

Linear Mixed Effects Regression Analysis to Explore the Prevalence of Eating Disorders Among Varying Generations and Ethnicities of Asian Americans

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1 Abstract

American culture has come to develop and perpetuate some of the most harmful and unattainable beauty standards in the world; manifestations of these are present everywhere in our everyday lives, and so it is no surprise to witness the emergence and rise of eating disorders in Americans. Another phenomena taking place in the United States is acculturation; the Asian American population is the fastest growing minority in the U.S. (Budiman), the first and second generations of which are the population of study in this paper. In this project, I explore the intersection between these two areas. I used Linear Mixed Effects models to investigate whether generation or ethnicity better model the prevalence of eating disorders among this population. Using generation and ethnicity as separate groups upon which the other predictors are conditioned, I developed the respective models for these two focal groups. In the end, I ultimately concluded that both groups had equal strength in modeling the eating disorder prevalences and getting close to the observed data.

2 Introduction

Eating disorders and acculturation are commonly thought to be related phenomena, especially in current times as discourse regarding both have become more widely discussed in mainstream media. It is no surprise that American culture and society hold very specific yet unattainable beauty ideals that are reinforced and perpetuated by celebrities, models, and entertainment media. Exposure to and immersion in these Western beauty standards are thus thought to influence prevalence of eating disorders among Asians such that the former increase the latter, as the more assimilated an individual is into American culture (eg. First Generation versus Second Generation), the more exposure to these ideals they accumulate. Additionally, the prevalence of eating disorders is thought to be greater among East Asians for similar reasons; populations living in industrial cultures (such as South Korea) are exposed to the same Western ideals that link thinness and appearance to success.

In this paper, I explore both generation and ethnicity as potential key factors that may influence the prevalence of eating disorders among first and second generation Asian Americans. To do so, I use a linear mixed effects model to develop two separate models for each respective key factor, then investigated the posterior predictive distributions and prediction accuracy to evaluate the models. With these models and evaluation, I aim to distinguish which, if either, have a stronger effect on eating disorder prevalence within the aforementioned group.

2.1 Data

The dataset that I chose to use for this project quantifies eating disorder severity and acculturation via two surveys conducted on a randomly sampled population that contains first and second generation Asian

Americans. These surveys were sent out on public platforms, including Reddit and Facebook, particularly in specific groups, from which the subjects were randomly selected to participate in the survey. The first survey, the Eating Disorder Examination Questionnaire (EDE-Q) measures whether the subjects have an eating disorder, and the second survey, General Ethnicity Questionnaire (GEQ) measures the extent of their acculturation. I conducted exploratory analysis and created visual summaries of the data compiled from this survey. The first six figures of the dataset are displayed in Figure 1.

Figure 1: Dataset

	generation	smas	restraint	eating	shape	weight	global
1	Second Generation	78	0.0	1.8	3.625	2.6	2.00625
2	Second Generation	81	1.0	1.4	2.750	3.4	2.13750
3	Second Generation	76	1.0	0.2	1.000	0.8	0.75000
4	Second Generation	88	3.2	5.0	5.125	4.2	4.38125
5	Second Generation	97	3.0	2.6	4.625	4.0	3.55625
6	First Generation	84	5.2	3.4	4.750	5.0	4.58750

According to the National Eating Disorders Association, there are a multitude of emotional and behavioral as well as physical symptoms of an eating disorder. The survey used to construct this dataset focuses on the emotional and behavioral indicators as quantitative subscores, namely restraint, concern with eating, concern with weight, and concern with shape. Additionally, this survey includes a global score that acts as an overall metric for the prevalence of the eating disorder. These variables are all measured on a numerical basis.

Figure 2 shows the averages of the four EDE-Q subscores, comparing them by generation. As previously stated, the average subscores of the second generation Asian Americans are expected to be greater than those of the first generation, as the second generation is likely more accultured and has had more exposure to American culture and beauty standards, having lived in the United States longer than their counterparts. However, this bar graph shows the opposite; there appears to be a trend in that all the subscores of the first generation are greater than than those of the second generation.

Figure 2: EDE-Q Subscores by Generation

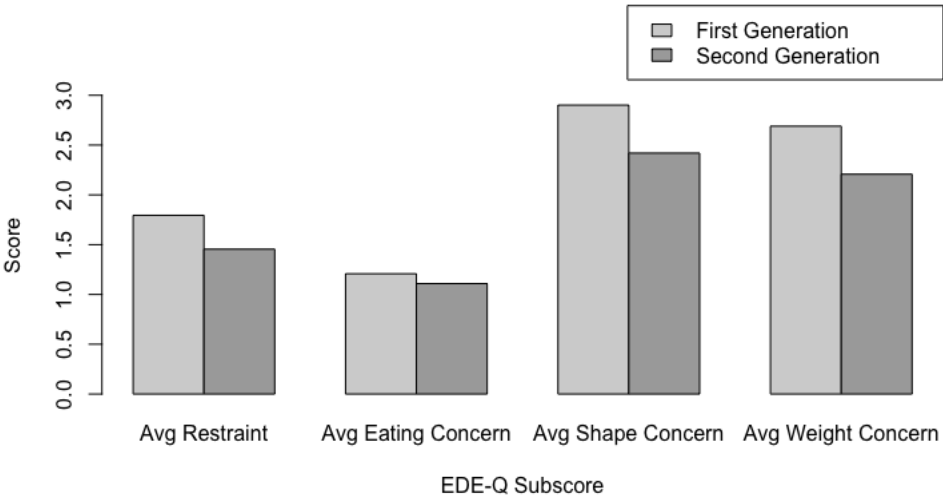
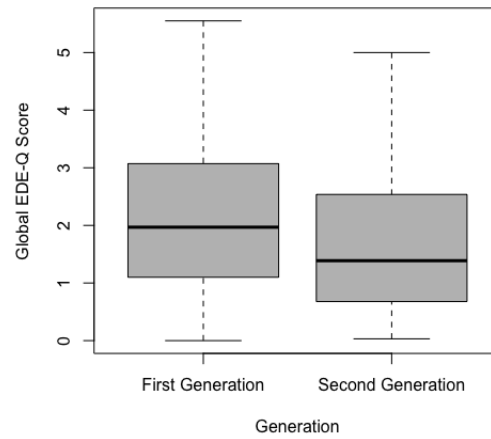


Figure 3 summarizes and compares the global scores from each generation. This boxplot reflects similar sentiments as Figure 2, showing that the prevalence of eating disorders is greater in the first generation than in the second generation. We can see clearly in Figure 3 that the first generation’s global scores have a higher interquartile range and mean compared to those of the second generation.

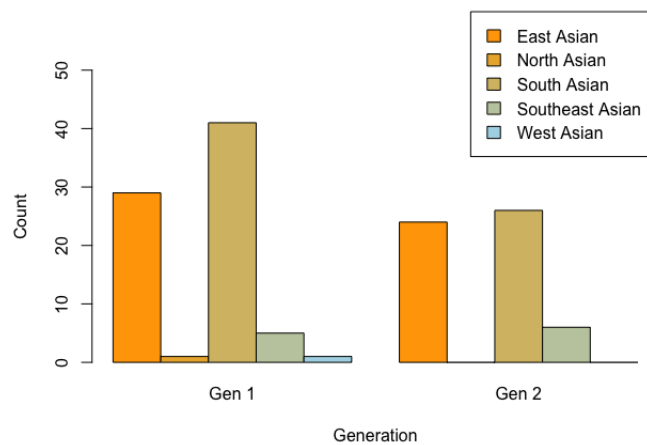
Figure 3: Global Scores by Generation



The second survey measures the extent of the subjects' acculturation, which is defined as the process through which people from one culture come to adopt the practices and values of a dominant culture (Cole). In this survey, it is gauged first via categorical questions about subjects' demographics, eg. their ethnicities and if they identify as First or Second Generations. It is also gauged via questions presented as a scale regarding how much or how little subjects agree with traditional American ideals versus their own ethnic ideals. In addition, this survey asked subjects what state they are from, though I chose to omit this variable in this paper as I deemed ethnicity to be of more relevance regarding geographical origins.

Figure 4 summarizes and compares the distribution of the major Asian ethnic regions represented in the dataset. The subjects of the survey identified roots from a multitude of ethnicities from various regions of the Asian continent, but for convenience for visual summary here I have grouped these into five major ethnic groups: East Asian, North Asian, South Asian, Southeast Asian, and West Asian. We can see from the bargraph that more Asian Americans of East, South, and Southeast Asian descent are present in the dataset than their North and West Asian counterparts.

