Effects of inflorescence architecture on within-individual variation in phenology and reproductive success of flowers in Lathyrus vernus

First analyses

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Contents

Load previously created objects>

```
load("output/models/mod_within_among_87.rda")
load("output/models/mod_within_among_88.rda")
load("output/models/mod_within_among_89.rda")
load("output/models/mod_within_among_frset_87.rda")
load("output/models/mod_within_among_frset_88.rda")
load("output/models/mod_within_among_frset_89.rda")
```

Read data for individual flowers

```
data_id_flowers <- read_csv("data/clean/data_id_flowers.csv")%>%
  mutate(year=as.factor(year))
```

Q1: Components of variation

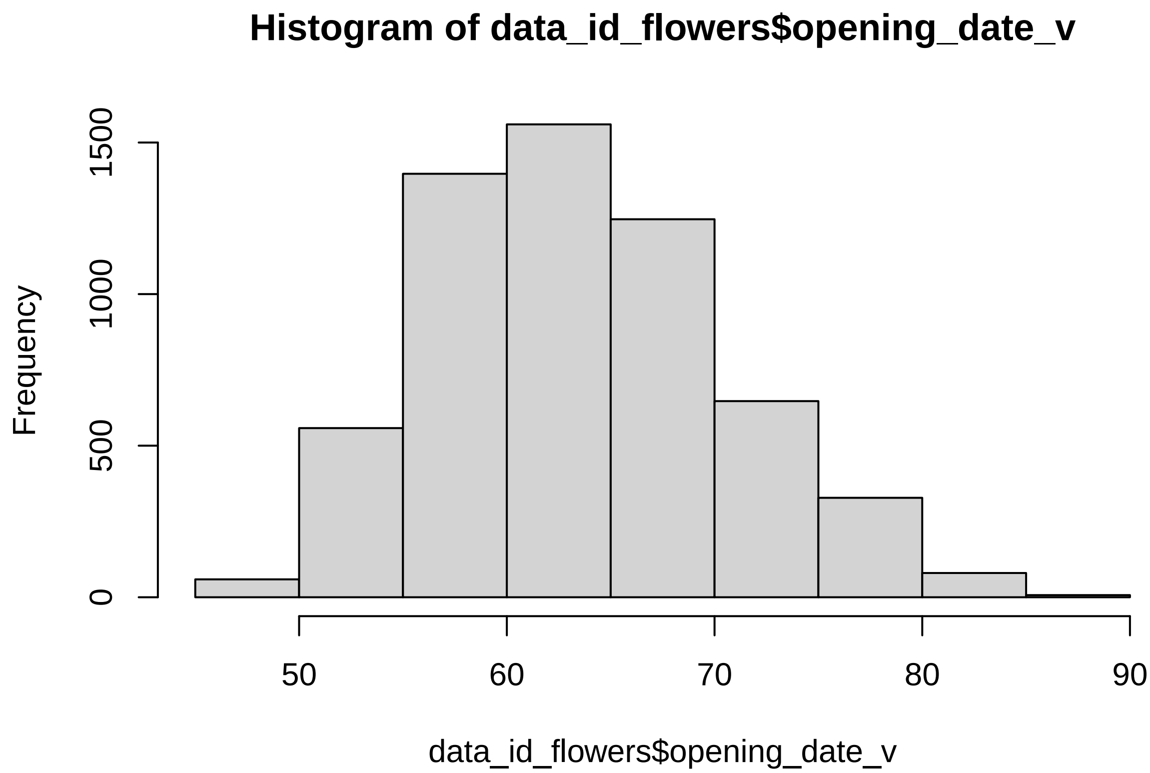
Opening date

How much variation in opening date of individual flowers can be attributed to among-individual variation among plants within the population, and to within-individual variation among flowers on the same plants?

How much of the within-individual variation can be attributed to variation among shoots within an individual, among racemes within a shoot, and among flowers within a raceme?

Check distribution of opening dates:

```
hist(data_id_flowers$opening_date_v)
```



Looks quite normal.

Variance partitioning:

```
v_id_87 <- (VarCorr(mod_within_among_87, summary=FALSE)$id$sd)^2
v_shoot_87 <- (VarCorr(mod_within_among_87, summary=FALSE)$`id:shoot_id`$sd)^2
v_raceme_87 <- (VarCorr(mod_within_among_87,
                        summary=FALSE)$`id:shoot_id:raceme_id`$sd)^2
v_flower_87 <- (VarCorr(mod_within_among_87, summary=FALSE)$residual$sd)^2
prop_v_id_87 <- as.mcmc(v_id_87 /
                          (v_id_87 + v_shoot_87 + v_raceme_87 + v_flower_87))
prop_v_shoot_87 <- as.mcmc(v_shoot_87 /
                             (v_id_87 + v_shoot_87 + v_raceme_87 + v_flower_87))
prop_v_raceme_87 <- as.mcmc(v_raceme_87 /
                              (v_id_87 + v_shoot_87 + v_raceme_87 + v_flower_87))
prop_v_flower_87 <- as.mcmc(v_flower_87 /
                              (v_id_87 + v_shoot_87 + v_raceme_87 + v_flower_87))
summary(prop_v_id_87)
```

```
##
## Iterations = 1:5600
## Thinning interval = 1
## Number of chains = 1
## Sample size per chain = 5600
##
## 1. Empirical mean and standard deviation for each variable,
```

```
##    plus standard error of the mean:
##
##           Mean             SD       Naive SE Time-series SE
##       0.087257       0.066006       0.000882       0.002257
##
## 2. Quantiles for each variable:
##
##      2.5%       25%       50%       75%     97.5%
## 0.0003967 0.0280650 0.0810510 0.1341770 0.2249283
```

```r
summary(prop_v_shoot_87)
```

```
##
## Iterations = 1:5600
## Thinning interval = 1
## Number of chains = 1
## Sample size per chain = 5600
##
## 1. Empirical mean and standard deviation for each variable,
##    plus standard error of the mean:
##
##           Mean             SD       Naive SE Time-series SE
##      0.0859478      0.0682617      0.0009122      0.0024958
##
## 2. Quantiles for each variable:
##
##      2.5%       25%       50%       75%     97.5%
## 0.0003343 0.0247046 0.0765306 0.1337936 0.2316648
```

```r
summary(prop_v_raceme_87)
```

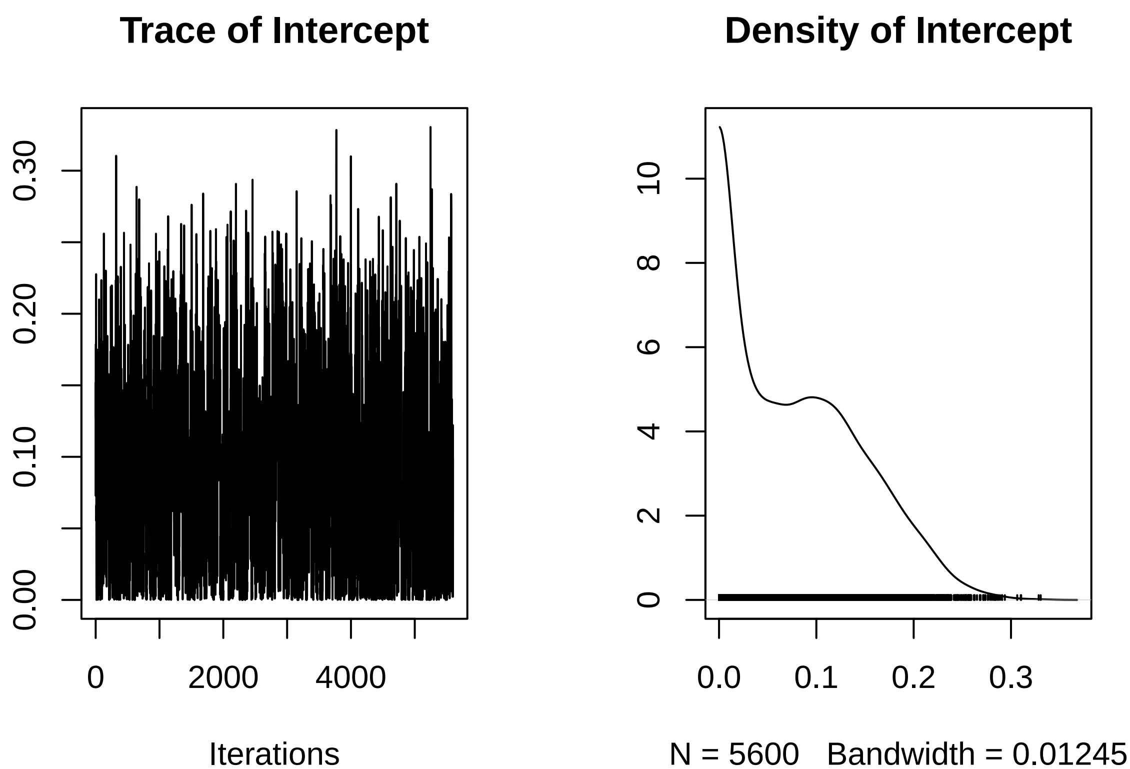
```
##
## Iterations = 1:5600
## Thinning interval = 1
## Number of chains = 1
## Sample size per chain = 5600
##
## 1. Empirical mean and standard deviation for each variable,
##    plus standard error of the mean:
##
##           Mean             SD       Naive SE Time-series SE
##      0.6818668      0.0527894      0.0007054      0.0012881
##
## 2. Quantiles for each variable:
##
##   2.5%    25%    50%    75%  97.5%
## 0.5793 0.6457 0.6826 0.7176 0.7850
```

```r
summary(prop_v_flower_87)
```

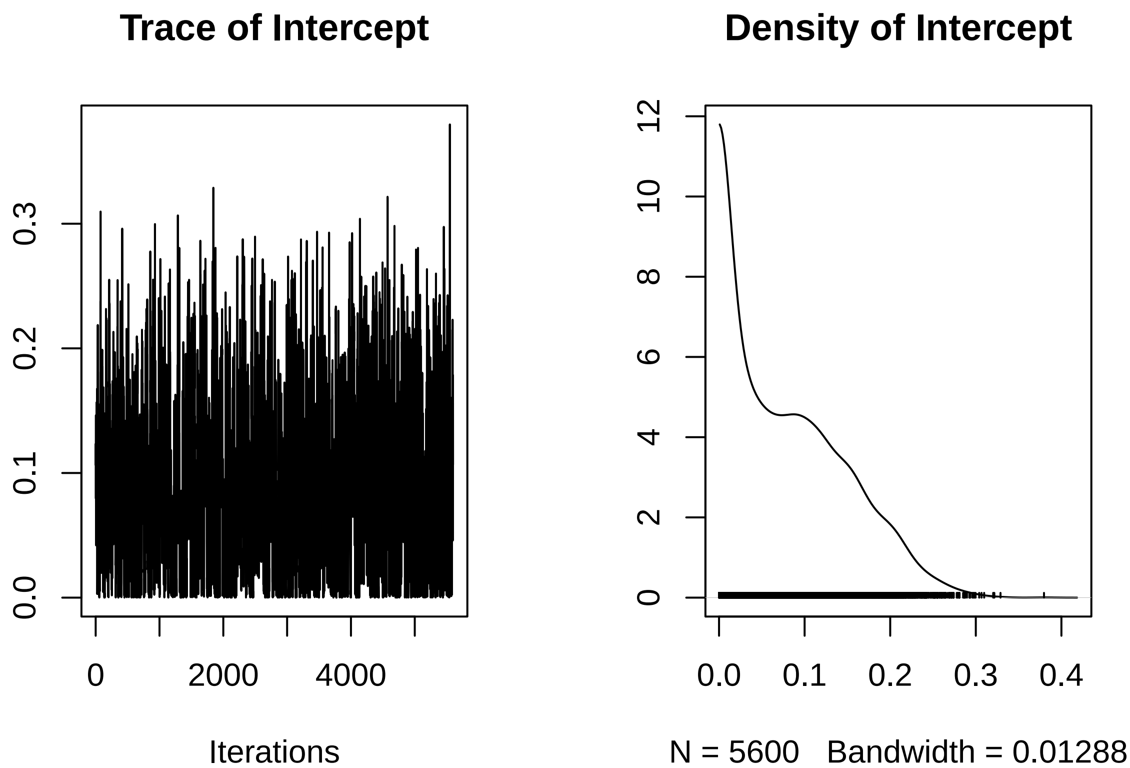
```
##
## Iterations = 1:5600
```

```
## Thinning interval = 1
## Number of chains = 1
## Sample size per chain = 5600
##
## 1. Empirical mean and standard deviation for each variable,
##    plus standard error of the mean:
##
##           Mean             SD       Naive SE Time-series SE
##      0.1449286      0.0101441      0.0001356      0.0001620
##
## 2. Quantiles for each variable:
##
##   2.5%    25%    50%    75%  97.5%
## 0.1254 0.1381 0.1448 0.1514 0.1656
```

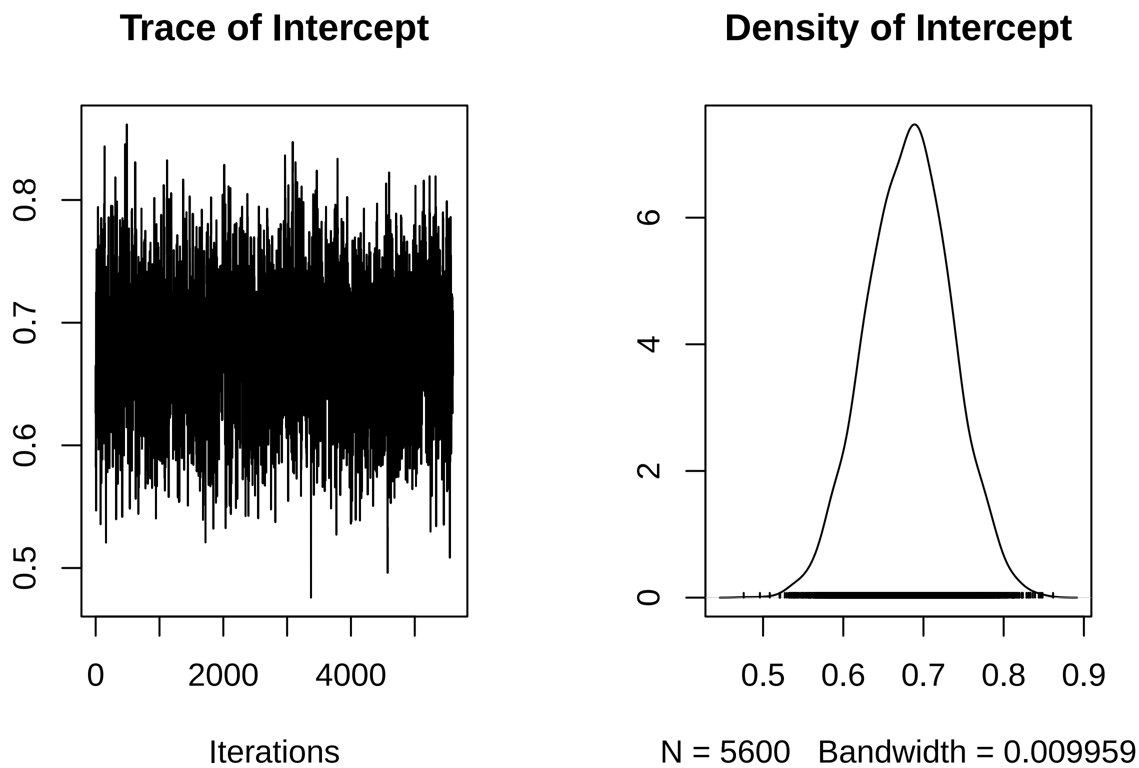
```r
plot(prop_v_id_87)
```



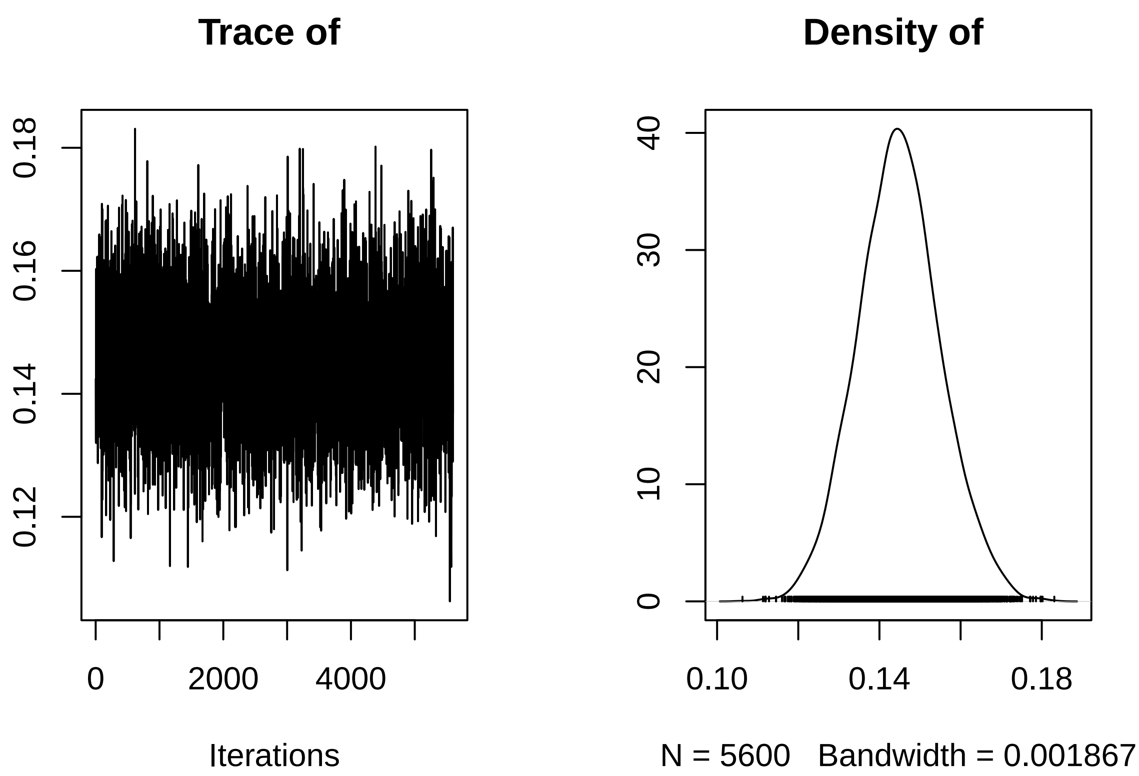

```r
plot(prop_v_shoot_87)
```




```r
plot(prop_v_raceme_87)
```




```r
plot(prop_v_flower_87)
```




```r
v_id_88 <- (VarCorr(mod_within_among_88, summary=FALSE)$id$sd)^2
v_shoot_88 <- (VarCorr(mod_within_among_88, summary=FALSE)$`id:shoot_id`$sd)^2
v_raceme_88 <- (VarCorr(mod_within_among_88,
                        summary=FALSE)$`id:shoot_id:raceme_id`$sd)^2
v_flower_88 <- (VarCorr(mod_within_among_88, summary=FALSE)$residual$sd)^2
prop_v_id_88 <- as.mcmc(v_id_88 /
                          (v_id_88 + v_shoot_88 + v_raceme_88 + v_flower_88))
prop_v_shoot_88 <- as.mcmc(v_shoot_88 /
                             (v_id_88 + v_shoot_88 + v_raceme_88 + v_flower_88))
prop_v_raceme_88 <- as.mcmc(v_raceme_88 /
                              (v_id_88 + v_shoot_88 + v_raceme_88 + v_flower_88))
prop_v_flower_88 <- as.mcmc(v_flower_88 /
                              (v_id_88 + v_shoot_88 + v_raceme_88 + v_flower_88))
summary(prop_v_id_88)
```

```
##
## Iterations = 1:5600
## Thinning interval = 1
## Number of chains = 1
## Sample size per chain = 5600
##
## 1. Empirical mean and standard deviation for each variable,
##    plus standard error of the mean:
##
##           Mean             SD       Naive SE Time-series SE
```

```
##      0.2658015      0.0691501      0.0009241      0.0016772
##
## 2. Quantiles for each variable:
##
##   2.5%    25%    50%    75%  97.5%
## 0.1196 0.2236 0.2700 0.3146 0.3903
```

```r
summary(prop_v_shoot_88)
```

```
##
## Iterations = 1:5600
## Thinning interval = 1
## Number of chains = 1
## Sample size per chain = 5600
##
## 1. Empirical mean and standard deviation for each variable,
##    plus standard error of the mean:
##
##           Mean             SD       Naive SE Time-series SE
##      0.0871077      0.0646490      0.0008639      0.0020441
##
## 2. Quantiles for each variable:
##
##      2.5%       25%       50%       75%     97.5%
## 0.0007575 0.0356066 0.0770383 0.1265230 0.2407471
```

```r
summary(prop_v_raceme_88)
```

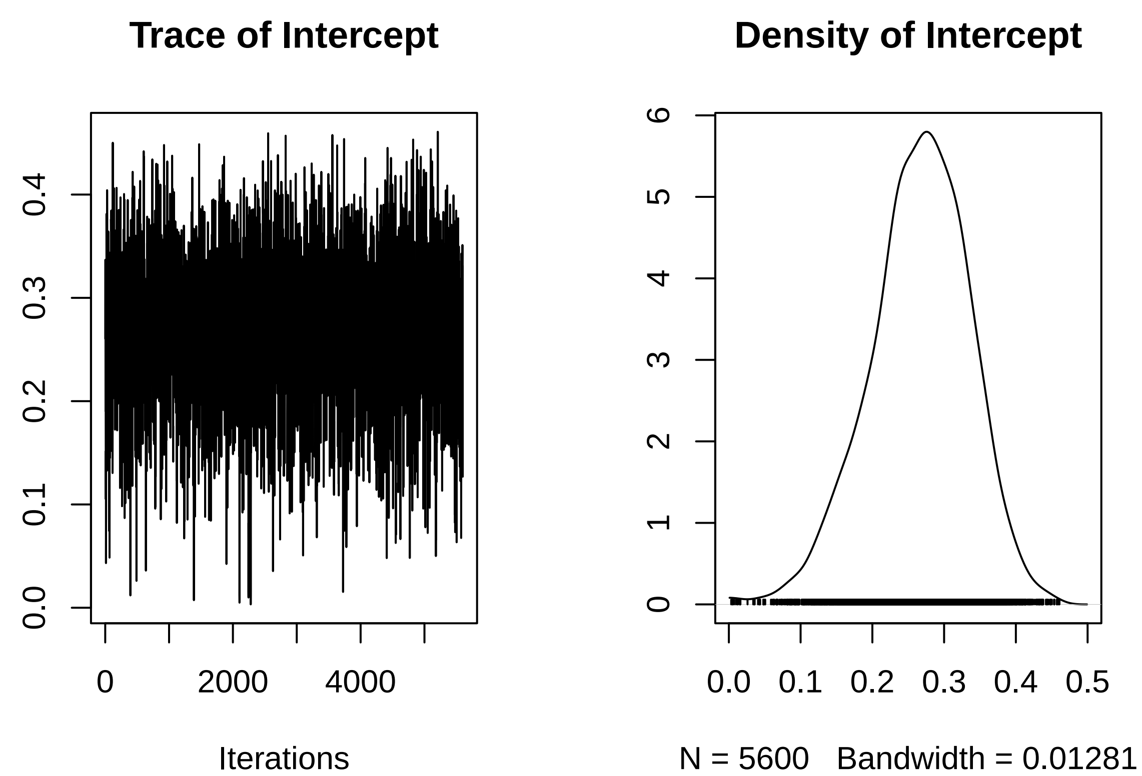
```
##
## Iterations = 1:5600
## Thinning interval = 1
## Number of chains = 1
## Sample size per chain = 5600
##
## 1. Empirical mean and standard deviation for each variable,
##    plus standard error of the mean:
##
##           Mean             SD       Naive SE Time-series SE
##      0.5155499      0.0455275      0.0006084      0.0007713
##
## 2. Quantiles for each variable:
##
##   2.5%    25%    50%    75%  97.5%
## 0.4287 0.4837 0.5152 0.5470 0.6071
```

```r
summary(prop_v_flower_88)
```

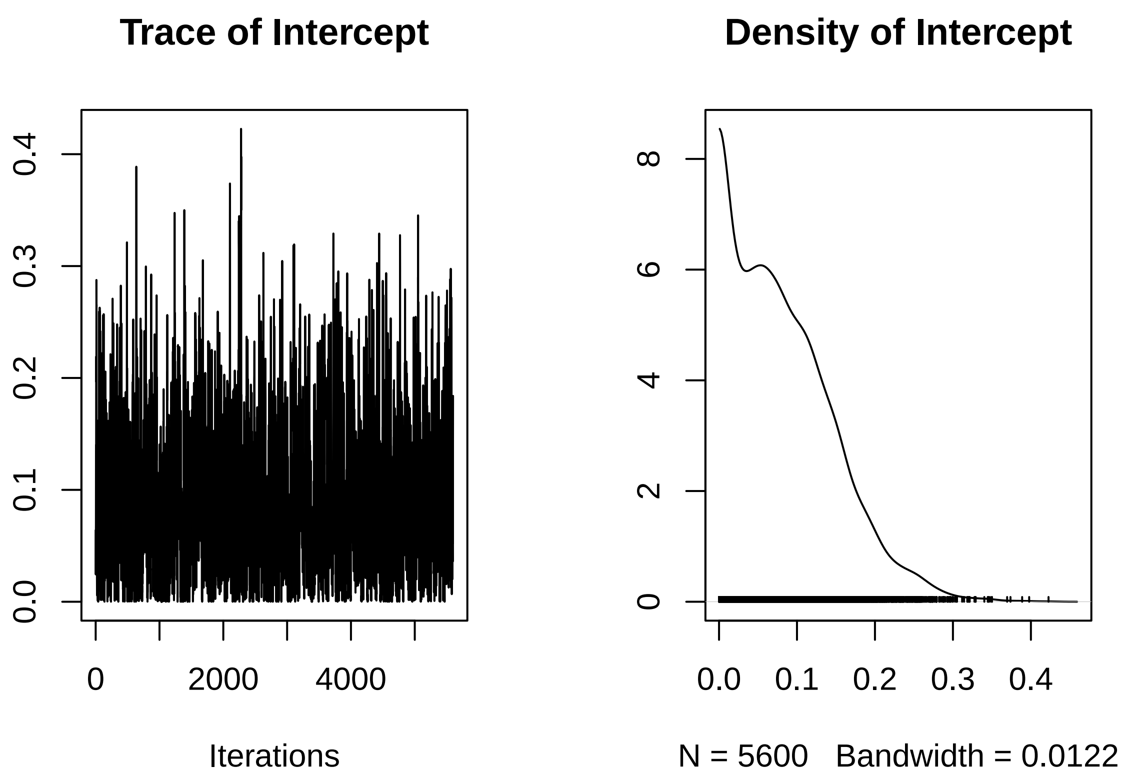
```
##
## Iterations = 1:5600
## Thinning interval = 1
## Number of chains = 1
## Sample size per chain = 5600
```

```
##
## 1. Empirical mean and standard deviation for each variable,
##    plus standard error of the mean:
##
##           Mean             SD       Naive SE Time-series SE
##      0.1315409      0.0089460      0.0001195      0.0001313
##
## 2. Quantiles for each variable:
##
##   2.5%    25%    50%    75%  97.5%
## 0.1141 0.1255 0.1315 0.1374 0.1497
```

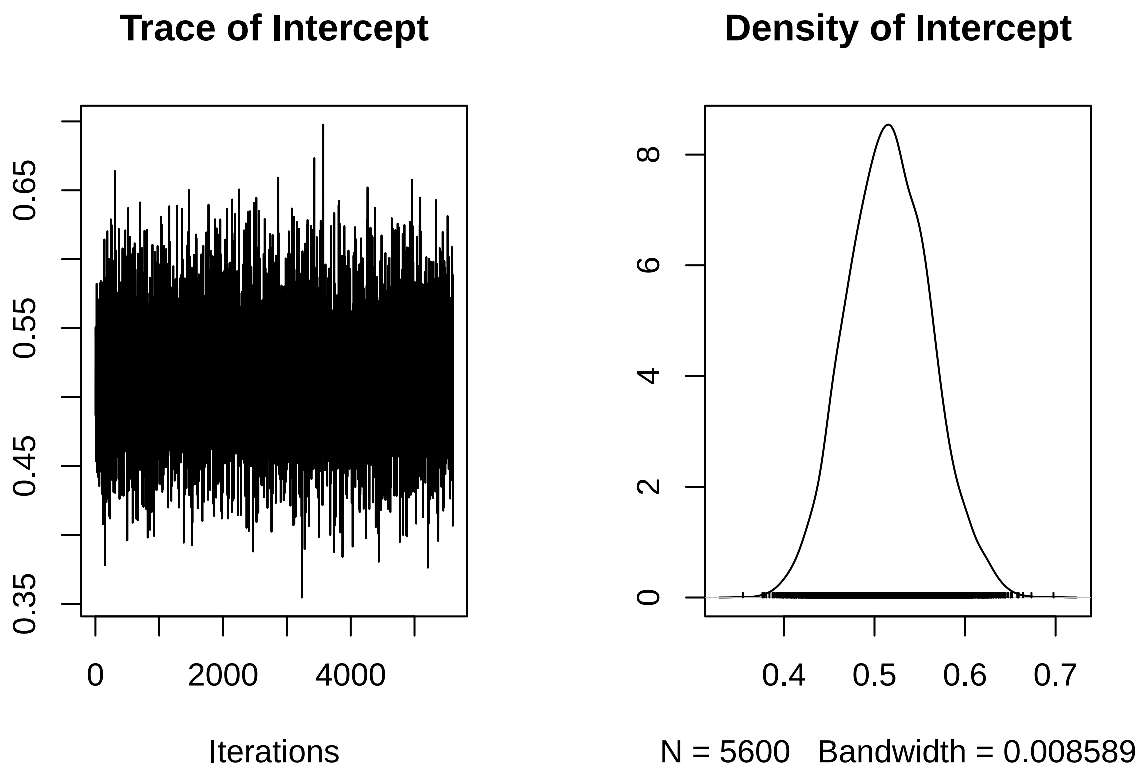
```r
plot(prop_v_id_88)
```



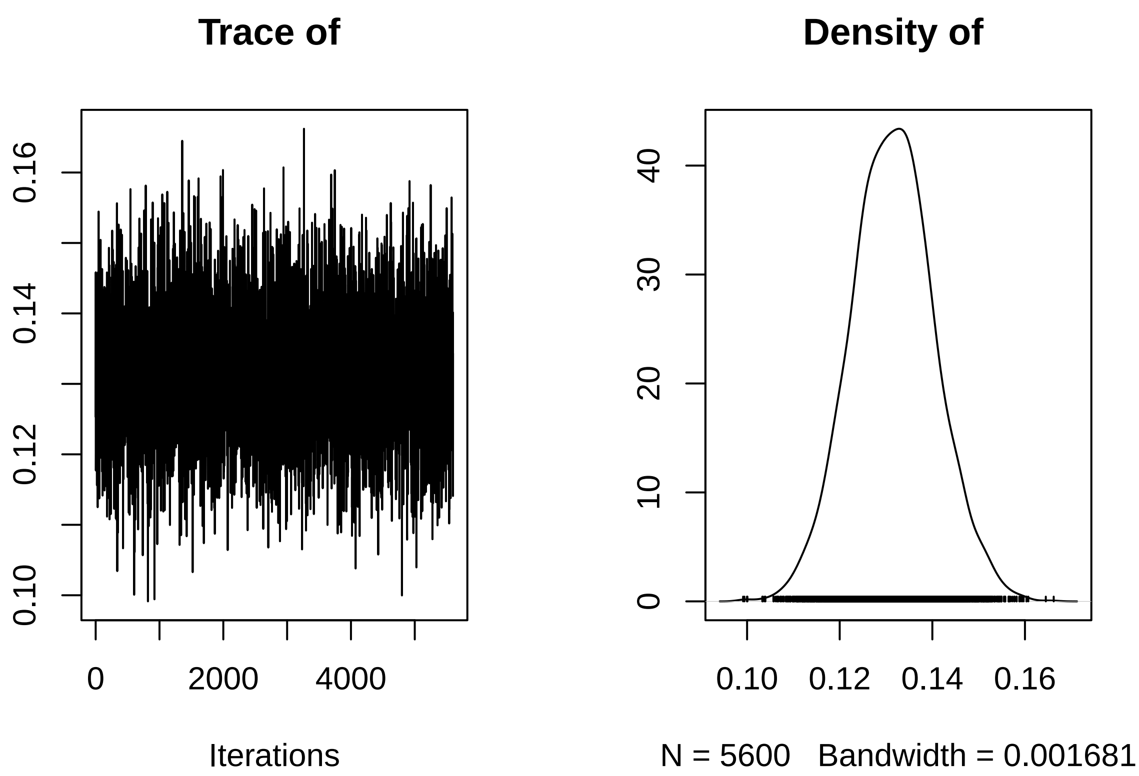

```r
plot(prop_v_shoot_88)
```




```r
plot(prop_v_raceme_88)
```




```
plot(prop_v_flower_88)
```




```
v_id_89 <- (VarCorr(mod_within_among_89, summary=FALSE)$id$sd)^2
v_shoot_89 <- (VarCorr(mod_within_among_89, summary=FALSE)$`id:shoot_id`$sd)^2
v_raceme_89 <- (VarCorr(mod_within_among_89,
                        summary=FALSE)$`id:shoot_id:raceme_id`$sd)^2
v_flower_89 <- (VarCorr(mod_within_among_89, summary=FALSE)$residual$sd)^2
prop_v_id_89 <- as.mcmc(v_id_89 /
                          (v_id_89 + v_shoot_89 + v_raceme_89 + v_flower_89))
prop_v_shoot_89 <- as.mcmc(v_shoot_89 /
                             (v_id_89 + v_shoot_89 + v_raceme_89 + v_flower_89))
prop_v_raceme_89 <- as.mcmc(v_raceme_89 /
                              (v_id_89 + v_shoot_89 + v_raceme_89 + v_flower_89))
prop_v_flower_89 <- as.mcmc(v_flower_89 /
                              (v_id_89 + v_shoot_89 + v_raceme_89 + v_flower_89))
summary(prop_v_id_89)
```

```
##
## Iterations = 1:5600
## Thinning interval = 1
## Number of chains = 1
## Sample size per chain = 5600
##
## 1. Empirical mean and standard deviation for each variable,
##    plus standard error of the mean:
##
##          Mean             SD       Naive SE Time-series SE
```

```
##      0.0767340      0.0502556      0.0006716      0.0011972
##
## 2. Quantiles for each variable:
##
##      2.5%       25%       50%       75%     97.5%
## 0.0009783 0.0376872 0.0730810 0.1092399 0.1854024
```

```r
summary(prop_v_shoot_89)
```

```
##
## Iterations = 1:5600
## Thinning interval = 1
## Number of chains = 1
## Sample size per chain = 5600
##
## 1. Empirical mean and standard deviation for each variable,
##    plus standard error of the mean:
##
##           Mean             SD       Naive SE Time-series SE
##      0.0368080      0.0417467      0.0005579      0.0011215
##
## 2. Quantiles for each variable:
##
##      2.5%       25%       50%       75%     97.5%
## 4.669e-05 4.818e-03 2.171e-02 5.559e-02 1.452e-01
```

```r
summary(prop_v_raceme_89)
```

