

Genetic differentiation on flowering time in *Cerastium fontanum* using a reciprocal transplant experiment

Analyses with FFD

Alicia Valdés

09 January, 2024

Contents

| | |
|---|-----------|
| Read clean data from .csv files | 2 |
| Distributions | 2 |
| TO DO: Check model diagnostics | 11 |
| Models FFD (OLD but USE?) | 11 |
| Temp mother + Temp father | 11 |
| Plots predicted effects | 15 |
| Heat zone (model1) | 15 |
| Temp at planting site (model2) | 16 |
| Interaction heat zone x temp father (model1) | 18 |
| Temp father (model2) | 20 |
| Interaction temp at planting site x temp of the father (model2) | 21 |
| Mean temp parents | 22 |
| Plots predicted effects | 25 |
| Heat zone (model1) | 26 |
| Temp at planting site (model2) | 27 |
| Interaction heat zone x mean temp parents (model1) | 29 |
| Mean temp parents (model2) | 31 |
| Interaction temp at planting site x mean temp of the parents (model2) | 32 |

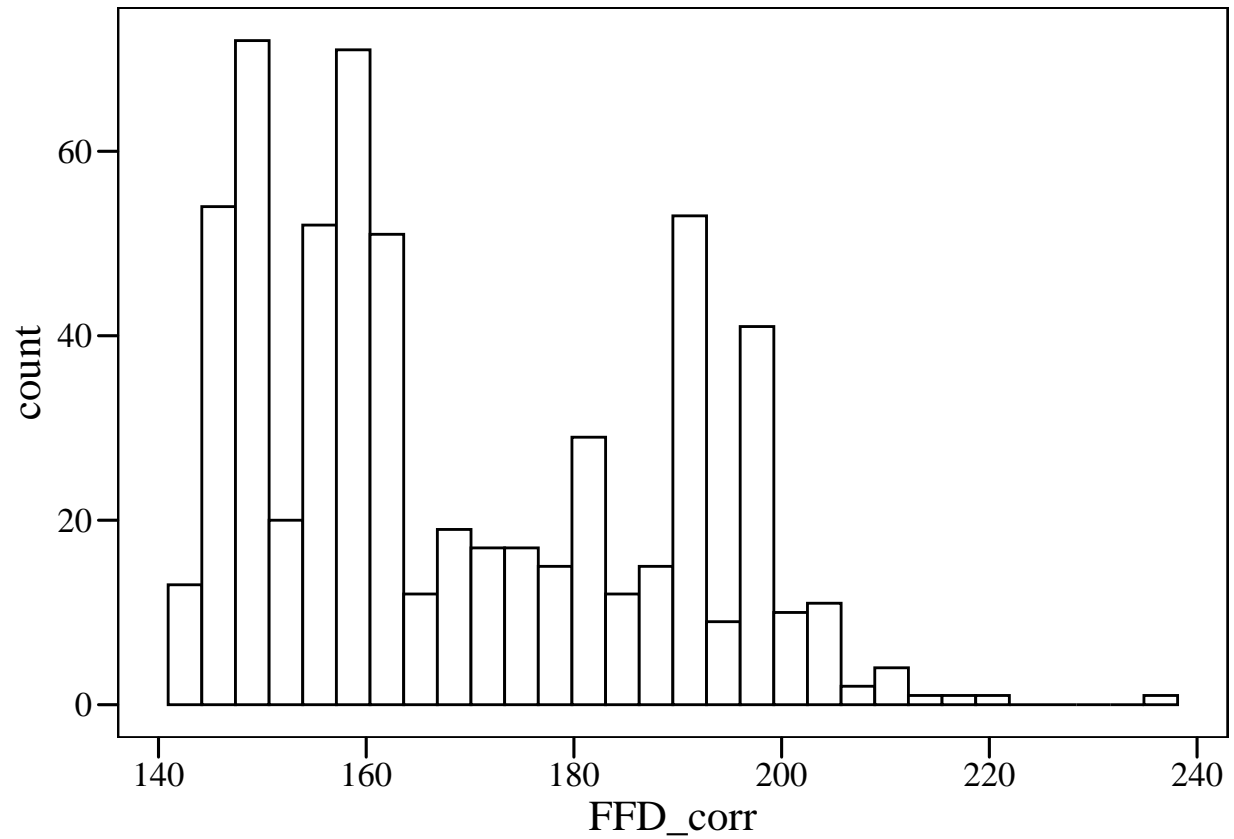
| | |
|--|-----------|
| Models similar to greenhouse paper | 33 |
| Prediction 1 | 33 |
| Models | 33 |
| Proportions of variance | 35 |
| Heritability and maternal effects | 36 |
| Table SM: LRTs for variance component | 38 |
| Table SM: LRTs for variance components | 38 |
| Prediction 2 | 39 |
| Models | 39 |
| Proportions of variance | 42 |
| Heritability and maternal effects | 42 |
| Table SM: LRTs for variance components | 44 |
| Figure 1 (Predictions 1-2) | 45 |
| Table 1 (Predictions 1-2) | 45 |
| Figure 2 (Prediction 2) | 45 |
| Prediction 3 | 48 |
| Models | 48 |
| Table 2 | 51 |
| Proportions of variance | 51 |
| Figure 3 | 53 |
| Models mid-parental values | 53 |
| Prediction 4 | 56 |
| Models | 56 |
| Table 3 | 60 |
| Figure 4 | 60 |
| Models mid-parental values | 60 |
| Predictions 3 and 4 with breeding values? | 68 |
| Session info | 68 |

Read clean data from .csv files

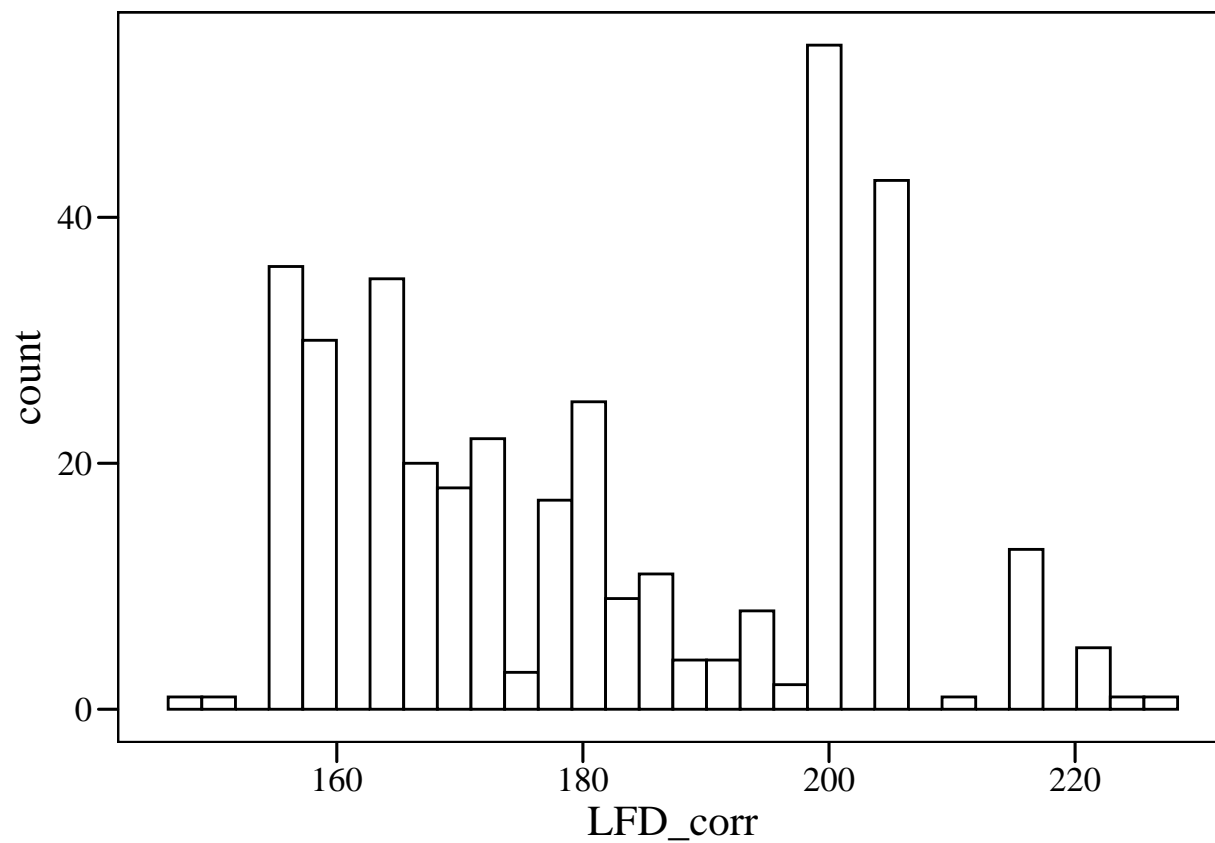
```
data_transplants <- read_csv("data/clean/data_transplants.csv")
```

Distributions

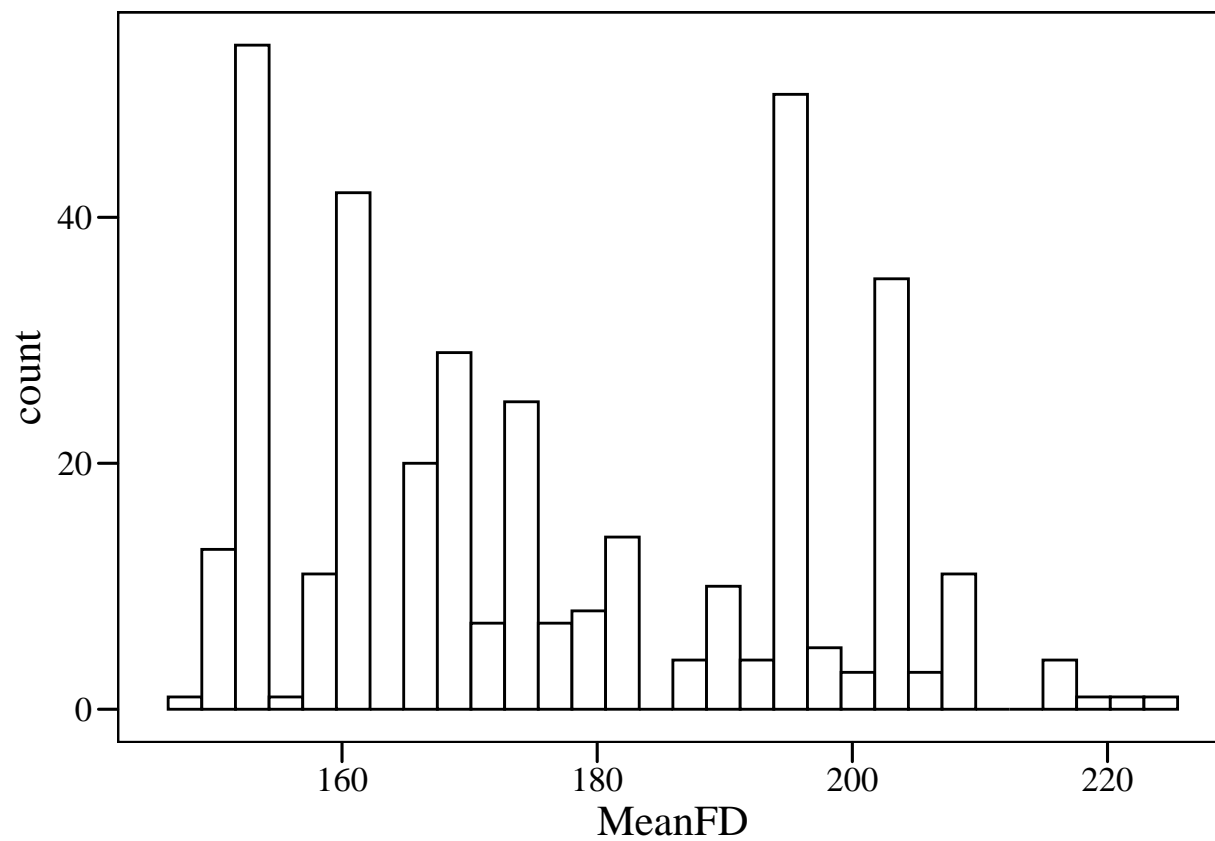
```
ggplot(data_transplants,aes(x=FFD_corr))+
  geom_histogram(color="black",fill="white")+
  my_theme()
```



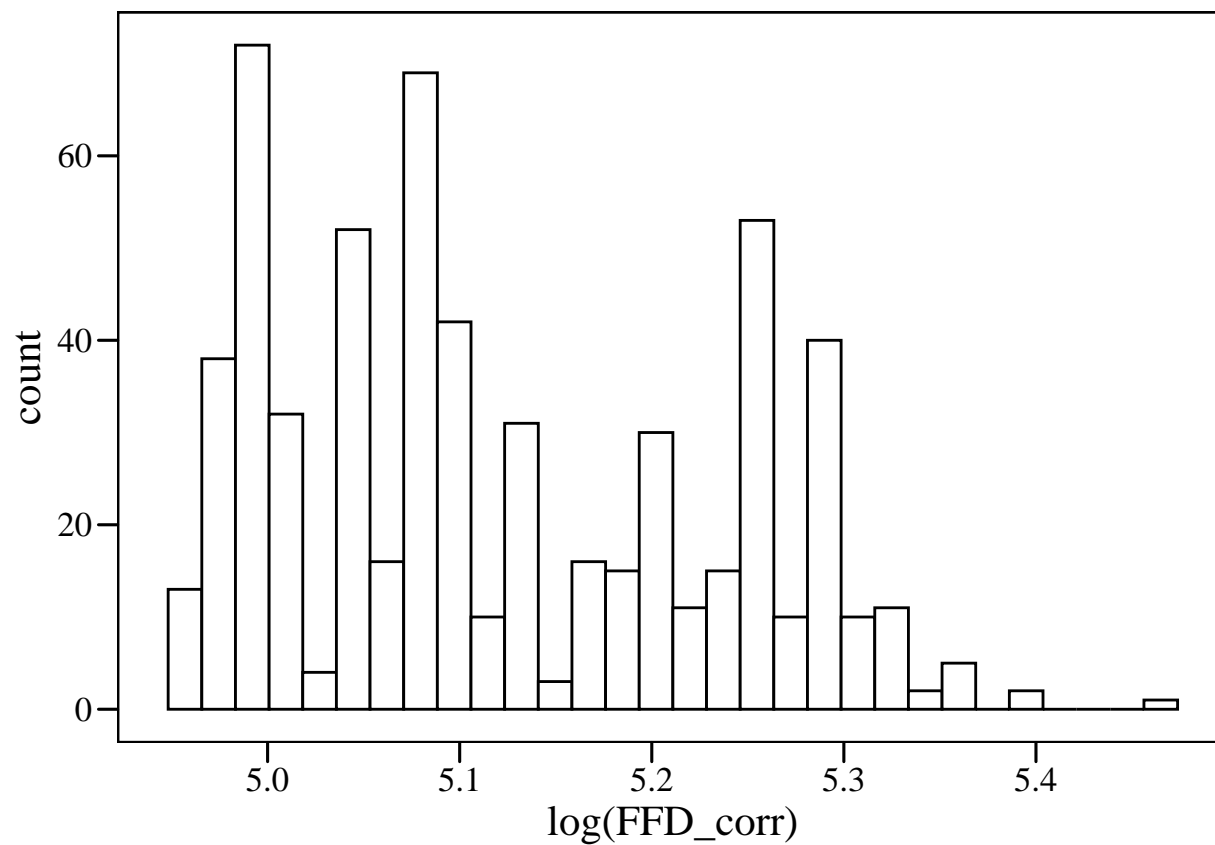
```
ggplot(data_transplants,aes(x=LFD_corr))+
  geom_histogram(color="black",fill="white")+
  my_theme()
```



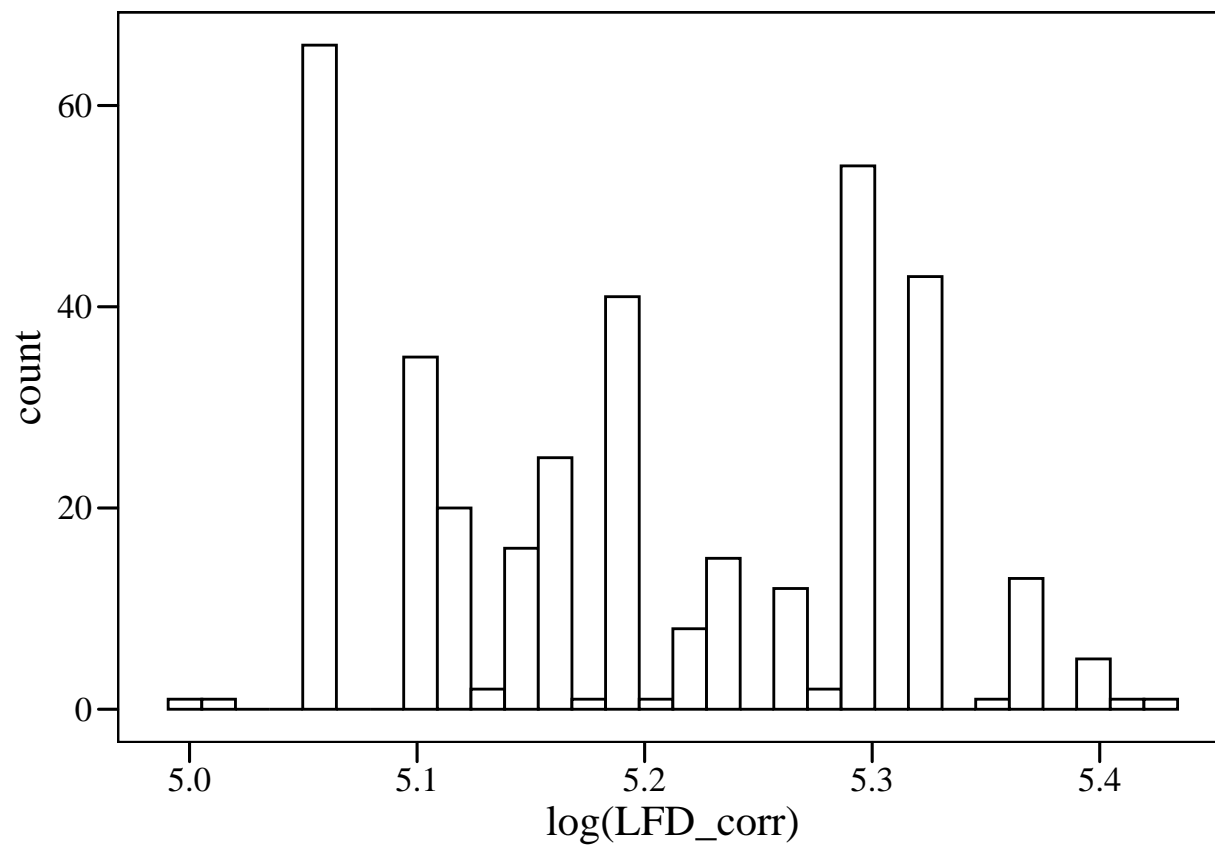
```
ggplot(data_transplants,aes(x=MeanFD))+  
  geom_histogram(color="black",fill="white")+  
  my_theme()
```



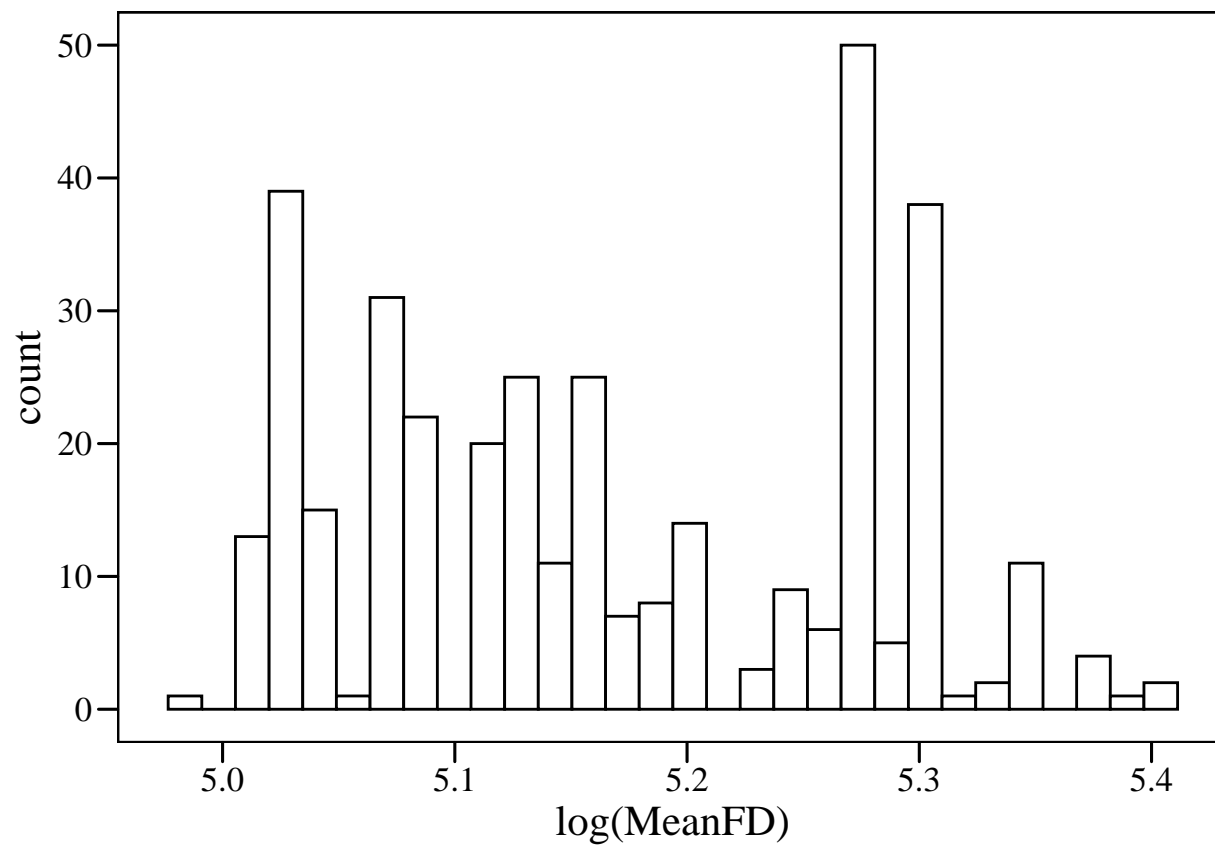
```
ggplot(data_transplants,aes(x=log(FFD_corr)))+  
  geom_histogram(color="black",fill="white")+  
  my_theme()
```



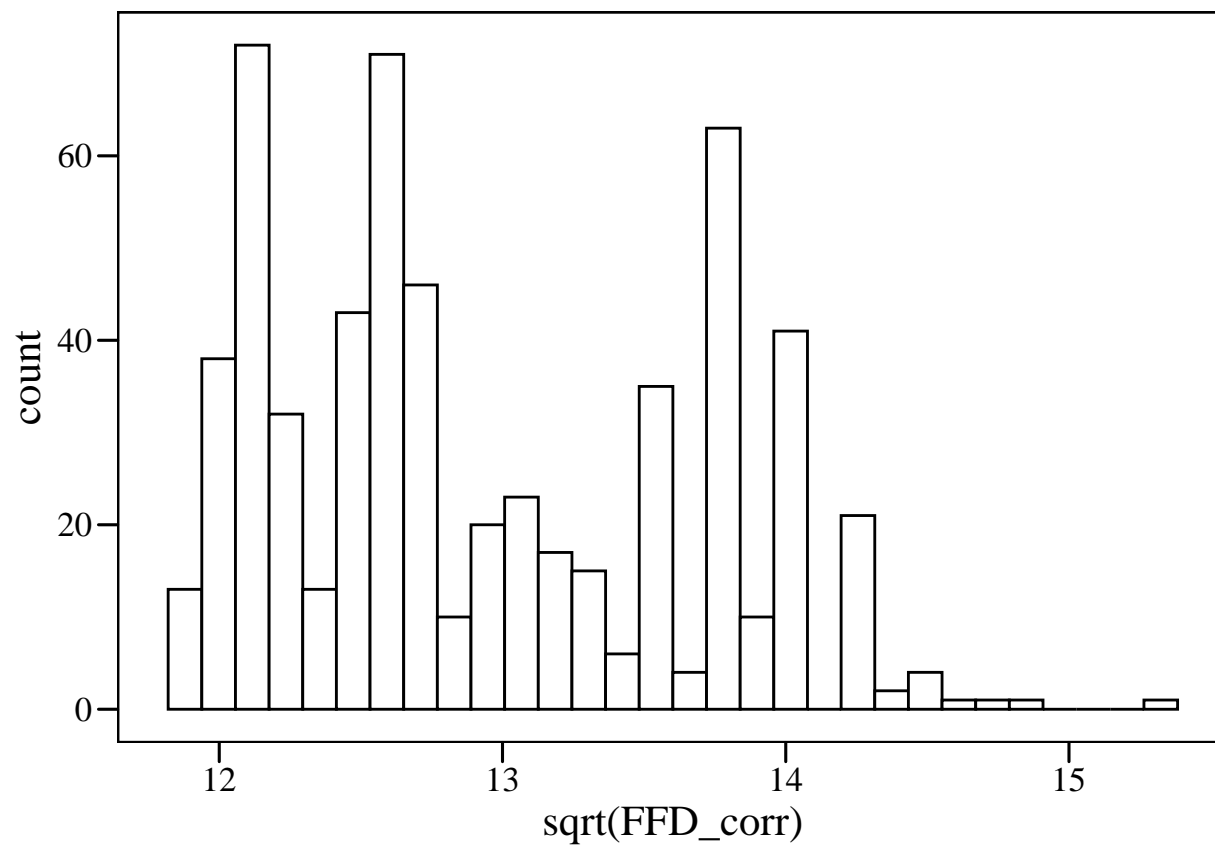
```
ggplot(data_transplants,aes(x=log(LFD_corr)))+  
  geom_histogram(color="black",fill="white")+  
  my_theme()
```



