

## Introduction

Obstructive sleep apnea (OSA) - recurrent partial or complete upper airway collapse during sleep - is common. Epidemiologic studies suggest that sleep apnea prevalence in adults is estimated to be 26% and increasing with the burgeoning obesity epidemic.<sup>1</sup> Sleep apnea is associated with increased healthcare costs, treatment-resistant hypertension, daytime sleepiness and fatigue, and decreased quality of life.

Sleep apnea is treatable. The most common treatment is continuous positive airway pressure therapy (CPAP), a device that blows air into the upper airway via a mask. CPAP effectively eliminates OSA breathing events. However, adherence has been notoriously poor.

CPAP adherence may be mediating improvements in functional outcomes such as quality of life and daytime symptoms. We conducted a secondary analysis of a randomized controlled trial of CPAP therapy to evaluate this relationship between CPAP adherence and functional outcomes, particularly overall quality of life, across the first 3 months of CPAP therapy.

## Question/hypothesis

What is the effect of adherence to CPAP on quality of life and other functional outcomes in the first 3 months of therapy? We hypothesize that increased adherence is associated with improvements in all functional outcomes at 3-month follow-up.

## Methods

### *Population and Variables*

Subjects were participants of the HomePAP Study<sup>2</sup>, a randomized open-label multicenter trial that compared home-based unattended portable obstructive sleep apnea (OSA) diagnosis and therapy titration (determination of appropriate settings for therapy) with (A) home sleep apnea testing and autotitrating CPAP and (B) polysomnography-diagnosed OSA and in-lab titration. The study included 373 participants aged 18 years and older, but only randomized those with moderate to severe OSA who accepted CPAP therapy (n = 187 in home group and n = 186 in in-lab group). OSA severity is defined by the apnea-hypopnea index, which is the number of complete or partial decreases in airflow per hour of sleep. Moderate to severe OSA is defined by an apnea hypopnea index of at least 15/hour.

The study had three primary outcomes: (1) CPAP acceptance, (2) time to treatment, and (3) CPAP adherence. The secondary outcomes were changes in Epworth Sleepiness Scale (ESS) and functional outcomes.<sup>2</sup> Baseline measurements were conducted from 2008-2010 and follow up assessments took place at 1 and 3 months after CPAP initiation. A comprehensive description of the HomePAP study's rationale, questions, and methods can be found elsewhere (Rosenet al., 2012).

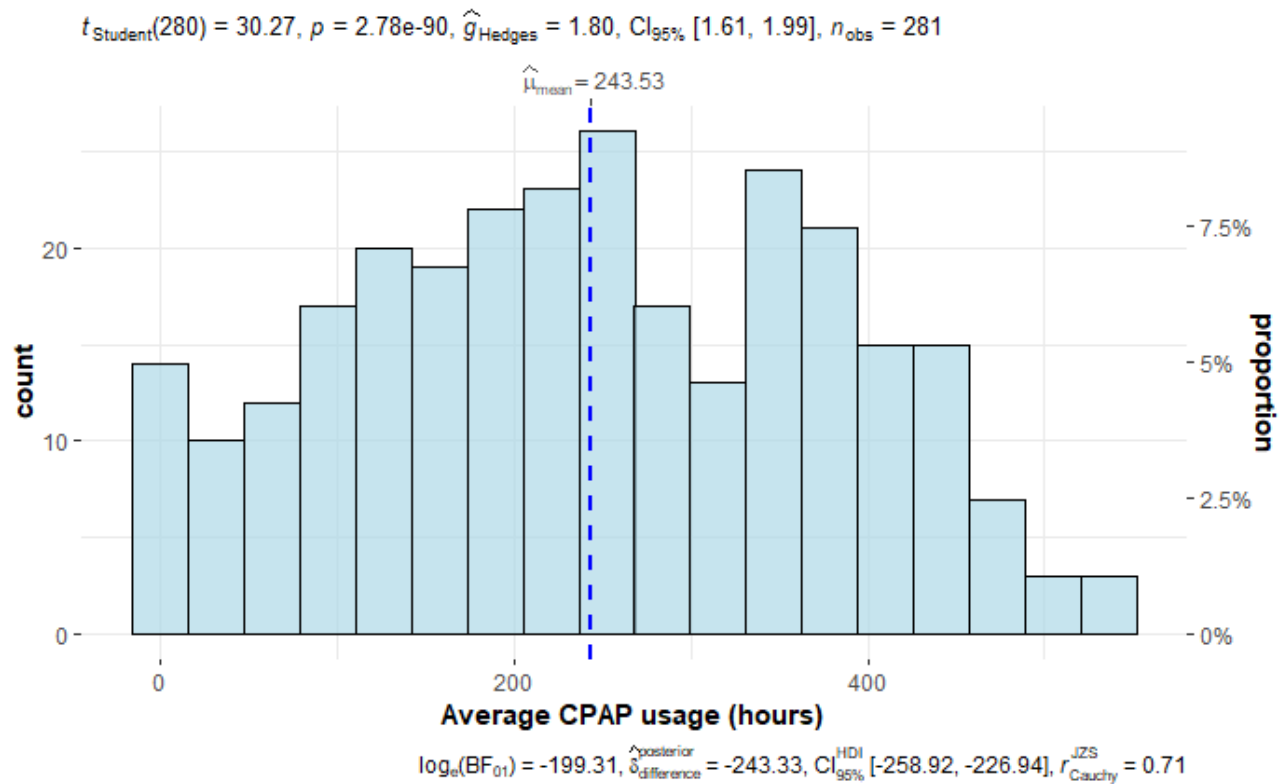
Data for the present study were drawn from baseline (n=373). Participants were included if they had any data on the main predictor, CPAP adherence, or outcome, global FOSQ score (n=154). Adherence was a continuous variable defined as average CPAP use per night. It was calculated as the total time of CPAP use divided by the total number of days in the interval in hours/night. A 30 minute increase in adherence is considered clinically meaningful. Functional outcomes, a continuous variable, was measured using the Functional Outcomes of Sleep Questionnaire

(FOSQ) Global Score.<sup>3,4</sup> Specifically, FOSQ Global assesses the impact on daily activities and sleep-related quality of life. Higher scores indicate better functional status.<sup>3</sup> We additionally assessed FOSQ subscale in secondary analyses. Other quality of life measures that are not disease-specific, the SF-36 physical functioning and SF-36 mental functioning, were used as sensitivity analyses.<sup>3</sup> Relationship between adherence and the Epworth Sleepiness Score was evaluated as a potential mediator in the relationship between adherence and quality of life.<sup>2,5,6</sup> We adjusted for the following covariates: age, race, sex, time to treatment, AHI, body mass index, and comorbidities (coronary heart disease, congestive heart failure, depression, and hypothyroidism). All analyses used R, version 4.04 and SAS, version 9.4.

### Exploratory analyses

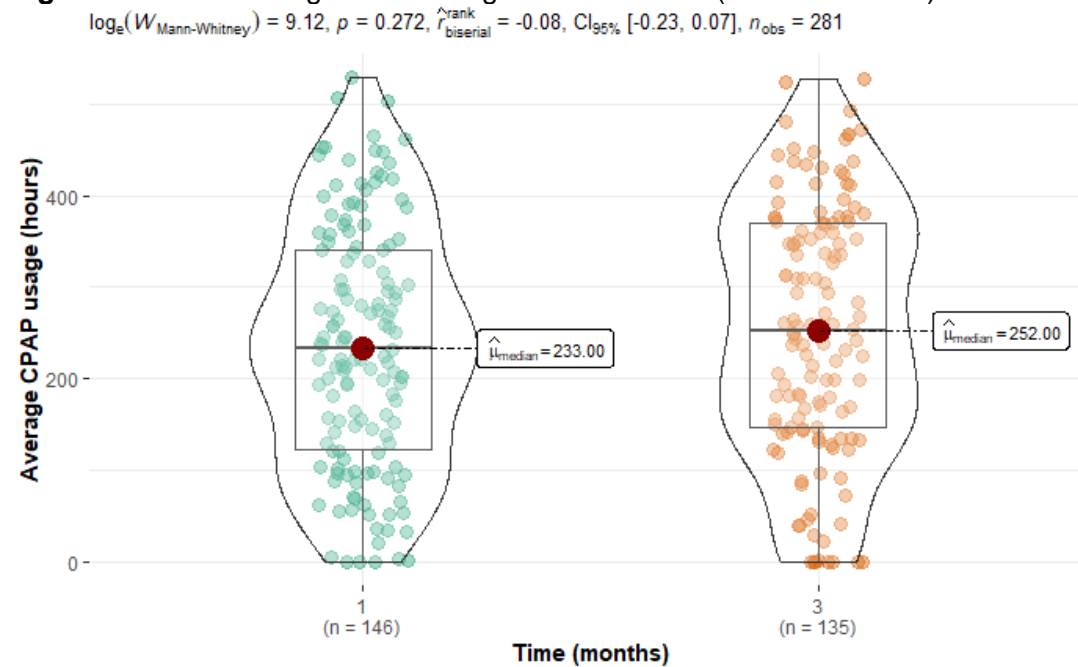
We first examined the distribution of the main predictor, CPAP adherence (Figure 1). There is a good spread of values across the spectrum of responses.

**Figure 1.** Histogram of CPAP use over all time points



There is a change in the distribution of adherence between the 1 and 3 month time points. Because of this we will include the interaction of adherence and time in the model to account for the time-varying nature of the adherence variable.

