

Appendix A

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Parameter table

Below is table with all parameter values.

Global parameters			
Parameter	Parameter description	Parameter value	Value description
Population size	The amount of students at the year/in the cohort	$N = 50$	The set value is based on the mean of the cohorts C18 and C19 compared in the paper
Studygroup size	The number of study groups in a population. Determines how many students are in each study group	$\text{Group}_{\text{nr}} = 10$	The value divided the population into 10 study groups with 5 students in each, as this was the most frequent number in the real data
Time	The number of ticks the ABM should run, where one tick equals one day in a semester.	$t_{\text{max}} = 180$	Removing holidays and weekends, one semester is approximately 60 days, and it is desired to see the network after 3 semesters
Daily meet-ups	Determines how many other students each student can meet in a day.	$\text{daily}_{\text{con}} = 3$	Each student meets 3 other students in a day, as an average covering that the student will meet less people some days and more people other days
Connection base probability	Sets a baseline threshold for how likely it is for a student to connect to another student. It is not set to 100% to reflect that you can meet a person without necessarily becoming better friends	$\text{baseline}_{\text{connect}} = 50$	The baseline connection value is set to 50 to reflect a 50/50 chance of getting better acquainted when meeting another student
Friendship threshold	Determines how many times two students must connect before a friendship tie has been established. This parameter is introduced to incorporate that it is possible to meet other students and be acquainted without being “friends”	$u = 23$	To form a friendship tie, the students must meet and connect more than 23 times. This value was chosen based on test runs of the ABM showing similarity to the real-world network structure
Lockdown ON/OFF	Operationalizes the lockdown into three main parts which are consequences of restrictions:	$v_{\text{lockdown}} = 10$	Global decrease in the meeting weight of all students

	1) Removing in-person lectures and classes 2) Adding a global penalty to the possibility of meeting other students, as interaction without one’s own social circle was discouraged 3) Downsizing the amount of meet-ups each students has each day to simulate an assembly ban The parameter, if turned on, will be active after 60 days, as first semester was not affected	Friday bars OFF	Removing the possibility of having Friday bars
		In-person lectures & classes OFF	Removing in-person lectures and classes
		daily _{con} = 1	Change the amount of other students each student meets a day from 3 to 1
In person lecture or class ON/OFF	Adds a lecture/class every two day, where the probability of meeting and connecting to people outside your own social circle increases. The parameter reflects the idea that in-person interaction increases the chance not only of meeting but also connecting (see Introduction)	freq _l = 2	Frequency of lectures or classes in days, set to reflect that classes and lectures are not present every day
		V _{lecture} = 10	A global weight added to all students, evening out the probabilities of meeting for all the students – calibrated to fit C18 networks
		V _{lecture_con} = 5	A global weight added to all students, increasing the chance of connecting to their peers. Calibrated to fit C18 networks
Friday bar ON/OFF	Friday bars are parties held at the university campus and occur approximately every three to four weeks. The Friday bars are a social event, and the parameter thus introduce an increase in the probability of meeting students outside your own social circle, as well as increase the chance of connecting due to a more social setting	freq _{fb} = 21	Frequency of Friday bars in days, set to be every three/four weeks
		V _{friday_bar} = 20	A global weight added to all students, evening out the probabilities of meeting for all the students. The weight is higher than at lectures, as it is expected that the probabilities of meeting become even more even -
		V _{fridaybar_con} = 5	A global weight added to all students, increasing the chance of connecting to their peers
Agent-centric parameters			

Parameter	Parameter description	Parameter value	Value description
Meeting baseline	Adding random variance in the probability for certain students to meet, to account for the possibility that some student run into each other more easily (also outside of school)	$v_{\text{meet}} = 3$	Assign a random weight between 1 and 3 in the meeting matrix to each possible pair of students.
Connecting baseline	Adding random variance in the probability for certain students to connect to account for the possibility that some student might form connections more easily, e.g. because of mutual interest (which may be unrelated to their study)	$v_{\text{con}} = 4$	Assign a random weight between 1 and 4 in the meeting matrix to each possible pair of students. The value is set a bit higher than for meeting, as connection probabilities are not normalized across students, but are weights summed to lie between 1-100
Social trait	Each student is assigned a random social trait which defines how social they are, based on a normal distribution. This is done to account for the possibility that not all students are equally social. The trait affects how easily the student connects to other students – the higher the social trait, the higher the chance of connecting	$\text{mean}_{\text{st}} = 0$	The mean of the normal distribution from which the traits are sampled
		$\text{SD}_{\text{st}} = 4$	The standard deviation of the distribution. The SD is set to be four to allow for a large spread in how social people are (some are hyper-social and some are asocial)
Study group	Adds a bonus weight of meeting to students who are in the same study group to increase the probability of meeting a student from the same study group compared to other students. The influence of the parameter decays over time, as studygroups become less important and friendship ties have a larger influence on who you connect to $\text{Weight} = v_{\text{studygroup}} * e^{-\frac{t}{\text{divider}}}$	$v_{\text{studygroup}} = 15$	Adds a weight to student pairs in the meeting matrix who are in the same study group.
		$\text{divider} = 100$	Regulates the decay of the study group weight
		t	The day out of t_{max} . Used to regulate the influence of the parameter to decrease over time
Friend of a friend	The “friend of a friend” parameter is based on social network theories suggesting that people are more likely to befriend other people who are close in their network (see Introduction). This is operationalized by calculating the network measure <i>geodesic distance</i> , which is length of the path between	$v_{\text{dist}} = 10$	Regulates the size of the weight added by the friend of a friend parameter
		$\delta = 0.35$	Regulates how much the weight differs between students who are far away in

	two nodes (students) in a network, and adding a bonus weight to students who are close in the network, using the following equation:		the network and students who are close
	$\text{Weight} = v_{\text{dist}} * \delta^{\text{dist}} * \log(t)$ <p>The δ^{dist} is the decay function specifying a smaller weight the further away in the network two students are from each other. The $\log(t)$ regulates the influence of the parameter to increase over time as networks emerges</p>	dist	The geodesic distance between the two nodes (students) at the given timepoint t
		t	The day out of t_{max} . Used to regulate the influence of the parameter to increase over time
Preferential attachment	Preferential attachment states that people who are popular (have more friends) will attract more friendships (See Introduction section) This is operationalized as the following equation, increasing the size of the weight the more degrees a student has:	degree	The number of friendship-ties each student has formed in the network
	$\text{Weight} = (\text{degree}_{\text{student}_i} * \alpha) (\text{degree}_{\text{student}_j} * \alpha)$ <p>The parameter is in the first days of the ABM, as no friendships have been formed yet</p>	$\alpha = 0.018$	Regulates the weight size of preferential attachment

Analysis 1:

Bayesian Analysis & SNA of empirical data

Data collection - The experiment

The experiment for acquiring the network data had three steps, and the questions posed to the 2018-year and 2019-year varied only in phrasing. Only the edge data from point 1 and 2 are used in the present study, as the weights for 2018 and 2019 were collected with different questions.

1. The friendship network:

Participants are asked “*Name up to 10 friends in your study program*”. As the original experiment was targeted at completely new students during the introduction weeks to understand the impact of study on future friendships, it was needed to control for who were already friends. Therefore, for each friend named, the question “*Did you know that person before starting your university degree? Rate on a scale from 1 to 7; 1 being not at all, and 7 being best friends*” was added. Here, most weights were 1 most of the time, because most students did not know each other before university.

A follow up version of the survey included the question “*How well do you know that person?*” with a rating from scale 1-7. As the 2018 year had these types of weights, and the 2019 year had the former types of weights, we only use the edge-data in this study.

2. The study network:

Participants are asked “*Name the students in your study group*”.

3. The network of social beliefs: (Not used in the current analysis)

Participants are asked the following question:

“*Here we would like to know more about you perceive your classmates.*”

The names of all students in the cohort are then presented. For each student, there are two variables of interest - ‘perceived as fun’ and ‘perceived as studious’ – those participants are asked to respond to on the following scales:

“*This person is really studious*”: No - I don’t know - Yes

“*This person is really fun*”: No - I don’t know - Yes

The 2019 year were asked with a different phrasing to make the scale more concrete:

“*This is a person I would definitely invite to a small party*”: No - I don’t know - Yes

This is a person I would ask about class topics if I had a doubt”: No - I don’t know - Yes

Prior simulations

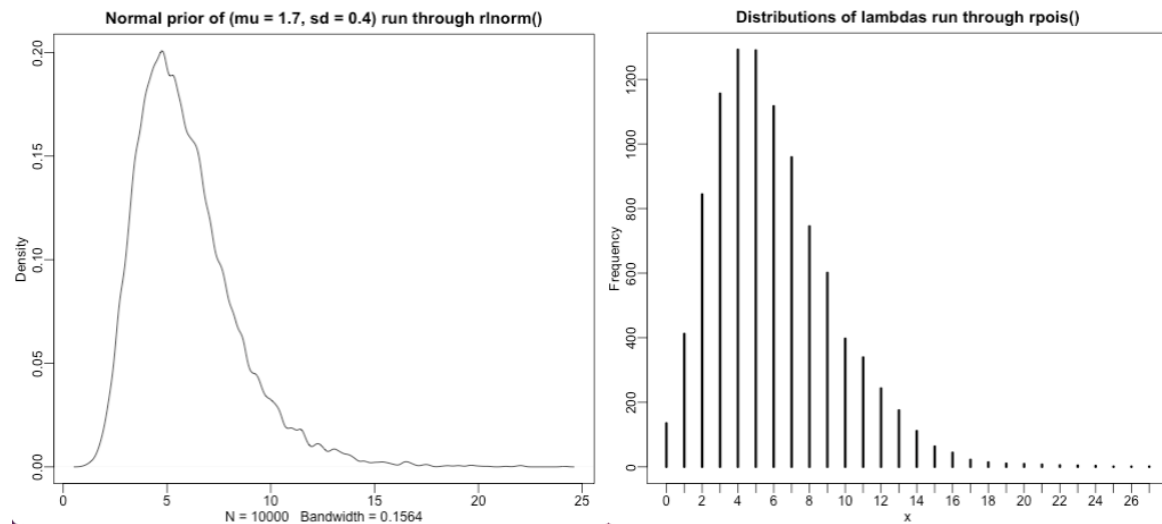


Figure 3: 1) Distribution of lambdas sampling from a lognormal distribution when setting a normal prior for beta to $M = 1.7$, $SD = 0.4$. 2) Using `rpois()` to sample 10.000 times from a Poisson distribution defined by the lambdas generated in 1). The plot illustrates that the set priors will most likely expect a Poisson distribution of network connections with a mean and variance around 4 or 5 connections in each of the four conditions

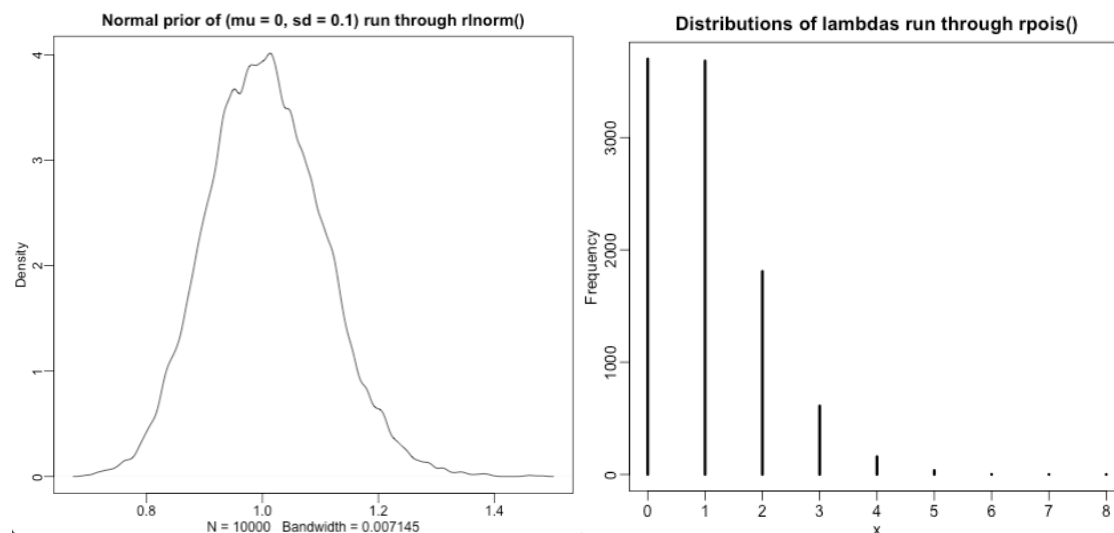


Figure 4: 1) Lognormal distribution of lambdas for varying effects when sampling from a normal distribution of $M = 0$, $SD = 0.1$. 2) Poisson distribution defined by lambdas generated from 1).