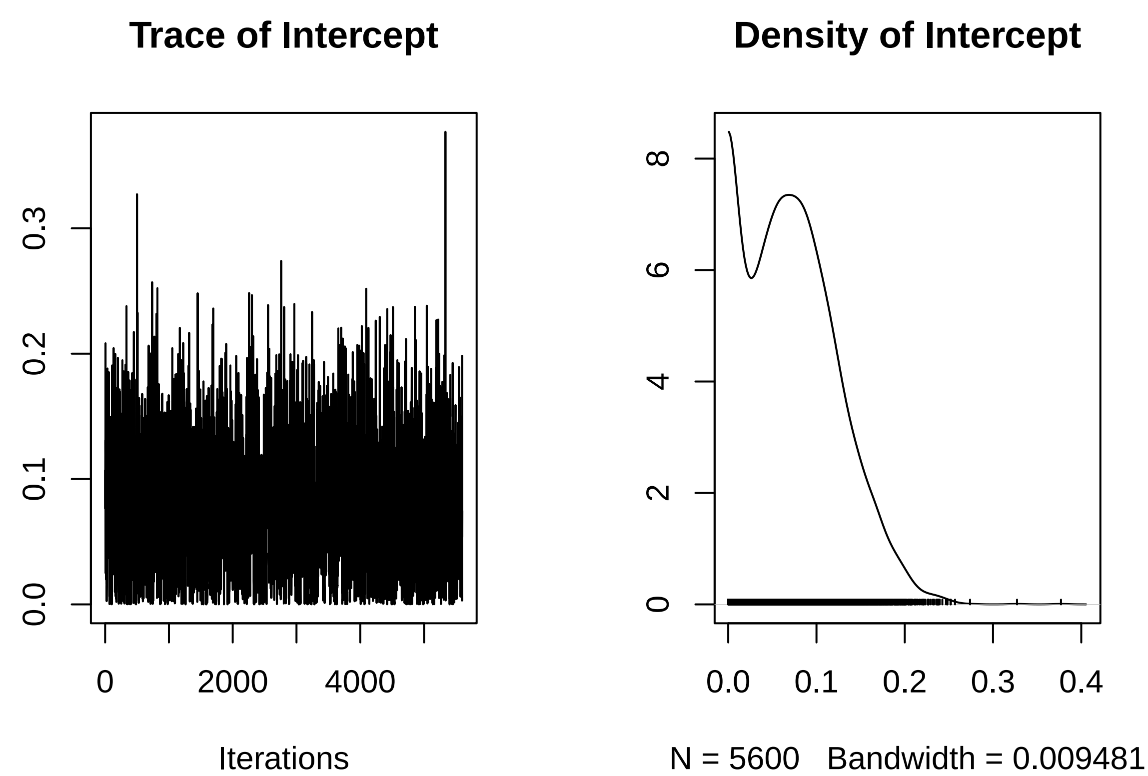
```
##
## Iterations = 1:5600
## Thinning interval = 1
## Number of chains = 1
## Sample size per chain = 5600
##
## 1. Empirical mean and standard deviation for each variable,
##    plus standard error of the mean:
##
##           Mean             SD       Naive SE Time-series SE
##      0.7177859      0.0491983      0.0006574      0.0011046
##
## 2. Quantiles for each variable:
##
##   2.5%    25%    50%    75%  97.5%
## 0.6177 0.6850 0.7193 0.7525 0.8095
```

```r
summary(prop_v_flower_89)
```

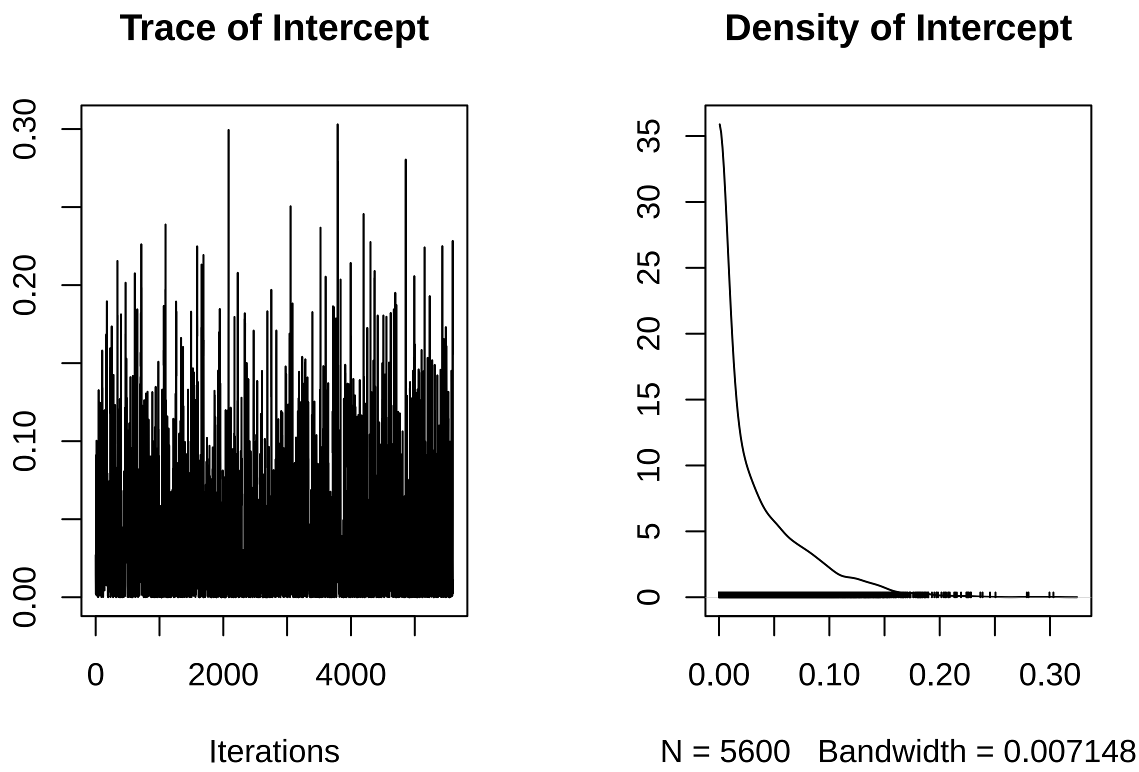
```
##
## Iterations = 1:5600
## Thinning interval = 1
## Number of chains = 1
## Sample size per chain = 5600
```

```
##
## 1. Empirical mean and standard deviation for each variable,
##    plus standard error of the mean:
##
##           Mean             SD       Naive SE Time-series SE
##      0.1686720      0.0136677      0.0001826      0.0002013
##
## 2. Quantiles for each variable:
##
##   2.5%    25%    50%    75%  97.5%
## 0.1431 0.1591 0.1685 0.1778 0.1959
```

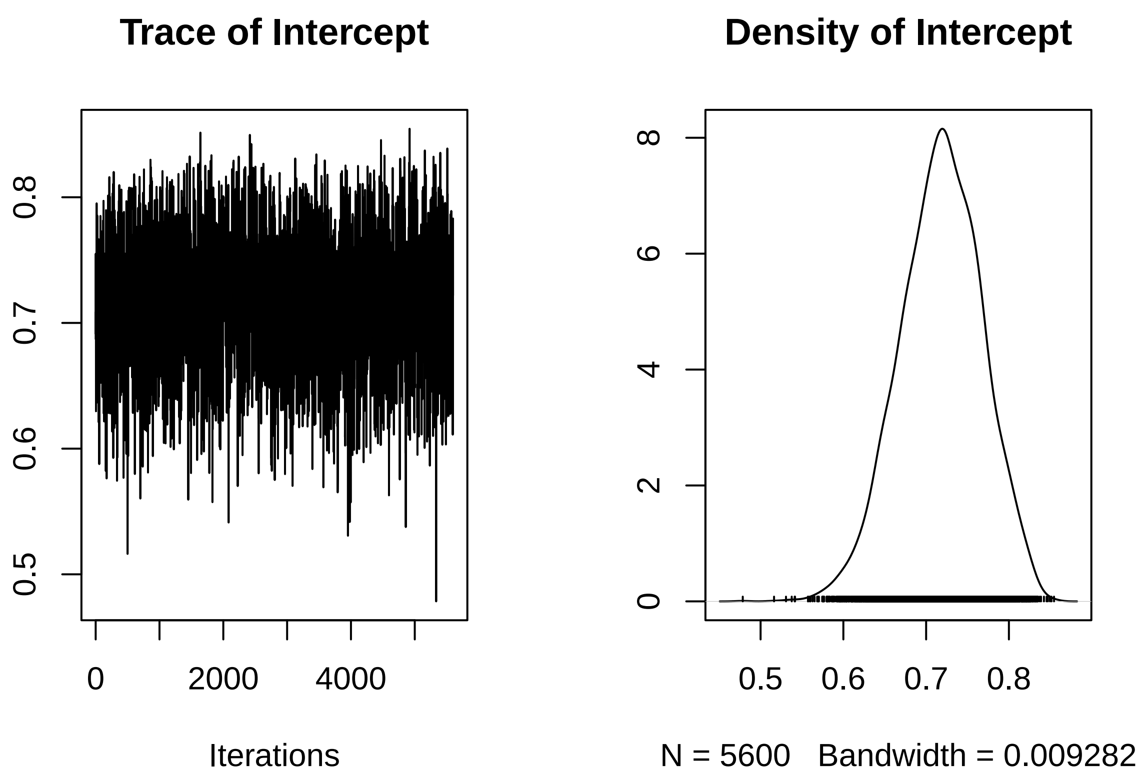
```r
plot(prop_v_id_89)
```



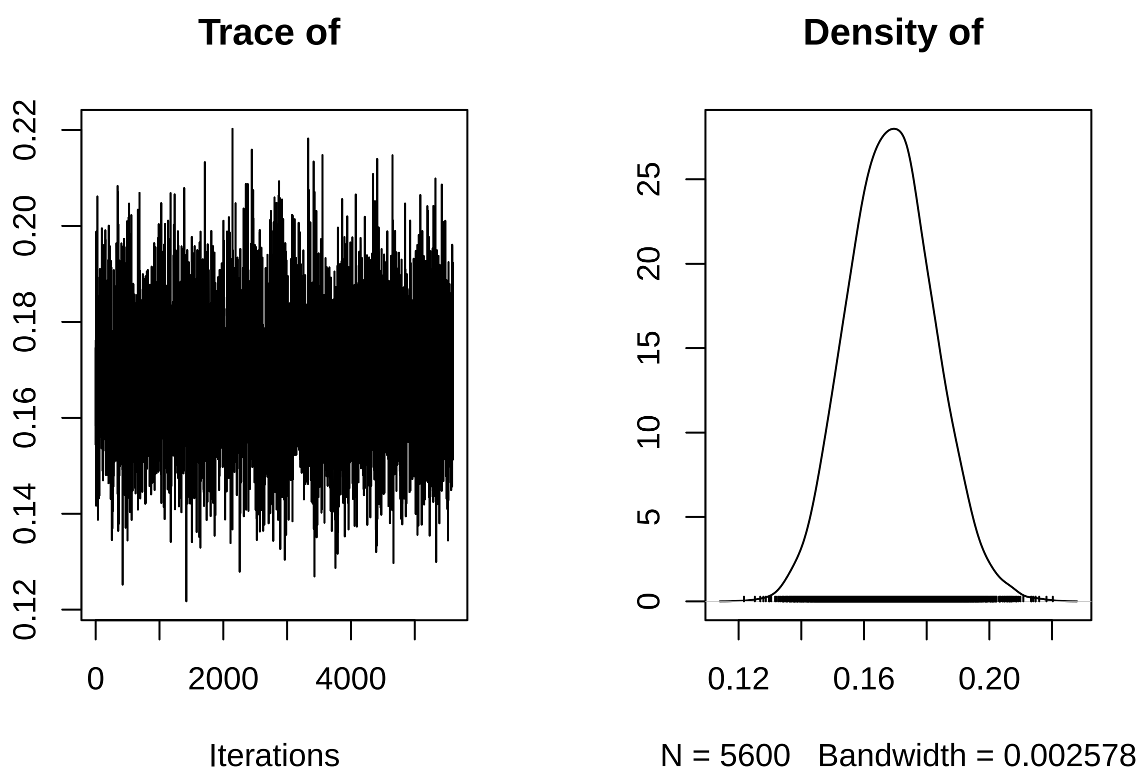

```r
plot(prop_v_shoot_89)
```




```
plot(prop_v_raceme_89)
```




```
plot(prop_v_flower_89)
```




```
data_props_87<-full_join(
  cbind(data.frame(id_mean=summary(prop_v_id_87)$statistics[1]),
        data.frame(shoot_mean=summary(prop_v_shoot_87)$statistics[1]),
        data.frame(raceme_mean=summary(prop_v_raceme_87)$statistics[1]),
        data.frame(flower_mean=summary(prop_v_flower_87)$statistics[1]))%>%
    pivot_longer(cols=c("id_mean","shoot_mean","raceme_mean","flower_mean"),
                 names_to="effect",values_to="mean",names_pattern="(.*)_mean"),
  cbind(data.frame(id_lower=coda::HPDinterval(prop_v_id_87)[1],
                   id_upper=coda::HPDinterval(prop_v_id_87)[2]),
        data.frame(shoot_lower=coda::HPDinterval(prop_v_shoot_87)[1],
                   shoot_upper=coda::HPDinterval(prop_v_shoot_87)[2]),
        data.frame(raceme_lower=coda::HPDinterval(prop_v_raceme_87)[1],
                   raceme_upper=coda::HPDinterval(prop_v_raceme_87)[2]),
        data.frame(flower_lower=coda::HPDinterval(prop_v_flower_87)[1],
                   flower_upper=coda::HPDinterval(prop_v_flower_87)[2]))%>%
    pivot_longer(cols=c("id_lower","id_upper",
                        "shoot_lower","shoot_upper",
                        "raceme_lower","raceme_upper",
                        "flower_lower","flower_upper"),
                 names_to=c("effect","cat"),names_sep="_",values_to="value")%>%
    pivot_wider(names_from="cat",values_from="value"))%>%
  mutate(year=1987)
data_props_88<-full_join(
  cbind(data.frame(id_mean=summary(prop_v_id_88)$statistics[1]),
        data.frame(shoot_mean=summary(prop_v_shoot_88)$statistics[1]),
        data.frame(raceme_mean=summary(prop_v_raceme_88)$statistics[1]),
```

```r
        data.frame(flower_mean=summary(prop_v_flower_88)$statistics[1]))%>%
    pivot_longer(cols=c("id_mean","shoot_mean","raceme_mean","flower_mean"),
                 names_to="effect",values_to="mean",names_pattern="(.*)_mean"),
  cbind(data.frame(id_lower=coda::HPDinterval(prop_v_id_88)[1],
                   id_upper=coda::HPDinterval(prop_v_id_88)[2]),
        data.frame(shoot_lower=coda::HPDinterval(prop_v_shoot_88)[1],
                   shoot_upper=coda::HPDinterval(prop_v_shoot_88)[2]),
        data.frame(raceme_lower=coda::HPDinterval(prop_v_raceme_88)[1],
                   raceme_upper=coda::HPDinterval(prop_v_raceme_88)[2]),
        data.frame(flower_lower=coda::HPDinterval(prop_v_flower_88)[1],
                   flower_upper=coda::HPDinterval(prop_v_flower_88)[2]))%>%
    pivot_longer(cols=c("id_lower","id_upper",
                        "shoot_lower","shoot_upper",
                        "raceme_lower","raceme_upper",
                        "flower_lower","flower_upper"),
                 names_to=c("effect","cat"),names_sep="_",values_to="value")%>%
    pivot_wider(names_from="cat",values_from="value"))%>%
  mutate(year=1988)
data_props_89<-full_join(
  cbind(data.frame(id_mean=summary(prop_v_id_89)$statistics[1]),
        data.frame(shoot_mean=summary(prop_v_shoot_89)$statistics[1]),
        data.frame(raceme_mean=summary(prop_v_raceme_89)$statistics[1]),
        data.frame(flower_mean=summary(prop_v_flower_89)$statistics[1]))%>%
    pivot_longer(cols=c("id_mean","shoot_mean","raceme_mean","flower_mean"),
                 names_to="effect",values_to="mean",names_pattern="(.*)_mean"),
  cbind(data.frame(id_lower=coda::HPDinterval(prop_v_id_89)[1],
                   id_upper=coda::HPDinterval(prop_v_id_89)[2]),
        data.frame(shoot_lower=coda::HPDinterval(prop_v_shoot_89)[1],
                   shoot_upper=coda::HPDinterval(prop_v_shoot_89)[2]),
        data.frame(raceme_lower=coda::HPDinterval(prop_v_raceme_89)[1],
                   raceme_upper=coda::HPDinterval(prop_v_raceme_89)[2]),
        data.frame(flower_lower=coda::HPDinterval(prop_v_flower_89)[1],
                   flower_upper=coda::HPDinterval(prop_v_flower_89)[2]))%>%
    pivot_longer(cols=c("id_lower","id_upper",
                        "shoot_lower","shoot_upper",
                        "raceme_lower","raceme_upper",
                        "flower_lower","flower_upper"),
                 names_to=c("effect","cat"),names_sep="_",values_to="value")%>%
    pivot_wider(names_from="cat",values_from="value"))%>%
  mutate(year=1989)
data_props<-rbind(data_props_87,data_props_88,data_props_89)%>%
  mutate(year=factor(year),
         effect=factor(effect,levels=c("id","shoot","raceme","flower")))
```

Probability of setting fruit

How much variation in reproductive success of individual flowers can be attributed to among-individual variation among plants within the population, and to within-individual variation among flowers on the same plants?

How much of the within-individual variation can be attributed to variation among shoots within an individual, among racemes within a shoot, and among flowers within a raceme?

Variance partitioning:

```r
v_id_87_frset <- (VarCorr(mod_within_among_frset_87, summary=FALSE)$id$sd)^2
v_shoot_87_frset <- (VarCorr(mod_within_among_frset_87,
                              summary=FALSE)$`id:shoot_id`$sd)^2
v_raceme_87_frset <- (VarCorr(mod_within_among_frset_87,
                               summary=FALSE)$`id:shoot_id:raceme_id`$sd)^2
v_flower_87_frset <- (VarCorr(mod_within_among_frset_87,
                               summary=FALSE)$residual$sd)^2
# No residual variance! OK?
prop_v_id_87_frset <- as.mcmc(v_id_87_frset /
                                (v_id_87_frset + v_shoot_87_frset +
                                   v_raceme_87_frset))
prop_v_shoot_87_frset <- as.mcmc(v_shoot_87_frset /
                                   (v_id_87_frset + v_shoot_87_frset +
                                      v_raceme_87_frset))
prop_v_raceme_87_frset <- as.mcmc(v_raceme_87_frset /
                                    (v_id_87_frset + v_shoot_87_frset +
                                       v_raceme_87_frset))
prop_v_flower_87_frset <- as.mcmc(v_flower_87_frset /
                                    (v_id_87_frset + v_shoot_87_frset +
                                       v_raceme_87_frset))
summary(prop_v_id_87_frset)
```

```
##
## Iterations = 1:5600
## Thinning interval = 1
## Number of chains = 1
## Sample size per chain = 5600
##
## 1. Empirical mean and standard deviation for each variable,
##    plus standard error of the mean:
##
##           Mean             SD       Naive SE Time-series SE
##       0.476956       0.327298       0.004374       0.009399
##
## 2. Quantiles for each variable:
##
##     2.5%      25%      50%      75%    97.5%
## 0.001609 0.156390 0.486747 0.782781 0.980859
```

```r
summary(prop_v_shoot_87_frset)
```

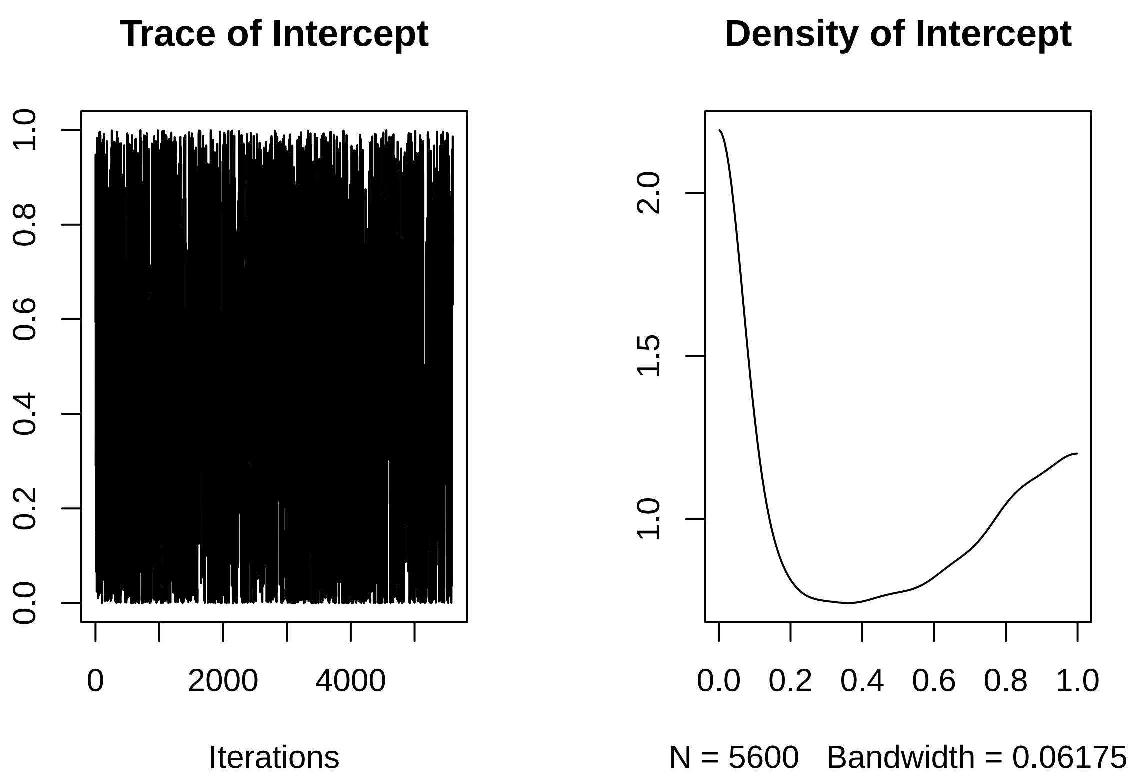
```
##
## Iterations = 1:5600
## Thinning interval = 1
## Number of chains = 1
## Sample size per chain = 5600
##
## 1. Empirical mean and standard deviation for each variable,
##    plus standard error of the mean:
##
##           Mean             SD       Naive SE Time-series SE
##       0.438764       0.327116       0.004371       0.009556
```

```
##
## 2. Quantiles for each variable:
##
##     2.5%      25%      50%      75%    97.5%
## 0.001222 0.120388 0.415223 0.739554 0.977682
```

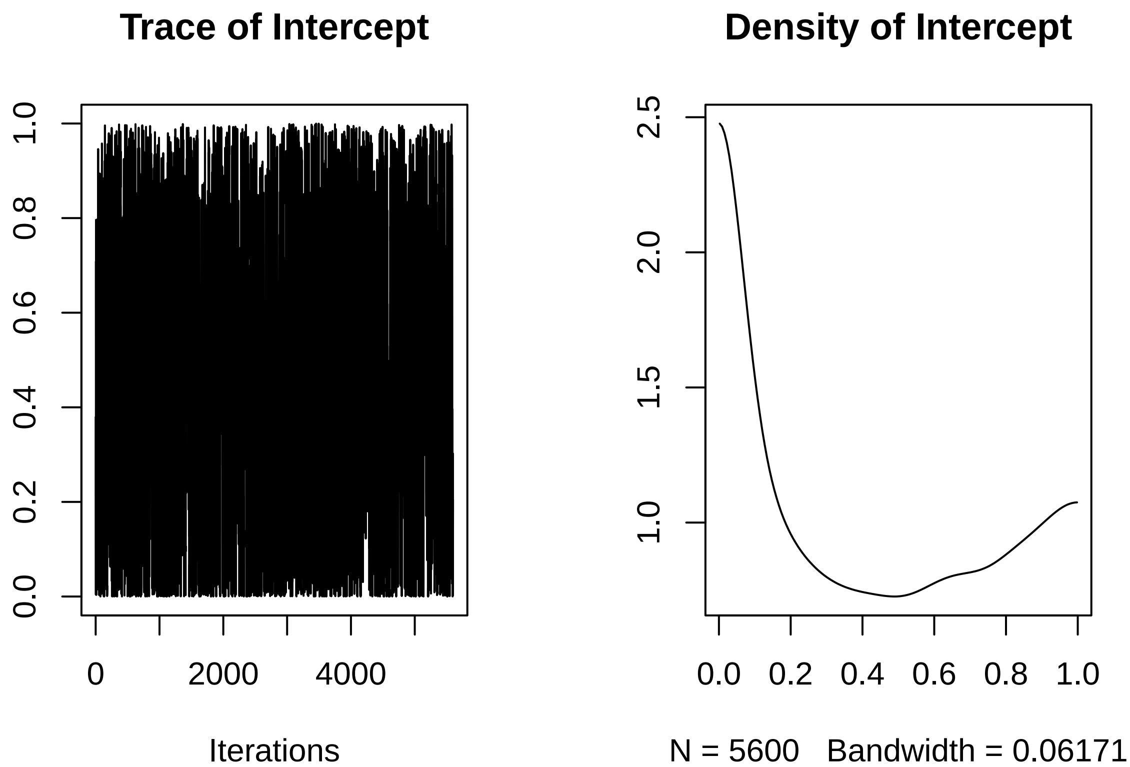
```r
summary(prop_v_raceme_87_frset)
```

```
##
## Iterations = 1:5600
## Thinning interval = 1
## Number of chains = 1
## Sample size per chain = 5600
##
## 1. Empirical mean and standard deviation for each variable,
##    plus standard error of the mean:
##
##           Mean             SD       Naive SE Time-series SE
##       0.084280       0.100843       0.001348       0.001486
##
## 2. Quantiles for each variable:
##
##      2.5%       25%       50%       75%     97.5%
## 0.0001082 0.0105237 0.0462467 0.1221818 0.3614010
```

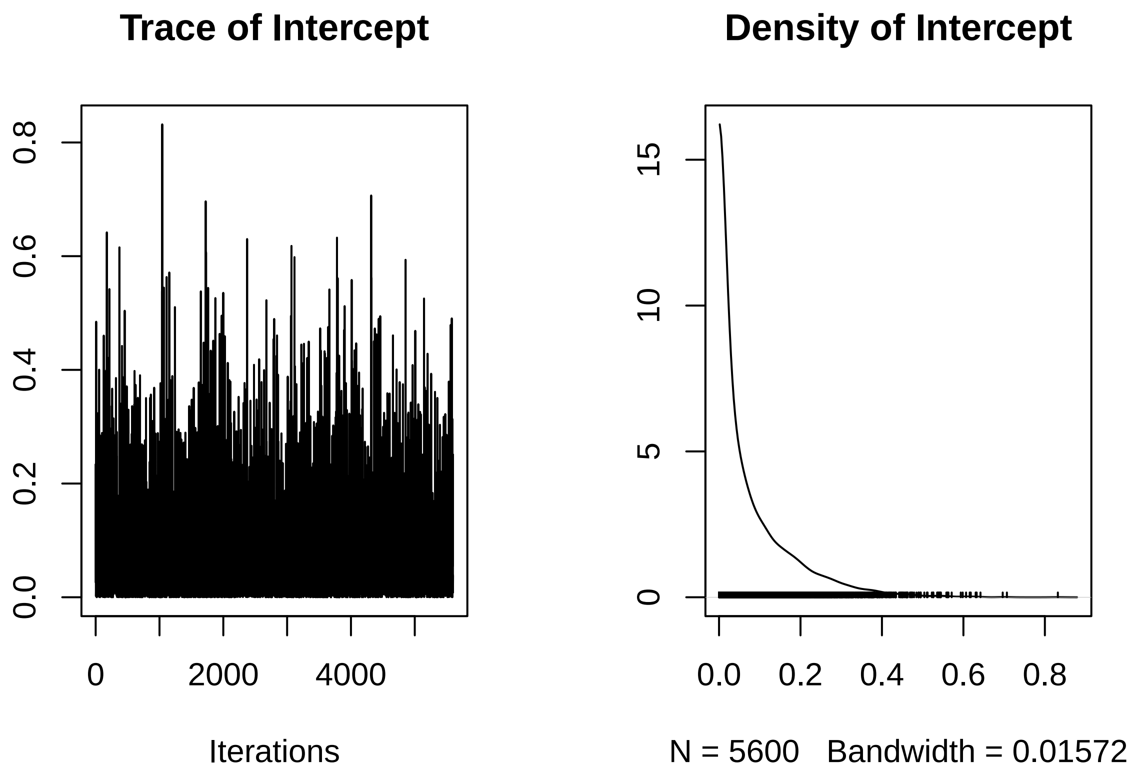
```r
plot(prop_v_id_87_frset)
```



```r
plot(prop_v_shoot_87_frset)
```




```r
plot(prop_v_raceme_87_frset)
```




```
v_id_88_frset <- (VarCorr(mod_within_among_frset_88, summary=FALSE)$id$sd)^2
v_shoot_88_frset <- (VarCorr(mod_within_among_frset_88,
                              summary=FALSE)$`id:shoot_id`$sd)^2
v_raceme_88_frset <- (VarCorr(mod_within_among_frset_88,
                               summary=FALSE)$`id:shoot_id:raceme_id`$sd)^2
v_flower_88_frset <- (VarCorr(mod_within_among_frset_88,
                               summary=FALSE)$residual$sd)^2
# No residual variance! OK?
prop_v_id_88_frset <- as.mcmc(v_id_88_frset /
                                 (v_id_88_frset + v_shoot_88_frset +
                                    v_raceme_88_frset))
prop_v_shoot_88_frset <- as.mcmc(v_shoot_88_frset /
                                    (v_id_88_frset + v_shoot_88_frset +
                                       v_raceme_88_frset))
prop_v_raceme_88_frset <- as.mcmc(v_raceme_88_frset /
                                     (v_id_88_frset + v_shoot_88_frset +
                                        v_raceme_88_frset))
summary(prop_v_id_88_frset)
```

```
##
## Iterations = 1:5600
## Thinning interval = 1
## Number of chains = 1
## Sample size per chain = 5600
##
```

```
## 1. Empirical mean and standard deviation for each variable,
##    plus standard error of the mean:
##
##           Mean             SD       Naive SE Time-series SE
##       0.866303       0.117894       0.001575       0.001877
##
## 2. Quantiles for each variable:
##
##   2.5%    25%    50%    75%  97.5%
## 0.5549 0.8118 0.8985 0.9546 0.9954
```