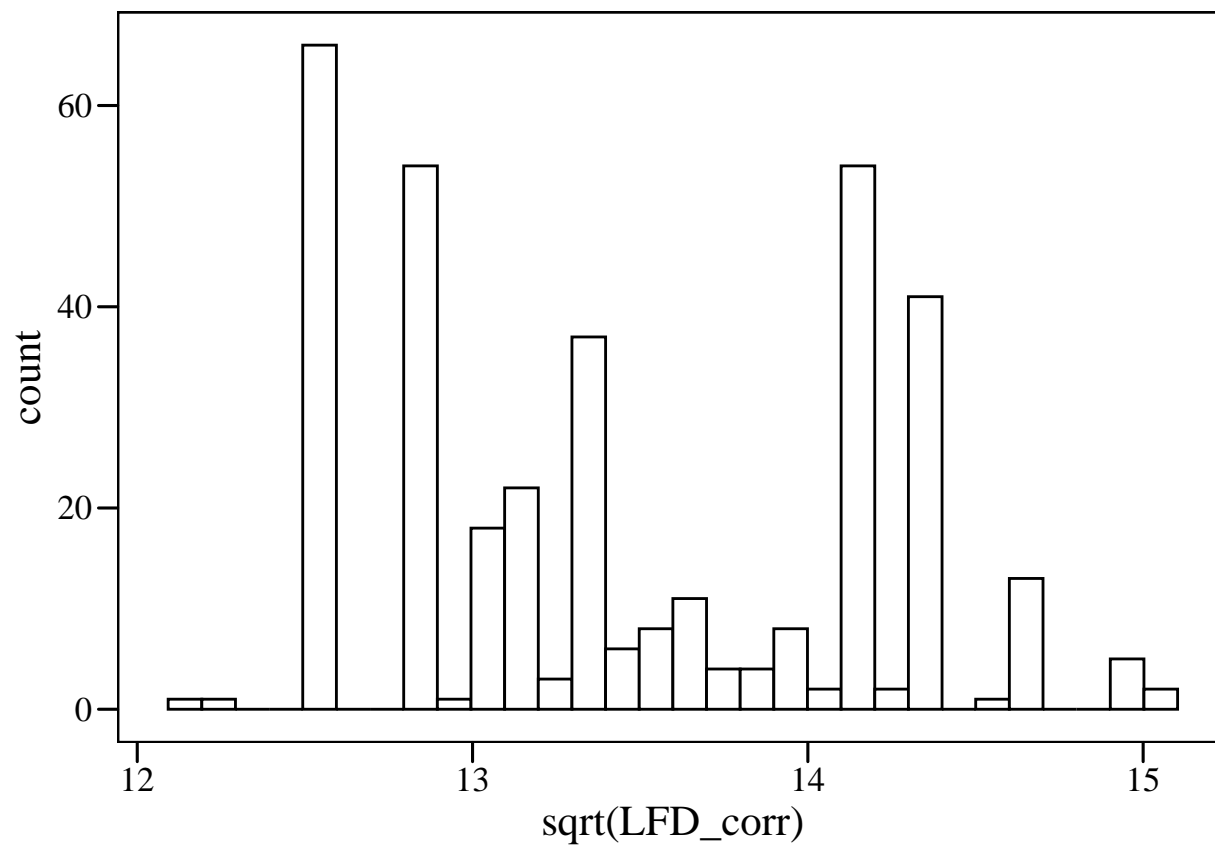
```
ggplot(data_transplants,aes(x=log(MeanFD)))+  
  geom_histogram(color="black",fill="white")+  
  my_theme()
```



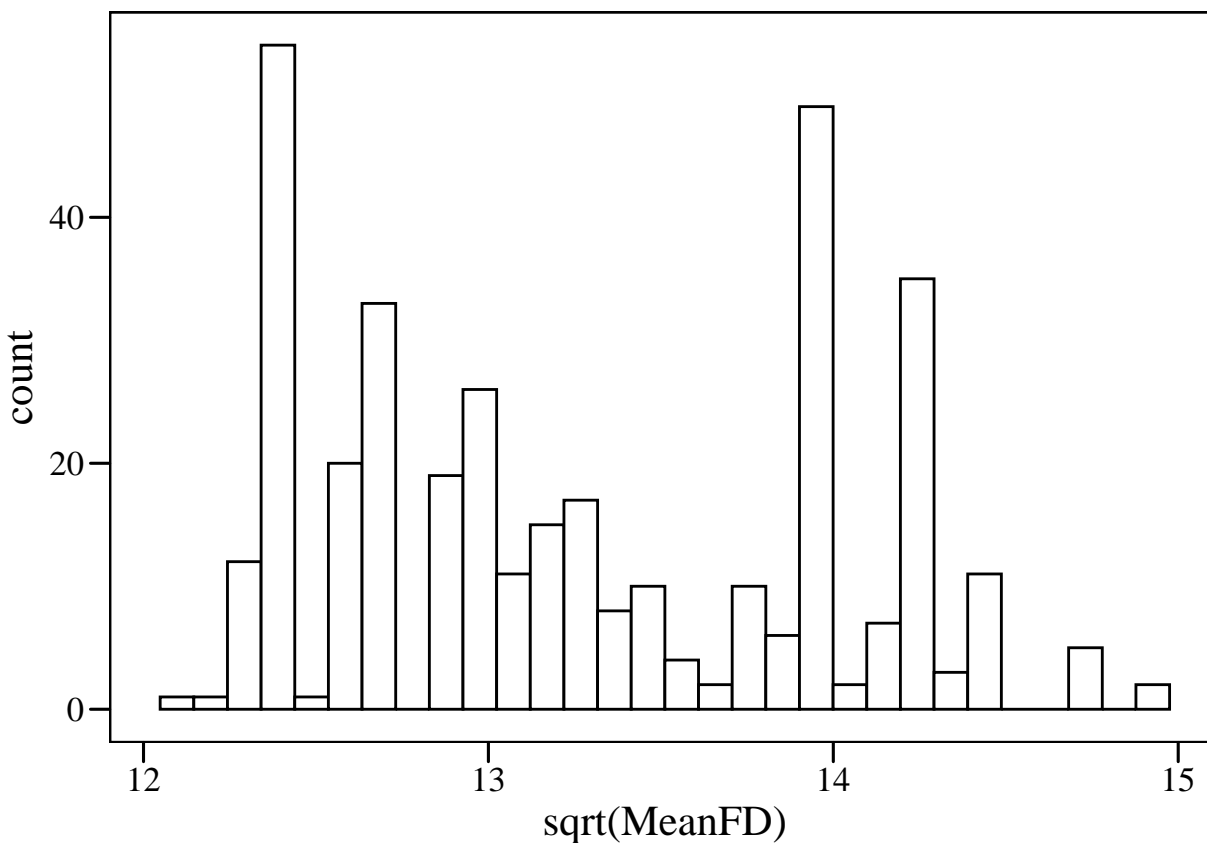
```
ggplot(data_transplants,aes(x=sqrt(FFD_corr)))+  
  geom_histogram(color="black",fill="white")+  
  my_theme()
```

```
ggplot(data_transplants,aes(x=sqrt(LFD_corr)))+  
  geom_histogram(color="black",fill="white")+  
  my_theme()
```



```
ggplot(data_transplants,aes(x=sqrt(MeanFD)))+  
  geom_histogram(color="black",fill="white")+  
  my_theme()
```



None of the distribution is looking super normal, but what else can we use?

TO DO: Check model diagnostics

Models FFD (OLD but USE?)

Temp mother + Temp father

```
data_transplants$heat_zone <- factor(data_transplants$heat_zone,
                                     levels=c("Cold", "Intermediate", "Hot"))
```

```
model_FFD1<-lmer(FFD_corr~(temp_mother+temp_father)*heat_zone+
                 (1|mother)+(1|father)+(1|crossing)+(1|plot),data_transplants)
model_FFD2<-lmer(FFD_corr~(temp_mother+temp_father)*temp+
                 (1|mother)+(1|father)+(1|crossing)+(1|plot),data_transplants)
# Both models with singular fit
# Because of low variance in some of the random effects?
```

```
tab_model(model_FFD1,model_FFD2,
          transform=NULL,show.ci=F,show.se=T,show.stat=T,digits=3,
          dv.labels=c("heat_zone", "temp"),
          title="Models FFD")
```

Models FFD

| | |
|-------------|--|
| heat_zone | |
| temp | |
| Predictors | |
| Estimates | |
| std. Error | |
| Statistic | |
| p | |
| Estimates | |
| std. Error | |
| Statistic | |
| p | |
| (Intercept) | |
| 194.764 | |
| 3.623 | |
| 53.760 | |
| <0.001 | |
| 188.950 | |
| 5.121 | |
| 36.900 | |
| <0.001 | |
| temp mother | |
| -0.011 | |
| 0.075 | |
| -0.146 | |
| 0.884 | |
| -0.011 | |
| 0.086 | |
| -0.128 | |
| 0.898 | |
| temp father | |
| -0.086 | |
| 0.054 | |
| -1.602 | |
| 0.110 | |

-0.180
 0.068
 -2.636
 0.009
 heat zone [Intermediate]
 -26.792
 4.469
 -5.995
 <0.001
 heat zone [Hot]
 -44.012
 4.531
 -9.714
 <0.001
 temp mother \times heat zone[Intermediate]
 0.086
 0.077
 1.118
 0.264
 temp mother \times heat zone[Hot]
 0.085
 0.081
 1.050
 0.294
 temp father \times heat zone[Intermediate]
 -0.042
 0.070
 -0.606
 0.545
 temp father \times heat zone[Hot]
 0.145
 0.076
 1.902
 0.058
 temp
 -0.899

0.095
 -9.442
 <0.001
 temp mother \times temp
 0.003
 0.003
 0.898
 0.370
 temp father \times temp
 0.006
 0.003
 2.033
 0.042
 Random Effects
 2
 54.30
 51.80
 00
 0.00 crossing
 0.00 crossing
 0.00 father
 0.17 father
 10.76 mother
 10.21 mother
 29.88 plot
 171.60 plot
 N
 63 mother
 63 mother
 64 father
 64 father
 131 crossing
 131 crossing
 8 plot
 8 plot
 Observations

603

603

Marginal R2 / Conditional R2

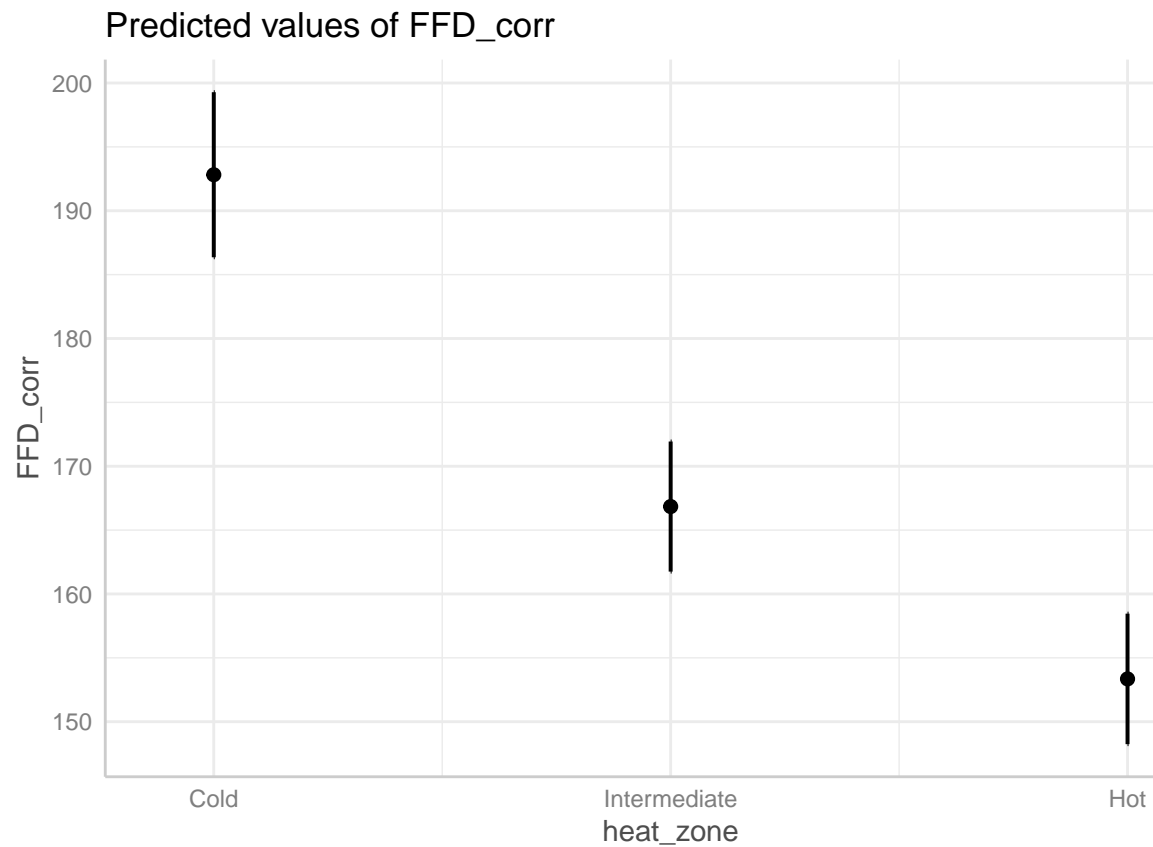
0.815 / NA

0.438 / NA

Save models as HTML table

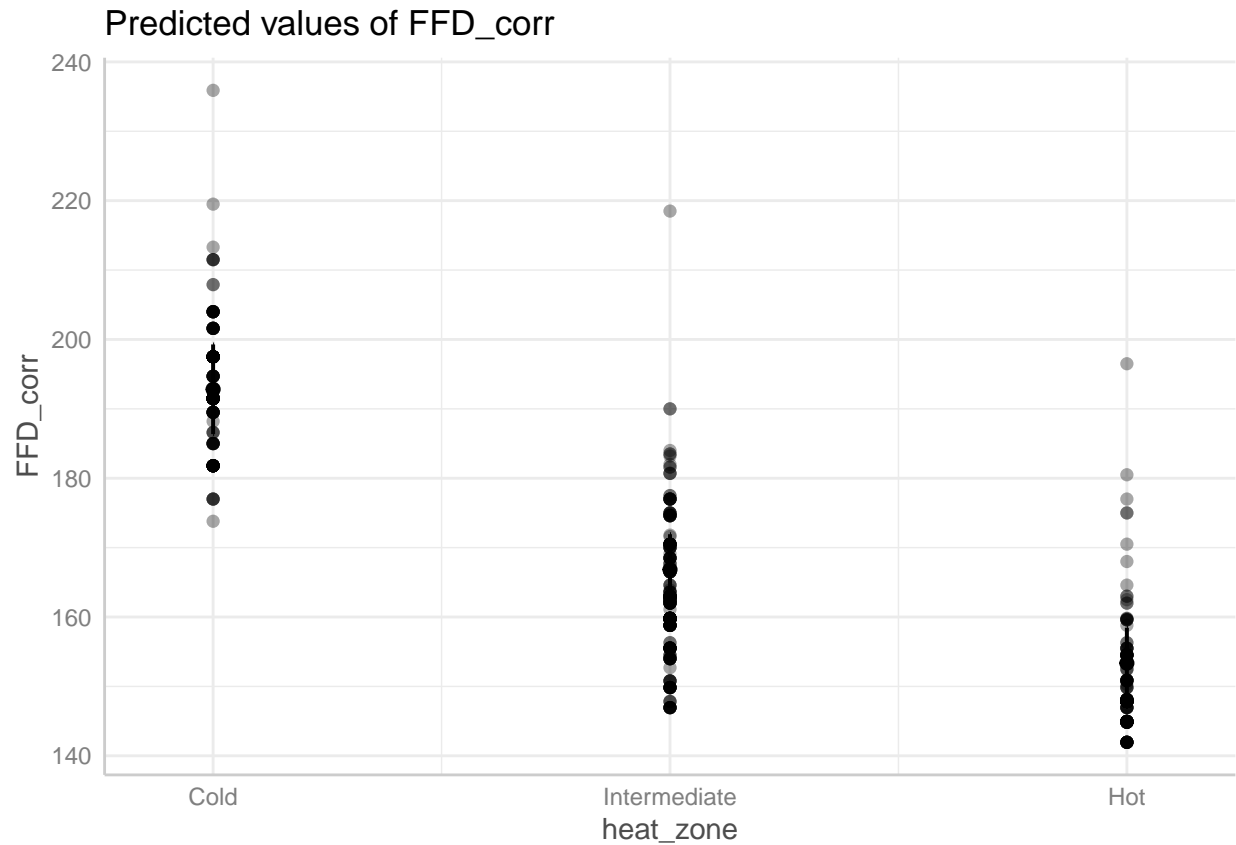
Plots predicted effects

```
plot(ggpredict(model_FFD1, terms=c("heat_zone")), add.data=F)
```



Heat zone (model1)

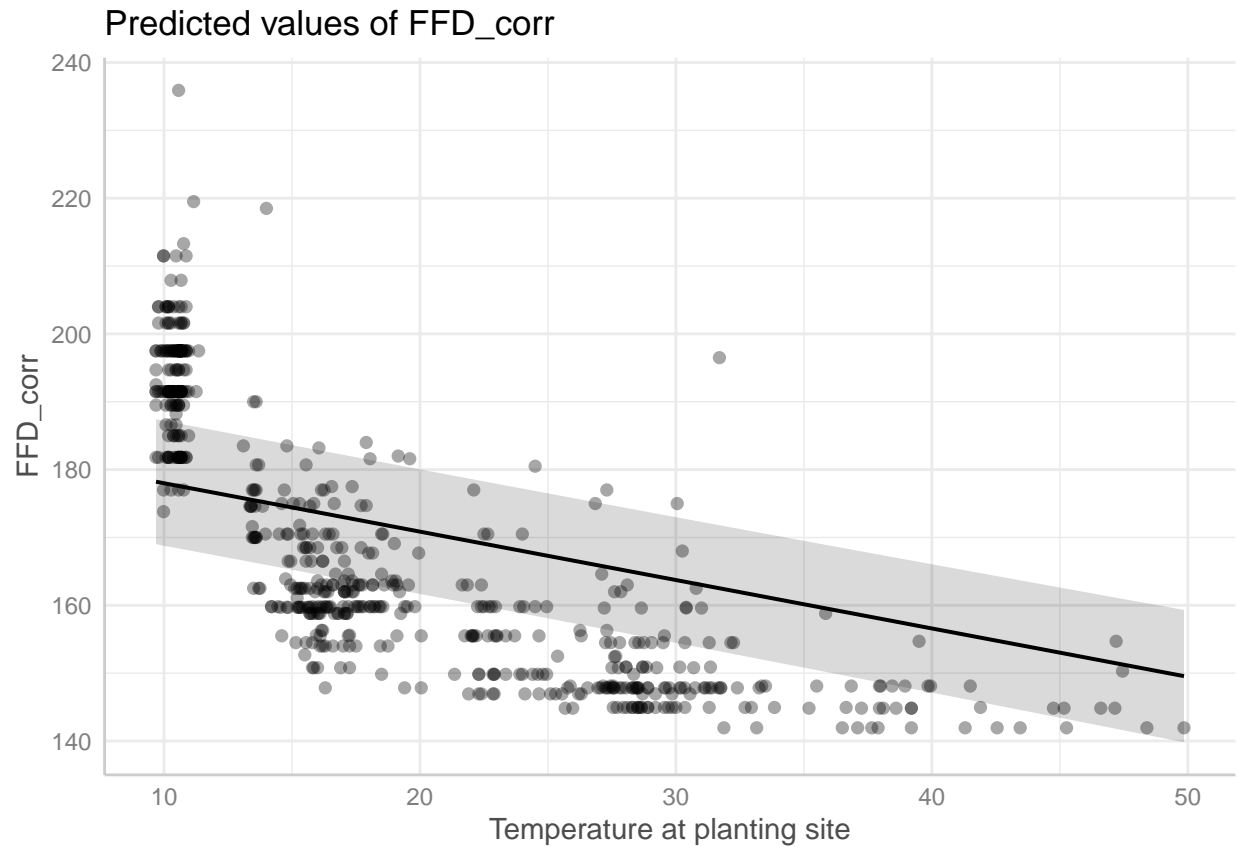
```
plot(ggpredict(model_FFD1, terms=c("heat_zone")), add.data=T)
```



There is plasticity in flowering time: individuals planted in warmer areas flower earlier.