Quality checks

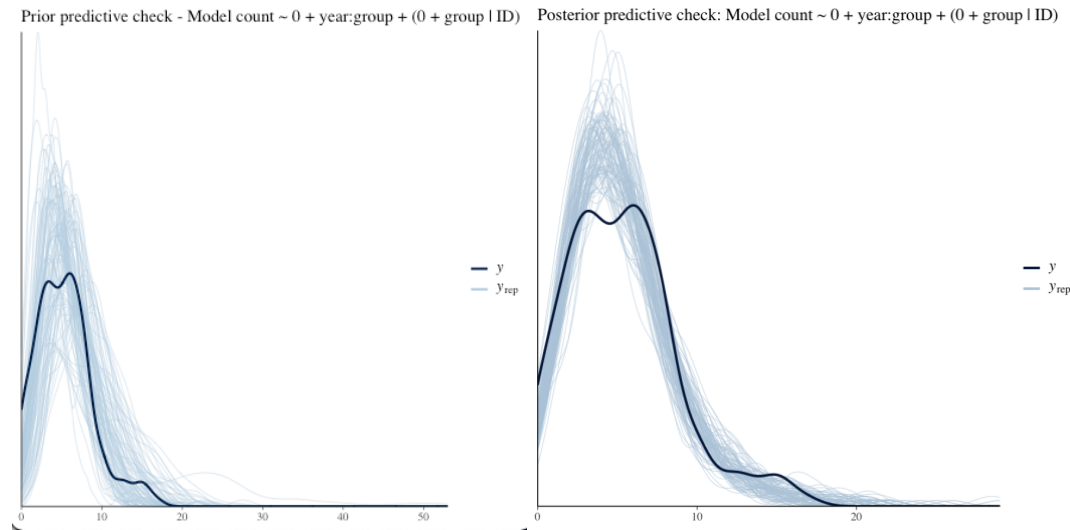


Figure 5: Prior predictive check (left) and posterior predictive check (right) for Model 1. The priors generate a few extreme predictions of up to 50 connections, which are not present in the posterior check. The data also display a bimodal property, which is to some extent captured in the posterior predictions. Comparing the two, it is visible that the model learns well from the data and thus generate estimates with a better fit to the data

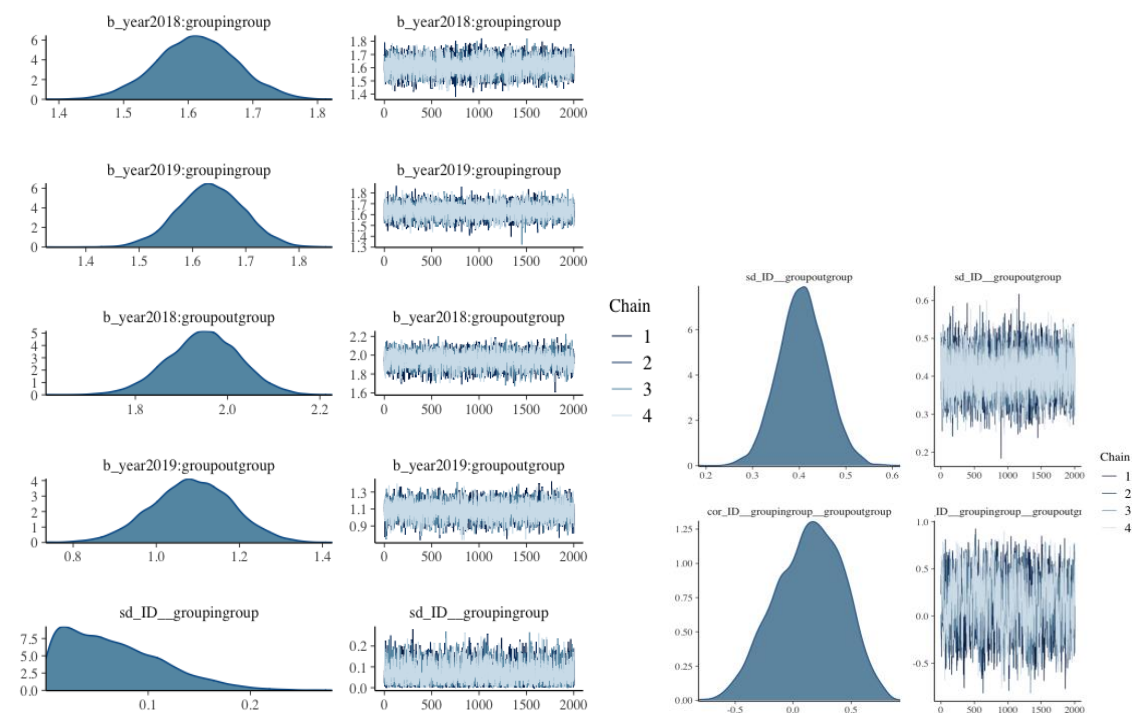


Figure 6: Trace plots for all parameters and their corresponding posterior distributions from Model 1. No problematic mixing is observed, but $\text{cor_ID_groupinggroup_groupoutgroup}$ initially had abnormalities, and its mixing improved by increasing iterations.

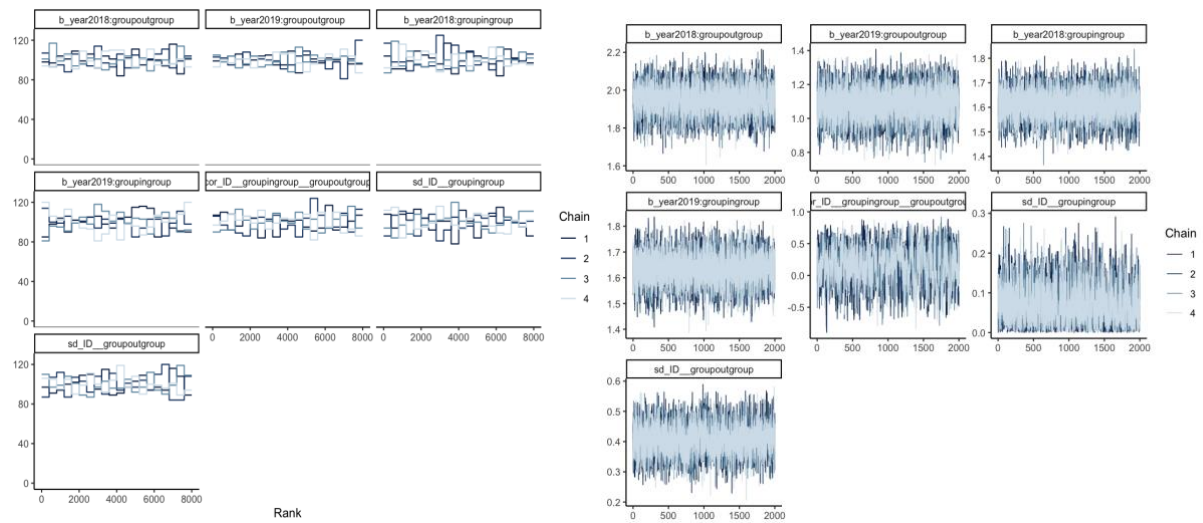


Figure 7: Trace- and rank plots for all parameters from Model 1.

Posterior learning plots

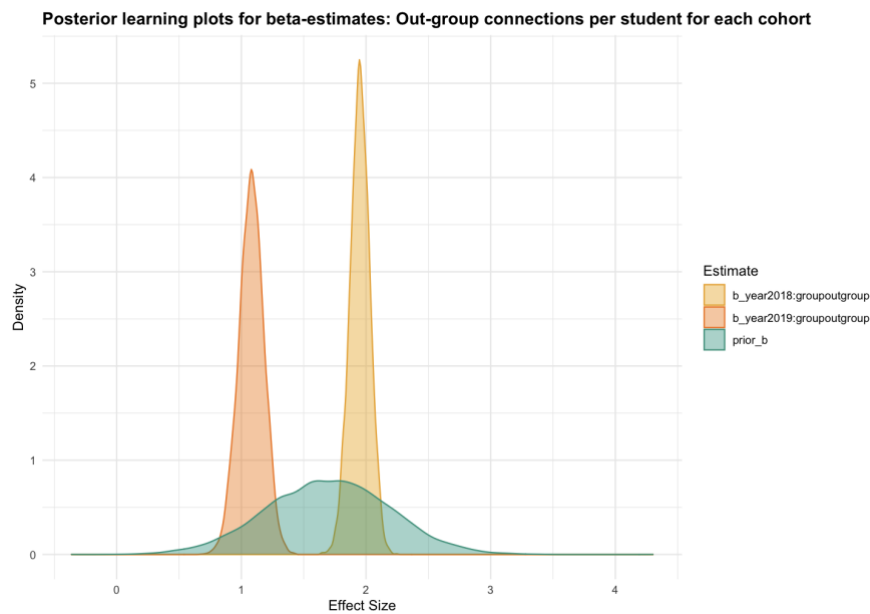


Figure 8: Posterior learning plot for the beta estimates for outgroup connections for C18 and C19. The two posteriors have increased in certainty and moved in opposite directions from the prior, suggesting that the model has learned a lot from the data.

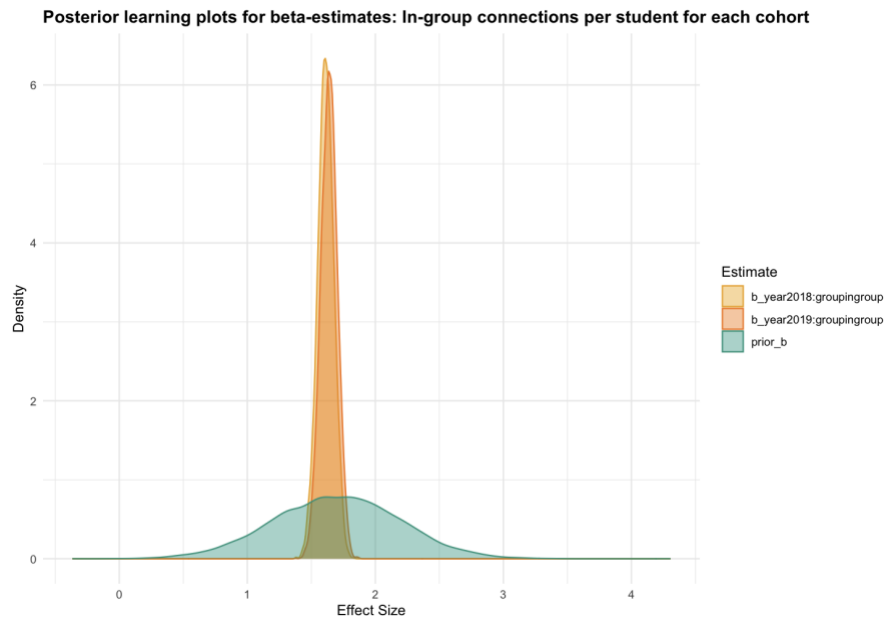


Figure 9: Posterior learning plot for the beta estimates for in-group connections for C18 and C19. Both posteriors have increased in certainty while remaining close to the mode of the prior, suggesting that the model have learned from the data.

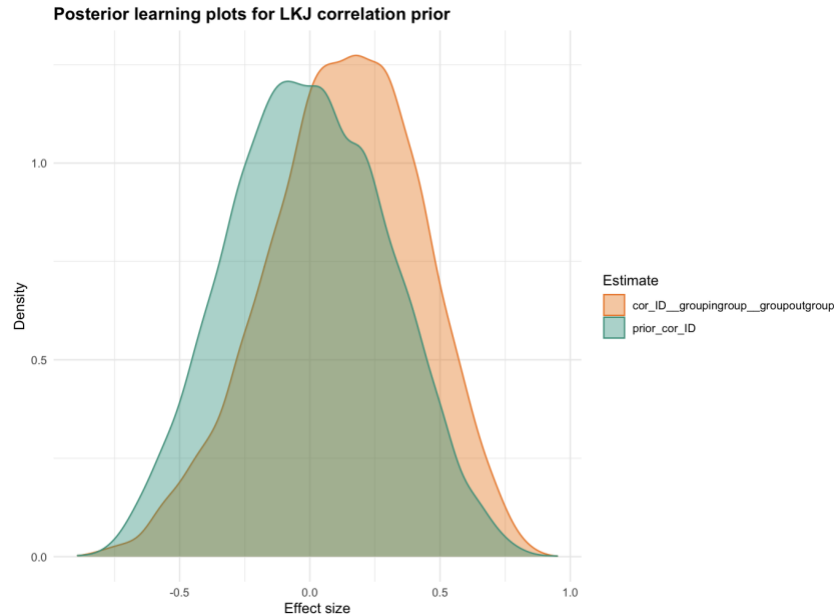


Figure 10: Posterior learning plot for the LKJ correlation-parameter. As the prior was set to be constraining of extreme correlations, the posterior does not deviate much from the prior.

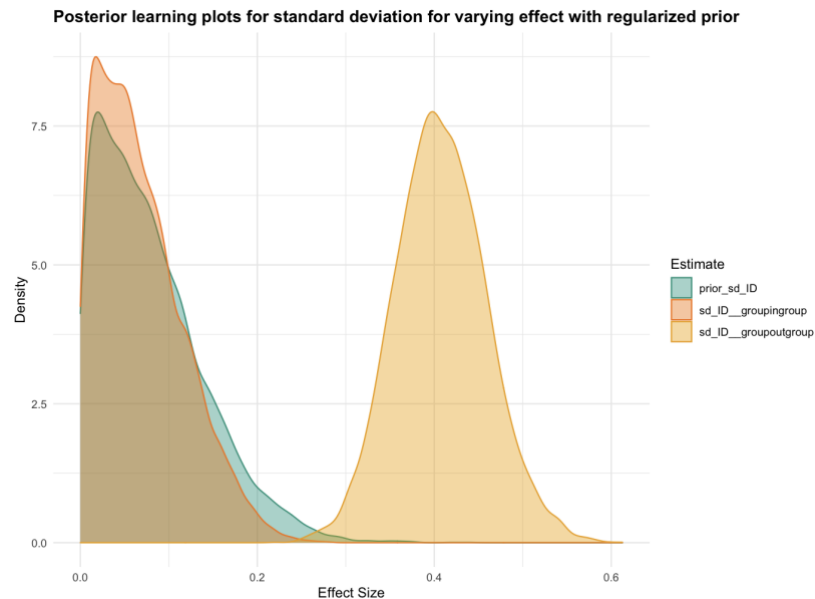


Figure 11: Posterior learning plot for the sd estimates for varying effects. As the prior was regularized, the posterior does not increase in certainty, but due to a large variation in number of outgroup-connections, the outgroup estimate is seen to be very influenced by the data

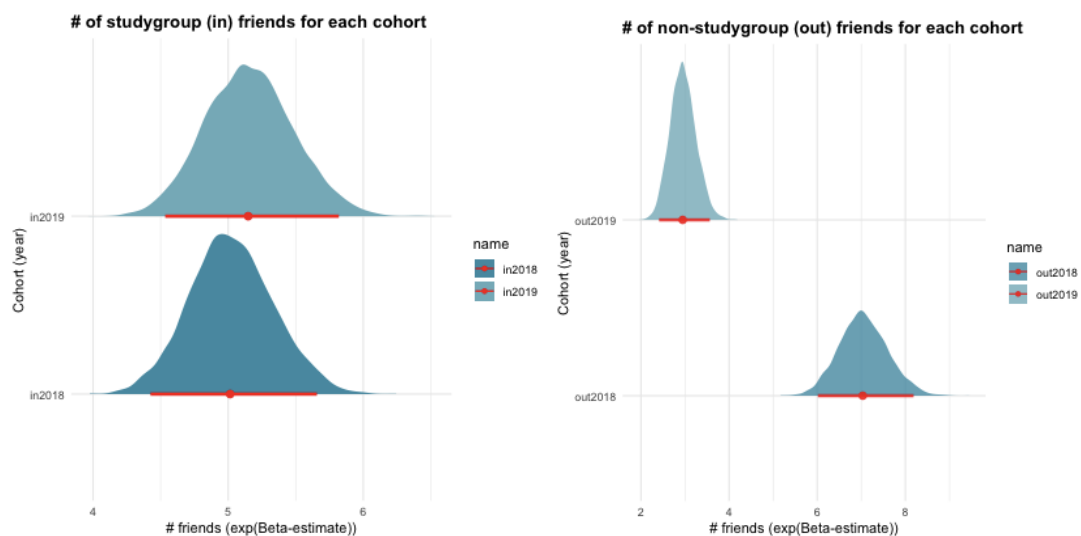


Figure 12: **1)** Distribution of possible estimates for number of studygroup friends (connections) for each cohort. The distributions overlap, suggesting no larger difference between the two conditions. **2)** Distribution of possible estimates for number of non-studygroup friends (connections) for each cohort. Here, no overlap is visible, suggesting a difference in the amount of non-studygroup friends between the two cohorts.

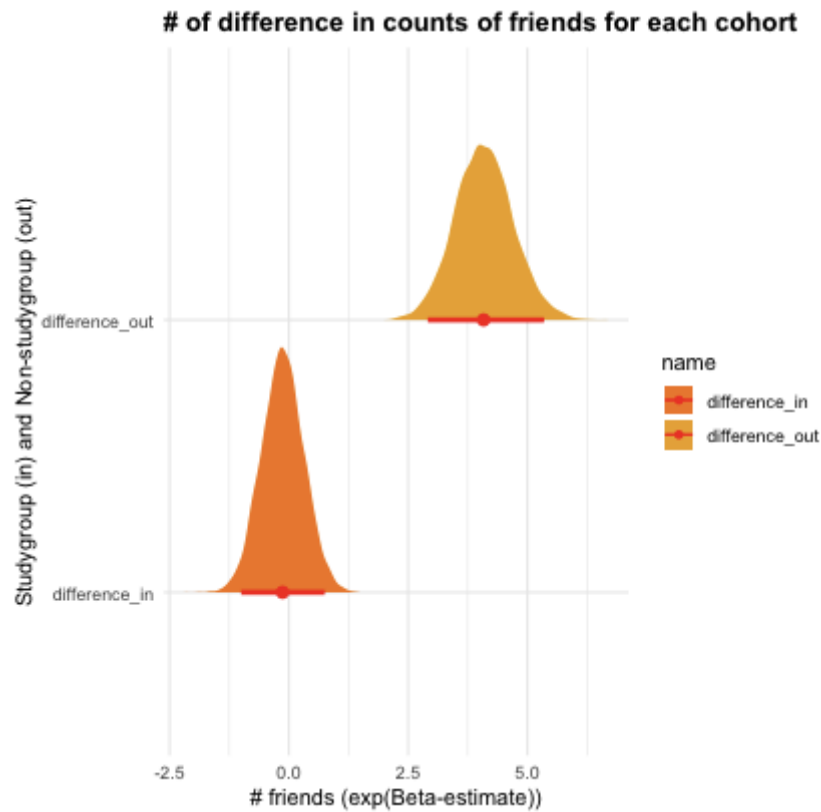


Figure 13: Difference distributions for studygroup- and non-studygroup friends (connection). For studygroup connections, the difference distribution is centered around 0, indication no difference between the two cohorts. For the outgroup connections the difference between C18 and C19 is around 4 connections, suggesting a large difference between the cohorts.

Prior & Posterior checks

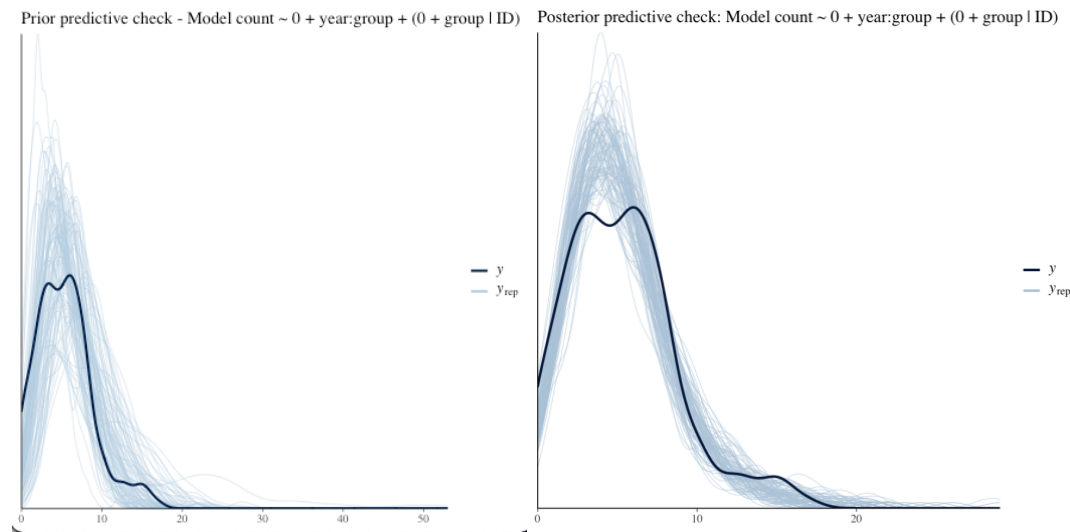


Figure 5: Prior predictive check (left) and posterior predictive check (right) for Model 1. The priors generate a few extreme predictions of up to 50 connections, which are not present in the posterior check. The data also display a bimodal property, which is to some extent captured in the posterior predictions. Comparing the two, it is visible that the model learns well from the data and thus generate estimates with a better fit to the data

Zooming in on influential points

Assessing which observations are the problematic ones has been done for all the models to be found in the Rmd.-file, but for brevity and as Model 1, the model decided on for use in the present analysis, was the better model, we will only include influential points analysis for this one model.

Using the `loo()` command, we can inspect directly the observations that are deemed too highly influential for our model. As can be seen on the plot below, there are 20 influential points (points with Pareto-k values > 0.7). These observations are found in *Table 7* below the plot.

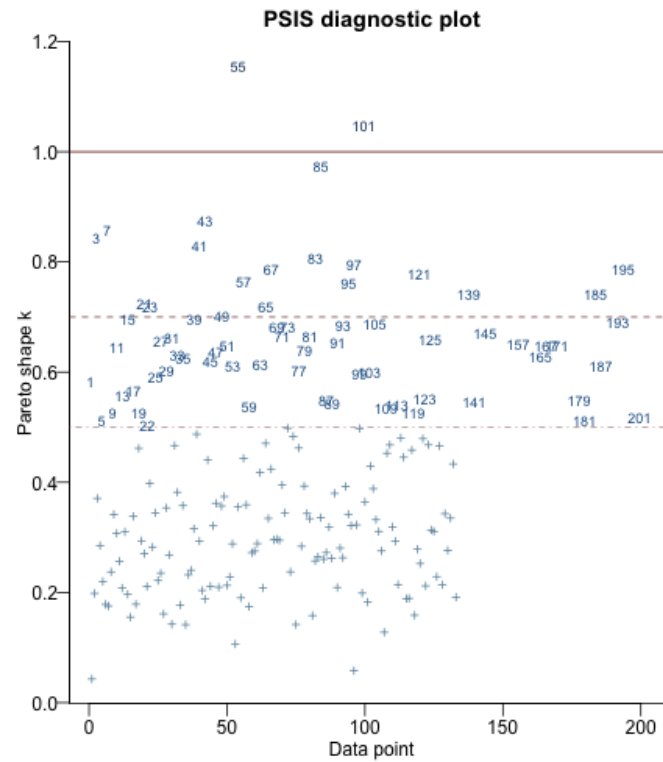


Figure 14: PSIS diagnostics plot used to inspect influential points

# Observation	Year	Group	Count
3	2018	outgroup	15
7	2018	outgroup	14
21	2018	outgroup	16
23	2018	outgroup	15
41	2018	outgroup	2
43	2018	outgroup	15
49	2018	outgroup	3
55	2018	outgroup	17
57	2018	outgroup	15
65	2018	outgroup	13
67	2018	outgroup	13
83	2018	outgroup	2

85	2018	outgroup	1
95	2018	outgroup	5
97	2018	outgroup	11
101	2019	outgroup	3
121	2019	outgroup	9
139	2019	outgroup	10
195	2019	outgroup	10

Table 7: Overview of influential observations

Quite visibly, all influential points are in the ‘outgroup’ level of the Group variable, and only 4/20 points are from the 2019 year, which was the year for the cohort that were subject to lockdown semesters. To test whether the effect found in the analysis above is robust, these influential points are removed, and the model is refitted to a dataset not containing these observations. The same priors are used but see the next section for a robustness check of the posterior with different priors. The model performs well and passes chain and summary checks with no issues.

Group-Level Effects:	Estimate	Est. Error	lower 95% CI	upper 95% CI	Rhat	Bulk_ESS	Tail_ESS
sd(groupingroup)	0.07	0.05	0.00	0.18	1.00	3366	4033
sd(groupoutgroup)	0.23	0.08	0.05	0.51	1.00	2639	2323
cor(groupingroup, groupoutgroup)	0.13	0.30	-0.49	0.67	1.00	3314	4504
year2018:groupingroup	1.61	0.06	1.49	1.73	1.00	14816	5804
year2019:groupingroup	1.63	0.06	1.51	1.75	1.00	13755	6174
year2018:groupoutgroup	1.88	0.08	1.72	2.02	1.00	9120	5927
year2019:groupoutgroup	1.03	0.09	0.84	1.21	1.00	11969	5485

Table 8: Model summary when excluding influential points

Assessing evidence reveals that the evidence is still highly in favor of the hypothesis that the 2018 outgroup connections estimate is higher than the 2019 outgroup connections estimate:

Hypothesis (Ingroup) (Dataset without influential observations)	Evidence ratio	Posterior Probability
Year2018_Ingroup > Year2019_Ingroup	0.65	0.39
Year2018_Ingroup = Year2019_Ingroup	5.91	0.86
Year2018_Ingroup < Year2019_Ingroup	1.54	0.61

Table 9: Hypothesis testing for ingroup effects when excluding influential points

Hypothesis (Outgroup) (Dataset without influential observations)	Evidence ratio	Posterior Probability
Year2018_Outgroup > Year2019_Outgroup	Inf	1
Year2018_Outgroup = Year2019_Outgroup	0	0
Year2018_Outgroup < Year2019_Outgroup	0	0

Table 10: Hypothesis testing for outgroup effects when excluding influential points

And we can make the same plots as we did in the analysis and visibly assess the effects, where we see the estimate has slightly changed, but as the tables above show, evidence is still in favor of both H1a, H1a_alternative, and H1b.