Figure 4: Distribution of Ethnicities



Regarding the extent of subjects' acculturation, the survey uses the Stephenson Multicultural Acculturation Scale (SMAS), asking questions that evaluate the developments and changes that occur when people interact with/assimilate into different cultures (Stephenson Multicultural Acculturation Scale). Responses to these questions are presented as numerical scales, and produce the SMAS scores that are recorded in the dataset. Figure 5 plots the distribution of these scores; the distribution of frequencies of the scores appears to be fairly normal.

Figure 6 then compares these scores by generation. We can see that SMAS scores are generally higher for second generation Asian Americans compared to first generation, as expected. The second generation has a higher interquartile range, mean, minimum, and maximum (excluding outliers) than the first generation.

Figure 5: Distribution of SMAS Scores

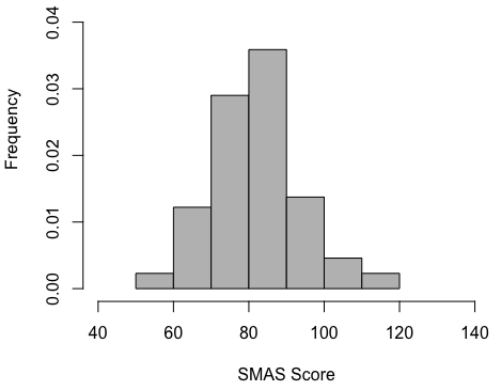
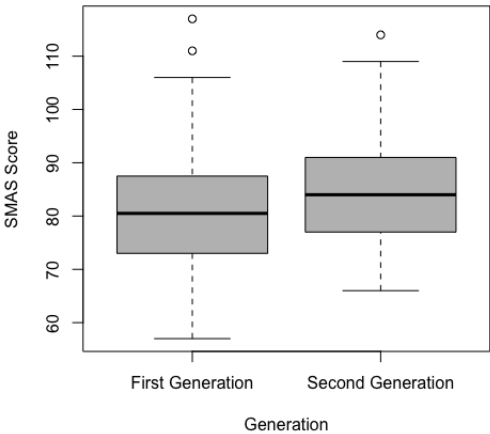


Figure 6: SMAS Scores by Generation

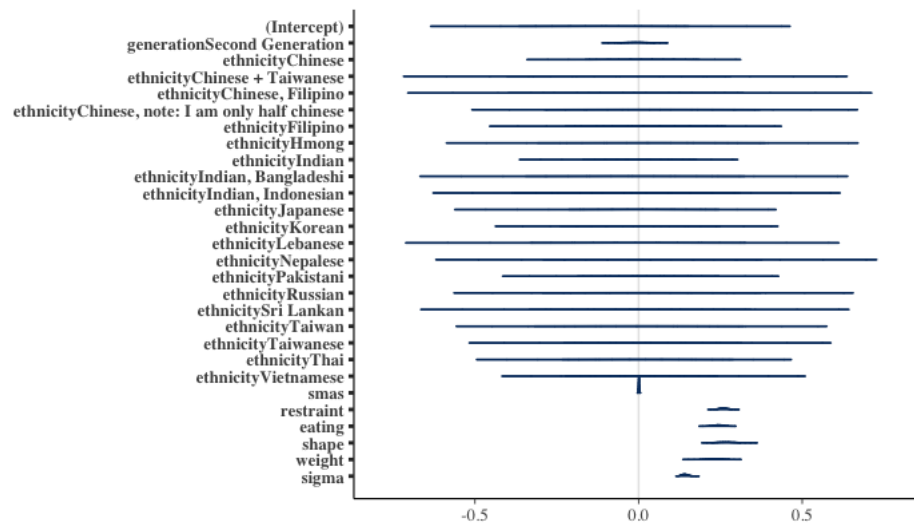


3 Analysis and Results

3.1 Horseshoe Priors

I first examined the horseshoe priors on the regression parameters by creating a simple linear model with all of the variables as predictors for the global score. In doing so, I aimed to calibrate my knowledge for myself by providing more insight into sensitivity analysis and to explore the effects of each of the variables in the dataset. The plot results as shown in Figure 7 show strong evidence that most of the coefficients of the variables, primarily those associated with generation and ethnicity are centered around 0, though a few variables are not. These nonzero variables are the EDE-Q subscores, which I would have predicted as influential indicators of eating disorders.

Figure 7: SMAS Scores by Generation



I then printed these coefficients and interval results into summary tables, Figures 8 and 9, respectively.

