HR_Va_h2_G2_2023

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```
#load pHRkages
library(lme4)
```

```
## Loading required package: Matrix
```

```
library(tidyverse)
```

```
## -- Attaching core tidyverse packages ------------------------ tidyverse 2.0.0 --
## v dplyr     1.1.4     v readr     2.1.5
## v forcats   1.0.0     v stringr   1.5.1
## v ggplot2   3.4.4     v tibble    3.2.1
## v lubridate 1.9.3     v tidyr     1.3.0
## v purrr     1.0.2
```

```
## -- Conflicts ------------------------------------------ tidyverse_conflicts() --
## x tidyr::expand() masks Matrix::expand()
## x dplyr::filter() masks stats::filter()
## x dplyr::lag()    masks stats::lag()
## x tidyr::pack()   masks Matrix::pack()
## x tidyr::unpack() masks Matrix::unpack()
## i Use the conflicted package (<http://conflicted.r-lib.org/>) to force all conflicts to become errors
```

```
library(lmerTest)
```

```
##
## Attaching package: 'lmerTest'
##
## The following object is masked from 'package:lme4':
##
##     lmer
##
## The following object is masked from 'package:stats':
##
##     step
```

```
library(car)
```

```
## Loading required package: carData
##
## Attaching package: 'car'
##
## The following object is masked from 'package:dplyr':
##
##     recode
##
```

```
## The following object is masked from 'package:purrr':
##
##     some
```

##########**2023**##########

Read in the data:

```
HR_23 <- read_csv(here::here("data_sheets", "compiled_sheets", "HR_mastersheet_Fitness-mains_2023.csv"))
```

```
## Rows: 781 Columns: 51
## -- Column specification --------------------------------------------------------
## Delimiter: ","
## chr   (6): Gen, Donor, Recipient, sample_ID_SEG, sample_ID, SegPos
## dbl  (35): Year, Transect, Sequence, Plant_ID, days_sow2flower, days_plant2f...
## lgl   (1): F_plant
## date  (9): Sow_Date, Plant_Date, FFD, LFD, F_Num_01, F_Num_02, F_Num_03, pho...
##
## i Use `spec()` to retrieve the full column specification for this data.
## i Specify the column types or set `show_col_types = FALSE` to quiet this message.
```

```
HR_23_fit <- HR_23 %>%
  filter(Gen == "G2")

HR_22_23_full <- read_csv(here::here("data_sheets", "compiled_sheets", "HR_22_23_full.csv"))
```

```
## Warning: One or more parsing issues, call `problems()` on your data frame for details,
## e.g.:
##   dat <- vroom(...)
##   problems(dat)
```

```
## Rows: 7684 Columns: 67
## -- Column specification --------------------------------------------------------
## Delimiter: ","
## chr   (9): Gen, Donor, Recipient, sample_ID_SEG, sample_ID, SegPos, Block, R...
## dbl  (45): Year, Transect, Sequence, Plant_ID, days_sow2flower, days_plant2f...
## lgl   (4): F_plant, F_Num_03, Rep_FitP, any_FitP
## date  (9): Sow_Date, Plant_Date, FFD, LFD, F_Num_01, F_Num_02, photo_date, p...
##
## i Use `spec()` to retrieve the full column specification for this data.
## i Specify the column types or set `show_col_types = FALSE` to quiet this message.
```

```
# Calculate the mean surv_to_flower for each group in AC_22_23_full and add it as a new column
HR_22_23_full <- HR_22_23_full %>%
  group_by(Year, Gen, Transect, Sequence, Donor, Recipient, SegPos) %>%
  mutate(prop_surv_to_flower = mean(surv_to_flower, na.rm = TRUE)) %>%
  ungroup()  # Remove grouping

HR_prop_sample <- HR_22_23_full %>%
  select(c(Year, Gen, Transect, Sequence, Donor, Recipient, SegPos, prop_surv_to_flower))  %>%
    distinct()

HR_23_fit <- HR_23_fit %>%
  left_join(HR_prop_sample %>% select(Year, Gen, Transect, Sequence, Donor, Recipient, SegPos, prop_surv
            by = c("Year", "Gen", "Transect", "Sequence", "Donor", "Recipient"))

# Create the new column
```

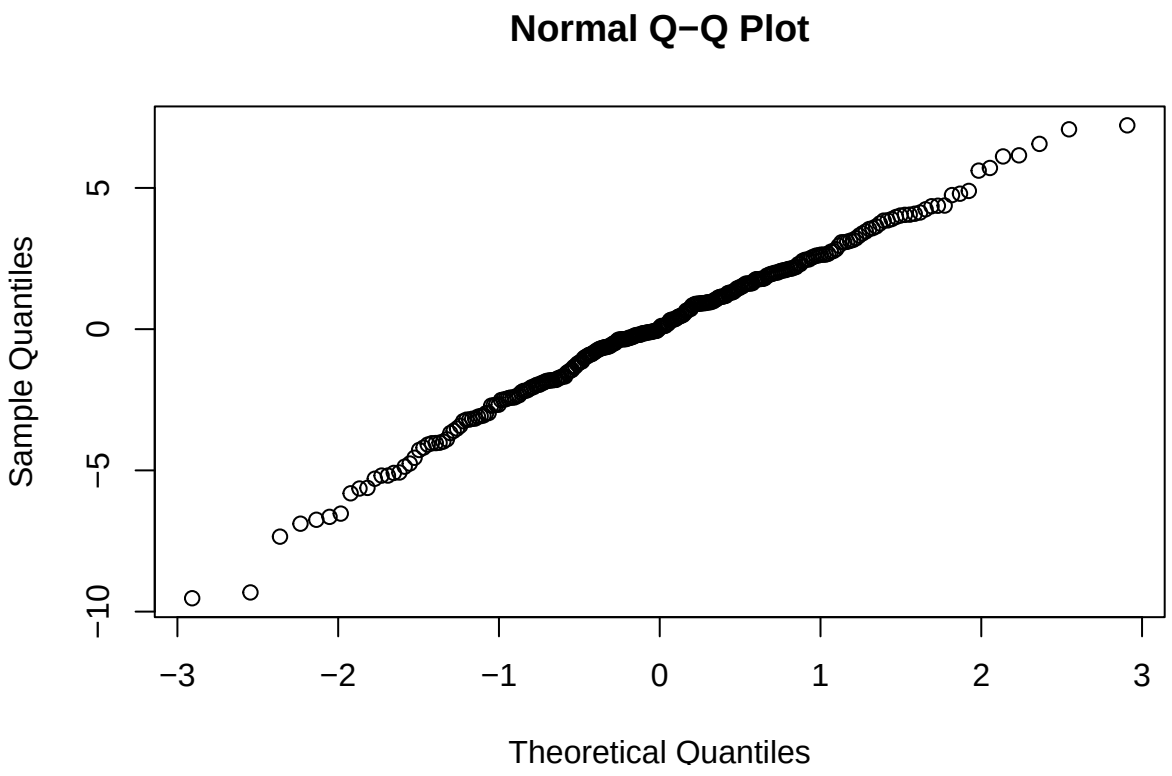
```r
HR_23_fit <- HR_23_fit %>%
  mutate(est_fitness = prop_surv_to_flower * est_fecundity)
```

```r
#log transform certain variables
HR_23_fit$skel_dryweight_mg_SEG <- log(HR_23_fit$skel_dryweight_mg_SEG)
HR_23_fit$SLA_SEG <- log(HR_23_fit$SLA_SEG)
HR_23_fit$est_fitness <- sqrt(HR_23_fit$est_fitness)

#mean center the traits of interest

traits <- c("corolla_diam_mm_SEG", "skel_dryweight_mg_SEG", "fl_duration", "est_fecundity", "msm_all",

# Mean center eHRh trait
for (trait in traits) {
  trait_mean <- mean(HR_23_fit[[trait]], na.rm = TRUE)
  HR_23_fit[[paste0(trait, "_centered")]] <- HR_23_fit[[trait]] - trait_mean
}
```

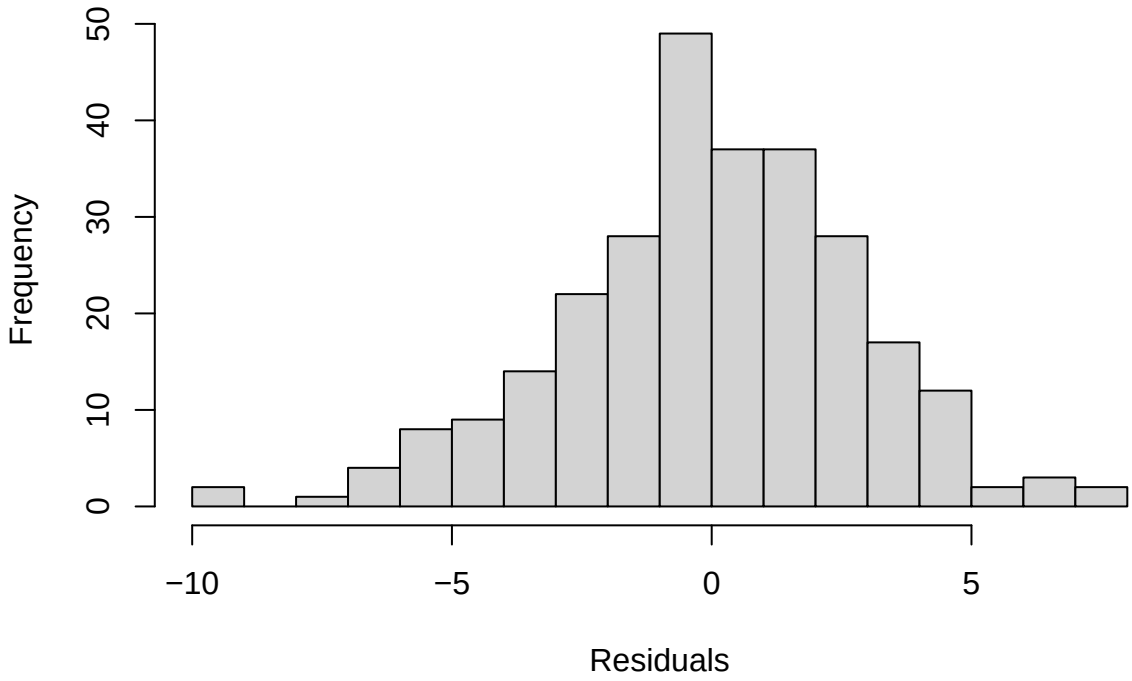
```r
# Create the mixed model for corolla area

corolla_model <- lmer(corolla_diam_mm_SEG_centered ~ (1 | Recipient) + (1 | Donor), data = HR_23_fit)

rand(corolla_model)
```

```
## ANOVA-like table for random-effects: Single term deletions
##
## Model:
## corolla_diam_mm_SEG_centered ~ (1 | Recipient) + (1 | Donor)
##                  npar  logLik    AIC     LRT Df Pr(>Chisq)
## <none>              4 -693.85 1395.7
## (1 | Recipient)     3 -694.07 1394.1 0.44563  1     0.5044
## (1 | Donor)         3 -693.86 1393.7 0.02542  1     0.8733
```

```r
# Get residuals from the model
residuals <- resid(corolla_model)

