# Model 1

```
brm(visits ~ autonomous_selfing_level + (1|net_id) + (1|gr(phylo, cov = A))
```

This model uses both quantitative and qualitative data of selfing levels which is grouped in 4 categories: "high", "medium", "low" and "none". The response variable is the integer of visits. Note that the quantitative measurement that we use is autonomous fruit production and is grouped as follows: 0=none, >0-25=low, >25-75=medium; >75-100=high.
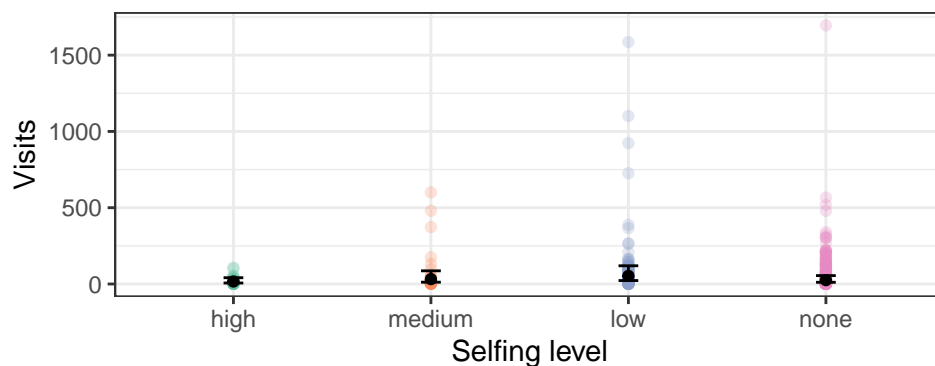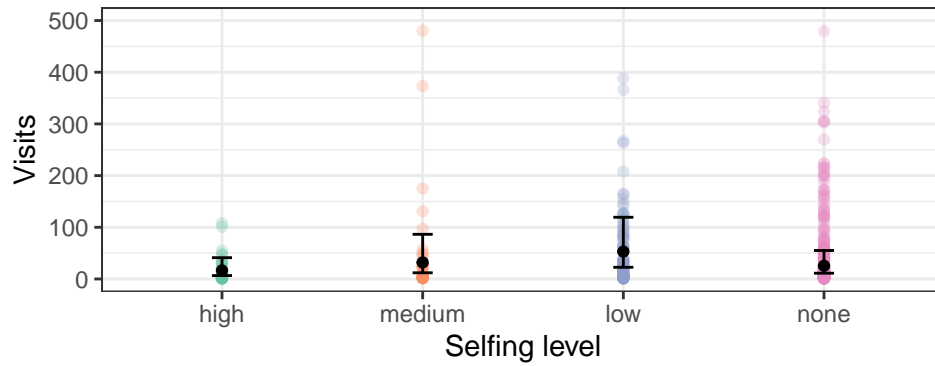
Check now the fit of the model:
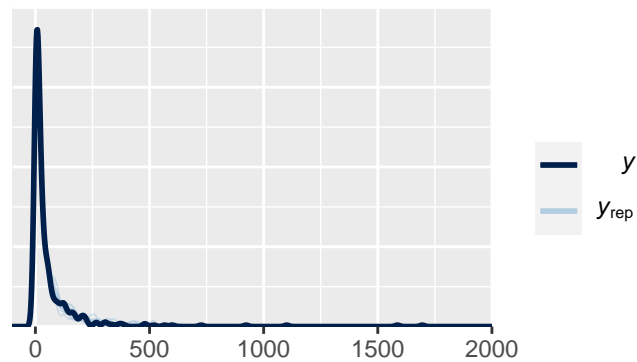


The fit seems right, check now estimates, se and credible intervals:

| autonomous_selfing_level | estimate___ | se___ | lower___ | upper___ |
|---|---|---|---|---|
| high | 16.46631 | 7.172786 | 6.54490 | 41.17418 |
| medium | 32.03038 | 15.992431 | 11.96357 | 86.43711 |
| low | 53.04246 | 22.171801 | 22.59104 | 119.38276 |
| none | 25.50623 | 10.137330 | 11.23013 | 55.09680 |

Plot output:

Set ylim max to 500 in order to improve visualization Some data points not shown.