Figure 8: Coefficients of Variables Results

```
> round(coef(fit), 2)
```

(Intercept)	-0.11	generationSecond Generation	-0.01
ethnicityChinese	0.01	ethnicityChinese + Taiwanese	-0.06
ethnicityChinese, Filipino	-0.03	ethnicityChinese, note: I am only half chinese	0.04
ethnicityFilipino	0.02	ethnicityHmong	0.05
ethnicityIndian	0.00	ethnicityIndian, Bangladeshi	-0.02
ethnicityIndian, Indonesian	-0.04	ethnicityJapanese	0.01
ethnicityKorean	0.01	ethnicityLebanese	0.00
ethnicityNepalese	0.04	ethnicityPakistani	0.02
ethnicityRussian	0.03	ethnicitySri Lankan	0.00
ethnicityTaiwan	0.00	ethnicityTaiwanese	0.04
ethnicityThai	0.03	ethnicityVietnamese	0.01
smas	0.00	restraint	0.26
eating	0.24	shape	0.27
weight	0.23		

Figure 9: Posterior Intervals of Variables Results

```
> round(posterior_interval(fit, prob=0.9), 2)
```

	5%	95%
(Intercept)	-0.31	0.11
generationSecond Generation	-0.06	0.04
ethnicityChinese	-0.13	0.16
ethnicityChinese + Taiwanese	-0.35	0.23
ethnicityChinese, Filipino	-0.33	0.26
ethnicityChinese, note: I am only half chinese	-0.23	0.31
ethnicityFilipino	-0.18	0.23
ethnicityHmong	-0.25	0.32
ethnicityIndian	-0.14	0.15
ethnicityIndian, Bangladeshi	-0.29	0.27
ethnicityIndian, Indonesian	-0.32	0.25
ethnicityJapanese	-0.17	0.21
ethnicityKorean	-0.20	0.21
ethnicityLebanese	-0.28	0.27
ethnicityNepalese	-0.23	0.32
ethnicityPakistani	-0.16	0.20
ethnicityRussian	-0.25	0.31
ethnicitySri Lankan	-0.28	0.29
ethnicityTaiwan	-0.27	0.27
ethnicityTaiwanese	-0.19	0.26
ethnicityThai	-0.19	0.25
ethnicityVietnamese	-0.18	0.20
smas	0.00	0.00
restraint	0.24	0.28
eating	0.22	0.27
shape	0.23	0.30
weight	0.20	0.27
sigma	0.13	0.16

I wasn't necessarily interested in eliminating variables, but was more interested in modeling all of them to see their impacts on global score, especially since there were a relatively small number of variables measured in the dataset. As such, I used this analysis to help me to understand the sensitivity and influences of the variables, and ultimately decided to use all of them in my models.

The code I wrote to produce these plot and outputs is as follows:

```
simplefit <- stan_glm(global ~ generation+ethnicity+smas+restraint+eating+shape+weight, data =
df, prior = normal(location = 1, scale = 1, autoscale = TRUE), prior_intercept = normal(location =
1, scale = 2.5, autoscale = TRUE), seed = 1, refresh = 0)
plot(simplefit, "areas", prob = 0.95, prob_outer = 1)
round(coef(simplefit), 2)
round(posterior_interval(simplefit, prob=0.9), 2)
```