# Q-Q plot for normality
qqnorm(residuals) #looks good
```




```r
# Histogram for normality
hist(residuals, breaks = 20, main = "Histogram of Residuals", xlab = "Residuals") #normal
```

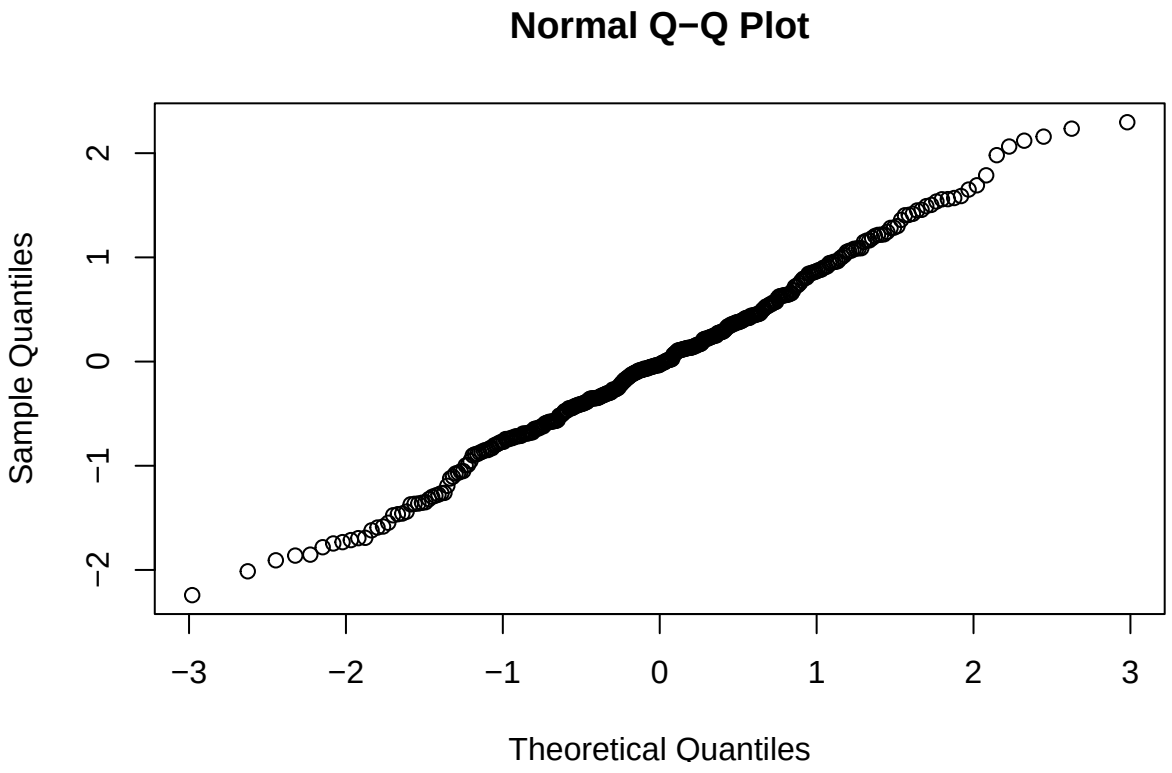



```r
# Create the mixed model for skeleton weight, with skeleton weight log transformed
skel_model <- lmer((skel_dryweight_mg_SEG_centered) ~ (1 | Transect) + (1 | Recipient) + (1 | Donor), da
```

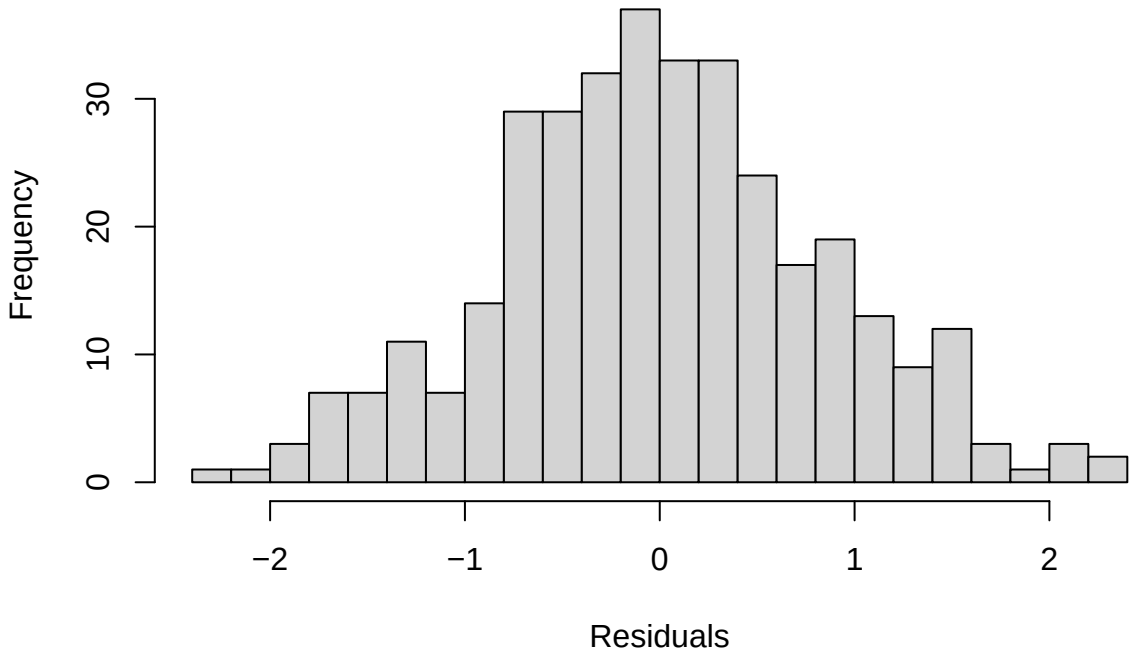
```r
rand(skel_model)
```

```
## ANOVA-like table for random-effects: Single term deletions
##
## Model:
## (skel_dryweight_mg_SEG_centered) ~ (1 | Transect) + (1 | Recipient) + (1 | Donor)
##                  npar  logLik    AIC    LRT Df Pr(>Chisq)
## <none>              5 -468.75 947.51
## (1 | Transect)      4 -472.41 952.82 7.3093  1    0.00686 **
## (1 | Recipient)     4 -469.26 946.53 1.0172  1    0.31319
## (1 | Donor)         4 -468.80 945.60 0.0856  1    0.76986
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