Try now to logit estimates, credible intervals and points, maybe improves visualization?
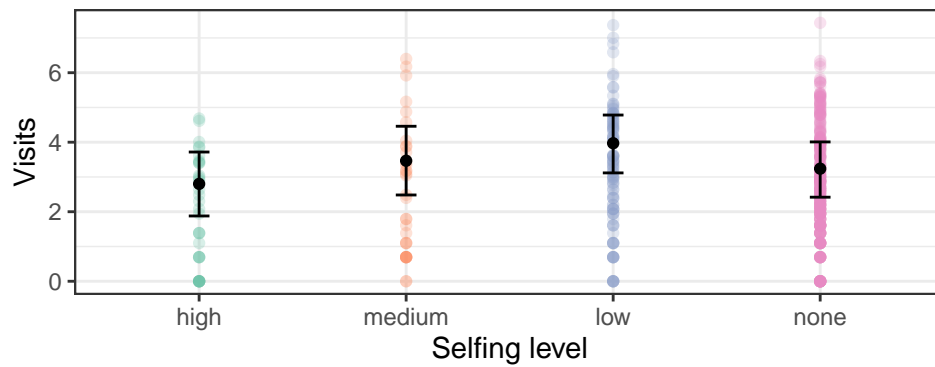


So far we haven't found big differences between groups. Also note that we have a greater number of low and none self species. This could be discussed. Keep in mind.

Now I´m going to exclude the dioecious and monoecioues species that were considered as non-selfers.

# Model 2 Excluding species with flowers with separated sexes

```
brm(visits ~ autonomous_selfing_level + (1|net_id) + (1|gr(phylo, cov = A))
```
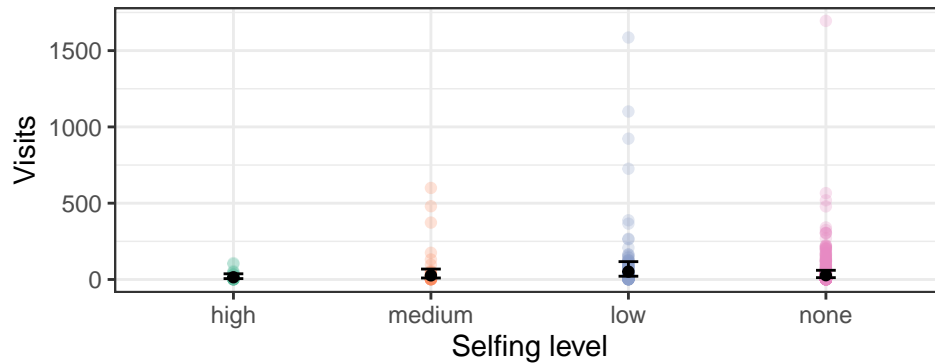
Check now the fit of the model:
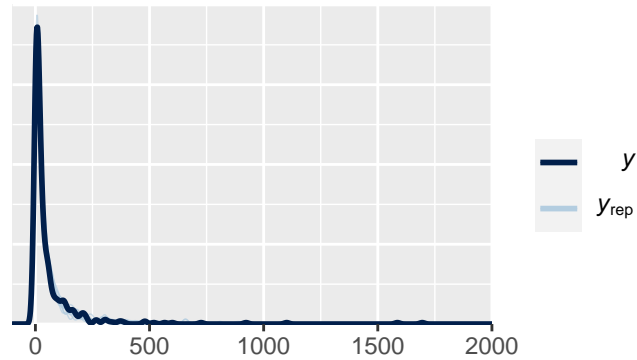


Again, the fit seems right, check now estimates, se and credible intervals:

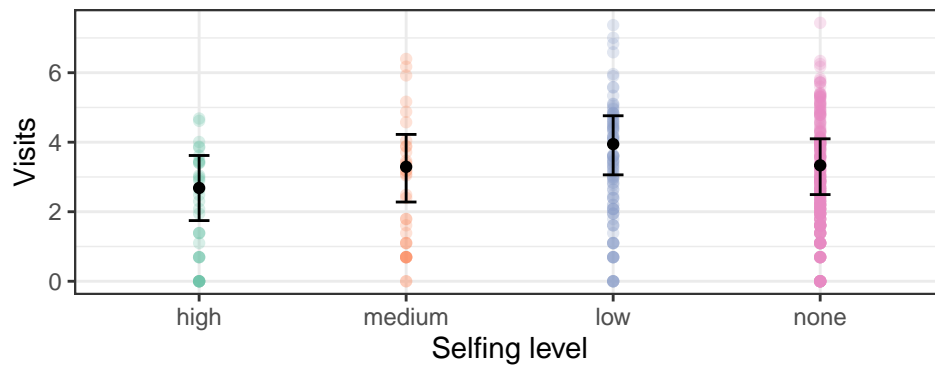| autonomous_selfing_level | estimate___ | se___ | lower___ | upper___ |
|---|---|---|---|---|
| high | 14.64717 | 6.555324 | 5.729252 | 37.28762 |
| medium | 26.89150 | 12.748789 | 9.772945 | 68.35116 |
| low | 51.69279 | 21.114401 | 21.363356 | 116.86905 |
| none | 28.07845 | 11.028904 | 12.107805 | 60.20638 |

Plot output:

Set ylim max to 500 in order to improve visualization Some data points not shown.
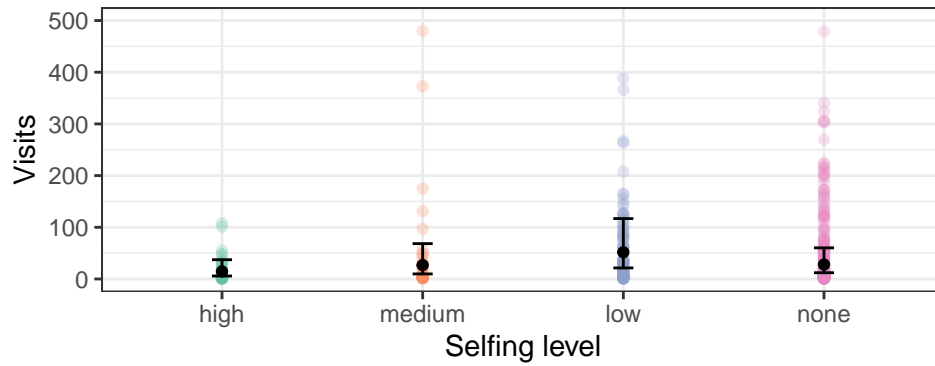


Logit estimates, credible intervals and points



Including or excluding dioecious and monoecious species does not make a very big differences in the models.

BAYES R2 Model 1 including all species

```
##      Estimate  Est.Error       Q2.5      Q97.5
## R2 0.2960526 0.07756711 0.1688188 0.4676823
```

```
##    autonomous_selfing_level    visits net_id phylo cond__ effect1__ estimate__
## 1                      high 65.47619     NA    NA      1      high   14.64717
## 2                    medium 65.47619     NA    NA      1    medium   26.89150
## 3                       low 65.47619     NA    NA      1       low   51.69279
## 4                      none 65.47619     NA    NA      1      none   28.07845
##        se__   lower__   upper__
## 1  6.555324  5.729252  37.28762
## 2 12.748789  9.772945  68.35116
```

```
## 3 21.114401 21.363356 116.86905

## 4 11.028904 12.107805  60.20638
```

BAYES R2 Model 1 without monoecious and dioecious species

```
##      Estimate  Est.Error      Q2.5      Q97.5
## R2 0.2478697 0.07965286 0.1252223 0.4299983

##   autonomous_selfing_level   visits net_id phylo cond__ effect1__ estimate__
## 1                     high 65.47619     NA    NA      1      high   14.64717
## 2                   medium 65.47619     NA    NA      1    medium   26.89150
## 3                      low 65.47619     NA    NA      1       low   51.69279
## 4                     none 65.47619     NA    NA      1      none   28.07845
##        se__    lower__   upper__
## 1  6.555324  5.729252  37.28762
## 2 12.748789  9.772945  68.35116
## 3 21.114401 21.363356 116.86905
## 4 11.028904 12.107805  60.20638
```

Because the qualitative data can add some noise to the analysis now I'm going to exclude it and just consider species that have quantitative information of the auntonomous selfing level.