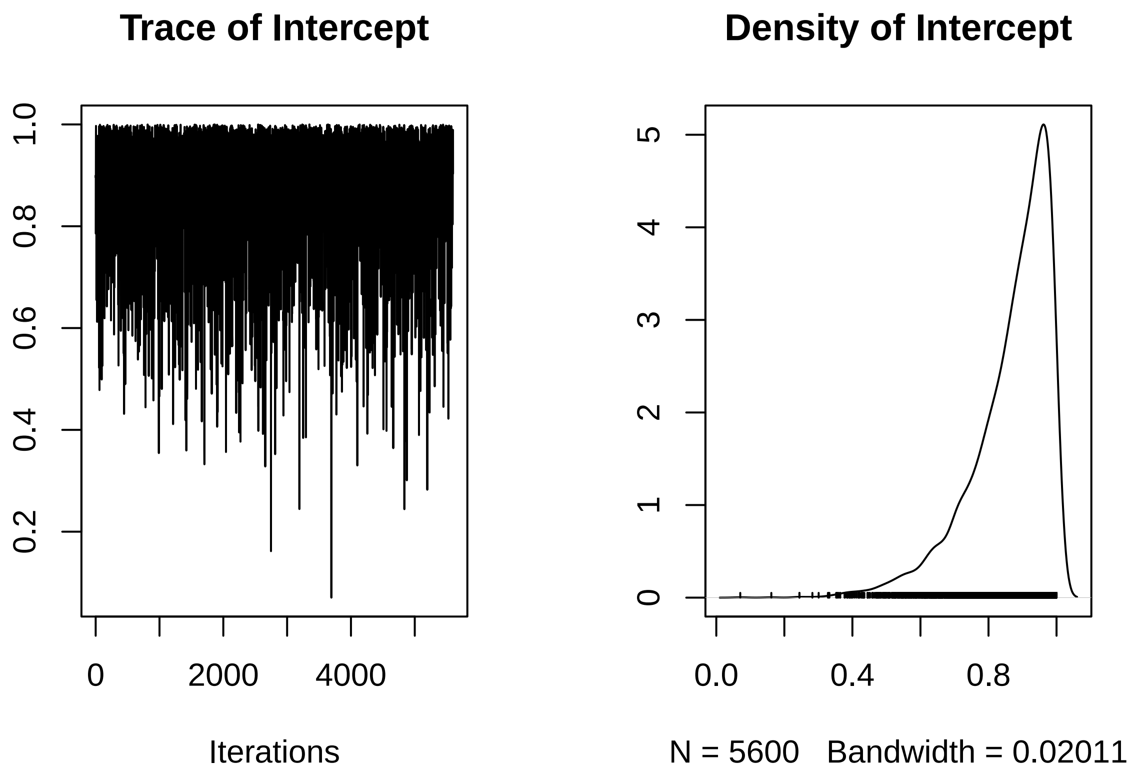
```
summary(prop_v_shoot_88_frset)
```

```
##
## Iterations = 1:5600
## Thinning interval = 1
## Number of chains = 1
## Sample size per chain = 5600
##
## 1. Empirical mean and standard deviation for each variable,
##    plus standard error of the mean:
##
##           Mean             SD       Naive SE Time-series SE
##       0.076484       0.097375       0.001301       0.001708
##
## 2. Quantiles for each variable:
##
##      2.5%       25%       50%       75%     97.5%
## 0.0001014 0.0096540 0.0383157 0.1068401 0.3514276
```

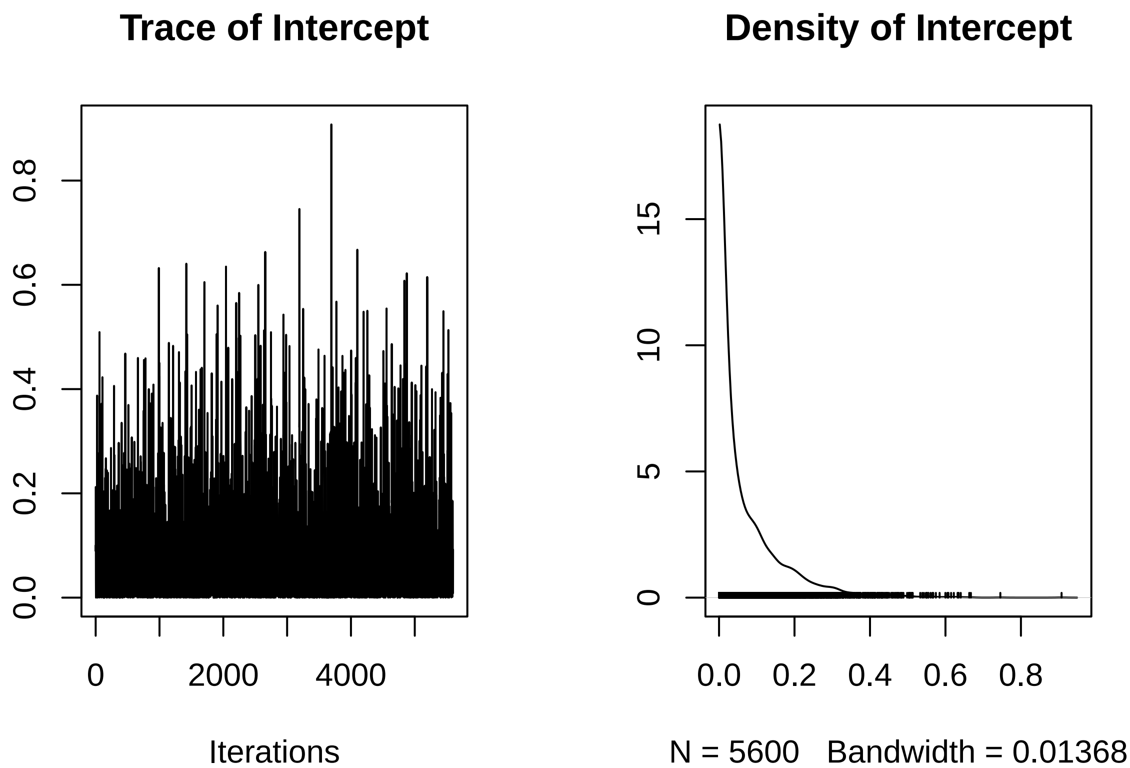
```
summary(prop_v_raceme_88_frset)
```

```
##
## Iterations = 1:5600
## Thinning interval = 1
## Number of chains = 1
## Sample size per chain = 5600
##
## 1. Empirical mean and standard deviation for each variable,
##    plus standard error of the mean:
##
##           Mean             SD       Naive SE Time-series SE
##      0.0572128      0.0725026      0.0009689      0.0010461
##
## 2. Quantiles for each variable:
##
##      2.5%       25%       50%       75%     97.5%
## 9.351e-05 6.849e-03 2.918e-02 7.983e-02 2.627e-01
```

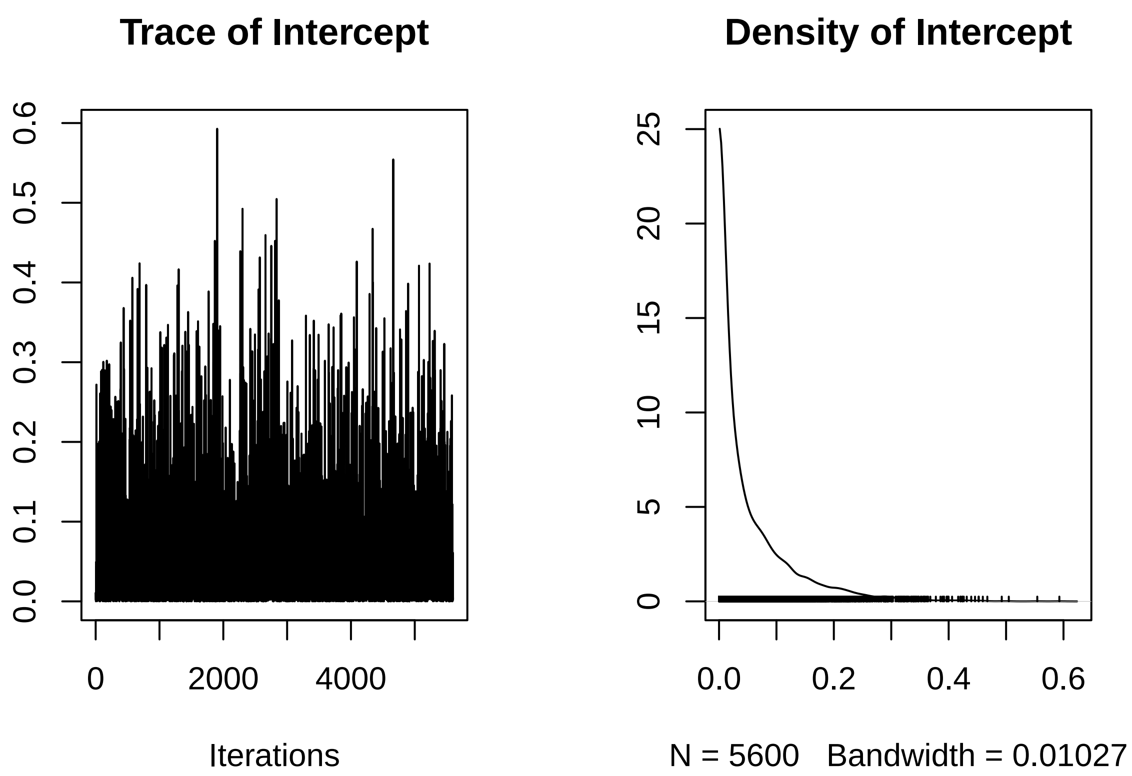
```
plot(prop_v_id_88_frset)
```




```
plot(prop_v_shoot_88_frset)
```




```
plot(prop_v_raceme_88_frset)
```




```
v_id_89_frset <- (VarCorr(mod_within_among_frset_89, summary=FALSE)$id$sd)^2
v_shoot_89_frset <- (VarCorr(mod_within_among_frset_89,
                              summary=FALSE)$`id:shoot_id`$sd)^2
v_raceme_89_frset <- (VarCorr(mod_within_among_frset_89,
                               summary=FALSE)$`id:shoot_id:raceme_id`$sd)^2
v_flower_89_frset <- (VarCorr(mod_within_among_frset_89,
                               summary=FALSE)$residual$sd)^2
# No residual variance! OK?
prop_v_id_89_frset <- as.mcmc(v_id_89_frset /
                                (v_id_89_frset + v_shoot_89_frset +
                                   v_raceme_89_frset))
prop_v_shoot_89_frset <- as.mcmc(v_shoot_89_frset /
                                   (v_id_89_frset + v_shoot_89_frset +
                                      v_raceme_89_frset))
prop_v_raceme_89_frset <- as.mcmc(v_raceme_89_frset /
                                    (v_id_89_frset + v_shoot_89_frset +
                                       v_raceme_89_frset))
summary(prop_v_id_89_frset)
```

```
##
## Iterations = 1:5600
## Thinning interval = 1
## Number of chains = 1
## Sample size per chain = 5600
##
```

```
## 1. Empirical mean and standard deviation for each variable,
##    plus standard error of the mean:
##
##           Mean             SD       Naive SE Time-series SE
##       0.655696       0.281758       0.003765       0.005766
##
## 2. Quantiles for each variable:
##
##    2.5%     25%     50%     75%   97.5%
## 0.02311 0.47795 0.73596 0.88823 0.98925
```

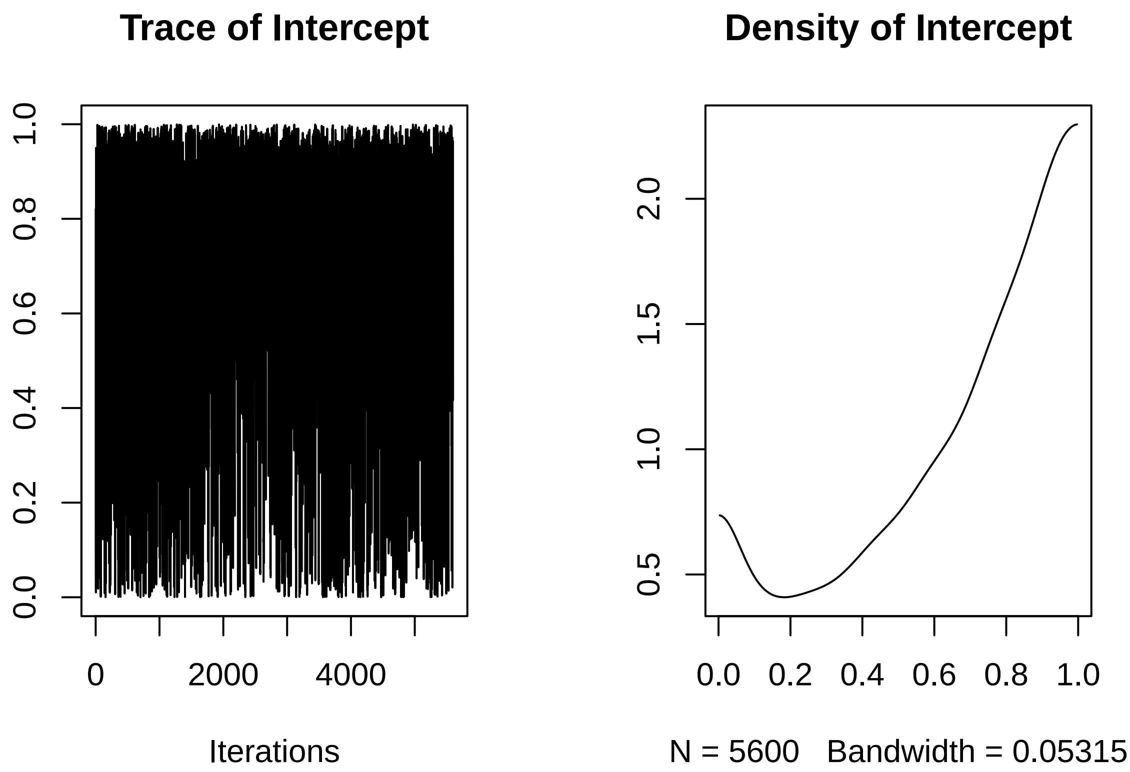
```r
summary(prop_v_shoot_89_frset)
```

```
##
## Iterations = 1:5600
## Thinning interval = 1
## Number of chains = 1
## Sample size per chain = 5600
##
## 1. Empirical mean and standard deviation for each variable,
##    plus standard error of the mean:
##
##           Mean             SD       Naive SE Time-series SE
##       0.264415       0.273355       0.003653       0.005714
##
## 2. Quantiles for each variable:
##
##     2.5%      25%      50%      75%    97.5%
## 0.000371 0.039216 0.161211 0.420806 0.923928
```

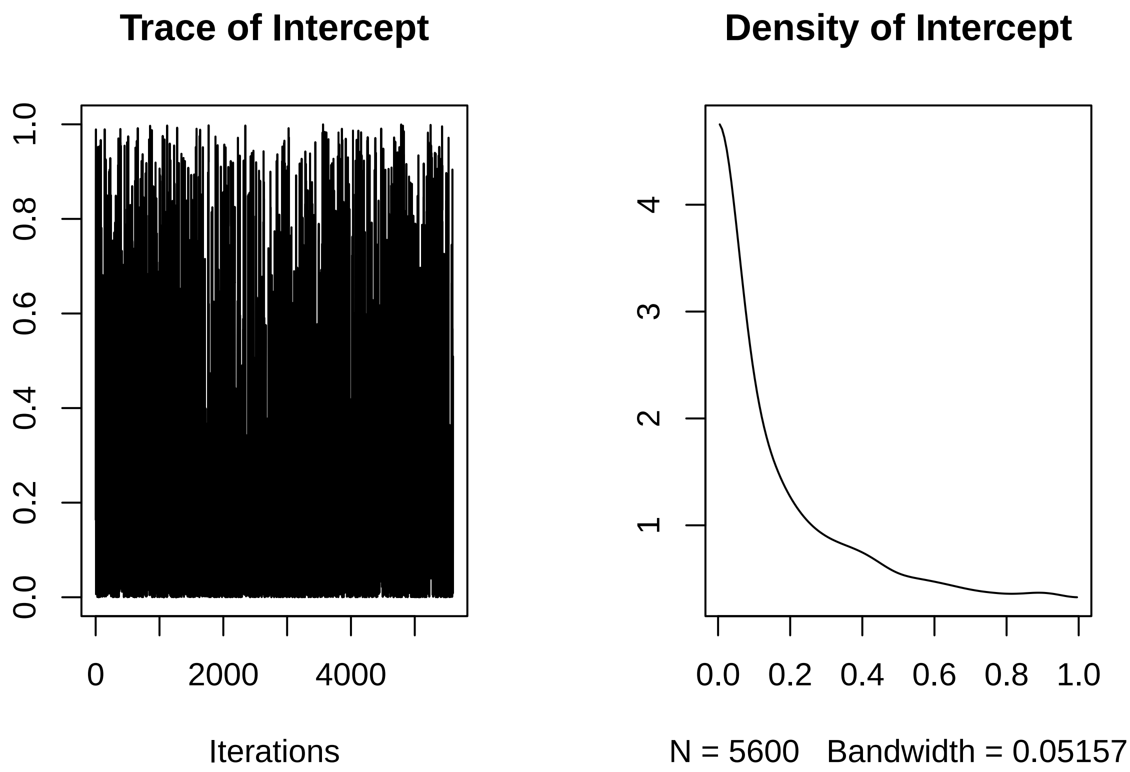
```r
summary(prop_v_raceme_89_frset)
```

```
##
## Iterations = 1:5600
## Thinning interval = 1
## Number of chains = 1
## Sample size per chain = 5600
##
## 1. Empirical mean and standard deviation for each variable,
##    plus standard error of the mean:
##
##           Mean             SD       Naive SE Time-series SE
##       0.079888       0.099770       0.001333       0.001374
##
## 2. Quantiles for each variable:
##
##      2.5%       25%       50%       75%     97.5%
## 0.0001039 0.0093747 0.0404745 0.1152912 0.3525675
```

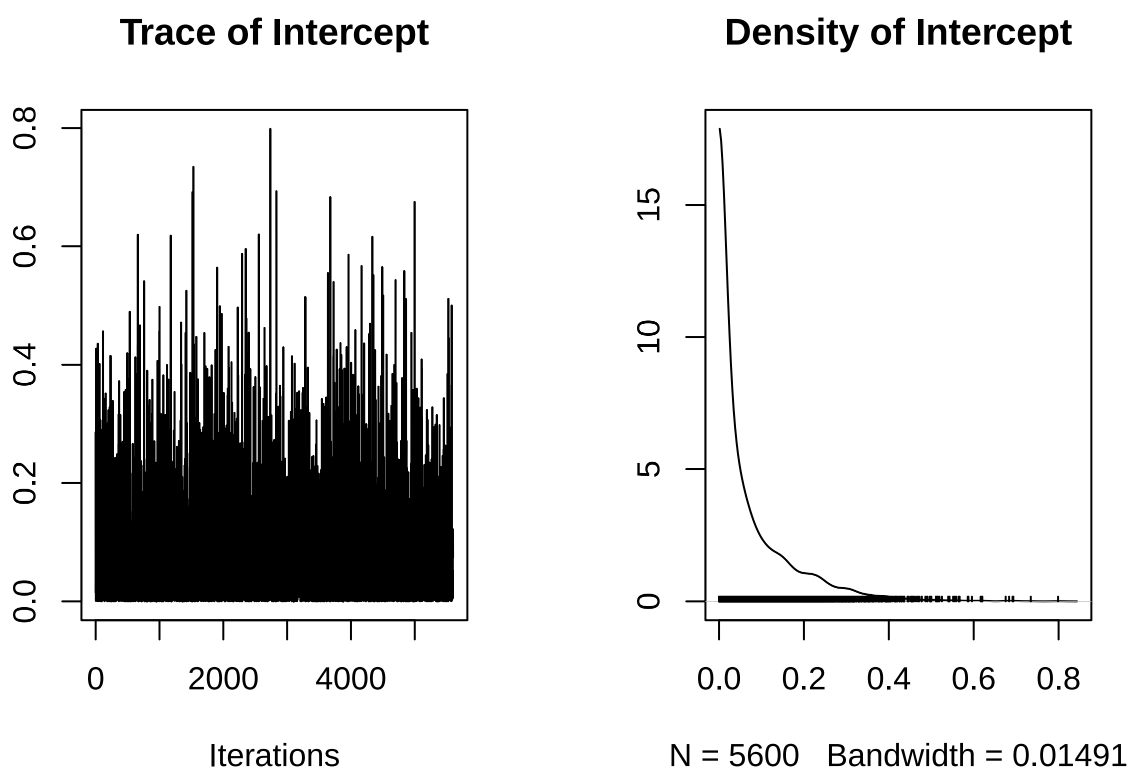
```r
plot(prop_v_id_89_frset)
```




```r
plot(prop_v_shoot_89_frset)
```




```r
plot(prop_v_raceme_89_frset)
```

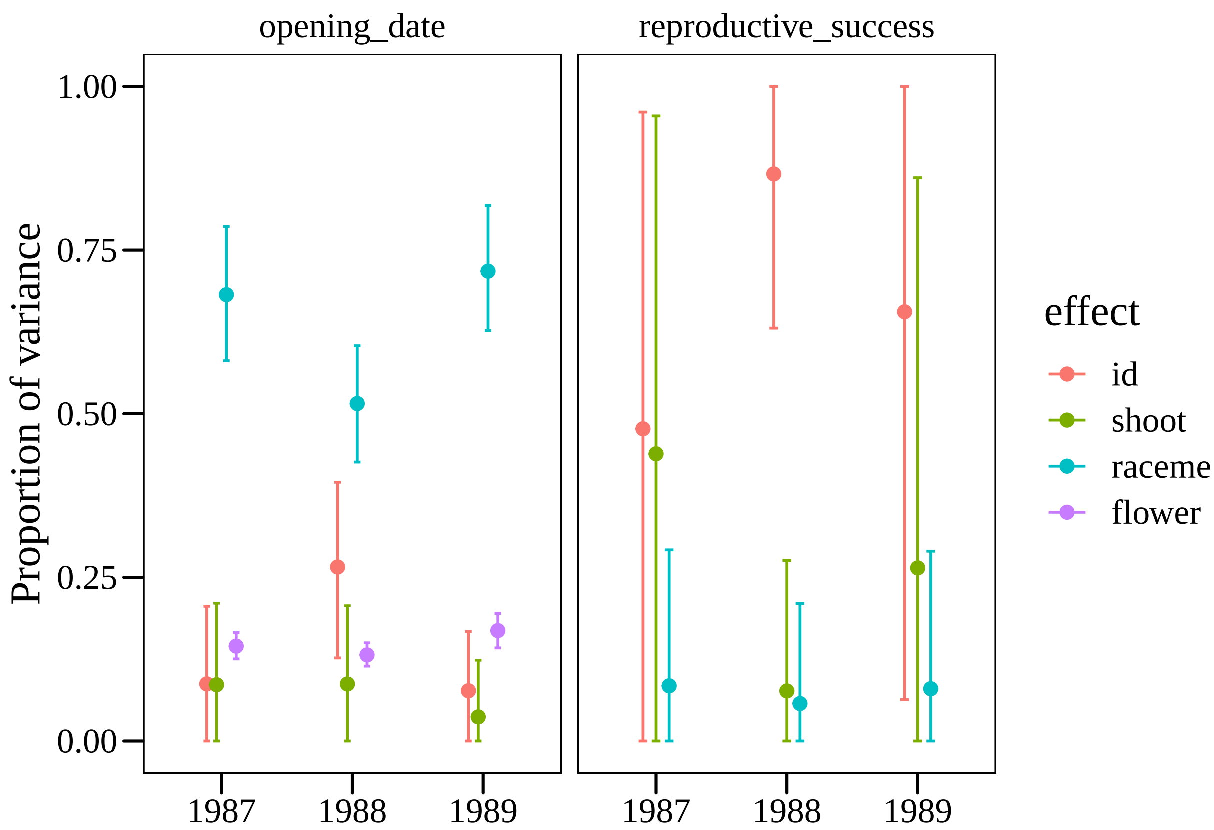



```
data_props_87_frset<-full_join(
  cbind(data.frame(id_mean=summary(prop_v_id_87_frset)$statistics[1]),
        data.frame(shoot_mean=summary(prop_v_shoot_87_frset)$statistics[1]),
        data.frame(raceme_mean=summary(prop_v_raceme_87_frset)$statistics[1]))%>%
    pivot_longer(cols=c("id_mean","shoot_mean","raceme_mean"),
                 names_to="effect",values_to="mean",names_pattern="(.*)_mean"),
  cbind(data.frame(id_lower=coda::HPDinterval(prop_v_id_87_frset)[1],
                   id_upper=coda::HPDinterval(prop_v_id_87_frset)[2]),
        data.frame(shoot_lower=coda::HPDinterval(prop_v_shoot_87_frset)[1],
                   shoot_upper=coda::HPDinterval(prop_v_shoot_87_frset)[2]),
        data.frame(raceme_lower=coda::HPDinterval(prop_v_raceme_87_frset)[1],
                   raceme_upper=coda::HPDinterval(prop_v_raceme_87_frset)[2]))%>%
    pivot_longer(cols=c("id_lower","id_upper",
                        "shoot_lower","shoot_upper",
                        "raceme_lower","raceme_upper"),
                 names_to=c("effect","cat"),names_sep="_",values_to="value")%>%
    pivot_wider(names_from="cat",values_from="value"))%>%
  mutate(year=1987)
data_props_88_frset<-full_join(
  cbind(data.frame(id_mean=summary(prop_v_id_88_frset)$statistics[1]),
        data.frame(shoot_mean=summary(prop_v_shoot_88_frset)$statistics[1]),
        data.frame(raceme_mean=summary(prop_v_raceme_88_frset)$statistics[1]))%>%
    pivot_longer(cols=c("id_mean","shoot_mean","raceme_mean"),
                 names_to="effect",values_to="mean",names_pattern="(.*)_mean"),
  cbind(data.frame(id_lower=coda::HPDinterval(prop_v_id_88_frset)[1],
                   id_upper=coda::HPDinterval(prop_v_id_88_frset)[2]),
```

```
       data.frame(shoot_lower=coda::HPDinterval(prop_v_shoot_88_frset)[1],
                  shoot_upper=coda::HPDinterval(prop_v_shoot_88_frset)[2]),
       data.frame(raceme_lower=coda::HPDinterval(prop_v_raceme_88_frset)[1],
                  raceme_upper=coda::HPDinterval(prop_v_raceme_88_frset)[2]))%>%
    pivot_longer(cols=c("id_lower","id_upper",
                        "shoot_lower","shoot_upper",
                        "raceme_lower","raceme_upper"),
                 names_to=c("effect","cat"),names_sep="_",values_to="value")%>%
    pivot_wider(names_from="cat",values_from="value"))%>%
  mutate(year=1988)
data_props_89_frset<-full_join(
  cbind(data.frame(id_mean=summary(prop_v_id_89_frset)$statistics[1]),
        data.frame(shoot_mean=summary(prop_v_shoot_89_frset)$statistics[1]),
        data.frame(raceme_mean=summary(prop_v_raceme_89_frset)$statistics[1]))%>%
    pivot_longer(cols=c("id_mean","shoot_mean","raceme_mean"),
                 names_to="effect",values_to="mean",names_pattern="(.*)_mean"),
  cbind(data.frame(id_lower=coda::HPDinterval(prop_v_id_89_frset)[1],
                  id_upper=coda::HPDinterval(prop_v_id_89_frset)[2]),
        data.frame(shoot_lower=coda::HPDinterval(prop_v_shoot_89_frset)[1],
                  shoot_upper=coda::HPDinterval(prop_v_shoot_89_frset)[2]),
        data.frame(raceme_lower=coda::HPDinterval(prop_v_raceme_89_frset)[1],
                  raceme_upper=coda::HPDinterval(prop_v_raceme_89_frset)[2]))%>%
    pivot_longer(cols=c("id_lower","id_upper",
                        "shoot_lower","shoot_upper",
                        "raceme_lower","raceme_upper"),
                 names_to=c("effect","cat"),names_sep="_",values_to="value")%>%
    pivot_wider(names_from="cat",values_from="value"))%>%
  mutate(year=1989)
data_props_frset<-rbind(data_props_87_frset,
                        data_props_88_frset,
                        data_props_89_frset)%>%
  mutate(year=factor(year),
         effect=factor(effect,levels=c("id","shoot","raceme")))
```

Figure 2

```
ggplot(rbind(data_props%>%mutate(type="opening_date"),
             data_props_frset%>%mutate(type="reproductive_success"))%>%
         mutate(type=factor(type,
                            levels=c("opening_date","reproductive_success"))),
       aes(x=year,y=mean,ymin=lower,ymax=upper,
                  color=effect))+
  geom_errorbar(linewidth=0.5,width=0.2,position=position_dodge(0.3))+
  geom_point(size=2,position=position_dodge(0.3))+facet_wrap(~type)+
  my_theme_legend()+xlab(NULL)+ylab("Proportion of variance")
```




```
ggsave(filename="output/figures/fig2.tiff",
       width=22,height=10,units="cm",dpi=300)
```

Q2: Effects of flower position on flowering phenology

Does opening date of individual flowers depend on flower position within and among the racemes?

