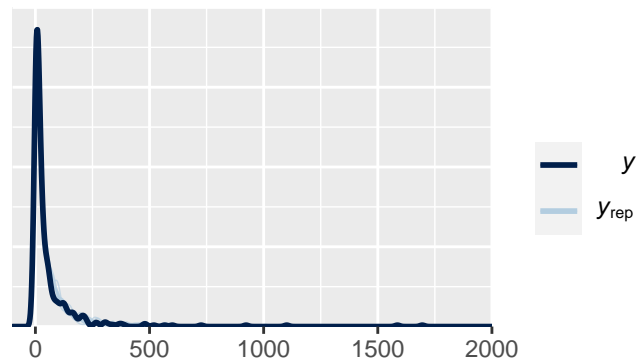


# Model 1

```
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.

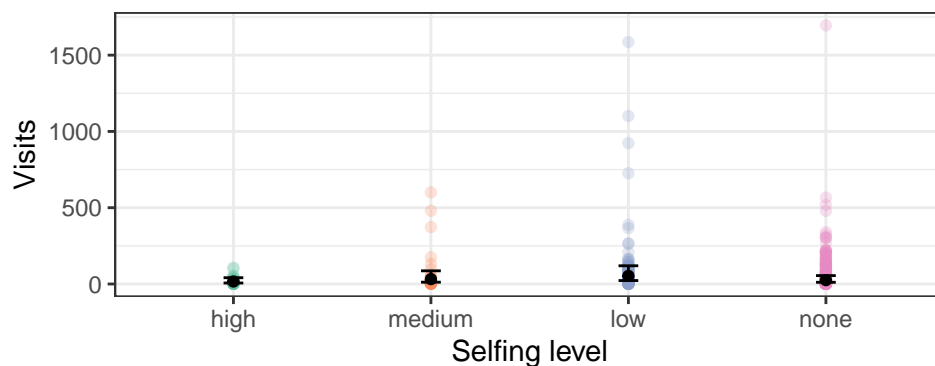
Check now the fit of the model:



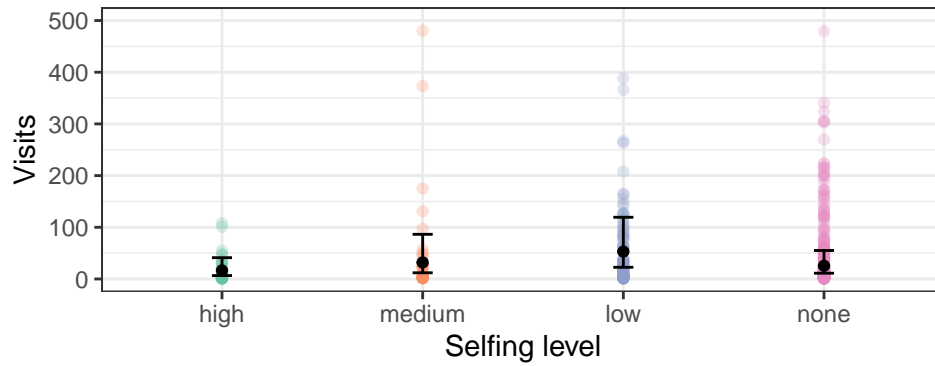
The fit seems right, check now estimates, se and credible intervals:

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

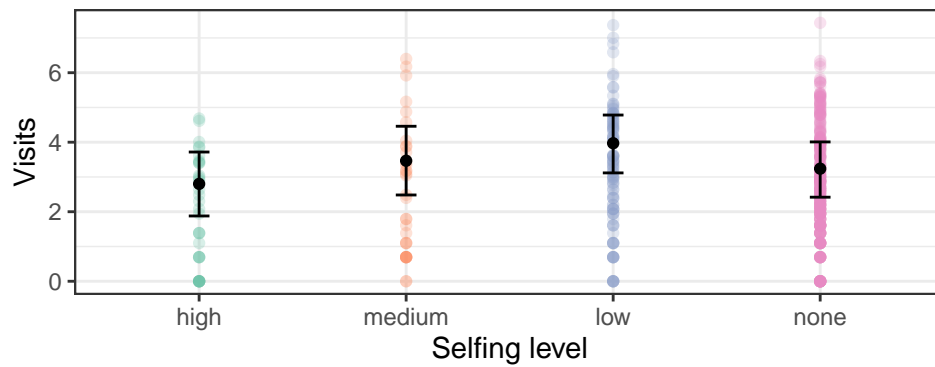
Plot output:



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?



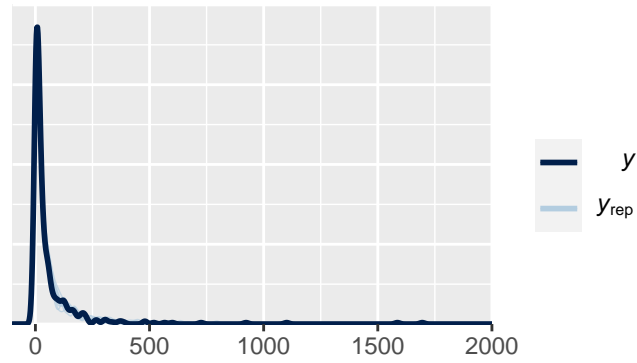
So far we haven't found big differences between groups. Also note that we have a greater number of low and none self species. This could be discussed. Keep in mind.

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

## Model 2

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

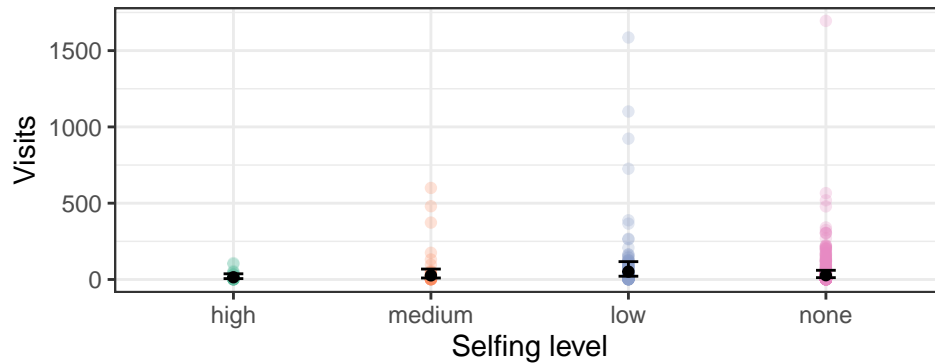
Check now the fit of the model:



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

autonomous_selfing_level	estimate__	se__	lower__	upper__
high	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.

