "Testing H0 no alpha vs alpha"
##    dLL dF      pvalue
## 1 3.62  1 0.007097729
```

```
## [1] "Testing H1 no alpha vs alpha"
##    dLL dDF     pvalue
## 1 2.85   1 0.01704348
## [1] "Testing H2 groupA no alpha vs alpha"
##   dLL dDF    pvalue
## 1 1.1   1 0.1372232
## [1] "Testing H2 groupB no alpha vs alpha"
##   dLL dDF     pvalue
## 1 2.8   1 0.01801596
## [1] "Testing H3 groupA no alpha vs alpha"
##    dLL dDF    pvalue
## 1 1.26   1 0.1127669
## [1] "Testing H3 groupB no alpha vs alpha"
##    dLL dDF     pvalue
## 1 2.83   1 0.01730355
## [1] "Testing H1 vs H0"
##    dLL dDF    pvalue
## 1 0.96   1 0.1657638
## [1] "Testing H2 vs H0"
##    dLL dDF    pvalue
## 1 0.33   3 0.8828548
## [1] "Testing H3 vs H1"
##    dLL dDF    pvalue
## 1 3.13   4 0.1810318
## [1] "Testing H3 vs H2"
##    dLL dDF     pvalue
## 1 3.76   2 0.02334086
```

```r
# Define or ensure MeanLoad is correctly defined
MeanLoad <- function(L1, alpha, HI) {
    # Placeholder formula: adjust based on actual functional form
    return(L1 + alpha * HI)  # Adjust this formula as necessary
}

# Calculate predicted mean using MeanLoad for H0
predicted_mean_H0 <- MeanLoad(L1 = 9.3545283, alpha = -0.2786233, HI = Field$HI)

# Assuming normal distribution
predicted_values_H0 <- rnorm(length(predicted_mean_H0),
                             mean = predicted_mean_H0, sd = 2.4458989)

