

```
## Linear mixed model fit by REML ['lmerMod']
## Formula: inverse_power_rt ~ number_of_words + readability + (1 | ID)
## Data: df
##
## REML criterion at convergence: -1480.2
##
## Scaled residuals:
##      Min       1Q   Median       3Q      Max
## -2.97808 -0.64371  0.06979  0.66357  3.02511
##
## Random effects:
## Groups Name Variance Std.Dev.
## ID      (Intercept) 0.001248 0.03532
## Residual              0.003717 0.06097
## Number of obs: 565, groups: ID, 24
##
## Fixed effects:
##              Estimate Std. Error t value
## (Intercept)    0.878968   0.007653 114.854
## number_of_words -0.005653   0.002585  -2.186
## readability    0.006260   0.002586   2.421
##
## Correlation of Fixed Effects:
##              (Intr) nmbr__
## nmbr_f_wrds  0.000
## readability  0.000 -0.115
```

Below I will transform the t-values into p-values.

```
t_values <- c(114.854, -2.186, 2.421)
dof <- 560
p_values <- 2 * pt(abs(t_values), df = dof, lower.tail = FALSE)
p_values
```

```
## [1] 0.00000000 0.02922893 0.01579475
```

The residuals have to be normally distributed because this is an assumption for mixed-effects models, therefore the p-value of the residuals has to be above the 0.05 threshold.

```
residuals_model_simple <- resid(model_simple)

# I will run a Shapiro-Wilk test to obtain the p-value.

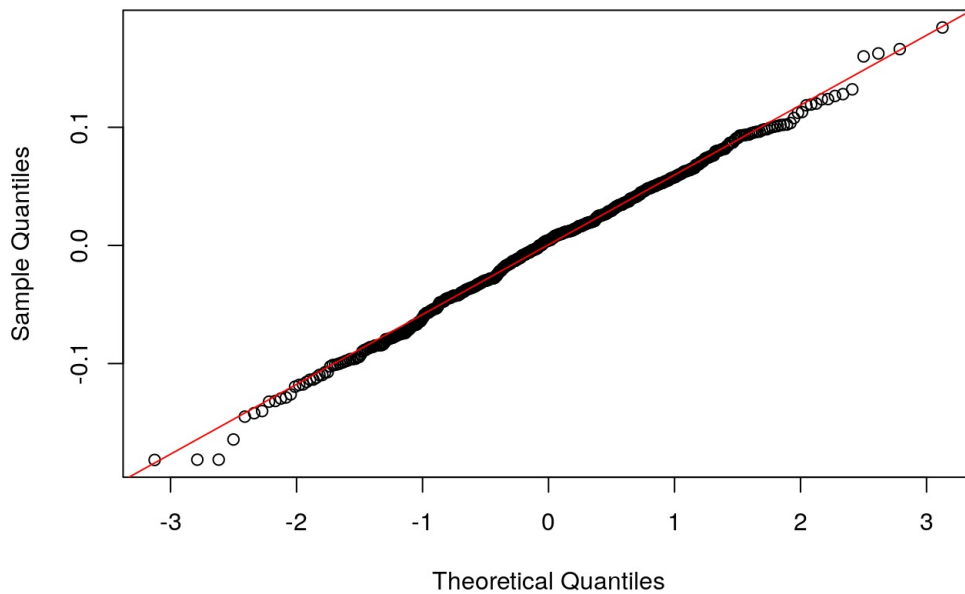
shapiro.test(residuals_model_simple)
```

```
##
## Shapiro-Wilk normality test
##
## data: residuals_model_simple
## W = 0.99699, p-value = 0.3839
```

Below is a QQ-plot of the residuals to see if they align with those of a theoretical normal distribution visually.

```
qqnorm(residuals_model_simple)
qqline(residuals_model_simple, col = "red")
```