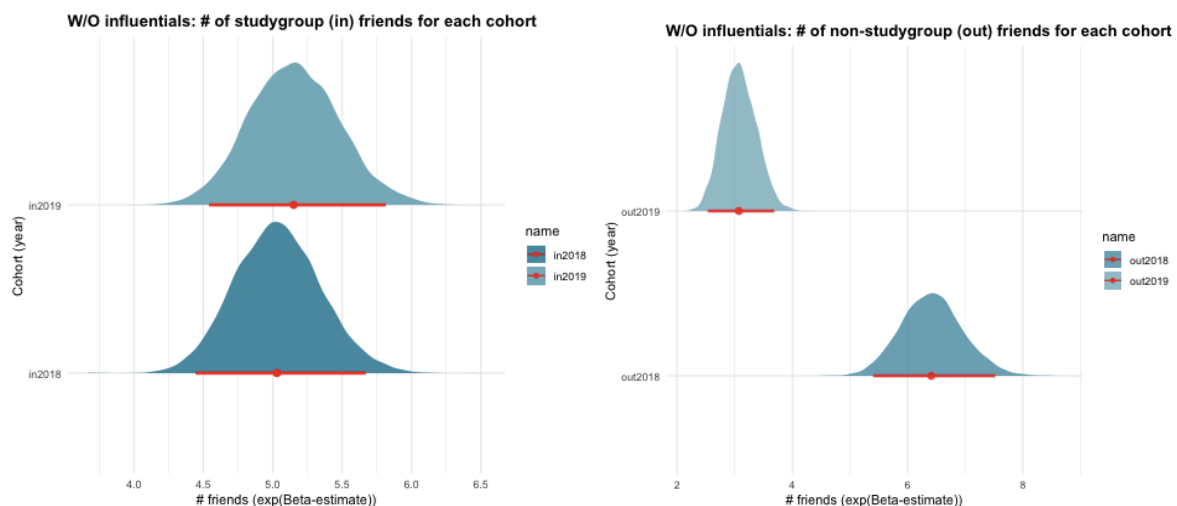


Figure 15: Distributions of possible estimates for number of studygroup and non-studygroup friends (connections) for each cohort when influential points are removed

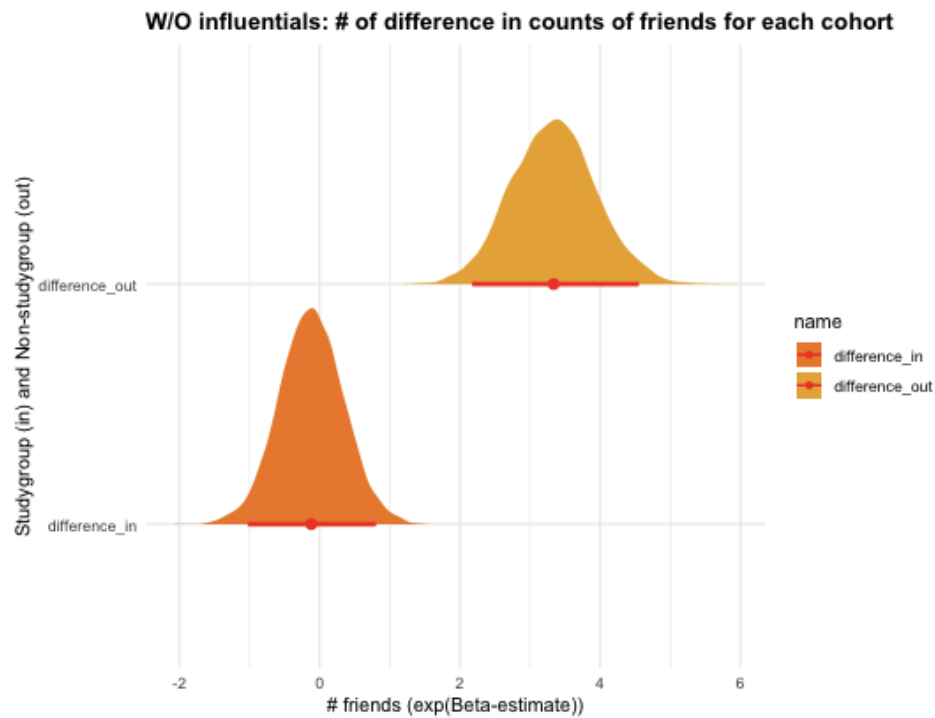


Figure 16: Difference distribution for studygroup and non-studygroup connections when influential observations are removed

Inspecting the two different beta-estimates for the 2018Outgroup, we can see that before removing influential data-points, an increment to this level of the variables would cause a factor of $\exp(1.95) = 7.02$ increase in the dependent variable, the rate of friend connections. (see Table 2 for all posterior estimates). After removal of influential data-points, that same increment would cause a factor of $\exp(1.88) = 6.55$ increase in the dependent variable, revealing the slight change to the estimates.

In conclusion, the difference of Beta2018Outgroup compared to the Beta2019Outgroup is substantial and still very much present after removing 20 influential data points. We will run robustness checks on this model to ensure that the posterior holds its own against different priors, so as to prove that the priors set in the present study did not drive the effect seen, but that the data mostly spoke for itself.

Robustness checks

As a last step, robustness checks were run running the Model from above several times with different priors. Included here are three robustness checks:

Test 1: Only changing the SD prior to be wider, setting it to normal(0,1.5)

This normal prior for the SD implies rates (lambdas) of 350 for the standard deviation in our varying effects, as can be seen to the left below, which on the right can be seen through the `rpois()`:

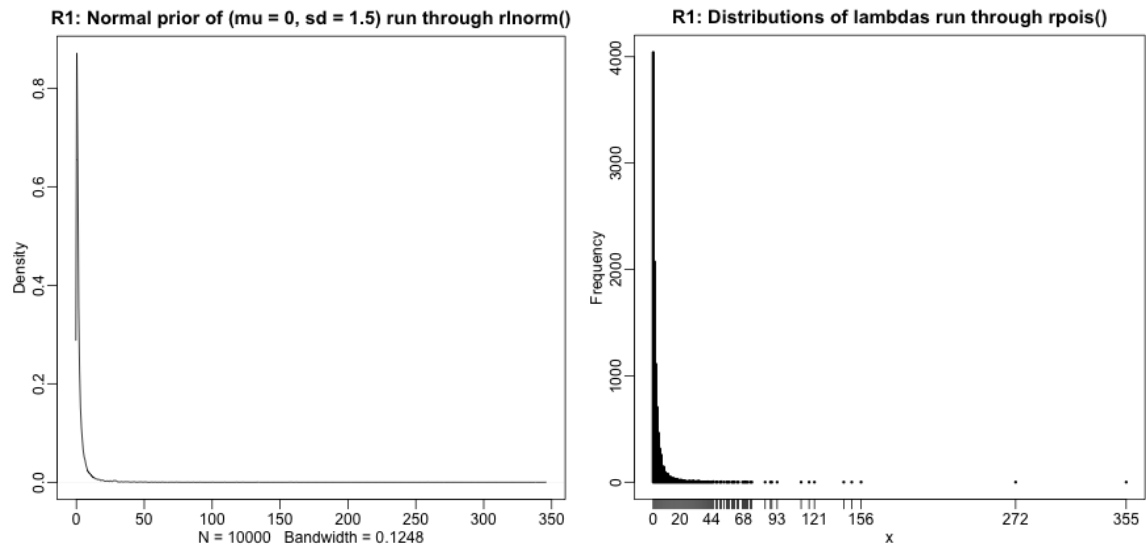


Figure 17: Simulating the expected lambdas of a vague prior with a wide standard deviation

The prior predictive check and posterior predictive check are plotted below:

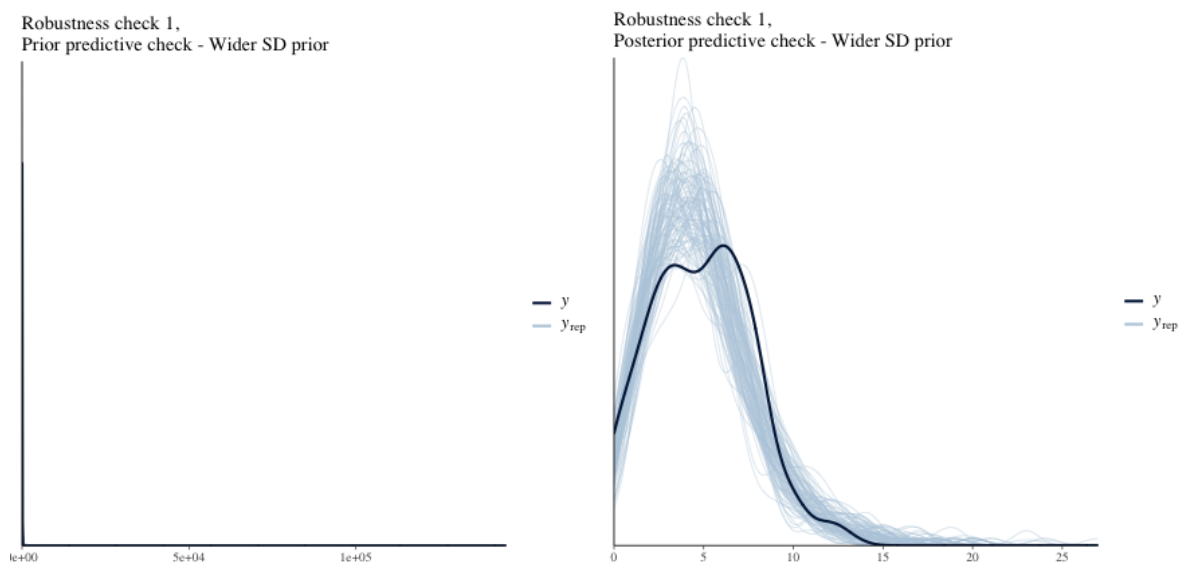


Figure 18: Predictive and posterior plot with a wide prior. The two plots illustrate how much the model learn from the data even with a very informative prior

Test 2: Only changing the Beta prior to be wider, setting it to normal(2,2)

Keeping the SD prior at normal(0,0.1), this new normal prior for the Beta implies rates (lambdas) of up to 15000 for the 2018/2019 in/outgroup conditions in our model, as can be seen to the left below, and on the right side again for what it implies for the Poisson distribution:

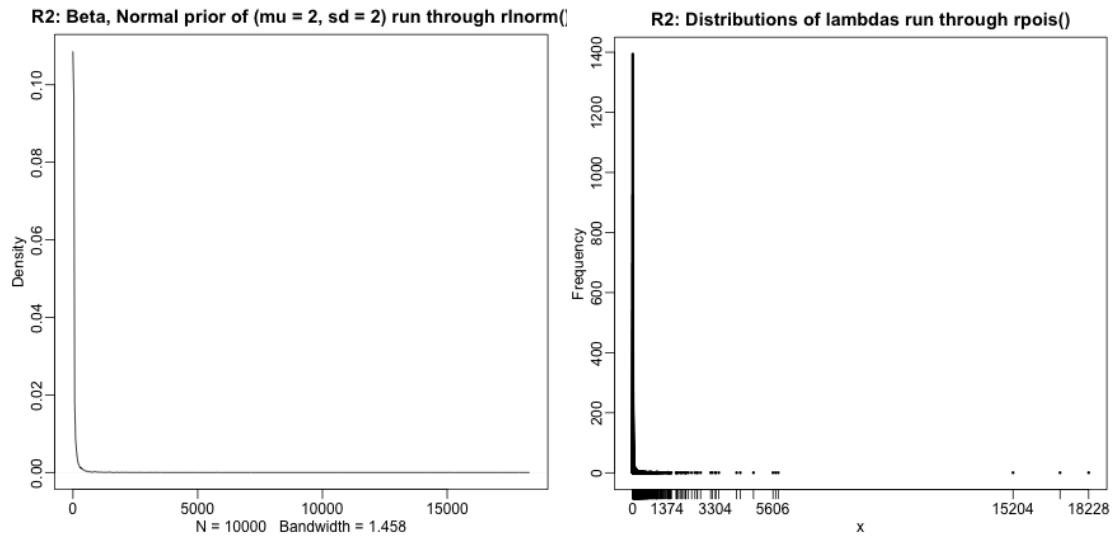


Figure 19: Simulating the expected lambdas of a vague normal prior, mean = 2, sd = 2

The prior predictive check and posterior predictive check are plotted below:

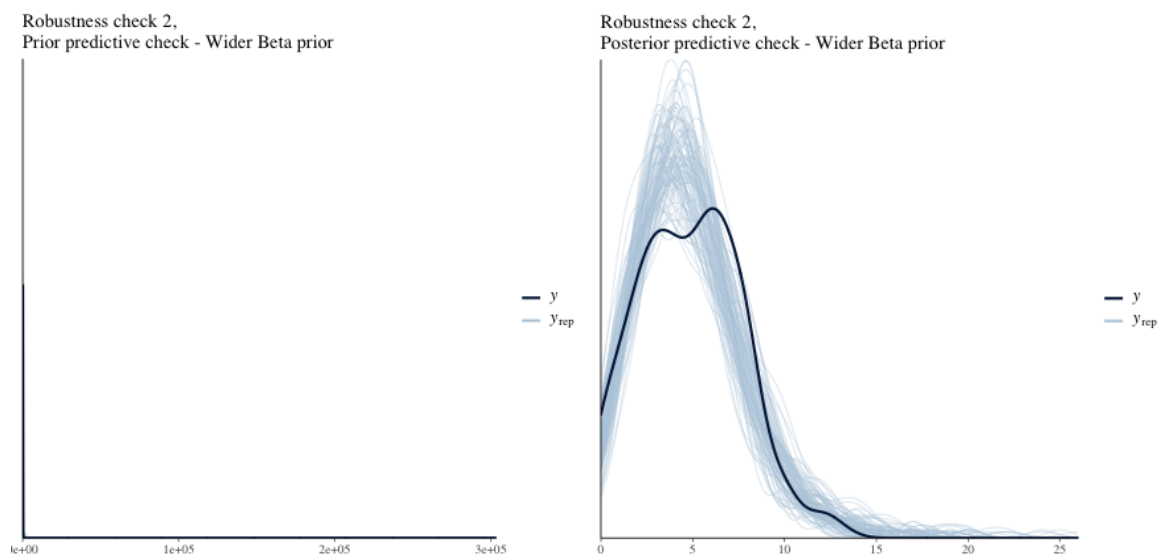


Figure 20: Prior and posterior check when using a different vague prior. The result is similar to that of the first vague prior illustrated in Figure 18

Test 3: Changing both Beta and SD to wider, combining wide priors from test 1 and 2

The prior predictive check and posterior predictive check are plotted below:

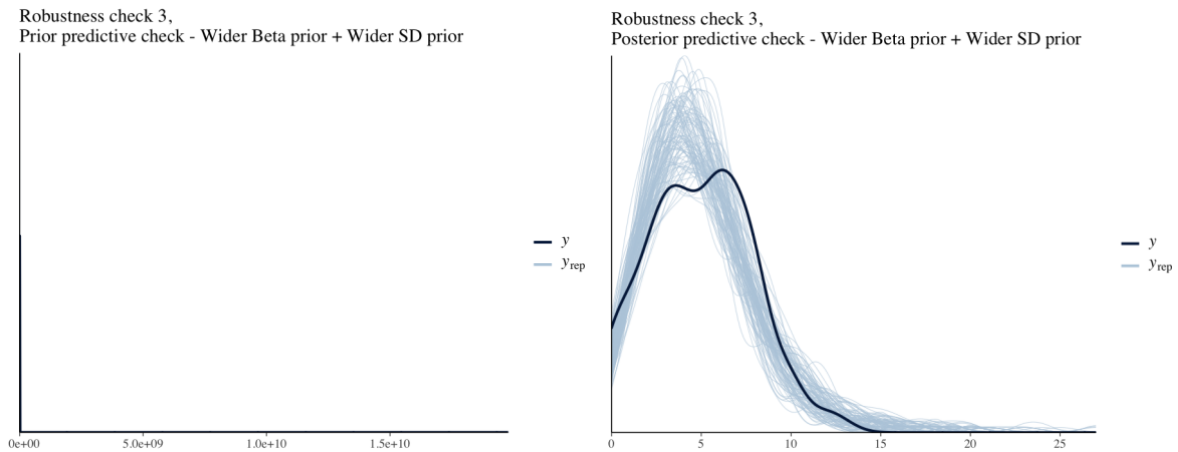


Figure 21: Prior and posterior checks for the third prior in the robustness check. The tendency is the same as for the previous priors: even with a very uninformative prior, the posterior still assimilates the data very well, when the model is allowed to learn from the data

The posterior distribution is quite robust regardless of prior set. This indicates the signal in the data is pretty clear, unless the model is overfit - but as shown in the section “Model comparison”, this seems to not be the case as this model was the best in terms of LOO-IC, an indicator out of sample performance, and stacking weights. In conclusion, the posterior seems robust against many different types of priors, and the effect seen is not due to qualities of the priors set.

Analysis 2: Bayesian Analysis of ABM-simulated Social Networks (Including Calibration, Model Validation & Model Exploration)

In order to investigate H2, an Agent Based Model simulating social networks at a university program was constructed. In this appendix, the simulated data will be compared against the real empirical data will be conducted in order to validate the ABM to validate its usefulness for the exploratory analysis. After successful validation, the exploratory analysis will be conducted.

The aim of the calibration was to simulate the “control” cohort’s social network, validate it, and then continue on with the exploratory analysis introducing lockdown.

Three parts: Calibration, Model Validation, Model Exploration.

1) Calibration

The model was calibrated to resemble the same patterns and amounts of degrees as in the real data for C18. This was done by adjusting values within the different parameters described in Table X, along with running several robustness and sensitivity checks. This was done by specifying different values for the different parameters, once a decent ‘default’ network was gotten. The model proved robust to the majority of parameters, but was sincerely sensitive to changes in parameters

- a) **Number of daily meet-ups**
- b) **Frequency of studygroup meetings**
- c) **Friendship connection threshold**
- d) **Preferential attachment (if the value is slightly larger, one person is allocated most of connections)**

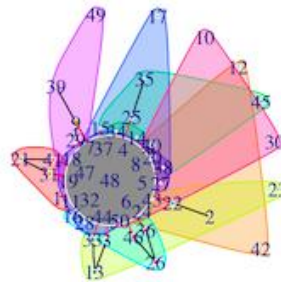
A recurring pattern found in the calibration was that the model has trouble capturing lower and higher tails, although it is mostly lower. This is potentially an artefact caused by instantiating only studygroup sizes of 5, see *Discussion*.

Robustness checks

To test robustness in the model and sensitivity to parameters, several robustness checks were conducted. Not all parameters were tested extensively due to lack of computational power and restricted access to better computers quite ironically, due to COVID-19. The most important parameters were therefore prioritized, and all of these pertained to the social theories reviewed in the introduction. All robustness checks conducted can be found in the code.

Of relevant checks, it was found the model was sincerely *sensitive* to or in the mechanisms of:

- 1) **Preferential attachment:** a tipping point somewhere between an alpha of 0.1-0.3 meant that the network became very unbalanced, allocating connections in the 15000's to one single person due to exponential rise in connections, pictured below:



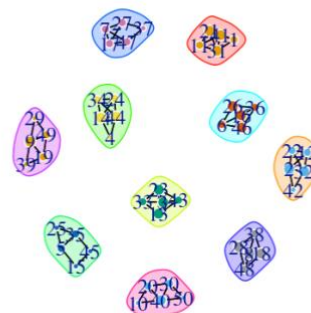
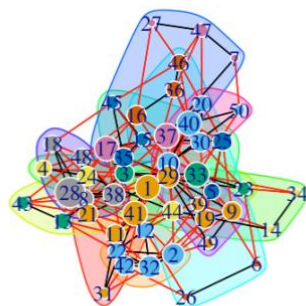
- 2) **Frequency of studygroup meetings:** The model run in LC (lockdown) was extremely sensitive to frequency of studygroup meetings. For every other day, the model returned a network almost completely similar to the NC model. For every day, the model returned a network completely disaggregated out in studygroups. Both these cases are respectively shown below, where the earlier mentioned compromise of 67% was found by a trial-and-error method, and was therefore deemed unreliable:

Studygroup meetings every 2nd day:

Studygroup meetings every day:

ABM_24MayHighSG_LOCK_v10

ABM_24MayHighSG_LOCK_v10_everyday



- 3) **Friendship threshold:** The model was sensitive to threshold of friendship connections, the amount of 23 chosen because model validation was deemed satisfactory at this point.

2) **Model validation:**

Comparing the C18_ABM output with C18_REAL

Model validation was done over several rounds to see whether the ABM calibration of the social network resembling our ‘control’ condition, that is, the real data for C18 (unaffected by lockdown) was successful. The results were fairly successful, although the ABM overshoots, see *Discussion*.

The goals of the model validation were to 1) check matching between simulated and real control data in terms of Total Degrees, which was our focal point for matching, as it is the essential measure in the analysis of the real data, where we split Total Degrees in in-studygroup/out-studygroup connections 2) check matching between simulated and real control data in terms of network measures using t-tests, 3) ‘exploratory’ check of whether the real and simulated dataset were matched in terms of in-studygroup/out-studygroup connections.

- a) **Validation 1:** Are C18_ABM and C18_REAL matched on Total Degrees? (**Core validation**)
Conclusion: Fairly successful.

Model summary output:

```
> # 6. Summary of model
> summary(model_TD_VAL_brm)
Family: poisson
Links: mu = log
Formula: degrees ~ 0 + type + (1 | ID)
Data: FakeAndRealC18 (Number of observations: 102)
Samples: 4 chains, each with iter = 3000; warmup = 1000; thin = 1;
        total post-warmup samples = 8000

Group-Level Effects:
~ID (Number of levels: 102)
      Estimate Est.Error l-95% CI u-95% CI Rhat Bulk_ESS Tail_ESS
sd(Intercept)    0.21     0.04    0.13    0.29 1.00    3289    3907

Population-Level Effects:
      Estimate Est.Error l-95% CI u-95% CI Rhat Bulk_ESS Tail_ESS
typeC18_ABM    2.56     0.05    2.46    2.66 1.00    5751    5524
typeC18_REAL    2.52     0.05    2.42    2.61 1.00    6415    5456

Samples were drawn using sample(hmc). For each parameter, Bulk_ESS
and Tail_ESS are effective sample size measures, and Rhat is the potential
scale reduction factor on split chains (at convergence, Rhat = 1).
> |
```

Validation 1 was run using Bayesian analysis to assess difference in Total Degrees between simulated and real data for C18. The validation was fairly successful, as evidence was found in favor of the real and simulated dataset for the ‘control’ cohort, C18, having similar Total Degrees. However, a smaller amount of evidence for the simulated data having more degrees than the real was also found. This means the ABM may have a tendency to overshoot amounts of degrees. This is also found by inspecting the spread of Total Degrees in C18_ABM and C18_REAL, which reveals that the ABM has trouble capturing the full spread of the data, even though it to a large extent *does* capture the spread:

```
> # Summaries for inspecting
> summary(C18_ABM_NetworkMetrics$degrees) # fake data
  Min. 1st Qu.  Median    Mean 3rd Qu.    Max.
  8.00  10.50   13.00   13.24  16.00   23.00
> summary(NetworkMetricsAndConnections_C18$degrees) # real data
  Min. 1st Qu.  Median    Mean 3rd Qu.    Max.
  1.00   8.75   13.00   12.81  18.00   23.00
> |
```

Nevertheless, the evidence magnitude and posterior probability was larger for the former hypothesis, meaning the former hypothesis is more likely. For this reason, the validation is considered passed for the case of the present analysis. However, this is obviously a discussion point. In sum, the datasets are matched on Total Degrees, but the ABM can tend to return slightly larger values in general than the real data. This can be due to the equally sized studygroups in the ABM, or random noise not being captured.


```

Hypothesis Tests for class b:
      Hypothesis Estimate Est.Error CI.Lower CI.Upper Evid.Ratio Post.Prob Star
1 (typeC18_ABM)-(ty... > 0      0.04      0.07    -0.07    0.16      2.54      0.72
2 (typeC18_ABM)-(ty... = 0      0.04      0.07    -0.10    0.18      8.83      0.90
3 (typeC18_ABM)-(ty... < 0      0.04      0.07    -0.07    0.16      0.39      0.28
---
'CI': 90%-CI for one-sided and 95%-CI for two-sided hypotheses.
'*': For one-sided hypotheses, the posterior probability exceeds 95%;
for two-sided hypotheses, the value tested against lies outside the 95%-CI.
Posterior probabilities of point hypotheses assume equal prior probabilities.
> |

```

- b) **Validation 2:** Are C18_ABM and C18_REAL matched on network measures such as *betweenness*, *transitivity* & *eigen-centrality*?

Conclusion: Fairly successful, w. 2/3 non-significant tests (3/3 non-significant desired).

Models' summary output:

```

> # T.test - betweenness (non-significant)
> t.test(betweenness ~ type, data = NetworkMetricsC18_both)

Welch Two Sample t-test

data: betweenness by type
t = -0.57184, df = 77.344, p-value = 0.5691
alternative hypothesis: true difference in means is not equal to 0
95 percent confidence interval:
 -29.52008 16.34715
sample estimates:
mean in group C18_ABM mean in group C18_REAL
      63.38000         69.96646

> # T.test - eigen centrality (non-significant)
> t.test(eigen_centrality ~ type, data = NetworkMetricsC18_both)

Welch Two Sample t-test

data: eigen_centrality by type
t = 1.5463, df = 81.095, p-value = 0.1259
alternative hypothesis: true difference in means is not equal to 0
95 percent confidence interval:
 -0.02094868 0.16707732
sample estimates:
mean in group C18_ABM mean in group C18_REAL
      0.5256316         0.4525672

> # T.test - transitivity (significant)
> t.test(transitivity ~ type, data = NetworkMetricsC18_both)

Welch Two Sample t-test

data: transitivity by type
t = -6.4452, df = 49.826, p-value = 4.49e-08
alternative hypothesis: true difference in means is not equal to 0
95 percent confidence interval:
 -0.2541562 -0.1333762
sample estimates:
mean in group C18_ABM mean in group C18_REAL
      0.04717905         0.24094524

```

Validation 2 was fairly successful, 2/3 of the network metrics (*betweenness*, *eigen_centrality*) returning non-significant t-tests for the differences in means between the real and simulated data for C18.

