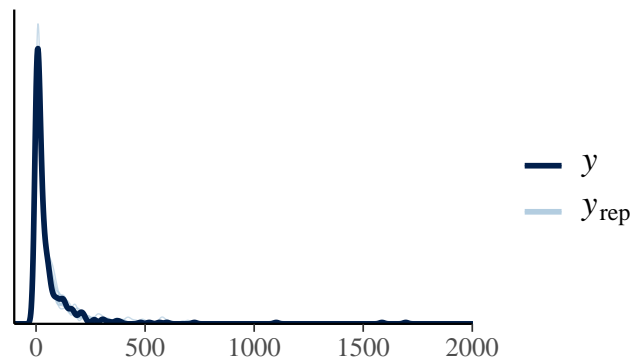


Model 1

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

This model contains both quantitative and qualitative data of selfing levels and the fixed effect is grouped in 4 categories of high, medium, low and none levels of selfing. The response variable is the integer of visits.

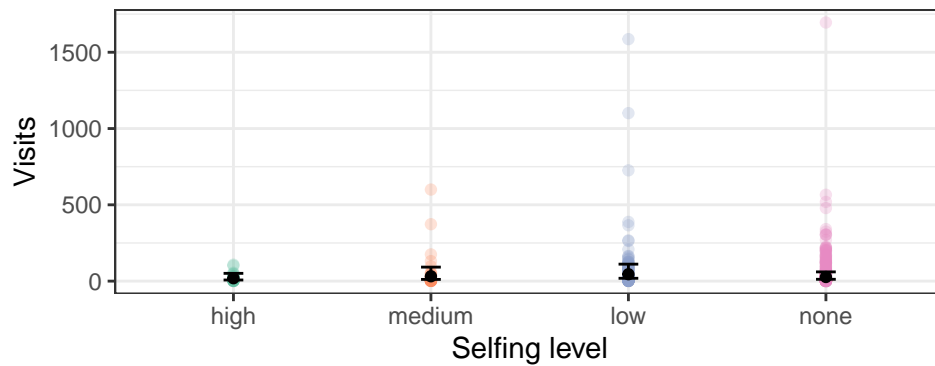
Check now the fit of the model:



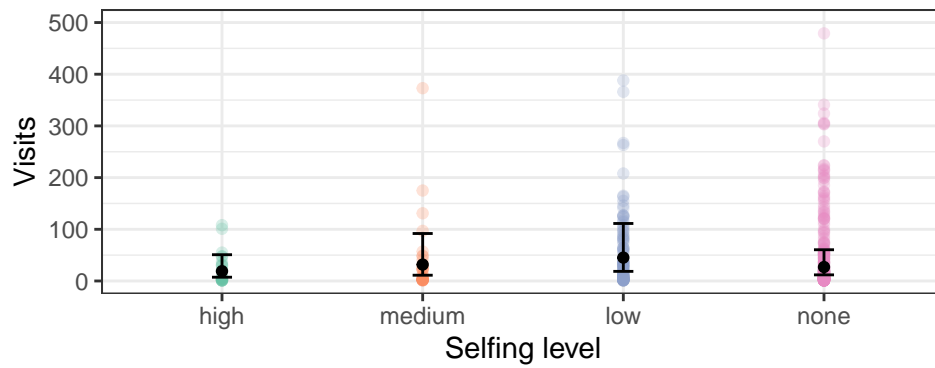
The fit seems right, check now estimates, se and credible intervals:

autonomous_selfing_level	estimate__	se__	lower__	upper__
high	18.95042	8.961369	7.276448	50.84844
medium	31.79574	15.794019	11.151221	91.82252
low	45.25257	20.163373	18.605345	111.24852
none	26.98599	10.901718	11.837674	60.44503

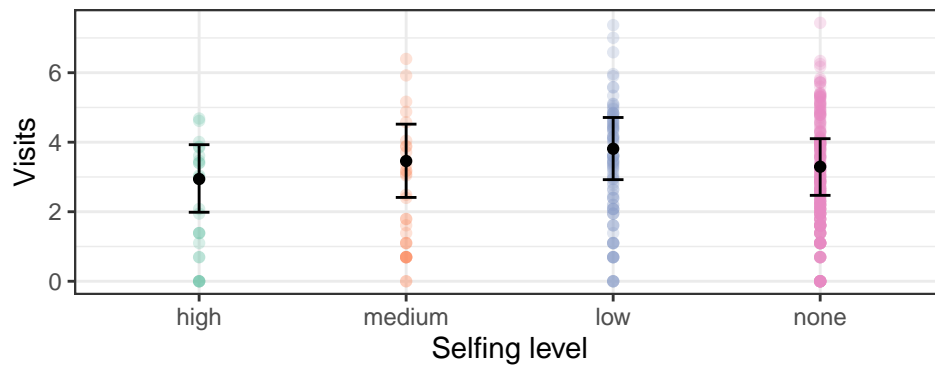
Plot output:



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?



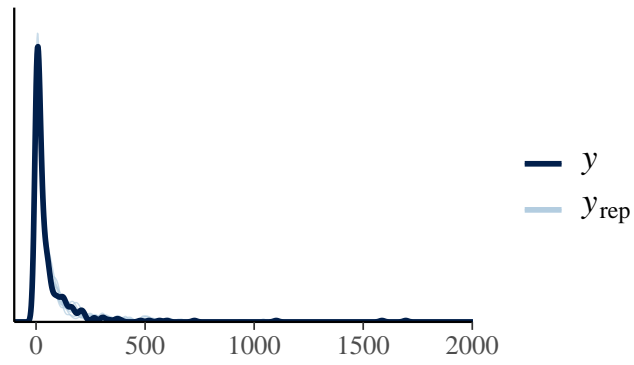
So far we haven't found big differences between groups. Also note that we have a greater number of low and none self species. This could be discussed. Keep in mind.

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	16.92305	7.681015	6.501945	43.88584
medium	25.96567	12.327886	9.656833	67.26103
low	47.81048	19.731773	20.626264	107.69210
none	31.69261	12.302849	13.612128	67.22745

Plot output:

