# 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.
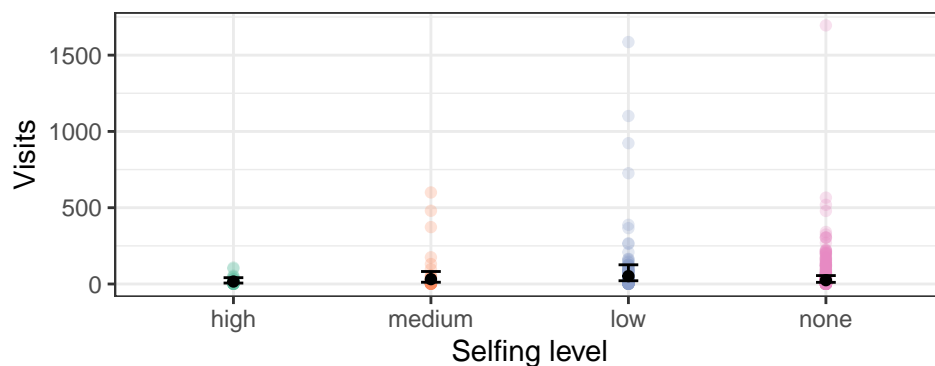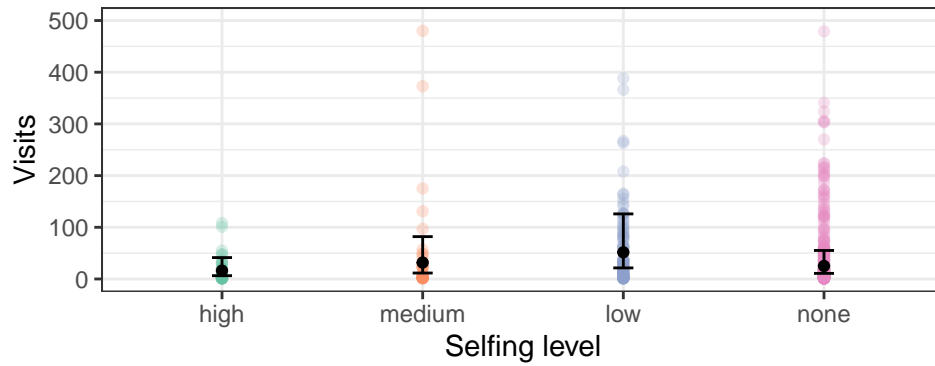
Check now the fit of the model:
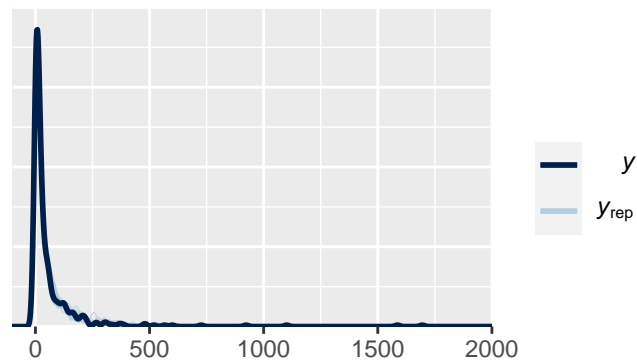
The fit seems right, check now estimates, se and credible intervals:

| autonomous_selfing_level	estimate___	se___	lower___	upper___
high	16.22890	7.237954	6.388558	41.40229
medium	31.81053	15.517126	11.542339	81.92444
low	51.62325	21.704897	21.417291	125.88574
none	25.07522	9.871306	10.825766	55.17484

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?
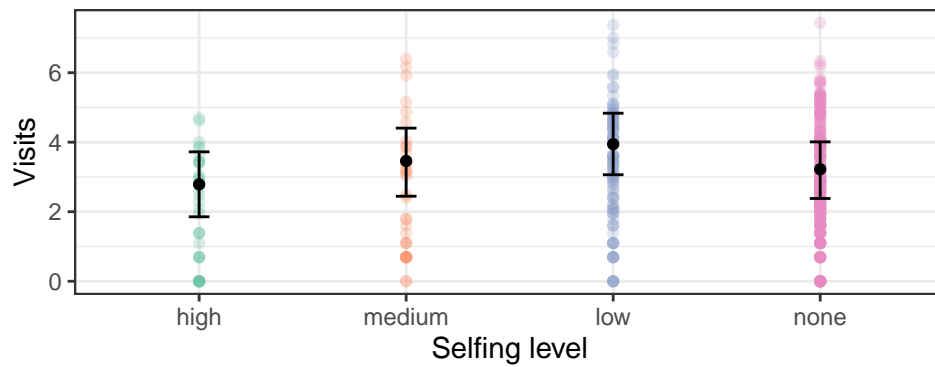

So far we haven't found big differences between groups. Also note that we have a greater number of low and none self species. This could be discussed. Keep in mind.