- c) **Validation 3:** Are C18_ABM and C18_REAL matched in-studygroup / out-studygroup connections?

Conclusion: Fairly successful, however, the ABM still overshoots slightly, as seen in Validation 1.

Model summary output:

```
> summary(model_ABM_C18_brm)
Family: poisson
Links: mu = log
Formula: count ~ 0 + condition:group + (0 + group | ID)
Data: FakeAndRealC18_INOUT_Long (Number of observations: 204)
Samples: 4 chains, each with iter = 3000; warmup = 1000; thin = 1;
        total post-warmup samples = 8000

Group-Level Effects:
~ID (Number of levels: 102)

              Estimate Est.Error l-95% CI u-95% CI Rhat Bulk_ESS Tail_ESS
sd(groupingroup)      0.06      0.05    0.00    0.17 1.00    3014    3499
sd(groupoutgroup)     0.27      0.05    0.17    0.36 1.00    2788    2076
cor(groupingroup,groupoutgroup) 0.12      0.30   -0.48    0.66 1.00    1170    2099

Population-Level Effects:
              Estimate Est.Error l-95% CI u-95% CI Rhat Bulk_ESS Tail_ESS
conditionABM:groupingroup      1.42      0.07    1.29    1.56 1.00    11896    6079
conditionREAL:groupingroup      1.61      0.06    1.49    1.74 1.00    11734    5683
conditionABM:groupoutgroup      2.17      0.06    2.04    2.28 1.00     6249    6259
conditionREAL:groupoutgroup      2.00      0.07    1.87    2.12 1.00     6572    5814

Samples were drawn using sample(hmc). For each parameter, Bulk_ESS
and Tail_ESS are effective sample size measures, and Rhat is the potential
scale reduction factor on split chains (at convergence, Rhat = 1).
```

Outgroup: Evidence was in favor of the real data having fewer outgroup connections than the simulated data. A smaller amount of evidence was found in favor of the two datasets having similar amounts of outgroup connections. As can be seen in the summary output above, the CI's also overlap between the two conditions.

```
> hypothesis(
+   model_ABM_C18_brm,
+   c(
+     "conditionREAL:groupoutgroup > conditionABM:groupoutgroup",
+     "conditionREAL:groupoutgroup = conditionABM:groupoutgroup",
+     "conditionREAL:groupoutgroup < conditionABM:groupoutgroup"
+   )
+ )
Hypothesis Tests for class b:
              Hypothesis Estimate Est.Error CI.Lower CI.Upper Evid.Ratio Post.Prob Star
1 (conditionREAL:gr... > 0   -0.17      0.09   -0.31   -0.03      0.03      0.02
2 (conditionREAL:gr... = 0   -0.17      0.09   -0.35      0.00      1.18      0.54  *
3 (conditionREAL:gr... < 0   -0.17      0.09   -0.31   -0.03     39.20      0.98  *
---
'CI': 90%-CI for one-sided and 95%-CI for two-sided hypotheses.
'*': For one-sided hypotheses, the posterior probability exceeds 95%;
for two-sided hypotheses, the value tested against lies outside the 95%-CI.
Posterior probabilities of point hypotheses assume equal prior probabilities.
```

Ingroup: Evidence is in favor of the real data having more ingroup connections than the simulated. Slight amount of speculative evidence was found in favor of the real and simulated data having similar amounts of ingroup connections. As can be seen in the summary output, the confidence intervals overlap.

```
> hypothesis(
+   model_ABM_C18_brm,
+   c(
+     "conditionREAL:groupinggroup > conditionABM:groupinggroup",
+     "conditionREAL:groupinggroup = conditionABM:groupinggroup",
+     "conditionREAL:groupinggroup < conditionABM:groupinggroup"
+   )
+ )
Hypothesis Tests for class b:
      Hypothesis Estimate Est.Error CI.Lower CI.Upper Evid.Ratio Post.Prob Star
1 (conditionREAL:gr... > 0      0.19      0.09      0.04      0.34      43.44      0.98  *
2 (conditionREAL:gr... = 0      0.19      0.09      0.00      0.37       0.97      0.49  *
3 (conditionREAL:gr... < 0      0.19      0.09      0.04      0.34       0.02      0.02
---
'CI': 90%-CI for one-sided and 95%-CI for two-sided hypotheses.
'*': For one-sided hypotheses, the posterior probability exceeds 95%;
for two-sided hypotheses, the value tested against lies outside the 95%-CI.
Posterior probabilities of point hypotheses assume equal prior probabilities.
>
```

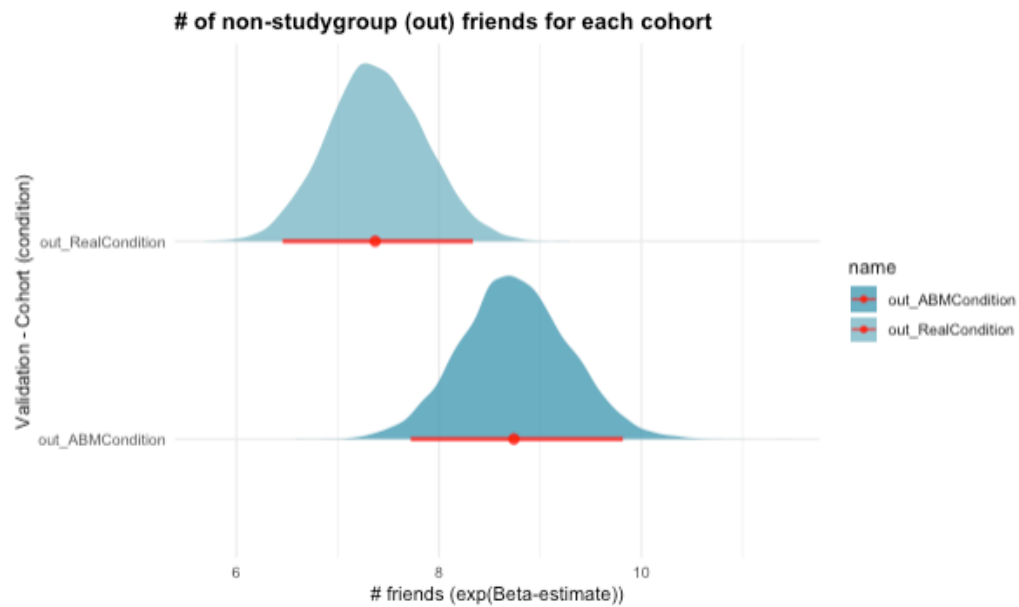
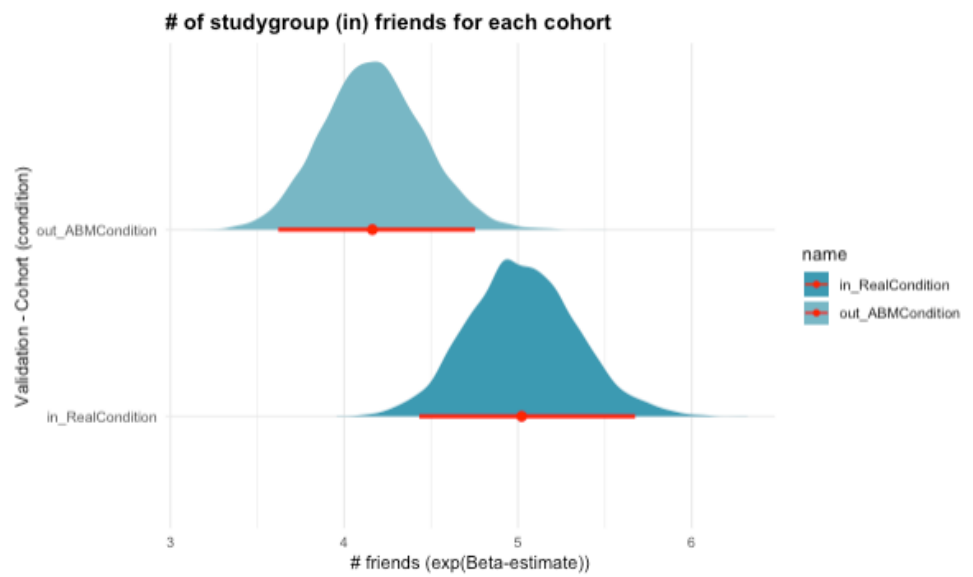
Assessing posterior samples reveals the undershoot/overshoot respectively done in Ingroup and Outgroup condition:

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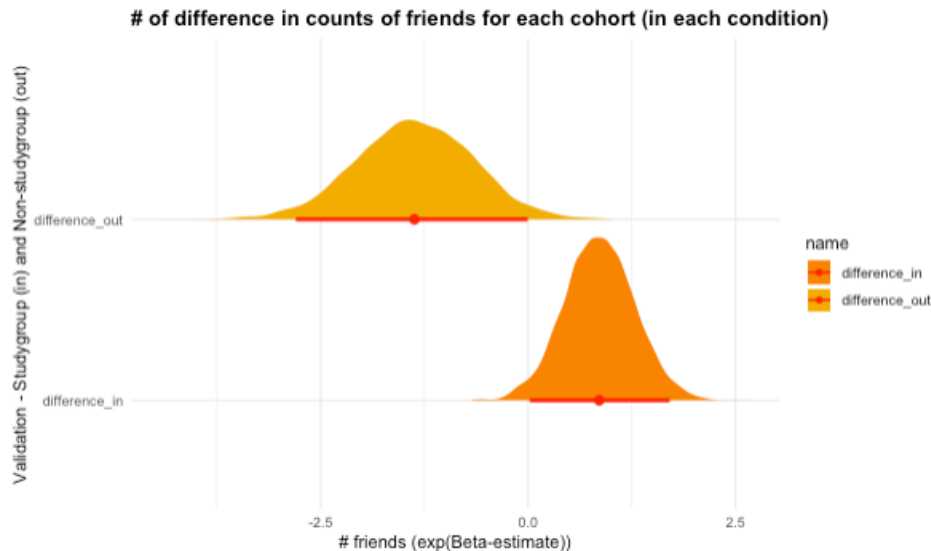
May 27, 2021

Klara Krøyer Fomsgaard | Student_no: 201906449, AUID648487

Course: *Social & Cultural Dynamics of Cognition*, Supervisor: *Riccardo Fusaroli*



The difference plot reveals the same point. Here, they should ideally have aligned completely if it matched up 100%:



Concluding on the validation checks

In conclusion, the validation checks were of varying degrees of success.

Validation 1 was fairly successful. It was run using Bayesian analysis which passed all quality checks to assess difference in Total Degrees between simulated and real data for C18. The validation was fairly successful, as evidence was found in favor of the real and simulated dataset for the ‘control’ cohort, C18, having similar Total Degrees. However, a smaller amount of evidence for the simulated data having more degrees than the real was also found. This means the ABM may have a tendency to overshoot amounts of degrees. This is also found by inspecting the spread of Total Degrees in C18_ABM. The ABM has trouble capturing the exact full spread of the data, even though it to a large extent does capture the spread. Nevertheless, the evidence magnitude and posterior probability was larger for the former hypothesis, meaning the former hypothesis is more likely. For this reason, the validation is considered passed for the case of the present analysis. However, this is obviously a discussion point. In sum, the datasets are matched on Total Degrees, but the ABM can tend to return slightly larger values in general than the real data. This can be due to the equally sized studygroups in the ABM, or random noise not being captured.

Validation 2 was fairly successful returning 2/3 desired non-significant t-tests for the differences in means between the real and simulated data for C18, passing the test for *betweenness* and *eigen-centrality*, however not for *transitivity*. This is obviously a discussion

point but since the network metrics are not used in the present analysis and are only used as proxies to deem matching success, 2/3 tests are deemed sufficing for the present analysis and the validation check is passed – although it was not perfect.

Validation 3 was fairly successful, although the ABM overshoots slightly, as seen in validation 1. **Ingroup:** Evidence was in favor of the real data having fewer outgroup connections than the simulated data. A smaller amount of evidence was found in favor of the two datasets having similar amounts of outgroup connections. CI's overlapped between the two Outgroup estimates. **Outgroup:** Evidence was in favor the real data having more ingroup connections than the simulated. Slight amount of speculative evidence was found in favor of the real and simulated data having similar amounts of ingroup connections. CI's overlapped between the two Ingroup estimates. This means the ABM can tend to predict lower values for Ingroup than the actual C18 data shows, and it predicts higher values for Outgroup than the actual C18 data shows (as also shown in the plots).

3) Model Exploration: Introducing lockdown in the ABM & Bayesian Analysis

Part A aims to validate the model to be used for further exploration. This consists of building the model, checking parameter functionalities and testing how well interactions between parameters and setting of the real-world exogenous parameters capture similar trends as in the real “control” data-set, C18. In line with the above conclusion, although validation checks were not perfect, they were all deemed fairly successful with room for improvement in some places. The validation checks suffice for the present purposes, as the goal is not necessarily to replicate all facets of the unique real empirical data of C18, but rather approximate it with a certain range of error, and then assess whether it, in the ABM world, makes a difference to introduce Lockdown to the model. This will be done followingly and analyzed with Bayesian multilevel modelling, the same model used as in Analysis 1, only with the data switched out.