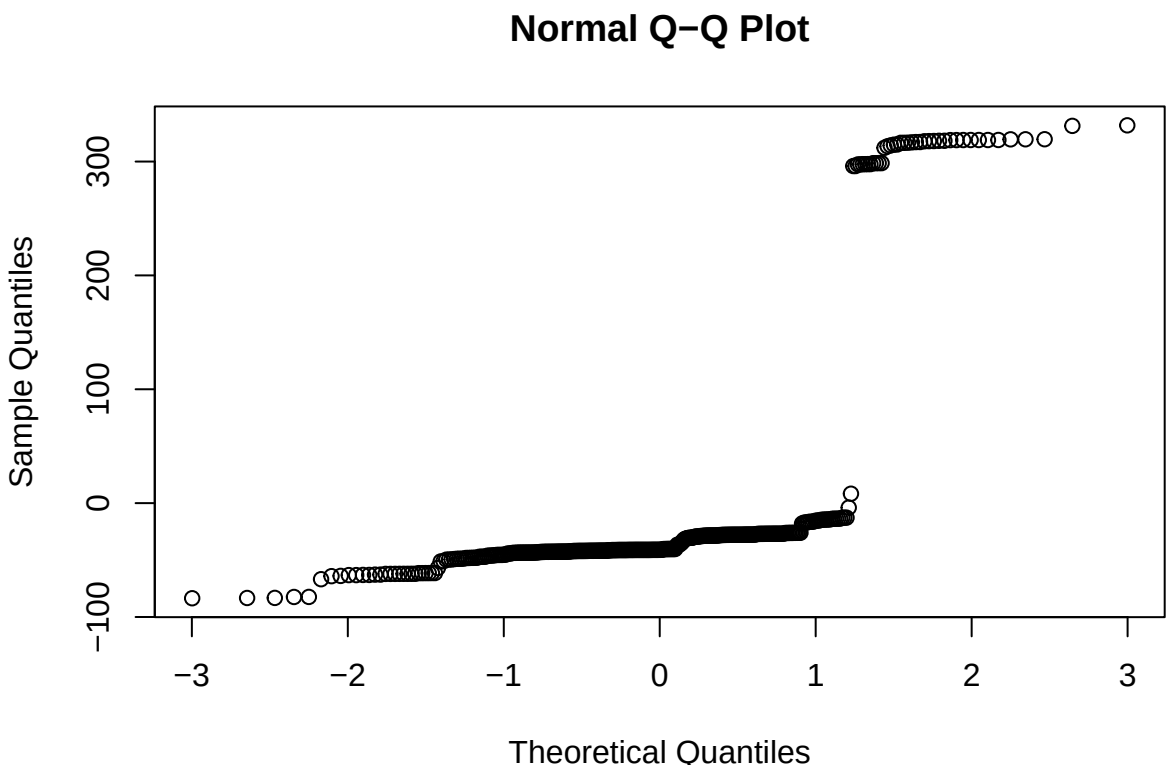
```r
# Get residuals from the model
residuals <- resid(skel_model)

# Q-Q plot for normality
qqnorm(residuals) #looks good
```



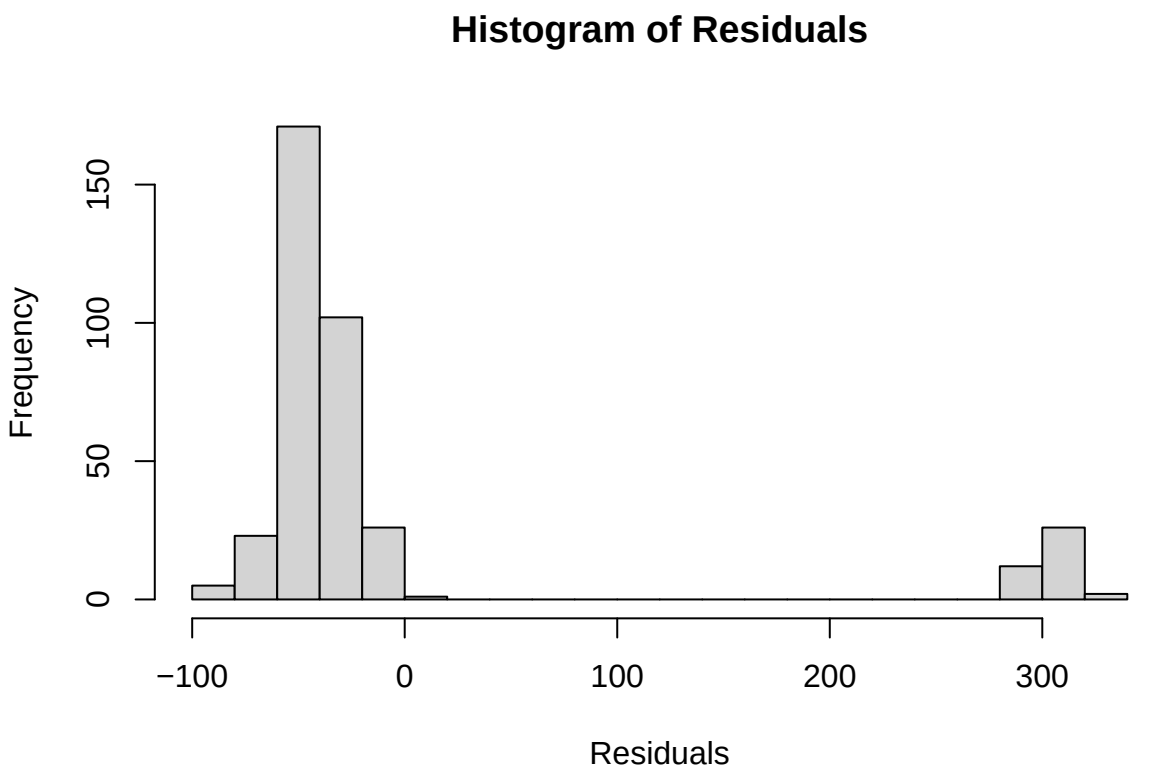

```r
# Histogram for normality
hist(residuals, breaks = 20, main = "Histogram of Residuals", xlab = "Residuals") #normal
```




```r
# Create the mixed model for flowering duration
fl_duration_model <- lmer(fl_duration_centered ~ (1 | Recipient) + (1 | Donor), data = HR_23_fit)

# Get residuals from the model
residuals <- resid(fl_duration_model)

# Q-Q plot for normality
qqnorm(residuals) #looks good
```




```
# Histogram for normality
hist(residuals, breaks = 20, main = "Histogram of Residuals", xlab = "Residuals") #normal
```




```
rand(fl_duration_model)
```

```
## ANOVA-like table for random-effects: Single term deletions
```

```
##
## Model:
## fl_duration_centered ~ (1 | Recipient) + (1 | Donor)
##                 npar  logLik    AIC     LRT Df Pr(>Chisq)
## <none>             4 -2270.1 4548.1
## (1 | Recipient)    3 -2270.5 4546.9 0.82563  1     0.3635
## (1 | Donor)        3 -2270.1 4546.1 0.00656  1     0.9355
```