# MODEL 3 JUST QUANTITATIVE DATA BUT GROUPED IN 4 CATEGORIES NONE, LOW, MEDIUM, HIGH.

Two distributions fit the data: **Negative binomial** and **skew gaussian** with logit transformation of visits and because for the negative binomial I have to to log transform the data in order to improve visualization. I'm going to keep from now on with a **skew gaussian** with the logit of visits (the output is quite similar).
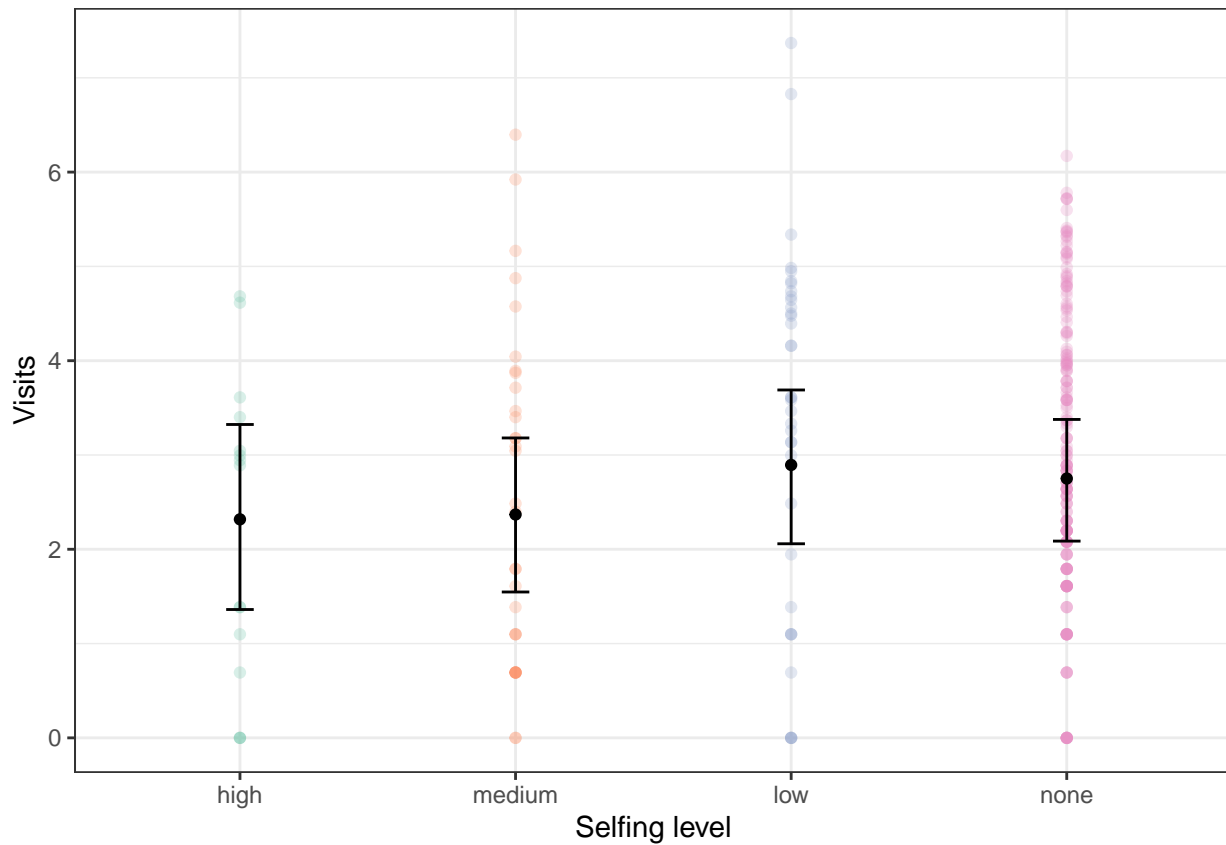
```
##       Estimate  Est.Error      Q2.5      Q97.5
## R2 0.3662231 0.07075732 0.2208557 0.4982124

##   autonomous_selfing_level log(visits)   visits net_id phylo cond__ effect1__
## 1                     high    4.106142 60.71206     NA    NA      1      high
## 2                   medium    4.106142 60.71206     NA    NA      1    medium
## 3                      low    4.106142 60.71206     NA    NA      1       low
## 4                     none    4.106142 60.71206     NA    NA      1      none
##   estimate__       se__   lower__   upper__
## 1   2.317643 0.4901701 1.361128 3.323500
## 2   2.368672 0.4046779 1.547036 3.180592
## 3   2.894266 0.4057195 2.058465 3.689323
## 4   2.750345 0.3171880 2.086709 3.376879
```