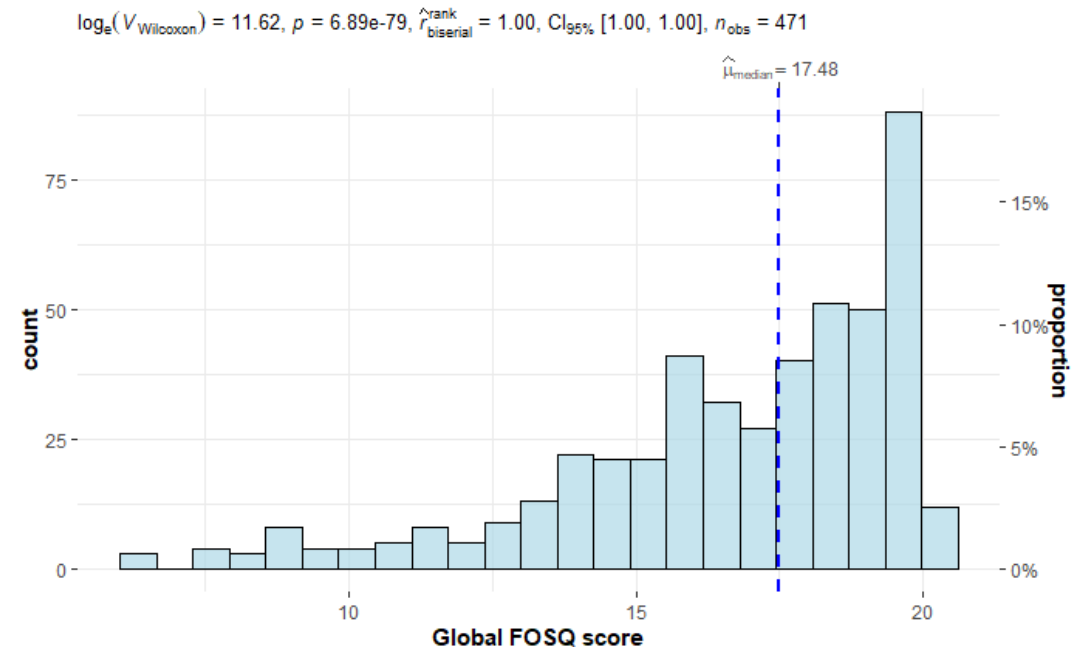
**Figure 2.** Plot of average CPAP usage based on time (1 and 3 months):



This change in the shape of the adherence violin plots over time indicates a potential interaction between adherence and time. We test this supposition more formally later on as well.

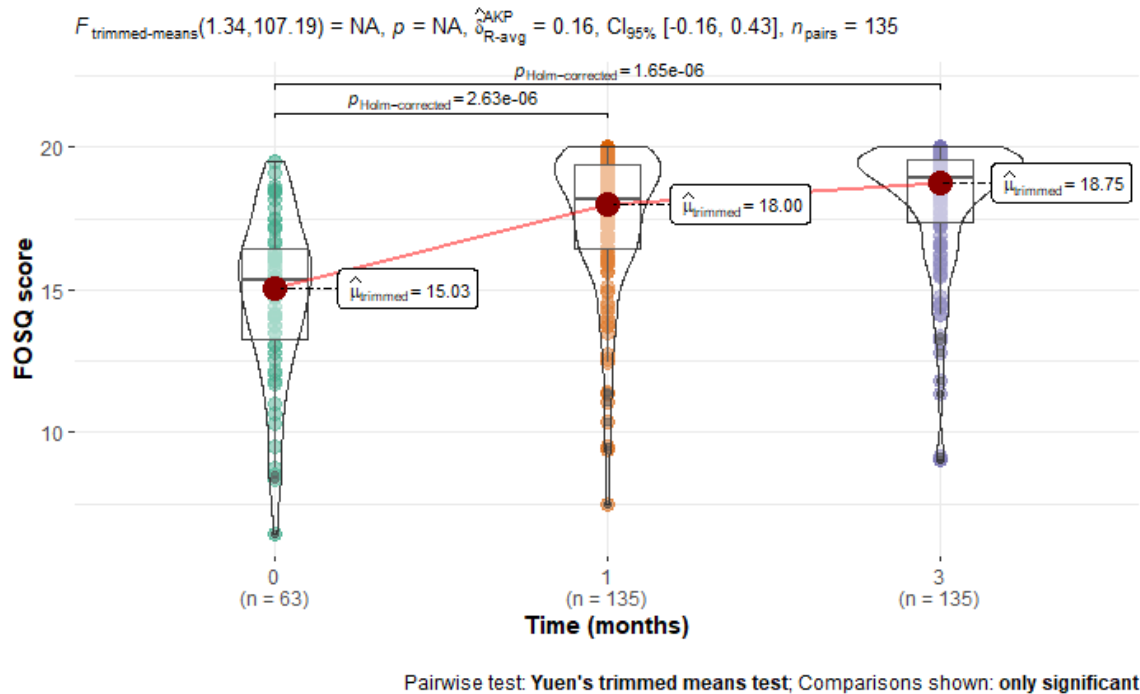
The primary outcome is the global score of the (FOSQ, a validated disease-specific quality of life measure. This questionnaire consists of 30 questions in 5 domains with an overall score range of 5-20. Low scores indicate poor sleep-related quality of life while higher scores correspond to few functional impairments. The distribution of this outcome over all time points is left-skewed with bunching at the top end of the scale (Figure 3).

**Figure 3.** FOSQ global score histogram



Looking at the FOSQ distribution over time, the distribution becomes increasingly skewed from baseline to 1 and 3 months post-therapy initiation (Figure 4).

**Figure 4.** Plot of FOSQ global score based on time



### Missing Data

After only including patients with at least one observed value for the main predictor, adherence, and the outcome, FOSQ global, there were 117 patients who had complete data for all 12 variables. The missing data pattern was shown to be nonmonotone or arbitrary as can be seen in Table A1 of the appendix. To address missingness, we decided to use multiple imputation. We chose multiple imputation because we used Little's test for missing completely at random, and there is strong evidence that our data is not missing completely at random. Therefore, complete case analysis would not be appropriate and we did not want to be limited by the bias associated with single imputation. Therefore, it was assumed that the data was missing at random. Missing at random assumes that the mechanism of the missing observation depends only on the observed covariates but not on the value for the variable itself.

To multiply impute arbitrary missing values, we had the choice to either use a Markov chain Monte Carlo (MCMC) method or a fully conditional specification (FCS) method (also known as multiple imputation by chained equations). We chose the FCS method because it assumes the existence of a joint distribution for all variables rather than multivariate normality. Thus, since we had a non-normally distributed and discrete response, the FCS assumption was much better based on its flexibility. For the continuous variables, we had the choice of using a regression method or predictive mean matching method. For model type selection, imputation was done with a combination of cart and predictive mean matching to avoid non-invertible regression predictor matrix if predictive mean matching was used for all variables (this occurs when some variables are linear combinations of other variables).

After the model type was specified, we did a separate imputation to use for model and covariance structure selection and main analysis. Because the mixed-effects model has time-dependent (e.g., body mass index) and time-independent variables (e.g. sex), we used multilevel predictive mean matching imputation with inclusion of time-dependent variable means, time-dependent variable deviations from the mean, and interactions within the time-dependent variables, between time-dependent and baseline variables, and within all baseline variables. We used an iterative updating approach where main effects are imputed first and then the interactions were calculated. Main effects are then updated based on the relationship between the interactions. This approach preserves the multilevel structure of longitudinal data. Provided that the highest percentage of a missing variable was 10%, the number of imputations was set to 10 for both imputations.

### **Modeling strategy**

Our overall strategy was to sequentially evaluate model parameters:

1. Fit of beta and gamma distributions vs. linear regression - standardized residuals and compare residuals to choose a model type
2. Select preliminary mean structure (unstructured)
3. Select preliminary random-effects structure
4. Select covariance structure
5. Evaluate reduction of random effects
6. Select the mean model

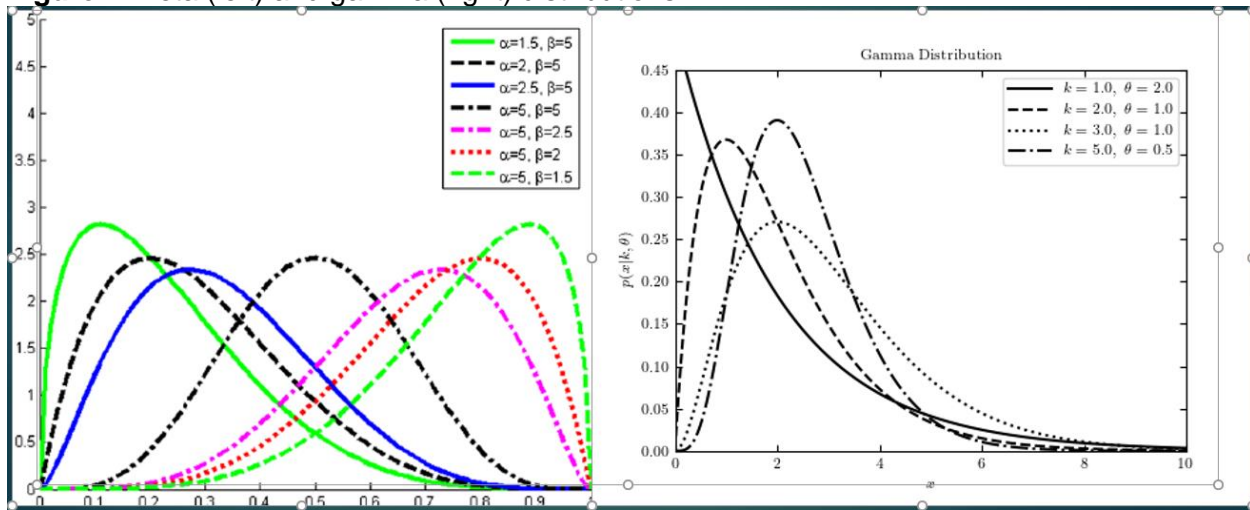
The final model will use CPAP adherence as a predictor and functional outcomes as the outcome. The primary analysis will focus on quality of life as measured by the FOSQ. Secondary analyses will evaluate sleepiness, SF-36 subscale scores, and blood pressure measurements. We will also conduct sensitivity analyses including home vs. lab grouping as used in the study as a predictor variable.

#### *Selecting a model type*

Because of the shape of the outcome distribution, in addition to linear models, we evaluated other distributions, namely the beta and gamma distributions (Figure 4). These distributions visually more closely approximated the FOSQ distribution within our study.

We constructed general estimating equations (GEE) models using the beta and gamma distributions. We compared these models to a linear mixed effects model (LME) with a random intercept. Comparison of the justification/advantages of each approach can be seen in Table 1.

**Figure 4.** Beta (left) and gamma (right) distributions.<sup>7,8</sup>



**Table 1.** Characteristics of the general estimating equations and linear mixed effects models. Italicized points apply to both models.