H: We expect that basal flowers open earlier than distal flowers within the raceme, and that flowers on basal racemes open earlier than flowers on distal racemes.

```
mod_phen_87<-glmmTMB(opening_date_v~relpos_fl*relpos_rac+
                       (1|id/shoot_id/raceme_id),
               subset(data_id_flowers,year==1987))
mod_phen_88<-glmmTMB(opening_date_v~relpos_fl*relpos_rac+
                       (1|id/shoot_id/raceme_id),
               subset(data_id_flowers,year==1988))
mod_phen_89<-glmmTMB(opening_date_v~relpos_fl*relpos_rac+
                       (1|id/shoot_id/raceme_id),
               subset(data_id_flowers,year==1989))
# OK with random factors and nesting?
summary(mod_phen_87)
```

```
##  Family: gaussian  ( identity )
## Formula:
```

```
## opening_date_v ~ relpos_fl * relpos_rac + (1 | id/shoot_id/raceme_id)
## Data: subset(data_id_flowers, year == 1987)
##
##      AIC      BIC   logLik deviance df.resid
##   7615.7   7660.1  -3799.8   7599.7     1905
##
## Random effects:
##
## Conditional model:
##  Groups                 Name        Variance Std.Dev.
##  raceme_id:shoot_id:id (Intercept)  4.160   2.040
##  shoot_id:id           (Intercept) 11.040   3.323
##  id                    (Intercept)  3.796   1.948
##  Residual                           1.290   1.136
## Number of obs: 1913, groups:
## raceme_id:shoot_id:id, 481; shoot_id:id, 239; id, 231
##
## Dispersion estimate for gaussian family (sigma^2): 1.29
##
## Conditional model:
##                      Estimate Std. Error z value Pr(>|z|)
## (Intercept)           60.0677     0.4202  142.94  < 2e-16 ***
## relpos_fl              5.4989     0.3196   17.20  < 2e-16 ***
## relpos_rac            15.3382     0.6509   23.57  < 2e-16 ***
## relpos_fl:relpos_rac   2.4474     0.6785    3.61  0.00031 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```r
summary(mod_phen_88)
```

```
##  Family: gaussian  ( identity )
## Formula:
## opening_date_v ~ relpos_fl * relpos_rac + (1 | id/shoot_id/raceme_id)
## Data: subset(data_id_flowers, year == 1988)
##
##      AIC      BIC   logLik deviance df.resid
##   9783.6   9830.3  -4883.8   9767.6     2513
##
## Random effects:
##
## Conditional model:
##  Groups                 Name        Variance Std.Dev.
##  raceme_id:shoot_id:id (Intercept)  2.221   1.490
##  shoot_id:id           (Intercept) 10.015   3.165
##  id                    (Intercept)  7.347   2.711
##  Residual                           1.214   1.102
## Number of obs: 2521, groups:
## raceme_id:shoot_id:id, 642; shoot_id:id, 337; id, 232
##
## Dispersion estimate for gaussian family (sigma^2): 1.21
##
## Conditional model:
##                      Estimate Std. Error z value Pr(>|z|)
## (Intercept)           53.7874     0.3538  152.04  < 2e-16 ***
```

```
## relpos_fl              6.9119     0.2765   25.00  < 2e-16 ***
## relpos_rac            15.2002     0.4731   32.13  < 2e-16 ***
## relpos_fl:relpos_rac  -2.5349     0.5792   -4.38  1.2e-05 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```r
summary(mod_phen_89)
```

```
##  Family: gaussian  ( identity )
## Formula:
## opening_date_v ~ relpos_fl * relpos_rac + (1 | id/shoot_id/raceme_id)
## Data: subset(data_id_flowers, year == 1989)
##
##      AIC      BIC   logLik deviance df.resid
##   5402.3   5444.6  -2693.2   5386.3     1441
##
## Random effects:
##
## Conditional model:
##  Groups                Name        Variance Std.Dev.
##  raceme_id:shoot_id:id (Intercept) 2.451    1.565
##  shoot_id:id           (Intercept) 6.388    2.527
##  id                    (Intercept) 2.211    1.487
##  Residual                          1.233    1.110
## Number of obs: 1449, groups:
## raceme_id:shoot_id:id, 317; shoot_id:id, 135; id, 95
##
## Dispersion estimate for gaussian family (sigma^2): 1.23
##
## Conditional model:
##                      Estimate Std. Error z value Pr(>|z|)
## (Intercept)           47.2051     0.4178  112.99  < 2e-16 ***
## relpos_fl              7.2003     0.3343   21.54  < 2e-16 ***
## relpos_rac            17.1235     0.6106   28.04  < 2e-16 ***
## relpos_fl:relpos_rac  -2.5454     0.7012   -3.63 0.000283 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

Interaction significant in all years.

Table 1

```r
tab_model(mod_phen_87,mod_phen_88,mod_phen_89,
          transform=NULL,show.intercept=F,show.ci=F,show.se=T,show.stat=T,
          show.r2=T,show.icc=F,show.re.var=F,show.ngroups=F,digits=3,
          dv.labels=c("1987","1988","1989"),
          file="output/tables/Table1.doc")
```

1987

1988

1989

Predictors

Estimates

std. Error

Statistic

p

Estimates

std. Error

Statistic

p

Estimates

std. Error

Statistic

p

relpos fl

5.499

0.320

17.204

<0.001

6.912

0.277

24.995

<0.001

7.200

0.334

21.540

<0.001

relpos rac

15.338

0.651

23.566

<0.001

15.200

0.473

32.128

<0.001

17.124

0.611

28.044

<0.001

relpos fl × relpos rac

2.447

0.679

3.607

<0.001

-2.535

0.579

-4.377

<0.001

-2.545

0.701

-3.630

<0.001

Observations

1913

2521

1449

Marginal R2 / Conditional R2

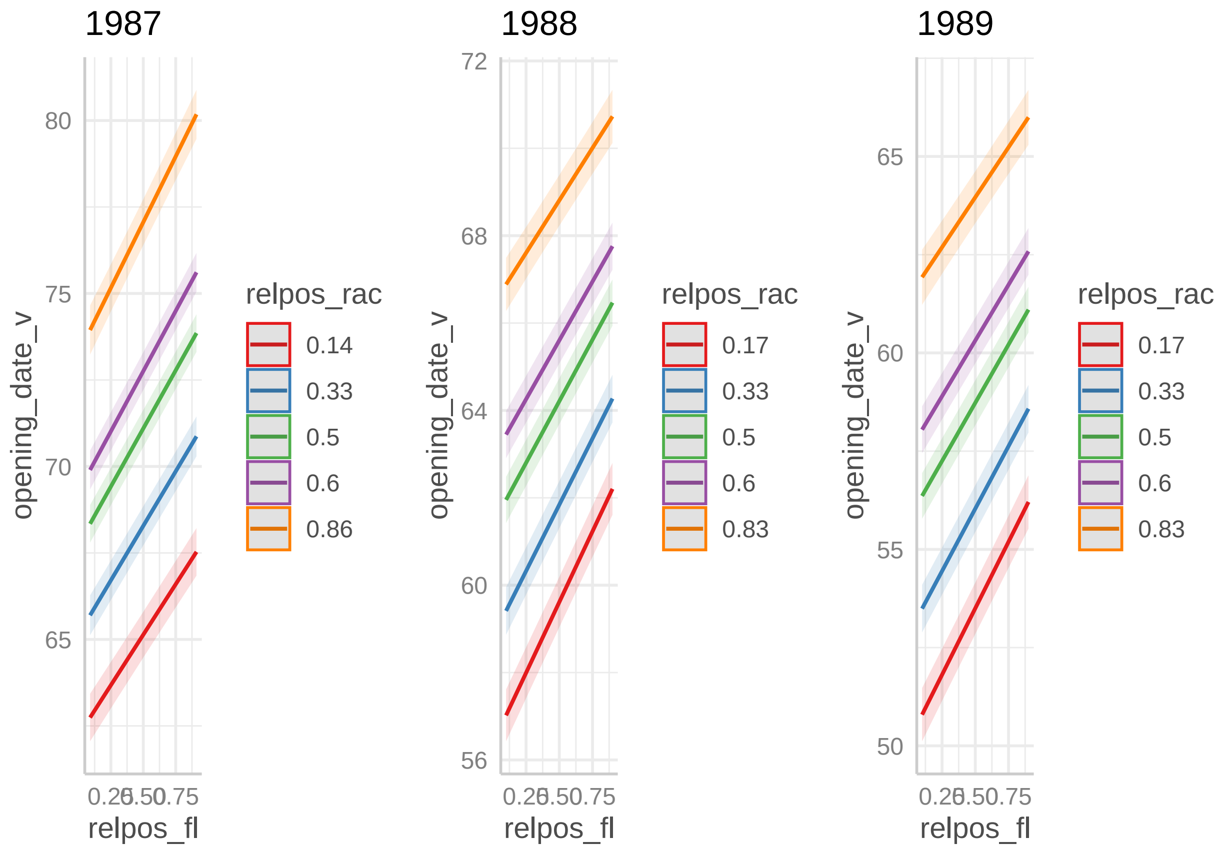
0.340 / 0.958

0.261 / 0.957

0.459 / 0.946

Figure 3

```
fig3<-grid.arrange(
  plot(ggpredict(mod_phen_87,terms=c("relpos_fl[quart]","relpos_rac[quart]")))+
    ggtitle("1987"),
  plot(ggpredict(mod_phen_88,terms=c("relpos_fl[quart]","relpos_rac[quart]")))+
    ggtitle("1988"),
  plot(ggpredict(mod_phen_89,terms=c("relpos_fl[quart]","relpos_rac[quart]")))+
    ggtitle("1989"),
  ncol=3)
```




```
ggsave(filename="output/figures/fig3.tiff",plot=fig3,
       width=28,height=8,units="cm",dpi=300)
```

Basal flowers (lower relpos_fl) open earlier than distal flowers within the raceme. Flowers on basal racemes (lower relpos_rac) open earlier than flowers on distal racemes.

Basal flowers on basal racemes (lower relpos_fl and lower relpos_rac) open the earliest, and distal flowers on distal racemes (higher relpos_fl and higher relpos_rac) open the latest.

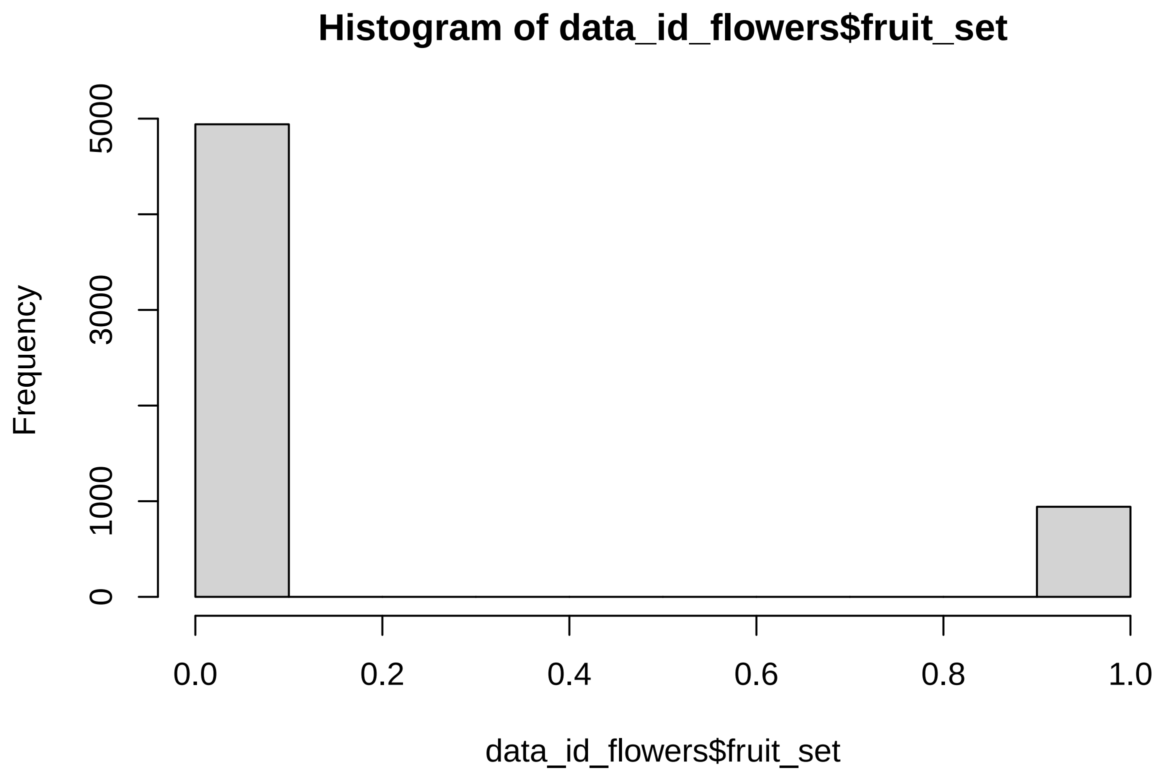
Q3: Effects of flower position on reproductive success

Does reproductive success of individual flowers depend on flower position within and among the racemes, and are effects of flower position due to different resource accessibility or to different phenologies of individual flowers?

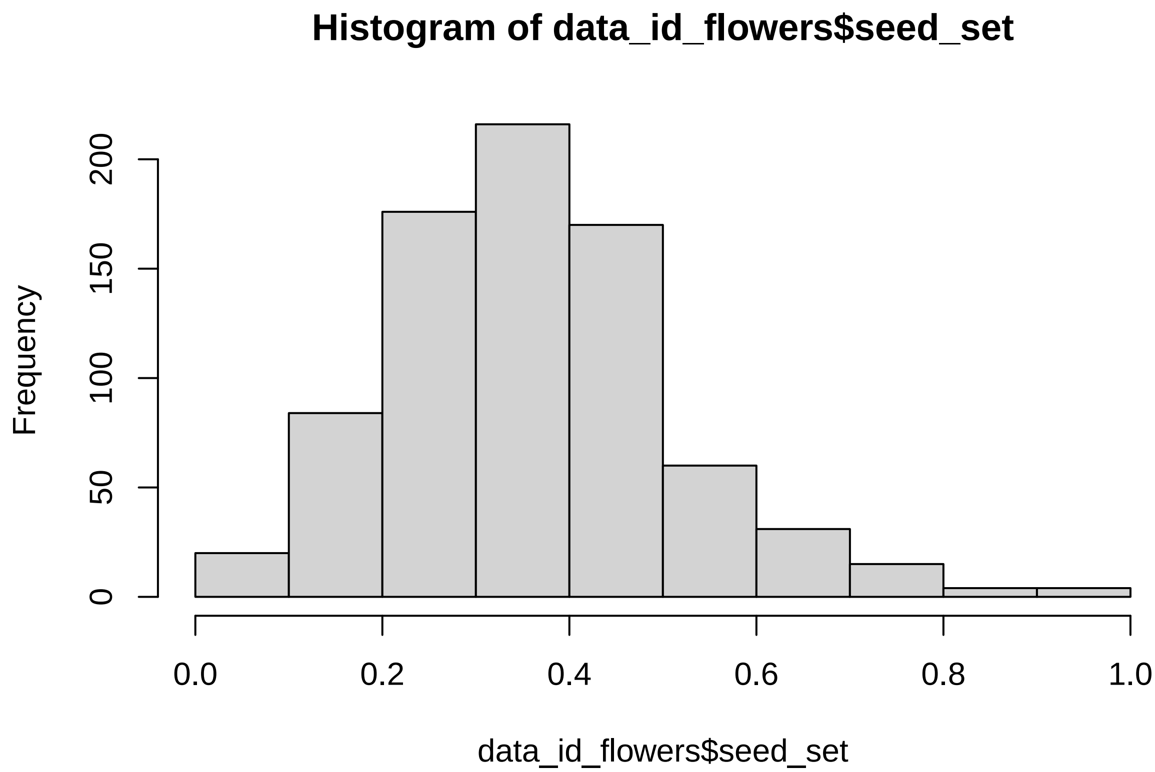
H: We expect that basal flowers have a higher probability of initiating and setting fruit and a higher seed set than distal flowers within the raceme, and that flowers on basal racemes have a higher probability of initiating and setting fruit and a higher seed set than flowers on distal racemes. We expect that effects of flower position on reproductive success are both due to different resource accessibility and to different phenologies of individual flowers.

Check distributions:

```
hist(data_id_flowers$fruit_set)
```




```
hist(data_id_flowers$seed_set)
```



Probability of initiating fruit

Without phenology

```
mod_frinit_87<-glmmTMB(initiated_fr~relpos_fl*relpos_rac+
                         (1|id/shoot_id/raceme_id),
                       subset(data_id_flowers,year==1987),family="binomial")
mod_frinit_88<-glmmTMB(initiated_fr~relpos_fl*relpos_rac+
                         (1|id/shoot_id/raceme_id),
                       subset(data_id_flowers,year==1988),family="binomial")
mod_frinit_89<-glmmTMB(initiated_fr~relpos_fl*relpos_rac+
                         (1|id/shoot_id/raceme_id),
                       subset(data_id_flowers,year==1989),family="binomial")
# OK with random factors and nesting?
summary(mod_frinit_87)
```

```
##  Family: binomial  ( logit )
## Formula:
## initiated_fr ~ relpos_fl * relpos_rac + (1 | id/shoot_id/raceme_id)
## Data: subset(data_id_flowers, year == 1987)
##
##      AIC      BIC   logLik deviance df.resid
##   2134.4   2173.3  -1060.2   2120.4     1906
```

```
##
## Random effects:
##
## Conditional model:
##  Groups                 Name        Variance  Std.Dev.
##  raceme_id:shoot_id:id (Intercept) 1.259e+00 1.1220413
##  shoot_id:id           (Intercept) 2.150e+00 1.4661726
##  id                    (Intercept) 5.333e-07 0.0007303
## Number of obs: 1913, groups:
## raceme_id:shoot_id:id, 481; shoot_id:id, 239; id, 231
##
## Conditional model:
##                      Estimate Std. Error z value Pr(>|z|)
## (Intercept)            4.5977     0.5359   8.580  < 2e-16 ***
## relpos_fl             -4.9525     0.8429  -5.875 4.22e-09 ***
## relpos_rac            -5.2110     1.0156  -5.131 2.88e-07 ***
## relpos_fl:relpos_rac   2.1153     1.7007   1.244    0.214
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
summary(mod_frinit_88)
```

```
##  Family: binomial  ( logit )
## Formula:
## initiated_fr ~ relpos_fl * relpos_rac + (1 | id/shoot_id/raceme_id)
## Data: subset(data_id_flowers, year == 1988)
##
##      AIC      BIC   logLik deviance df.resid
##   2917.7   2958.5  -1451.9   2903.7     2514
##
## Random effects:
##
## Conditional model:
##  Groups                 Name        Variance Std.Dev.
##  raceme_id:shoot_id:id (Intercept) 1.3541   1.1636
##  shoot_id:id           (Intercept) 0.3962   0.6294
##  id                    (Intercept) 1.4749   1.2145
## Number of obs: 2521, groups:
## raceme_id:shoot_id:id, 642; shoot_id:id, 337; id, 232
##
## Conditional model:
##                      Estimate Std. Error z value Pr(>|z|)
## (Intercept)            2.6154     0.4329   6.041 1.53e-09 ***
## relpos_fl             -1.5654     0.6781  -2.308   0.0210 *
## relpos_rac            -1.5645     0.8357  -1.872   0.0612 .
## relpos_fl:relpos_rac  -2.7645     1.4092  -1.962   0.0498 *
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
summary(mod_frinit_89)
```

```
##  Family: binomial  ( logit )
## Formula:
```

```
## initiated_fr ~ relpos_fl * relpos_rac + (1 | id/shoot_id/raceme_id)
## Data: subset(data_id_flowers, year == 1989)
##
##      AIC      BIC   logLik deviance df.resid
##   1656.1   1693.1   -821.1   1642.1     1442
##
## Random effects:
##
## Conditional model:
##  Groups                 Name        Variance Std.Dev.
##  raceme_id:shoot_id:id (Intercept) 1.0108   1.0054
##  shoot_id:id           (Intercept) 0.7798   0.8831
##  id                    (Intercept) 0.6365   0.7978
## Number of obs: 1449, groups:
## raceme_id:shoot_id:id, 317; shoot_id:id, 135; id, 95
##
## Conditional model:
##                       Estimate Std. Error z value Pr(>|z|)
## (Intercept)           2.147168   0.506751   4.237 2.26e-05 ***
## relpos_fl             0.003934   0.796142   0.005 0.996057
## relpos_rac           -0.796483   0.980811  -0.812 0.416754
## relpos_fl:relpos_rac -5.563312   1.678277  -3.315 0.000917 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

Interaction only significant in 1989 (marginally significant in 1988). Refit models for 1987 and 1988 without interaction.

```r
mod_frinit_87<-glmmTMB(initiated_fr~relpos_fl+relpos_rac+
                      (1|id/shoot_id/raceme_id),
                    subset(data_id_flowers,year==1987),family="binomial")
mod_frinit_88<-glmmTMB(initiated_fr~relpos_fl+relpos_rac+
                      (1|id/shoot_id/raceme_id),
                    subset(data_id_flowers,year==1988),family="binomial")
# OK with random factors and nesting?
summary(mod_frinit_87)
```

```
##  Family: binomial  ( logit )
## Formula:
## initiated_fr ~ relpos_fl + relpos_rac + (1 | id/shoot_id/raceme_id)
## Data: subset(data_id_flowers, year == 1987)
##
##      AIC      BIC   logLik deviance df.resid
##   2133.9   2167.3  -1061.0   2121.9     1907
##
## Random effects:
##
## Conditional model:
##  Groups                 Name        Variance  Std.Dev.
##  raceme_id:shoot_id:id (Intercept) 1.256e+00 1.1207451
##  shoot_id:id           (Intercept) 2.142e+00 1.4636946
##  id                    (Intercept) 4.012e-07 0.0006334
## Number of obs: 1913, groups:
```

```
## raceme_id:shoot_id:id, 481; shoot_id:id, 239; id, 231
##
## Conditional model:
##             Estimate Std. Error z value Pr(>|z|)
## (Intercept)   4.0973     0.3439  11.916  < 2e-16 ***
## relpos_fl    -3.9895     0.3134 -12.732  < 2e-16 ***
## relpos_rac   -4.1281     0.5093  -8.106 5.23e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
summary(mod_frinit_88)
```

```
##  Family: binomial  ( logit )
## Formula:
## initiated_fr ~ relpos_fl + relpos_rac + (1 | id/shoot_id/raceme_id)
## Data: subset(data_id_flowers, year == 1988)
##
##      AIC      BIC   logLik deviance df.resid
##   2919.6   2954.6  -1453.8   2907.6     2515
##
## Random effects:
##
## Conditional model:
##  Groups                Name        Variance Std.Dev.
##  raceme_id:shoot_id:id (Intercept) 1.3429   1.1588
##  shoot_id:id           (Intercept) 0.3965   0.6297
##  id                    (Intercept) 1.4645   1.2101
## Number of obs: 2521, groups:
## raceme_id:shoot_id:id, 642; shoot_id:id, 337; id, 232
##
## Conditional model:
##             Estimate Std. Error z value Pr(>|z|)
## (Intercept)   3.2512     0.2943  11.049  < 2e-16 ***
## relpos_fl    -2.8171     0.2464 -11.435  < 2e-16 ***
## relpos_rac   -2.9623     0.4447  -6.661 2.72e-11 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

Basal flowers (lower relpos_fl) have a higher probability of initiating fruit than distal flowers within the raceme. Flowers on basal racemes (lower relpos_rac) have a higher probability of initiating fruit than flowers on distal racemes. In 1989, basal flowers on basal racemes (lower relpos_fl and lower relpos_rac) have the highest probabilities of initiating fruit, and distal flowers on distal racemes (higher relpos_fl and higher relpos_rac) the lowest.

With phenology

Fit the same models as before but including opening_date_v.

```
mod_frinit_phen_87<-glmmTMB(initiated_fr~relpos_fl+relpos_rac+opening_date_v+
                      (1|id/shoot_id/raceme_id),
                    subset(data_id_flowers,year==1987),family="binomial")
mod_frinit_phen_88<-glmmTMB(initiated_fr~relpos_fl+relpos_rac+opening_date_v+
```

```r
                      (1|id/shoot_id/raceme_id),
                    subset(data_id_flowers,year==1988),family="binomial")
mod_frinit_phen_89<-glmmTMB(initiated_fr~relpos_fl*relpos_rac+opening_date_v+
                      (1|id/shoot_id/raceme_id),
                    subset(data_id_flowers,year==1989),family="binomial")
# OK with random factors and nesting?
summary(mod_frinit_phen_87)
```

```
##  Family: binomial  ( logit )
## Formula:
## initiated_fr ~ relpos_fl + relpos_rac + opening_date_v + (1 |
##     id/shoot_id/raceme_id)
## Data: subset(data_id_flowers, year == 1987)
##
##      AIC      BIC   logLik deviance df.resid
##   2073.9   2112.8  -1030.0   2059.9     1906
##
## Random effects:
##
## Conditional model:
##  Groups                Name        Variance Std.Dev.
##  raceme_id:shoot_id:id (Intercept) 1.01842  1.0092
##  shoot_id:id           (Intercept) 0.03901  0.1975
##  id                    (Intercept) 1.68507  1.2981
## Number of obs: 1913, groups:
## raceme_id:shoot_id:id, 481; shoot_id:id, 239; id, 231
##
## Conditional model:
##                Estimate Std. Error z value Pr(>|z|)
## (Intercept)    15.92000    1.61459   9.860  < 2e-16 ***
## relpos_fl      -2.62770    0.33148  -7.927 2.24e-15 ***
## relpos_rac     -0.83488    0.60820  -1.373     0.17
## opening_date_v -0.19978    0.02586  -7.725 1.12e-14 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```r
summary(mod_frinit_phen_88)
```

```
##  Family: binomial  ( logit )
## Formula:
## initiated_fr ~ relpos_fl + relpos_rac + opening_date_v + (1 |
##     id/shoot_id/raceme_id)
## Data: subset(data_id_flowers, year == 1988)
##
##      AIC      BIC   logLik deviance df.resid
##   2874.5   2915.3  -1430.2   2860.5     2514
##
## Random effects:
##
## Conditional model:
##  Groups                Name        Variance Std.Dev.
##  raceme_id:shoot_id:id (Intercept) 1.2683   1.1262
```

```
##  shoot_id:id           (Intercept) 0.3064   0.5536
##  id                    (Intercept) 1.4414   1.2006
## Number of obs: 2521, groups:
## raceme_id:shoot_id:id, 642; shoot_id:id, 337; id, 232
##
## Conditional model:
##                Estimate Std. Error z value Pr(>|z|)
## (Intercept)    11.29804    1.27852   8.837  < 2e-16 ***
## relpos_fl      -1.98432    0.26684  -7.436 1.04e-13 ***
## relpos_rac     -0.95477    0.51533  -1.853   0.0639 .
## opening_date_v -0.14795    0.02232  -6.628 3.41e-11 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```r
summary(mod_frinit_phen_89)
```

```
##  Family: binomial  ( logit )
## Formula:
## initiated_fr ~ relpos_fl * relpos_rac + opening_date_v + (1 |
##     id/shoot_id/raceme_id)
## Data: subset(data_id_flowers, year == 1989)
##
##      AIC      BIC   logLik deviance df.resid
##   1614.0   1656.2   -799.0   1598.0     1441
##
## Random effects:
##
## Conditional model:
##  Groups                Name        Variance Std.Dev.
##  raceme_id:shoot_id:id (Intercept) 0.9707   0.9853
##  shoot_id:id           (Intercept) 0.2786   0.5278
##  id                    (Intercept) 0.5880   0.7668
## Number of obs: 1449, groups:
## raceme_id:shoot_id:id, 317; shoot_id:id, 135; id, 95
##
## Conditional model:
##                      Estimate Std. Error z value Pr(>|z|)
## (Intercept)          12.63674    1.68796   7.486 7.08e-14 ***
## relpos_fl             1.59300    0.83432   1.909 0.056219 .
## relpos_rac            2.98398    1.11876   2.667 0.007648 **
## opening_date_v       -0.22336    0.03362  -6.643 3.08e-11 ***
## relpos_fl:relpos_rac -6.10319    1.68902  -3.613 0.000302 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

Flowers opening earlier have a higher probability of initiating fruit.

1987 and 1988: Basal flowers (lower relpos_fl) have a higher probability of initiating fruit than distal flowers within the raceme.

1989: When including opening date in the model, the interaction is still significant, but in this case distal flowers on distal racemes (higher relpos_fl and higher relpos_rac) have the lowest probabilities of intiating fruit, and basal flowers on distal racemes (lower relpos_fl and higher relpos_rac) the highest (the lines cross). The contribution of the effect of flower position among racemes to the interaction changes when including opening date in the model. Does this indicate that the effect of flower position among racemes is mainly due to different phenologies of individual flowers?

The effect of flower position among racemes seems to be mainly due to different phenologies of individual flowers, and the effect of flower position within the raceme seems to be mainly due to different resource accessibility.

Probability of setting fruit

Without phenology

```
mod_frset_87<-glmmTMB(fruit_set~relpos_fl*relpos_rac+
                      (1|id/shoot_id/raceme_id),
                    subset(data_id_flowers,year==1987),family="binomial")
mod_frset_88<-glmmTMB(fruit_set~relpos_fl*relpos_rac+
                      (1|id/shoot_id/raceme_id),
                    subset(data_id_flowers,year==1988),family="binomial")
mod_frset_89<-glmmTMB(fruit_set~relpos_fl*relpos_rac+
                      (1|id/shoot_id/raceme_id),
                    subset(data_id_flowers,year==1989),family="binomial")
# OK with random factors and nesting?
summary(mod_frset_87)
```

```
##  Family: binomial  ( logit )
## Formula:
## fruit_set ~ relpos_fl * relpos_rac + (1 | id/shoot_id/raceme_id)
## Data: subset(data_id_flowers, year == 1987)
##
##      AIC      BIC   logLik deviance df.resid
##   1445.3   1484.2   -715.6   1431.3     1906
##
## Random effects:
##
## Conditional model:
##  Groups                Name        Variance  Std.Dev.
##  raceme_id:shoot_id:id (Intercept) 1.029e-07 0.0003208
##  shoot_id:id           (Intercept) 4.614e-01 0.6792378
##  id                    (Intercept) 6.188e-01 0.7866148
## Number of obs: 1913, groups:
## raceme_id:shoot_id:id, 481; shoot_id:id, 239; id, 231
##
## Conditional model:
##                       Estimate Std. Error z value Pr(>|z|)
## (Intercept)             2.2561     0.4532   4.978 6.41e-07 ***
## relpos_fl              -7.2697     1.0511  -6.916 4.63e-12 ***
## relpos_rac             -4.2106     0.9805  -4.294 1.75e-05 ***
## relpos_fl:relpos_rac    4.7397     2.2488   2.108   0.0351 *
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```r
summary(mod_frset_88)
```

```
##  Family: binomial  ( logit )
## Formula:
## fruit_set ~ relpos_fl * relpos_rac + (1 | id/shoot_id/raceme_id)
## Data: subset(data_id_flowers, year == 1988)
##
##      AIC      BIC   logLik deviance df.resid
##   1847.8   1888.6   -916.9   1833.8     2514
##
## Random effects:
##
## Conditional model:
##  Groups                 Name        Variance  Std.Dev.
##  raceme_id:shoot_id:id (Intercept) 1.168e-08 0.0001081
##  shoot_id:id           (Intercept) 1.183e-08 0.0001088
##  id                    (Intercept) 8.785e-01 0.9373088
## Number of obs: 2521, groups:
## raceme_id:shoot_id:id, 642; shoot_id:id, 337; id, 232
##
## Conditional model:
##                      Estimate Std. Error z value Pr(>|z|)
## (Intercept)            1.1116     0.3927   2.830  0.00465 **
## relpos_fl             -4.5798     0.8799  -5.205 1.94e-07 ***
## relpos_rac            -2.4738     0.8527  -2.901  0.00372 **
## relpos_fl:relpos_rac   0.7843     1.9539   0.401  0.68811
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```r
summary(mod_frset_89)
```

```
##  Family: binomial  ( logit )
## Formula:
## fruit_set ~ relpos_fl * relpos_rac + (1 | id/shoot_id/raceme_id)
## Data: subset(data_id_flowers, year == 1989)
##
##      AIC      BIC   logLik deviance df.resid
##   1035.0   1071.9   -510.5   1021.0     1442
##
## Random effects:
##
## Conditional model:
##  Groups                 Name        Variance  Std.Dev.
##  raceme_id:shoot_id:id (Intercept) 1.302e-08 0.0001141
##  shoot_id:id           (Intercept) 6.747e-02 0.2597418
##  id                    (Intercept) 6.276e-01 0.7922373
## Number of obs: 1449, groups:
## raceme_id:shoot_id:id, 317; shoot_id:id, 135; id, 95
##
## Conditional model:
##                      Estimate Std. Error z value Pr(>|z|)
## (Intercept)            1.1010     0.4632   2.377   0.0175 *
```

```
## relpos_fl             -4.9039     1.1168  -4.391 1.13e-05 ***
## relpos_rac            -1.5088     1.0038  -1.503   0.1328
## relpos_fl:relpos_rac  -1.4651     2.5367  -0.578   0.5636
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

Interaction only significant in 1987. Refit models for 1988 and 1989 without interaction.