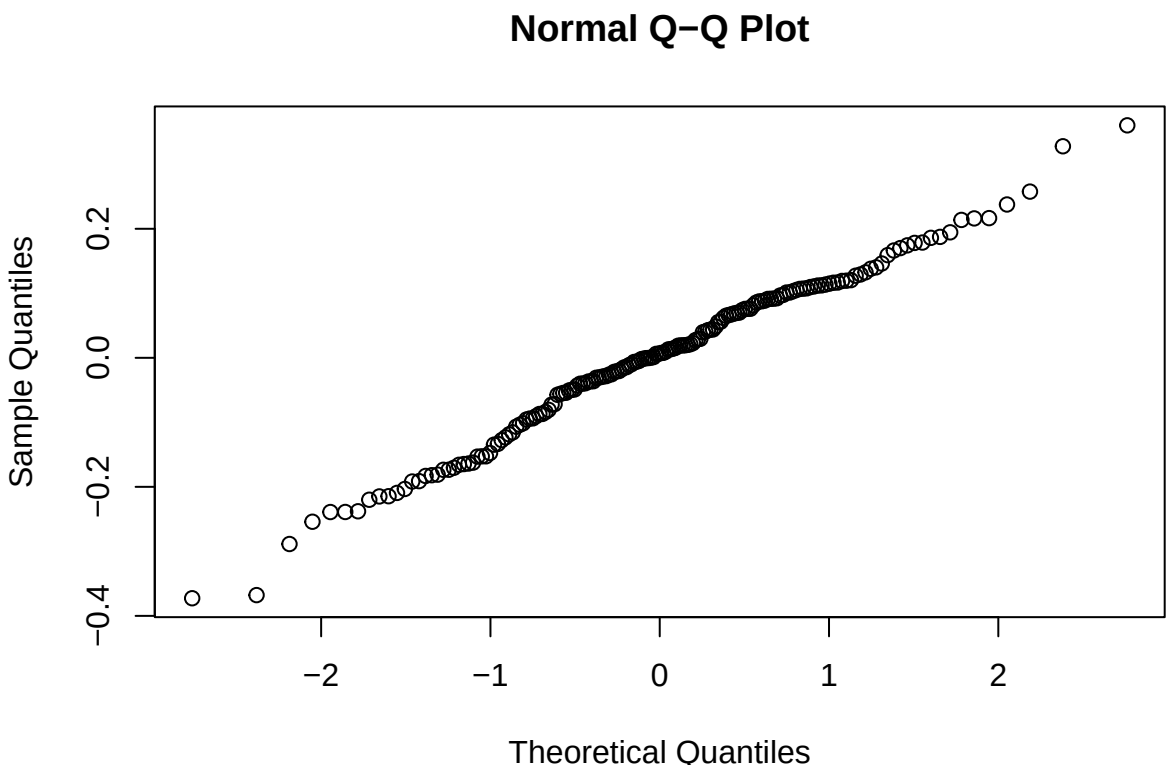
```
# Create the mixed model for estimated fecundity, sqrt transforming estimated fecundity
#est_fecundity_model <- lmer((est_fecundity_centered) ~ (1 | Recipient) + (1 | Donor), data = HR_23_fit

# Create the mixed model for estimated fecundity, sqrt transforming estimated fecundity
#est_fecundity_model_2 <- lmer((est_fecundity_centered) ~ (1 | Donor), data = HR_23_fit) #singular
```

```
#Fix MSM

# Create the mixed model for mean seed mass, log transformed mean seed mass
#msm_model <- lmer((msm_all_centered) ~ (1 | Recipient) + (1 | Donor), data = HR_23_fit) #singular
```

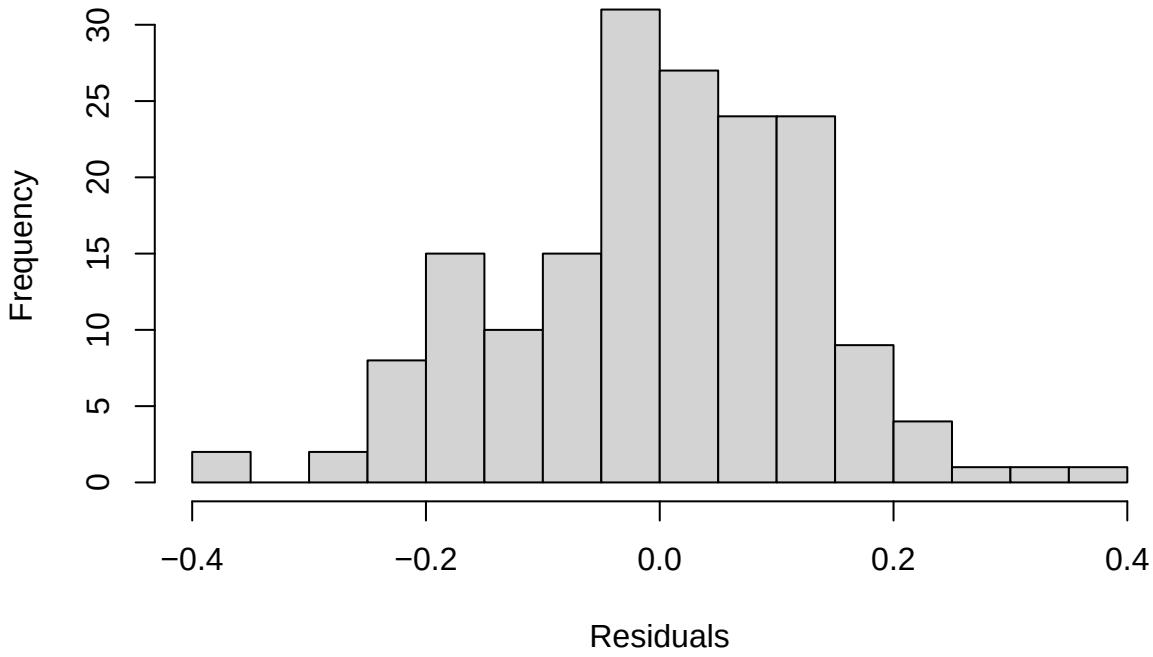
```
# Create the mixed model for SLA
#SLA_model <- lmer((SLA_SEG_centered) ~ (1 | Recipient) + (1 | Donor), data = HR_23_fit) #Singular

##adding in transect##
# Create the mixed model for SLA
SLA_model <- lmer((SLA_SEG_centered) ~ (1 | Transect) + (1 | Donor), data = HR_23_fit)

rand(SLA_model)
```

```
## ANOVA-like table for random-effects: Single term deletions
##
## Model:
## (SLA_SEG_centered) ~ (1 | Transect) + (1 | Donor)
##                 npar logLik     AIC    LRT Df Pr(>Chisq)
## <none>             4 87.247 -166.49
## (1 | Transect)     3 86.489 -166.98 1.5161  1     0.2182
## (1 | Donor)        3 85.386 -164.77 3.7222  1     0.0537 .
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
# Get residuals from the model
residuals <- resid(SLA_model)

# Q-Q plot for normality
qqnorm(residuals) #okay..
```




```
# Histogram for normality
hist(residuals, breaks = 20, main = "Histogram of Residuals", xlab = "Residuals") #definitely a few out
```