3.2 Method: Linear Mixed Effects Model

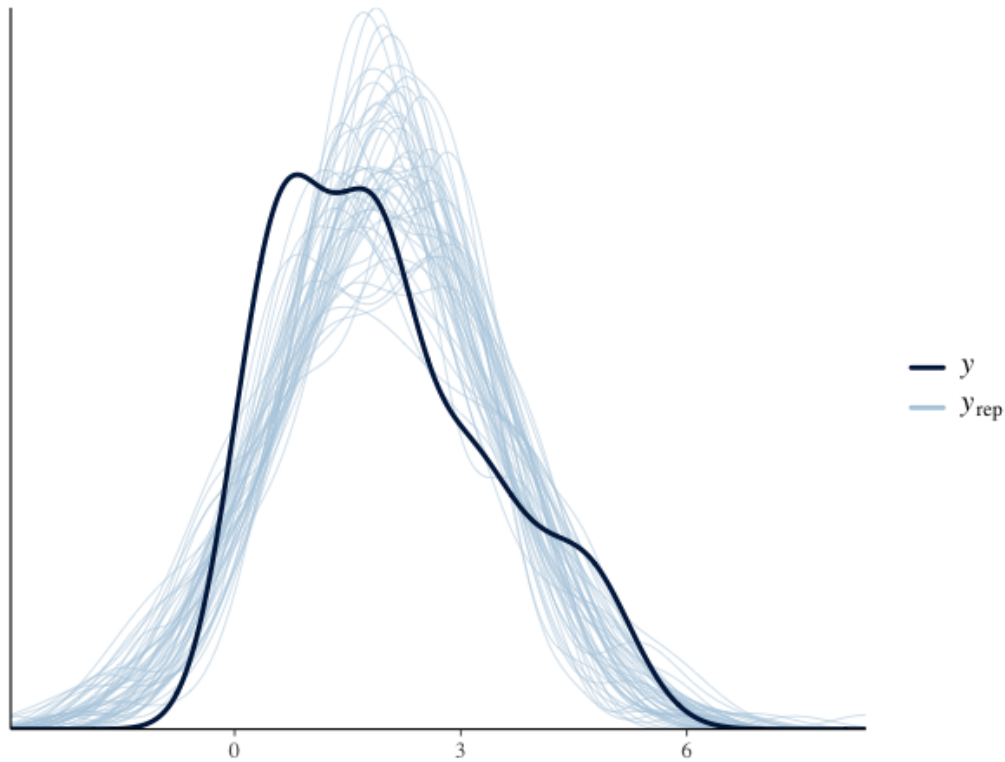
I chose to use a linear mixed effects model to model my data and explore the possible impacts of generation and ethnicity on eating disorders. The different generations and ethnicities are the top levels, under which the subjects within these levels are measured. The observations of SMAS, EDE-Q, and global scores then represent the next level on these subjects. This hierarchical structure implies non independence in the data, with the mixed model allowing for the inclusion of both the random effect of groups (namely generation and ethnicity) and explanatory variables defined at these group levels. Furthermore, I chose the linear mixed effects model as opposed to the generalized linear mixed effect model because the data I used does not include binary outcome, and so I thought the LME model to be more appropriate. Using the stanlmer function of the rstanarm package, I obtained a Bayesian fit for these linear mixed effects regression models.

The first model I fit used generation as the group; I initially included only SMAS as a fixed effect and SMAS conditioned on generation as the random effect, as shown in the code below; I also used the default priors. Using a posterior predictive check, I evaluated the fit of this first trial model (Figure 10). Looking

at Figure 10, we can clearly see that the proposed model does not adequately fit the observed data, and so I refit the model with more fixed parameters, a new random effect, and subjective priors informed by my own beliefs regarding SMAS and the influences of acculturation on eating disorders.

```
oldfit ← stan_lmer(global ~ smas + (smas|generation), data = df, seed = 345)
pp_check(oldfit)
```