A comparative analysis between two runs of the ABM to create two simulated social networks, that are essentially ‘fake’ cohorts, which we call NormalCondition (NC), resembling the case of C18, and LockdownCondition (LC), resembling the case of C19. Both models run for the full 3 semesters (180 ticks), NC having 3/3 & LC having 1/3 normal semesters. The latter thus had 2/3 lockdown semesters. Both models have their ID's assigned to studygroups of 5, who have studygroup meetings every other

day the whole time, and both have the same settings at 1st semester. The lockdown set in place for the one cohort, LC, caused the following parameter changes to reflect true exogenous circumstances during this time:

- a) Lockdown starts after 60 ticks (days)
 - a. Then, Friday bars are ‘switched off’ and do not happen anymore
 - b. Then, In-person teaching is ‘switched off’ and does not happen anymore
 - c. The general rate of daily meetups with others is **reduced** from the normal factor of 3, to 1

The analysis of the simulated cohorts is exactly the same as for Analysis 1, modeling the differences in Ingroup/Outgroup connections using Bayesian multilevel modelling, and all code can be found in the Rmd-documents. The same model formula and same priors were used, as the means for the ABM-data were still finely captured by the original vague priors for the real data. The model passed all quality checks.

Model summary output:

```
> summary(model_ABM_brm)
Family: poisson
Links: mu = log
Formula: count ~ 0 + condition:group + (0 + group | ID)
Data: Cohorts_ABM_long (Number of observations: 200)
Samples: 4 chains, each with iter = 3000; warmup = 1000; thin = 1;
         total post-warmup samples = 8000

Group-Level Effects:
~ID (Number of levels: 100)

              Estimate Est.Error l-95% CI u-95% CI Rhat Bulk_ESS Tail_ESS
sd(groupingroup)      0.05      0.04   0.00   0.14 1.00    5475    4706
sd(groupoutgroup)     0.07      0.05   0.00   0.17 1.00    3765    4824
cor(groupingroup,groupoutgroup) -0.02    0.30  -0.59   0.56 1.00   12654    5679

Population-Level Effects:
              Estimate Est.Error l-95% CI u-95% CI Rhat Bulk_ESS Tail_ESS
conditionLockdown:groupingroup    1.43    0.07   1.29   1.56 1.00   19520    5529
conditionNormal:groupingroup       1.43    0.07   1.29   1.56 1.00   20446    5786
conditionLockdown:groupoutgroup    1.43    0.07   1.28   1.56 1.00   17779    5687
conditionNormal:groupoutgroup      2.20    0.05   2.10   2.29 1.00   18292    5391

Samples were drawn using sample(hmc). For each parameter, Bulk_ESS
and Tail_ESS are effective sample size measures, and Rhat is the potential
scale reduction factor on split chains (at convergence, Rhat = 1).
```

Evidence 1/2:

Conclusion 1/2: Evidence is highly in favor of the Normal condition having more outgroup connections than the Lockdown condition.


```
> hypothesis(
+   model_ABM_brm,
+   c(
+     "conditionNormal:groupoutgroup > conditionLockdown:groupoutgroup",
+     "conditionNormal:groupoutgroup = conditionLockdown:groupoutgroup",
+     "conditionNormal:groupoutgroup < conditionLockdown:groupoutgroup"
+   )
+ )
Hypothesis Tests for class b:
      Hypothesis Estimate Est.Error CI.Lower CI.Upper Evid.Ratio Post.Prob Star
1 (conditionNormal:... > 0      0.77      0.08    0.63    0.91      Inf        1      *
2 (conditionNormal:... = 0      0.77      0.08    0.61    0.94        0        0      *
3 (conditionNormal:... < 0      0.77      0.08    0.63    0.91        0        0
---
'CI': 90%-CI for one-sided and 95%-CI for two-sided hypotheses.
'*': For one-sided hypotheses, the posterior probability exceeds 95%;
for two-sided hypotheses, the value tested against lies outside the 95%-CI.
Posterior probabilities of point hypotheses assume equal prior probabilities.
> |
```

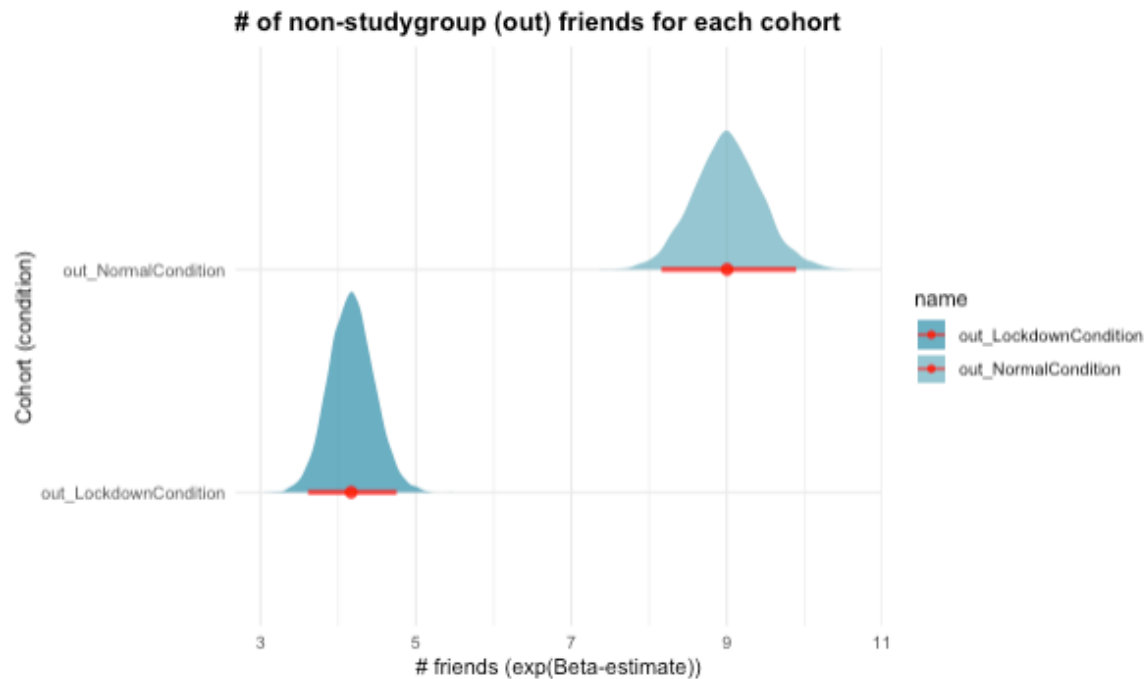
Evidence 2/2:

Conclusion 2/2: Evidence is largely in favor of the Normal and Lockdown condition having similar ingroup connections, however a slight amount of evidence for the Normal condition having fewer connections ingroup than the Lockdown condition is also present, though with a smaller posterior probability.

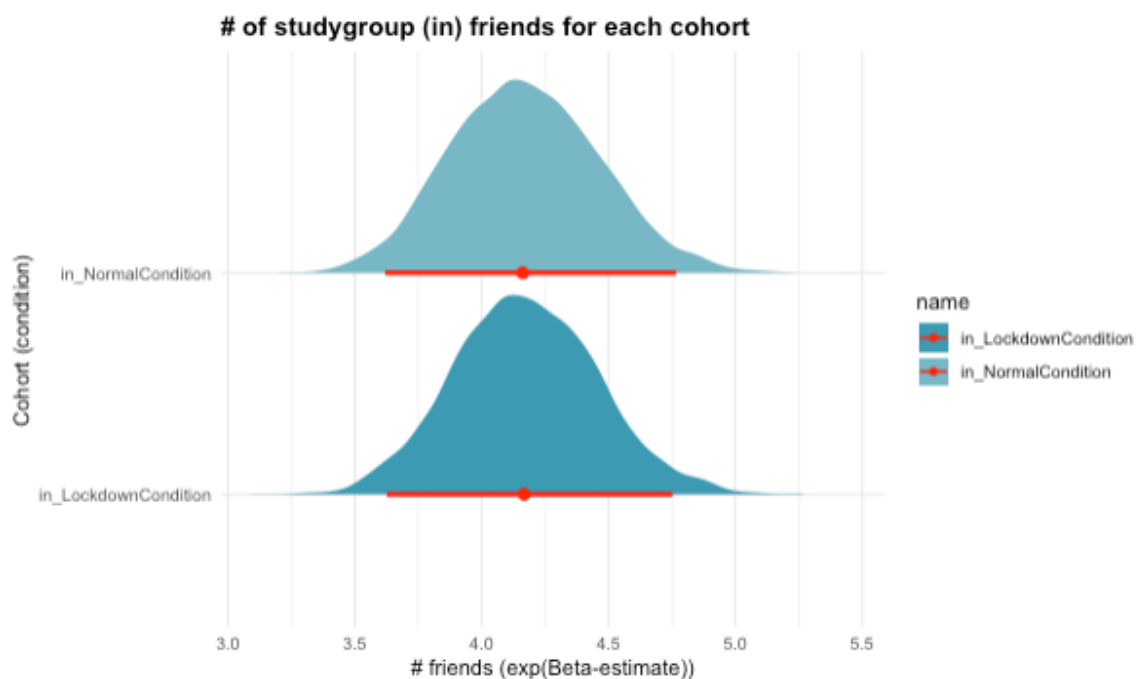
```
> hypothesis(
+   model_ABM_brm,
+   c(
+     "conditionNormal:groupingroup > conditionLockdown:groupingroup",
+     "conditionNormal:groupingroup = conditionLockdown:groupingroup",
+     "conditionNormal:groupingroup < conditionLockdown:groupingroup"
+   )
+ )
Hypothesis Tests for class b:
      Hypothesis Estimate Est.Error CI.Lower CI.Upper Evid.Ratio Post.Prob Star
1 (conditionNormal:... > 0      0      0.1   -0.16    0.16    0.99    0.50
2 (conditionNormal:... = 0      0      0.1   -0.19    0.19    6.95    0.87
3 (conditionNormal:... < 0      0      0.1   -0.16    0.16    1.01    0.50
---
'CI': 90%-CI for one-sided and 95%-CI for two-sided hypotheses.
'*': For one-sided hypotheses, the posterior probability exceeds 95%;
for two-sided hypotheses, the value tested against lies outside the 95%-CI.
Posterior probabilities of point hypotheses assume equal prior probabilities.
> |
```

Taking posterior samples and plotting differences reveals the same patterns seen in the summary and evidence ratios.

Below is the difference between Normal- and Lockdown-condition in Outgroup ties:



Below is the difference between Normal- and Lockdown-condition in Ingroup ties:



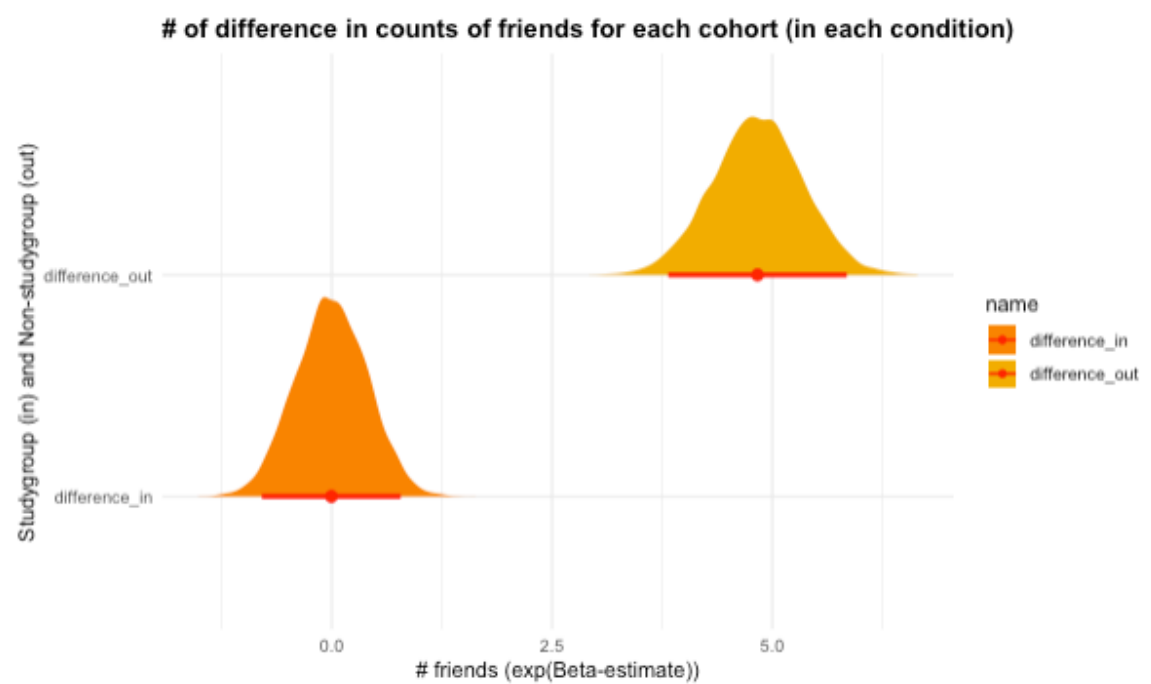
As the plot and model summary shows, the Ingroup posterior estimates and distributions are extremely similar down to the second decimal, around 4.16. Because of this, the model was run again, to reveal similar results. A similar differential pattern was found introducing lockdown in a different way, by tuning up the frequency of studygroup meetings to 67% instead of every other day (50%),

yielding similar relations. However, this way of introducing lockdown was deemed inferior to the other because of a) data cannot be found to support that choosing to see ones studygroup more was a central effect of students or young people during the lockdown in DK, however, there is data supporting that people did limit their daily meetings with others, along with b), the model was extremely sensitive to changes in frequency of meetings with studygroup in lockdown.