```
mod_frset_88<-glmmTMB(fruit_set~relpos_fl+relpos_rac+
                      (1|id/shoot_id/raceme_id),
                    subset(data_id_flowers,year==1988),family="binomial")
mod_frset_89<-glmmTMB(fruit_set~relpos_fl+relpos_rac+
                      (1|id/shoot_id/raceme_id),
                    subset(data_id_flowers,year==1989),family="binomial")
# OK with random factors and nesting?
summary(mod_frset_88)
```

```
##  Family: binomial  ( logit )
## Formula:
## fruit_set ~ relpos_fl + relpos_rac + (1 | id/shoot_id/raceme_id)
## Data: subset(data_id_flowers, year == 1988)
##
##      AIC      BIC   logLik deviance df.resid
##     1846     1881     -917     1834     2515
##
## Random effects:
##
## Conditional model:
##  Groups                Name        Variance  Std.Dev.
##  raceme_id:shoot_id:id (Intercept) 1.256e-09 3.544e-05
##  shoot_id:id           (Intercept) 2.347e-08 1.532e-04
##  id                    (Intercept) 8.770e-01 9.365e-01
## Number of obs: 2521, groups:
## raceme_id:shoot_id:id, 642; shoot_id:id, 337; id, 232
##
## Conditional model:
##             Estimate Std. Error z value Pr(>|z|)
## (Intercept)   0.9850     0.2329   4.230 2.34e-05 ***
## relpos_fl    -4.2525     0.3222 -13.197  < 2e-16 ***
## relpos_rac   -2.1697     0.3872  -5.603 2.10e-08 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
summary(mod_frset_89)
```

```
##  Family: binomial  ( logit )
## Formula:
## fruit_set ~ relpos_fl + relpos_rac + (1 | id/shoot_id/raceme_id)
## Data: subset(data_id_flowers, year == 1989)
##
##      AIC      BIC   logLik deviance df.resid
##   1033.3   1065.0   -510.7   1021.3     1443
```

```
##
## Random effects:
##
## Conditional model:
##  Groups                 Name        Variance  Std.Dev.
##  raceme_id:shoot_id:id (Intercept) 1.118e-08 0.0001057
##  shoot_id:id           (Intercept) 7.237e-02 0.2690247
##  id                    (Intercept) 6.267e-01 0.7916478
## Number of obs: 1449, groups:
## raceme_id:shoot_id:id, 317; shoot_id:id, 135; id, 95
##
## Conditional model:
##             Estimate Std. Error z value Pr(>|z|)
## (Intercept)   1.3114     0.2898   4.525 6.05e-06 ***
## relpos_fl    -5.5002     0.4513 -12.189  < 2e-16 ***
## relpos_rac   -2.0245     0.4683  -4.323 1.54e-05 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

Basal flowers (lower relpos_fl) have a higher probability of setting fruit than distal flowers within the raceme. Flowers on basal racemes (lower relpos_rac) have a higher probability of setting fruit than flowers on distal racemes. In 1987, basal flowers on basal racemes (lower relpos_fl and lower relpos_rac) have the highest probabilities of setting fruit, and distal flowers on distal racemes (higher relpos_fl and higher relpos_rac) the lowest.

With phenology

Fit the same models as before but including opening_date_v.

```
mod_frset_phen_87<-glmmTMB(fruit_set~relpos_fl*relpos_rac+opening_date_v+
                      (1|id/shoot_id/raceme_id),
                    subset(data_id_flowers,year==1987),family="binomial")
mod_frset_phen_88<-glmmTMB(fruit_set~relpos_fl+relpos_rac+opening_date_v+
                      (1|id/shoot_id/raceme_id),
                    subset(data_id_flowers,year==1988),family="binomial")
mod_frset_phen_89<-glmmTMB(fruit_set~relpos_fl+relpos_rac+opening_date_v+
                      (1|id/shoot_id/raceme_id),
                    subset(data_id_flowers,year==1989),family="binomial")
# OK with random factors and nesting?
summary(mod_frset_phen_87)
```

```
##  Family: binomial  ( logit )
## Formula:
## fruit_set ~ relpos_fl * relpos_rac + opening_date_v + (1 | id/shoot_id/raceme_id)
## Data: subset(data_id_flowers, year == 1987)
##
##      AIC      BIC   logLik deviance df.resid
##   1418.0   1462.4   -701.0   1402.0     1905
##
## Random effects:
##
## Conditional model:
##  Groups                 Name        Variance  Std.Dev.
```

```
##  raceme_id:shoot_id:id (Intercept) 1.248e-08 0.0001117
##  shoot_id:id           (Intercept) 8.221e-08 0.0002867
##  id                    (Intercept) 1.174e+00 1.0833769
## Number of obs: 1913, groups:
## raceme_id:shoot_id:id, 481; shoot_id:id, 239; id, 231
##
## Conditional model:
##                     Estimate Std. Error z value Pr(>|z|)
## (Intercept)         10.28358    1.67491   6.140 8.26e-10 ***
## relpos_fl           -6.84621    1.07660  -6.359 2.03e-10 ***
## relpos_rac          -2.54709    1.03768  -2.455   0.0141 *
## opening_date_v      -0.13219    0.02623  -5.040 4.66e-07 ***
## relpos_fl:relpos_rac  5.49703    2.30650   2.383   0.0172 *
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```r
summary(mod_frset_phen_88)
```

```
##  Family: binomial  ( logit )
## Formula:
## fruit_set ~ relpos_fl + relpos_rac + opening_date_v + (1 | id/shoot_id/raceme_id)
## Data: subset(data_id_flowers, year == 1988)
##
##      AIC      BIC   logLik deviance df.resid
##   1789.4   1830.2   -887.7   1775.4     2514
##
## Random effects:
##
## Conditional model:
##  Groups                Name        Variance  Std.Dev.
##  raceme_id:shoot_id:id (Intercept) 1.403e-10 1.184e-05
##  shoot_id:id           (Intercept) 2.053e-08 1.433e-04
##  id                    (Intercept) 6.776e-01 8.231e-01
## Number of obs: 2521, groups:
## raceme_id:shoot_id:id, 642; shoot_id:id, 337; id, 232
##
## Conditional model:
##                Estimate Std. Error z value Pr(>|z|)
## (Intercept)     8.65079    1.06004   8.161 3.33e-16 ***
## relpos_fl      -3.46205    0.33113 -10.455  < 2e-16 ***
## relpos_rac     -0.27645    0.45384  -0.609    0.542
## opening_date_v -0.14212    0.01904  -7.464 8.39e-14 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```r
summary(mod_frset_phen_89)
```

```
##  Family: binomial  ( logit )
## Formula:
## fruit_set ~ relpos_fl + relpos_rac + opening_date_v + (1 | id/shoot_id/raceme_id)
## Data: subset(data_id_flowers, year == 1989)
##
##      AIC      BIC   logLik deviance df.resid
```

```
##    1020.6   1057.6   -503.3   1006.6     1442
##
## Random effects:
##
## Conditional model:
##  Groups                Name        Variance  Std.Dev.
##  raceme_id:shoot_id:id (Intercept) 3.123e-12 1.767e-06
##  shoot_id:id           (Intercept) 8.721e-08 2.953e-04
##  id                    (Intercept) 5.274e-01 7.263e-01
## Number of obs: 1449, groups:
## raceme_id:shoot_id:id, 317; shoot_id:id, 135; id, 95
##
## Conditional model:
##                Estimate Std. Error z value Pr(>|z|)
## (Intercept)     6.85991    1.47424   4.653 3.27e-06 ***
## relpos_fl      -4.74325    0.47726  -9.938  < 2e-16 ***
## relpos_rac     -0.16654    0.66326  -0.251 0.801748
## opening_date_v -0.11765    0.03062  -3.842 0.000122 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

Flowers opening earlier have a higher probability of setting fruit.

1987: When including opening date in the model, the interaction is still significant, but in this case basal flowers on basal racemes (lower relpos_fl and lower relpos_rac) have the highest probabilities of setting fruit, and distal flowers on basal racemes (higher relpos_fl and lower relpos_rac) the lowest (the lines cross). The contribution of the effect of flower position among racemes to the interaction changes when including opening date in the model. Does this indicate that the effect of flower position among racemes is mainly due to different phenologies of individual flowers?

1988 and 1989: Basal flowers (lower relpos_fl) have a higher probability of initiating fruit than distal flowers within the raceme.

The effect of flower position among racemes seems to be mainly due to different phenologies of individual flowers, and the effect of flower position within the raceme seems to be mainly due to different resource accessibility.

Seed set

Without phenology

```r
mod_seedset_87<-glmmTMB(cbind(n_seeds,n_ovules-n_seeds)~relpos_fl*relpos_rac+
                          (1|id/shoot_id/raceme_id),
                        subset(data_id_flowers,year==1987),family="binomial")
mod_seedset_88<-glmmTMB(cbind(n_seeds,n_ovules-n_seeds)~relpos_fl*relpos_rac+
                          (1|id/shoot_id/raceme_id),
                        subset(data_id_flowers,year==1988),family="binomial")
mod_seedset_89<-glmmTMB(cbind(n_seeds,n_ovules-n_seeds)~relpos_fl*relpos_rac+
                          (1|id/shoot_id/raceme_id),
                        subset(data_id_flowers,year==1989),family="binomial")
summary(mod_seedset_87)
```

```
##  Family: binomial  ( logit )
```

```
## Formula:
## cbind(n_seeds, n_ovules - n_seeds) ~ relpos_fl * relpos_rac +
##     (1 | id/shoot_id/raceme_id)
## Data: subset(data_id_flowers, year == 1987)
##
##      AIC      BIC   logLik deviance df.resid
##   1016.3   1040.8   -501.2   1002.3      237
##
## Random effects:
##
## Conditional model:
##  Groups                Name        Variance  Std.Dev.
##  raceme_id:shoot_id:id (Intercept) 2.658e-12 1.630e-06
##  shoot_id:id           (Intercept) 1.812e-08 1.346e-04
##  id                    (Intercept) 2.642e-01 5.140e-01
## Number of obs: 244, groups:
## raceme_id:shoot_id:id, 157; shoot_id:id, 105; id, 102
##
## Conditional model:
##                      Estimate Std. Error z value Pr(>|z|)
## (Intercept)           -0.5735     0.2602  -2.204   0.0275 *
## relpos_fl              0.2349     0.7113   0.330   0.7412
## relpos_rac             0.3692     0.5930   0.623   0.5336
## relpos_fl:relpos_rac  -1.6500     1.6299  -1.012   0.3114
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```r
summary(mod_seedset_88)
```

```
##  Family: binomial  ( logit )
## Formula:
## cbind(n_seeds, n_ovules - n_seeds) ~ relpos_fl * relpos_rac +
##     (1 | id/shoot_id/raceme_id)
## Data: subset(data_id_flowers, year == 1988)
##
##      AIC      BIC   logLik deviance df.resid
##   1266.1   1292.2   -626.1   1252.1      298
##
## Random effects:
##
## Conditional model:
##  Groups                Name        Variance  Std.Dev.
##  raceme_id:shoot_id:id (Intercept) 1.156e-09 0.000034
##  shoot_id:id           (Intercept) 1.085e-01 0.329373
##  id                    (Intercept) 9.294e-02 0.304867
## Number of obs: 305, groups:
## raceme_id:shoot_id:id, 210; shoot_id:id, 150; id, 127
##
## Conditional model:
##                      Estimate Std. Error z value Pr(>|z|)
## (Intercept)           -0.5122     0.2328  -2.201   0.0278 *
## relpos_fl             -0.1952     0.5952  -0.328   0.7429
## relpos_rac             0.3594     0.5202   0.691   0.4896
## relpos_fl:relpos_rac  -0.2242     1.3560  -0.165   0.8687
```

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

```r
summary(mod_seedset_89)
```

```
##  Family: binomial  ( logit )
## Formula:
## cbind(n_seeds, n_ovules - n_seeds) ~ relpos_fl * relpos_rac +
##     (1 | id/shoot_id/raceme_id)
## Data: subset(data_id_flowers, year == 1989)
##
##      AIC      BIC   logLik deviance df.resid
##    921.6    945.7   -453.8    907.6      224
##
## Random effects:
##
## Conditional model:
##  Groups                Name        Variance  Std.Dev.
##  raceme_id:shoot_id:id (Intercept) 1.747e-08 0.0001322
##  shoot_id:id           (Intercept) 2.701e-02 0.1643603
##  id                    (Intercept) 6.925e-02 0.2631500
## Number of obs: 231, groups:
## raceme_id:shoot_id:id, 143; shoot_id:id, 81; id, 66
##
## Conditional model:
##                      Estimate Std. Error z value Pr(>|z|)
## (Intercept)           -0.3377     0.2415  -1.399    0.162
## relpos_fl             -0.8827     0.6526  -1.352    0.176
## relpos_rac            -0.6622     0.5323  -1.244    0.213
## relpos_fl:relpos_rac   2.2552     1.4459   1.560    0.119
```

Interaction not significant in any of the years. Refit models without interaction.

```r
mod_seedset_87<-glmmTMB(cbind(n_seeds,n_ovules-n_seeds)~relpos_fl+relpos_rac+
                          (1|id/shoot_id/raceme_id),
                        subset(data_id_flowers,year==1987),family="binomial")
mod_seedset_88<-glmmTMB(cbind(n_seeds,n_ovules-n_seeds)~relpos_fl+relpos_rac+
                          (1|id/shoot_id/raceme_id),
                        subset(data_id_flowers,year==1988),family="binomial")
mod_seedset_89<-glmmTMB(cbind(n_seeds,n_ovules-n_seeds)~relpos_fl+relpos_rac+
                          (1|id/shoot_id/raceme_id),
                        subset(data_id_flowers,year==1989),family="binomial")
summary(mod_seedset_87)
```

```
##  Family: binomial  ( logit )
## Formula:
## cbind(n_seeds, n_ovules - n_seeds) ~ relpos_fl + relpos_rac +
##     (1 | id/shoot_id/raceme_id)
## Data: subset(data_id_flowers, year == 1987)
##
##      AIC      BIC   logLik deviance df.resid
##   1015.4   1036.3   -501.7   1003.4      238
```

```
##
## Random effects:
##
## Conditional model:
##  Groups                Name        Variance  Std.Dev.
##  raceme_id:shoot_id:id (Intercept) 1.077e-16 1.038e-08
##  shoot_id:id           (Intercept) 1.828e-08 1.352e-04
##  id                    (Intercept) 2.612e-01 5.110e-01
## Number of obs: 244, groups:
## raceme_id:shoot_id:id, 157; shoot_id:id, 105; id, 102
##
## Conditional model:
##             Estimate Std. Error z value Pr(>|z|)
## (Intercept)  -0.3628     0.1561  -2.324   0.0201 *
## relpos_fl    -0.4425     0.2438  -1.815   0.0695 .
## relpos_rac   -0.1571     0.2860  -0.549   0.5827
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```r
summary(mod_seedset_88)
```

```
##  Family: binomial  ( logit )
## Formula:
## cbind(n_seeds, n_ovules - n_seeds) ~ relpos_fl + relpos_rac +
##     (1 | id/shoot_id/raceme_id)
## Data: subset(data_id_flowers, year == 1988)
##
##      AIC      BIC   logLik deviance df.resid
##   1264.1   1286.5   -626.1   1252.1      299
##
## Random effects:
##
## Conditional model:
##  Groups                Name        Variance  Std.Dev.
##  raceme_id:shoot_id:id (Intercept) 1.711e-09 4.136e-05
##  shoot_id:id           (Intercept) 1.092e-01 3.305e-01
##  id                    (Intercept) 9.200e-02 3.033e-01
## Number of obs: 305, groups:
## raceme_id:shoot_id:id, 210; shoot_id:id, 150; id, 127
##
## Conditional model:
##             Estimate Std. Error z value Pr(>|z|)
## (Intercept)  -0.4807     0.1335  -3.601 0.000317 ***
## relpos_fl    -0.2879     0.1995  -1.444 0.148873
## relpos_rac    0.2819     0.2247   1.254 0.209769
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```r
summary(mod_seedset_89)
```

```
##  Family: binomial  ( logit )
## Formula:
## cbind(n_seeds, n_ovules - n_seeds) ~ relpos_fl + relpos_rac +
```

```
##     (1 | id/shoot_id/raceme_id)
## Data: subset(data_id_flowers, year == 1989)
##
##      AIC      BIC   logLik deviance df.resid
##    922.0    942.7   -455.0    910.0      225
##
## Random effects:
##
## Conditional model:
##  Groups                Name        Variance Std.Dev.
##  raceme_id:shoot_id:id (Intercept) 0.004986 0.07061
##  shoot_id:id           (Intercept) 0.018888 0.13743
##  id                    (Intercept) 0.077870 0.27905
## Number of obs: 231, groups:
## raceme_id:shoot_id:id, 143; shoot_id:id, 81; id, 66
##
## Conditional model:
##             Estimate Std. Error z value Pr(>|z|)
## (Intercept) -0.63968    0.14561  -4.393 1.12e-05 ***
## relpos_fl    0.05652    0.25058   0.226    0.822
## relpos_rac   0.06582    0.25492   0.258    0.796
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

No significant effects on seed set.

Not fitting models with phenology because we found no effects of flower position on seed set.

Table 2

```r
tab_model(mod_frinit_87,mod_frinit_88,mod_frinit_89,
          transform=NULL,show.intercept=F,show.ci=F,show.se=T,show.stat=T,
          show.r2=T,show.icc=F,show.re.var=F,show.ngroups=F,digits=3,
          dv.labels=c("1987","1988","1989"),title="Fruit initiation",
          file="output/tables/Table2a.doc")
```

Fruit initiation

1987

1988

1989

Predictors

Log-Odds

std. Error

Statistic

p

Log-Odds

std. Error

Statistic

p

Log-Odds

std. Error

Statistic

p

relpos fl

-3.990

0.313

-12.732

<0.001

-2.817

0.246

-11.435

<0.001

0.004

0.796

0.005

0.996

relpos rac

-4.128

0.509

-8.106

<0.001

-2.962

0.445

-6.661

<0.001

-0.796

0.981

-0.812

0.417

relpos fl × relpos rac

-5.563

1.678

-3.315

0.001

Observations

1913

2521

1449

Marginal R2 / Conditional R2

0.287 / NA

0.092 / 0.540

0.124 / 0.496

```r
tab_model(mod_frinit_phen_87,mod_frinit_phen_88,mod_frinit_phen_89,
          transform=NULL,show.intercept=F,show.ci=F,show.se=T,show.stat=T,
          show.r2=T,show.icc=F,show.re.var=F,show.ngroups=F,digits=3,
          dv.labels=c("1987","1988","1989"),title="Fruit initiation",
          file="output/tables/Table2b.doc")
```

Fruit initiation

1987

1988

1989

Predictors

Log-Odds

std. Error

Statistic

p

Log-Odds

std. Error

Statistic

p

Log-Odds

std. Error

Statistic

p

relpos fl

-2.628

0.331

-7.927

<0.001

-1.984

0.267

-7.436

<0.001

1.593

0.834

1.909

0.056

relpos rac

-0.835

0.608

-1.373

0.170

-0.955

0.515

-1.853

0.064

2.984

1.119

2.667

0.008

opening date v

-0.200

0.026

-7.725

<0.001

-0.148

0.022

-6.628

<0.001

-0.223

0.034

-6.643

<0.001

relpos fl × relpos rac

-6.103

1.689

-3.613

<0.001

Observations

1913

2521

1449

Marginal R2 / Conditional R2

0.244 / 0.588

0.142 / 0.552

0.207 / 0.491

```
tab_model(mod_frset_87,mod_frset_88,mod_frset_89,
          transform=NULL,show.intercept=F,show.ci=F,show.se=T,show.stat=T,
          show.r2=T,show.icc=F,show.re.var=F,show.ngroups=F,digits=3,
          dv.labels=c("1987","1988","1989"),title="Fruit set",
          file="output/tables/Table2c.doc")
```

Fruit set

1987

1988

1989

Predictors

Log-Odds

std. Error

Statistic

p

Log-Odds

std. Error

Statistic

p

Log-Odds

std. Error

Statistic

p

relpos fl

-7.270

1.051

-6.916

<0.001

-4.252

0.322

-13.197

<0.001

-5.500

0.451

-12.189

<0.001

relpos rac

-4.211

0.980

-4.294

<0.001

-2.170

0.387

-5.603

<0.001

-2.024

0.468

-4.323

<0.001

relpos fl × relpos rac

4.740

2.249

2.108

0.035

Observations

1913

2521

1449

Marginal R2 / Conditional R2

0.314 / NA

0.243 / NA

0.353 / NA

```r
tab_model(mod_frset_phen_87,mod_frset_phen_88,mod_frset_phen_89,
          transform=NULL,show.intercept=F,show.ci=F,show.se=T,show.stat=T,
          show.r2=T,show.icc=F,show.re.var=F,show.ngroups=F,digits=3,
          dv.labels=c("1987","1988","1989"),title="Fruit set",
          file="output/tables/Table2d.doc")
```

Fruit set

1987

1988

1989

Predictors

Log-Odds

std. Error

Statistic

p

Log-Odds

std. Error

Statistic

p

Log-Odds

std. Error

Statistic

p

relpos fl

-6.846

1.077

-6.359

<0.001

-3.462

0.331

-10.455

<0.001

-4.743

0.477

-9.938

<0.001

relpos rac

-2.547

1.038

-2.455

0.014

-0.276

0.454

-0.609

0.542

-0.167

0.663

-0.251

0.802

opening date v

-0.132

0.026

-5.040

<0.001

-0.142

0.019

-7.464

<0.001

-0.118

0.031

-3.842

<0.001

relpos fl × relpos rac

5.497

2.307

2.383

0.017

Observations

1913

2521

1449

Marginal R2 / Conditional R2

0.363 / NA

0.302 / NA

0.367 / NA

```
tab_model(mod_seedset_87,mod_seedset_88,mod_seedset_89,
          transform=NULL,show.intercept=F,show.ci=F,show.se=T,show.stat=T,
          show.r2=T,show.icc=F,show.re.var=F,show.ngroups=F,digits=3,
          dv.labels=c("1987","1988","1989"),title="Seed set",
          file="output/tables/Table2e.doc")
```

Seed set

1987

1988

1989

Predictors

Log-Odds

std. Error

Statistic

p

Log-Odds

std. Error

Statistic

p

Log-Odds

std. Error

Statistic

p

relpos fl

-0.443

0.244

-1.815

0.070

-0.288

0.199

-1.444

0.149

0.057

0.251

0.226

0.822

relpos rac

-0.157

0.286

-0.549

0.583

0.282

0.225

1.254

0.210

0.066

0.255

0.258

0.796

Observations

244

305

231

Marginal R2 / Conditional R2

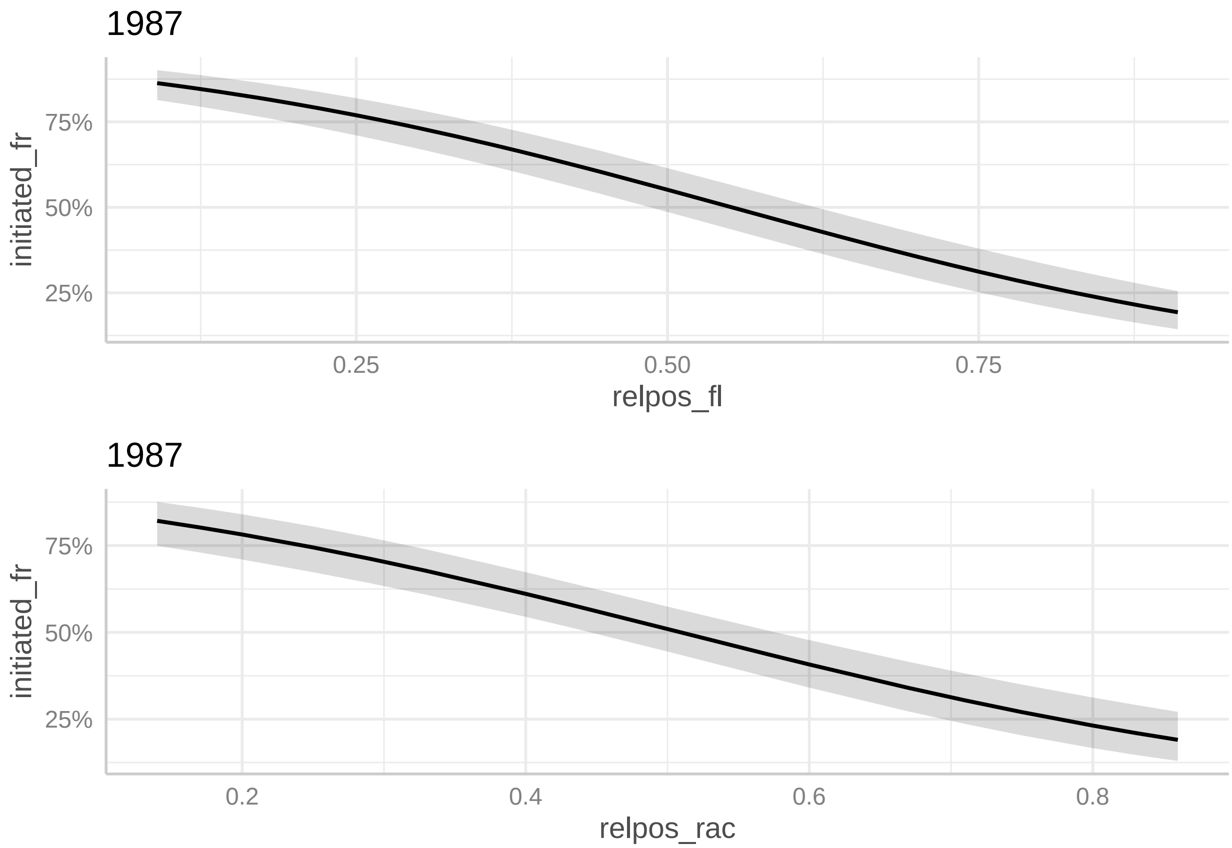
0.002 / NA

0.002 / NA

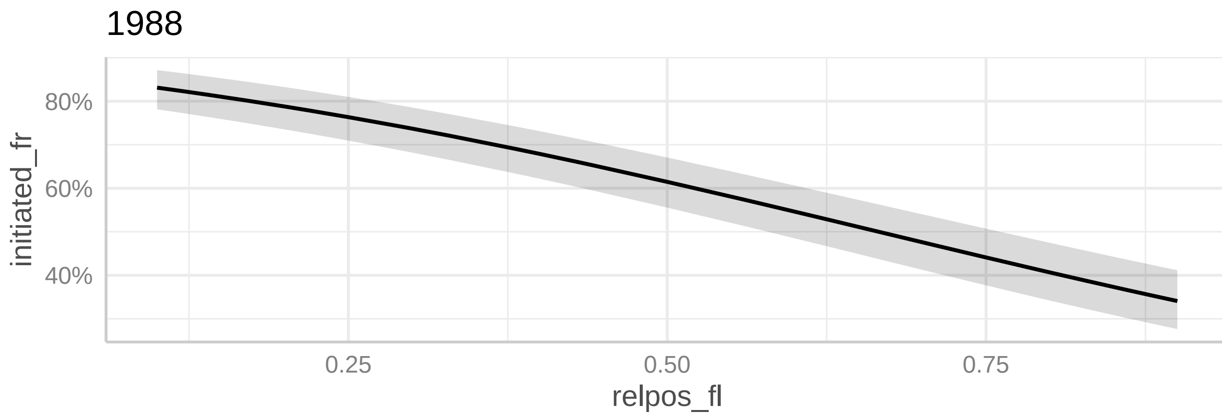
0.000 / 0.030

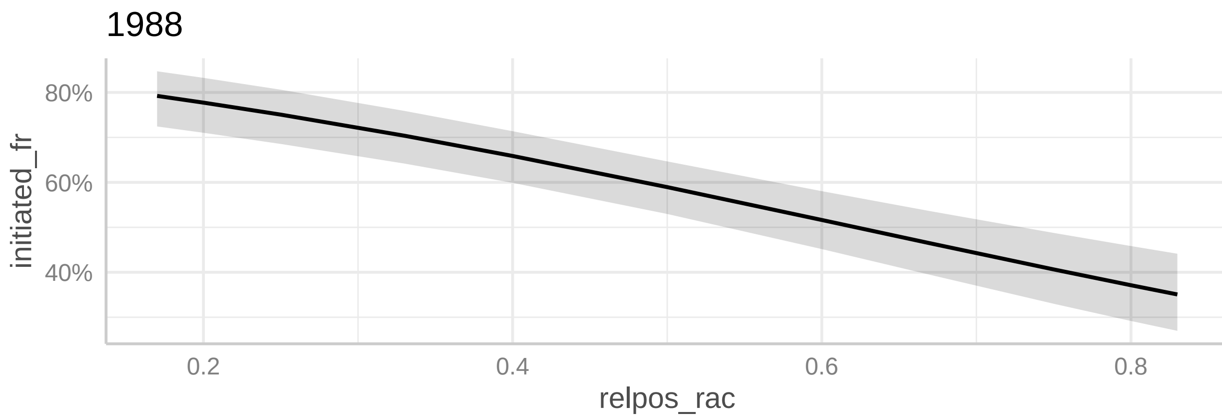
Figures 4-5

```
# Fruit initiation, without opening date
plot_fr_init_87<-grid.arrange(
  plot(ggpredict(mod_frinit_87,terms="relpos_fl[all]"))+ggtitle("1987"),
  plot(ggpredict(mod_frinit_87,terms="relpos_rac[all]"))+ggtitle("1987"),
  ncol=1)
```




```
plot_fr_init_88<-grid.arrange(
  plot(ggpredict(mod_frinit_88,terms="relpos_fl[all]"))+ggtitle("1988"),
  plot(ggpredict(mod_frinit_88,terms="relpos_rac[all]"))+ggtitle("1988"),
  ncol=1)
```

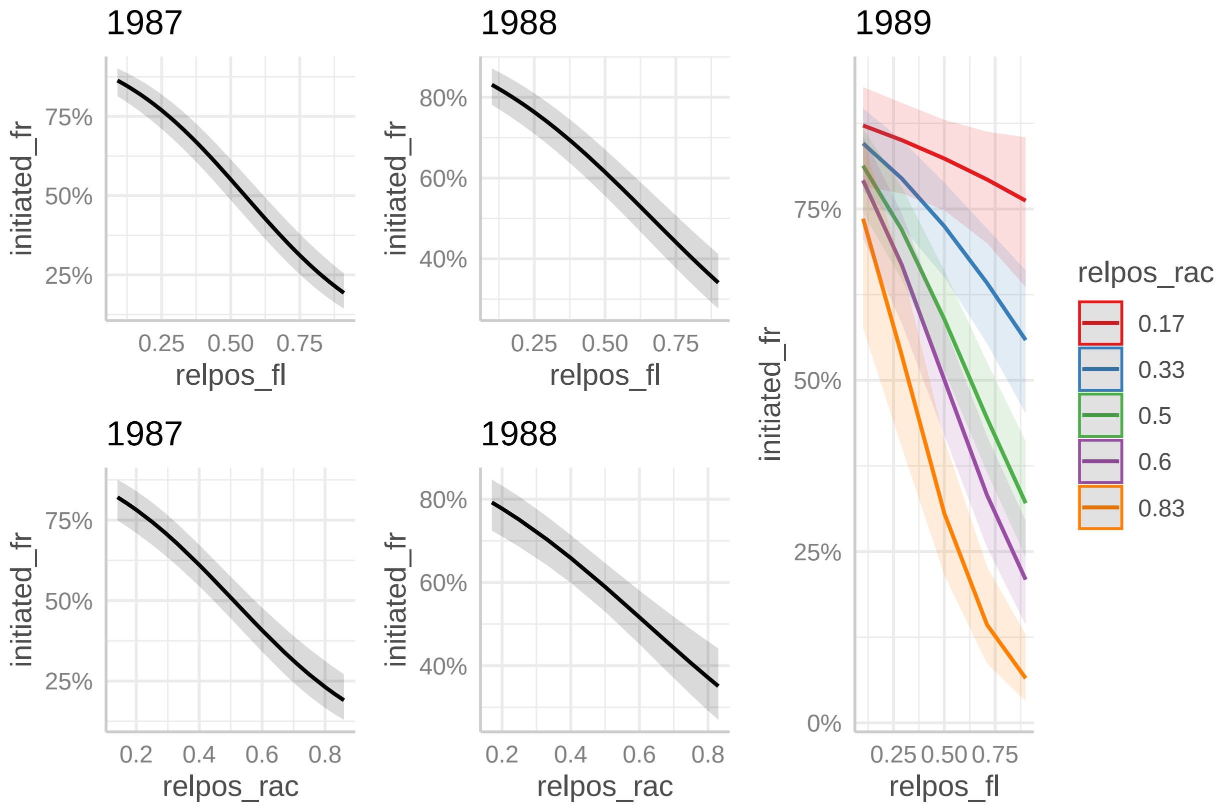




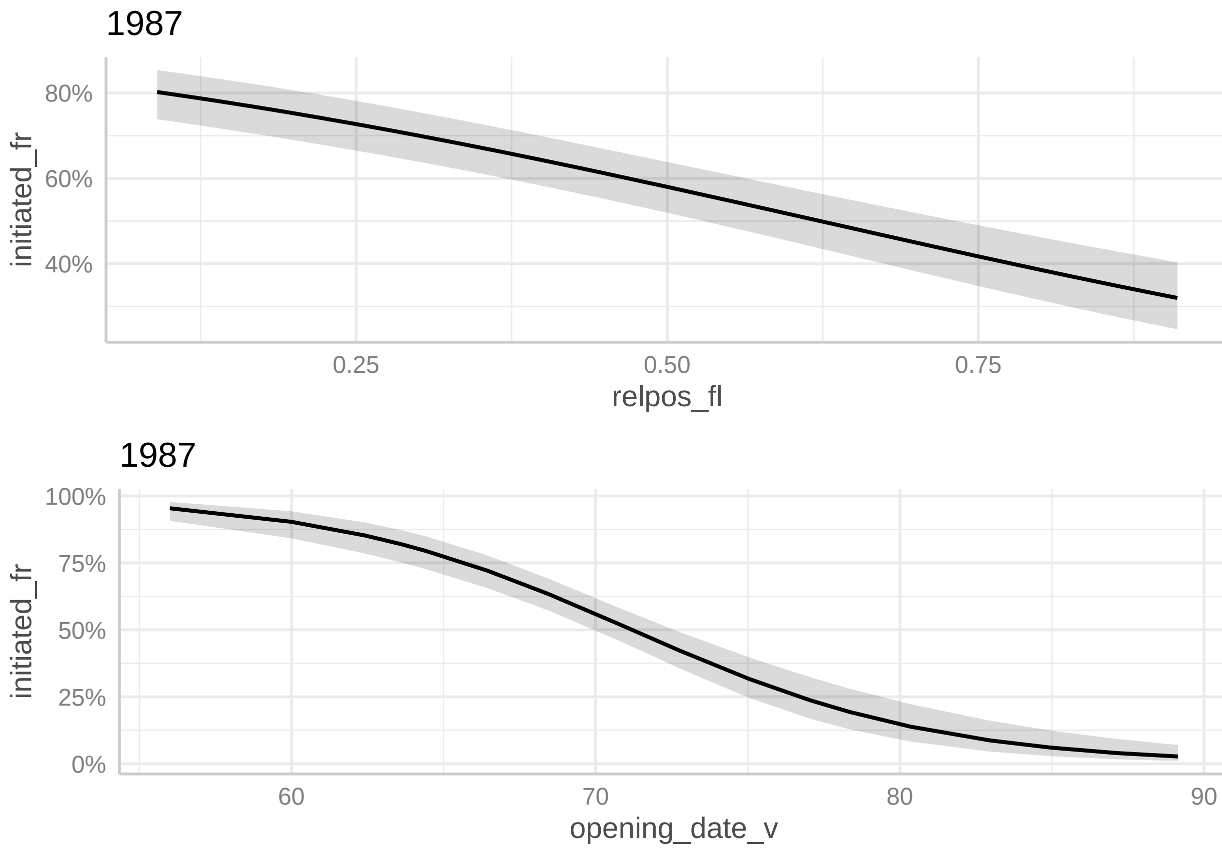

```
plot_fr_init_89<-plot(ggpredict(mod_frinit_89,
                              terms=c("relpos_fl[quart]",
                                      "relpos_rac[quart]")))+ggtitle("1989")

plot_fr_init<-grid.arrange(plot_fr_init_87,plot_fr_init_88,plot_fr_init_89,
                          ncol=3,widths=c(0.75,0.75,1),
                          top="A) Fruit initiation, without opening date")
```