	GEE	LME
<b>Justification</b>	<ul style="list-style-type: none"> <li>Accommodates non-normally distributed data for a continuous outcome</li> <li><i>Answered research question</i></li> </ul>	<ul style="list-style-type: none"> <li>Robust to the assumption of normally distributed data</li> <li><i>Answered research question</i></li> </ul>
<b>Advantages</b>	<ul style="list-style-type: none"> <li><i>Results can be interpreted at an individual or population level</i></li> <li><i>Does not require common measurement times</i></li> <li><i>Can handle imbalance due to missing data in the response variables.</i></li> <li>almost as precise/efficient as MLE for many longitudinal design</li> <li>Full distribution does not need to be specified, so although the standard errors may be inaccurate, the coefficient</li> </ul>	<ul style="list-style-type: none"> <li><i>Results can be interpreted at an individual or population level</i></li> <li><i>Does not require common measurement times</i></li> <li><i>Can handle imbalance due to missing data in the response variables.</i></li> <li>Uses maximum likelihood approach, thus models can be compared using AIC, BIC, and LRT</li> <li>If data not imputed, assumes missing at random</li> <li>Can account for heterogeneity in the</li> </ul>

	GEE	LME
	<p>estimates can still be accurate. Can separate the interpretation of the regression coefficients and the covariance structure</p> <ul style="list-style-type: none"> <li>• If the mean model is correct, the 'empirical or 'sandwich' estimator correctly models the variance of beta hat</li> </ul>	<p>population with random effects</p> <ul style="list-style-type: none"> <li>• Can evaluate multiple covariance structures</li> <li>• Can use REML or ML. REML will be less seriously biased than the ML because ML acts as if our estimated beta was the true value of beta. REML separates the part of the data used to measure sigma from that used for estimating beta.</li> <li>• Valid standard errors for the <math>\hat{\beta}</math> can be based on the "sandwich" estimator of <math>\text{cov}(\hat{\beta})</math>. Then, if the covariance structure is misspecified, the standard errors are robust to that</li> <li>• The covariances among the longitudinal responses are expressed as a function of time. Unlike covariance pattern models (e.g., AR1, exponential, CS, ARH(1), LMEs explicitly distinguish between-subject and within-subject sources of variability</li> <li>• Unlike many covariance pattern models that make strong assumptions about variance being the same over time, random effects covariance structure allows for the variance and covariance to</li> </ul>

	GEE	LME
		<p>increase or decrease as a function of the times of measurement</p> <ul style="list-style-type: none"> <li>Account for the covariance among repeated measures in a parsimonious way (i.e. the induced random effects covariance structure is described with only a few parameters regardless of the number of measurements)</li> <li>incorporates measurement error</li> </ul>
<b>Disadvantages</b>	<ul style="list-style-type: none"> <li>Most computer software for beta distribution with GEE only allows for an unstructured covariance matrix</li> <li>Widely available software assume that the scale parameter for the variance of <math>Y_{ij}</math> is time invariant</li> <li>Uses quasi-likelihood to be flexible for model types other than identity (which is the linear model) to compare models</li> <li>Strong assumption of MCAR if data not imputed</li> </ul>	<ul style="list-style-type: none"> <li>Must specify a full distribution</li> <li>An important issue in LME is the “centering” of time measurements</li> </ul>
<b>Assumptions</b>	<ul style="list-style-type: none"> <li>The expectation of the response depends on the covariates through a link function, which for beta regression, was the log.</li> <li>The variance of each</li> </ul>	<ul style="list-style-type: none"> <li>The responses are distributed as multivariate normal</li> <li>Normally distributed errors</li> <li>Assumes that the repeated responses depend on a</li> </ul>

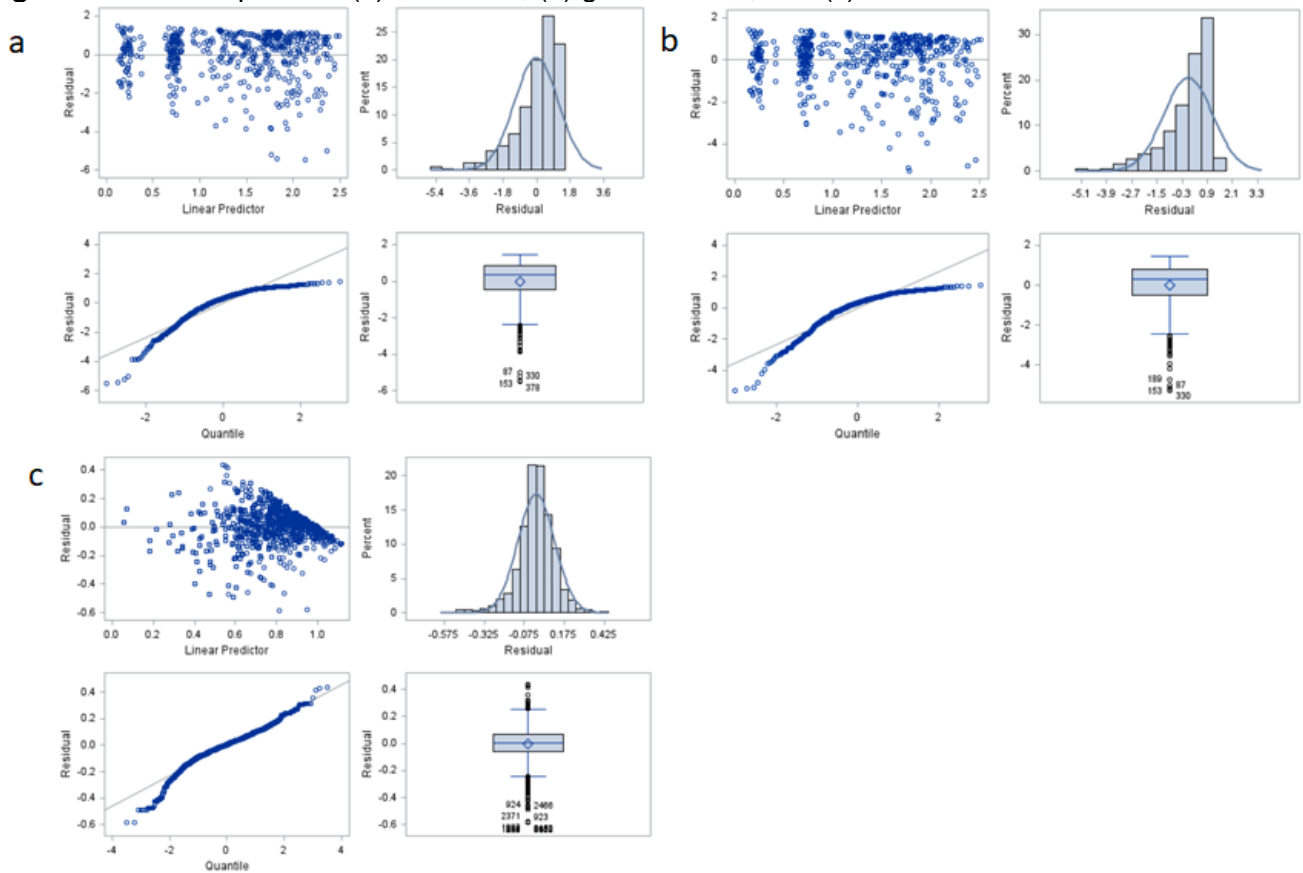


	GEE	LME
	<p>of the repeated outcomes depends on the mean according to</p> $\text{Var}(Y_{ij} X_{ij}) = \phi v(\mu_{ij})$ <ul style="list-style-type: none"> <li>The two-way within-subject association among the vector of outcomes, is assumed to be a function of the means, <math>\mu_{ij}</math>, and an additional set of within-subject association parameters, alpha. The term “working” correlation matrix addresses our uncertainty about the assumed model for the within subject correlations and variances.</li> </ul>	<p>combination of population characteristics (fixed effects denoted by beta) and subject specific effects (random effects)</p> <ul style="list-style-type: none"> <li>Both the subject effect and measurement effect are assumed to be random with a mean of zero and with variances</li> </ul> $\text{Var}(b_i) = \sigma_b^2 \text{ and } \text{Var}(\epsilon_{ij})$ <ul style="list-style-type: none"> <li>Conditional independence assumption: given the random effects, <math>b_i</math>, the measurement errors are independently distributed with a common variance <math>\sigma^2</math></li> <li>The subject effect and measurement error are independent of one another</li> </ul>

To evaluate the model fit, we constructed and evaluated plots of standardized residuals from each model (Figure 6).

As can be seen in Figure 6, the beta and gamma residuals do not conform to a normal distribution. Both histograms show a substantial left skew and the Q-Q plot is much more curved than what would be expected in a well-fitting model. The LME residuals, on the other hand, do approximate a normal distribution with perhaps an overabundance of points in the very middle. The Q-Q line for the LME residuals also much more closely fit the predicted QQ line for a normal distribution of residuals. ~~Based on this, the LME seems to be the better-fitting model for this dataset.~~ Therefore, all the rest of model selection is done with the LME models.

**Figure 6.** Residual plots for (a) beta GEE, (b) gamma GEE, and (c) LME



### Working Covariance Structure

We next explored several covariance structures on the fully elaborated model specified in the mean model structure section (model 6 in Table 3) with random intercept and slope (time), namely variance components and unstructured. We considered other covariance structures, but found them less desirable than these two based on Table 2.

**Table 2.** Possible covariance structures for linear mixed effects models and their appropriateness for our dataset

Covariance Structure	Description	Appropriate to model our dataset?
<b>Compound Symmetry</b>	<p>Variance is constant across occasions</p> <p>Unrealistic assumptions:                      Randomization argument                      Correlation between any pair of measurements is the same regardless of the time interval (expected to decay with time)</p>	<p>No, because there is a very strong assumption of equal correlation.</p> <p>Also, in mixed effects models, the introduction of a random subject effect induces correlation among repeated measures. Thus, this</p>

Covariance Structure	Description	Appropriate to model our dataset?
		structure is not usually appropriate
<b>Variance component</b>	Allows for different variances, but there will be zero correlation between the random intercept and random slope	Yes, will be evaluated
<b>Unstructured</b>	Allows for nonzero correlation between random intercept & random slope	Yes, will be evaluated

An unstructured model (type= un) and variance components (type = vc) model were compared using a likelihood ratio test (LRT). The code and output can be seen in table A2 of the appendix. The LRT statistic is 67 on 5 degrees of freedom (parameters in un - parameters in vc). Since the critical value (for alpha=0.05) is 11.1, which is less than our LRT statistic, we reject the null hypothesis that the reduced model (vc) is adequate relative to the unstructured model. Thus, the data suggest that we need a more complex model than vc to describe the covariance structure, however this does not necessarily mean that we need the unstructured model (there could be something in between). For all subsequent analyses, the unstructured model was used as the covariance structure.

### *Random effects structure*

Next, we evaluated whether the random effects structure could be reduced. We tested the full mean model (specified in mean model selection (model 6 in Table 3) with several random effects structures: (A) no random effects, (B) random intercept only, and (C) both random intercept and random slope (time).