Figure 10: Posterior Predictive Check for Model 1



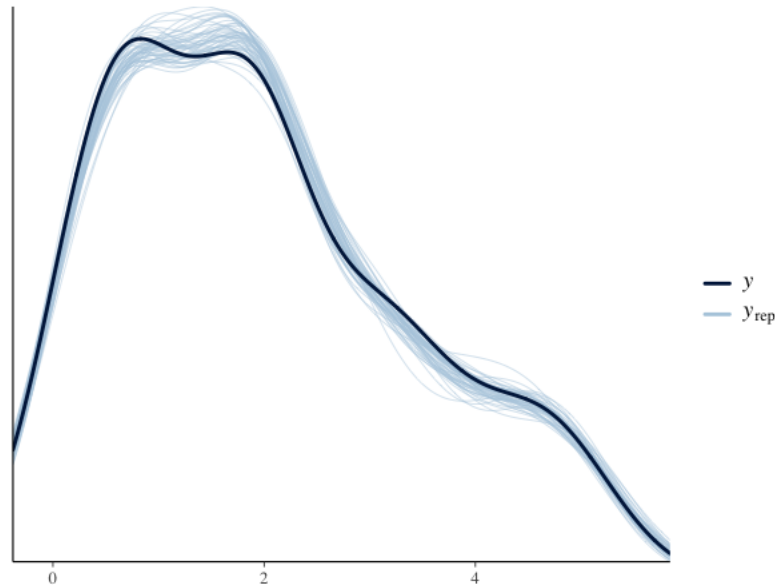
In the next model, I added several additional predictors, including the four EDE-Q subscores since these were shown to be statistically significant to the global scores based on the horseshoe priors as previously discussed. I added these variables both as fixed effects and into the mixed effect variable. For the mixed effects, I added SMAS and these four subscores as conditioned on generation. Furthermore, I added subjective priors. Because I predicted the second generation subjects to have higher global scores, I set a positive prior in which a significant mass of the probability distribution would be on positive values with, accordingly, a smaller mass on negative values. This positive prior also appropriately applies to the EDE-Q subscores since the horseshoe priors demonstrated positive coefficients for these variables. As such, I chose a prior with location 1 and scale 1 to in essence force the model to reflect my beliefs of the predominantly positive coefficients. For the prior intercept, I chose a flatter, less informative prior since I didn't have extensive prior knowledge about the global response variable. I wanted this prior to be more noninformative yet still numerically stable for computations, and so I selected a location of 1 and scale of 2.5 for the prior intercept. Finally, I set a seed to ensure I obtained the same reproducible results for randomization each time I ran the code. Figure 11 shows the posterior predictive check of this model, and demonstrates that this proposed model fits the data much better than the first model. The leave one out-type notion associated with this method of checking holds that the distributions should look very similar to each other if the predictive model is good, and the distributions in this Figure indeed are very similar.

```

newfit1 ← stan_lmer(global ~ smas + restraint + eating + shape + weight + (smas + restraint +
eating + shape + weight|generation), data = df, prior = normal(location = 1, scale = 1, autoscale =
TRUE), prior_intercept = normal(location = 1, scale = 2.5, autoscale = TRUE), seed = 345)
pp_check(newfit1)
summary(newfit1)

```

Figure 11: Posterior Predictive Check for New Model 1



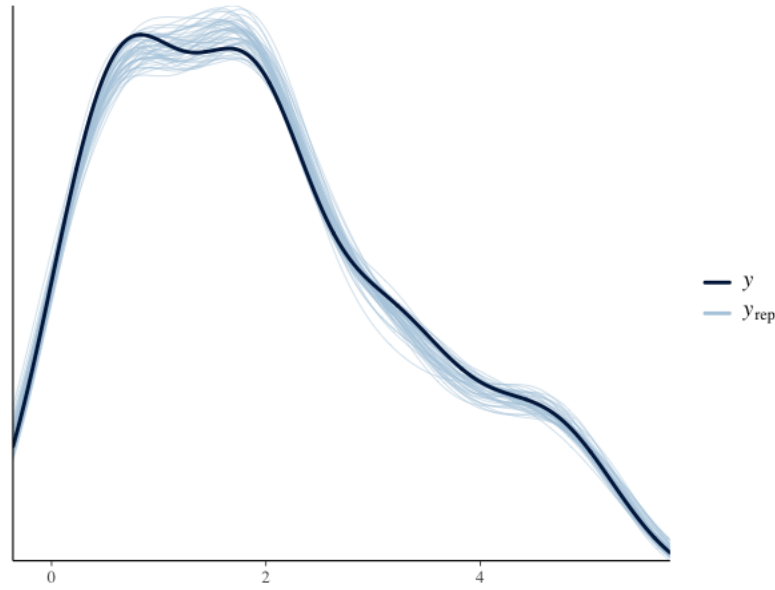
After establishing this foundation for modeling with important predictors that helped to significantly improve my model that used generation as the group, I then created a similar model using ethnicity rather than generation as the groups across which the intercepts/slopes of the random effects varied. Because I didn't believe ethnicity to be as strong an influence on eating disorders as generation, I selected a slightly flatter distribution with location 1 and scale 2.5. Here the prior distribution still has a significant mass on positive values, but not to the extent as selected in the model with generation. I used the same prior intercept values and seed value as the first model, then conducted the posterior predictive check as before. Looking at this distribution, we can see that this model fits the data fairly well.

```

newfit2 ← stan_lmer(global ~ smas + restraint + eating + shape + weight + (smas + restraint + eating +
shape + weight|ethnicity.factored), data = df2, prior = normal(location = 1, scale = 2.5, autoscale =
TRUE), prior_intercept = normal(location = 1, scale = 2.5, autoscale = TRUE), seed = 345)
pp_check(newfit2)

```


Figure 12: Posterior Predictive Check for New Model 2



I conducted further evaluation of my final two models by plotting the convergence traceplots, Figures 13 and 14, to confirm that the program computed the Bayes Theorem correctly. Here, I used SMAS as the parameter because this is the variable thought to be most varied by group. Neither traceplot shows extreme anomalies.