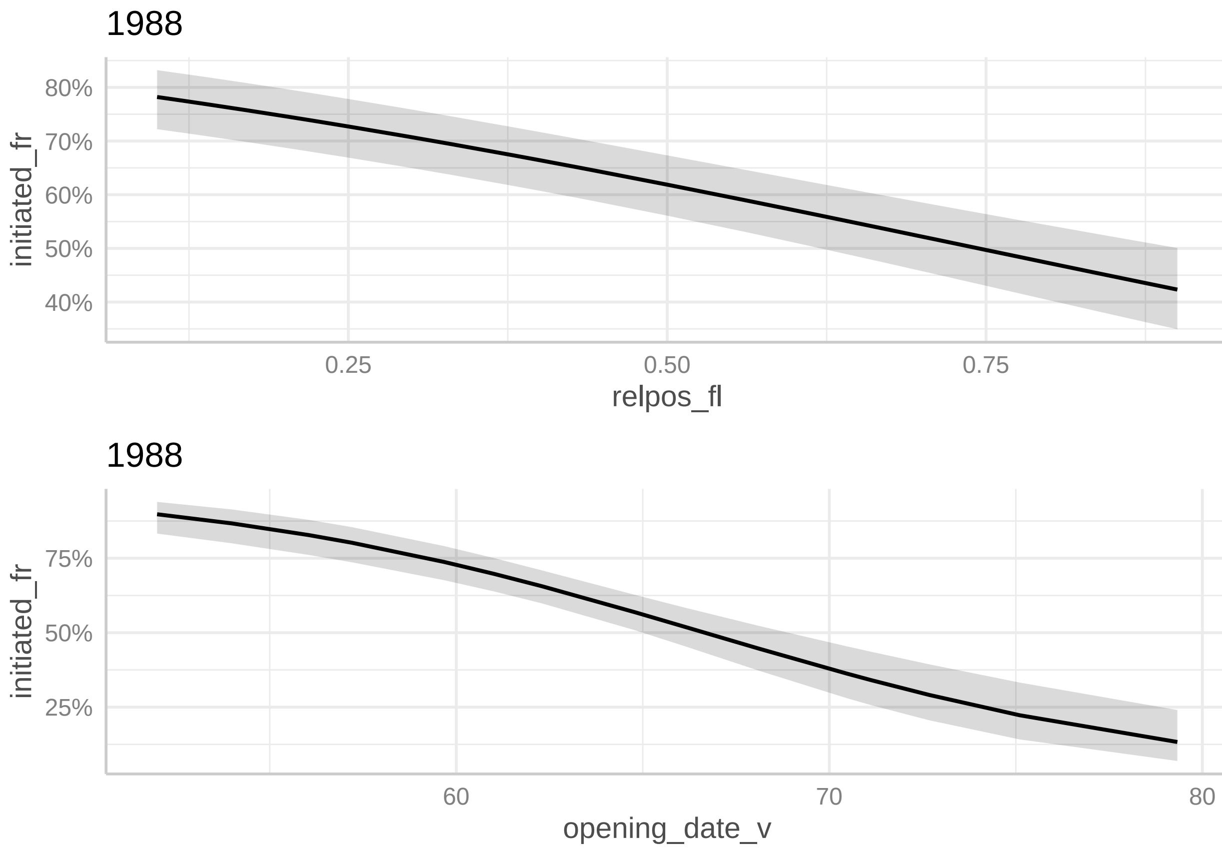
A) Fruit initiation, without opening date



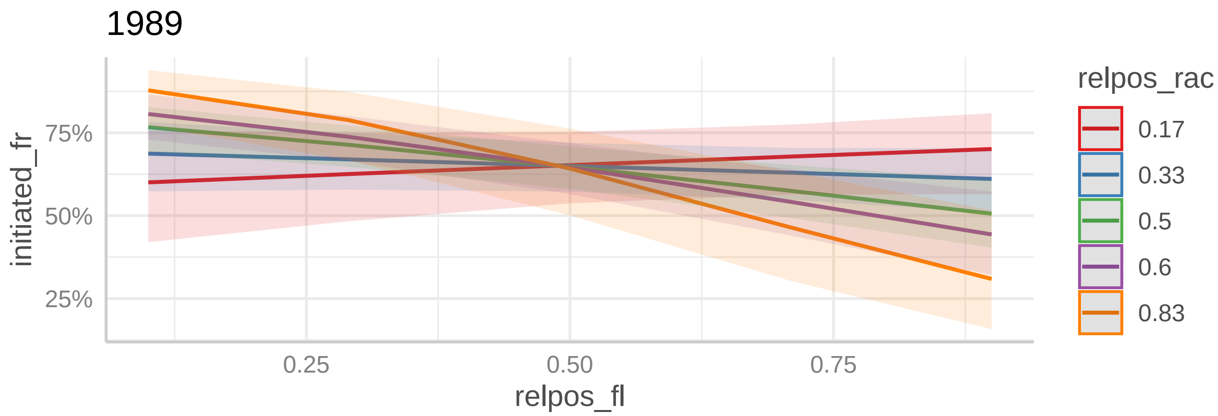

```
# Fruit initiation, with opening date
plot_fr_init_phen_87<-grid.arrange(
  plot(ggpredict(mod_frinit_phen_87,terms="relpos_fl[all]"))+
    ggtitle("1987"),
  plot(ggpredict(mod_frinit_phen_87,terms="opening_date_v[all]"))+
    ggtitle("1987"),
  ncol=1)
```

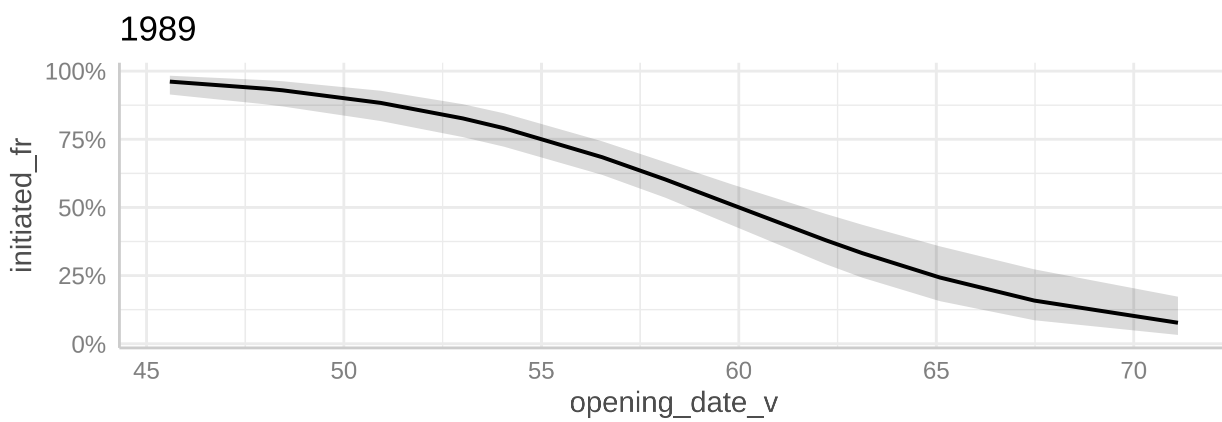



```
plot_fr_init_phen_88<-grid.arrange(
  plot(ggpredict(mod_frinit_phen_88,terms="relpos_fl[all]"))+
    ggtitle("1988"),
  plot(ggpredict(mod_frinit_phen_88,terms="opening_date_v[all]"))+
    ggtitle("1988"),
  ncol=1)
```

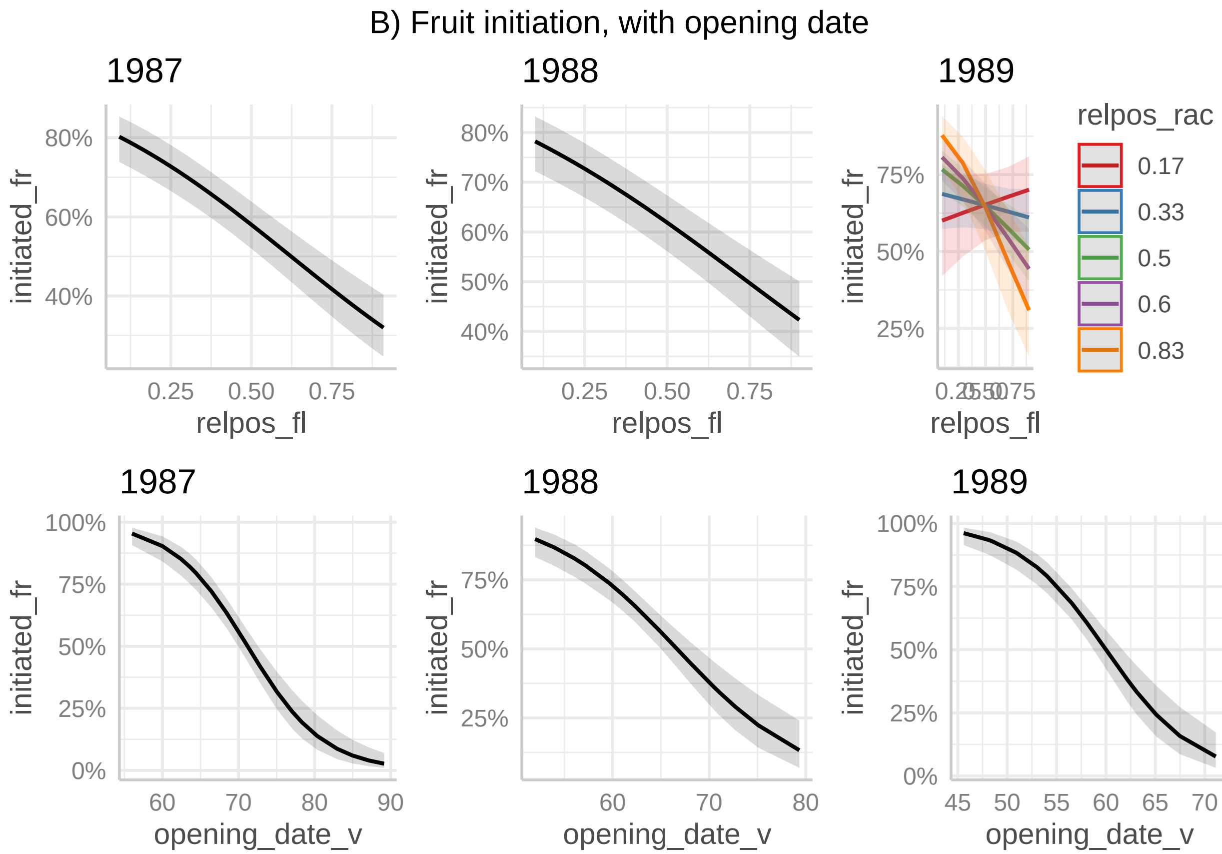



```
plot_fr_init_phen_89<-grid.arrange(
  plot(ggpredict(mod_frinit_phen_89,
                 terms=c("relpos_fl[quart]","relpos_rac[quart]")))+
    ggtitle("1989"),
  plot(ggpredict(mod_frinit_phen_89,terms="opening_date_v[all]"))+
    ggtitle("1989"),
  ncol=1)
```

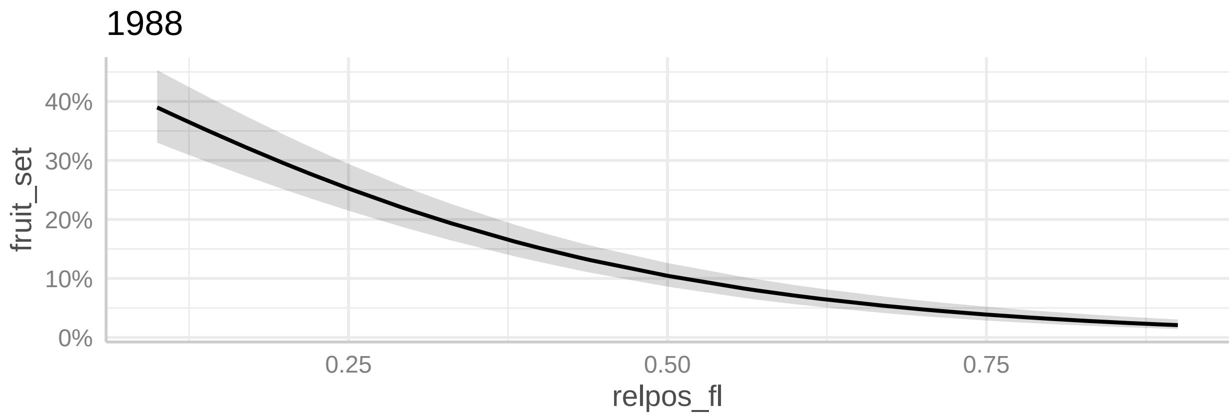


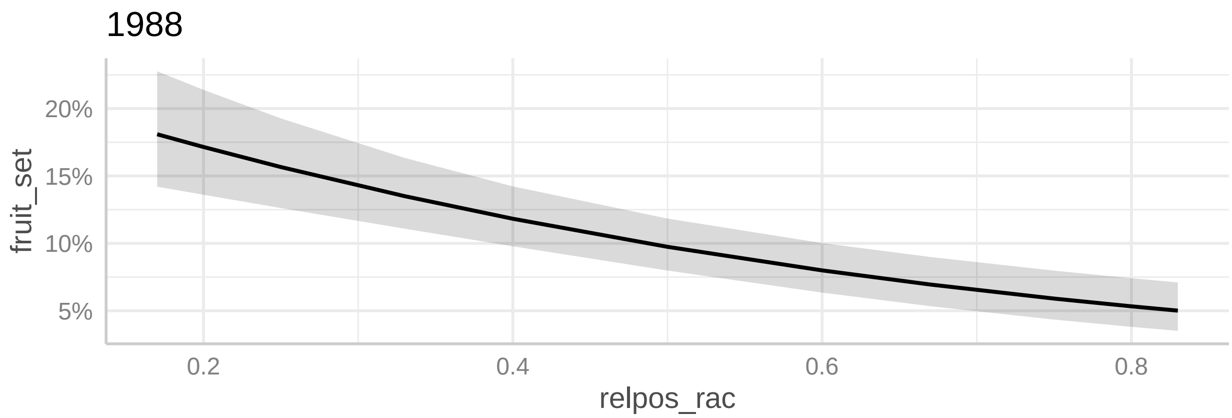



```
plot_fr_init_phen<-grid.arrange(plot_fr_init_phen_87,plot_fr_init_phen_88,
                                plot_fr_init_phen_89,
                          ncol=3,
                          top="B) Fruit initiation, with opening date")
```

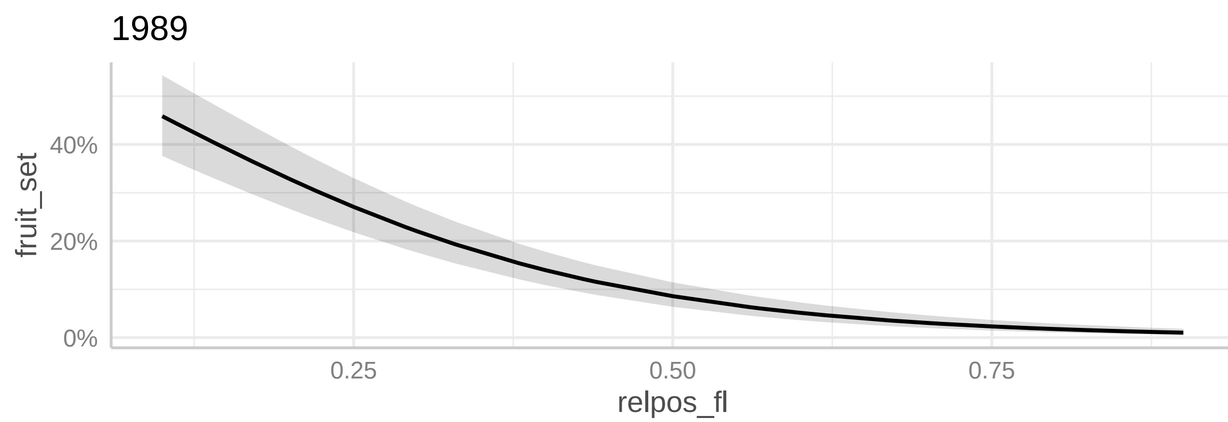


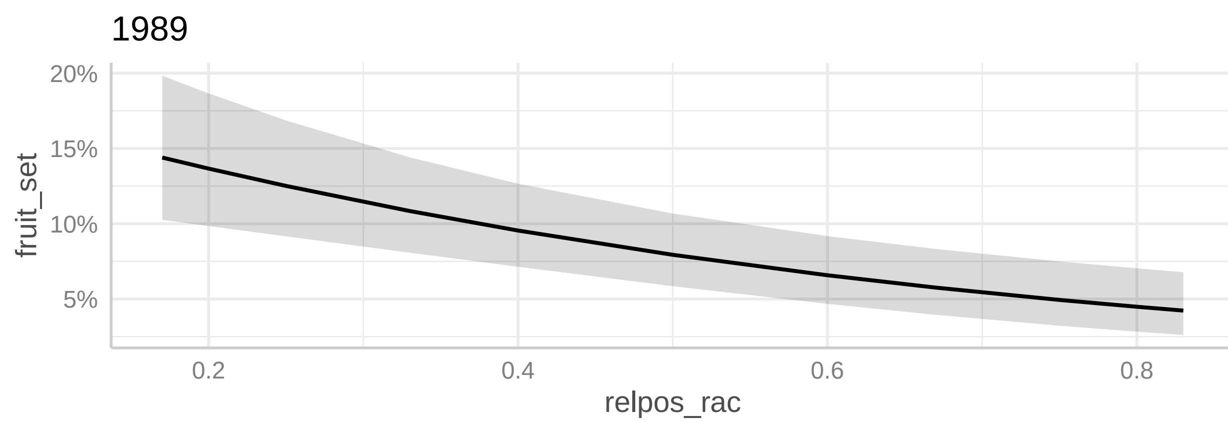

```
# Fruit set, without opening date
plot_fr_set_87<-plot(ggpredict(mod_frset_87,
                              terms=c("relpos_fl[quart]",
                                      "relpos_rac[quart]")))+ggtitle("1987")
plot_fr_set_88<-grid.arrange(
  plot(ggpredict(mod_frset_88,terms="relpos_fl[all]"))+ggtitle("1988"),
  plot(ggpredict(mod_frset_88,terms="relpos_rac[all]"))+ggtitle("1988"),
  ncol=1)
```



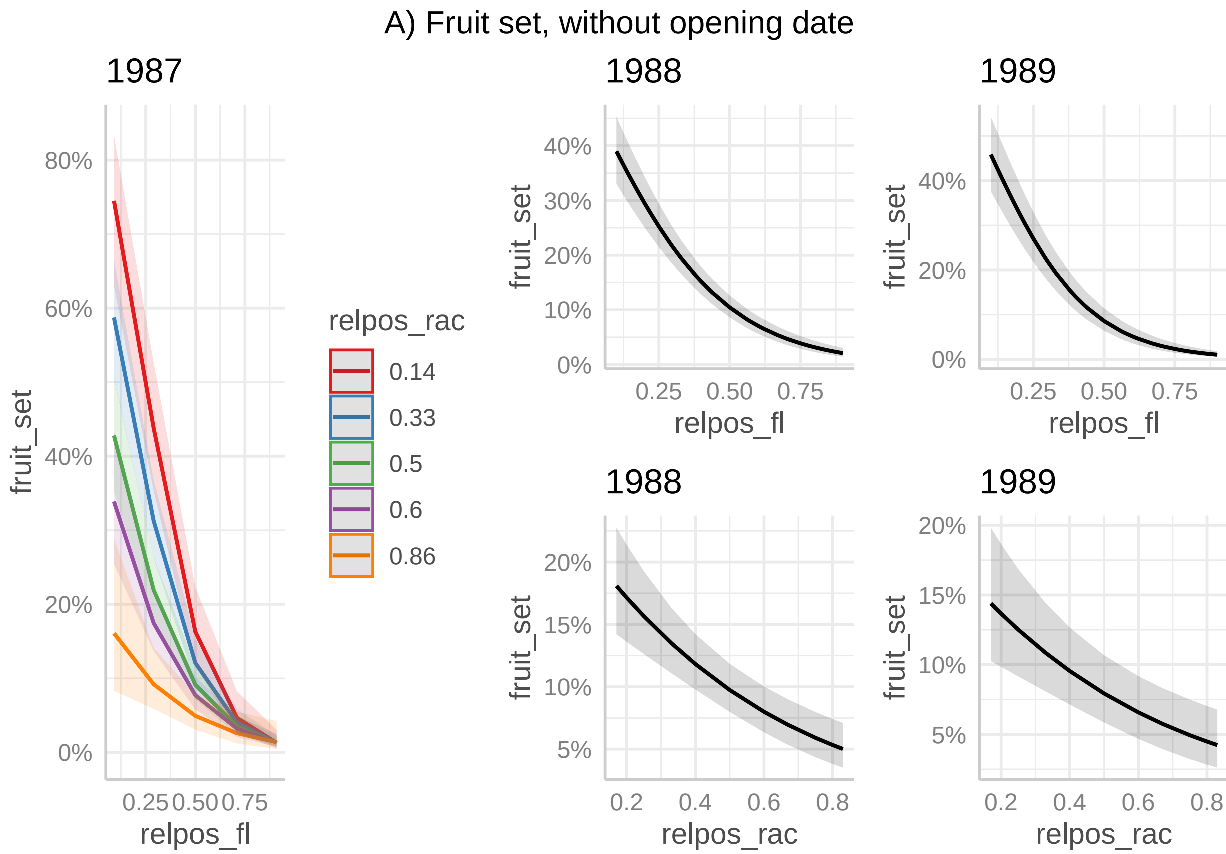



```
plot_fr_set_89<-grid.arrange(
  plot(ggpredict(mod_frset_89,terms="relpos_fl[all]"))+ggtitle("1989"),
  plot(ggpredict(mod_frset_89,terms="relpos_rac[all]"))+ggtitle("1989"),
  ncol=1)
```

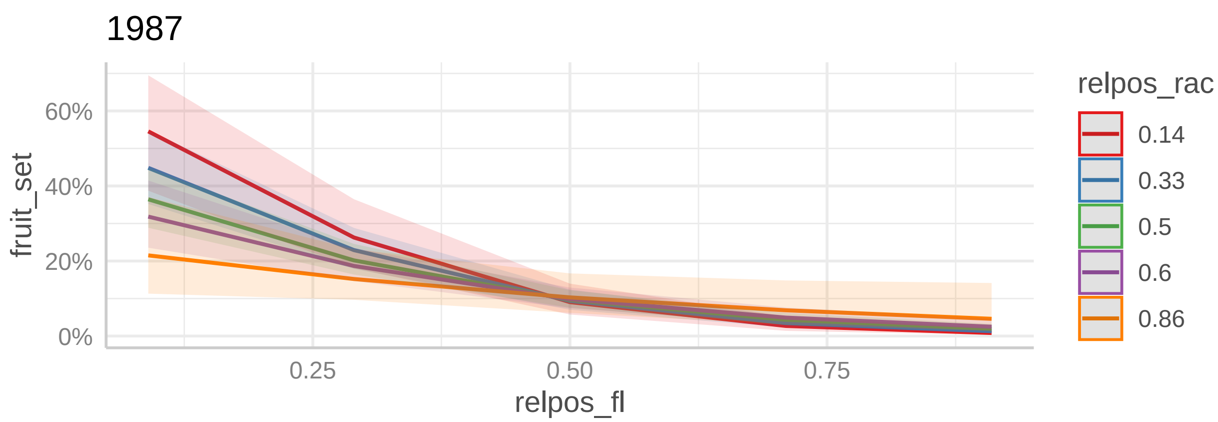


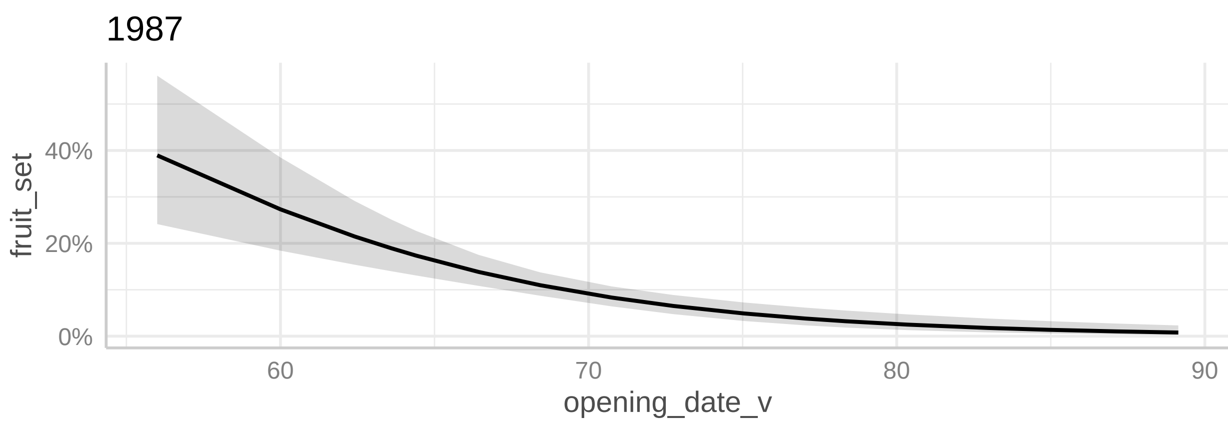



```
plot_fr_set<-grid.arrange(plot_fr_set_87,plot_fr_set_88,plot_fr_set_89,
                          ncol=3,widths=c(1,0.75,0.75),
                          top="A) Fruit set, without opening date")
```

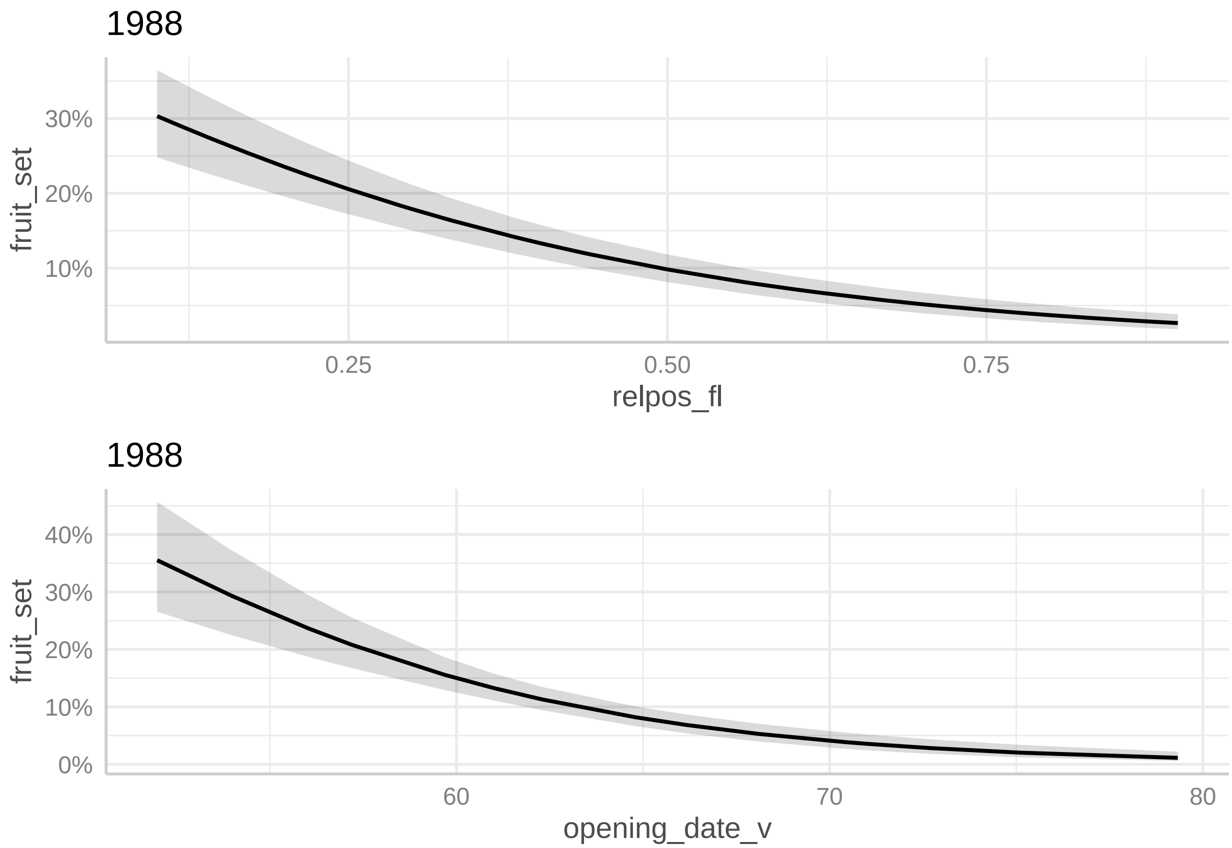



```
# Fruit set, with opening date
plot_fr_set_phen_87<-grid.arrange(
  plot(ggpredict(mod_frset_phen_87,
                terms=c("relpos_fl[quart]","relpos_rac[quart]")))+
    ggtitle("1987"),
  plot(ggpredict(mod_frset_phen_87,terms="opening_date_v[all]"))+
    ggtitle("1987"),
  ncol=1)
```