We computed the -2 log likelihood for each of the three models and used LRT to test among them. The chi-squared statistic was 36.7 for the difference between model B and model A. This is substantially higher than the critical value, which means that the model with fixed effects only is insufficient compared to one with fixed effects and a random intercept. The critical chi-square value for comparison of intercept and slope relative to only intercept random effect is 5.14. Since  $5.28 > 5.14$ , we have evidence that the random intercept is insufficient compared to the random intercept and slope. All further models will use the random intercept and slope as the random structure.

### *Model mean structure*

Variable selection proceeded in several steps. First, we used structural equation modeling to make an interconnected model from all available (and some unavailable but influential) variables based on prior research and biologic plausibility related to PAP adherence and quality of life in the dataset. Based on adjusting for confounders of the relationship between adherence

and quality of life while avoiding adjusting colliders and mediators of the relationship, the following variables were selected for inclusion in the initial full model (other than quality of life and adherence): age, sex, race, heart failure (HF), coronary heart disease (CHD), depression, hypothyroidism, time to treatment, and sleep apnea severity (the apnea-hypopnea index). This is the model that was used for model type and covariance structure selection.

We built several nested LME models (Table 3) to determine optimal variables to include in the analysis. All of these models were created using maximum likelihood; REML could not be used because they have different residuals because of the differences in their mean structure. These models were compared with the Wald test to determine whether there was evidence that the restricted model did not describe the data as well as the more elaborated model at  $\alpha = 0.05$ .

**Table 3.** Evaluation of nested mean models. The compactor column indicates the model of comparison for the Wald p-value (e.g., p-value 0.58 for model 5 relative to model 6) and df is the degrees of freedom of the full - restricted model

#	Parameters	Comparator(s)	F-value Test statistic	df	Wald p-value
1	Intercept only	2	116	2	< 0.0001
2	Adherence + time	3	11.0	1	0.001
3	Adherence + time + adherence * time	4	2.08	5	0.08
4	Model 3 + age + sex + race	5	5.98	4	0.0001
5	Model 4 + HF + CHD + depression + hypothyroidism	6	0.91	2	0.40
6	Model 5 + time to treatment + sleep apnea severity	7	0.98	9	0.45
7	Adherence + time + adherence * time + depression	3	23.95	1	< 0.0001

Based on Table 3 we conclude that model 7 is optimal for this dataset. Because model 6 includes all intermediate predictor models between model 7 and model 6, there is no need to test nested models with more than model 7 but fewer than model 6 parameters. If any of those models improved the fit, then the p-value for the comparison between model 6 and model 7 would be expected to be less than 0.05 (but it's not,  $p = 0.45$ ).

### Analysis

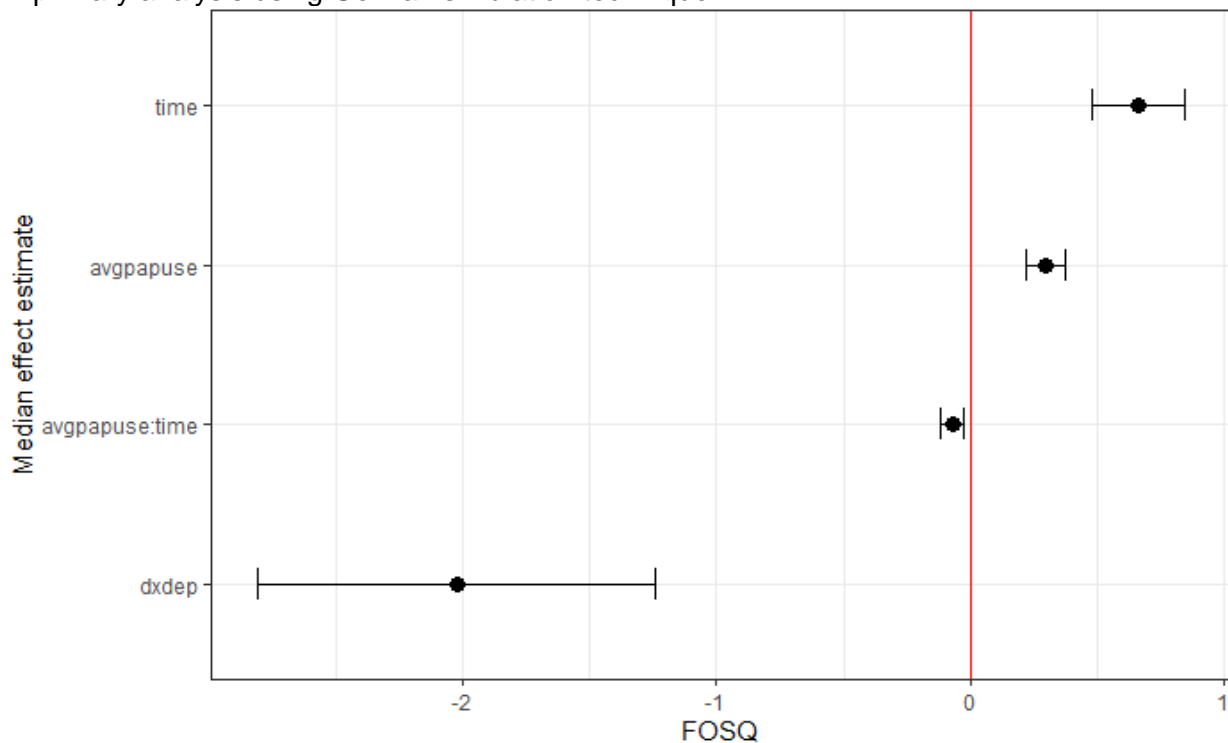
Now, we have a mean model, a random effects model, and a covariance structure. We're set to actually do our analysis evaluating the association between adherence and functional outcomes. For all of our secondary analyses, we will use the same random effects and covariance structure as in the primary analysis. We evaluated associations of CPAP adherence with FOSQ global score as the primary analysis. Secondary analyses included subscale score, SF-36 mental functioning and physical functioning subscores. For mediation analyses, we

evaluated whether Epworth sleepiness score was a mediator of the relationship between adherence and FOSQ. Therefore, we constructed two additional models: (1) predictor variables of the primary analysis and ESS as the outcome and (2) a model with FOSQ global score as the outcome and ESS, time, and depression as fixed effects.

## Results

Based on our linear mixed effects model, we conclude that CPAP use is associated with improvement in FOSQ global score by 0.30 per hour increase in sleep (95% CI: 0.22, 0.38; t-value 7.5;  $p < 0.001$ ). The interaction of time and CPAP use decreases FOSQ by -0.07 per hour sleep \* month (95% CI: -0.11, -0.02; t-value = 3.0,  $p = 0.003$ ). This may indicate a stronger effect of CPAP adherence early in therapy which wanes with time. Depression had the biggest effect in the model and decreased global FOSQ scores by -2.06 (95% CI: -2.90, -1.23; t-value -4.8;  $p < 0.001$ ). These results are presented graphically in Figure 7.

**Figure 7.** Visual representation of effect estimates and 95% confidence interval of model effects in primary analysis using Gelman simulation technique



## Subscales

The FOSQ score is made up of 5 subscales: activity level, vigilance, intimacy, general productivity, and social functioning. Improvements in adherence increased each of the subscales, but all increases were less than 0.1 points for each hour or CPAP use (Table 4).

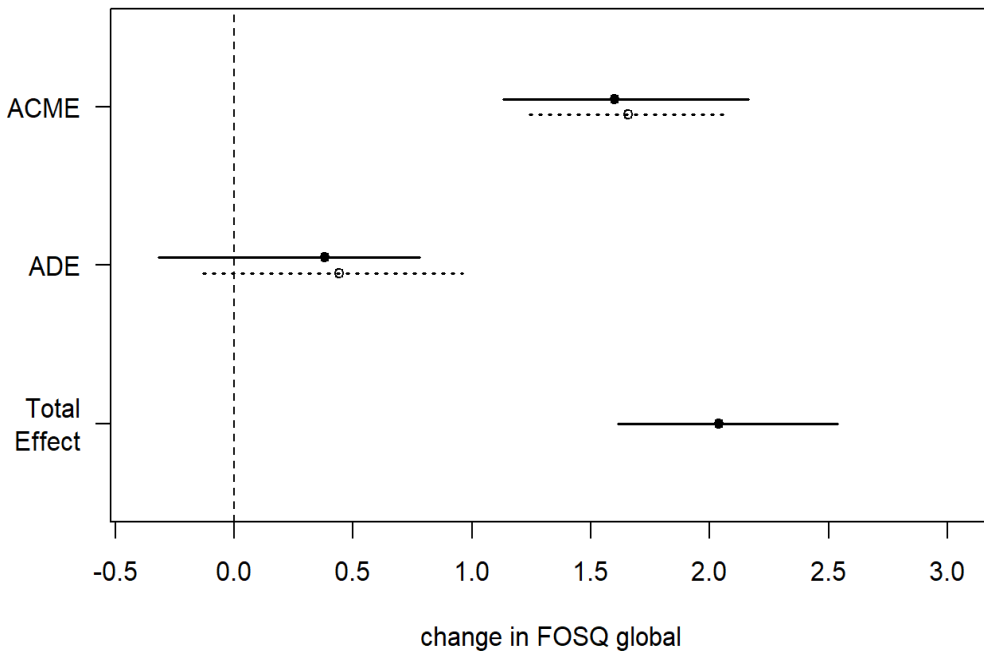
**Table 4.** Results of longitudinal analysis of the relationship between PAP adherence and individual FOSQ subscales

Subscale	Estimate (95% CI)	t-value	p-value
activity level	0.095 (0.068, 0.121)	7.02	<0.001
vigilance	0.095 (0.070, 0.121)	7.30	<0.001
intimacy	0.054 (0.016, 0.091)	2.82	0.005
general productivity	0.078 (0.056, 0.100)	6.93	<0.001
social	0.068 (0.040, 0.096)	4.78	<0.001

*Mediation analysis*

We evaluated the possibility that the ESS mediated relationship between PAP adherence and FOSQ global score by using 50 simulations on the imputed datasets and then merging the results. For this analysis, the primary predictor had to be a categorical measure. Therefore, we dichotomized the continuous PAP adherence into <4 hours use per night and  $\geq 4$  hours use per night. This threshold is the standard measure of whether someone is adherent and used by payers to determine coverage for continued PAP therapy. Therefore, this is a clinically meaningful threshold. The majority of the relationship between PAP adherence and FOSQ was mediated by the ESS (Figure 8). The average causal mediation effect = 1.63, 95% CI: 1.21-2.02, which corresponds to a proportion mediated is 0.80, 95% CI: 0.795-0.80`.