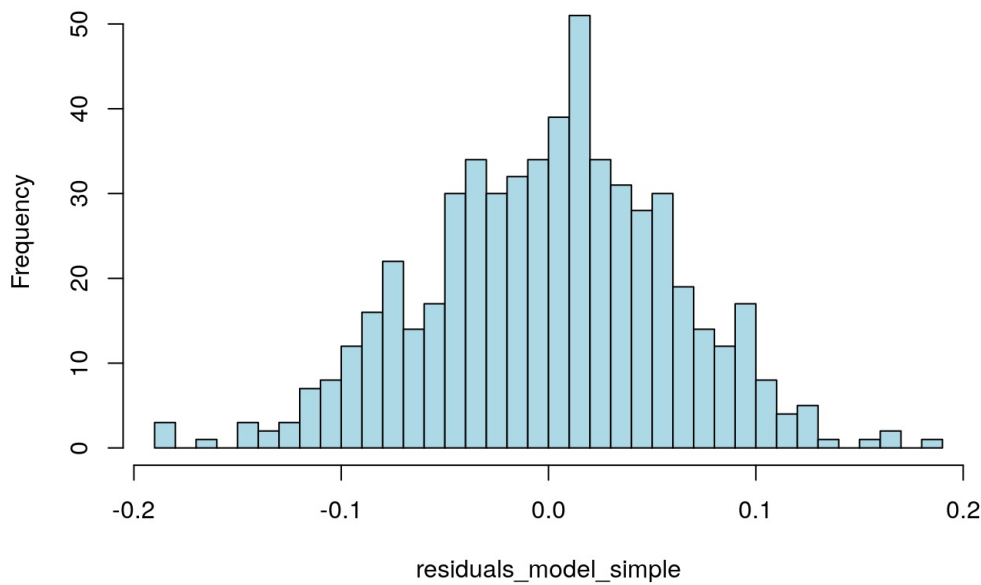
Normal Q-Q Plot



I will create a histogram of residuals to visually inspect the residuals.

```
hist(residuals_model_simple, main = "Histogram of Residuals", breaks = 50, col = "lightblue", border = "black")
```

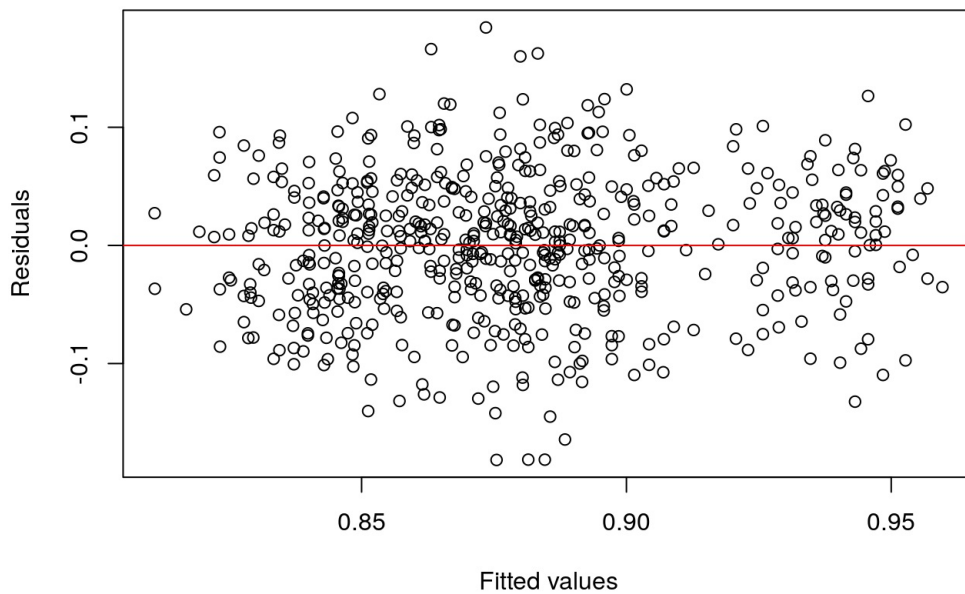
Histogram of Residuals



Below is a residuals vs fitted values plot to check if the data is homoscedastic and the relationship between the dependent variables and the independent variables is linear. For these assumptions to be met, there must not be a specific shape in the plot (they should be scattered randomly).

```
plot(fitted(model_simple), resid(model_simple),
     main = "Residuals vs Fitted",
     xlab = "Fitted values",
     ylab = "Residuals")
abline(h = 0, col = "red")
```