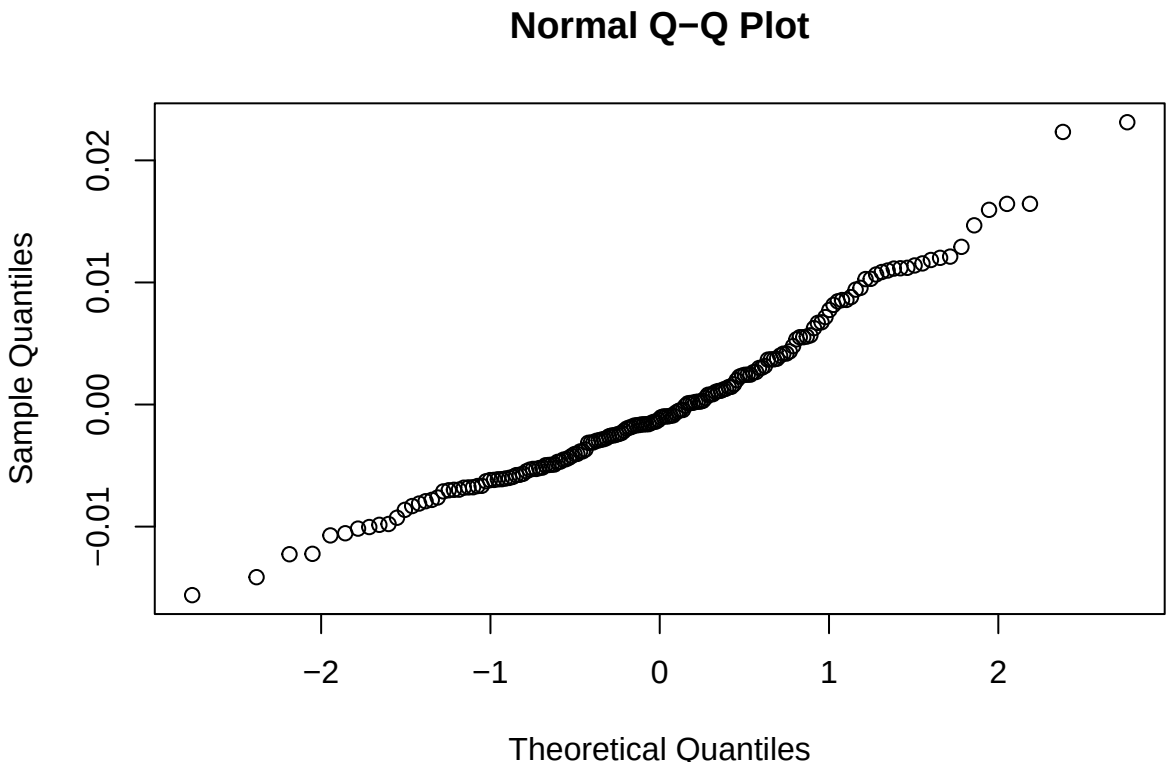



```
# Create the mixed model for mean seed mass, log transformed mean seed mass
#LMA_model <- lmer(LMA_SEG_centered ~ (1 | Recipient) + (1 | Donor), data = HR_23_fit) #Singular
```

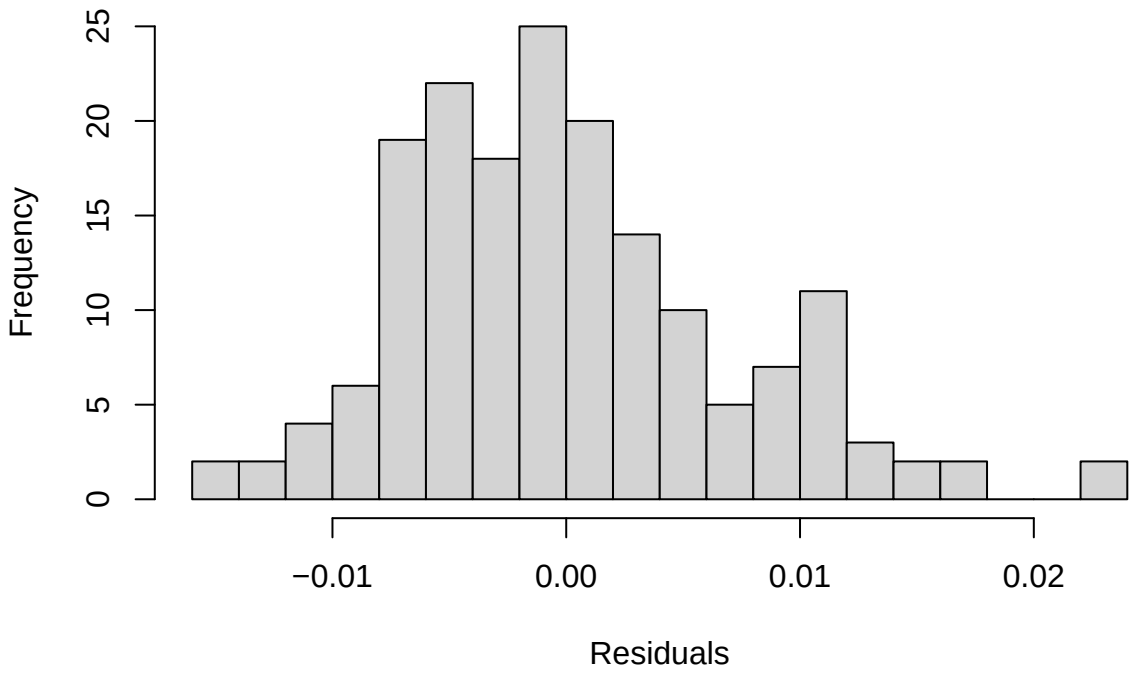
```r
LMA_model <- lmer(LMA_SEG_centered ~ (1 | Donor), data = HR_23_fit)

rand(LMA_model)
```

```
## ANOVA-like table for random-effects: Single term deletions
##
## Model:
## LMA_SEG_centered ~ (1 | Donor)
##             npar logLik     AIC   LRT Df Pr(>Chisq)
## <none>         3 594.30 -1182.6
## (1 | Donor)    2 592.16 -1180.3 4.281  1    0.03854 *
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```r
# Get residuals from the model
residuals <- resid(LMA_model)

# Q-Q plot for normality
qqnorm(residuals) #good enough
```



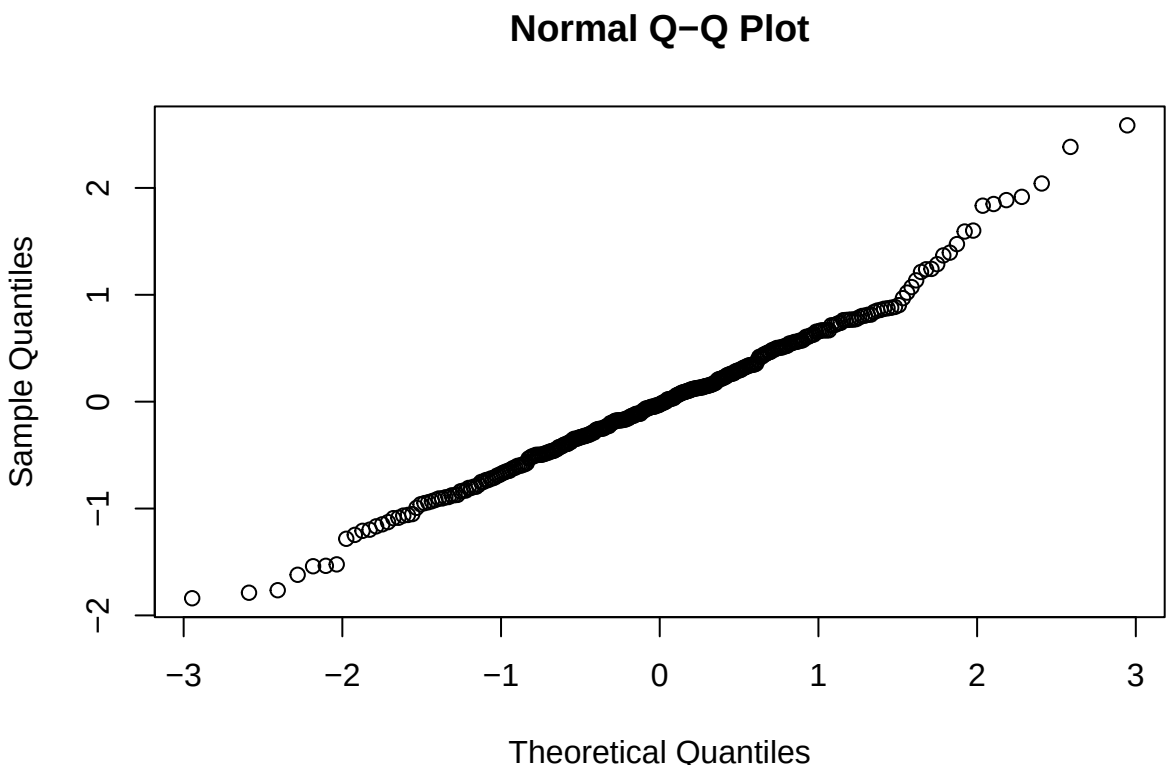

```r
# Histogram for normality
hist(residuals, breaks = 20, main = "Histogram of Residuals", xlab = "Residuals") #normal-ish
```



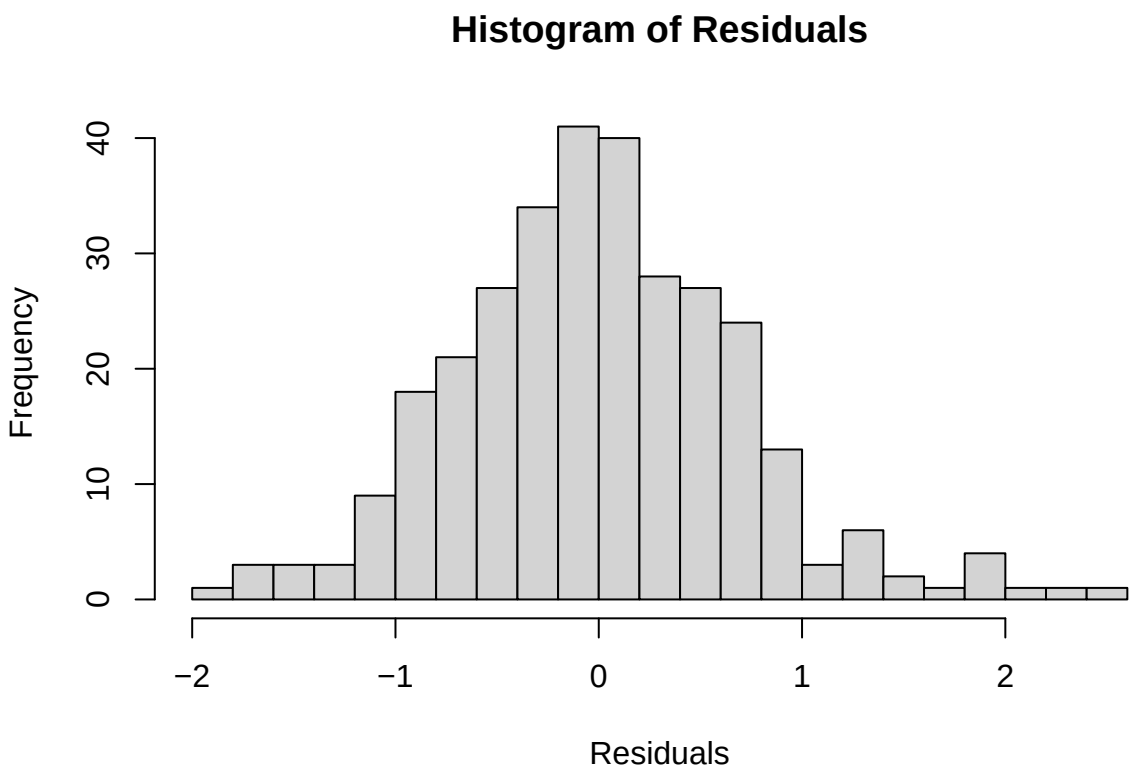

```
# Create the mixed model for d13C, log transformed mean seed mass
d13C_model <- lmer(d13C_SEG_centered ~ (1 | Recipient) + (1 | Donor), data = HR_23_fit)

rand(d13C_model)
```

```
## ANOVA-like table for random-effects: Single term deletions
##
## Model:
## d13C_SEG_centered ~ (1 | Recipient) + (1 | Donor)
##                  npar  logLik    AIC      LRT Df Pr(>Chisq)
## <none>              4 -349.04 706.08
## (1 | Recipient)     3 -349.19 704.38 0.297283  1     0.5856
## (1 | Donor)         3 -349.07 704.15 0.069552  1     0.7920
```

```
# Get residuals from the model
residuals <- resid(d13C_model)

# Q-Q plot for normality
qqnorm(residuals) #good enough
```




```
# Histogram for normality
hist(residuals, breaks = 20, main = "Histogram of Residuals", xlab = "Residuals") #normal-ish
```




```
# Create the mixed model for d13C, log transformed mean seed mass
#est_fitness_model <- lmer(est_fitness_centered ~ (1 | Donor), data = HR_23_fit) #singular
```

```r
# Function to Get variance components and calculate required values
calculate_variances <- function(model, trait_name) {
  var_components <- as.data.frame(VarCorr(model))

  # Initialize variables
  Va_mat <- NA
  Va_sd_mat <- NA
  Va_pat <- NA
  Va_sd_pat <- NA
  res_var <- NA
  Vp <- NA
  Vp_sd <- NA
  h2 <- NA

  # Check if "Recipient" is included as a random effect
  if ("Recipient" %in% var_components$grp) {
    Va_mat <- (var_components$vcov[var_components$grp == "Recipient"]) * 4
    Va_sd_mat <- sqrt(Va_mat)
  }

  # Calculate other variance components
  if ("Donor" %in% var_components$grp) {
    Va_pat <- (var_components$vcov[var_components$grp == "Donor"]) * 16
    Va_sd_pat <- sqrt(Va_pat)
  }

  if ("Residual" %in% var_components$grp) {
    res_var <- (var_components$vcov[var_components$grp == "Residual"])
  }

  # Calculate total phenotypic variance and narrow-sense heritability if components are available
  if (!is.na(Va_mat) & !is.na(Va_pat) & !is.na(res_var)) {
    Vp <- Va_mat + Va_pat + res_var
    Vp_sd <- sqrt(Vp)
    h2 <- (Va_pat) / Vp  # assumed calculation
  }

  # Create the dataframe and add the traits column
  df <- data.frame(traits = trait_name, Va_mat, Va_sd_mat, Va_pat, Va_sd_pat, Vp, Vp_sd, h2)

  return(df)
}

# Calculate variances for eHRh model and add trait names
corolla_variances <- calculate_variances(corolla_model, 'corolla_diameter')
skel_variances <- calculate_variances(skel_model, "skel_biomass_mg")
#est_fecundity_variances <- calculate_variances(est_fecundity_model, "estimated_fecundity")
#msm_variances <- calculate_variances(msm_model, "mean_seed_mass")
SLA_variances <- calculate_variances(SLA_model, "SLA")
LMA_variances <- calculate_variances(LMA_model, "LMA")
fl_duration_variances <- calculate_variances(fl_duration_model, "flowering duration")
d13C_variances <- calculate_variances(d13C_model, "delta_C_13")
```

```r
# Combine the results into a single dataframe
variance_HR_2023_G2 <- rbind(
  corolla_variances,
  skel_variances,
  fl_duration_variances,
  LMA_variances,
  SLA_variances,
  #msm_variances,
  #est_fecundity_variances
  d13C_variances
)

# Print the dataframe
print(variance_HR_2023_G2)
```

```
##               traits       Va_mat  Va_sd_mat       Va_pat   Va_sd_pat
## 1   corolla_diameter 2.199941e+00  1.4832197 1.145152e+00  1.07011779
## 2    skel_biomass_mg 2.423888e-01  0.4923299 1.552907e-01  0.39406937
## 3 flowering duration 3.222108e+03 56.7636141 6.926749e+02 26.31871748
## 4                LMA           NA         NA 1.251931e-04  0.01118897
## 5                SLA           NA         NA 4.097050e-02  0.20241171
## 6         delta_C_13 9.559901e-02  0.3091909 9.054189e-02  0.30090180
##             Vp       Vp_sd         h2
## 1 1.183638e+01   3.4404047 0.09674847
## 2 1.174448e+00   1.0837194 0.13222442
## 3 1.670486e+04 129.2472676 0.04146548
## 4           NA          NA         NA
## 5           NA          NA         NA
## 6 7.044457e-01   0.8393126 0.12852928
```

```r
#Save the csv file if you want
write_csv(x = variance_HR_2023_G2, here::here("data_sheets", "compiled_sheets", "HR_Va_h2_R_2023.csv"))
```