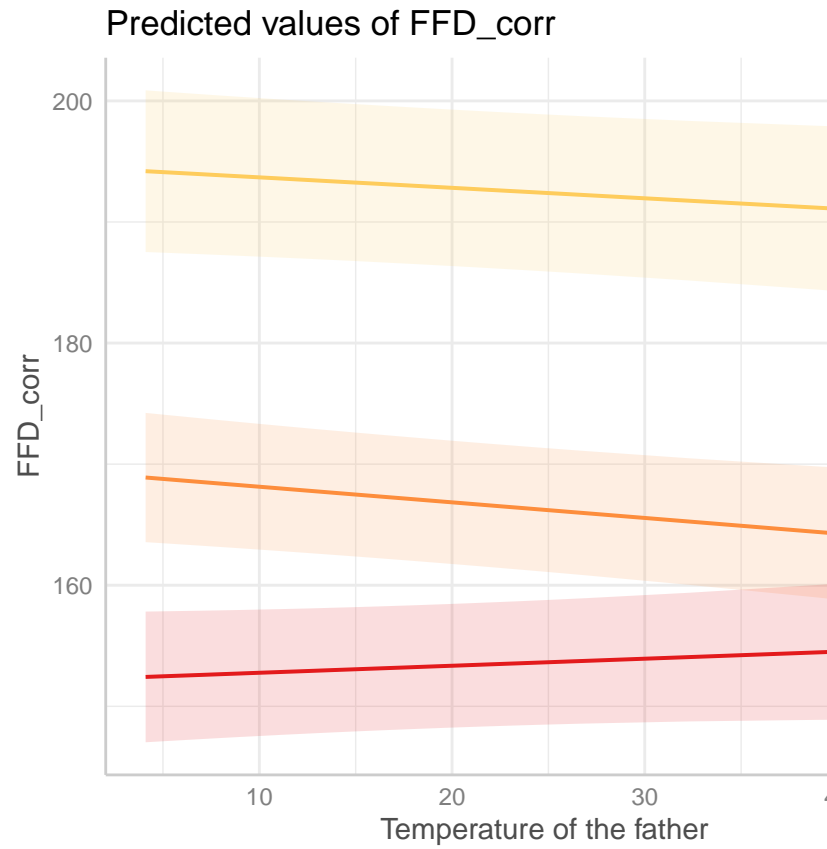
Temp at planting site (model2) Non-linear effect?

```
plot(ggpredict(model_FFD2, terms=c("temp[all]")), add.data=T) +
  xlab("Temperature at planting site")
```

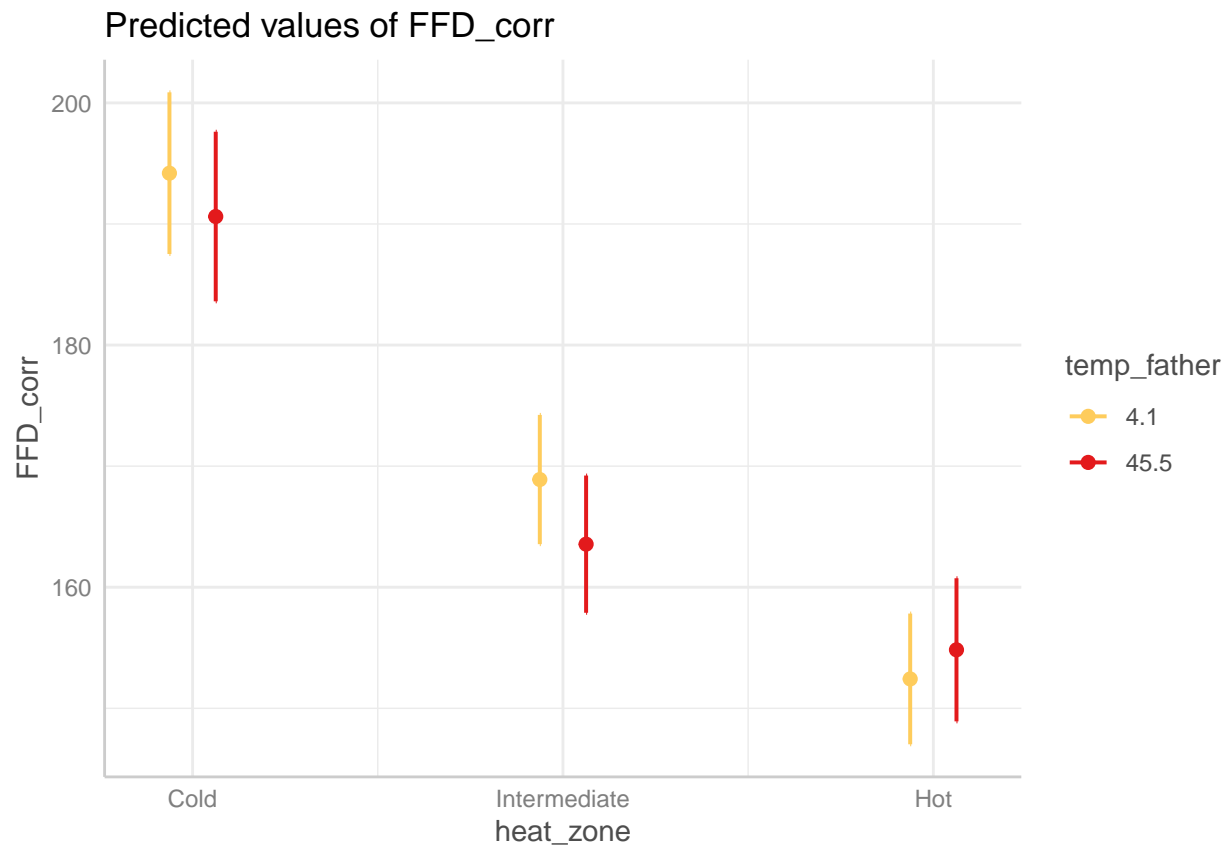
There is plasticity in flowering time: individuals planted in warmer areas flower earlier.

```
plot(ggpredict(model_FFD1, terms=c("temp_father[all]", "heat_zone")), add.data=F) +
  scale_color_manual(values = c("#fecc5c", "#fd8d3c", "#e31a1c")) +
  scale_fill_manual(values = c("#fecc5c", "#fd8d3c", "#e31a1c")) +
  xlab("Temperature of the father")
```

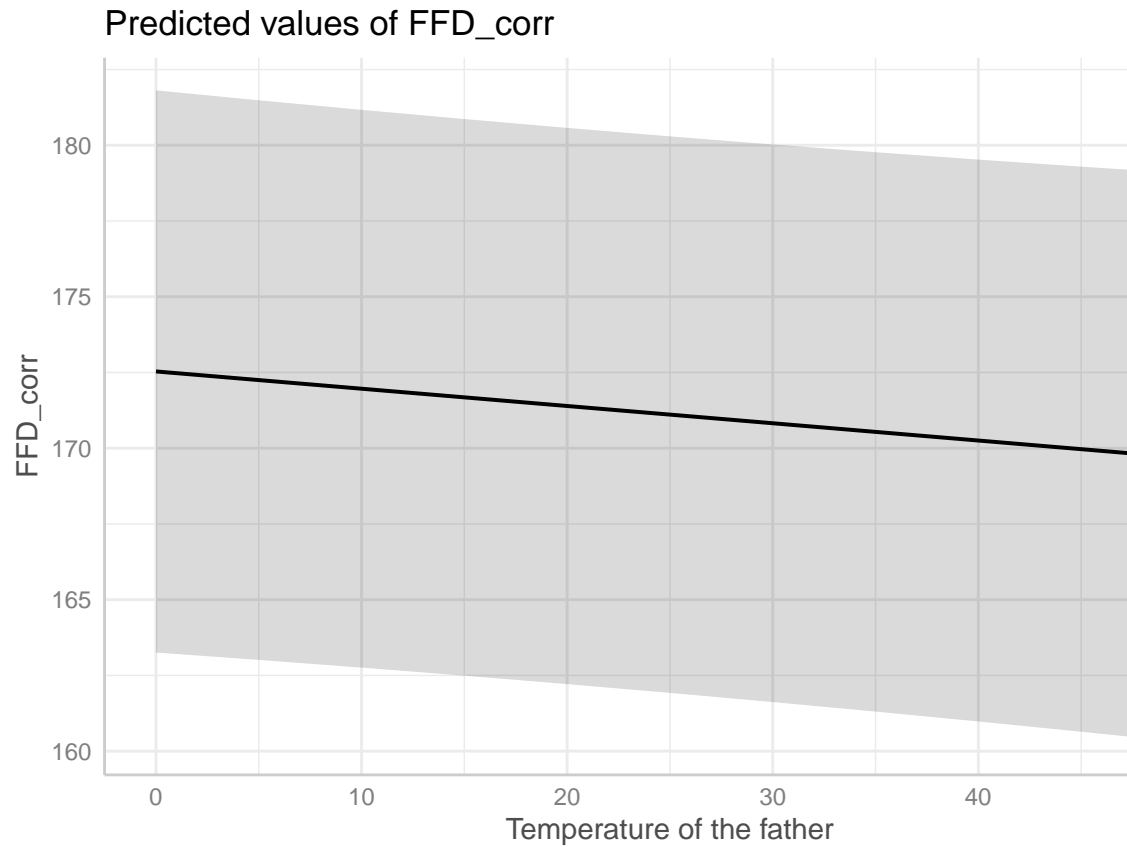


Interaction heat zone x temp father (model1)

```
plot(ggpredict(model_FFD1,terms=c("heat_zone","temp_father[minmax]")),add.data=F)+  
  scale_color_manual(values = c("#fecc5c", "#e31a1c"))
```



```
plot(ggpredict(model_FFD2, terms=c("temp_father")), add.data=F) +  
  xlab("Temperature of the father")
```

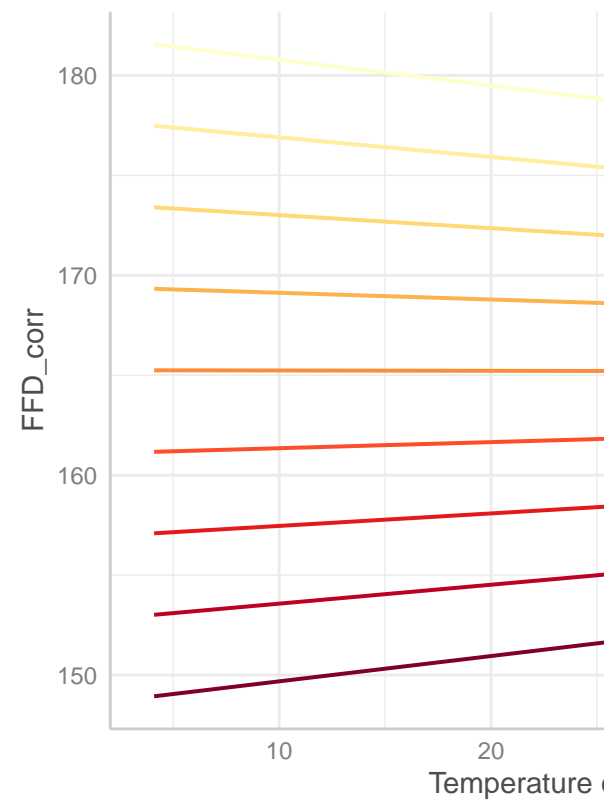


Temp father (model2)

I was expecting that this effect would go in the opposite direction, and that plants with fathers from colder origins would flower on average earlier. But maybe we should not really interpret this main effect, because the interaction with temperature at planting site is significant?

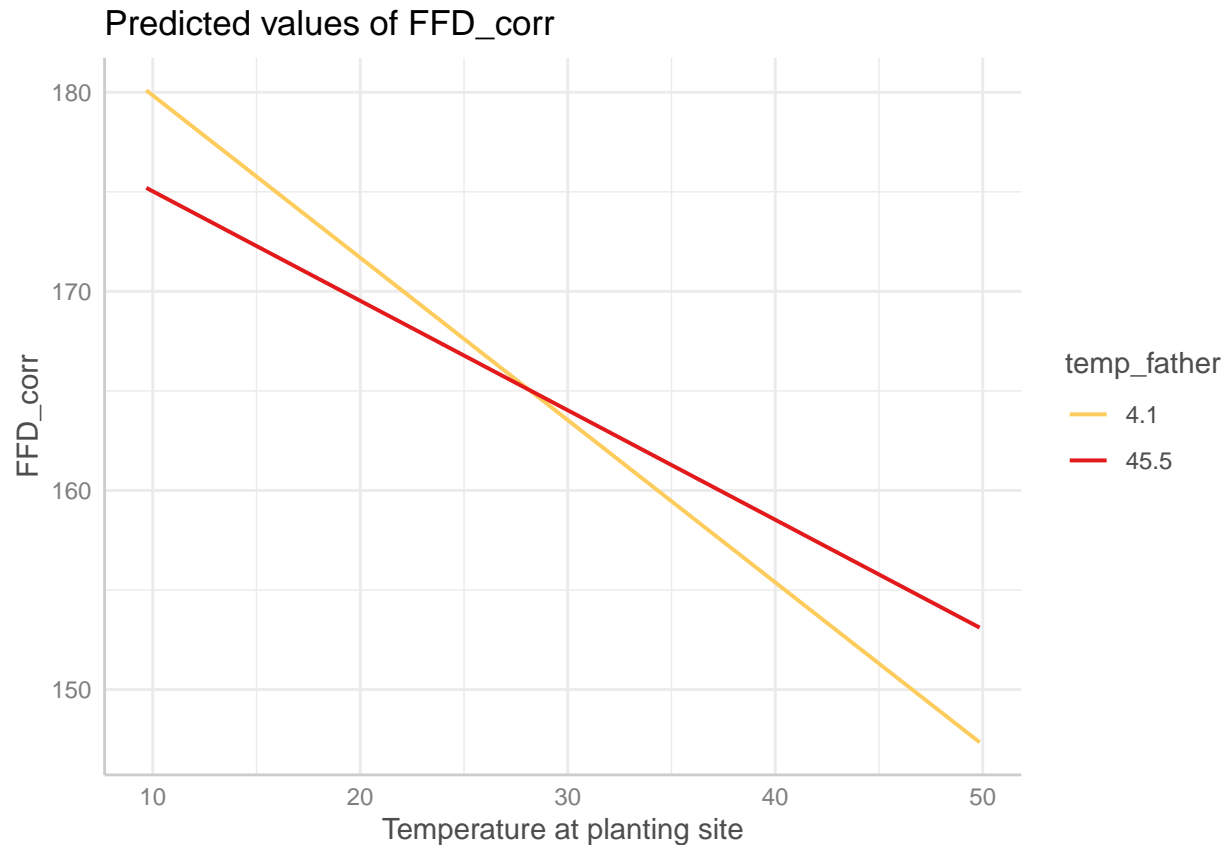
```
plot(ggpredict(model_FFD2, terms=c("temp_father[all]", "temp[7.9:49.7 by=5]")), add.data=F, ci=F) +  
  scale_color_brewer(palette="YlOrRd") +  
  xlab("Temperature of the father")
```

Predicted values of FFD_corr



Interaction temp at planting site x temp of the father (model2)

```
plot(ggpredict(model_FFD2,terms=c("temp[all]","temp_father[minmax]")),add.data=F,ci=F)+
  scale_color_manual(values = c("#fecc5c", "#e31a1c"))+
  xlab("Temperature at planting site")
```



Plants with fathers from colder origins flower on average earlier when planted on warmer areas, and on average later when planted on colder areas. Plasticity varies between temperatures of origin of the father: the differences in FFD between planting sites are larger for plants with fathers from colder origin than for plants with fathers from warmer origin.

Mean temp parents

```
data_transplants<-data_transplants%>%
  mutate(mean_temp_parents=(temp_mother+temp_father)/2)
```

```
model_FFD1_mean<-lmer(FFD_corr~mean_temp_parents*heat_zone+
  (1|mother)+(1|father)+(1|crossing)+(1|plot),data_transplants)
model_FFD2_mean<-lmer(FFD_corr~mean_temp_parents*temp+
  (1|mother)+(1|father)+(1|crossing)+(1|plot),data_transplants)
```

```
tab_model(model_FFD1_mean,model_FFD2_mean,
  transform=NULL,show.ci=F,show.se=T,show.stat=T,digits=3,
  dv.labels=c("heat_zone","temp"),
  title="Models FFD mean temp parents")
```

Models FFD mean temp parents

heat_zone

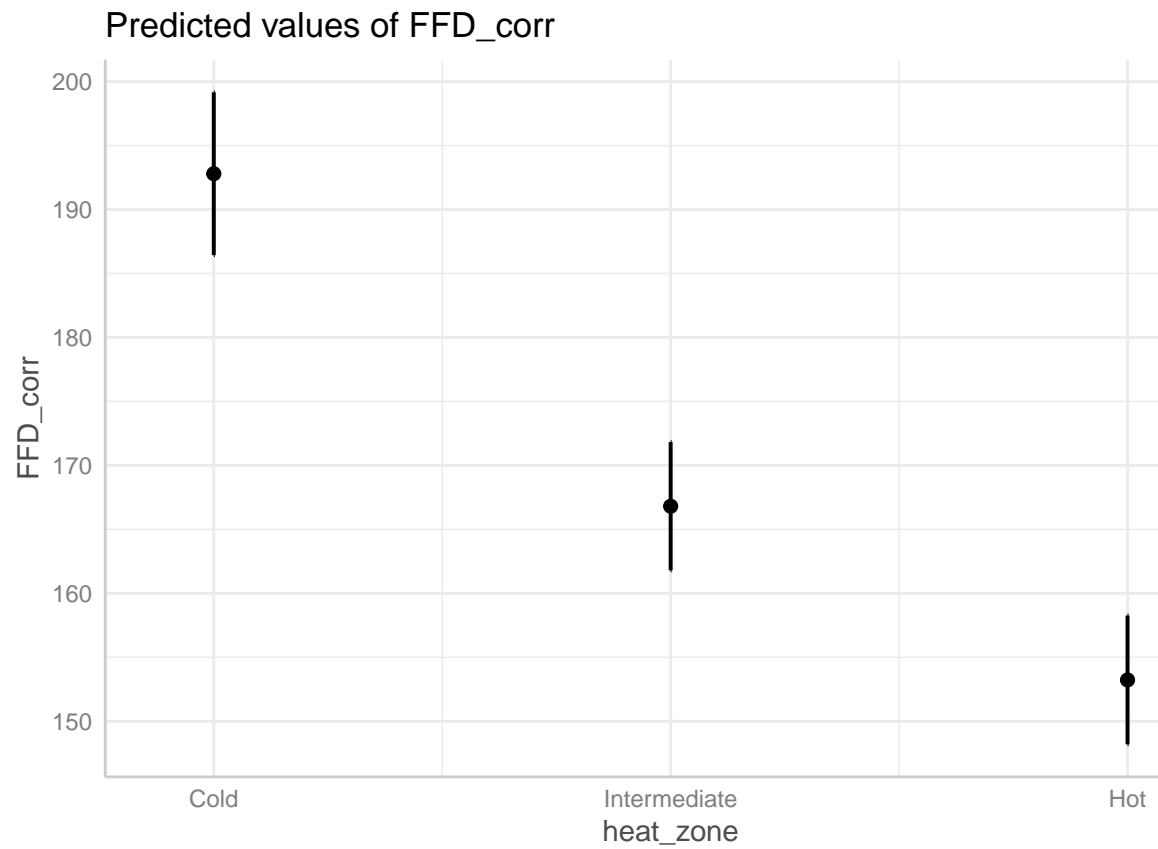
| temp |
|--------------------------|
| Predictors |
| Estimates |
| std. Error |
| Statistic |
| p |
| Estimates |
| std. Error |
| Statistic |
| p |
| (Intercept) |
| 195.507 |
| 3.528 |
| 55.411 |
| <0.001 |
| 189.786 |
| 5.079 |
| 37.369 |
| <0.001 |
| mean temp parents |
| -0.137 |
| 0.071 |
| -1.930 |
| 0.054 |
| -0.235 |
| 0.089 |
| -2.640 |
| 0.009 |
| heat zone [Intermediate] |
| -26.728 |
| 4.410 |
| -6.061 |
| <0.001 |
| heat zone [Hot] |
| -44.167 |
| 4.473 |

-9.875
 <0.001
 mean temp parents \times heatzone [Intermediate]
 0.037
 0.087
 0.431
 0.667
 mean temp parents \times heatzone [Hot]
 0.233
 0.095
 2.464
 0.014
 temp
 -0.906
 0.095
 -9.526
 <0.001
 mean temp parents \times temp
 0.010
 0.004
 2.436
 0.015
 Random Effects
 2
 54.55
 51.89
 00
 0.00 crossing
 0.00 crossing
 0.00 father
 0.25 father
 10.57 mother
 9.88 mother
 28.89 plot
 170.95 plot
 ICC

0.42
0.78
N
63 mother
63 mother
64 father
64 father
131 crossing
131 crossing
8 plot
8 plot
Observations
603
603
Marginal R2 / Conditional R2
0.719 / 0.837
0.148 / 0.810
Save models as HTML table

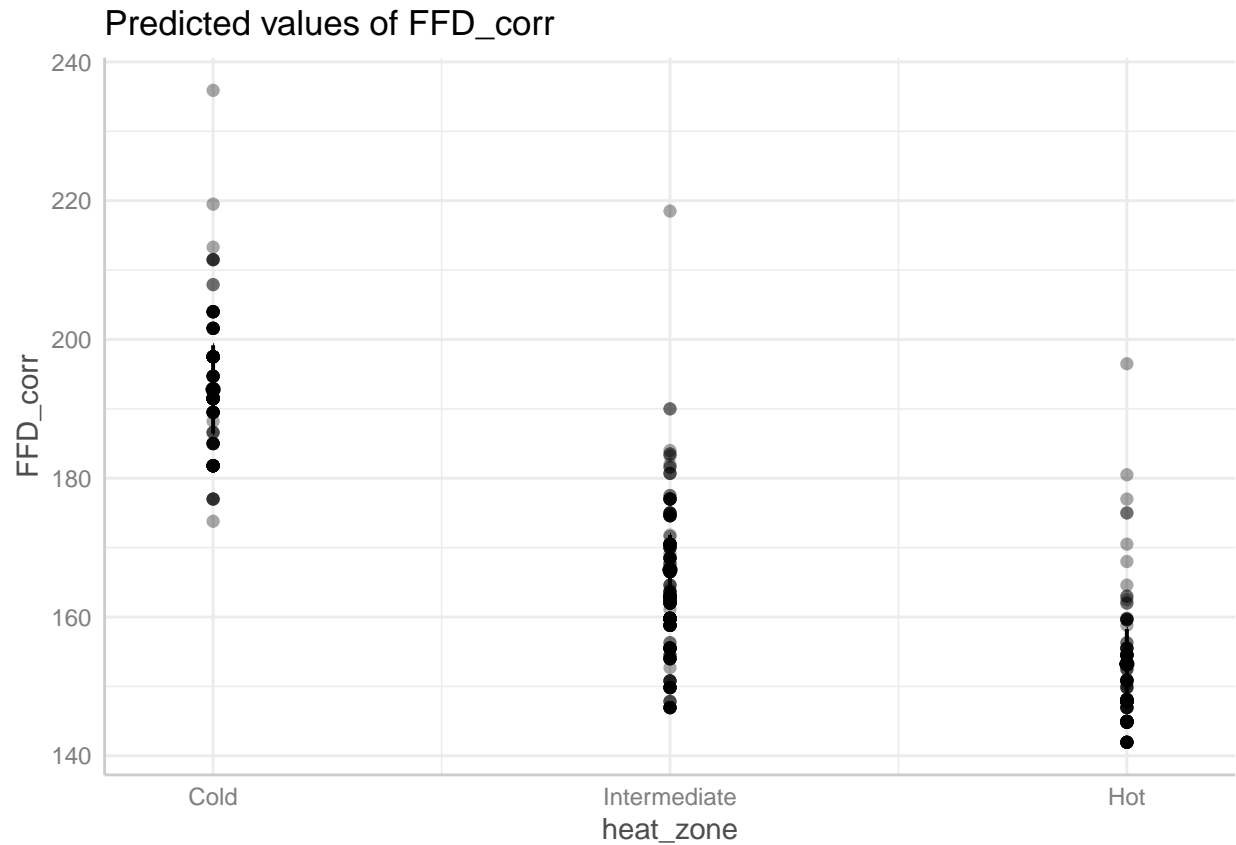
Plots predicted effects

```
plot(ggpredict(model_FFD1_mean, terms=c("heat_zone")), add.data=F)
```



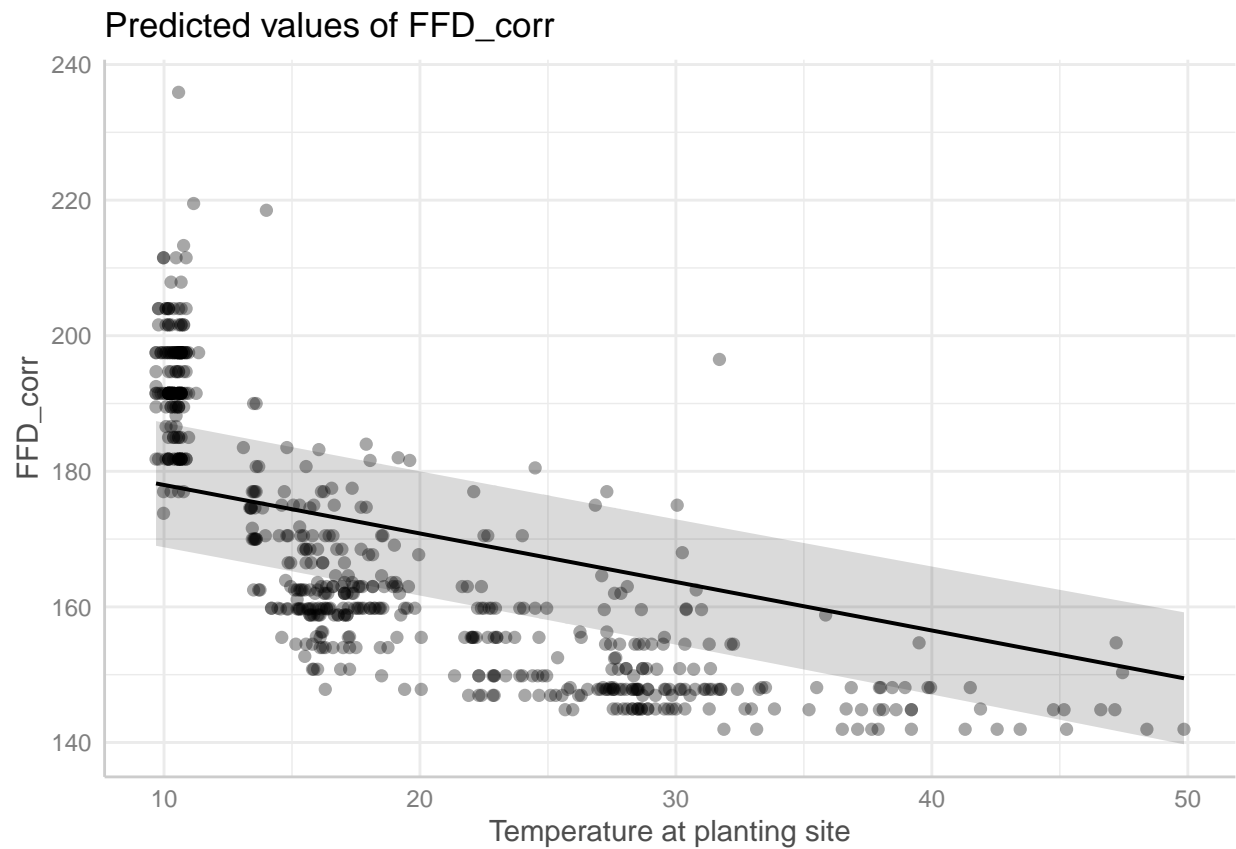
Heat zone (model1)

```
plot(ggpredict(model_FFD1_mean, terms=c("heat_zone")), add.data=T)
```