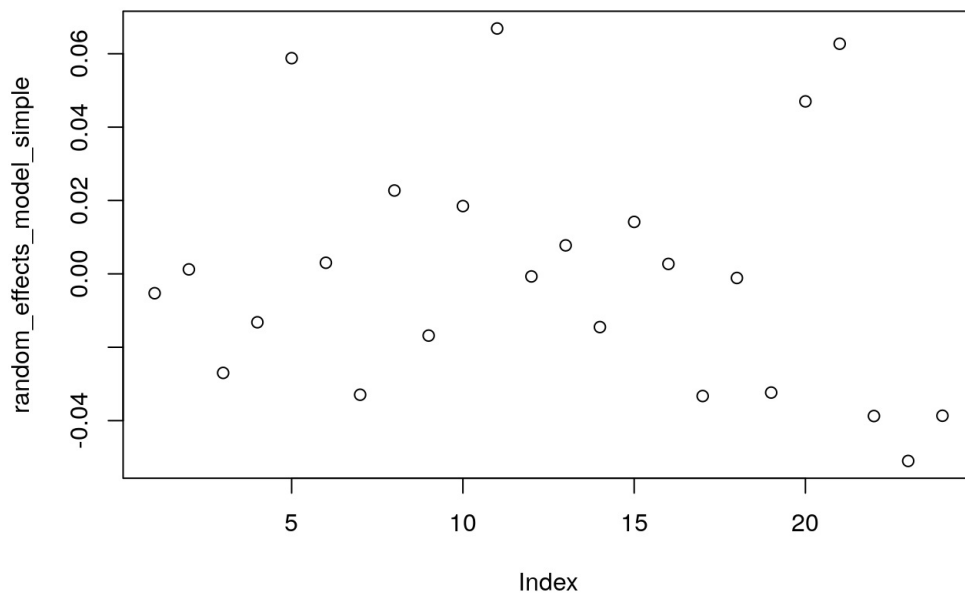
Residuals vs Fitted



One assumption is that the random intercepts have to be normal. Below I will get the random intercepts of my model and plot them using a histogram and a QQ-plot to see if they are normally distributed visually. Then I will run a Shapiro-Wilk test to confirm the normality if the p-value is above the conventional threshold of 0.05. I will also check that the mean of the random intercepts is 0 as this is another assumption.

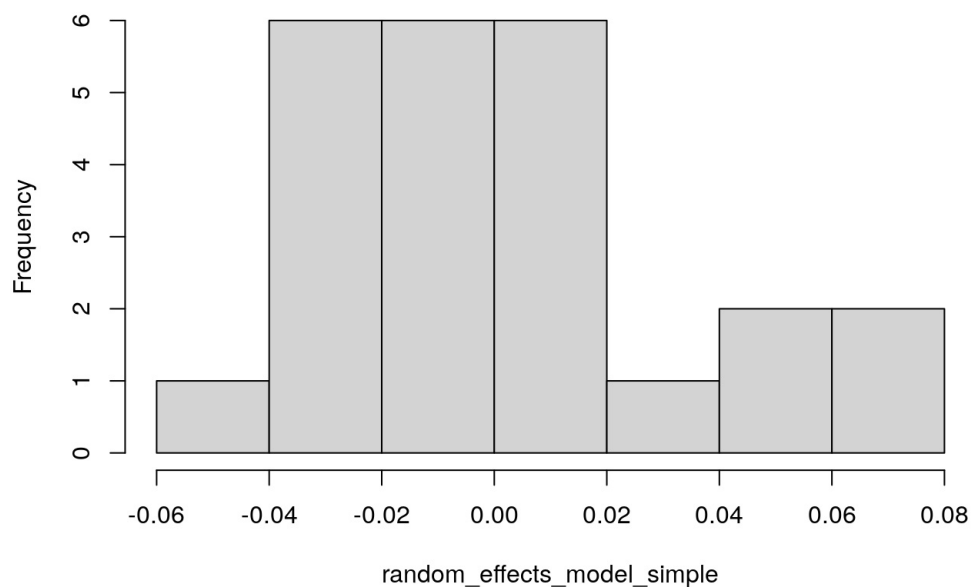
```
random_effects_model_simple <- ranef(model_simple)$ID[, 1]
random_effects_model_simple <- as.numeric(random_effects_model_simple)

plot(random_effects_model_simple)
```



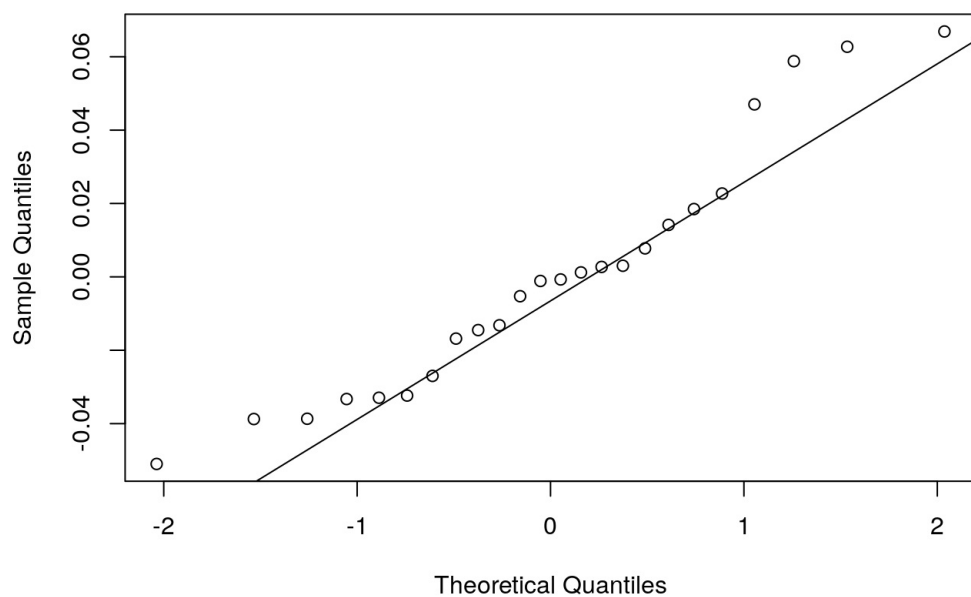
```
hist(random_effects_model_simple)
```

Histogram of random_effects_model_simple



```
qqnorm(random_effects_model_simple)
qqline(random_effects_model_simple)
```

Normal Q-Q Plot



```
mean(random_effects_model_simple)
```

```
## [1] -5.991843e-15
```

```
shapiro.test(random_effects_model_simple)
```

```
##
##  Shapiro-Wilk normality test
##
## data:  random_effects_model_simple
## W = 0.93462, p-value = 0.1237
```

```
AIC(model_simple)
```

```
## [1] -1470.153
```

```
BIC(model_simple)
```

```
## [1] -1448.469
```

```
# This model meets all the assumptions required for a mixed-effects model.
```

```
# The model without polarity and subjectivity fits the data better. I know this because of the REML value of -1480.2, the AIC value of -1470.15 and the BIC value of -1448.47, which are lower in all cases.
```

```
# The following model is the model I have constructed with the lowest REML, AIC and BIC values.
```

```
model_slope <- lmer(inverse_power_rt ~ readability + (number_of_words|ID), data = df)
```

```
summary(model_slope)
```

```
## Linear mixed model fit by REML ['lmerMod']
## Formula: inverse_power_rt ~ readability + (number_of_words | ID)
##      Data: df
##
## REML criterion at convergence: -1485.8
##
## Scaled residuals:
##      Min       1Q   Median       3Q      Max
## -3.01402 -0.63247  0.06985  0.68290  2.98981
##
## Random effects:
##  Groups      Name                Variance Std.Dev. Corr
##  ID          (Intercept)         1.247e-03 0.035317
##             number_of_words 2.595e-05 0.005094 -0.17
##  Residual                        3.716e-03 0.060960
## Number of obs: 565, groups: ID, 24
##
## Fixed effects:
##              Estimate Std. Error t value
## (Intercept) 0.878028   0.007639 114.947
## readability 0.005715   0.002571   2.223
##
## Correlation of Fixed Effects:
##              (Intr)
## readability -0.006
```

```
# Below I will transform the t-values into p-values.
```

```
t_values <- c(114.854, -2.186, 2.421)
dof <- 560
p_values <- 2 * pt(abs(t_values), df = dof, lower.tail = FALSE)
p_values
```

```
## [1] 0.00000000 0.02922893 0.01579475
```

```
# The residuals have to be normally distributed because this is an assumption for mixed-effects models, therefore the p-value of the residuals has to be above the 0.05 threshold.
```

```
residuals_model_slope <- resid(model_slope)
```

```
# I will run a Shapiro-Wilk test to obtain the p-value.
```

```
shapiro.test(residuals_model_slope)
```

```
##
## Shapiro-Wilk normality test
##
## data: residuals_model_slope
## W = 0.99654, p-value = 0.2635
```

```
# Below is a QQ-plot of the residuals to see if they align with those of a theoretical normal distribution visually.
```

```
qqnorm(residuals_model_slope)
qqline(residuals_model_slope, col = "red")
```