# Calculate residuals
observed_values <- Field$predicted_WL
residuals_H0 <- observed_values - predicted_values_H0

# Histogram of residuals
hist(residuals_H0, main="Histogram of Residuals for H0", xlab="Residuals")
```
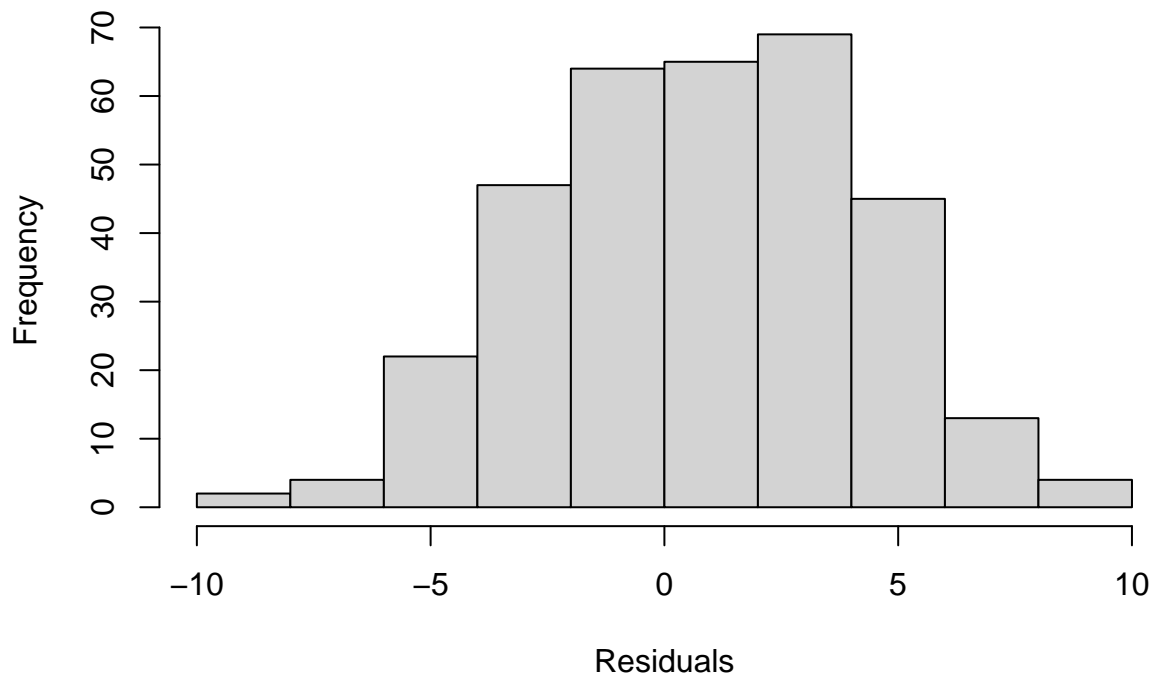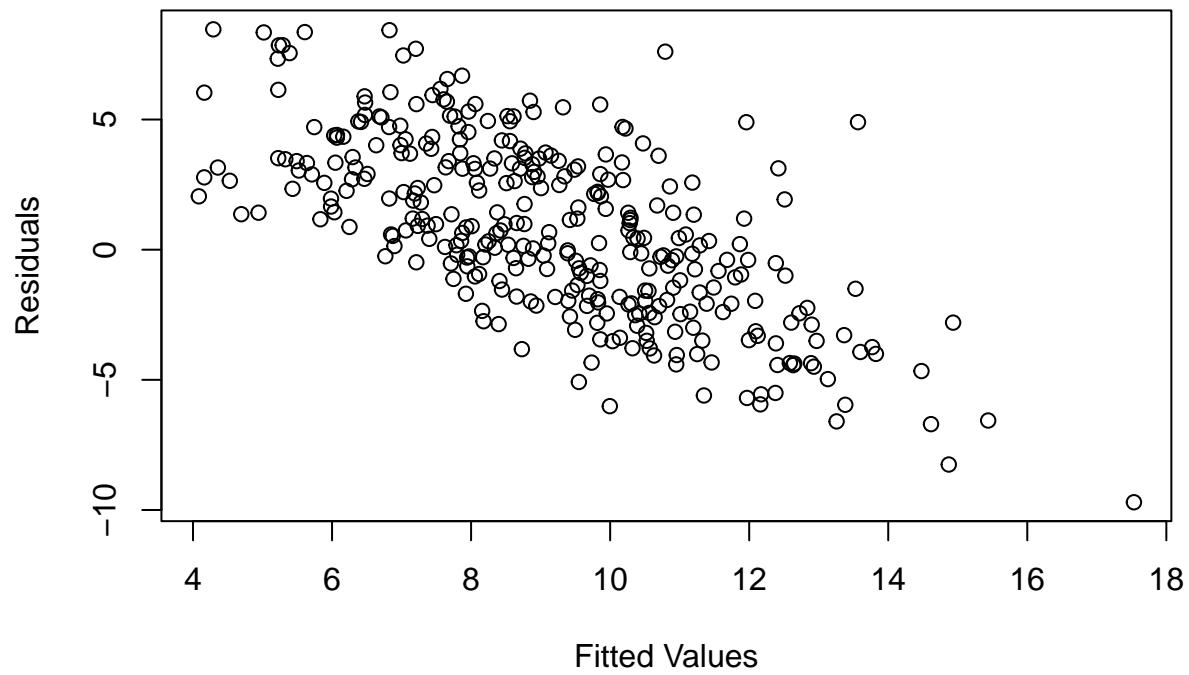
Histogram of Residuals for H0


```r
# Shapiro-Wilk test for normality
shapiro.test(residuals_H0)
```

```
##
##  Shapiro-Wilk normality test
##
## data:  residuals_H0
## W = 0.99382, p-value = 0.1898
```

```r
# Plotting residuals against fitted values
plot(predicted_values_H0, residuals_H0, main="Residual vs. Fitted Plot for H0",
     xlab="Fitted Values", ylab="Residuals")
```

Residual vs. Fitted Plot for H0


```
# Generating a Q-Q plot for normality check
qqnorm(residuals_H0, main="Q-Q Plot for Normality Check of H0 Residuals")
```

Q–Q Plot for Normality Check of H0 Residuals