**Figure 8.** Graphical display of mediation analysis with ESS as the mediator between PAP adherence and FOSQ global score. Grey bars are nonadherent individuals and black bars are adherent individuals. ADE = average direct effect, ACME = average causal mediation effect (i.e., indirect effect), and total effect is the combination of ADE and ACME.



### *SF-36*

For the SF-36 mental health summary score, an additional hour of PAP use increases SF-36 mental health summary score by 0.87 (95% CI: 0.47, 1.28; t-value = 4.39,  $p < 0.001$ ). Each additional hour of PAP use increases the SF-36 physical summary score by 0.54 (95% CI: 0.22, 0.87; t-value = 3.26;  $p = 0.001$ ).

## Discussion

Increases in adherence in those with moderate-severe OSA initiating on CPAP therapy are associated with better quality of life, both when measured on a disease specific questionnaire (FOSQ) and a general questionnaire (SF-36). Furthermore, mediation analysis revealed the majority of the quality of life improvement was mediated by improvements in sleepiness as measured by the Epworth Sleepiness Scale. PAP adherence also had a stronger association early in therapy (1 month) with attenuation at 3 months of therapy.

The FOSQ minimally clinically important difference is 1/20 points. None of our estimates rose to this level. Therefore, even though there is a statistically significant relationship between adherence and quality of life, it is not a clinically meaningful one. The story is much the same with SF-36: the minimally clinically important difference is estimated to be 8-11, a value an order of magnitude larger than the effect seen in this study.

### *Limitations*

There are several limitations to this study. First, this is a secondary analysis and, as such, should be considered hypothesis-generating. Additional work including a more diverse racial mix - other than primarily white and black people - would make the findings more generalizable. In addition, this study was conducted in a single Midwestern city and may not be representative of other parts of the country (due to potential differences in cultural norms, beliefs, and behaviors). The study follow-up period was rather short - follow-up ended 3 months after CPAP initiation. This study, therefore, can't speak to long-term changes to quality of life associated with CPAP use. Mild sleep apnea patients, which are a large proportion of the clinical population treated for sleep apnea, were excluded from the study. The results may not be generalizable to these individuals, particularly if they are less symptomatic (e.g. less sleepy). Overall, this was a secondary analysis of a rigorously- conducted randomized controlled trial with systematic data collection and good retention of participants.

On a more technical note, data were presumed to be missing at random (MAR). However, it is quite possible that those people that did not have improvements in their symptoms or quality of life were more likely to not complete the study procedures. In addition, certain variables may have been missing not at random. If this is true, multiple imputation does not alleviate bias since it does not account for this type of missingness. Usage of all available covariates may have improved multiple imputation procedures. However, since we chose the most biologically and clinically salient factors, inclusion of other variables may have led to more accurate modeling of noise (i.e. more noise because the variables are not informative but the algorithm uses them in modeling nonetheless).

### *Future directions*

This initial exploration of associations between CPAP adherence and quality of life needs to be additionally validated in larger and more diverse cohorts. We examined the population-level effect. However, it is possible that the heterogeneity of effect is the more interesting measure. Perhaps some people benefit greatly while others hardly benefit at all. In this situation, although

the population-level effect may be meager, the effect for those that benefit is large. It is also possible that for some their quality of life decreases secondary to the burdens of CPAP therapy. Identification of subgroups for whom CPAP therapy may yield large gains in quality of life while avoiding this therapy in those that do not benefit may be more clinically meaningful than evaluating the average effect. Longer-term follow-up of 6 - 12 months may be more meaningful as well compared to the relatively short 3-month follow-up of this study. Longer follow-up may also be more indicative of long-term changes in quality of life and symptomatology secondary to CPAP therapy.



## References

1. Peppard, P. E. *et al.* Increased Prevalence of Sleep-Disordered Breathing in Adults. *American Journal of Epidemiology* **177**, 1006–1014 (2013).
2. Rosen, C. L. *et al.* A Multisite Randomized Trial of Portable Sleep Studies and Positive Airway Pressure Autotitration Versus Laboratory-Based Polysomnography for the Diagnosis and Treatment of Obstructive Sleep Apnea: The HomePAP Study. *Sleep* **35**, 757–767 (2012).
3. Silva, G. E., Goodwin, J. L., Vana, K. D. & Quan, S. F. Obstructive Sleep Apnea and Quality of Life: Comparison of the SAQLI, FOSQ, and SF-36 Questionnaires. *Southwest J Pulm Crit Care* **13**, 137–149 (2016).
4. Omachi, T. A. Measuring Sleep in Rheumatologic Diseases: The ESS, FOSQ, ISI, and PSQI. *Arthritis Care Res (Hoboken)* **63**, S287–S296 (2011).
5. Patel, S. *et al.* The Epworth Sleepiness Scale: Minimum Clinically Important Difference in Obstructive Sleep Apnea. *Am. J. Respir. Crit. Care Med.* **197**, 961–963 (2018).
6. Ayas, N. T. & Marra, C. Continuous Positive Airway Pressure Therapy for Obstructive Sleep Apnea Syndrome: Do the Dollars Make Sense? *Sleep* **28**, 1211–1213 (2005).
7. Lin, L. & Goodrich, M. A Bayesian approach to modeling lost person behaviors based on terrain features in Wilderness Search and Rescue. *Computational & Mathematical Organization Theory* **16**, 300–323 (2010).
8. Example of a Gamma distribution — astroML 0.4 documentation.  
[https://www.astroml.org/book\\_figures/chapter3/fig\\_gamma\\_distribution.html](https://www.astroml.org/book_figures/chapter3/fig_gamma_distribution.html).

# Appendix 1

**Table A1.** Missing Data structure

Group	fosq1	fosq2	fosq3	adh2	adh3	ttt	gender	race_f	ahi	bmi	chd	chf	age	dep	hypothy	Freq	Percent
1	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	117	67.24
2	X	X	X	X	X	X	X	X	X	X	X	X	X	X	.	1	0.57
3	X	X	X	X	X	X	X	X	X	X	X	X	X	.	X	4	2.30
4	X	X	X	X	X	X	X	X	X	X	.	X	X	X	X	1	0.57
5	X	X	X	X	X	X	X	X	X	X	.	X	X	.	X	1	0.57
6	X	X	X	X	X	X	X	X	X	.	X	X	X	X	X	1	0.57
7	X	X	X	X	.	X	X	X	X	X	X	X	X	X	X	4	2.30
8	X	X	X	X	.	X	X	X	X	.	X	X	X	X	X	1	0.57
9	X	X	X	.	X	X	X	X	X	X	X	X	X	X	X	6	3.45
10	X	X	.	X	.	X	X	X	X	X	X	X	X	X	X	1	0.57
11	X	X	.	X	.	X	X	X	X	.	X	X	X	X	X	13	7.47
12	X	X	.	X	.	X	X	X	X	.	X	X	X	.	X	1	0.57
13	X	X	.	.	.	X	X	X	X	.	X	X	X	X	X	4	2.30
14	X	.	X	X	X	X	X	X	X	X	X	X	X	X	X	1	0.57
15	X	.	X	.	X	X	X	X	X	X	X	X	X	X	X	2	1.15
16	X	.	X	.	X	X	X	X	X	.	X	X	X	X	X	1	0.57
17	X	.	X	.	.	X	X	X	X	X	X	X	X	X	X	2	1.15

An "X" means that the variable is observed and a "." means that the variable is missing

**Table A2.** Comparison of the unstructured (UN) and variance components (VC) variance structures fit to our elaborated linear mixed effects model over 5 different imputed datasets; LL = -2 log likelihood for each imputation

Covariance Model	# of Paramaters	LL1	LL 2	LL3	LL4	LL5	Average LL	
UN	8	2302.8	2300.6	2303.6	2290.7	2298.1	2299.16	
VC	3	2369.1	2358.7	2358.8	2363.8	2356.1	2361.3	
							difference LL	62.14
							df	5
							p-value	<0.001

*Code Used to compare covariance structures:*

```

title "Unstructured, random int, random month, all covariates";
proc mixed method=REML data=multimp;
  class _Imputation_ nsrrid race_f gender dep chf chd hypothy time;
  model fosq_global = adherence month month*adherence ttt bmi ahi age race_f gender dep chf chd
  hypothy/ solution;
  random int month / subject = nsrrid;
  repeated time / subject=nsrrid type = UN(1);
  by _Imputation_;
  ods output SolutionF = mixslope;
run;

```

```

title "VC, random slope& int";
proc mixed method=REML data=multimp;
  class _Imputation_ nsrrid race_f gender dep chf chd hypothy time;
  model fosq_global = adherence month month*adherence ttt bmi ahi age race_f gender dep chf chd
  hypothy/ solution;
  random int month / subject = nsrrid;
  repeated time / subject=nsrrid type = VC;
  by _Imputation_;
run;

```

The -2 loglikelihood fit statistics were averaged for each iteration.

**Code for the rest of the analysis attached.**

## Appendix 2: R code for project

```
1 Load data
2 Overview
3 Table 1
4 Missingness
5 mice
6 Linear mixed effects model lme
7 ICC
```

# Longitudinal project: model type selection

Anna M. May & Lindsay Petrenchik

2021-05-06

`/fontfamily{'Calibri'}`

## 0.1 Preliminaries

## 0.2 Functions

`paste(colnames(hiv), collapse = "+")`

```
#paste(colnames(hiv), collapse = "+ ")
anna.qq = function(v) {
  # qqnorm(fitted(v), pch = 1, frame = TRUE)
  # qqline(fitted(v), col = "steelblue", lwd = 2)
  car::qqPlot(fitted(v),
              main = v)
}
anna.standardized = function(v) {
  res = residuals(v)
  st.res = res/sd(res)
  plot(st.res ~ fitted(v), main = v)
}
```

```

library(ggplot2)

# ***** Base theme *****
base_theme <- theme(
  plot.margin = unit(rep(1, 3), "cm"),
  plot.title = element_text(size = 24,
                             face = "bold",
                             color = "#22292F",
                             margin = margin(b = 8)),
  plot.subtitle = element_text(size = 16,
                                lineheight = 1.1,
                                color = "#22292F",
                                margin = margin(b = 25)),
  plot.caption = element_text(size = 12,
                               margin = margin(t = 25),
                               color = "#3D4852"),
  axis.title.x = element_text(margin = margin(t = 15)),
  axis.title.y = element_text(margin = margin(r = 15)),
  axis.text = element_text(color = "#22292F")
)

set_base_theme <- function() {
  theme_set(theme_minimal(base_size = 18) +
            base_theme)
}

# ***** Set flat theme *****
flat_theme <- theme(
  panel.grid = element_line(color = "#cacfd2", linetype = "dashed"),
  axis.line = element_line(color = "#606F7B")
)

set_flat_theme <- function() {
  theme_set(theme_minimal(base_size = 18,
                          base_family = "Segoe UI") +
            base_theme +
            flat_theme)
}

set_flat_theme()