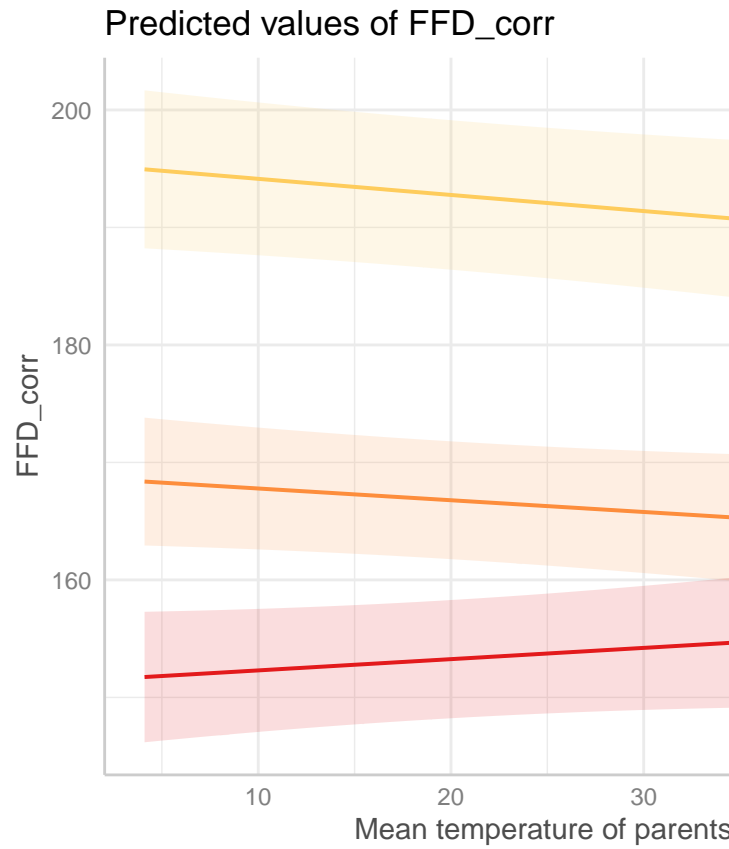


Temp at planting site (model2) Non-linear effect?

```
plot(ggpredict(model_FFD2_mean, terms=c("temp[all]")), add.data=T) +  
  xlab("Temperature at planting site")
```

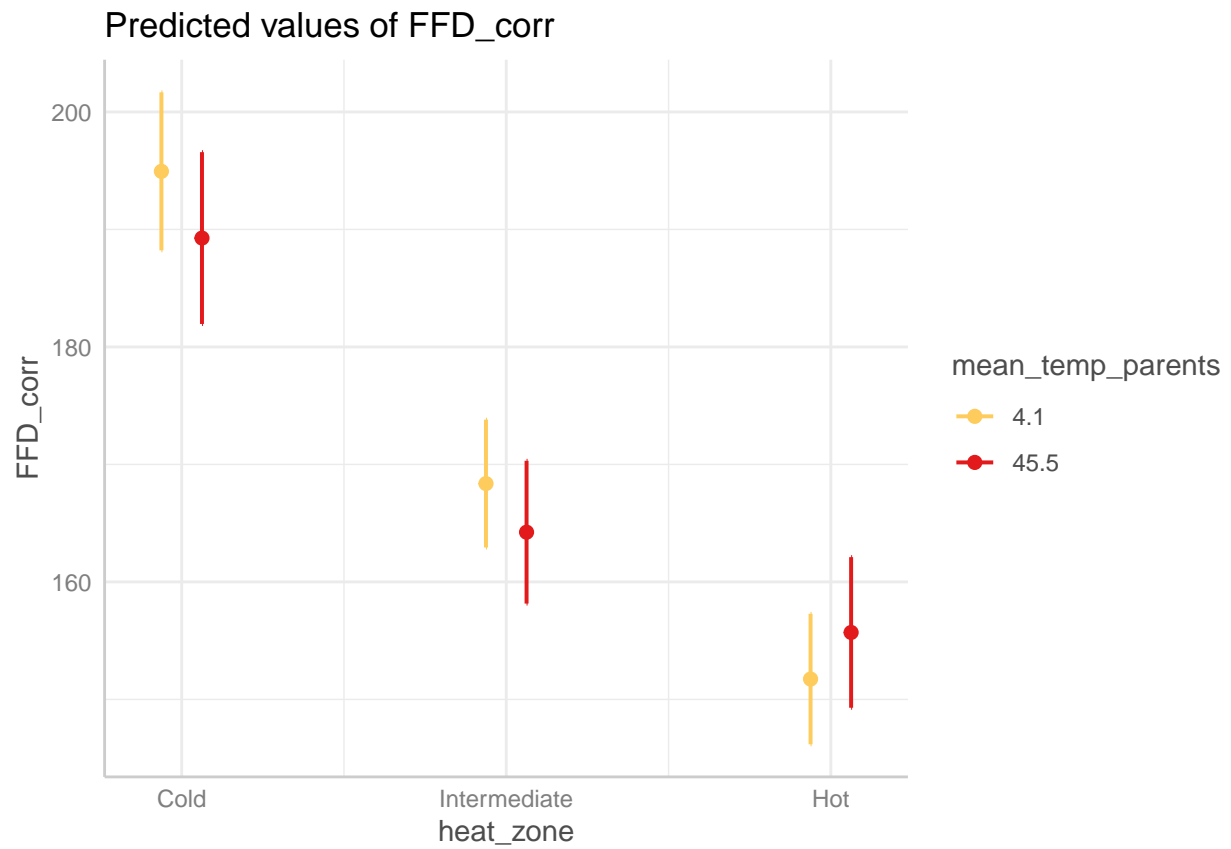


```
plot(ggpredict(model_FFD1_mean, terms=c("mean_temp_parents[all]", "heat_zone")), add.data=F) +
  scale_color_manual(values = c("#fecc5c", "#fd8d3c", "#e31a1c")) +
  scale_fill_manual(values = c("#fecc5c", "#fd8d3c", "#e31a1c")) +
  xlab("Mean temperature of parents")
```

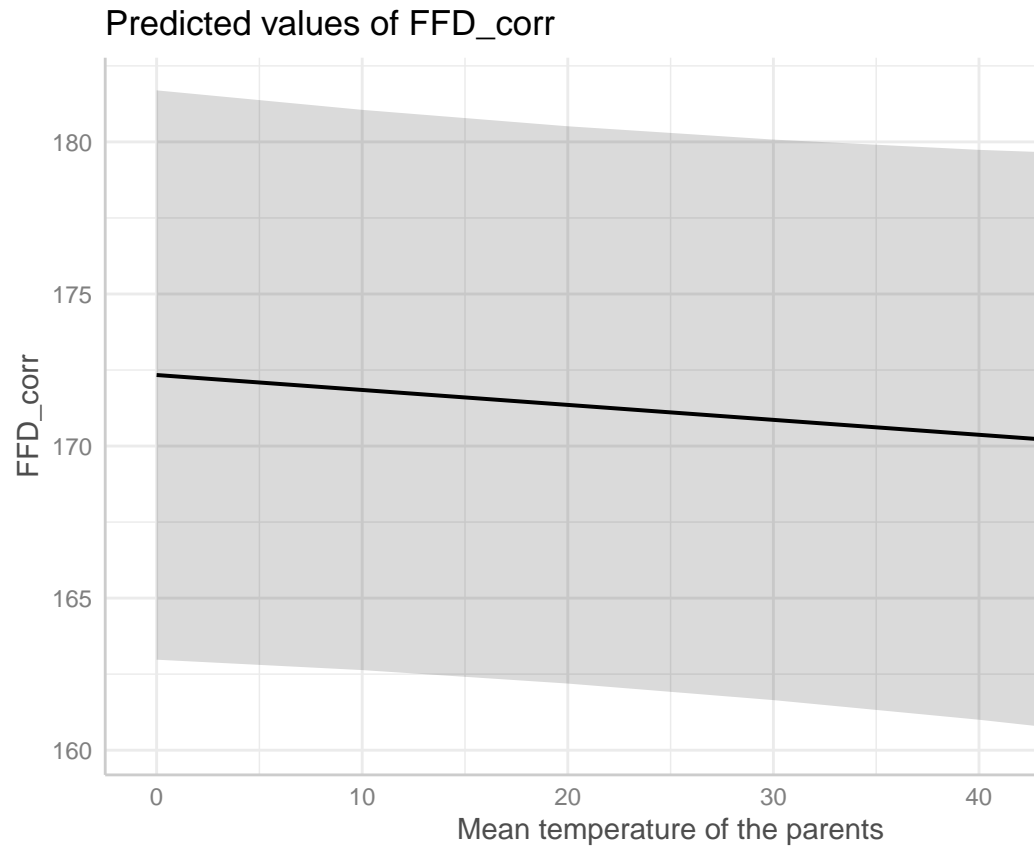


Interaction heat zone x mean temp parents (model1)

```
plot(ggpredict(model_FFD1_mean, terms=c("heat_zone", "mean_temp_parents[minmax]")), add.data=F) +
  scale_color_manual(values = c("#fecc5c", "#e31a1c"))
```

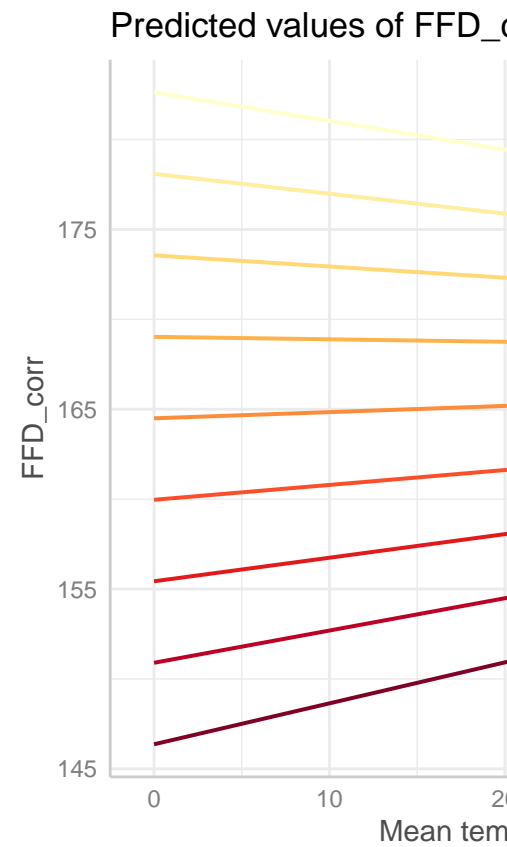


```
plot(ggpredict(model_FFD2_mean, terms=c("mean_temp_parents")), add.data=F) +  
  xlab("Mean temperature of the parents")
```



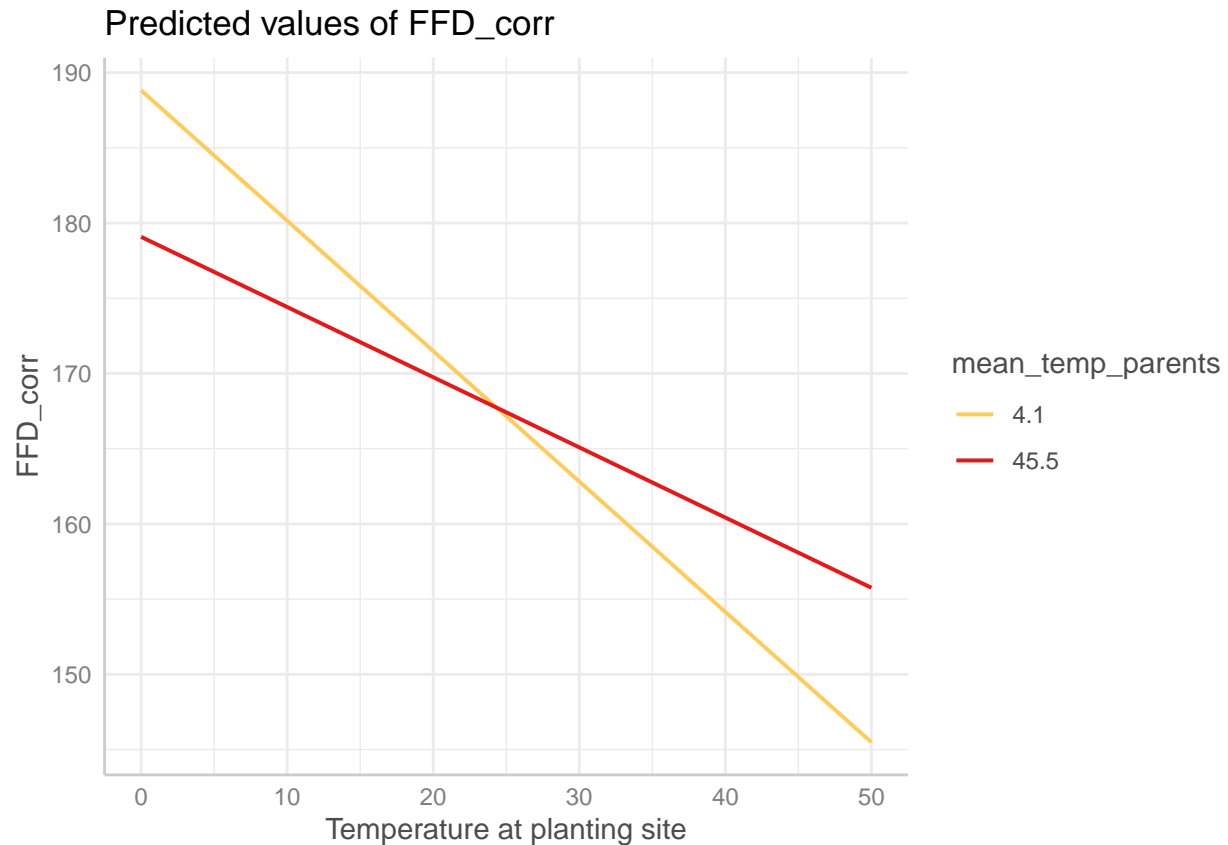
Mean temp parents (model2)

```
plot(ggpredict(model_FFD2_mean, terms=c("mean_temp_parents", "temp[7.9:49.7 by=5]")),  
     add.data=F, ci=F) +  
  scale_color_brewer(palette="YlOrRd") +  
  xlab("Mean temperature of the parents")
```



Interaction temp at planting site x mean temp of the parents (model2)

```
plot(ggpredict(model_FFD2_mean, terms=c("temp", "mean_temp_parents[minmax]")), add.data=F, ci=F) +
  scale_color_manual(values = c("#fecc5c", "#e31a1c")) +
  xlab("Temperature at planting site")
```

Models similar to greenhouse paper

Prediction 1

Models

```
modell1_FFD<-lmer(FFD_corr~1+(1|father)+(1|mother)+(1|father:mother)+(1|plot),
  data_transplants)
modell1_LFD<-lmer(LFD_corr~1+(1|father)+(1|mother)+(1|father:mother)+(1|plot),
  data_transplants)
modell1_MeanFD<-lmer(MeanFD~1+(1|father)+(1|mother)+(1|father:mother)+(1|plot),
  data_transplants)
summary(modell1_FFD)
```

```
## Linear mixed model fit by REML. t-tests use Satterthwaite's method [
## lmerModLmerTest]
## Formula: FFD_corr ~ 1 + (1 | father) + (1 | mother) + (1 | father:mother) +
## (1 | plot)
## Data: data_transplants
##
## REML criterion at convergence: 4349.2
##
```

```
## Scaled residuals:
##      Min       1Q   Median       3Q      Max
## -2.2029 -0.6613 -0.0692  0.5486  5.0403
##
## Random effects:
##   Groups      Name      Variance Std.Dev.
## father:mother (Intercept)  0.00000  0.0000
## father        (Intercept)  0.06272  0.2504
## mother        (Intercept)  8.83030  2.9716
## plot          (Intercept) 333.09746 18.2510
## Residual                69.36945  8.3288
## Number of obs: 603, groups:
## father:mother, 131; father, 64; mother, 63; plot, 8
##
## Fixed effects:
##              Estimate Std. Error      df t value Pr(>|t|)
## (Intercept)  172.338      6.486    7.077   26.57 2.37e-08 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
## optimizer (nloptwrap) convergence code: 0 (OK)
## boundary (singular) fit: see help('isSingular')
```

```
summary(model1_LFD)
```

```
## Linear mixed model fit by REML. t-tests use Satterthwaite's method [
## lmerModLmerTest]
## Formula: LFD_corr ~ 1 + (1 | father) + (1 | mother) + (1 | father:mother) +
##      (1 | plot)
##      Data: data_transplants
##
## REML criterion at convergence: 2653.9
##
## Scaled residuals:
##      Min       1Q   Median       3Q      Max
## -2.3988 -0.7025 -0.0959  0.4784  4.5886
##
## Random effects:
##   Groups      Name      Variance Std.Dev.
## father:mother (Intercept) 2.459e-07 4.959e-04
## mother        (Intercept) 6.380e+00 2.526e+00
## father        (Intercept) 5.210e+00 2.282e+00
## plot          (Intercept) 3.077e+02 1.754e+01
## Residual                7.034e+01 8.387e+00
## Number of obs: 364, groups:
## father:mother, 120; mother, 59; father, 59; plot, 8
##
## Fixed effects:
##              Estimate Std. Error      df t value Pr(>|t|)
## (Intercept)  183.185      6.258    7.126   29.27 1.09e-08 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
## optimizer (nloptwrap) convergence code: 0 (OK)
## boundary (singular) fit: see help('isSingular')
```

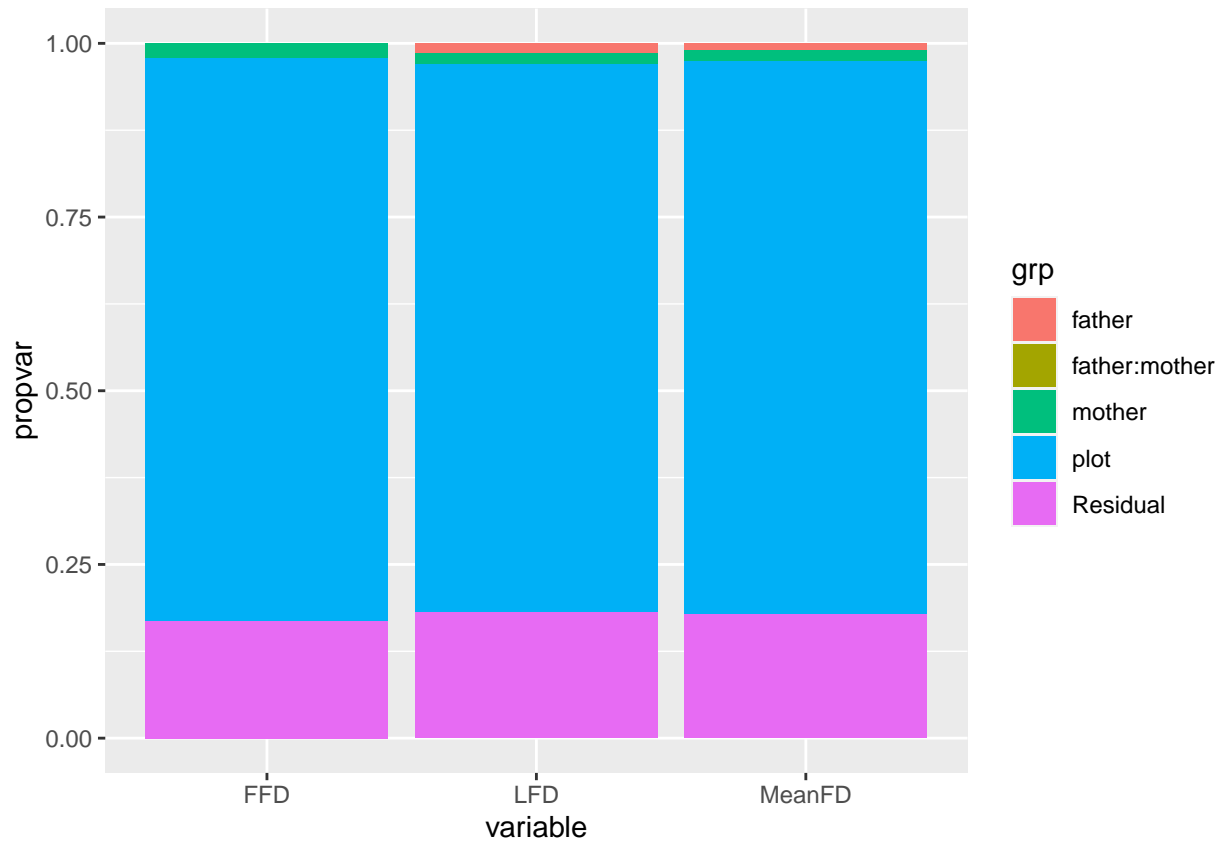
```
summary(model1_MeanFD)
```

```
## Linear mixed model fit by REML. t-tests use Satterthwaite's method [
## lmerModLmerTest]
## Formula: MeanFD ~ 1 + (1 | father) + (1 | mother) + (1 | father:mother) +
##      (1 | plot)
##      Data: data_transplants
##
## REML criterion at convergence: 2644.5
##
## Scaled residuals:
##      Min       1Q   Median       3Q      Max
## -2.2400 -0.7146 -0.0838  0.5046  4.6854
##
## Random effects:
##      Groups       Name             Variance Std.Dev.
## father:mother (Intercept)    0.000    0.000
## mother        (Intercept)    6.517    2.553
## father        (Intercept)    3.443    1.855
## plot          (Intercept)  310.767   17.629
## Residual                        69.280    8.323
## Number of obs: 364, groups:
## father:mother, 120; mother, 59; father, 59; plot, 8
##
## Fixed effects:
##              Estimate Std. Error      df t value Pr(>|t|)
## (Intercept)  178.253      6.285    7.110   28.36 1.41e-08 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
## optimizer (nloptwrap) convergence code: 0 (OK)
## boundary (singular) fit: see help('isSingular')
```

Proportions of variance

```
Variance_FFD<-as.data.frame(VarCorr(model1_FFD))[,c(1,4)]
Variance_LFD<-as.data.frame(VarCorr(model1_LFD))[,c(1,4)]
Variance_MeanFD<-as.data.frame(VarCorr(model1_MeanFD))[,c(1,4)]
# Intra-class correlations
PropVar_FFD <- Variance_FFD%>%mutate(propvar=vcov/sum(vcov))%>%
  mutate(variable="FFD")
PropVar_LFD <- Variance_LFD%>%mutate(propvar=vcov/sum(vcov))%>%
  mutate(variable="LFD")
PropVar_MeanFD <- Variance_MeanFD%>%mutate(propvar=vcov/sum(vcov))%>%
  mutate(variable="MeanFD")
Props_var<-rbind(PropVar_FFD,PropVar_LFD,PropVar_MeanFD)

ggplot(Props_var,aes(x=variable,y=propvar,fill=grp))+
  geom_col()
```



Heritability and maternal effects

```
# h^2 (paternal effects)
her_FFD<-as.numeric(4*subset(PropVar_FFD,grp=="father")[3])
her_LFD<-as.numeric(4*subset(PropVar_LFD,grp=="father")[3])
her_MeanFD<-as.numeric(4*subset(PropVar_MeanFD,grp=="father")[3])
# Because the additive genetic variance, VA,
# is expected to be four times the among pollen-donor variance
# (Falconer & Mackay, 1996; Lynch & Walsh, 1998)
her<-data.frame(value=rbind(her_FFD,her_LFD,her_MeanFD))%>%
  rownames_to_column()%>%
  mutate(variable=c("FFD","LFD","MeanFD"),
    effect="Heritability")
```

```
# maternal effects

# Maternal - paternal
# -----
# summed effects

# Because the pollen-recipient variance component contains a combination of
# genetic and environmental effects, we subtracted the additive genetic
# (pollen donor) component from the pollen-recipient variance component
# before dividing the resulting estimate by VP to estimate
```

```

# m2 (m2 = (Vpollen recipient - Vpollen donor)/VP).

# But what about the interaction?

mat_FFD<-((Variance_FFD%>%filter(grp=="mother"))$vcov-
  (Variance_FFD%>%filter(grp=="father"))$vcov)/
  as.numeric(Variance_FFD%>%summarise(sum(vcov)))
mat_LFD<-((Variance_LFD%>%filter(grp=="mother"))$vcov-
  (Variance_LFD%>%filter(grp=="father"))$vcov)/
  as.numeric(Variance_LFD%>%summarise(sum(vcov)))
mat_MeanFD<-((Variance_MeanFD%>%filter(grp=="mother"))$vcov-
  (Variance_MeanFD%>%filter(grp=="father"))$vcov)/
  as.numeric(Variance_MeanFD%>%summarise(sum(vcov)))

mat<-data.frame(value=rbind(mat_FFD))%>%
  rownames_to_column()%>%
  mutate(variable=c("FFD"),
    effect="Maternal effects")
mat<-data.frame(value=rbind(mat_FFD,mat_LFD,mat_MeanFD))%>%
  rownames_to_column()%>%
  mutate(variable=c("FFD", "LFD", "MeanFD"),
    effect="Maternal effects")

her_mat<-rbind(her,mat)
her_mat

```

```

##      rowname      value variable      effect
## 1  her_FFD 0.0006099264      FFD  Heritability
## 2  her_LFD 0.0534828146      LFD  Heritability
## 3 her_MeanFD 0.0353088400  MeanFD  Heritability
## 4  mat_FFD 0.0213136300      FFD Maternal effects
## 5  mat_LFD 0.0030046180      LFD Maternal effects
## 6 mat_MeanFD 0.0078827217  MeanFD Maternal effects