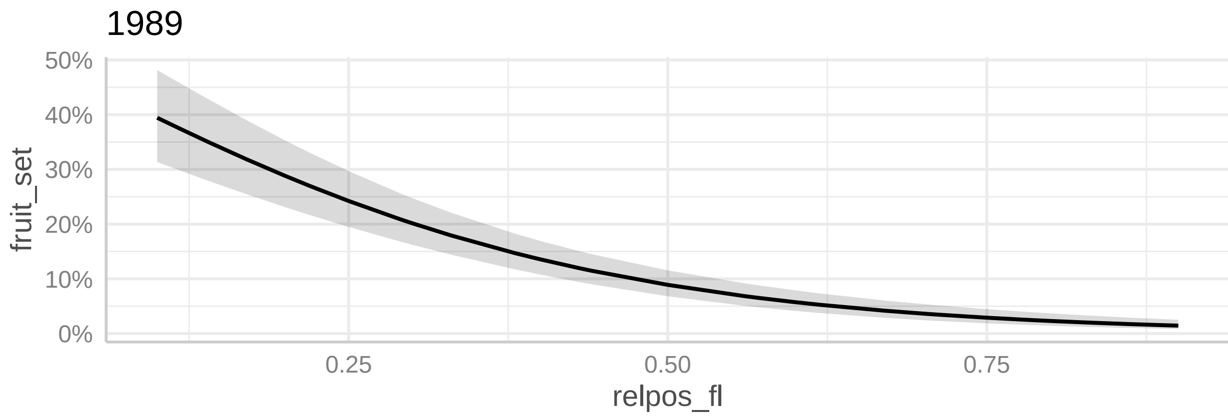


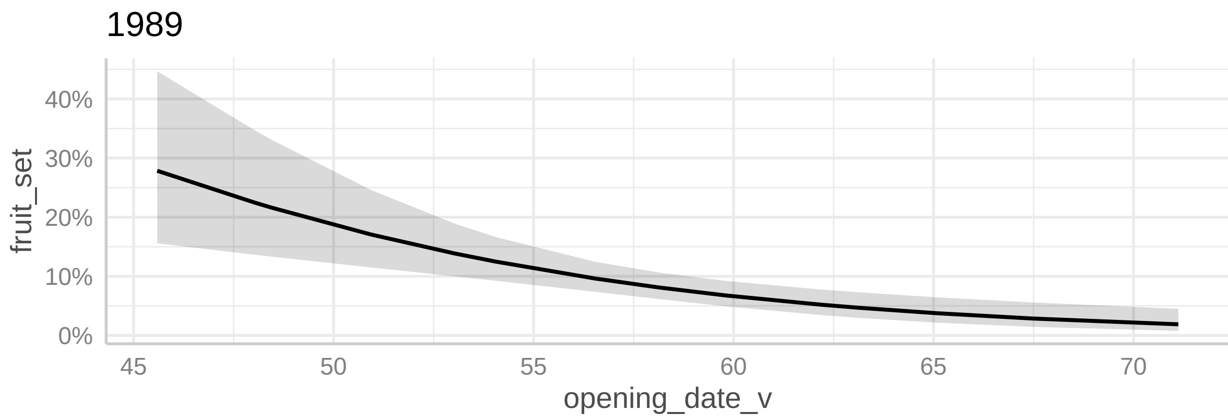



```
plot_fr_set_phen_88<-grid.arrange(
  plot(ggpredict(mod_frset_phen_88,terms="relpos_fl[all]"))+
    ggtitle("1988"),
  plot(ggpredict(mod_frset_phen_88,terms="opening_date_v[all]"))+
    ggtitle("1988"),
  ncol=1)
```

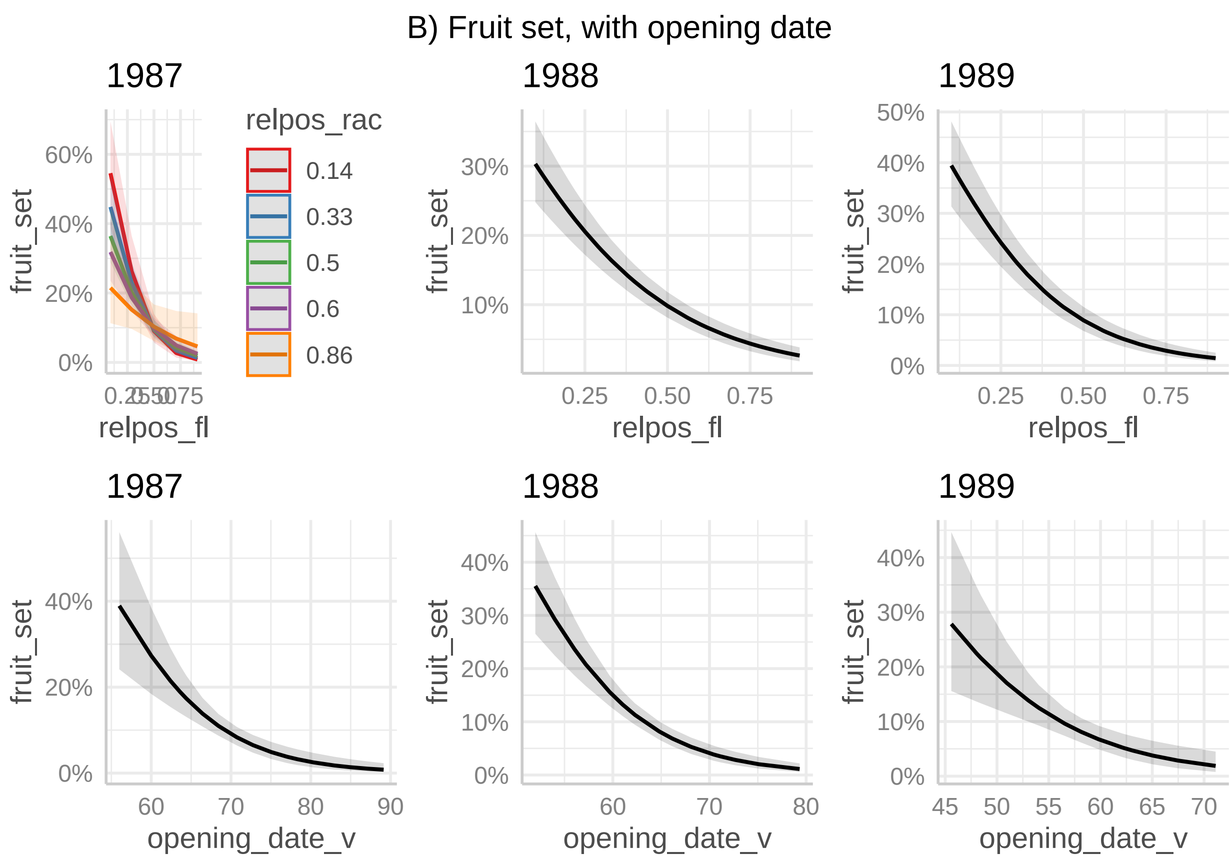



```
plot_fr_set_phen_89<-grid.arrange(
  plot(ggpredict(mod_frset_phen_89,terms="relpos_fl[all]"))+
    ggtitle("1989"),
  plot(ggpredict(mod_frset_phen_89,terms="opening_date_v[all]"))+
    ggtitle("1989"),
  ncol=1)
```

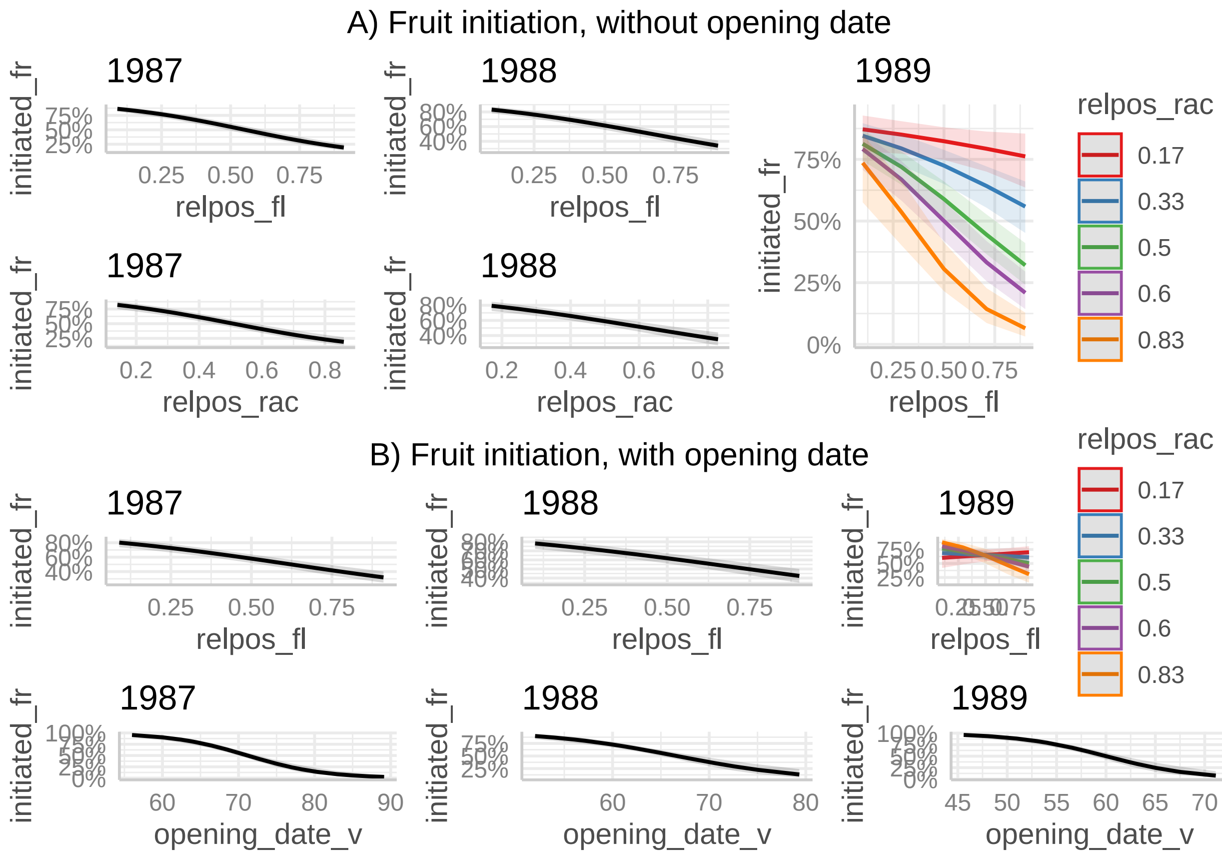





```
plot_fr_set_phen<-grid.arrange(plot_fr_set_phen_87,plot_fr_set_phen_88,
                               plot_fr_set_phen_89,
                               ncol=3,
                               top="B) Fruit set, with opening date")
```




```
fig4<-grid.arrange(plot_fr_init,plot_fr_init_phen,ncol=1)
```

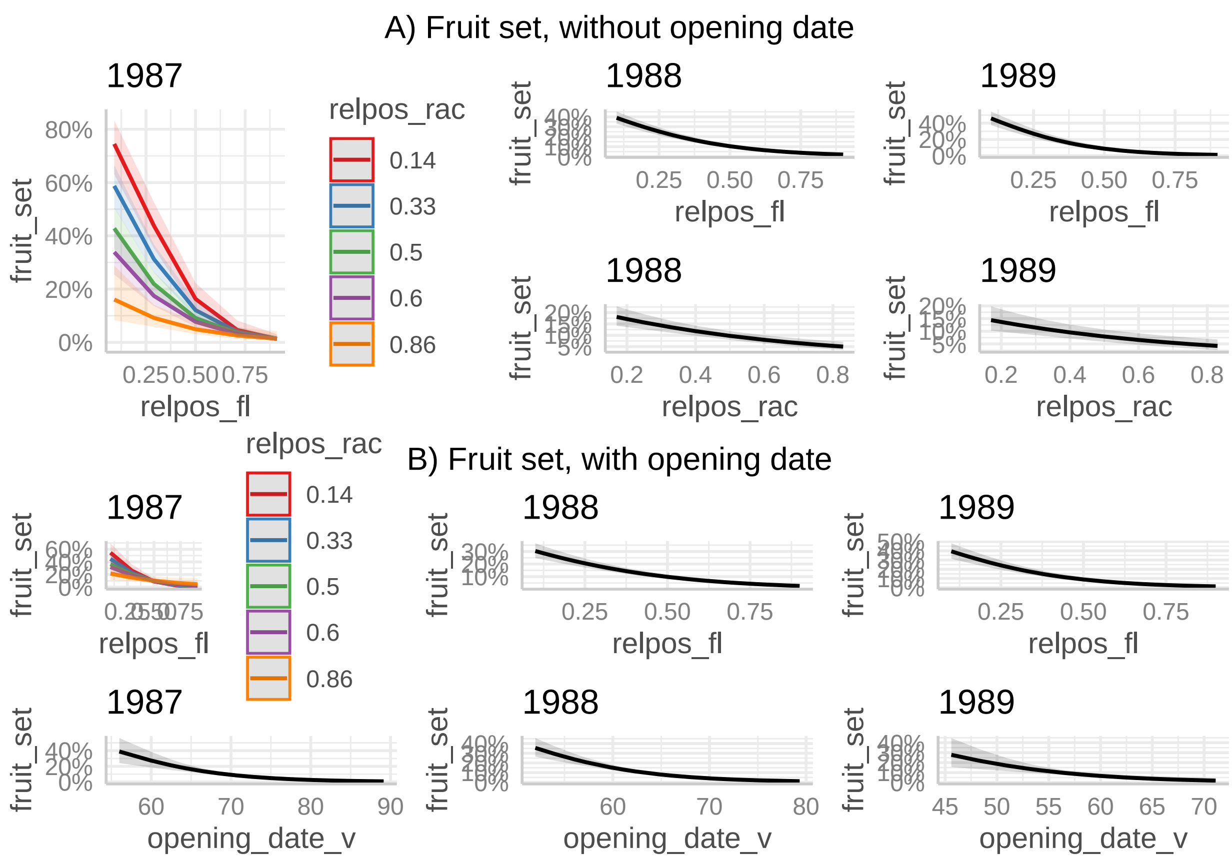



```
fig4
```

```
## TableGrob (2 x 1) "arrange": 2 grobs
##   z     cells    name            grob
## 1 1 (1-1,1-1) arrange gtable[arrange]
## 2 2 (2-2,1-1) arrange gtable[arrange]
```

```
ggsave(filename="output/figures/fig4.tiff",plot=fig4,
       width=30,height=30,units="cm",dpi=300)
```

```
fig5<-grid.arrange(plot_fr_set,plot_fr_set_phen,ncol=1)
```




```
fig5
```

```
## TableGrob (2 x 1) "arrange": 2 grobs
##   z     cells    name           grob
## 1 1 (1-1,1-1) arrange gtable[arrange]
## 2 2 (2-2,1-1) arrange gtable[arrange]
```

```
ggsave(filename="output/figures/fig5.tiff",plot=fig5,
       width=30,height=30,units="cm",dpi=300)
```

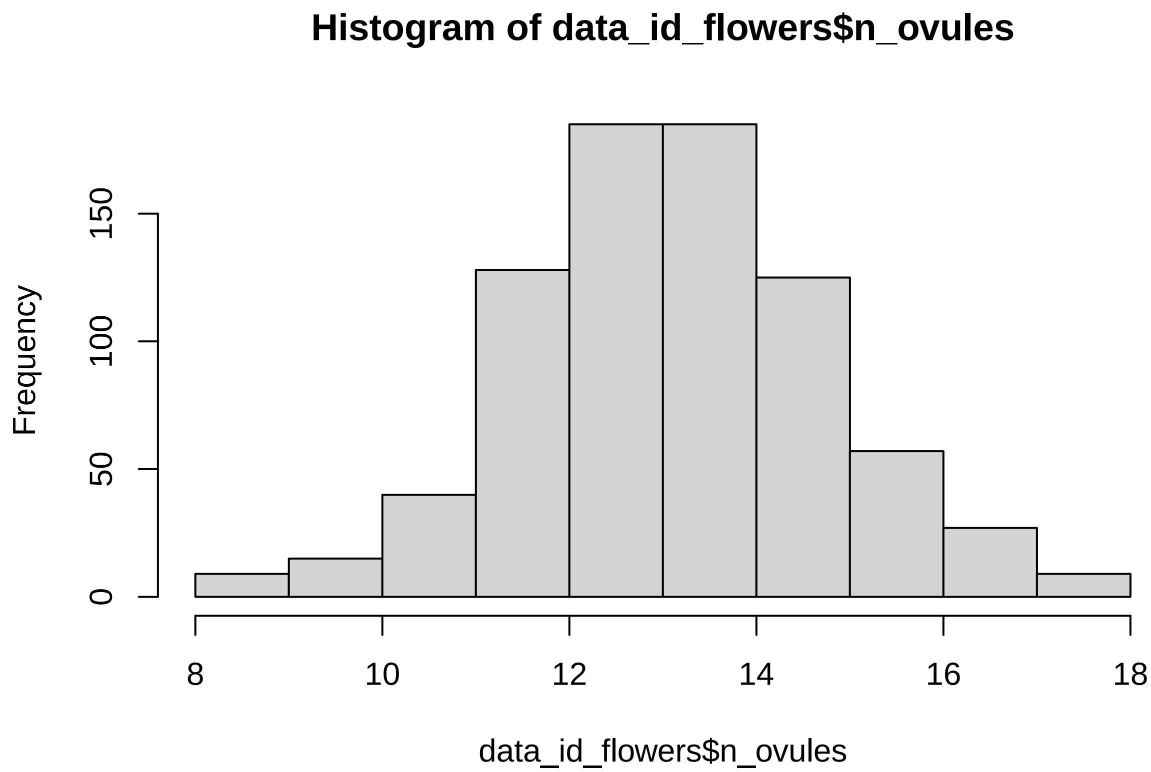
Q4: Effects of flower position on ovule number

Does ovule number of individual flowers depend on flower position within and among the raceme?

H: We expect that basal flowers have a higher ovule number than distal flowers within the raceme, and that flowers on basal racemes have a higher ovule number than flowers on distal racemes.

Check distribution:

```
hist(data_id_flowers$n_ovules)
```



Looks quite normal

```
mod_ov_87<-glmmTMB(n_ovules~relpos_fl*relpos_rac+
                        (1|id/shoot_id/raceme_id),
                subset(data_id_flowers,year==1987))
mod_ov_88<-glmmTMB(n_ovules~relpos_fl*relpos_rac+
                        (1|id/shoot_id/raceme_id),
                subset(data_id_flowers,year==1988))
mod_ov_89<-glmmTMB(n_ovules~relpos_fl*relpos_rac+
                        (1|id/shoot_id/raceme_id),
                subset(data_id_flowers,year==1989))
# OK with random factors and nesting?
summary(mod_ov_87)
```

```
##  Family: gaussian  ( identity )
## Formula:
## n_ovules ~ relpos_fl * relpos_rac + (1 | id/shoot_id/raceme_id)
## Data: subset(data_id_flowers, year == 1987)
##
##      AIC      BIC   logLik deviance df.resid
##    974.4   1002.4   -479.2    958.4      236
##
## Random effects:
##
## Conditional model:
##  Groups                Name        Variance  Std.Dev.
```

```
##  raceme_id:shoot_id:id (Intercept) 8.128e-09 9.016e-05
##  shoot_id:id           (Intercept) 5.859e-07 7.654e-04
##  id                    (Intercept) 1.521e+00 1.233e+00
##  Residual                          2.000e+00 1.414e+00
## Number of obs: 244, groups:
## raceme_id:shoot_id:id, 157; shoot_id:id, 105; id, 102
##
## Dispersion estimate for gaussian family (sigma^2):    2
##
## Conditional model:
##                      Estimate Std. Error z value Pr(>|z|)
## (Intercept)           13.3682     0.6467  20.671   <2e-16 ***
## relpos_fl              0.8461     1.7448   0.485    0.628
## relpos_rac            -0.1456     1.4484  -0.100    0.920
## relpos_fl:relpos_rac  -3.2357     3.9266  -0.824    0.410
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
summary(mod_ov_88)
```

```
##  Family: gaussian  ( identity )
## Formula:
## n_ovules ~ relpos_fl * relpos_rac + (1 | id/shoot_id/raceme_id)
## Data: subset(data_id_flowers, year == 1988)
##
##      AIC      BIC   logLik deviance df.resid
##   1018.1   1047.9   -501.0   1002.1      297
##
## Random effects:
##
## Conditional model:
##  Groups                Name        Variance Std.Dev.
##  raceme_id:shoot_id:id (Intercept) 0.3014   0.5490
##  shoot_id:id           (Intercept) 0.1290   0.3592
##  id                    (Intercept) 1.2256   1.1071
##  Residual                          0.6522   0.8076
## Number of obs: 305, groups:
## raceme_id:shoot_id:id, 210; shoot_id:id, 150; id, 127
##
## Dispersion estimate for gaussian family (sigma^2): 0.652
##
## Conditional model:
##                      Estimate Std. Error z value Pr(>|z|)
## (Intercept)           14.0609     0.4000   35.16   <2e-16 ***
## relpos_fl              1.3075     0.9819    1.33    0.183
## relpos_rac            -0.1296     0.8754   -0.15    0.882
## relpos_fl:relpos_rac  -4.7439     2.2627   -2.10    0.036 *
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
summary(mod_ov_89)
```

```
##  Family: gaussian  ( identity )
```

```
## Formula:
## n_ovules ~ relpos_fl * relpos_rac + (1 | id/shoot_id/raceme_id)
## Data: subset(data_id_flowers, year == 1989)
##
##      AIC      BIC   logLik deviance df.resid
##       NA       NA       NA       NA      223
##
## Random effects:
##
## Conditional model:
##  Groups                Name        Variance  Std.Dev.
##  raceme_id:shoot_id:id (Intercept) 3.286e-09 5.732e-05
##  shoot_id:id           (Intercept) 1.063e-07 3.261e-04
##  id                    (Intercept) 1.204e+00 1.097e+00
##  Residual                          9.831e-01 9.915e-01
## Number of obs: 231, groups:
## raceme_id:shoot_id:id, 143; shoot_id:id, 81; id, 66
##
## Dispersion estimate for gaussian family (sigma^2): 0.983
##
## Conditional model:
##                       Estimate Std. Error z value Pr(>|z|)
## (Intercept)            15.1606     0.4584   33.07  < 2e-16 ***
## relpos_fl              -3.9002     1.1859   -3.29  0.00101 **
## relpos_rac             -2.9094     0.9551   -3.05  0.00232 **
## relpos_fl:relpos_rac    5.4481     2.6182    2.08  0.03744 *
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

Interaction significant in 1988 and 1989. Refit model for 1987 without interaction.

```
mod_ov_87<-glmmTMB(n_ovules~relpos_fl+relpos_rac+
                       (1|id/shoot_id/raceme_id),
               subset(data_id_flowers,year==1987))
# OK with random factors and nesting?
summary(mod_ov_87)
```

```
##  Family: gaussian  ( identity )
## Formula:
## n_ovules ~ relpos_fl + relpos_rac + (1 | id/shoot_id/raceme_id)
## Data: subset(data_id_flowers, year == 1987)
##
##      AIC      BIC   logLik deviance df.resid
##       NA       NA       NA       NA      237
##
## Random effects:
##
## Conditional model:
##  Groups                Name        Variance  Std.Dev.
##  raceme_id:shoot_id:id (Intercept) 2.206e-23 4.697e-12
##  shoot_id:id           (Intercept) 6.227e-07 7.891e-04
##  id                    (Intercept) 1.499e+00 1.224e+00
##  Residual                          2.017e+00 1.420e+00
```

```
## Number of obs: 244, groups:
## raceme_id:shoot_id:id, 157; shoot_id:id, 105; id, 102
##
## Dispersion estimate for gaussian family (sigma^2): 2.02
##
## Conditional model:
##              Estimate Std. Error z value Pr(>|z|)
## (Intercept)  13.7970     0.3885   35.51   <2e-16 ***
## relpos_fl    -0.5067     0.6056   -0.84   0.4028
## relpos_rac   -1.1948     0.6963   -1.72   0.0862 .
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

Table 3

```r
tab_model(mod_ov_87,mod_ov_88,mod_ov_89,
          transform=NULL,show.intercept=F,show.ci=F,show.se=T,show.stat=T,
          show.r2=T,show.icc=F,show.re.var=F,show.ngroups=F,digits=3,
          dv.labels=c("1987","1988","1989"),
          file="output/tables/Table3.doc")
```

1987

1988

1989

Predictors

Estimates

std. Error

Statistic

p

Estimates

std. Error

Statistic

p

Estimates

std. Error

Statistic

p

relpos fl

-0.507

0.606

-0.837

0.403

1.307

0.982

1.332

0.183

-3.900

1.186

-3.289

0.001

relpos rac

-1.195

0.696

-1.716

0.086

-0.130

0.875

-0.148

0.882

-2.909

0.955

-3.046

0.002

relpos fl × relpos rac

-4.744

2.263

-2.097

0.036

5.448

2.618

2.081

0.037

Observations

244

305

231

Marginal R2 / Conditional R2

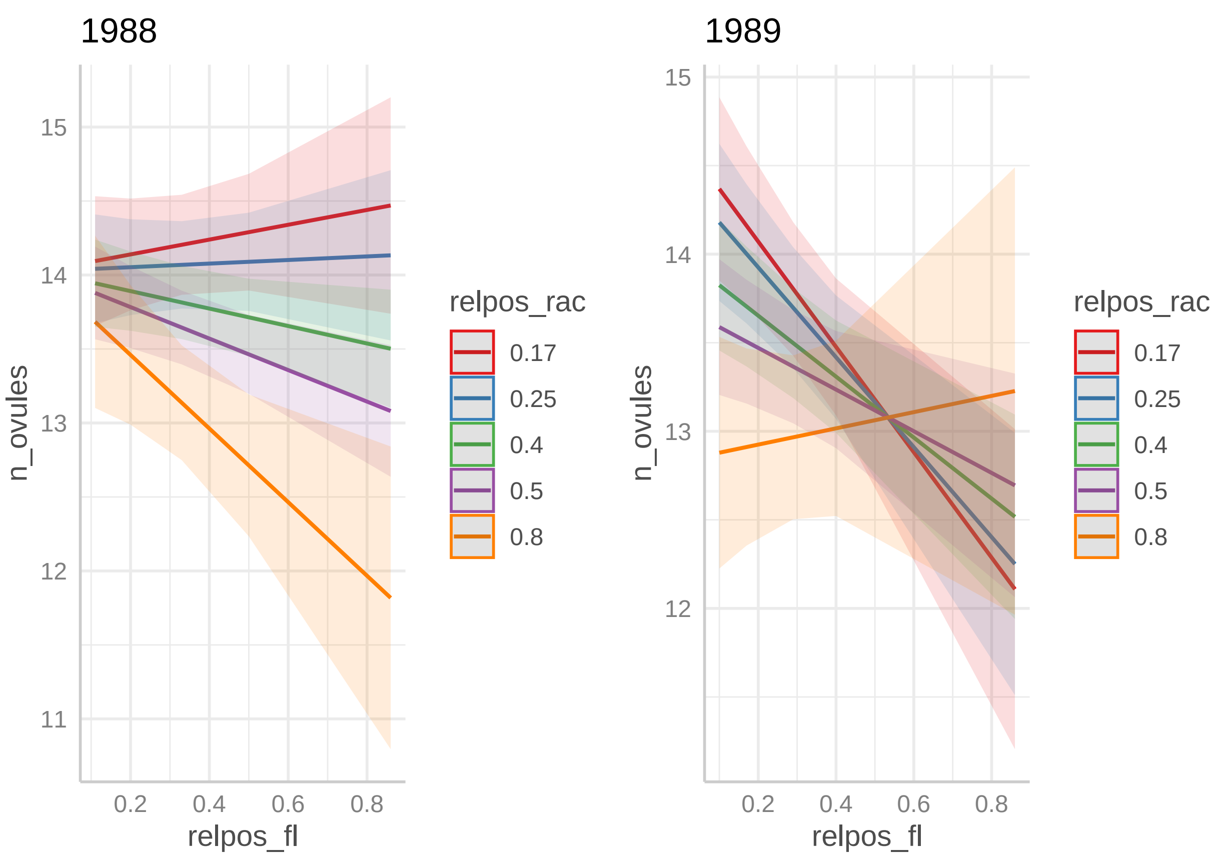
0.021 / NA

0.051 / 0.732

0.125 / NA

Figure 6

```
fig6<-grid.arrange(
  plot(ggpredict(mod_ov_88,
                 terms=c("relpos_fl[quart]","relpos_rac[quart]")))+
    ggtitle("1988"),
  plot(ggpredict(mod_ov_89,
                 terms=c("relpos_fl[quart]","relpos_rac[quart]")))+
    ggtitle("1989"),
  ncol=2)
```




```
ggsave(filename="output/figures/fig6.tiff",plot=fig6,
       width=18,height=8,units="cm",dpi=300)
```

No significant effects on ovule number in 1987. Main effects non-significant but interaction significant in 1988. Main effects and interaction significant in 1989.

Q5: Effects of flower position on seed predation

Does seed predation of individual flowers depend on flower position within and among the racemes?

H: We expect that basal flowers have a higher seed predation than distal flowers within the raceme, and that flowers on basal racemes have a higher seed predation than flowers on distal racemes.

Proportion of predated seeds

```
mod_seedpred_87<-glmmTMB(cbind(n_pred_seeds,n_seeds)~relpos_fl*relpos_rac+
                           (1|id/shoot_id/raceme_id),
                         subset(data_id_flowers,year==1987),family="binomial")
mod_seedpred_88<-glmmTMB(cbind(n_pred_seeds,n_seeds)~relpos_fl*relpos_rac+
                           (1|id/shoot_id/raceme_id),
                         subset(data_id_flowers,year==1988),family="binomial")
mod_seedpred_89<-glmmTMB(cbind(round(n_pred_seeds),n_seeds)~relpos_fl*relpos_rac+
                           (1|id/shoot_id/raceme_id),
                         subset(data_id_flowers,year==1989),family="binomial")
summary(mod_seedpred_87)
```

```
##  Family: binomial  ( logit )
## Formula:          cbind(n_pred_seeds, n_seeds) ~ relpos_fl * relpos_rac + (1 |
##     id/shoot_id/raceme_id)
## Data: subset(data_id_flowers, year == 1987)
##
##      AIC      BIC   logLik deviance df.resid
##    258.6    283.0   -122.3    244.6      237
##
## Random effects:
##
## Conditional model:
##  Groups                Name        Variance  Std.Dev.
##  raceme_id:shoot_id:id (Intercept) 8.039e-09 8.966e-05
##  shoot_id:id           (Intercept) 2.533e-06 1.591e-03
##  id                    (Intercept) 2.440e+01 4.939e+00
## Number of obs: 244, groups:
## raceme_id:shoot_id:id, 157; shoot_id:id, 105; id, 102
##
## Conditional model:
##                      Estimate Std. Error z value Pr(>|z|)
## (Intercept)            -6.559      1.591  -4.123 3.74e-05 ***
## relpos_fl               1.036      3.537   0.293    0.770
## relpos_rac              0.170      2.511   0.068    0.946
## relpos_fl:relpos_rac   -7.250      9.525  -0.761    0.447
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
summary(mod_seedpred_88)
```

```
##  Family: binomial  ( logit )
## Formula:          cbind(n_pred_seeds, n_seeds) ~ relpos_fl * relpos_rac + (1 |
```

```
##     id/shoot_id/raceme_id)
## Data: subset(data_id_flowers, year == 1988)
##
##      AIC      BIC   logLik deviance df.resid
##    953.3    979.3   -469.7    939.3      298
##
## Random effects:
##
## Conditional model:
##  Groups                Name        Variance  Std.Dev.
##  raceme_id:shoot_id:id (Intercept) 1.629e-10 1.276e-05
##  shoot_id:id           (Intercept) 5.955e-09 7.717e-05
##  id                    (Intercept) 2.291e-01 4.786e-01
## Number of obs: 305, groups:
## raceme_id:shoot_id:id, 210; shoot_id:id, 150; id, 127
##
## Conditional model:
##                     Estimate Std. Error z value Pr(>|z|)
## (Intercept)          -0.4066     0.3115  -1.306    0.192
## relpos_fl            -1.0059     0.8209  -1.225    0.220
## relpos_rac           -0.7246     0.6966  -1.040    0.298
## relpos_fl:relpos_rac   1.2001     1.8637   0.644    0.520
```

```r
summary(mod_seedpred_89)
```

```
##  Family: binomial  ( logit )
## Formula:
## cbind(round(n_pred_seeds), n_seeds) ~ relpos_fl * relpos_rac +
##     (1 | id/shoot_id/raceme_id)
## Data: subset(data_id_flowers, year == 1989)
##
##      AIC      BIC   logLik deviance df.resid
##    517.7    541.8   -251.8    503.7      225
##
## Random effects:
##
## Conditional model:
##  Groups                Name        Variance Std.Dev.
##  raceme_id:shoot_id:id (Intercept) 0.1721   0.4148
##  shoot_id:id           (Intercept) 0.2529   0.5029
##  id                    (Intercept) 1.6151   1.2709
## Number of obs: 232, groups:
## raceme_id:shoot_id:id, 143; shoot_id:id, 81; id, 66
##
## Conditional model:
##                     Estimate Std. Error z value Pr(>|z|)
## (Intercept)         -2.09866    0.68584  -3.060  0.00221 **
## relpos_fl           -0.03327    1.95706  -0.017  0.98644
## relpos_rac           0.87108    1.47357   0.591  0.55443
## relpos_fl:relpos_rac -3.61863    4.48923  -0.806  0.42020
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

Interaction not significant in any of the years. Refit models without interaction.