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))
```
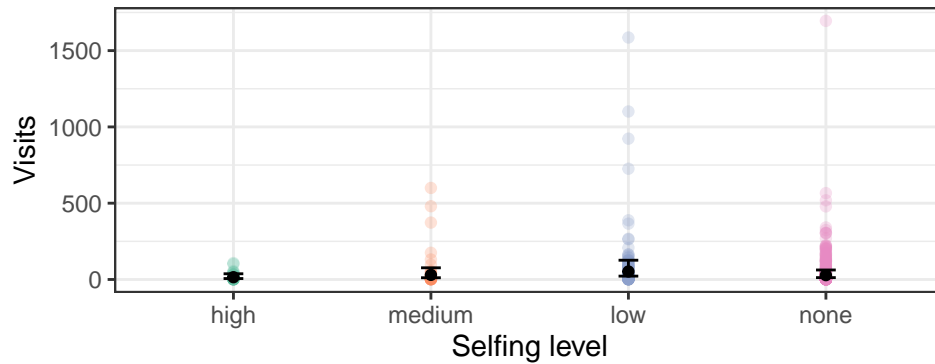
Check now the fit of the model:
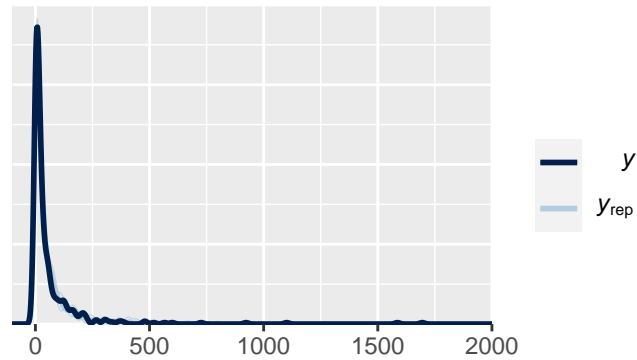
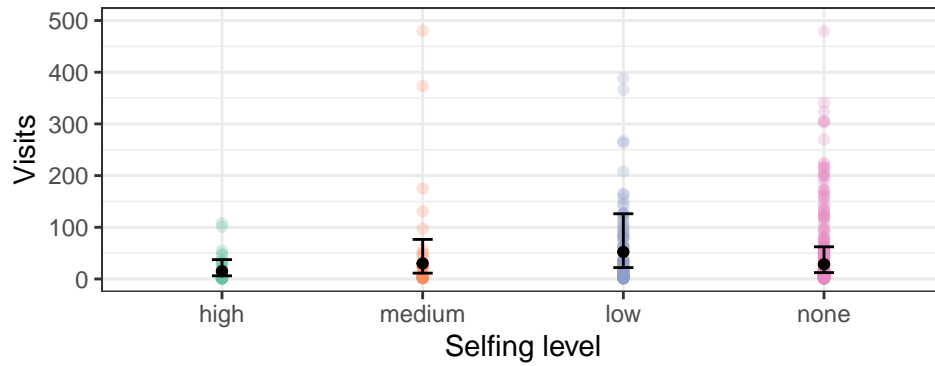Again, the fit seems right, check now estimates, se and credible intervals:

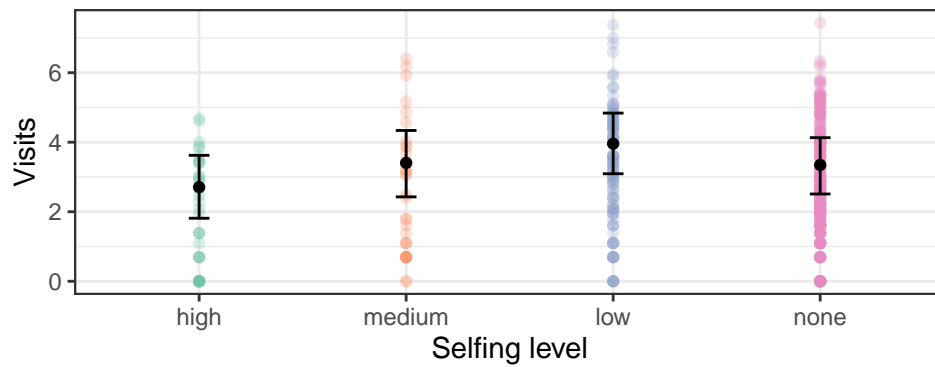| autonomous_selfing_level	estimate___	se___	lower___	upper___
high	14.99806	6.823373	6.126669	37.44073
medium	30.11032	14.079376	11.333166	76.56629
low	52.28513	21.083391	22.036199	126.20680
none	28.43006	10.913705	12.308011	62.22853

Plot output:

3

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  0.296992  0.07886342  0.1680863  0.4678135
```

```
##    autonomous_selfing_level   visits net_id phylo cond__ effect1__ estimate__
## 1                      high 65.28024     NA    NA      1      high   14.99806
## 2                    medium 65.28024     NA    NA      1    medium   30.11032
## 3                       low 65.28024     NA    NA      1       low   52.28513
## 4                      none 65.28024     NA    NA      1      none   28.43006
##         se__    lower__    upper__
## 1   6.823373   6.126669   37.44073
## 2  14.079376  11.333166   76.56629
```

```
## 3 21.083391 22.036198 126.20680

## 4 10.913705 12.308011  62.22853
```