Figure 13: Traceplot for New Model 1

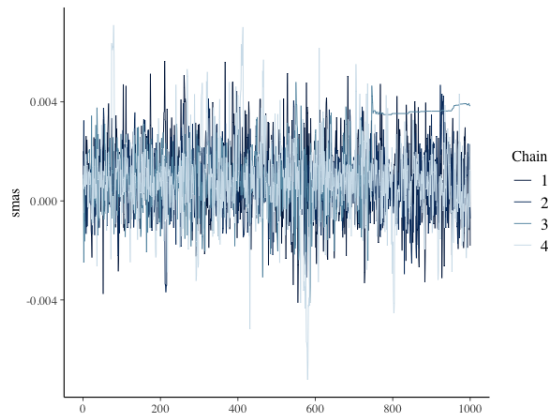
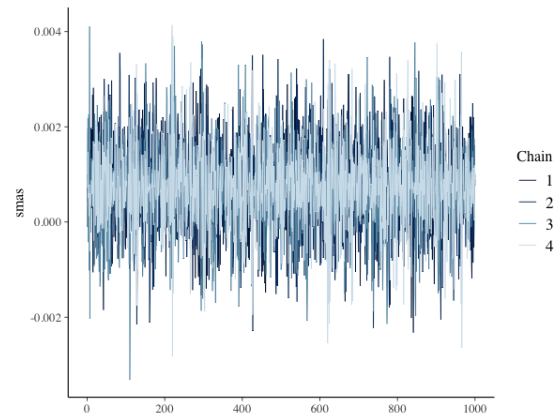


Figure 14: Traceplot for New Model 2



Continuing my comparison of these models, I used the Leave One Out method and compared the expected log pointwise prediction (ELPD) values of each model. The two ELPD values were very similar, as reflected by the comparison table (Table 1). Because these models have such similar ELPDs, I concluded that there was not one model that was stronger than the other.

Table 1: LOO Comparison

	<i>elpd_diff</i>	<i>elpd_diff</i>
newfit2	0.0	0.0
newfit1	-0.1	0.1

Examining the posterior predictive checks, convergence traceplots, and LOO ELPD values, I saw that both models performed well based on these measures, and also performed in a similar manner, getting fairly equally close to the data. As such, I concluded that both generation and ethnicity had similar strengths as the groups upon which their respective models are built.

4 Discussion

Because my results indicated that generation and ethnicity were both equally strong in modeling the data, this may lead to the necessity of further exploration into other exterior factors that may more strongly influence the prevalence of eating disorders among Asian Americans than these two. There are a multitude of environmental or confounding factors that are not measured in this survey and that could have potent impacts on the models, such as socioeconomic status.

Furthermore, there are limitations in the survey study due to the nature of data collection; the surveys were posted onto public forums, introducing response bias. Subjects frequenting these forums and forum subgroups may be more inclined to respond to the survey if they feel more strongly about or identify more strongly with eating disorders. Furthermore, in the survey itself, particularly the EDE-Q survey, questions that have similar implications may have resulted in similarities among subscores. For instance, if a subject answered a question that indicated a strong concern about their shape, it is likely that a following question that serves as a measure of concern about weight would be answered in a similar manner. This in turn may result in risk of collinearity between the shape and weight subscores. Because of these limitations, it is possible that the data used may result in overfitting of the model.

In order to minimize the harm of these limitations, the survey could be distributed to a more randomly selected group of subjects, rather than being posted on public sites to the general public to decide whether or not to engage with the study. Furthermore, the scale on which global score is comprised could possibly be altered to account for the potential relation between shape and weight concern; for instance, these two scores combined could be weighed equally as the other two individual scores.

5 References

- [1] Budiman, Abby, and Neil G. Ruiz. "Asian Americans Are the Fastest-Growing Racial or Ethnic Group in the U.S." *Pew Research Center*, Pew Research Center, 16 May 2021, <https://www.pewresearch.org/fact-tank/2021/04/09/asian-americans-are-the-fastest-growing-racial-or-ethnic-group-in-the-u-s/>.
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[4] “Stephenson Multigroup Acculturation Scale (SMAS).” *PSYCHOLOGICAL SCALES*, 17 Mar. 2022, <https://scales.arabpsychology.com/s/stephenson-multigroup-acculturation-scale-smas/>.

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