```r
mod_seedpred_87<-glmmTMB(cbind(n_pred_seeds,n_seeds)~relpos_fl+relpos_rac+
                           (1|id/shoot_id/raceme_id),
                         subset(data_id_flowers,year==1987),family="binomial")
mod_seedpred_88<-glmmTMB(cbind(n_pred_seeds,n_seeds)~relpos_fl+relpos_rac+
                           (1|id/shoot_id/raceme_id),
                         subset(data_id_flowers,year==1988),family="binomial")
mod_seedpred_89<-glmmTMB(cbind(round(n_pred_seeds),n_seeds)~relpos_fl+relpos_rac+
                           (1|id/shoot_id/raceme_id),
                         subset(data_id_flowers,year==1989),family="binomial")
summary(mod_seedpred_87)
```

```
##  Family: binomial  ( logit )
## Formula:          cbind(n_pred_seeds, n_seeds) ~ relpos_fl + relpos_rac + (1 |
##     id/shoot_id/raceme_id)
## Data: subset(data_id_flowers, year == 1987)
##
##      AIC      BIC   logLik deviance df.resid
##    257.2    278.1   -122.6    245.2      238
##
## Random effects:
##
## Conditional model:
##  Groups                Name        Variance  Std.Dev.
##  raceme_id:shoot_id:id (Intercept) 7.049e-11 8.396e-06
##  shoot_id:id           (Intercept) 5.109e-09 7.148e-05
##  id                    (Intercept) 2.549e+01 5.049e+00
## Number of obs: 244, groups:
## raceme_id:shoot_id:id, 157; shoot_id:id, 105; id, 102
##
## Conditional model:
##             Estimate Std. Error z value Pr(>|z|)
## (Intercept)   -6.079      1.439  -4.224  2.4e-05 ***
## relpos_fl     -1.565      1.095  -1.430    0.153
## relpos_rac    -1.487      1.270  -1.171    0.242
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```r
summary(mod_seedpred_88)
```

```
##  Family: binomial  ( logit )
## Formula:          cbind(n_pred_seeds, n_seeds) ~ relpos_fl + relpos_rac + (1 |
##     id/shoot_id/raceme_id)
## Data: subset(data_id_flowers, year == 1988)
##
##      AIC      BIC   logLik deviance df.resid
##    951.7    974.0   -469.9    939.7      299
##
## Random effects:
##
## Conditional model:
##  Groups                Name        Variance  Std.Dev.
##  raceme_id:shoot_id:id (Intercept) 7.210e-11 8.491e-06
```

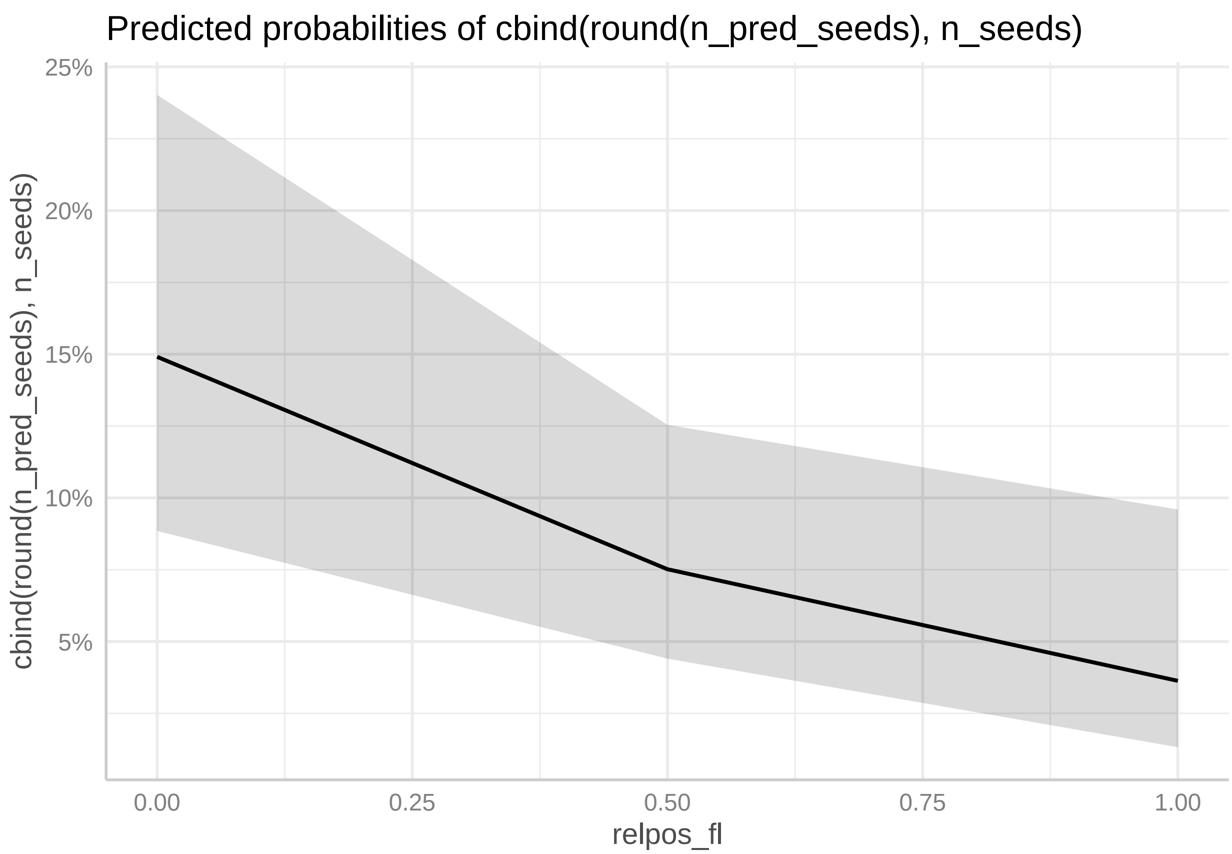
```
##  shoot_id:id           (Intercept) 4.734e-09 6.881e-05
##  id                    (Intercept) 2.289e-01 4.784e-01
## Number of obs: 305, groups:
## raceme_id:shoot_id:id, 210; shoot_id:id, 150; id, 127
##
## Conditional model:
##             Estimate Std. Error z value Pr(>|z|)
## (Intercept)  -0.5709     0.1791  -3.188  0.00143 **
## relpos_fl    -0.5086     0.2753  -1.848  0.06466 .
## relpos_rac   -0.3216     0.3057  -1.052  0.29281
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```r
summary(mod_seedpred_89)
```

```
##  Family: binomial  ( logit )
## Formula:
## cbind(round(n_pred_seeds), n_seeds) ~ relpos_fl + relpos_rac +
##     (1 | id/shoot_id/raceme_id)
## Data: subset(data_id_flowers, year == 1989)
##
##      AIC      BIC   logLik deviance df.resid
##    516.3    537.0   -252.2    504.3      226
##
## Random effects:
##
## Conditional model:
##  Groups                Name        Variance Std.Dev.
##  raceme_id:shoot_id:id (Intercept) 0.1722   0.4150
##  shoot_id:id           (Intercept) 0.2508   0.5008
##  id                    (Intercept) 1.6442   1.2823
## Number of obs: 232, groups:
## raceme_id:shoot_id:id, 143; shoot_id:id, 81; id, 66
##
## Conditional model:
##             Estimate Std. Error z value Pr(>|z|)
## (Intercept)  -1.6617     0.4181  -3.974 7.06e-05 ***
## relpos_fl    -1.5366     0.6355  -2.418   0.0156 *
## relpos_rac   -0.1955     0.6553  -0.298   0.7654
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

Only significant effect of relpos_fl in 1989

```r
plot(ggpredict(mod_seedpred_89,terms="relpos_fl"))
```



In 1989, basal flowers (lower relpos_fl) have a higher seed predation than distal flowers within the raceme.

Seed predation y/n

```
mod_seedpred_yn_87<-glmmTMB(seed_predation~relpos_fl*relpos_rac+
                          (1|id/shoot_id/raceme_id),
                        subset(data_id_flowers,year==1987),family="binomial")
mod_seedpred_yn_88<-glmmTMB(seed_predation~relpos_fl*relpos_rac+
                          (1|id/shoot_id/raceme_id),
                        subset(data_id_flowers,year==1988),family="binomial")
mod_seedpred_yn_89<-glmmTMB(seed_predation~relpos_fl*relpos_rac+
                          (1|id/shoot_id/raceme_id),
                        subset(data_id_flowers,year==1989),family="binomial")
# OK with random factors and nesting?
summary(mod_seedpred_yn_87)
```

```
##  Family: binomial  ( logit )
## Formula:
## seed_predation ~ relpos_fl * relpos_rac + (1 | id/shoot_id/raceme_id)
## Data: subset(data_id_flowers, year == 1987)
##
##      AIC      BIC   logLik deviance df.resid
##    134.6    159.1    -60.3    120.6      237
##
```

```
## Random effects:
##
## Conditional model:
##  Groups                Name        Variance  Std.Dev.
##  raceme_id:shoot_id:id (Intercept) 2.455e-09 4.955e-05
##  shoot_id:id           (Intercept) 9.804e-07 9.902e-04
##  id                    (Intercept) 3.688e+02 1.920e+01
## Number of obs: 244, groups:
## raceme_id:shoot_id:id, 157; shoot_id:id, 105; id, 102
##
## Conditional model:
##                       Estimate Std. Error z value Pr(>|z|)
## (Intercept)             -9.076      2.672  -3.396 0.000683 ***
## relpos_fl                5.237      7.903   0.663 0.507579
## relpos_rac               3.085      6.997   0.441 0.659284
## relpos_fl:relpos_rac   -36.840     28.638  -1.286 0.198304
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```r
summary(mod_seedpred_yn_88)
```

```
##  Family: binomial  ( logit )
## Formula:
## seed_predation ~ relpos_fl * relpos_rac + (1 | id/shoot_id/raceme_id)
## Data: subset(data_id_flowers, year == 1988)
##
##      AIC      BIC   logLik deviance df.resid
##    259.8    285.9   -122.9    245.8      298
##
## Random effects:
##
## Conditional model:
##  Groups                Name        Variance  Std.Dev.
##  raceme_id:shoot_id:id (Intercept) 4.047e+02 2.012e+01
##  shoot_id:id           (Intercept) 3.397e-11 5.828e-06
##  id                    (Intercept) 4.282e+01 6.544e+00
## Number of obs: 305, groups:
## raceme_id:shoot_id:id, 210; shoot_id:id, 150; id, 127
##
## Conditional model:
##                       Estimate Std. Error z value Pr(>|z|)
## (Intercept)             13.957      6.578   2.122   0.0339 *
## relpos_fl               -3.433     10.777  -0.318   0.7501
## relpos_rac              11.627     13.730   0.847   0.3971
## relpos_fl:relpos_rac   -34.786     27.185  -1.280   0.2007
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```r
summary(mod_seedpred_yn_89)
```

```
##  Family: binomial  ( logit )
## Formula:
## seed_predation ~ relpos_fl * relpos_rac + (1 | id/shoot_id/raceme_id)
```

```
## Data: subset(data_id_flowers, year == 1989)
##
##      AIC      BIC   logLik deviance df.resid
##    269.3    293.5   -127.7    255.3      225
##
## Random effects:
##
## Conditional model:
##  Groups                 Name        Variance Std.Dev.
##  raceme_id:shoot_id:id (Intercept) 2.539    1.593
##  shoot_id:id           (Intercept) 2.325    1.525
##  id                    (Intercept) 9.310    3.051
## Number of obs: 232, groups:
## raceme_id:shoot_id:id, 143; shoot_id:id, 81; id, 66
##
## Conditional model:
##                        Estimate Std. Error z value Pr(>|z|)
## (Intercept)           -0.09369    1.80116  -0.052    0.959
## relpos_fl             -1.15858    5.12698  -0.226    0.821
## relpos_rac             0.82627    3.91008   0.211    0.833
## relpos_fl:relpos_rac -6.46984   11.76885  -0.550    0.582
```

Interaction not significant in any of the years. Refit models without interaction.

```r
mod_seedpred_yn_87<-glmmTMB(seed_predation~relpos_fl+relpos_rac+
                      (1|id/shoot_id/raceme_id),
                    subset(data_id_flowers,year==1987),family="binomial")
mod_seedpred_yn_88<-glmmTMB(seed_predation~relpos_fl+relpos_rac+
                      (1|id/shoot_id/raceme_id),
                    subset(data_id_flowers,year==1988),family="binomial")
mod_seedpred_yn_89<-glmmTMB(seed_predation~relpos_fl+relpos_rac+
                      (1|id/shoot_id/raceme_id),
                    subset(data_id_flowers,year==1989),family="binomial")
# OK with random factors and nesting?
summary(mod_seedpred_yn_87)
```

```
##  Family: binomial  ( logit )
## Formula:
## seed_predation ~ relpos_fl + relpos_rac + (1 | id/shoot_id/raceme_id)
## Data: subset(data_id_flowers, year == 1987)
##
##      AIC      BIC   logLik deviance df.resid
##    135.0    156.0    -61.5    123.0      238
##
## Random effects:
##
## Conditional model:
##  Groups                 Name        Variance  Std.Dev.
##  raceme_id:shoot_id:id (Intercept) 4.226e-01 6.501e-01
##  shoot_id:id           (Intercept) 3.537e-07 5.948e-04
##  id                    (Intercept) 3.372e+02 1.836e+01
## Number of obs: 244, groups:
## raceme_id:shoot_id:id, 157; shoot_id:id, 105; id, 102
```

```
##
## Conditional model:
##             Estimate Std. Error z value Pr(>|z|)
## (Intercept)   -6.215      1.874  -3.316 0.000913 ***
## relpos_fl     -5.715      2.905  -1.967 0.049157 *
## relpos_rac    -5.882      3.597  -1.635 0.101982
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
summary(mod_seedpred_yn_88)
```

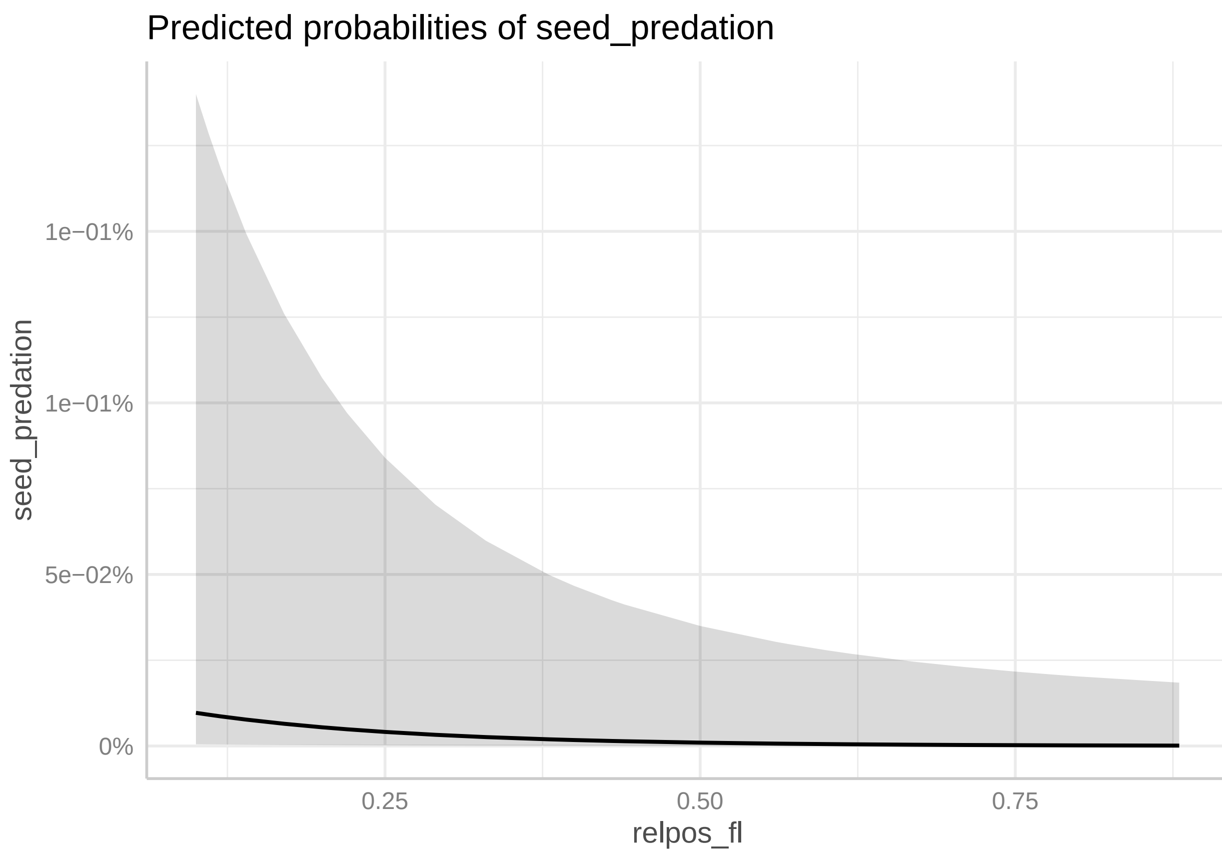
```
##  Family: binomial  ( logit )
## Formula:
## seed_predation ~ relpos_fl + relpos_rac + (1 | id/shoot_id/raceme_id)
## Data: subset(data_id_flowers, year == 1988)
##
##      AIC      BIC   logLik deviance df.resid
##    259.4    281.7   -123.7    247.4      299
##
## Random effects:
##
## Conditional model:
##  Groups                Name        Variance Std.Dev.
##  raceme_id:shoot_id:id (Intercept) 370.419  19.246
##  shoot_id:id           (Intercept)   8.047   2.837
##  id                    (Intercept)  41.655   6.454
## Number of obs: 305, groups:
## raceme_id:shoot_id:id, 210; shoot_id:id, 150; id, 127
##
## Conditional model:
##             Estimate Std. Error z value Pr(>|z|)
## (Intercept)   20.322      5.347   3.801 0.000144 ***
## relpos_fl    -16.537      4.924  -3.358 0.000784 ***
## relpos_rac    -4.768      5.805  -0.821 0.411505
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
summary(mod_seedpred_yn_89)
```

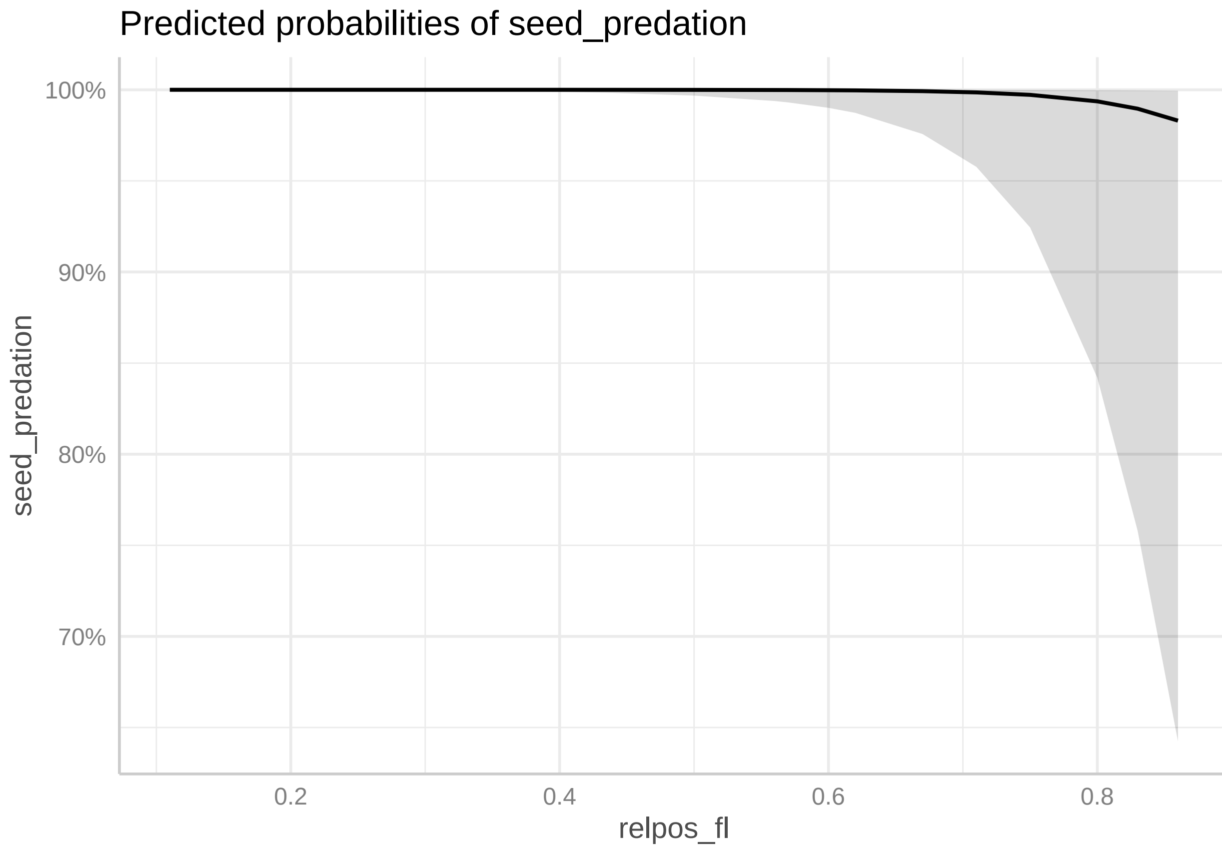
```
##  Family: binomial  ( logit )
## Formula:
## seed_predation ~ relpos_fl + relpos_rac + (1 | id/shoot_id/raceme_id)
## Data: subset(data_id_flowers, year == 1989)
##
##      AIC      BIC   logLik deviance df.resid
##    267.6    288.3   -127.8    255.6      226
##
## Random effects:
##
## Conditional model:
##  Groups                Name        Variance Std.Dev.
##  raceme_id:shoot_id:id (Intercept) 2.652    1.629
##  shoot_id:id           (Intercept) 2.608    1.615
```

```
##  id                    (Intercept) 9.273    3.045
## Number of obs: 232, groups:
## raceme_id:shoot_id:id, 143; shoot_id:id, 81; id, 66
##
## Conditional model:
##             Estimate Std. Error z value Pr(>|z|)
## (Intercept)   0.6794     1.1681   0.582   0.5608
## relpos_fl    -3.8277     1.9881  -1.925   0.0542 .
## relpos_rac   -1.0806     1.9172  -0.564   0.5730
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

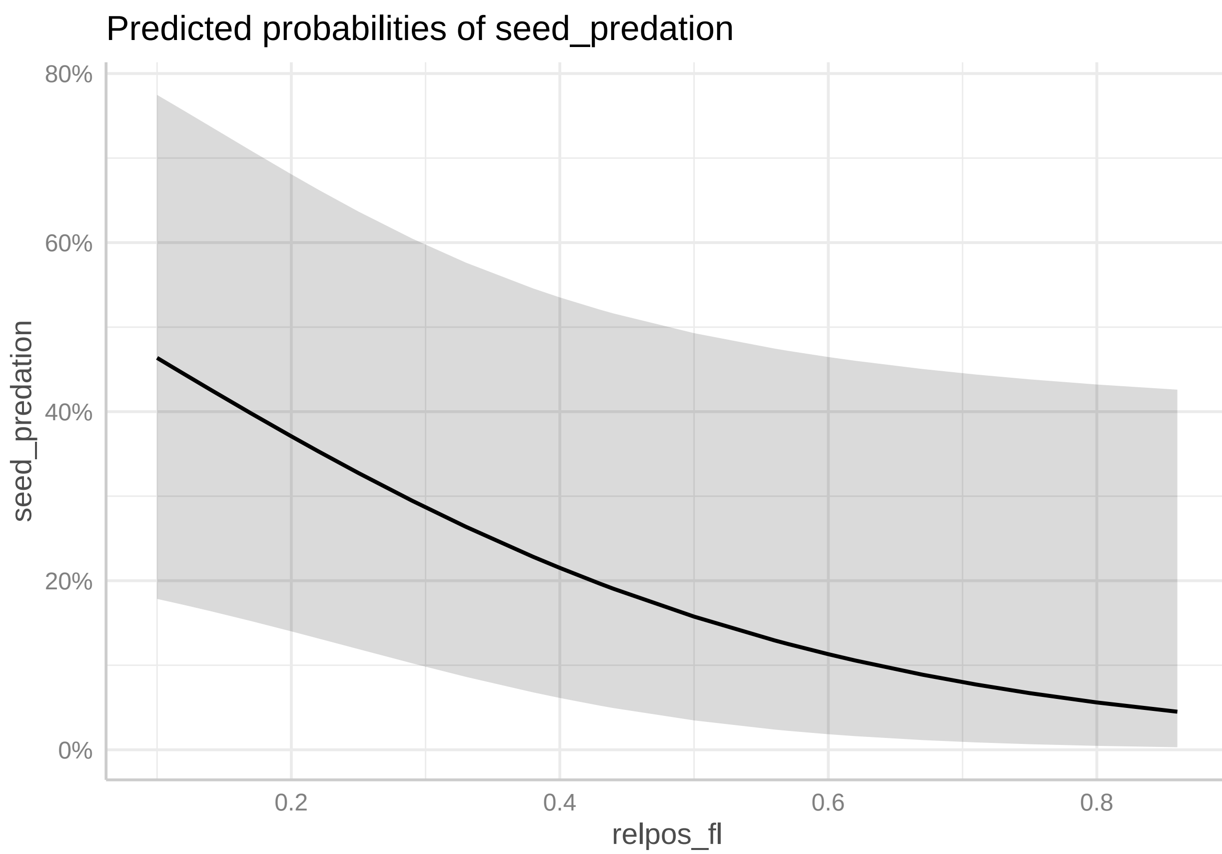
```
plot(ggpredict(mod_seedpred_yn_87,terms="relpos_fl[all]"
               ,allow.new.levels=T))
```




```
plot(ggpredict(mod_seedpred_yn_88,terms="relpos_fl[all]",
               allow.new.levels=T))
```




```r
plot(ggpredict(mod_seedpred_yn_89,terms="relpos_fl[all]",
                allow.new.levels=T)) # p=0.0542
```



Basal flowers (lower relpos_fl) have a higher probability of being attacked by seed predators than distal flowers within the raceme (marginally significant in 1989).

Session info

```r
sessionInfo()
```

```
## R version 4.3.0 (2023-04-21 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_0.10.4 lmerTest_3.1-3     lme4_1.1-33
##  [5] Matrix_1.5-4       gridExtra_2.3      sjPlot_2.8.14      glmmTMB_1.1.7
##  [9] ggeffects_1.2.2    brms_2.19.0        Rcpp_1.0.10        ggridges_0.5.4
## [13] ggthemes_4.2.4     RColorBrewer_1.1-3 moments_0.14.1     readxl_1.4.2
## [17] lubridate_1.9.2    forcats_1.0.0      stringr_1.5.0      dplyr_1.1.2
## [21] purrr_1.0.1        readr_2.1.4        tidyr_1.3.0        tibble_3.2.1
## [25] ggplot2_3.4.2      tidyverse_2.0.0
##
## loaded via a namespace (and not attached):
##   [1] tensorA_0.36.2       rstudioapi_0.14      jsonlite_1.8.4
##   [4] datawizard_0.7.1     magrittr_2.0.3       TH.data_1.1-2
##   [7] estimability_1.4.1   farver_2.1.1         nloptr_2.0.3
##  [10] rmarkdown_2.21       ragg_1.2.5           vctrs_0.6.2
##  [13] minqa_1.2.5          effectsize_0.8.3     base64enc_0.1-3
##  [16] htmltools_0.5.5      haven_2.5.2          distributional_0.3.2
##  [19] curl_5.0.0           broom_1.0.4          cellranger_1.1.0
##  [22] sjmisc_2.8.9         StanHeaders_2.26.26  htmlwidgets_1.6.2
##  [25] plyr_1.8.8           sandwich_3.0-2       emmeans_1.8.6
##  [28] zoo_1.8-12           TMB_1.9.4            igraph_1.4.3
##  [31] mime_0.12            lifecycle_1.0.3      pkgconfig_2.0.3
##  [34] colourpicker_1.2.0   sjlabelled_1.2.0     R6_2.5.1
##  [37] fastmap_1.1.1        shiny_1.7.4          digest_0.6.31
##  [40] numDeriv_2016.8-1.1  colorspace_2.1-0     ps_1.7.5
##  [43] textshaping_0.3.6    crosstalk_1.2.0      labeling_0.4.2
##  [46] fansi_1.0.4          timechange_0.2.0     abind_1.4-5
##  [49] compiler_4.3.0       bit64_4.0.5          withr_2.5.0
##  [52] backports_1.4.1      inline_0.3.19        shinystan_2.6.0
##  [55] highr_0.10           pkgbuild_1.4.0       MASS_7.3-58.4
##  [58] sjstats_0.18.2       gtools_3.9.4         loo_2.6.0
##  [61] tools_4.3.0          httpuv_1.6.11        threejs_0.3.3
##  [64] glue_1.6.2           callr_3.7.3          nlme_3.1-162
##  [67] promises_1.2.0.1     grid_4.3.0           checkmate_2.2.0
##  [70] reshape2_1.4.4       generics_0.1.3       gtable_0.3.3
##  [73] tzdb_0.4.0           hms_1.1.3            utf8_1.2.3
##  [76] pillar_1.9.0         markdown_1.7         vroom_1.6.3
##  [79] posterior_1.4.1      later_1.3.1          splines_4.3.0
##  [82] lattice_0.21-8       bit_4.0.5            survival_3.5-5
##  [85] tidyselect_1.2.0     miniUI_0.1.1.1       knitr_1.43
##  [88] V8_4.3.0             stats4_4.3.0         xfun_0.39
##  [91] bridgesampling_1.1-2 matrixStats_0.63.0   DT_0.28
##  [94] rstan_2.26.22        stringi_1.7.12       yaml_2.3.7
##  [97] boot_1.3-28.1        evaluate_0.21        codetools_0.2-19
## [100] cli_3.6.1            RcppParallel_5.1.7   parameters_0.21.1
## [103] systemfonts_1.0.4    shinythemes_1.2.0    xtable_1.8-4
## [106] munsell_0.5.0        processx_3.8.1       modelr_0.1.11
## [109] coda_0.19-4          parallel_4.3.0       rstantools_2.3.1
## [112] ellipsis_0.3.2       prettyunits_1.1.1    bayestestR_0.13.1
## [115] dygraphs_1.1.1.6     bayesplot_1.10.0     Brobdingnag_1.2-9
## [118] mvtnorm_1.1-3        scales_1.2.1         xts_0.13.1
```

```
## [121] insight_0.19.2       crayon_1.5.2         rlang_1.1.1
## [124] multcomp_1.4-23      shinyjs_2.1.0
```