```

```

ggplot(her_mat,aes(x=variable,y=value,fill=effect))+
  geom_bar(stat="identity",position="dodge")

```

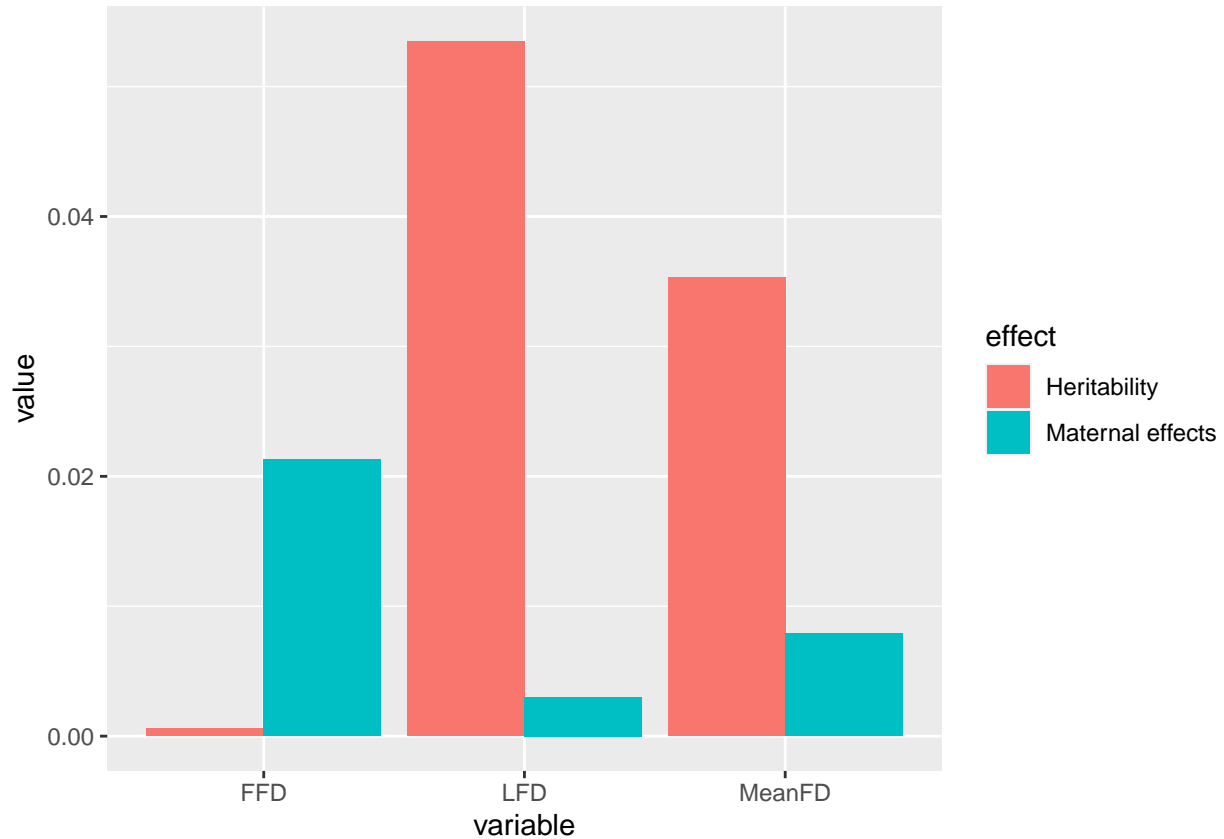


Table SM: LRTs for variance component

Table SM: LRTs for variance components

(These results could be used to add asterisks to the previous plot).

```
ranova(model1_FFD)
```

```
## ANOVA-like table for random-effects: Single term deletions
##
## Model:
## FFD_corr ~ (1 | father) + (1 | mother) + (1 | father:mother) + (1 | plot)
##
```

| | npars | logLik | AIC | LRT | Df | Pr(>Chisq) |
|---------------------|-------|---------|--------|--------|----|-------------|
| <none> | 6 | -2174.6 | 4361.2 | | | |
| (1 father) | 5 | -2174.6 | 4359.2 | 0.00 | 1 | 0.97164 |
| (1 mother) | 5 | -2179.4 | 4368.9 | 9.73 | 1 | 0.00181 ** |
| (1 father:mother) | 5 | -2174.6 | 4359.2 | 0.00 | 1 | 1.00000 |
| (1 plot) | 5 | -2636.2 | 5282.3 | 923.18 | 1 | < 2e-16 *** |

```
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
ranova(model1_LFD)
```

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

```
##
## Model:
## LFD_corr ~ (1 | father) + (1 | mother) + (1 | father:mother) + (1 | plot)
##               npar logLik   AIC    LRT Df Pr(>Chisq)
## <none>          6 -1326.9 2665.9
## (1 | father)     5 -1327.9 2665.8   1.95  1    0.16266
## (1 | mother)     5 -1328.6 2667.2   3.35  1    0.06712 .
## (1 | father:mother) 5 -1326.9 2663.9   0.00  1    1.00000
## (1 | plot)       5 -1590.8 3191.7 527.80  1    < 2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
ranova(model1_MeanFD)
```

```
## ANOVA-like table for random-effects: Single term deletions
##
## Model:
## MeanFD ~ (1 | father) + (1 | mother) + (1 | father:mother) + (1 | plot)
##               npar logLik   AIC    LRT Df Pr(>Chisq)
## <none>          6 -1322.2 2656.5
## (1 | father)     5 -1322.7 2655.5   0.99  1    0.31864
## (1 | mother)     5 -1323.9 2657.7   3.24  1    0.07178 .
## (1 | father:mother) 5 -1322.2 2654.5   0.00  1    1.00000
## (1 | plot)       5 -1591.3 3192.7 538.20  1    < 2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

Prediction 2

Models

```
model2_FFD<-lmer(FFD_corr~temp+(1|father)+(1|mother)+(1|father:mother)+(1|plot)+
  (1|temp:father)+(1|temp:mother),
  data_transplants)
model2_LFD<-lmer(LFD_corr~temp+(1|father)+(1|mother)+(1|father:mother)+(1|plot)+
  (1|temp:father)+(1|temp:mother),
  data_transplants)
model2_MeanFD<-lmer(MeanFD~temp+(1|father)+(1|mother)+(1|father:mother)+(1|plot)+
  (1|temp:father)+(1|temp:mother),
  data_transplants)
summary(model2_FFD)
```

```
## Linear mixed model fit by REML. t-tests use Satterthwaite's method [
## lmerModLmerTest]
## Formula: FFD_corr ~ temp + (1 | father) + (1 | mother) + (1 | father:mother) +
## (1 | plot) + (1 | temp:father) + (1 | temp:mother)
## Data: data_transplants
##
## REML criterion at convergence: 4192.4
##
## Scaled residuals:
```

```
##      Min      1Q  Median      3Q      Max
## -2.2868 -0.5248 -0.0903  0.4013  5.0763
##
## Random effects:
## Groups      Name      Variance Std.Dev.
## temp:father (Intercept) 1.874e-05 0.004329
## temp:mother (Intercept) 1.365e+01 3.693937
## father:mother (Intercept) 0.000e+00 0.000000
## father      (Intercept) 9.208e-01 0.959563
## mother      (Intercept) 8.925e+00 2.987438
## plot        (Intercept) 1.705e+02 13.057191
## Residual                3.891e+01 6.237921
## Number of obs: 603, groups:
## temp:father, 561; temp:mother, 554; father:mother, 131; father, 64; mother, 63; plot, 8
##
## Fixed effects:
##              Estimate Std. Error      df t value Pr(>|t|)
## (Intercept) 185.16683    4.75241    7.66150   38.96 4.35e-10 ***
## temp        -0.71624     0.05285  525.59618  -13.55 < 2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Correlation of Fixed Effects:
##      (Intr)
## temp -0.198
## optimizer (nloptwrap) convergence code: 0 (OK)
## boundary (singular) fit: see help('isSingular')
```

```
summary(model2_LFD)
```

```
## Linear mixed model fit by REML. t-tests use Satterthwaite's method [
## lmerModLmerTest]
## Formula: LFD_corr ~ temp + (1 | father) + (1 | mother) + (1 | father:mother) +
##      (1 | plot) + (1 | temp:father) + (1 | temp:mother)
##      Data: data_transplants
##
## REML criterion at convergence: 2562.4
##
## Scaled residuals:
##      Min      1Q  Median      3Q      Max
## -1.97513 -0.37245 -0.09377  0.27358  2.79436
##
## Random effects:
## Groups      Name      Variance Std.Dev.
## temp:father (Intercept) 6.972e-05 0.00835
## temp:mother (Intercept) 4.171e+01 6.45864
## father:mother (Intercept) 0.000e+00 0.00000
## mother      (Intercept) 9.389e+00 3.06409
## father      (Intercept) 0.000e+00 0.00000
## plot        (Intercept) 1.483e+02 12.17863
## Residual                1.729e+01 4.15756
## Number of obs: 364, groups:
## temp:father, 342; temp:mother, 336; father:mother, 120; mother, 59; father, 59; plot, 8
##
```



```
## Fixed effects:
##           Estimate Std. Error      df t value Pr(>|t|)
## (Intercept) 197.33622    4.60845   8.64466  42.821 2.27e-11 ***
## temp        -0.80639    0.08378 320.71741  -9.626 < 2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Correlation of Fixed Effects:
##      (Intr)
## temp -0.319
## optimizer (nloptwrap) convergence code: 0 (OK)
## boundary (singular) fit: see help('isSingular')
```

```
summary(model2_MeanFD)
```

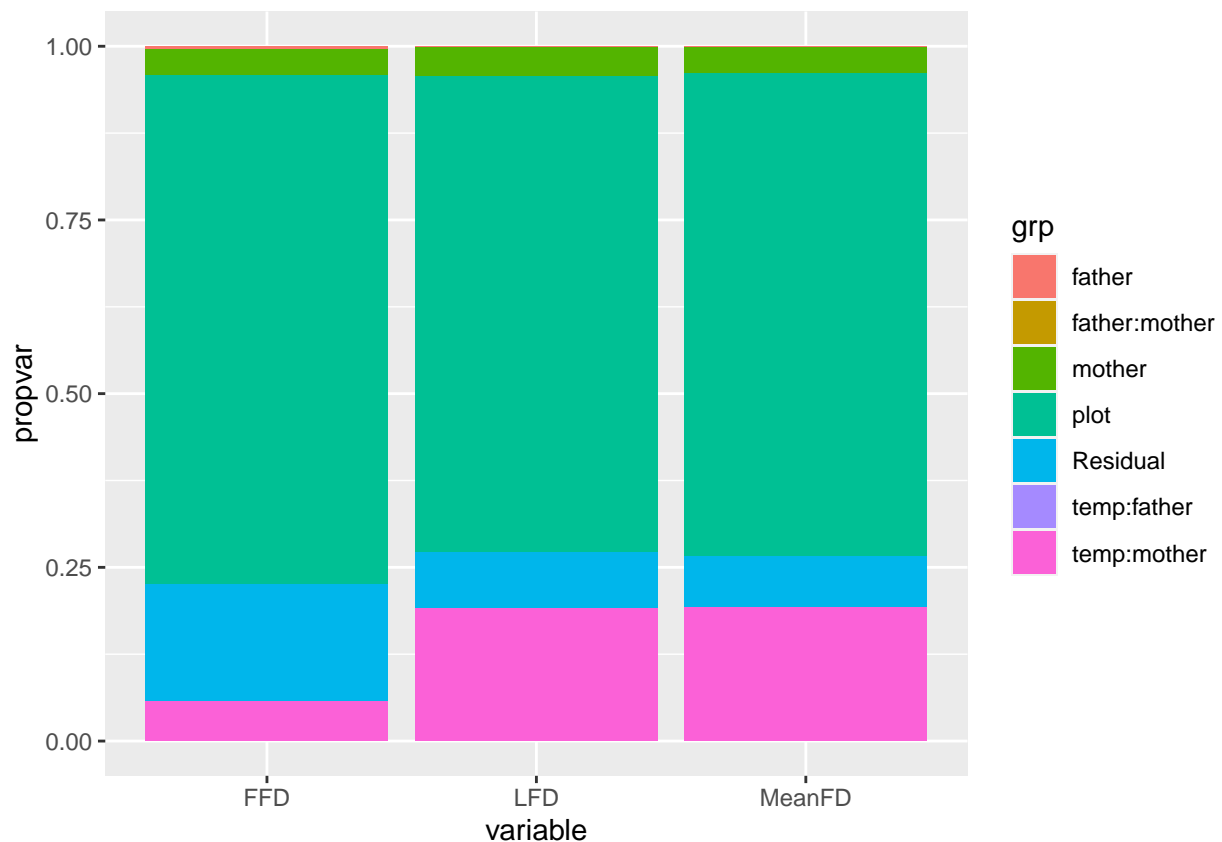
```
## Linear mixed model fit by REML. t-tests use Satterthwaite's method [
## lmerModLmerTest]
## Formula: MeanFD ~ temp + (1 | father) + (1 | mother) + (1 | father:mother) +
##      (1 | plot) + (1 | temp:father) + (1 | temp:mother)
## Data: data_transplants
##
## REML criterion at convergence: 2550.5
##
## Scaled residuals:
##      Min       1Q   Median       3Q      Max
## -1.89766 -0.33496 -0.07523  0.23820  2.78731
##
## Random effects:
## Groups      Name      Variance Std.Dev.
## temp:father (Intercept)  0.225   0.4744
## temp:mother (Intercept) 41.581   6.4483
## father:mother (Intercept) 0.000   0.0000
## mother      (Intercept)  8.297   2.8805
## father      (Intercept)  0.000   0.0000
## plot        (Intercept) 150.637  12.2734
## Residual                15.812   3.9764
## Number of obs: 364, groups:
## temp:father, 342; temp:mother, 336; father:mother, 120; mother, 59; father, 59; plot, 8
##
## Fixed effects:
##           Estimate Std. Error      df t value Pr(>|t|)
## (Intercept) 192.32468    4.63037   8.56536  41.536 3.52e-11 ***
## temp        -0.80056    0.08272 320.78688  -9.678 < 2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Correlation of Fixed Effects:
##      (Intr)
## temp -0.313
## optimizer (nloptwrap) convergence code: 0 (OK)
## boundary (singular) fit: see help('isSingular')
```

Singular fit: variances for some random effects are zero.

Proportions of variance

```
# extract variance components
Variance_FFD_temp <- as.data.frame(VarCorr(model2_FFD))[,c(1,4)]
Variance_LFD_temp <- as.data.frame(VarCorr(model2_LFD))[,c(1,4)]
Variance_MeanFD_temp <- as.data.frame(VarCorr(model2_MeanFD))[,c(1,4)]
# Intra-class correlation
PropVar_FFD_temp <- Variance_FFD_temp%>%
  mutate(propvar=vcov/sum(vcov))%>%mutate(variable="FFD")
PropVar_LFD_temp <- Variance_LFD_temp%>%
  mutate(propvar=vcov/sum(vcov))%>%mutate(variable="LFD")
PropVar_MeanFD_temp <- Variance_MeanFD_temp%>%
  mutate(propvar=vcov/sum(vcov))%>%mutate(variable="MeanFD")
# Proportional variance
Props_var_temp<-rbind(PropVar_FFD_temp,PropVar_LFD_temp,PropVar_MeanFD_temp)

ggplot(Props_var_temp,aes(x=variable,y=propvar,fill=grp))+
  geom_col()
```



Heritability and maternal effects

Are these heritability and maternal effects of the SLOPE of RNs?

```

# h^2 (paternal effects)
her_FFD_temp<-4*subset(PropVar_FFD_temp,grp=="temp:father")[3]
her_LFD_temp<-4*subset(PropVar_LFD_temp,grp=="temp:father")[3]
her_MeanFD_temp<-4*subset(PropVar_MeanFD_temp,grp=="temp:father")[3]
# Because the additive genetic variance, VA,
# is expected to be four times the among pollen-donor variance
# (Falconer & Mackay, 1996; Lynch & Walsh, 1998)
her_temp<-data.frame(value=rbind(her_FFD_temp,her_LFD_temp,her_MeanFD_temp))%>%
  mutate(variable=c("FFD","LFD","MeanFD"),
    effect="Heritability")%>%
  rename(value=propvar)

```

```

# maternal effects

# Maternal - paternal
# -----
# summed effects

# Because the pollen-recipient variance component contains a combination of
# genetic and environmental effects, we subtracted the additive genetic
# (pollen donor) component from the pollen-recipient variance component
# before dividing the resulting estimate by VP to estimate
# m2 (m2 = (Vpollen recipient - Vpollen donor)/VP).

mat_FFD_temp<-(subset(Variance_FFD_temp,grp=="temp:mother")[2]-
  subset(Variance_FFD_temp,grp=="temp:father")[2])/
  Variance_FFD_temp%>%summarise(sum(vcov))
mat_LFD_temp<-(subset(Variance_LFD_temp,grp=="temp:mother")[2]-
  subset(Variance_LFD_temp,grp=="temp:father")[2])/
  Variance_LFD_temp%>%summarise(sum(vcov))
mat_MeanFD_temp<-(subset(Variance_MeanFD_temp,grp=="temp:mother")[2]-
  subset(Variance_MeanFD_temp,grp=="temp:father")[2])/
  Variance_MeanFD_temp%>%summarise(sum(vcov))
mat_temp<-data.frame(value=rbind(mat_FFD_temp,mat_LFD_temp,mat_MeanFD_temp))%>%
  mutate(variable=c("FFD","LFD","MeanFD"),
    effect="Maternal effects")%>%
  rename(value=vcov)

```

```

her_mat_temp<-rbind(her_temp,mat_temp)
her_mat_temp

```

| ## | value | variable | effect |
|-------|--------------|----------|------------------|
| ## 1 | 3.219373e-07 | FFD | Heritability |
| ## 2 | 1.286938e-06 | LFD | Heritability |
| ## 3 | 4.156414e-03 | MeanFD | Heritability |
| ## 23 | 5.858988e-02 | FFD | Maternal effects |
| ## 21 | 1.924901e-01 | LFD | Maternal effects |
| ## 22 | 1.909732e-01 | MeanFD | Maternal effects |

```

ggplot(her_mat_temp,aes(x=variable,y=value,fill=effect))+
  geom_bar(stat="identity",position="dodge")

```

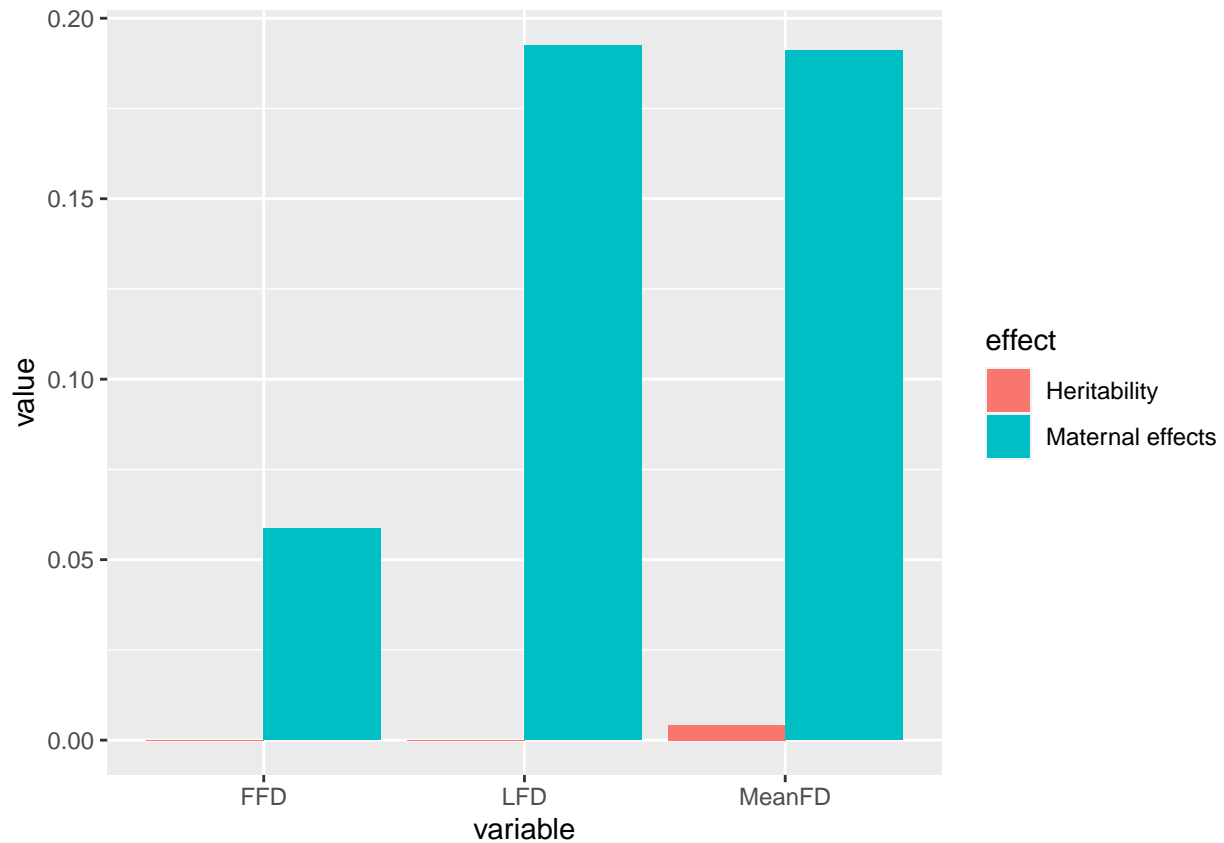


Table SM: LRTs for variance components

```
ranova(model2_FFD)
```

```
## ANOVA-like table for random-effects: Single term deletions
##
## Model:
## FFD_corr ~ temp + (1 | father) + (1 | mother) + (1 | father:mother) + (1 | plot) + (1 | temp:father)
##
```

| | npars | logLik | AIC | LRT | Df | Pr(>Chisq) |
|---------------------|-------|---------|--------|--------|----|---------------|
| <none> | 9 | -2096.2 | 4210.4 | | | |
| (1 father) | 8 | -2096.4 | 4208.8 | 0.41 | 1 | 0.5232570 |
| (1 mother) | 8 | -2103.1 | 4222.2 | 13.76 | 1 | 0.0002078 *** |
| (1 father:mother) | 8 | -2096.2 | 4208.4 | 0.00 | 1 | 1.0000000 |
| (1 plot) | 8 | -2325.2 | 4666.4 | 458.00 | 1 | < 2.2e-16 *** |
| (1 temp:father) | 8 | -2096.2 | 4208.4 | 0.00 | 1 | 1.0000000 |
| (1 temp:mother) | 8 | -2096.9 | 4209.8 | 1.40 | 1 | 0.2362381 |

```
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
ranova(model2_LFD)
```

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

```
## Model:
## LFD_corr ~ temp + (1 | father) + (1 | mother) + (1 | father:mother) + (1 | plot) + (1 | temp:father)
##               npar  logLik    AIC      LRT Df Pr(>Chisq)
## <none>          9 -1281.2 2580.4
## (1 | father)     8 -1281.2 2578.4   0.000   1 1.0000000
## (1 | mother)     8 -1286.7 2589.4  11.054   1 0.0008848 ***
## (1 | father:mother) 8 -1281.2 2578.4   0.000   1 1.0000000
## (1 | plot)       8 -1397.4 2810.9 232.524   1 < 2.2e-16 ***
## (1 | temp:father) 8 -1281.2 2578.4   0.000   1 1.0000000
## (1 | temp:mother) 8 -1287.0 2590.0  11.686   1 0.0006299 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
ranova(model2_MeanFD)
```

```
## ANOVA-like table for random-effects: Single term deletions
##
## Model:
## MeanFD ~ temp + (1 | father) + (1 | mother) + (1 | father:mother) + (1 | plot) + (1 | temp:father) +
##               npar  logLik    AIC      LRT Df Pr(>Chisq)
## <none>          9 -1275.2 2568.5
## (1 | father)     8 -1275.2 2566.5   0.000   1 1.0000000
## (1 | mother)     8 -1280.1 2576.2   9.672   1 0.0018715 **
## (1 | father:mother) 8 -1275.2 2566.5   0.000   1 1.0000000
## (1 | plot)       8 -1395.7 2807.4 240.873   1 < 2.2e-16 ***
## (1 | temp:father) 8 -1275.2 2566.5   0.002   1 0.9605368
## (1 | temp:mother) 8 -1281.3 2578.6  12.124   1 0.0004976 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