```

## 1 Load data

```

pap.base = read_csv(here::here("homepap", "datasets", "homepap-baseline-dataset-0.1.0.csv"))
pap.1mo = read_csv(here::here("homepap", "datasets", "homepap-month1-dataset-0.1.0.csv"))
pap.3mo = read_csv(here::here("homepap", "datasets", "homepap-month3-dataset-0.1.0.csv"))

dim(pap.base)

```

```
## [1] 373 104
```

```
dim(pap.1mo)
```

```
## [1] 373 31
```

```
dim(pap.3mo)
```

```
## [1] 373 33
```

Let's check out the variables in each dataset.

```
names(pap.base)
```

```
## [1] "nsrrid"      "clusterid"   "visit"       "treatmentarm"
## [5] "age"         "gender"      "race3"       "ethnicity"
## [9] "heightcm"   "weightkg"    "bmi"         "neckcm"
## [13] "waistcm"    "systolic"    "diastolic"   "cal_total"
## [17] "esstotal"   "fosq_genprd" "fosq_socout" "fosq_actlev"
## [21] "fosq_vigiln" "fosq_sexual" "fosq_global" "pf_norm"
## [25] "rp_norm"    "bp_norm"     "gh_norm"     "vt_norm"
## [29] "sf_norm"    "re_norm"     "mh_norm"     "agg_phys"
## [33] "agg_ment"   "sf36_pcs"    "sf36_mcs"    "dxasth"
## [37] "dxadhd"     "dxca"        "dxcatyp"     "dxchf"
## [41] "dxchd"     "dxdep"       "dxdiab"      "dxemph"
## [45] "dxgerd"     "dxhay"       "dxhich"      "dxhtn"
## [49] "dxhyperthy" "dxhypothy"   "dxkidney"    "dxliver"
## [53] "dxplhtn"   "dxseiz"      "dxstroke"    "slpprdp"
## [57] "slpeffp"    "tmstg1p"     "tmstg2p"     "tmstg34p"
## [61] "tmremp"    "avghr"       "pctsa90h"    "pctstg1_d"
## [65] "pctstg2_d" "pctstg34_d"  "pctrem_d"    "slpprd_d"
## [69] "slpeff_d"   "pctstg1_t"   "pctstg2_t"   "pctstg34_t"
## [73] "pctrem_t"   "slpprd_t"    "slpeff_t"    "avgsao2_d"
## [77] "avgsao2_t" "avghr_d"     "avghr_t"     "avgsao2"
## [81] "ahi_full"   "ahi_d"       "ahi_t"       "index_time"
## [85] "aphypi"     "avgsat"      "satlt90p"    "avgbpn"
## [89] "pressure"   "ablation"    "ahi"         "crossover"
## [93] "ttt"        "diagnostic"  "ahige15"     "eligible"
## [97] "titrated"   "acceptance"  "completedm1" "completedm3"
## [101] "completedm1m3" "diagtype"    "pctsa90p_d"  "pctsa90p_t"
```

```
names(pap.1mo)
```

```
## [1] "nsrrid"      "clusterid"   "visit"       "treatmentarm" "age"
## [6] "gender"      "race3"       "ethnicity"    "systolic"     "diastolic"
## [11] "cal_total"   "esstotal"    "fosq_genprd" "fosq_socout"  "fosq_actlev"
## [16] "fosq_vigiln" "fosq_sexual" "fosq_global" "pf_norm"      "rp_norm"
## [21] "bp_norm"     "gh_norm"     "vt_norm"     "sf_norm"      "re_norm"
## [26] "mh_norm"     "agg_phys"    "agg_ment"    "sf36_pcs"     "sf36_mcs"
## [31] "avgpapuse"
```

```
names(pap.3mo)
```

```
## [1] "nsrrid"      "clusterid"   "visit"       "treatmentarm" "age"
## [6] "gender"      "race3"       "ethnicity"    "weightkg"     "bmi"
## [11] "systolic"    "diastolic"   "cal_total"    "esstotal"     "fosq_genprd"
## [16] "fosq_socout" "fosq_actlev" "fosq_vigiln" "fosq_sexual"  "fosq_global"
## [21] "pf_norm"     "rp_norm"     "bp_norm"     "gh_norm"      "vt_norm"
## [26] "sf_norm"     "re_norm"     "mh_norm"     "agg_phys"     "agg_ment"
## [31] "sf36_pcs"    "sf36_mcs"    "avgpapuse"
```

## 1.0.1 Wide dataset

Merge datasets on nsrrid into a wide view. In the wide dataset, I don't include baseline adherence measures at all (because they don't exist).

```
# for each adherence that is NA that was taken as 0 adherence; this is a reasonable estimate since
# there is no report if the patient didn't use their machine
recurrent = c("esstotal", "bmi", "avgpapuse",
              "fosq_genprd", "fosq_socout", "fosq_genprd",
              "fosq_socout", "fosq_actlev", "fosq_vigiln", "fosq_sexual",
              "fosq_global",
              # "pf_norm", "rp_norm", "bp_norm", "gh_norm", "vt_norm",
              # "sf_norm", "re_norm", "mh_norm", "agg_phys", "agg_ment",
              "sf36_pcs", "sf36_mcs")
recur.base = paste0(recurrent, ".0")
recur.1 = paste0(recurrent, ".1")
recur.3 = paste0(recurrent, ".3")
#the diagnoses we want
diags = c("dxchf", "dxchd", "dxhypothy", "dxdep")
constants = c("nsrrid", "age", "gender", "race.f", "diags", "ttt", "cal_total",
              "desat", "pressure", "ahi")

### levels levels

outcome =c("esstotal",
           "fosq_genprd", "fosq_socout", "fosq_genprd",
           "fosq_socout", "fosq_actlev", "fosq_vigiln", "fosq_sexual",
           "fosq_global",
           # "pf_norm", "rp_norm", "bp_norm", "gh_norm", "vt_norm",
           # "sf_norm", "re_norm", "mh_norm", "agg_phys", "agg_ment",
           "sf36_pcs", "sf36_mcs")
level1 = c(recurrent[recurrent %nin% outcome])

level2 = c("treat.f", "age", "gender", "race.f", "ttt", "ahi",
           "dxchf", "dxchd", "dxdep", "dxhypothy",
           "desat", "pressure")
```

```

pap = pap.base %>%
  mutate(
    race.f = factor(race3),
    female.f = factor(gender, levels = 1:0, labels = c("male", "female")),
    treat.f = factor(treatmentarm, levels = 1:2, labels = c("lab", "home")),
    avgpapuse = 0,
    desat = case_when(!is.na(pctsa90h) ~ pctsa90h,
                      !is.na(pctsa90p_d) ~ pctsa90p_d,
                      TRUE ~ NA_real_)
  ) %>%
  rename_with(~paste0(".", ".0"), recurrent) %>%
  filter(acceptance == 1) %>%
  select(nsrrid, treat.f, ttt, age, gender, race.f,
         #systolic, diastolic, cal_total,
         diags, desat,
         pressure, ahi, recur.base) %>%
  left_join(
    pap.1mo %>%
      mutate(bmi = NA) %>%
      rename_with(~paste0(".", ".1"), recurrent) %>%
      select(nsrrid, recur.1), by="nsrrid") %>%
  left_join(
    pap.3mo %>%
      rename_with(~paste0(".", ".3"), recurrent) %>%
      select(nsrrid, recur.3), by="nsrrid") %>%
  rowwise(.) %>%
  mutate(
    total.f = #get rid of all peeps with missing adherence x 2 or missing fosq_global x 3
              length(which(is.na(c_across(contains("sc_fosq_global"))))),
    total.p =
              length(which(is.na(c_across(contains("avgpapuse"))))) %>%
  filter(total.f < 3 & total.p < 2) %>%
  mutate(across(contains("avgpap"), ~.x/60)) %>%
  select(nsrrid, treat.f, age, gender, race.f, ttt, starts_with("dx"), desat, pressure, ahi, en
ds_with(".0"), ends_with(".1"),
         everything()) %>%
  select(-total.f, -total.p)

write.csv(pap, file = "papwide.csv")
#SASxport::write.xport(pap, file = "papwide.xpt")

```

## 1.0.2 Long dataset

Now do the same thing with a long view. Here we have to make something up for the adherence measures. NA doesn't work well. I think maybe setting everyone to zero (0) may work ok. I thought I needed this but we're imputing on wide...so, don't need it.



```

pap.long = rbind(
  pap.base %>%
    mutate(
      race.f = factor(race3),
      female.f = factor(gender, levels =1:0, labels = c("male", "female")),
      treat.f = factor(treatmentarm, levels = 1:2, labels = c("lab", "home")),
      time = 0,
      avgpapuse = 0
    ) %>%
    filter(acceptance == 1) %>%
    select(nsrrid, treat.f, time, systolic, diastolic, avgpapuse, recurrent),
  pap.lmo %>%
    mutate(treat.f = factor(treatmentarm, levels = 1:2, labels = c("lab", "home")),
           female.f = factor(gender, levels =1:0, labels = c("male", "female")),
           bmi = NA,
           time = 1) %>%
    select(nsrrid, treat.f, time, systolic, diastolic, avgpapuse, recurrent),
  pap.3mo %>%
    mutate(treat.f = factor(treatmentarm, levels = 1:2, labels = c("lab", "home")),
           female.f = factor(gender, levels =1:0, labels = c("male", "female")),
           avgpapuse.3 = avgpapuse,
           time = 3) %>%
    select(nsrrid, treat.f,time, systolic, diastolic, avgpapuse, recurrent)) %>%
  mutate(
    across(
      contains("fosq"),
      ~((.x-min(.x, na.rm = TRUE))/(max(.x, na.rm = TRUE)-min(.x, na.rm = TRUE))),
      .names = "sc.{.col}"),
    across(contains("sc."),
           ~case_when(.x ==1 ~.x - 0.0001,
                      .x == 0 ~.x + 0.0001,
                      TRUE ~ .x))
  ) %>%
  group_by(nsrrid) %>%
  filter(sum(is.na(fosq_global)) != 3 & sum(is.na(avgpapuse)) !=2) %>% # get rid of everyone tha
t has all fosq or all adherence missing
  ungroup() %>%
  mutate(across(contains("avgpap"), ~.x/60))%>%
  left_join(pap %>% select(nsrrid, level2), by = "nsrrid" )

write.csv(pap.long, file = "paplong.csv")
#SASxport::write.xport(pap.long, file ="paplong.xpt")

```

## 2 Overview

The HomePAP study randomized 373 adult patients from 2008-2010 at 7 study sites to either receive diagnosis and therapy titration for sleep apnea at home or in the laboratory (the gold standard). The original study had 3 co-primary outcomes (1) CPAP (the main therapy for sleep apnea) acceptance, (2) therapy adherence and (3) time time to treatment initiation. The study manual of procedures is attached, and the most relevant page is 13 which lists all the instruments administered longitudinally (baseline, 1 month, and 3 moths). One exciting thing about this randomized controlled trial is that it was coordinated by Cleveland sleep docs.