This constitutes robustness checks that show that the differential patterns of having networks and ties predicted mainly by your studygroups in the simulated LC cohort can be attributed to either:

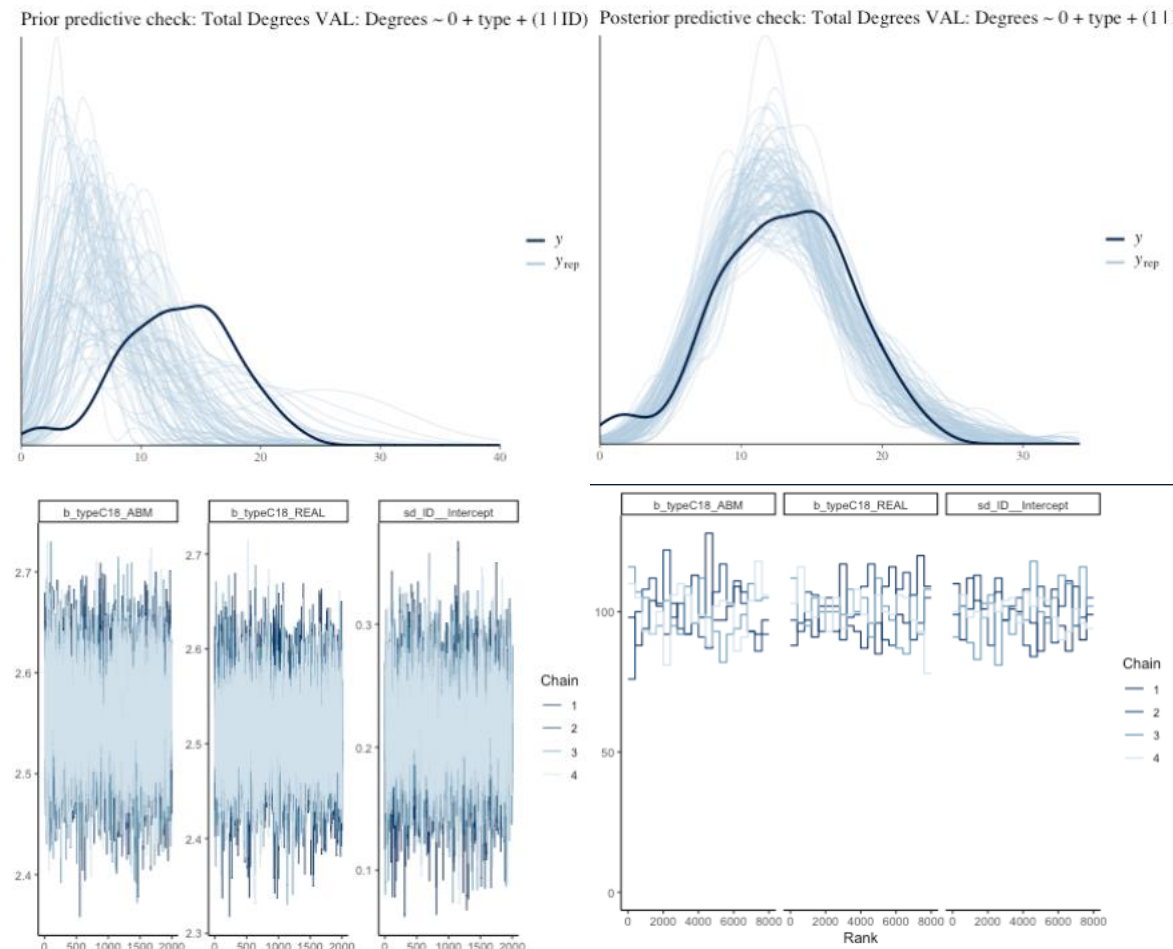
- 1) a general reduction in daily meetups with other people, meaning the agents sampled fewer people in general, which ended up causing a higher likelihood for sampling someone the agent was in a constrained relationship with (because that someone had a higher weight tied to them because of the constrained relationship, than say, a classmate from another group, who the agent was not likely to need scheduled meetings with)
- 2) more frequent meetings with your studygroup.

Because of the assembly ban, along with the fact that the university encouraged work in studygroups to continue, arguably, 1) is more likely to resemble what happened during lockdown, as people were advised to restrict their physical meetings to only those that were completely necessary, and data shows that young people including students *did* follow the restrictions.



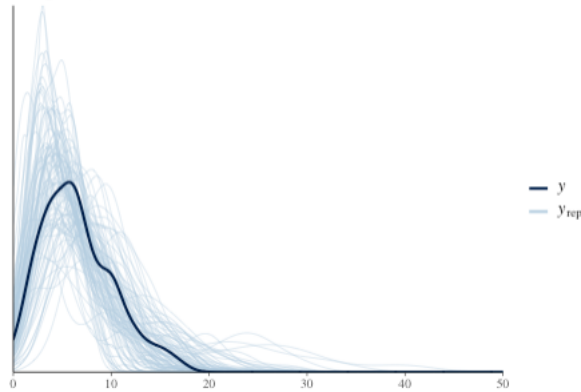
Prior, Posterior & Quality chain checks for validations

Validation 1:

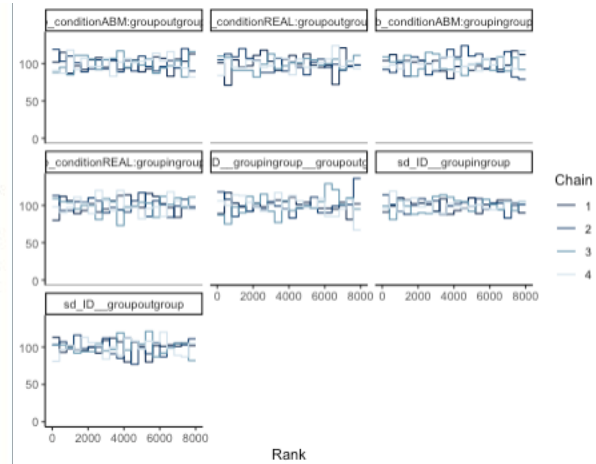
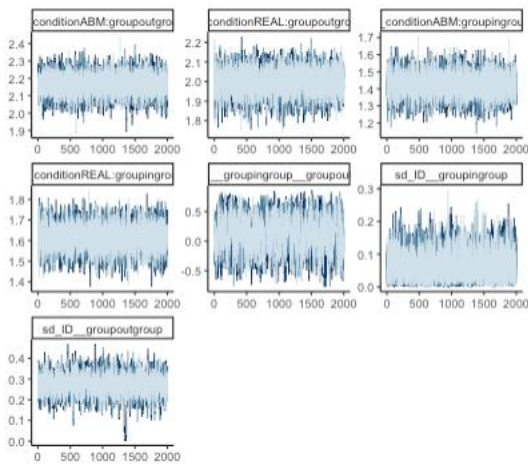
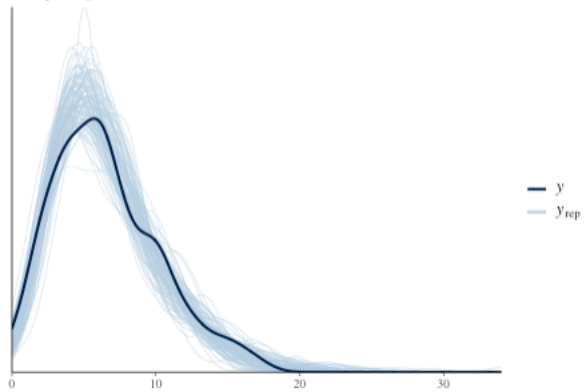


Validation 3:

Prior predictive check, Validation of Model count $\sim 0 + \text{condition:group} + (0 + \text{group} | \text{ID})$, comparing C18_AB_M with C18_Real

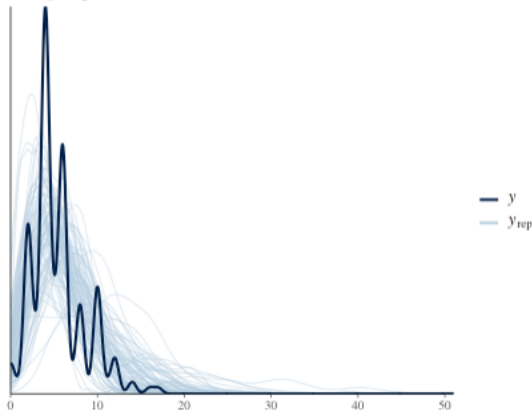


Posterior predictive check: Validation of Model count $\sim 0 + \text{condition:group} + (0 + \text{group} | \text{ID})$, comparing C18_AB_M with C18_Real

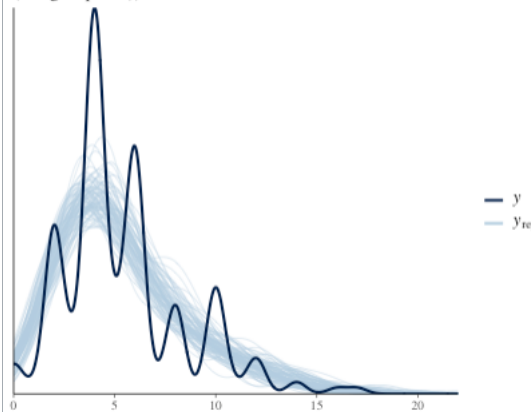


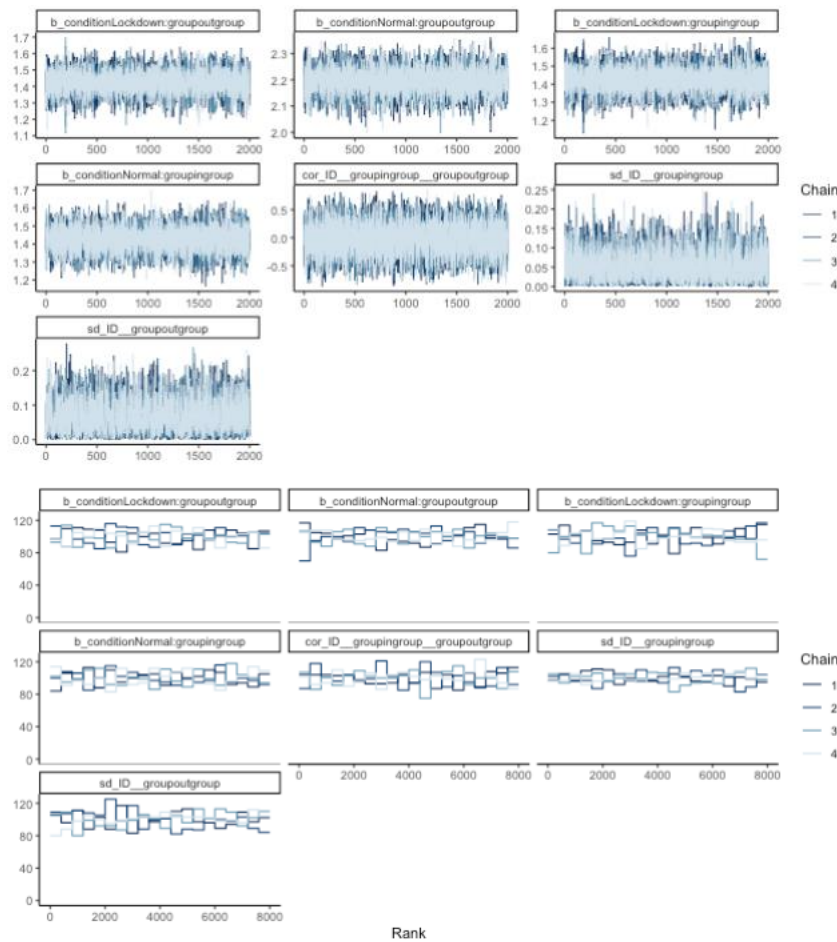
Prior, Posterior & Quality chain checks for Model Exploration: Analysis

Prior predictive check: ABM_Model count $\sim 0 + \text{condition:group} + (0 + \text{group} | \text{ID})$



Posterior predictive check: ABM_Model count $\sim 0 + \text{condition:group} + (0 + \text{group} | \text{ID})$

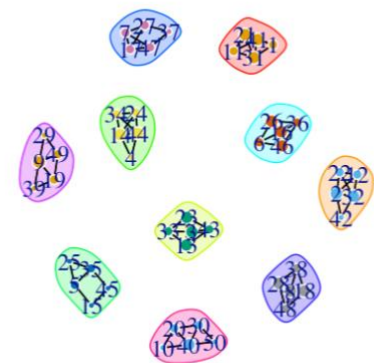




Example of robustness check of ABM

The plot below is a result of an ABM with set studygroup meetings every day:

ABM_24MayHighSG_LOCK_v10_everyday



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The plot below is then a result of an ABM with set studygroup meetings every **other** day, revealing the sensitivity:

