

7dpf

LR

2023-04-21

```
A.7.totaldist <-
  readRDS("A.7.totaldist.rds") %>%
  mutate(MPS = "A",
         Age = "7",
         Genotype = fct_relevel(Genotype,"wt",
                                "het", "hom")) %>%
  dplyr::mutate(Genotype = recode_factor(Genotype, 'wt' = '+/+', 'het' = '+/S387Lfs', 'hom' = 'S387Lfs/'))

A.7.fullldata <-
  readRDS("A.7.fullldata.rds") %>%
  mutate(MPS = "A",
         Age = "7",
         Genotype = fct_relevel(Genotype,"wt",
                                "het", "hom")) %>%
  dplyr::mutate(Genotype = recode_factor(Genotype, 'wt' = '+/+', 'het' = '+/S387Lfs', 'hom' = 'S387Lfs/'))

#B7
B.7.totaldist <-
  readRDS("B.7.totaldist.rds") %>%
  mutate(MPS = "B",
         Age = "7",
         Genotype = fct_relevel(Genotype,"wt",
                                "het", "hom")) %>%
  dplyr::mutate(Genotype = recode_factor(Genotype, 'wt' = '+/+', 'het' = '+/A603Efs', 'hom' = 'A603Efs/'))

B.7.fullldata <-
  readRDS("B.7.fullldata.rds") %>%
  mutate(MPS = "B",
         Age = "7",
         Genotype = fct_relevel(Genotype,"wt",
                                "het", "hom")) %>%
  dplyr::mutate(Genotype = recode_factor(Genotype, 'wt' = '+/+', 'het' = '+/A603Efs', 'hom' = 'A603Efs/'))

#C7
C.7.totaldist <-
  readRDS("C.7.totaldist.rds") %>%
  mutate(MPS = "C",
         Age = "7",
         Genotype = fct_relevel(Genotype,"wt",
```

```

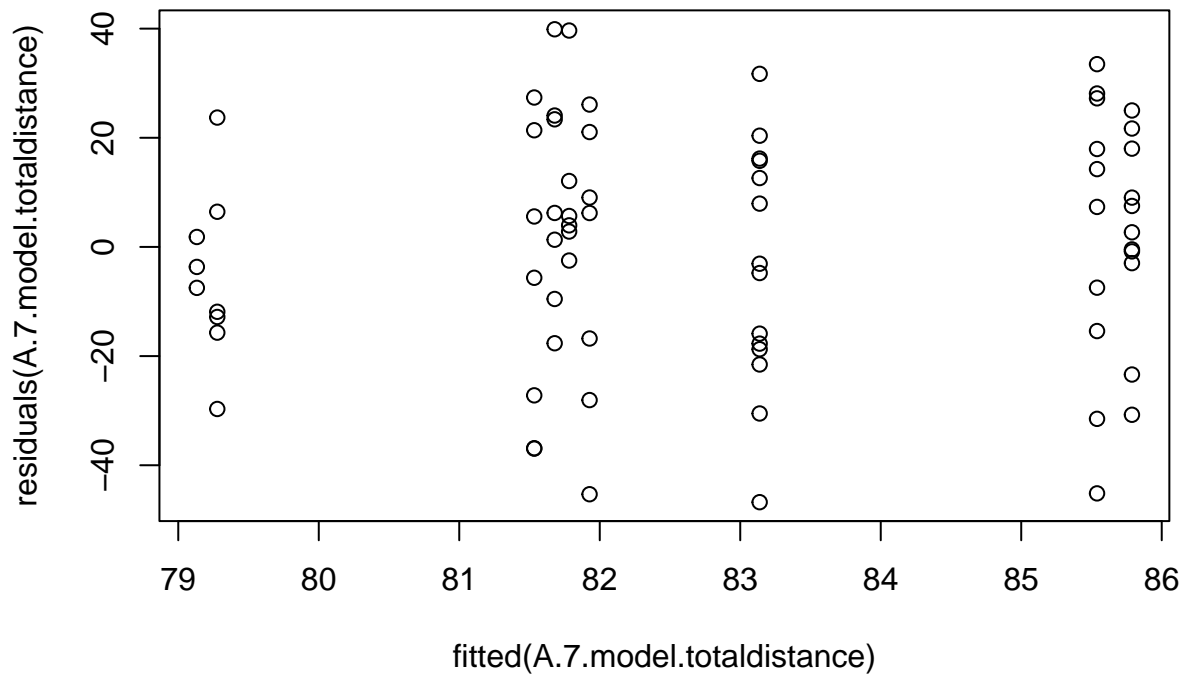
      "het", "hom"))%>%
dplyr::mutate(Genotype = recode_factor(Genotype, 'wt' = '+/+', 'het' = '+/G557fs', 'hom' = 'G557fs/G557fs'))

C.7.fulldata <-
  readRDS("C.7.fulldata.rds") %>%
  mutate(MPS = "C",
         Age = "7",
         Genotype = fct_relevel(Genotype, "wt",
                                "het", "hom"))%>%
  dplyr::mutate(Genotype = recode_factor(Genotype, 'wt' = '+/+', 'het' = '+/G557fs', 'hom' = 'G557fs/G557fs'))

#A model----
A.7.model.totaldistance <- A.7.totaldist %>%
  droplevels() %>%
  lmer(formula = sqrt(Total_distance) ~ Genotype + (1|Trial))

plot(residuals(A.7.model.totaldistance) ~ fitted(A.7.model.totaldistance))

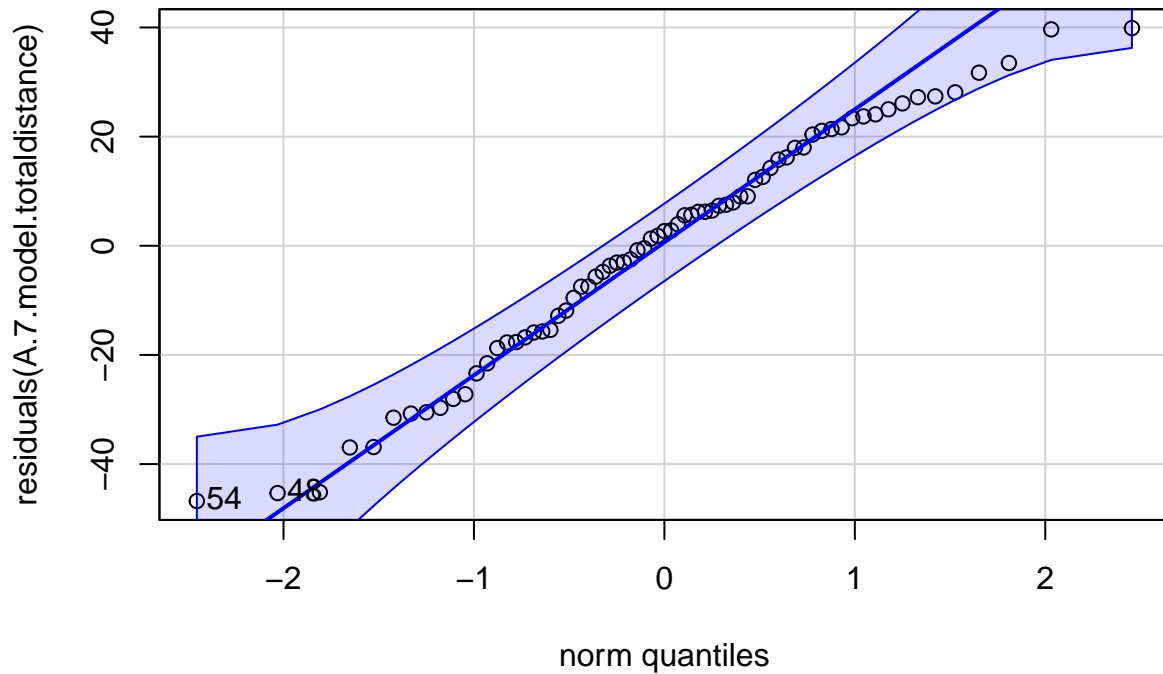
```



```
qqPlot(residuals(A.7.model.totaldistance))
```

Table 1: Type II Wald chisquare test of LME

	Chisq	Df	pval
Genotype	0.5641852	2	0.7542038

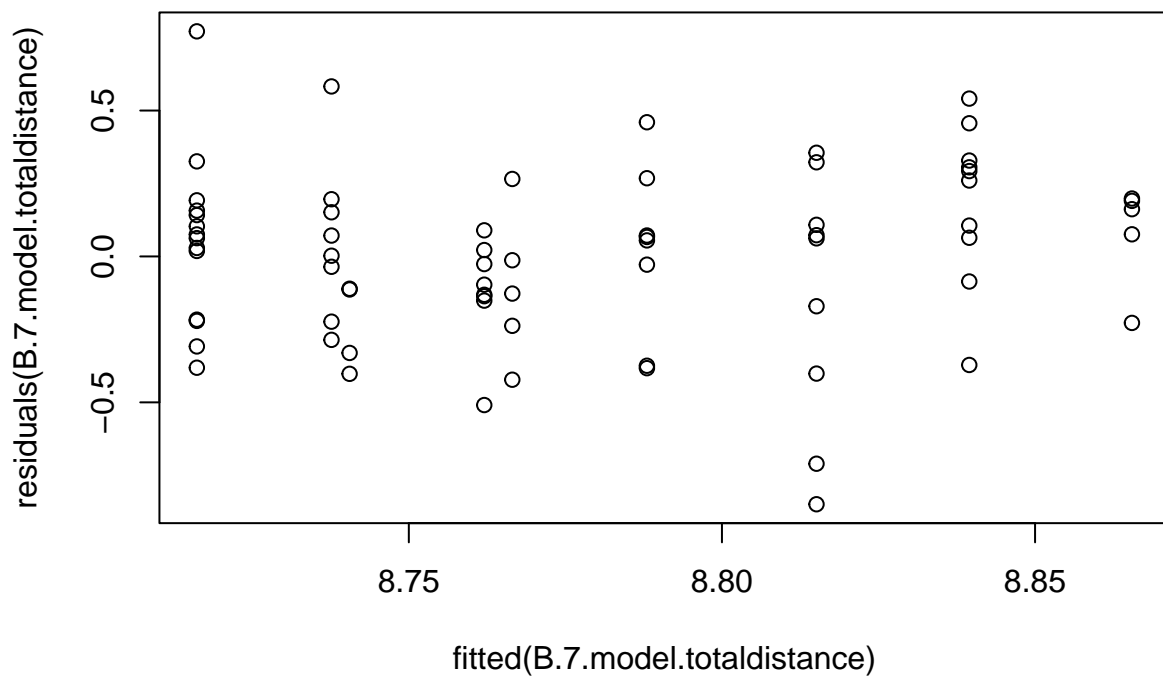


```
## [1] 54 48
```

```
Anova(A.7.model.totaldistance) %>%
  as.data.frame() %>%
  dplyr::rename(pval = `Pr(>Chisq)`) %>%
  kable(caption = "Type II Wald chisquare test of LME") %>%
  kable_styling()
```

```
#B model-----
B.7.model.totaldistance <- B.7.totaldist %>%
  droplevels() %>%
  lmer(formula = log(Total_distance) ~ Genotype + (1|Trial))

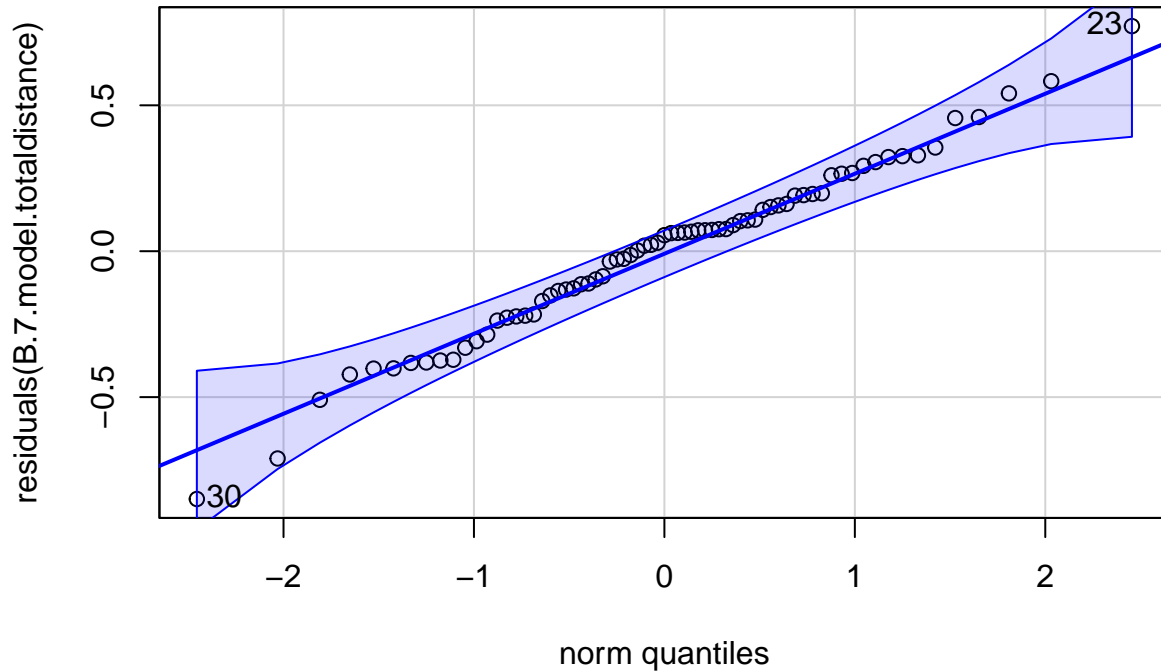
plot(residuals(B.7.model.totaldistance) ~ fitted(B.7.model.totaldistance))
```



```
qqPlot(residuals(B.7.model.totaldistance))
```

Table 2: Type II Wald chisquare test of LME

	Chisq	Df	pval
Genotype	0.3178061	2	0.8530791



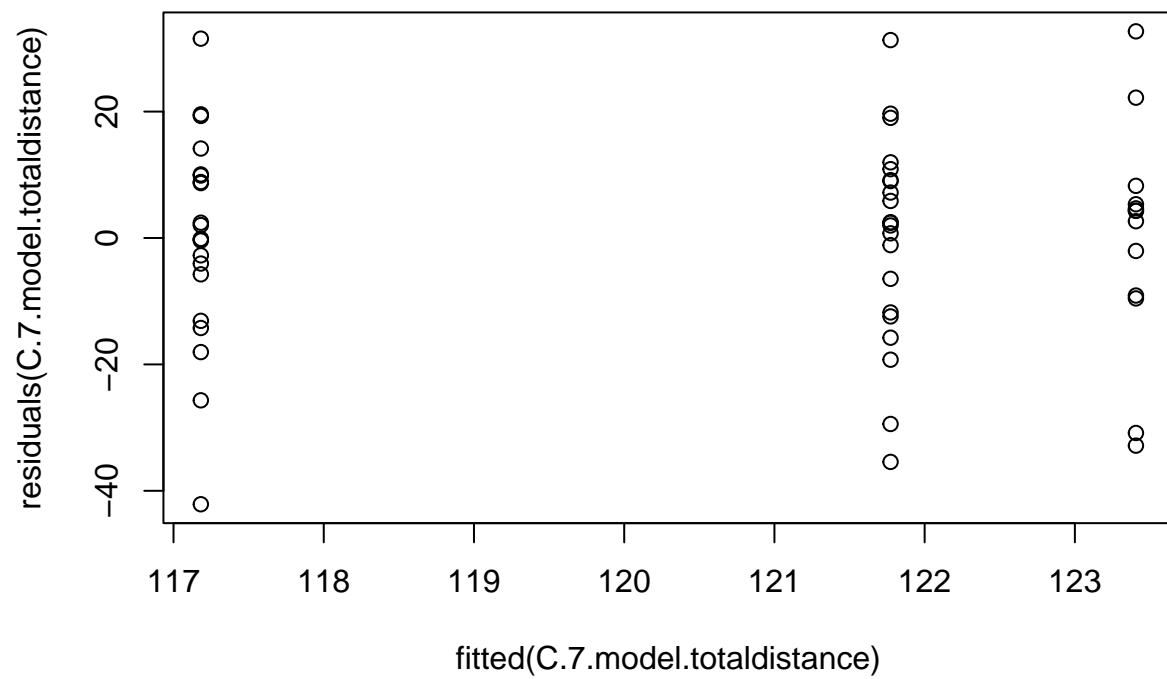
```
## [1] 30 23
```

```
Anova(B.7.model.totaldistance) %>%
  as.data.frame() %>%
  dplyr::rename(pval = `Pr(>Chisq)`) %>%
  kable(caption = "Type II Wald chisquare test of LME") %>%
  kable_styling()
```

```
#C model----
C.7.model.totaldistance <- C.7.totaldist %>%
  droplevels() %>%
  lmer(formula = sqrt(Total_distance) ~ Genotype + (1|Trial))
```

```
## boundary (singular) fit: see help('isSingular')
```

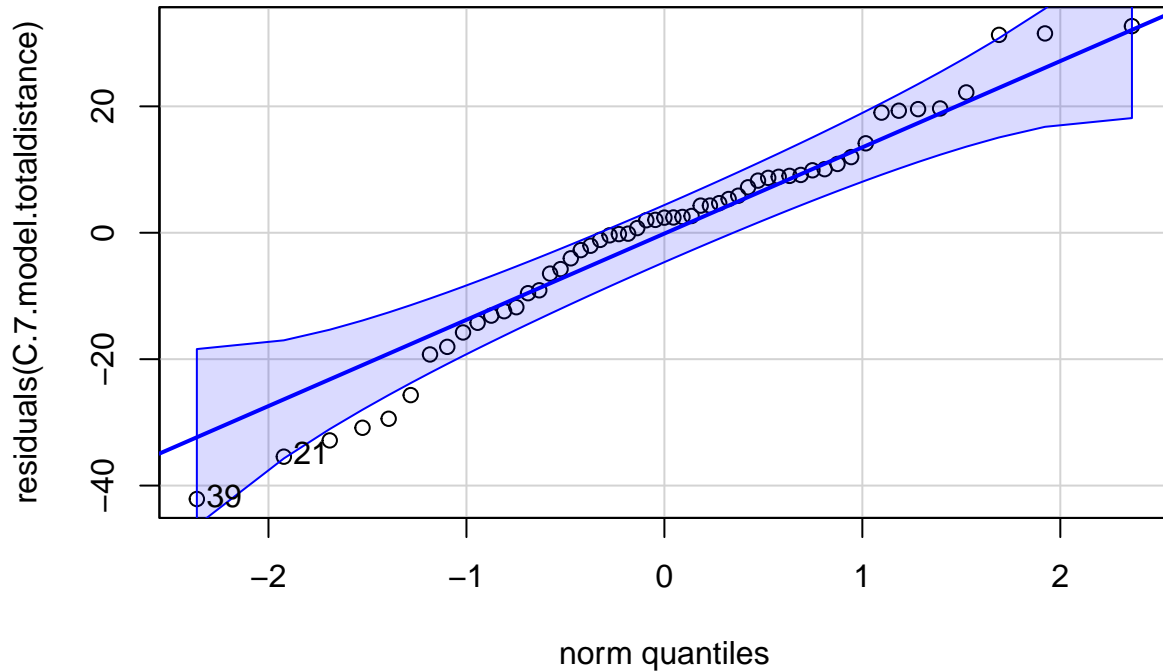
```
plot(residuals(C.7.model.totaldistance) ~ fitted(C.7.model.totaldistance))
```



```
qqPlot(residuals(C.7.model.totaldistance))
```

Table 3: Type II Wald chisquare test of LME

	Chisq	Df	pval
Genotype	1.31851	2	0.5172366



```
## [1] 39 21
```

```
Anova(C.7.model.totaldistance) %>%
  as.data.frame() %>%
  dplyr::rename(pval = `Pr(>Chisq)`) %>%
  kable(caption = "Type II Wald chisquare test of LME") %>%
  kable_styling()
```

```
A.7.model.20minbin <- A.7.fulldata %>%
  mutate(fish_id = as.character(fish_id)) %>%
  droplevels() %>%
  lmer(formula = sqrt(Distance_travelled) ~ (Bin*Genotype) + (1|Trial) + (1|fish_id),
       data = .)
```

Table 4: Type II Wald chisquare test of LME

	Chisq	Df	pval
Bin	73.0644181	2	0.0000000
Genotype	0.5915920	2	0.7439392
Bin:Genotype	0.6535028	4	0.9569367

```
Anova(A.7.model.20minbin) %>%
  as.data.frame() %>%
  dplyr::rename(pval = `Pr(>Chisq)`) %>%
  kable(caption = "Type II Wald chisquare test of LME") %>%
  kable_styling()
```

```
B.7.model.20minbin <- B.7.fulldata %>%
  mutate(fish_id = as.character(fish_id)) %>%
  droplevels() %>%
  lmer(formula = log(Distance_travelled) ~ (Bin*Genotype) + (1|Trial) + (1|fish_id),
        data = .)

plot(residuals(B.7.model.20minbin) ~ fitted(B.7.model.20minbin))
```

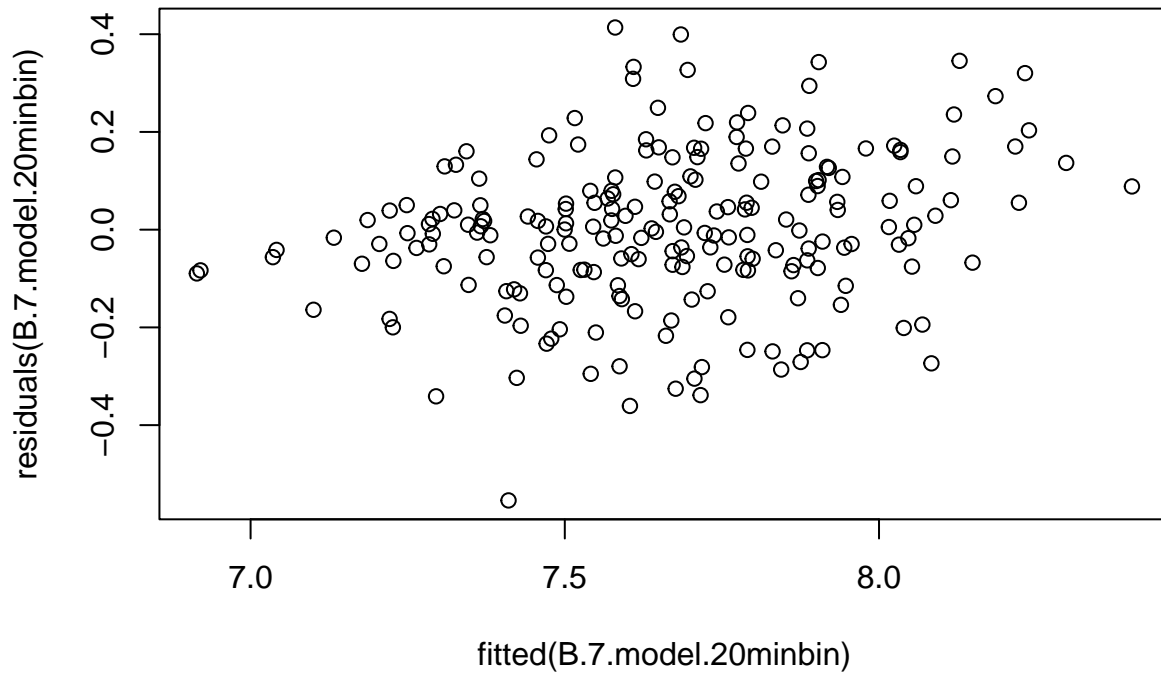
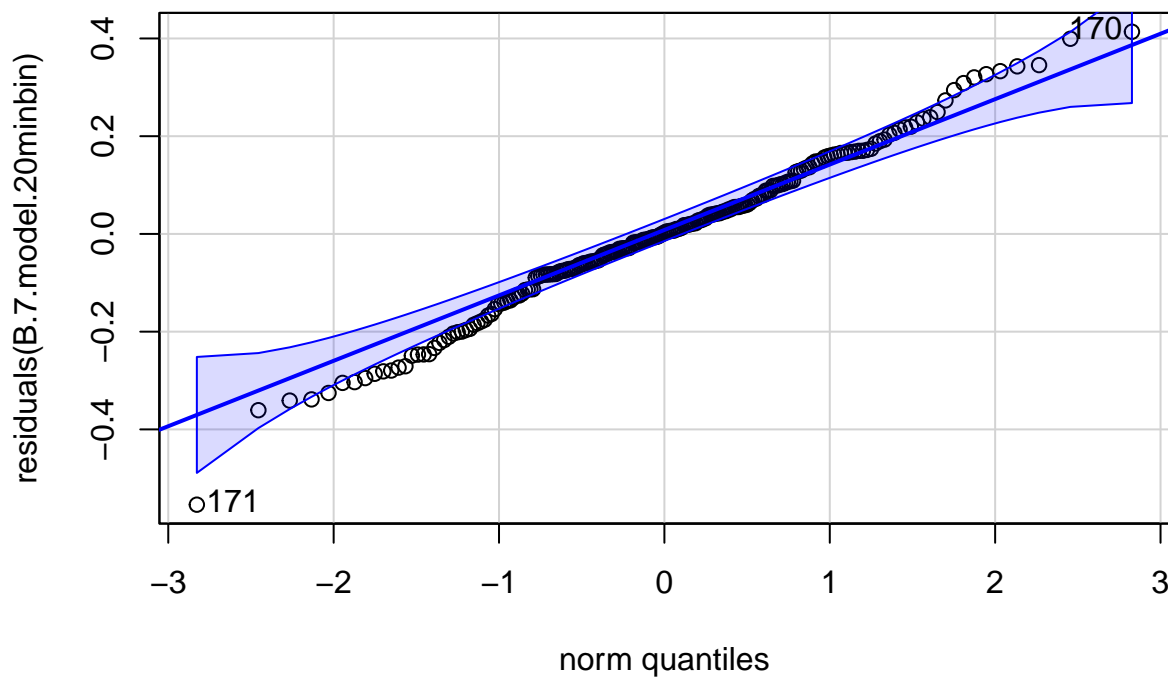


Table 5: Type II Wald chisquare test of LME

	Chisq	Df	pval
Bin	47.5664047	2	0.0000000
Genotype	0.2786811	2	0.8699317
Bin:Genotype	2.9060823	4	0.5736633

```
qqPlot(residuals(B.7.model.20minbin))
```



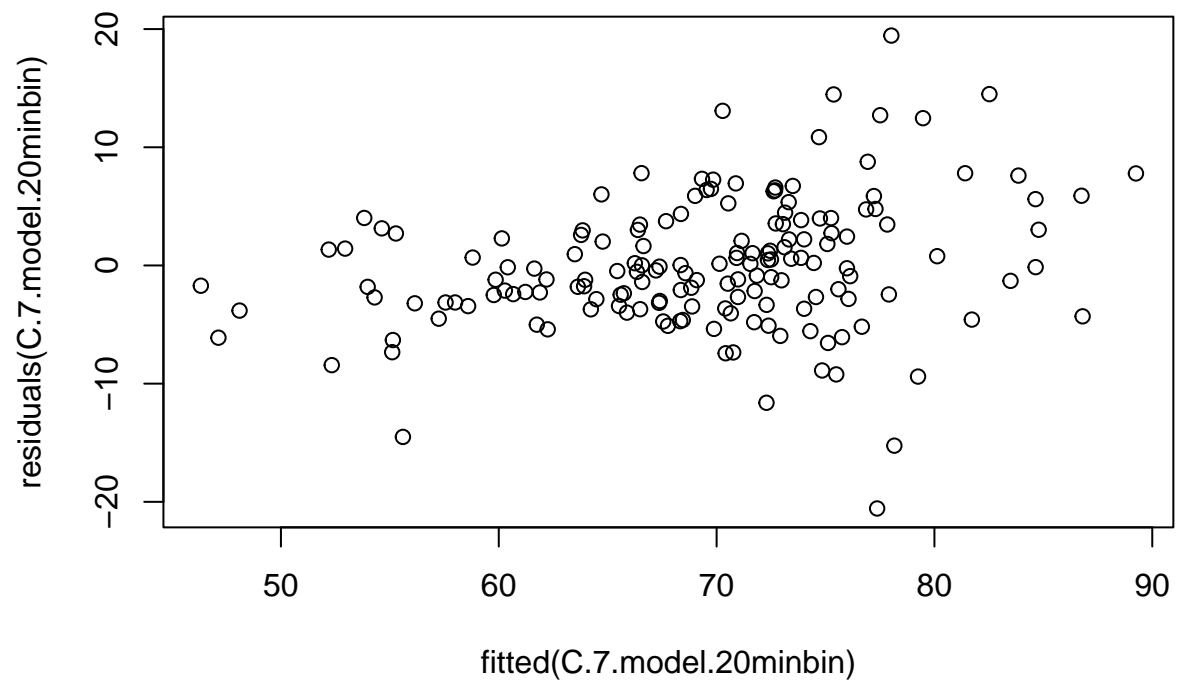
```
## [1] 171 170
```

```
Anova(B.7.model.20minbin) %>%
  as.data.frame() %>%
  dplyr::rename(pval = `Pr(>Chisq)`) %>%
  kable(caption = "Type II Wald chisquare test of LME") %>%
  kable_styling()
```

```
C.7.model.20minbin <- C.7.fulldata %>%
  mutate(fish_id = as.character(fish_id)) %>%
  droplevels() %>%
  lmer(formula = sqrt(Distance_travelled) ~ (Bin*Genotype) + (1|Trial) + (1|fish_id),
       data = .)
```

```
## boundary (singular) fit: see help('isSingular')
```

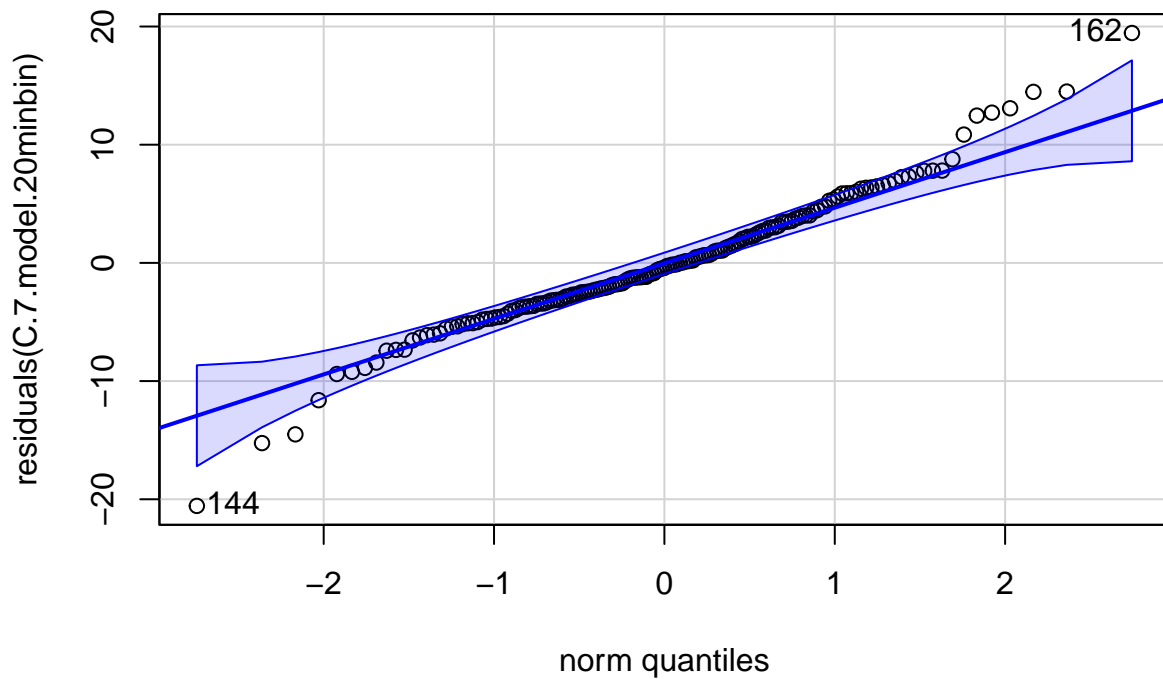
```
plot(residuals(C.7.model.20minbin) ~ fitted(C.7.model.20minbin))
```



```
qqPlot(residuals(C.7.model.20minbin))
```

Table 6: Type II Wald chisquare test of LME

	Chisq	Df	pval
Bin	0.5486277	2	0.7600935
Genotype	1.2459687	2	0.5363414
Bin:Genotype	4.5920463	4	0.3317723

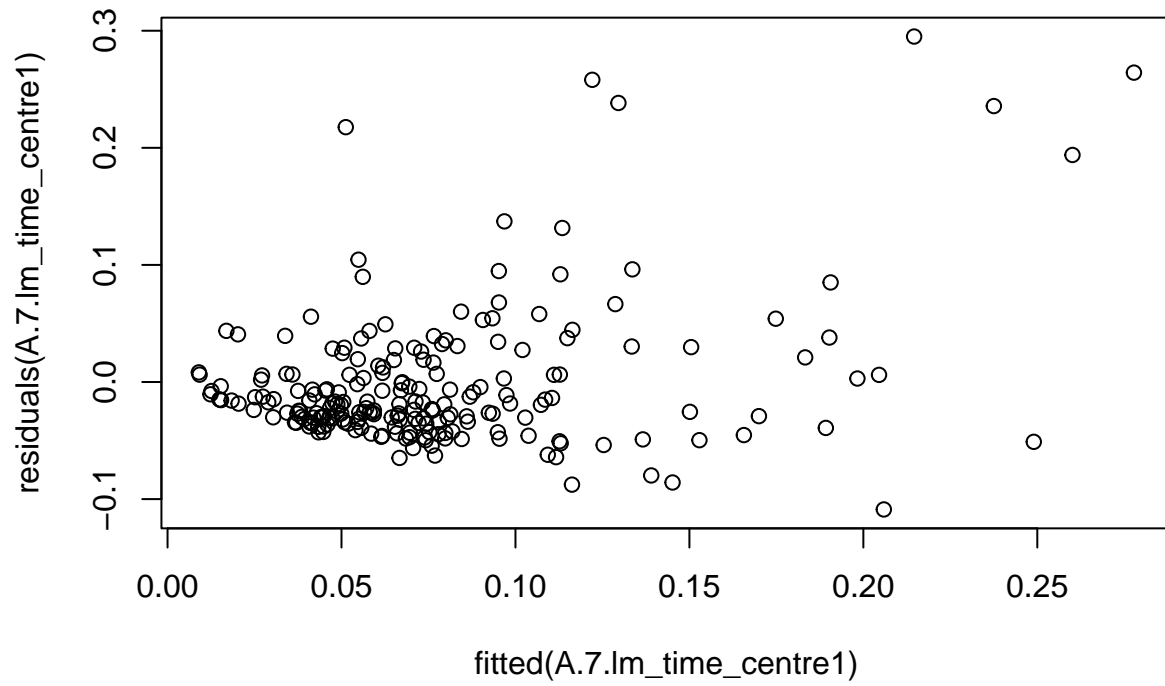


```
## [1] 144 162
```

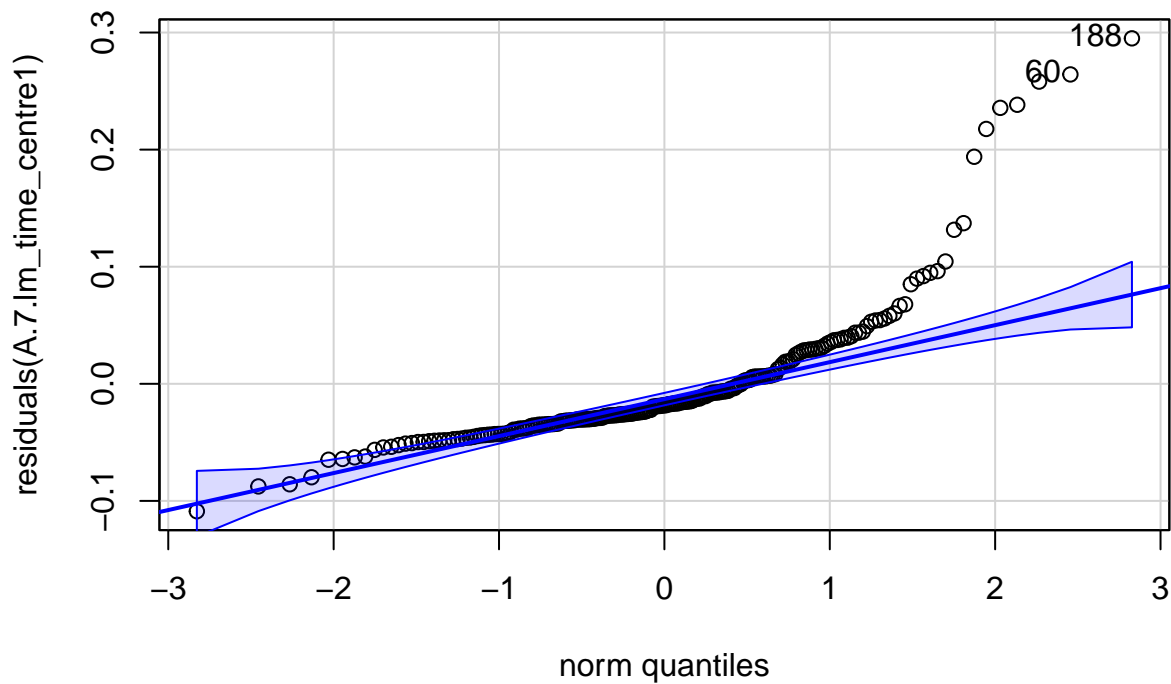
```
Anova(C.7.model.20minbin) %>%
  as.data.frame() %>%
  dplyr::rename(pval = `Pr(>Chisq)`) %>%
  kable(caption = "Type II Wald chisquare test of LME") %>%
  kable_styling()
```

```
A.7.lm_time_centre1 <-
  A.7.fulldata %>%
  group_by(fish_id) %>%
  dplyr::mutate(Time_in_centre = replace(Time_in_centre, Time_in_centre == 0, 0.0000001)) %>%
  glmmTMB(formula = Time_in_centre/1200 ~ (Genotype*Bin) + (1|Trial) + (1|fish_id),
    data = .,
    family = beta_family(link = "logit"))
```

```
plot(residuals(A.7.lm_time_centre1) ~ fitted(A.7.lm_time_centre1))
```



```
qqPlot(residuals(A.7.lm_time_centre1))
```



```
## [1] 188 60
```

```
Anova(A.7.lm_time_centre1)
```

```
## Analysis of Deviance Table (Type II Wald chisquare tests)
##
## Response: Time_in_centre/1200
##           Chisq Df Pr(>Chisq)
## Genotype    3.7507  2  0.1533030
## Bin        18.1137  2  0.0001166 ***
## Genotype:Bin  8.5283  4  0.0740336 .
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
B.7.lm_time_centre1 <-
  B.7.fullldata %>%
  group_by(fish_id) %>%
  dplyr::mutate(Time_in_centre = replace(Time_in_centre, Time_in_centre == 0, 0.0000001)) %>%
  glmmTMB(formula = Time_in_centre/1200 ~ (Genotype*Bin) + (1|Trial) + (1|fish_id),
    data = .,
    family = beta_family(link = "logit"))
```

```

C.7.lm_time_centre1 <-
  C.7.fullldata %>%
  group_by(fish_id) %>%
  dplyr::mutate(Time_in_centre = replace(Time_in_centre, Time_in_centre == 0, 0.0000001)) %>%
  glmmTMB(formula = Time_in_centre/1200 ~ (Genotype*Bin) + (1|Trial) + (1|fish_id),
    data = .,
    family = beta_family(link = "logit"))

Anova(C.7.lm_time_centre1)

```

```

## Analysis of Deviance Table (Type II Wald chisquare tests)
##
## Response: Time_in_centre/1200
##           Chisq Df Pr(>Chisq)
## Genotype    2.2471  2  0.3251171
## Bin         3.3039  2  0.1916722
## Genotype:Bin 22.2205  4  0.0001812 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

```

```

A.7.lm.freq <-
  A.7.fullldata %>%
  dplyr::mutate(fish_id = as.character(fish_id)) %>%
  glmer.nb(Freq_in_centre ~ (Bin*Genotype) + (1|Trial) + (1|fish_id),
    data = .,
    family = Poisson (link = "log"))

```

```
## boundary (singular) fit: see help('isSingular')
```

```

B.7.lm.freq <-
  B.7.fullldata %>%
  dplyr::mutate(fish_id = as.character(fish_id)) %>%
  glmer.nb(Freq_in_centre ~ (Bin*Genotype) + (1|Trial) + (1|fish_id),
    data = .,
    family = Poisson (link = "log"))

```

```
## boundary (singular) fit: see help('isSingular')
```

```

C.7.lm.freq <-
  C.7.fullldata %>%
  dplyr::mutate(fish_id = as.character(fish_id)) %>%
  glmer.nb(Freq_in_centre ~ Bin + Genotype + (1|Trial) + (1|fish_id),
    data = .,
    family = Poisson (link = "log"))

```

```
## boundary (singular) fit: see help('isSingular')
```

```
Anova(C.7.lm.freq)
```

```
## Analysis of Deviance Table (Type II Wald chisquare tests)
##
## Response: Freq_in_centre
##           Chisq Df Pr(>Chisq)
## Bin       1.7525 2    0.4163
## Genotype  2.8122 2    0.2451
```