We plan to evaluate whether *adherence to CPAP* is associated with *functional outcomes* over a 3-month time horizon. We plan to construct a mixed effects model incorporating CPAP adherence as a predictor and functional outcomes as the outcome. The primary analysis will focus on quality of life as measured by the FOSQ. Secondary analyses will evaluate sleepiness, SF-36 subscale scores, and blood pressure measurements. We will also conduct sensitivity analyses including home vs. lab grouping as used in the study as a predictor variable.

Multiple regressions and concern about familywise error rate Consider using the SAQLI for quality of life use general

health perception, social functioning, and vitality as outcome or as time-dependent covariate? Albert re: SAS or R

main predictor:avgpapuse (min) main outcomes: FOSQ global secondary outcomes: FOSQ subscales (activity level, general productivity, social outcome, vigilance, sexual activity), aggregate mental score, aggregate physical score SF-36, general health perception, vitality, social functioning, diastolic BP, systolic BP, ESS covariates: time to treatment (ttt), treatment arm (treatmentarm), age, gender, race (race3), ethnicity?, BMI, ahi, past history

### 3 Table 1

```
vars = c("bmi", "ttt", "age", "gender",
"race.f", "systolic", "diastolic", "cal_total", "ess.base", "dxchf",
"dxchd", "dxhyperthy", "dxdep", "desat", "pressure", "ahi",
"esstotal.base", "fosq_genprd.base", "fosq_socout.base", "fosq_actlev.base",
"fosq_vigiln.base", "fosq_sexual.base", "fosq_global.base", "pf_norm.base",
"rp_norm.base", "bp_norm.base", "gh_norm.base", "vt_norm.base",
"sf_norm.base", "re_norm.base", "mh_norm.base", "agg_phys.base",
"agg_ment.base", "sf36_pcs.base", "sf36_mcs.base")

factorVars = c("gender",
"race.f", "dxchf",
"dxchd", "dxhyperthy", "dxdep")

t1 = CreateTableOne(vars = vars,
                    factorVars = factorVars,
                    strata = c("treat.f"),
                    data = pap,
                    addOverall = TRUE)

t1.print = print(t1,
                 nonnormal = c("ttt", "desat", "pressure", "ahi",
                               "fosq_genprd.base", "fosq_socout.base",
                               "fosq_sexual.base", "fosq_global.base",
                               "pf_norm.base", "rp_norm.base", "bp_norm.base",
                               "vt_norm.base", "gh_norm.base",
                               "sf_norm.base", "re_norm.base", "mh_norm.base",
                               "agg_phys.base", "agg_ment.base", "sf36_mcs.base"
                               ),
                 noSpaces = T, test = TRUE, smd = TRUE)
```

```
##          Stratified by treat.f
##          Overall          lab
##          n                155          69
##          ttt (median [IQR]) 24.00 [15.00, 42.00] 28.00 [17.00, 51.00]
##          age (mean (SD))   48.94 (12.07)  49.72 (12.15)
##          gender = 1 (%)    99 (63.9)    47 (68.1)
##          race.f (%)
##            1                113 (72.9)    55 (79.7)
##            2                 29 (18.7)    10 (14.5)
##            3                 13 (8.4)     4 (5.8)
##          dxchf = 1 (%)     5 (3.2)     4 (5.8)
##          dxchd = 1 (%)    14 (9.2)     8 (11.9)
##          dxdep = 1 (%)    37 (24.8)    12 (17.9)
##          desat (median [IQR]) 15.65 [5.08, 40.88] 20.80 [5.80, 47.20]
##          pressure (median [IQR]) 10.00 [9.00, 12.00] 10.00 [9.00, 12.00]
##          ahi (median [IQR])  35.50 [23.30, 62.70] 44.00 [25.80, 66.80]
##          Stratified by treat.f
##          home          p      test      SMD
##          n                86
##          ttt (median [IQR]) 22.00 [14.00, 34.75] 0.088 nonnorm 0.253
##          age (mean (SD))   48.31 (12.04)  0.471          0.117
##          gender = 1 (%)    52 (60.5)    0.414          0.160
##          race.f (%)
##            1                58 (67.4)
##            2                 19 (22.1)
##            3                 9 (10.5)
##          dxchf = 1 (%)     1 (1.2)     0.244          0.255
##          dxchd = 1 (%)     6 (7.0)     0.439          0.170
##          dxdep = 1 (%)    25 (30.5)    0.115          0.297
##          desat (median [IQR]) 5.30 [2.35, 13.15] 0.002 nonnorm 0.727
##          pressure (median [IQR]) 10.00 [9.00, 12.00] 0.978 nonnorm 0.004
##          ahi (median [IQR])  33.70 [21.38, 58.30] 0.058 nonnorm 0.354
```

```
t2 = CreateTableOne(vars = vars,
                    factorVars = factorVars,
                    strata = c("treat.f"),
                    data = pap,
                    addOverall = TRUE,
                    includeNA = TRUE)
t2.print = print(t2, nonnormal = c("ttt", "desat", "pressure", "ahi",
                                   "fosq_genprd.base", "fosq_socout.base",
                                   "fosq_sexual.base", "fosq_global.base",
                                   "pf_norm.base", "rp_norm.base", "bp_norm.base",
                                   "vt_norm.base", "gh_norm.base",
                                   "sf_norm.base", "re_norm.base", "mh_norm.base",
                                   "agg_phys.base", "agg_ment.base", "sf36_mcs.base"),
                  noSpaces = T, test = TRUE, smd = TRUE)
```

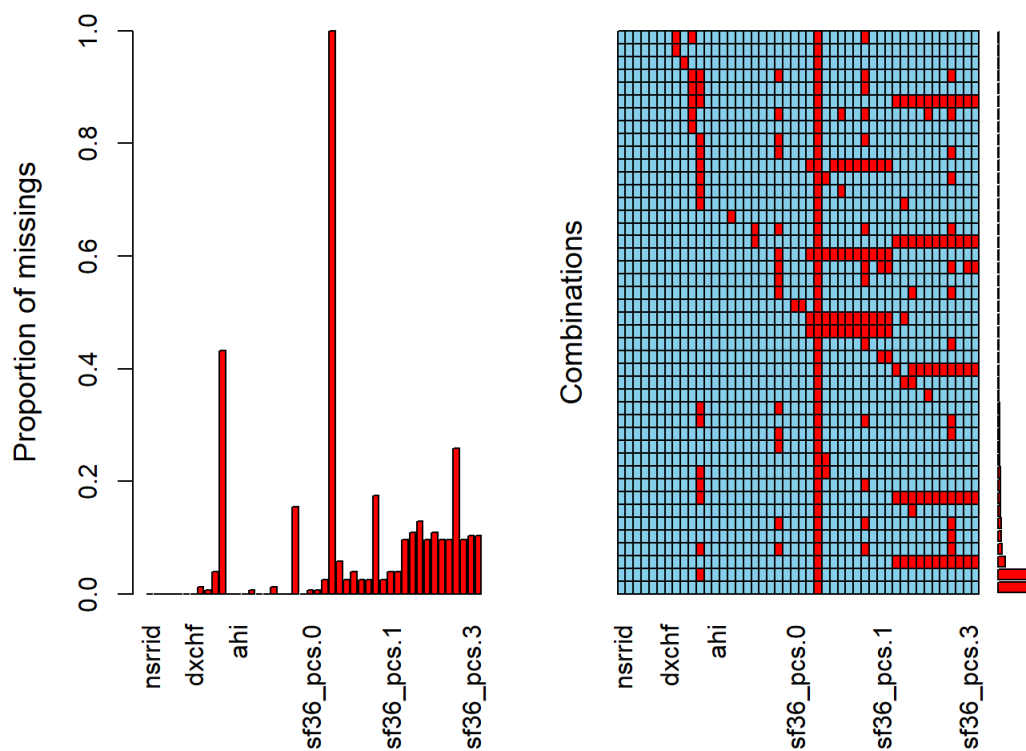
```
##                               Stratified by treat.f
##                               Overall          lab
##   n                          155            69
##   ttt (median [IQR])         24.00 [15.00, 42.00] 28.00 [17.00, 51.00]
##   age (mean (SD))            48.94 (12.07)      49.72 (12.15)
##   gender = 1 (%)             99 (63.9)         47 (68.1)
##   race.f (%)
##     1                        113 (72.9)        55 (79.7)
##     2                        29 (18.7)        10 (14.5)
##     3                        13 (8.4)         4 (5.8)
##   dxchf = 1 (%)              5 (3.2)         4 (5.8)
##   dxchd (%)
##     0                        139 (89.7)       59 (85.5)
##     1                        14 (9.0)         8 (11.6)
##     NA                        2 (1.3)         2 (2.9)
##   dxdep (%)
##     0                        112 (72.3)       55 (79.7)
##     1                        37 (23.9)       12 (17.4)
##     NA                        6 (3.9)         2 (2.9)
##   desat (median [IQR])       15.65 [5.08, 40.88] 20.80 [5.80, 47.20]
##   pressure (median [IQR])    10.00 [9.00, 12.00] 10.00 [9.00, 12.00]
##   ahi (median [IQR])         35.50 [23.30, 62.70] 44.00 [25.80, 66.80]
##                               Stratified by treat.f
##                               home           p      test      SMD
##   n                          86
##   ttt (median [IQR])         22.00 [14.00, 34.75] 0.088 nonnorm 0.253
##   age (mean (SD))            48.31 (12.04)      0.471          0.117
##   gender = 1 (%)             52 (60.5)         0.414          0.160
##   race.f (%)                 0.227            0.284
##     1                        58 (67.4)
##     2                        19 (22.1)
##     3                        9 (10.5)
##   dxchf = 1 (%)              1 (1.2)           0.244          0.255
##   dxchd (%)                 0.162            0.299
##     0                        80 (93.0)
##     1                        6 (7.0)
##     NA                        0 (0.0)
##   dxdep (%)                 0.178            0.306
##     0                        57 (66.3)
##     1                        25 (29.1)
##     NA                        4 (4.7)
##   desat (median [IQR])       5.30 [2.35, 13.15] 0.002 nonnorm 0.727
##   pressure (median [IQR])    10.00 [9.00, 12.00] 0.978 nonnorm 0.004
##   ahi (median [IQR])         33.70 [21.38, 58.30] 0.058 nonnorm 0.354
```

```
write.csv(t1.print, "WholeTable1.csv")
write.csv(naniar::miss_var_summary(pap, order = FALSE), "missingness.csv")

naniar::miss_var_summary(pap, order = TRUE)
```