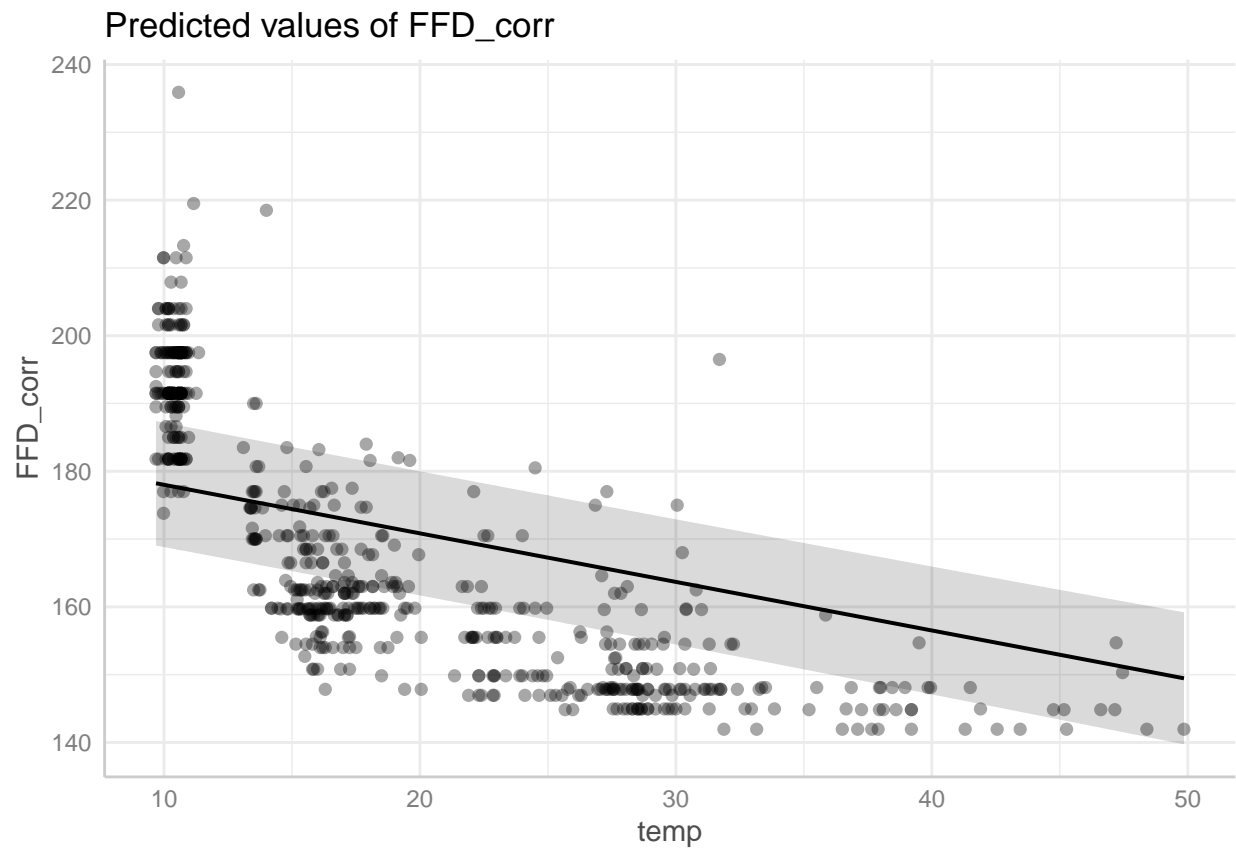
Figure 1 (Predictions 1-2)

Table 1 (Predictions 1-2)

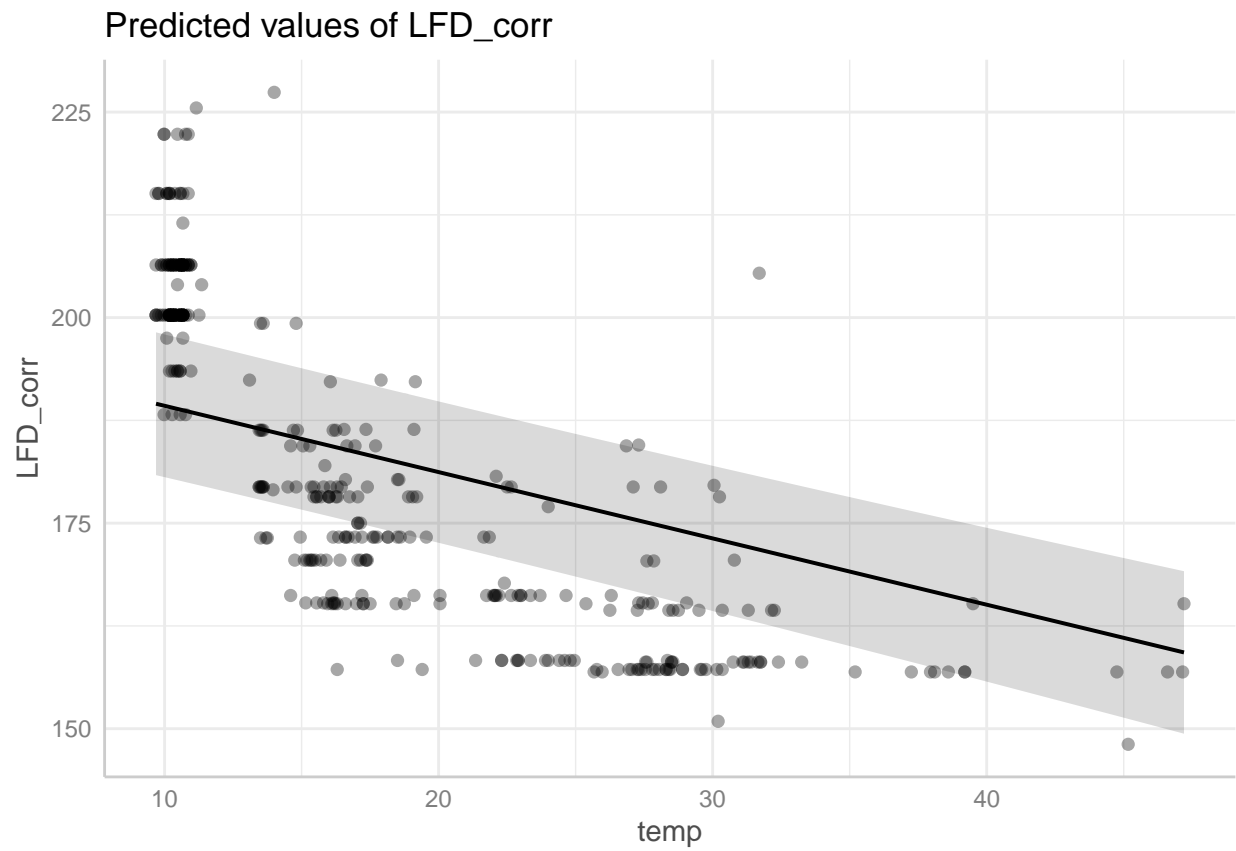
Figure 2 (Prediction 2)

Main effect of temperature significant for FFD, LFD and MeanFD.

```
plot(ggpredict(model2_FFD, terms="temp[all]"), add.data=T)
```

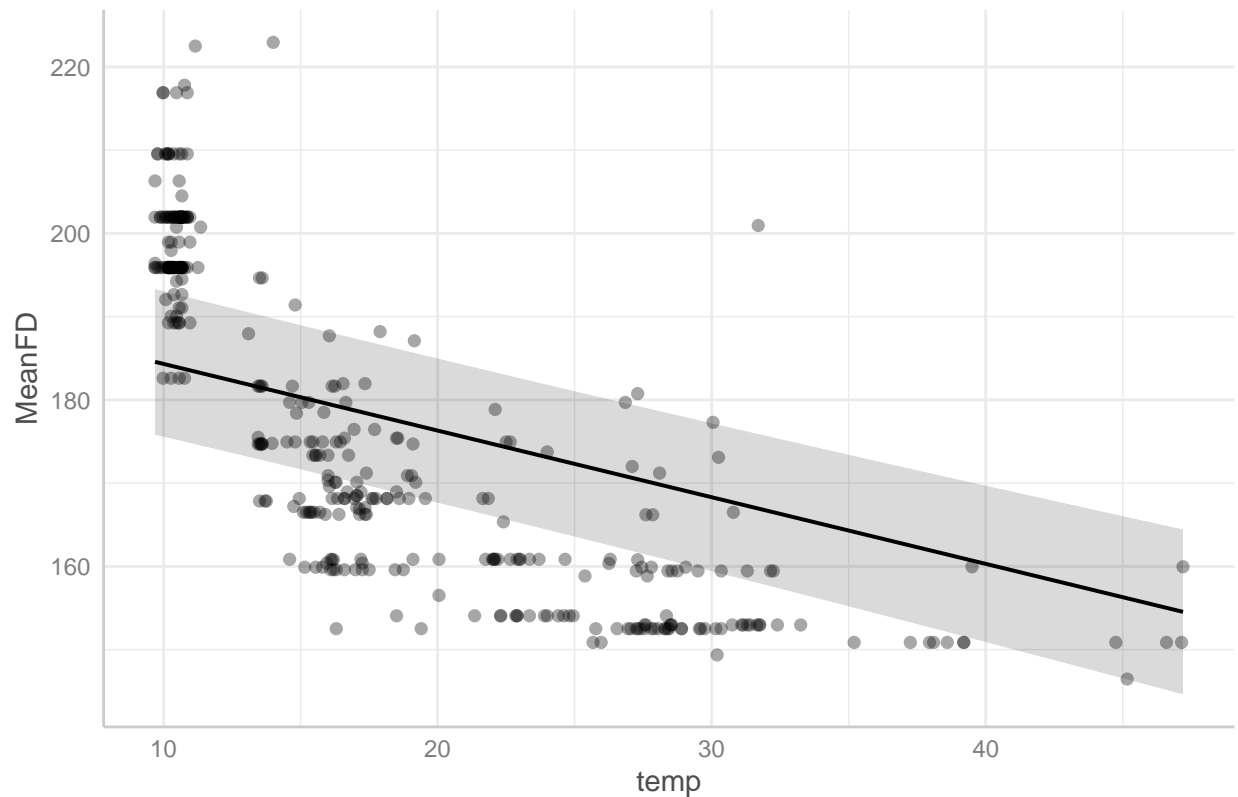


```
plot(ggpredict(model12_LFD, terms="temp[all]"), add.data=T)
```



```
plot(ggpredict(model12_MeanFD, terms="temp[all]"), add.data=T)
```

Predicted values of MeanFD



Prediction 3

Models

```
model3_FFD<-lmer(FFD_corr~temp_father+temp_mother+
  (1|father)+(1|mother)+(1|father:mother)+(1|plot),
  subset(data_transplants,!is.na(FFD_corr)))
model3_LFD<-lmer(LFD_corr~temp_father+temp_mother+
  (1|father)+(1|mother)+(1|father:mother)+(1|plot),
  subset(data_transplants,!is.na(LFD_corr)))
model3_MeanFD<-lmer(MeanFD~temp_father+temp_mother+
  (1|father)+(1|mother)+(1|father:mother)+(1|plot),
  subset(data_transplants,!is.na(MeanFD)))
summary(model3_FFD)

## Linear mixed model fit by REML. t-tests use Satterthwaite's method [
## lmerModLmerTest]
## Formula: FFD_corr ~ temp_father + temp_mother + (1 | father) + (1 | mother) +
## (1 | father:mother) + (1 | plot)
## Data: subset(data_transplants, !is.na(FFD_corr))
##
## REML criterion at convergence: 4354.6
##
```



```
## Scaled residuals:
##      Min       1Q   Median       3Q      Max
## -2.2256 -0.6720 -0.0671  0.5574  5.0480
##
## Random effects:
##   Groups      Name      Variance Std.Dev.
## father:mother (Intercept)  0.000    0.00
## father        (Intercept)  0.000    0.00
## mother        (Intercept)  9.799    3.13
## plot          (Intercept) 334.175   18.28
## Residual                68.897    8.30
## Number of obs: 603, groups:
## father:mother, 131; father, 64; mother, 63; plot, 8
##
## Fixed effects:
##              Estimate Std. Error      df t value Pr(>|t|)
## (Intercept) 172.75479    6.60103    7.54165  26.171 1.12e-08 ***
## temp_father  -0.06680    0.03745   537.69661  -1.784   0.075 .
## temp_mother   0.04900    0.05918   45.26370   0.828   0.412
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Correlation of Fixed Effects:
##              (Intr) tmp_ft
## temp_father -0.061
## temp_mother -0.138 -0.306
## optimizer (nloptwrap) convergence code: 0 (OK)
## boundary (singular) fit: see help('isSingular')
```

```
summary(model3_LFD)
```

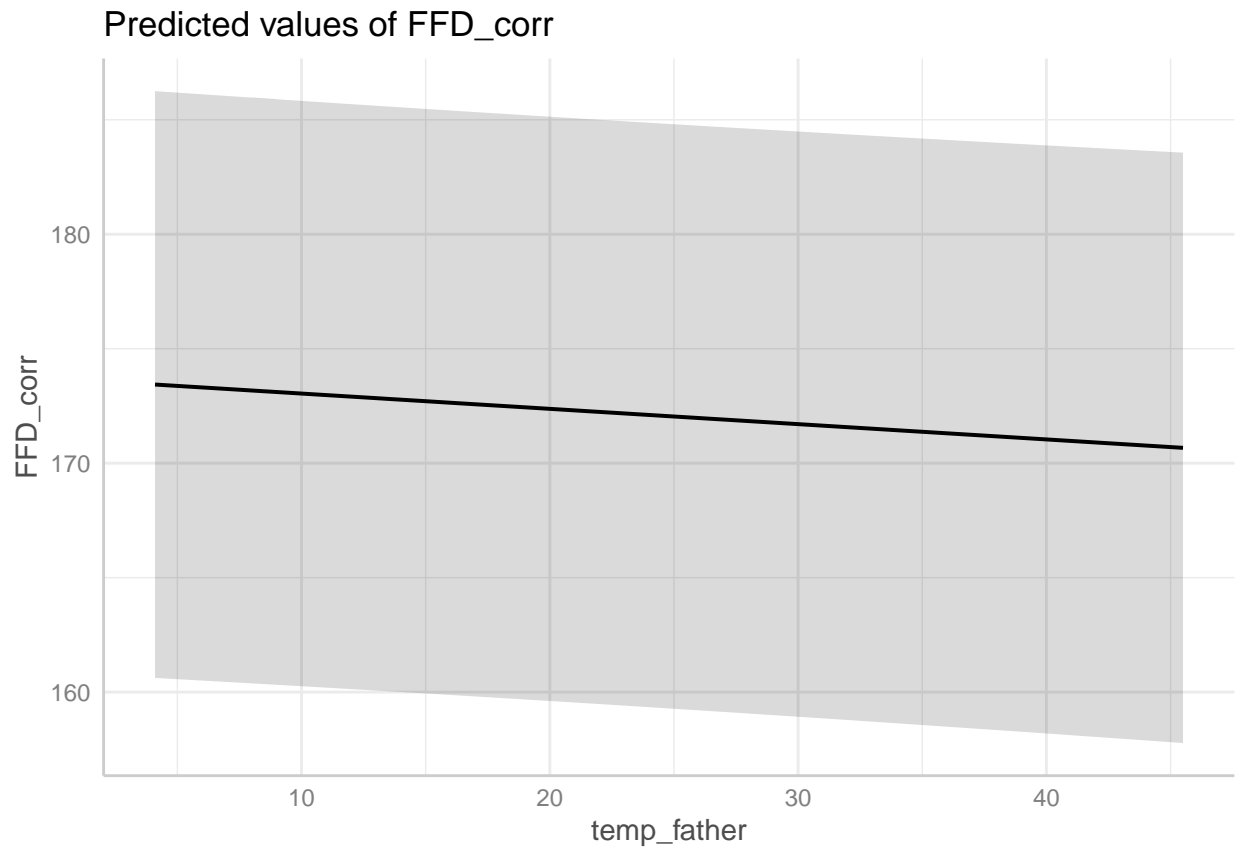
```
## Linear mixed model fit by REML. t-tests use Satterthwaite's method [
## lmerModLmerTest]
## Formula: LFD_corr ~ temp_father + temp_mother + (1 | father) + (1 | mother) +
##          (1 | father:mother) + (1 | plot)
## Data: subset(data_transplants, !is.na(LFD_corr))
##
## REML criterion at convergence: 2660.5
##
## Scaled residuals:
##      Min       1Q   Median       3Q      Max
## -2.4220 -0.6954 -0.0682  0.4691  4.5709
##
## Random effects:
##   Groups      Name      Variance Std.Dev.
## father:mother (Intercept) 3.390e-08 1.841e-04
## mother        (Intercept) 7.147e+00 2.673e+00
## father        (Intercept) 4.951e+00 2.225e+00
## plot          (Intercept) 3.087e+02 1.757e+01
## Residual                7.033e+01 8.386e+00
## Number of obs: 364, groups:
## father:mother, 120; mother, 59; father, 59; plot, 8
##
## Fixed effects:
```

```
##           Estimate Std. Error      df t value Pr(>|t|)
## (Intercept) 184.30929    6.42265   7.85179  28.697 3.11e-09 ***
## temp_father  -0.04725    0.05937  21.97361  -0.796   0.435
## temp_mother  -0.01094    0.06935  37.49581  -0.158   0.876
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Correlation of Fixed Effects:
##           (Intr) tmp_ft
## temp_father -0.108
## temp_mother -0.136 -0.366
## optimizer (nloptwrap) convergence code: 0 (OK)
## boundary (singular) fit: see help('isSingular')
```

```
summary(model3_MeanFD)
```

```
## Linear mixed model fit by REML. t-tests use Satterthwaite's method [
## lmerModLmerTest]
## Formula: MeanFD ~ temp_father + temp_mother + (1 | father) + (1 | mother) +
##          (1 | father:mother) + (1 | plot)
## Data: subset(data_transplants, !is.na(MeanFD))
##
## REML criterion at convergence: 2651.3
##
## Scaled residuals:
##      Min       1Q   Median       3Q      Max
## -2.2674 -0.7053 -0.0638  0.5218  4.6725
##
## Random effects:
## Groups      Name      Variance Std.Dev.
## father:mother (Intercept)  0.000   0.000
## mother        (Intercept)  7.256   2.694
## father        (Intercept)  3.300   1.817
## plot          (Intercept) 311.676  17.654
## Residual                69.224   8.320
## Number of obs: 364, groups:
## father:mother, 120; mother, 59; father, 59; plot, 8
##
## Fixed effects:
##           Estimate Std. Error      df t value Pr(>|t|)
## (Intercept) 179.257285    6.439242   7.783427  27.838 4.48e-09 ***
## temp_father  -0.046804    0.055558  20.373893  -0.842   0.409
## temp_mother  -0.004862    0.068192  40.370321  -0.071   0.944
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Correlation of Fixed Effects:
##           (Intr) tmp_ft
## temp_father -0.098
## temp_mother -0.138 -0.360
## optimizer (nloptwrap) convergence code: 0 (OK)
## boundary (singular) fit: see help('isSingular')
```

```
plot(ggpredict(model3_FFD, terms=c("temp_father[all]")))
```



In FFD NS effect of temp_father (but $p=0.075$), and the sign goes in the opposite direction as expected! (earlier FFD at a given temperature in individuals with fathers from warmer soils). All other effects of origin temperatures are NS.

Table 2

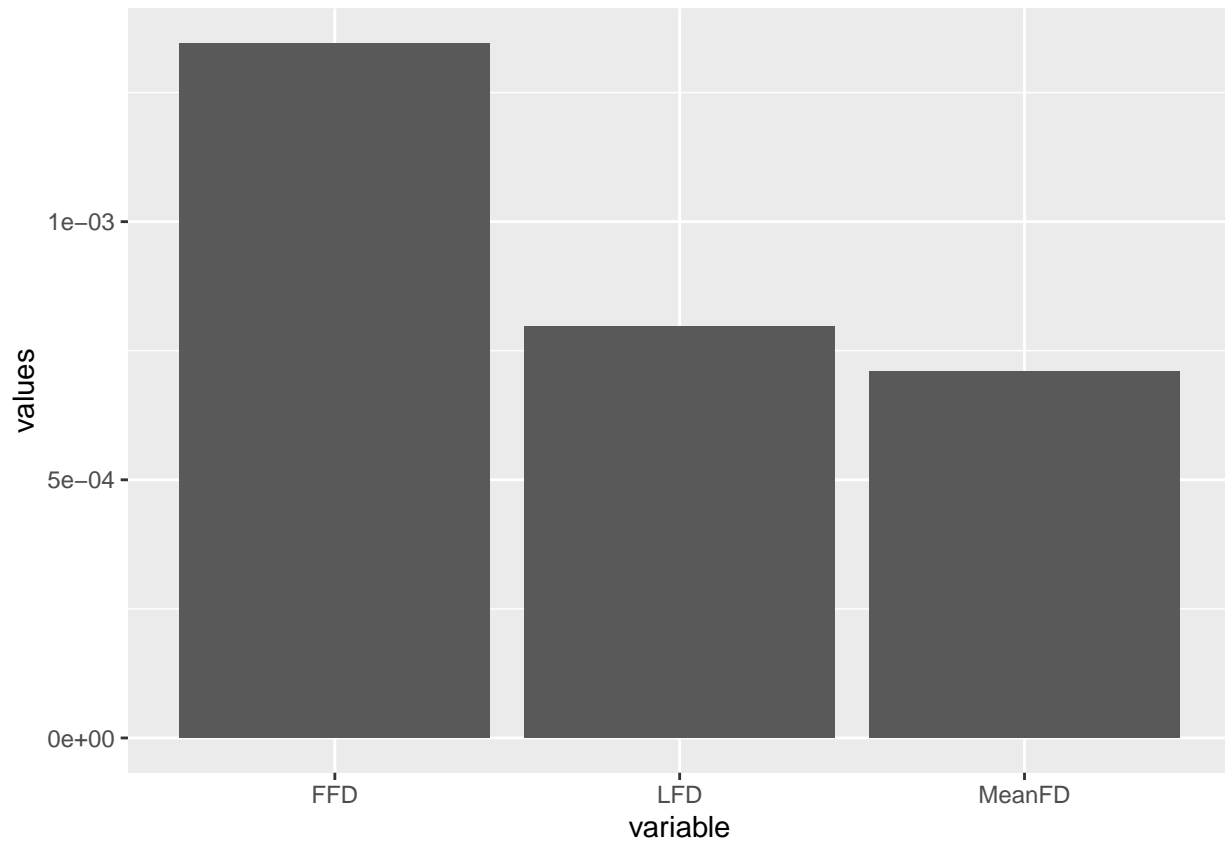
Proportions of variance

Proportion of variance explained by temperature of origin of fathers and mothers = proportion of variance explained by fixed effects: marginal R².

```
PropVar_FFD_temp_origin<-as.numeric(r2_nakagawa(model3_FFD,
                                                tolerance=1e-324)$R2_marginal)
PropVar_LFD_temp_origin<-as.numeric(r2_nakagawa(model3_LFD)$R2_marginal)
PropVar_MeanFD_temp_origin<-as.numeric(r2_nakagawa(model3_MeanFD,
                                                    tolerance=1e-324)$R2_marginal)

Props_var_temp_origin<-data.frame(
  values=c(PropVar_FFD_temp_origin,PropVar_LFD_temp_origin,
          PropVar_MeanFD_temp_origin),variable=c("FFD","LFD","MeanFD"))
```

```
ggplot(Props_var_temp_origin,aes(x=variable,y=values))+
  geom_bar(stat="identity",position="dodge")
```



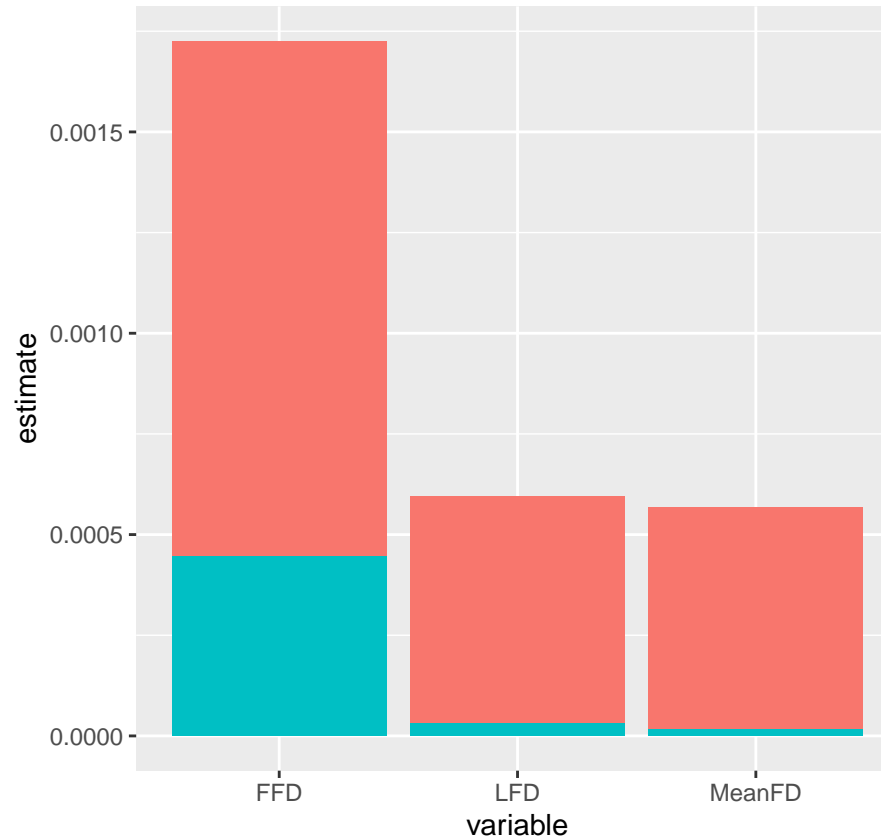
Fixed singular fit problems (because of some variance components equalling zero) by increasing tolerance:
can we trust these proportions of variance (for MFD, heated, and veg, unheated)?

```
load("output/models/partR2_model13_FFD.rda")
load("output/models/partR2_model13_LFD.rda")
load("output/models/partR2_model13_MeanFD.rda")
```

```
Props_var_temp_mf<-
  rbind(
    partR2_model13_FFD$R2%>%mutate(variable="FFD"),
    partR2_model13_LFD$R2%>%mutate(variable="LFD"),
    partR2_model13_MeanFD$R2%>%mutate(variable="MeanFD")
  )
```

```
ggplot(Props_var_temp_mf%>%
  filter(term!="temp_father+temp_mother"&term!="Full"))%>%
```

```
mutate(term=factor(term,levels=c("temp_father","temp_mother"),
                                labels=c("Temperature father",
                                           "Temperature mother"))),
aes(x=variable,y=estimate,ymin=CI_lower,ymax=CI_upper,
    fill=term))+
geom_bar(stat="identity")
```



Temperature mother and father: partR2

Figure 3

Models mid-parental values

```
model13_FFD_midP<-lmer(FFD_corr~mean_temp_parents+
                        (1|father)+(1|mother)+(1|mother:father)+(1|plot),
                        data_transplants)
model13_LFD_midP<-lmer(LFD_corr~mean_temp_parents+
                        (1|father)+(1|mother)+(1|mother:father)+(1|plot),
                        data_transplants)
model13_MeanFD_midP<-lmer(MeanFD~mean_temp_parents+
                           (1|father)+(1|mother)+(1|mother:father)+(1|plot),
                           data_transplants)
summary(model13_FFD_midP)
```

Linear mixed model fit by REML. t-tests use Satterthwaite's method [

```
## lmerModLmerTest]
## Formula: FFD_corr ~ mean_temp_parents + (1 | father) + (1 | mother) +
##      (1 | mother:father) + (1 | plot)
##      Data: data_transplants
##
## REML criterion at convergence: 4352.1
##
## Scaled residuals:
##      Min       1Q   Median       3Q      Max
## -2.2370 -0.6714 -0.0730  0.5611  5.0286
##
## Random effects:
##      Groups      Name      Variance Std.Dev.
## mother:father (Intercept)  0.000    0.000
## father        (Intercept)  0.000    0.000
## mother        (Intercept)  9.446    3.073
## plot          (Intercept) 333.637  18.266
## Residual                69.168   8.317
## Number of obs: 603, groups:
## mother:father, 131; father, 64; mother, 63; plot, 8
##
## Fixed effects:
##              Estimate Std. Error      df t value Pr(>|t|)
## (Intercept)    173.44932    6.57655    7.45522   26.37 1.24e-08 ***
## mean_temp_parents -0.05577    0.05313  161.67501   -1.05  0.295
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Correlation of Fixed Effects:
##              (Intr)
## mn_tmp_prnt -0.160
## optimizer (nloptwrap) convergence code: 0 (OK)
## boundary (singular) fit: see help('isSingular')
```

```
summary(model3_LFD_midP)
```

```
## Linear mixed model fit by REML. t-tests use Satterthwaite's method [
## lmerModLmerTest]
## Formula: LFD_corr ~ mean_temp_parents + (1 | father) + (1 | mother) +
##      (1 | mother:father) + (1 | plot)
##      Data: data_transplants
##
## REML criterion at convergence: 2656.6
##
## Scaled residuals:
##      Min       1Q   Median       3Q      Max
## -2.4077 -0.6877 -0.0738  0.4574  4.5687
##
## Random effects:
##      Groups      Name      Variance Std.Dev.
## mother:father (Intercept) 9.754e-09 9.876e-05
## mother        (Intercept) 6.700e+00 2.588e+00
## father        (Intercept) 4.874e+00 2.208e+00
## plot          (Intercept) 3.085e+02 1.756e+01
```

```
## Residual                7.041e+01 8.391e+00
## Number of obs: 364, groups:
## mother:father, 120; mother, 59; father, 59; plot, 8
##
## Fixed effects:
##              Estimate Std. Error      df t value Pr(>|t|)
## (Intercept)    184.37510     6.41529    7.82297  28.740 3.25e-09 ***
## mean_temp_parents -0.06218     0.07135   63.61790   -0.872    0.387
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Correlation of Fixed Effects:
##              (Intr)
## mn_tmp_prnt -0.214
## optimizer (nloptwrap) convergence code: 0 (OK)
## boundary (singular) fit: see help('isSingular')
```

```
summary(model3_MeanFD_midP)
```

```
## Linear mixed model fit by REML. t-tests use Satterthwaite's method [
## lmerModLmerTest]
## Formula: MeanFD ~ mean_temp_parents + (1 | father) + (1 | mother) + (1 |
## mother:father) + (1 | plot)
## Data: data_transplants
##
## REML criterion at convergence: 2647.3
##
## Scaled residuals:
##      Min       1Q   Median       3Q      Max
## -2.2515 -0.7071 -0.0588  0.5261  4.6670
##
## Random effects:
## Groups      Name      Variance Std.Dev.
## mother:father (Intercept) 3.626e-08 1.904e-04
## mother      (Intercept) 6.858e+00 2.619e+00
## father      (Intercept) 3.167e+00 1.780e+00
## plot        (Intercept) 3.116e+02 1.765e+01
## Residual                6.933e+01 8.326e+00
## Number of obs: 364, groups:
## mother:father, 120; mother, 59; father, 59; plot, 8
##
## Fixed effects:
##              Estimate Std. Error      df t value Pr(>|t|)
## (Intercept)    179.36013     6.43021    7.74376  27.893 4.75e-09 ***
## mean_temp_parents -0.05787     0.06846   59.65815   -0.845    0.401
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Correlation of Fixed Effects:
##              (Intr)
## mn_tmp_prnt -0.205
## optimizer (nloptwrap) convergence code: 0 (OK)
## boundary (singular) fit: see help('isSingular')
```

Mid-parental temperature always NS.

Prediction 4

Models

```
model14_FFD<-lmer(FFD_corr~temp*(temp_father+temp_mother)+
                  (1|father)+(1|mother)+(1|father:mother)+(1|plot),
                  data_transplants)
model14_LFD<-lmer(LFD_corr~temp*(temp_father+temp_mother)+
                  (1|father)+(1|mother)+(1|father:mother)+(1|plot),
                  data_transplants)
model14_MeanFD<-lmer(MeanFD~temp*(temp_father+temp_mother)+
                     (1|father)+(1|mother)+(1|father:mother)+(1|plot),
                     data_transplants)
summary(model14_FFD)

## Linear mixed model fit by REML. t-tests use Satterthwaite's method [
## lmerModLmerTest]
## Formula: FFD_corr ~ temp * (temp_father + temp_mother) + (1 | father) +
##          (1 | mother) + (1 | father:mother) + (1 | plot)
## Data: data_transplants
##
## REML criterion at convergence: 4212.8
##
## Scaled residuals:
##      Min       1Q   Median       3Q      Max
## -2.4131 -0.6276 -0.0775  0.4469  5.9576
##
## Random effects:
## Groups           Name             Variance Std.Dev.
## father:mother    (Intercept)      0.000    0.0000
## father           (Intercept)      0.172    0.4147
## mother           (Intercept)     10.206    3.1947
## plot             (Intercept)    171.599   13.0996
## Residual                51.804    7.1975
## Number of obs: 603, groups:
## father:mother, 131; father, 64; mother, 63; plot, 8
##
## Fixed effects:
##              Estimate Std. Error      df t value Pr(>|t|)
## (Intercept)   188.950129   5.120614  10.195792  36.900 3.43e-12 ***
## temp          -0.899010   0.095217  544.201171  -9.442 < 2e-16 ***
## temp_father   -0.180436   0.068461  198.647298  -2.636  0.00906 **
## temp_mother   -0.011005   0.085981  226.295232  -0.128  0.89827
## temp:temp_father  0.006411  0.003153  536.187938   2.033  0.04251 *
## temp:temp_mother  0.002946  0.003281  532.585778   0.898  0.36965
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Correlation of Fixed Effects:
##              (Intr) temp    tmp_ft tmp_mt tmp:tmp_f
```



```
## temp          -0.347
## temp_father -0.179  0.413
## temp_mother -0.258  0.403 -0.272
## tmp:tmp_fth  0.176 -0.499 -0.869  0.180
## tmp:tmp_mth  0.190 -0.532  0.230 -0.752 -0.238
## optimizer (nloptwrap) convergence code: 0 (OK)
## boundary (singular) fit: see help('isSingular')
```

```
summary(model4_LFD)
```

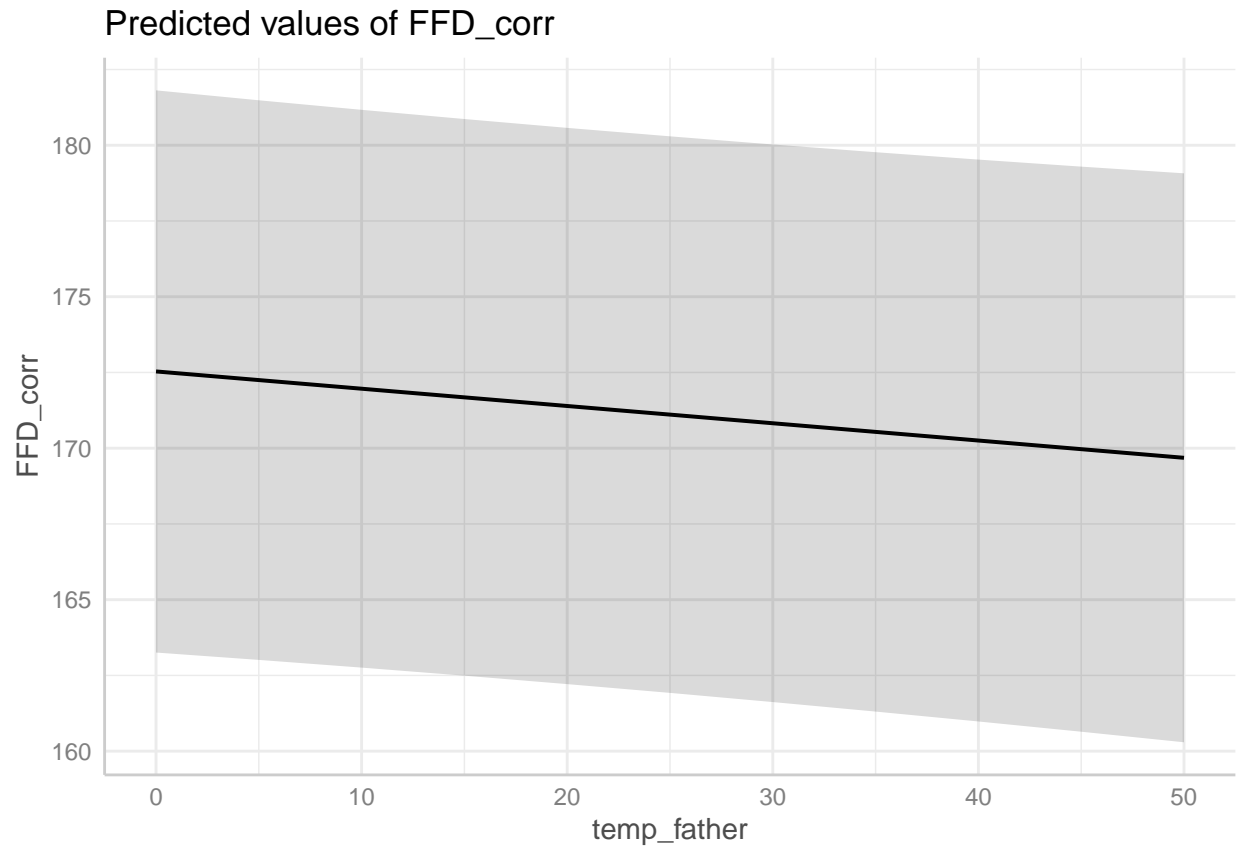
```
## Linear mixed model fit by REML. t-tests use Satterthwaite's method [
## lmerModLmerTest]
## Formula: LFD_corr ~ temp * (temp_father + temp_mother) + (1 | father) +
##          (1 | mother) + (1 | father:mother) + (1 | plot)
## Data: data_transplants
##
## REML criterion at convergence: 2596.1
##
## Scaled residuals:
##      Min       1Q   Median       3Q      Max
## -2.1918 -0.6293 -0.1117  0.4479  5.3030
##
## Random effects:
## Groups      Name                Variance Std.Dev.
## father:mother (Intercept)    0.000    0.000
## mother       (Intercept)    8.071    2.841
## father        (Intercept)    1.256    1.121
## plot          (Intercept) 145.212   12.050
## Residual                    57.143    7.559
## Number of obs: 364, groups:
## father:mother, 120; mother, 59; father, 59; plot, 8
##
## Fixed effects:
##              Estimate Std. Error      df t value Pr(>|t|)
## (Intercept)   202.146240   5.171920  14.240382  39.085 6.81e-16 ***
## temp          -1.041818   0.145984  329.793041  -7.137 6.12e-12 ***
## temp_father   -0.124554   0.095528  218.775041  -1.304  0.194
## temp_mother   -0.125597   0.117452  250.358226  -1.069  0.286
## temp:temp_father  0.005890   0.004679  314.065671   1.259  0.209
## temp:temp_mother  0.005986   0.005778  327.935861   1.036  0.301
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Correlation of Fixed Effects:
##              (Intr) temp    tmp_ft tmp_mt tmp:tmp_f
## temp          -0.492
## temp_father   -0.221  0.332
## temp_mother   -0.311  0.447 -0.353
## tmp:tmp_fth   0.205 -0.396 -0.869  0.309
## tmp:tmp_mth   0.253 -0.524  0.311 -0.835 -0.371
## optimizer (nloptwrap) convergence code: 0 (OK)
## boundary (singular) fit: see help('isSingular')
```

```
summary(model4_MeanFD)
```

```
## Linear mixed model fit by REML. t-tests use Satterthwaite's method [
## lmerModLmerTest]
## Formula: MeanFD ~ temp * (temp_father + temp_mother) + (1 | father) +
##      (1 | mother) + (1 | father:mother) + (1 | plot)
## Data: data_transplants
##
## REML criterion at convergence: 2586.1
##
## Scaled residuals:
##      Min       1Q   Median       3Q      Max
## -2.0332 -0.6273 -0.1003  0.4274  5.4430
##
## Random effects:
## Groups          Name          Variance Std.Dev.
## father:mother (Intercept)    0.0000  0.0000
## mother        (Intercept)    7.6064  2.7580
## father        (Intercept)    0.5984  0.7736
## plot          (Intercept)  147.5907 12.1487
## Residual                56.0534  7.4869
## Number of obs: 364, groups:
## father:mother, 120; mother, 59; father, 59; plot, 8
##
## Fixed effects:
##              Estimate Std. Error      df t value Pr(>|t|)
## (Intercept)   196.504555   5.172773  13.829918  37.988 2.18e-15 ***
## temp          -1.007407   0.144287  330.379753  -6.982 1.60e-11 ***
## temp_father   -0.114285   0.093538  231.267272  -1.222  0.223
## temp_mother   -0.100849   0.115615  257.797730  -0.872  0.384
## temp:temp_father  0.005526   0.004628  314.743459   1.194  0.233
## temp:temp_mother  0.004730   0.005710  329.163755   0.828  0.408
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Correlation of Fixed Effects:
##              (Intr) temp    tmp_ft tmp_mt tmp:tmp_f
## temp          -0.485
## temp_father  -0.215  0.335
## temp_mother  -0.307  0.449 -0.353
## tmp:tmp_fth   0.202 -0.396 -0.878  0.311
## tmp:tmp_mth   0.249 -0.524  0.316 -0.840 -0.372
## optimizer (nloptwrap) convergence code: 0 (OK)
## boundary (singular) fit: see help('isSingular')
```

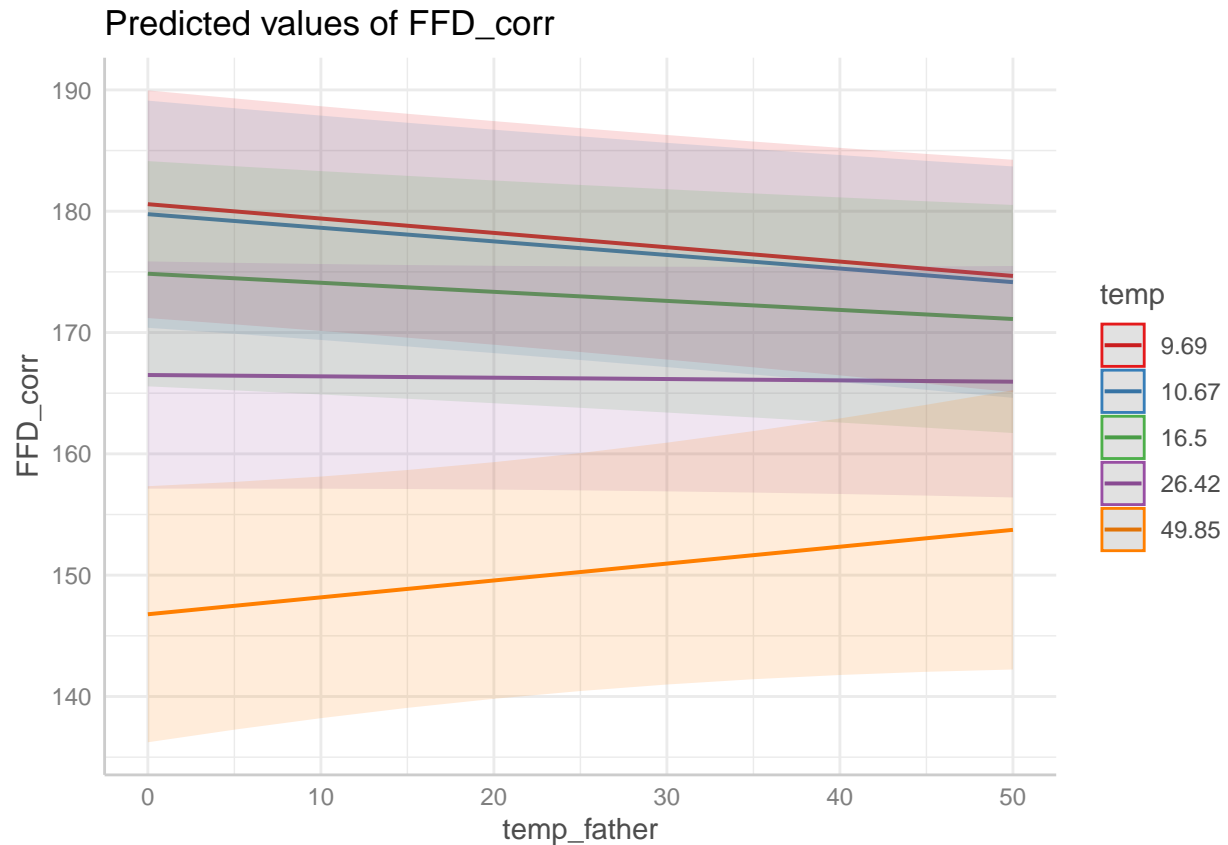
Interaction temp:temp_father is significant for FFD. There are temperature-related differences among fathers in the response to temperature of the planting site = Genetic differentiation related to origin temperature of the father in the slope of RNs?

```
plot(ggpredict(model4_FFD, terms=c("temp_father")))
```



The sign of temp_father goes in the opposite direction as expected! (earlier FFD at a given temperature in individuals with fathers from warmer soils). But maybe we should not interpret this main effect, as the interaction with temp is significant??

```
plot(ggpredict(model4_FFD, terms=c("temp_father", "temp[quart]")))
```



As predicted: differences in phenology between high and low soil temperatures are predicted to be smaller for plants with fathers from warm soils than for plants with fathers from colder soils.

Table 3

Figure 4

Models mid-parental values

```
model4_FFD_midP<-lmer(FFD_corr~temp*mean_temp_parents+
  (1|father)+(1|mother)+(1|father:mother)+(1|plot),
  data_transplants)
model4_LFD_midP<-lmer(LFD_corr~temp*mean_temp_parents+
  (1|father)+(1|mother)+(1|father:mother)+(1|plot),
  data_transplants)
model4_MeanFD_midP<-lmer(MeanFD~temp*mean_temp_parents+
  (1|father)+(1|mother)+(1|father:mother)+(1|plot),
  data_transplants)
summary(model4_FFD_midP)

## Linear mixed model fit by REML. t-tests use Satterthwaite's method [
## lmerModLmerTest]
## Formula: FFD_corr ~ temp * mean_temp_parents + (1 | father) + (1 | mother) +
```

```
##      (1 | father:mother) + (1 | plot)
##      Data: data_transplants
##
## REML criterion at convergence: 4200.2
##
## Scaled residuals:
##      Min       1Q   Median       3Q      Max
## -2.4568 -0.6145 -0.0779  0.4629  5.9683
##
## Random effects:
##      Groups             Name             Variance Std.Dev.
## father:mother (Intercept) 3.226e-08 1.796e-04
## father        (Intercept) 2.488e-01 4.988e-01
## mother        (Intercept) 9.882e+00 3.144e+00
## plot          (Intercept) 1.709e+02 1.307e+01
## Residual                        5.189e+01 7.203e+00
## Number of obs: 603, groups:
## father:mother, 131; father, 64; mother, 63; plot, 8
##
## Fixed effects:
##
##              Estimate Std. Error      df t value Pr(>|t|)
## (Intercept)    189.785668    5.078642    9.941874  37.369 5.05e-12 ***
## temp           -0.906470    0.095153   545.614449  -9.526 < 2e-16 ***
## mean_temp_parents -0.235270    0.089124   278.792352  -2.640 0.00876 **
## temp:mean_temp_parents 0.009669    0.003969   539.510956   2.436 0.01518 *
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Correlation of Fixed Effects:
##              (Intr) temp    mn_tm_
## temp          -0.346
## mn_tm_prnt -0.350  0.693
## tmp:mn_tm_  0.295 -0.835 -0.833
## optimizer (nloptwrap) convergence code: 0 (OK)
## boundary (singular) fit: see help('isSingular')
```

```
summary(model4_LFD_midP)
```

```
## Linear mixed model fit by REML. t-tests use Satterthwaite's method [
## lmerModLmerTest]
## Formula: LFD_corr ~ temp * mean_temp_parents + (1 | father) + (1 | mother) +
##      (1 | father:mother) + (1 | plot)
##      Data: data_transplants
##
## REML criterion at convergence: 2582.8
##
## Scaled residuals:
##      Min       1Q   Median       3Q      Max
## -2.1857 -0.6284 -0.1182  0.4479  5.3142
##
## Random effects:
##      Groups             Name             Variance Std.Dev.
## father:mother (Intercept)  0.000    0.000
## mother        (Intercept)  7.922    2.815
```

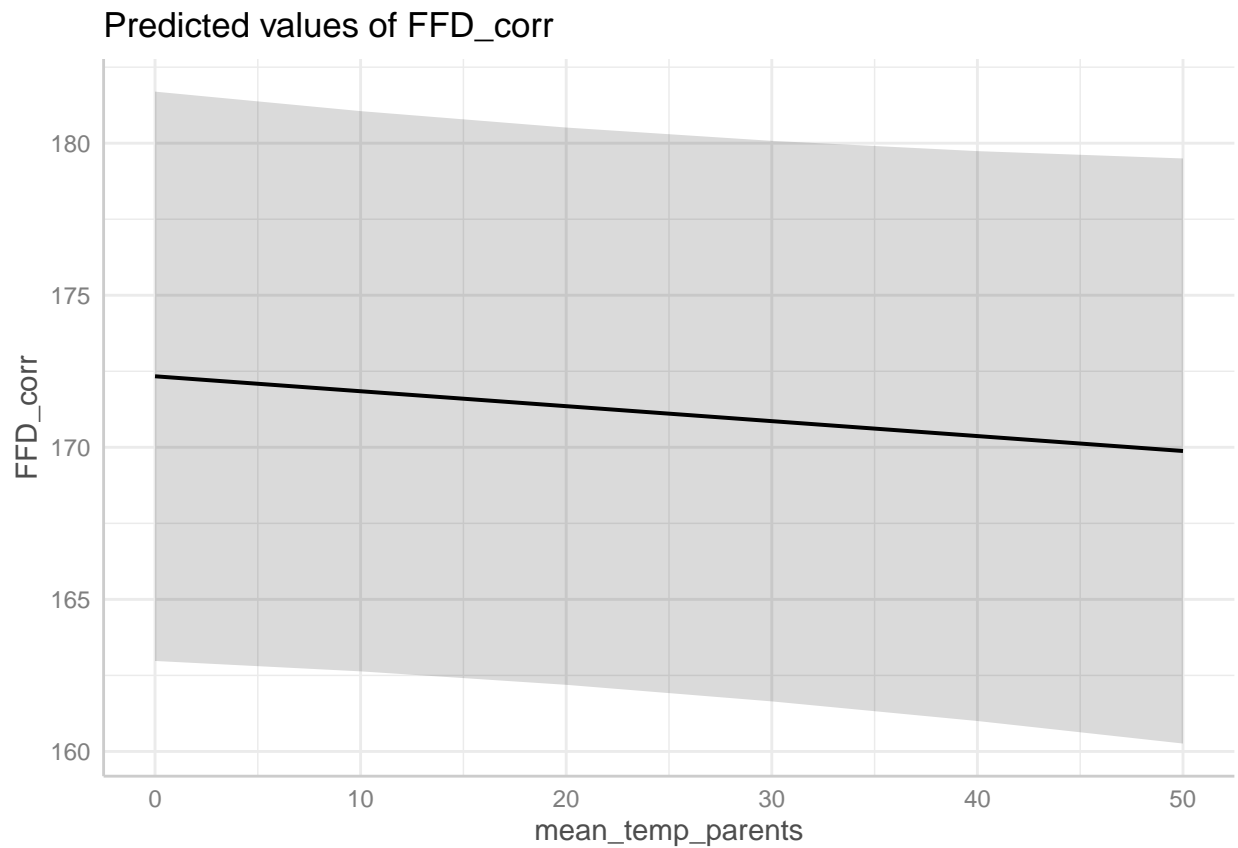
```
## father      (Intercept)    1.102    1.050
## plot        (Intercept) 145.028   12.043
## Residual                    56.968    7.548
## Number of obs: 364, groups:
## father:mother, 120; mother, 59; father, 59; plot, 8
##
## Fixed effects:
##              Estimate Std. Error      df t value Pr(>|t|)
## (Intercept)    202.152861   5.140611  13.943462  39.325  1.1e-15 ***
## temp           -1.042049   0.144340  330.853067  -7.219  3.6e-12 ***
## mean_temp_parents -0.249707   0.118947  298.674903  -2.099   0.0366 *
## temp:mean_temp_parents  0.011842   0.005769  330.637645   2.052   0.0409 *
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Correlation of Fixed Effects:
##              (Intr) temp    mn_tm_
## temp          -0.490
## mn_tm_prnt -0.463  0.689
## tmp:mn_tm_  0.409 -0.821 -0.856
## optimizer (nloptwrap) convergence code: 0 (OK)
## boundary (singular) fit: see help('isSingular')
```

```
summary(model4_MeanFD_midP)
```

```
## Linear mixed model fit by REML. t-tests use Satterthwaite's method [
## lmerModLmerTest]
## Formula: MeanFD ~ temp * mean_temp_parents + (1 | father) + (1 | mother) +
##          (1 | father:mother) + (1 | plot)
## Data: data_transplants
##
## REML criterion at convergence: 2572.6
##
## Scaled residuals:
##      Min       1Q   Median       3Q      Max
## -2.0273 -0.6318 -0.1043  0.4343  5.4612
##
## Random effects:
## Groups      Name                Variance Std.Dev.
## father:mother (Intercept)    0.000    0.0000
## mother        (Intercept)    7.441    2.7277
## father        (Intercept)    0.481    0.6936
## plot          (Intercept) 147.515   12.1456
## Residual                    55.879    7.4753
## Number of obs: 364, groups:
## father:mother, 120; mother, 59; father, 59; plot, 8
##
## Fixed effects:
##              Estimate Std. Error      df t value Pr(>|t|)
## (Intercept)    196.532947   5.141740  13.525104  38.223  3.56e-15 ***
## temp           -1.009431   0.142670  331.529077  -7.075  8.92e-12 ***
## mean_temp_parents -0.216483   0.116681  300.010168  -1.855   0.0645 .
## temp:mean_temp_parents  0.010356   0.005701  331.699274   1.816   0.0702 .
## ---
```

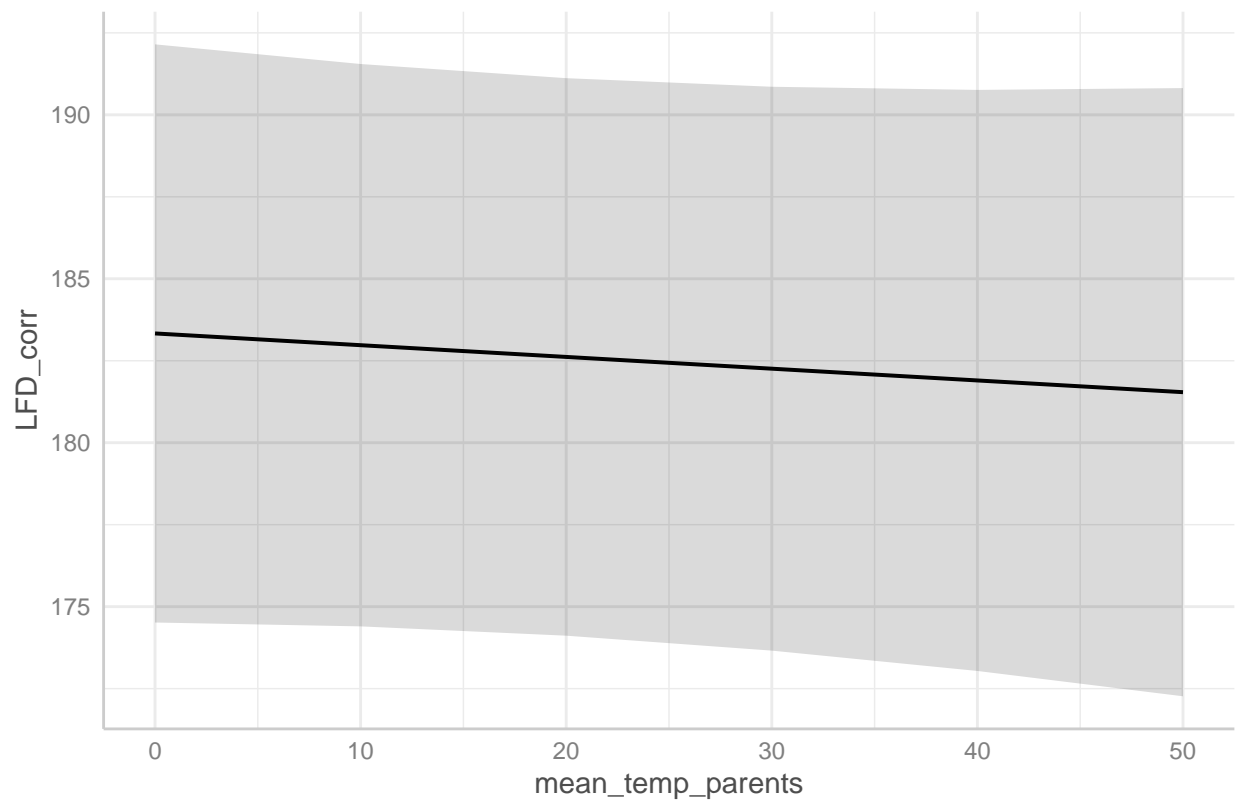
```
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Correlation of Fixed Effects:
##          (Intr) temp  mn_tm_
## temp      -0.483
## mn_tmp_prnt -0.453  0.694
## tmp:mn_tmp_  0.404 -0.821 -0.863
## optimizer (nloptwrap) convergence code: 0 (OK)
## boundary (singular) fit: see help('isSingular')
```

```
plot(ggpredict(model4_FFD_midP, terms=c("mean_temp_parents")))
```



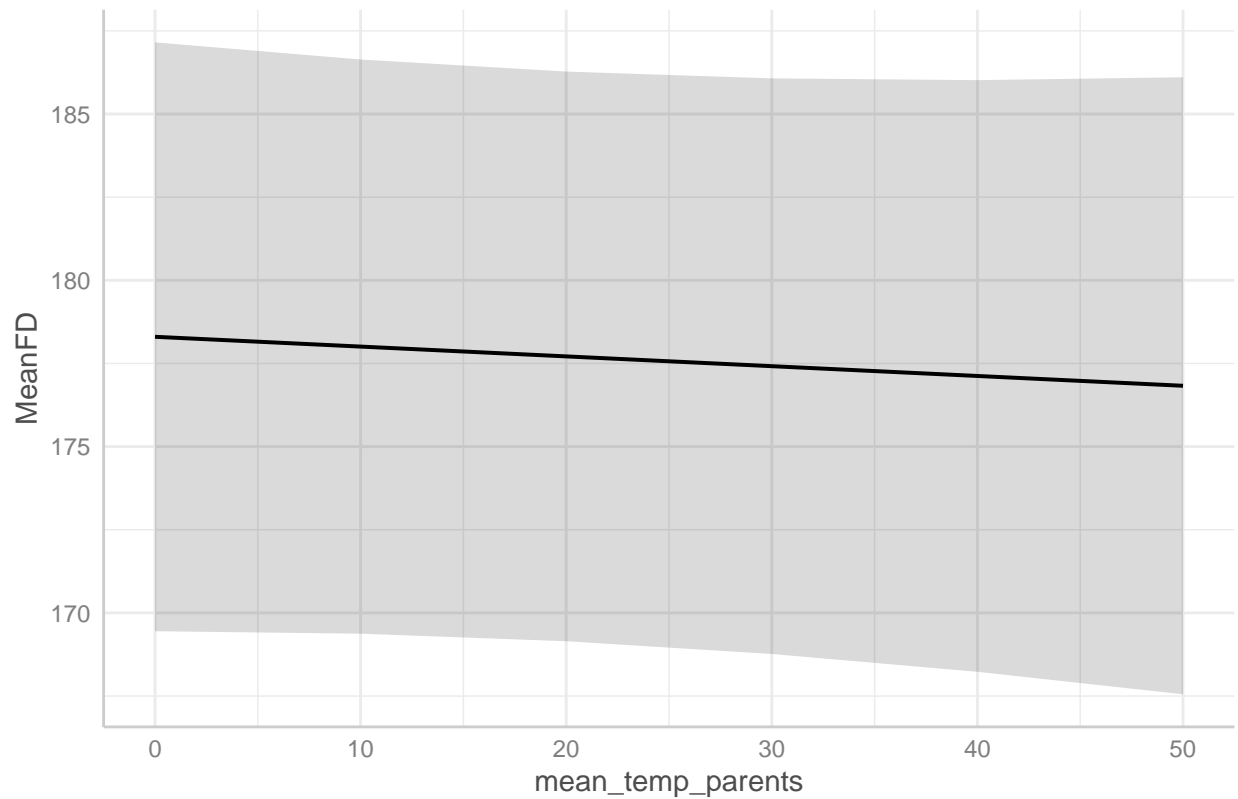
```
plot(ggpredict(model4_LFD_midP, terms=c("mean_temp_parents")))
```

Predicted values of LFD_corr



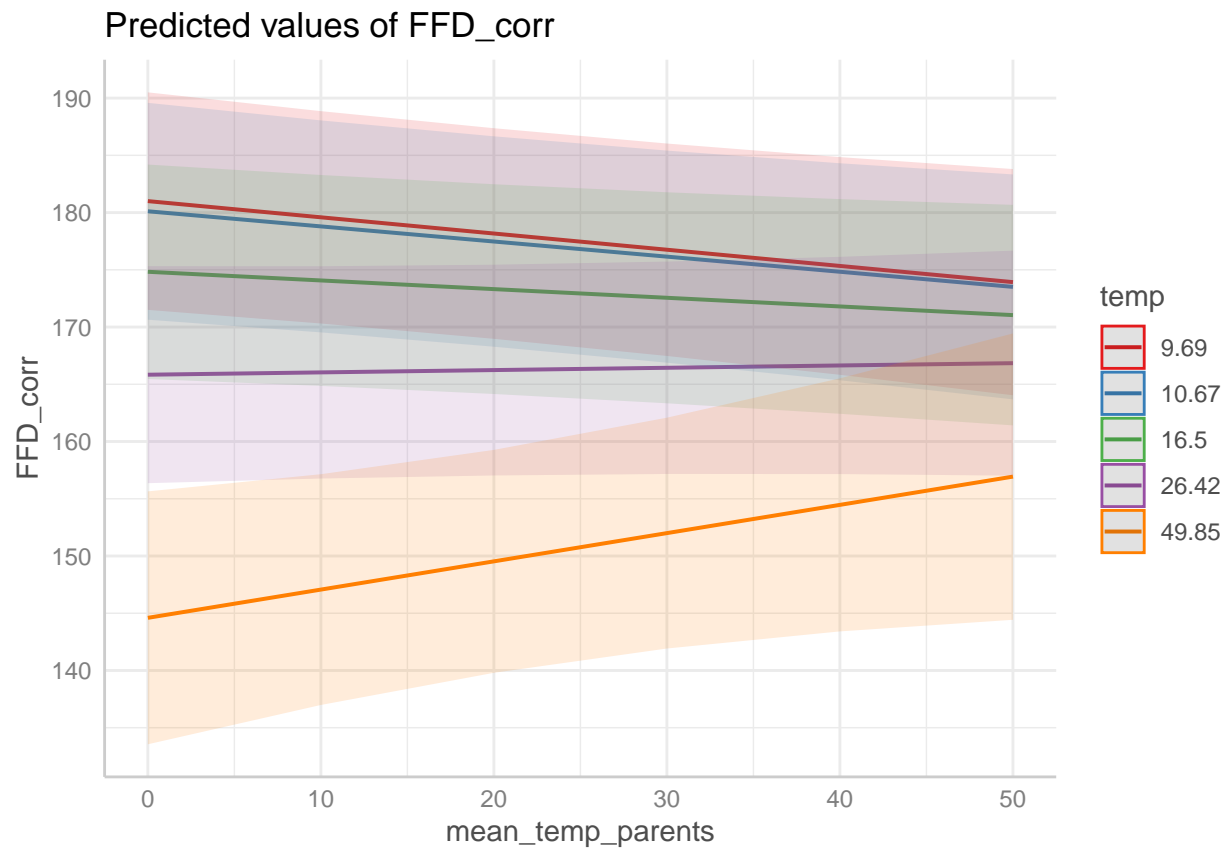
```
plot(ggpredict(model4_MeanFD_midP, terms=c("mean_temp_parents")) # Marginally *
```


Predicted values of MeanFD

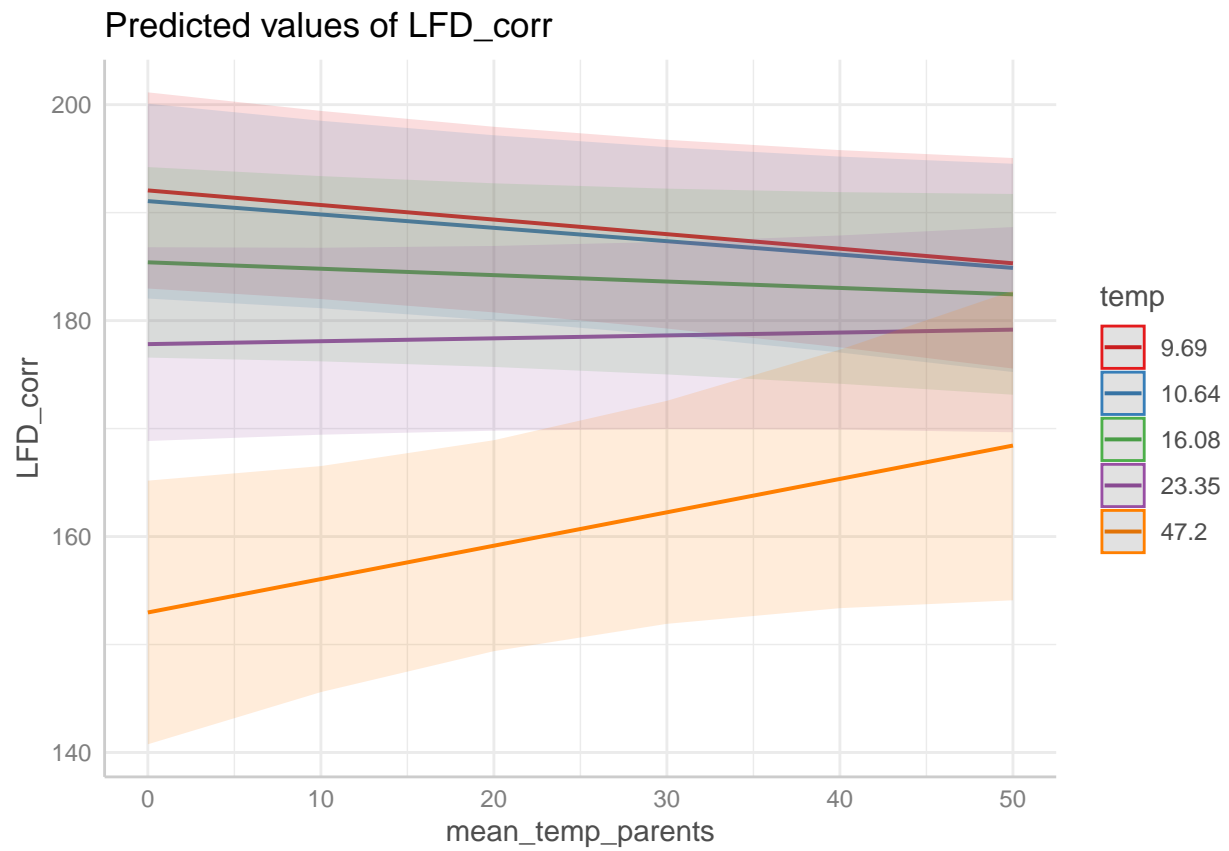


The sign of mean_temp_parents goes in the opposite direction as expected! (earlier FFD/LFD/meanFD at a given temperature in individuals with parents from warmer soils). But maybe we should not interpret this main effect, as the interaction with temp is significant??

```
plot(ggpredict(model4_FFD_midP, terms=c("mean_temp_parents", "temp[quart]")))
```

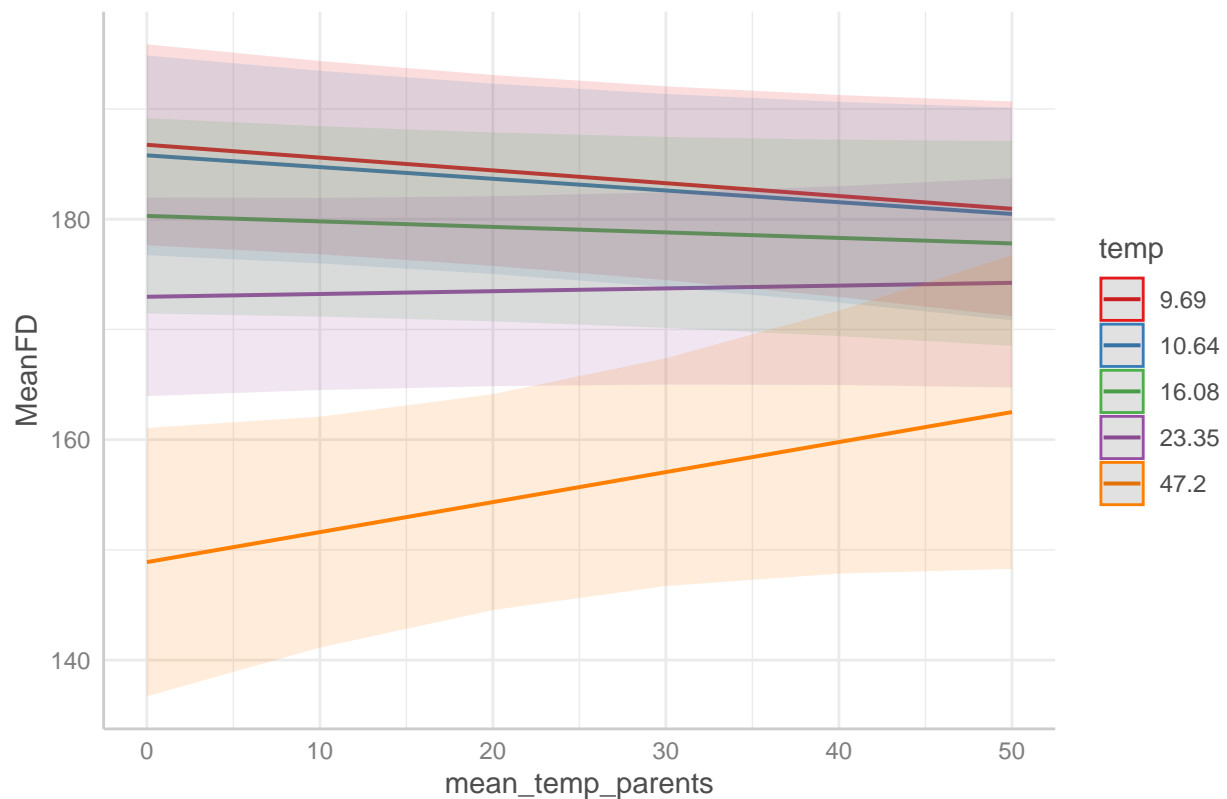


```
plot(ggpredict(model14_LFD_midP, terms=c("mean_temp_parents", "temp[quart]")))
```



```
plot(ggpredict(model4_MeanFD_midP, terms=c("mean_temp_parents", "temp[quart]"))) # Marginally *
```

Predicted values of MeanFD



As predicted: differences in phenology between high and low soil temperatures are predicted to be smaller for plants with parents from warm soils than for plants with parents from colder soils.

Predictions 3 and 4 with breeding values?

Session info

```
sessionInfo()
```

```
## R version 4.3.2 (2023-10-31 ucrt)
## Platform: x86_64-w64-mingw32/x64 (64-bit)
## Running under: Windows 11 x64 (build 22621)
##
## Matrix products: default
##
## locale:
## [1] LC_COLLATE=English_United States.utf8
## [2] LC_CTYPE=English_United States.utf8
## [3] LC_MONETARY=English_United States.utf8
## [4] LC_NUMERIC=C
## [5] LC_TIME=English_United States.utf8
```

```

##
## time zone: Europe/Madrid
## tzcode source: internal
##
## attached base packages:
## [1] stats      graphics  grDevices  utils      datasets  methods   base
##
## other attached packages:
## [1] partR2_0.9.1.9000  performance_0.10.8 ggeffects_1.3.4    sjPlot_2.8.15
## [5] car_3.1-2          carData_3.0-5      lmerTest_3.1-3     lme4_1.1-35.1
## [9] Matrix_1.6-4       glmmTMB_1.1.8      ggthemes_5.0.0     knitr_1.45
## [13] RColorBrewer_1.1-3 readxl_1.4.3       lubridate_1.9.3    forcats_1.0.0
## [17] stringr_1.5.1      dplyr_1.1.4        purrr_1.0.2        readr_2.1.4
## [21] tidyr_1.3.0        tibble_3.2.1       ggplot2_3.4.4      tidyverse_2.0.0
##
## loaded via a namespace (and not attached):
## [1] tidyselect_1.2.0    sjlabelled_1.2.0    farver_2.1.1
## [4] fastmap_1.1.1       TH.data_1.1-2      bayestestR_0.13.1
## [7] sjstats_0.18.2      digest_0.6.33      estimability_1.4.1
## [10] timechange_0.2.0    lifecycle_1.0.4    survival_3.5-7
## [13] magrittr_2.0.3      compiler_4.3.2     rlang_1.1.2
## [16] tools_4.3.2         utf8_1.2.4         yaml_2.3.8
## [19] labeling_0.4.3      bit_4.0.5          multcomp_1.4-25
## [22] abind_1.4-5         withr_2.5.2        numDeriv_2016.8-1.1
## [25] datawizard_0.9.0    grid_4.3.2         fansi_1.0.6
## [28] xtable_1.8-4        colorspace_2.1-0   emmeans_1.9.0
## [31] scales_1.3.0        MASS_7.3-60        insight_0.19.7
## [34] cli_3.6.2           mvtnorm_1.2-4      crayon_1.5.2
## [37] rmarkdown_2.25      generics_0.1.3     rstudioapi_0.15.0
## [40] modelr_0.1.11       tzdb_0.4.0         parameters_0.21.3
## [43] minqa_1.2.6         splines_4.3.2      parallel_4.3.2
## [46] effectsize_0.8.6    cellranger_1.1.0   vctrs_0.6.5
## [49] boot_1.3-28.1       sandwich_3.1-0     hms_1.1.3
## [52] bit64_4.0.5         glue_1.6.2         nloptr_2.0.3
## [55] codetools_0.2-19    stringi_1.8.3      gtable_0.3.4
## [58] munsell_0.5.0       pillar_1.9.0       htmltools_0.5.7
## [61] R6_2.5.1            TMB_1.9.10         vroom_1.6.5
## [64] evaluate_0.23       lattice_0.22-5     haven_2.5.4
## [67] highr_0.10          backports_1.4.1    broom_1.0.5
## [70] Rcpp_1.0.11         coda_0.19-4        nlme_3.1-164
## [73] mgcv_1.9-0          xfun_0.41          zoo_1.8-12
## [76] sjmisc_2.8.9        pkgconfig_2.0.3

```