BAYES R2 Model 1 without monoecious and dioecious species

```
##    Estimate  Est.Error      Q2.5     Q97.5
## R2 0.246085 0.07870143 0.1224886 0.4225047
```

```
##   autonomous_selfing_level   visits net_id phylo cond__ effect1__ estimate__
## 1                     high 65.28024    NA    NA      1      high   14.99806
## 2                   medium 65.28024    NA    NA      1    medium   30.11032
## 3                      low 65.28024    NA    NA      1       low   52.28513
## 4                     none 65.28024    NA    NA      1      none   28.43006
##         se__   lower__   upper__
## 1   6.823373  6.126669  37.44073
## 2  14.079376 11.333166  76.56629
## 3  21.083391 22.036198 126.20680
## 4  10.913705 12.308011  62.22853
```

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).
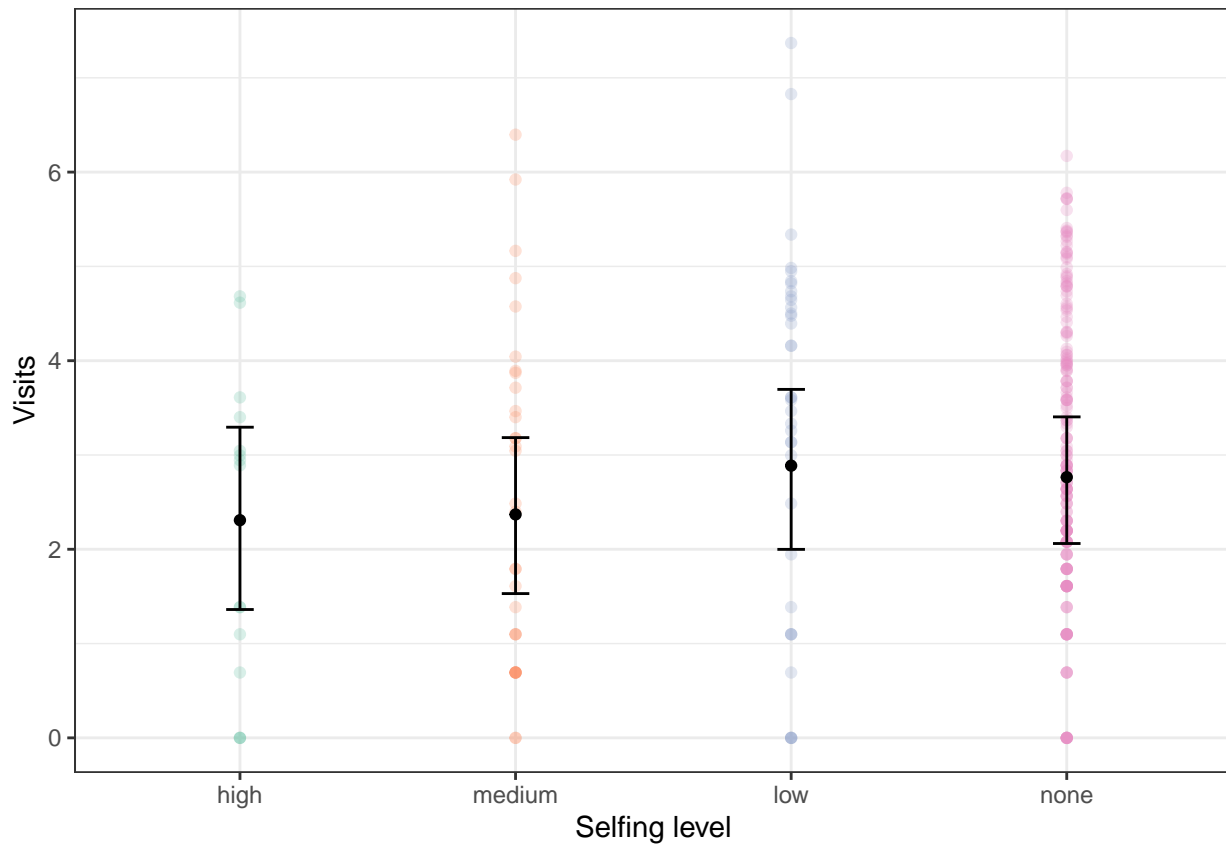
```
##      Estimate   Est.Error      Q2.5     Q97.5
## R2 0.3663574 0.07309651 0.2143842 0.499171

##   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   2.308604 0.4979512 1.361141 3.294633
## 2   2.369555 0.3962446 1.530127 3.184184
## 3   2.886825 0.4158274 1.998978 3.695772
## 4   2.764756 0.3249095 2.061301 3.404092
```