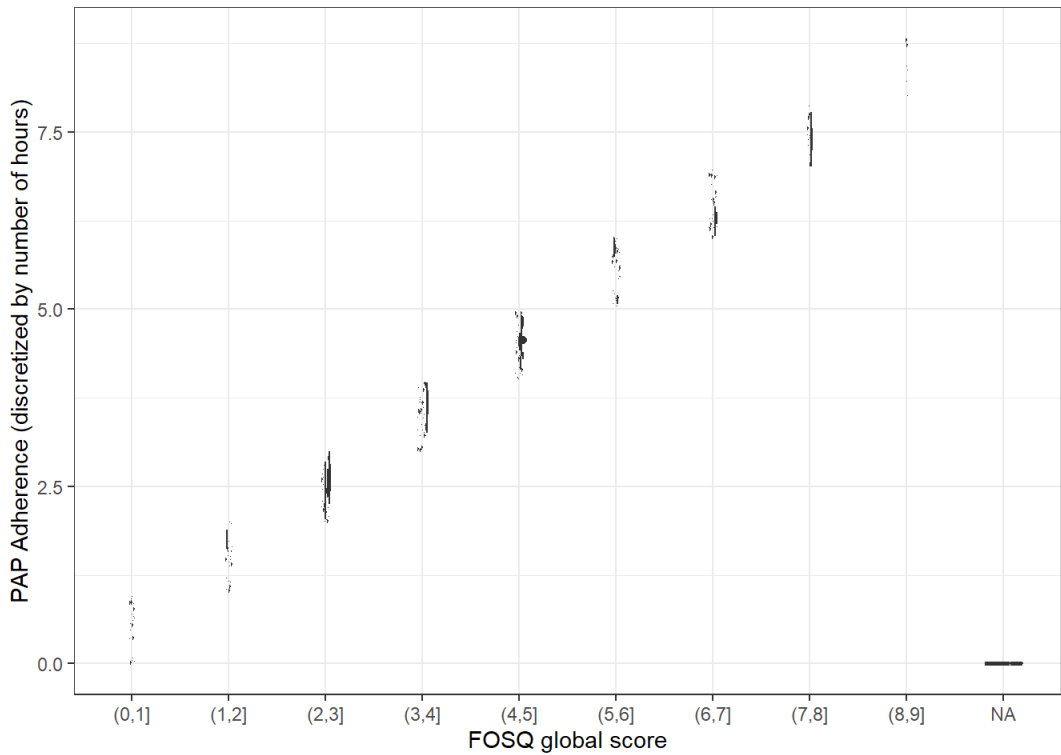
```
## # A tibble: 46 x 3
##   variable      n_miss pct_miss
##   <chr>         <int> <dbl>
## 1 bmi.1           155    100
## 2 desat            67    43.2
## 3 fosq_sexual.3   40    25.8
## 4 fosq_sexual.1   27    17.4
## 5 fosq_sexual.0   24    15.5
## 6 avgpapuse.3    20    12.9
## 7 bmi.3           17    11.0
## 8 fosq_socout.3  17    11.0
## 9 sf36_pcs.3     16    10.3
## 10 sf36_mcs.3     16    10.3
## # ... with 36 more rows
```

```
VIM::aggr(pap)
```



```
#Exploratory analyses adherence distribution
```

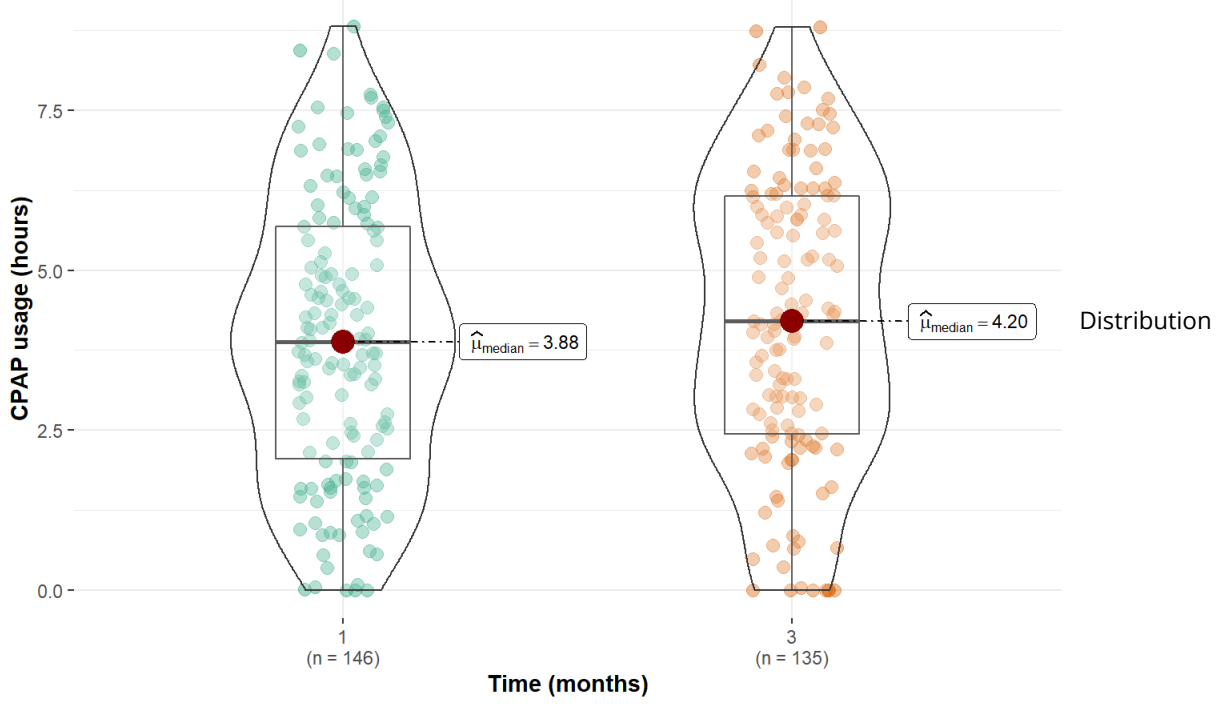
```
ggplot(mutate(pap.long,
  quints = cut(avgpapuse, breaks = seq(0,10, 1))),
  aes(x = factor(quints),
      y = avgpapuse,
      fill = factor(fosq_global))) +
  geom_boxplot(varwidth = TRUE) +
  theme_bw() +
  guides(fill = FALSE) +
  labs(x = "FOSQ global score",
      y = "PAP Adherence (discretized by number of hours)") +
  scale_fill_brewer(palette = "Spectral", direction =1)
```



Distribution of adherence over two time periods

```
ggstatsplot::ggbetweenstats(
  data = I(pap.long %>% filter(time != 0)),
  x = time,
  y = avgpapuse,
  ylab = "CPAP usage (hours)",
  xlab = "Time (months)",
  type = "np")
```

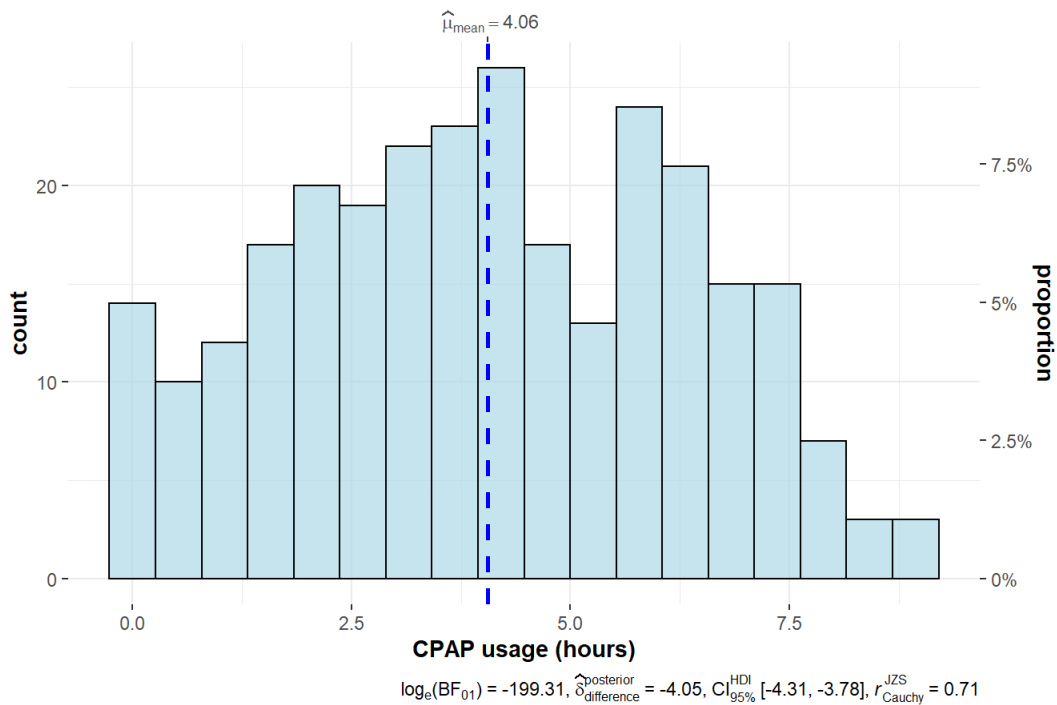
$\log_e(W_{\text{Mann-Whitney}}) = 9.12, p = 0.272, \hat{r}_{\text{biserial}}^{\text{rank}} = -0.08, \text{CI}_{95\%} [-0.19, 0.06], n_{\text{obs}} = 281$



adherence histogram

```
ggstatsplot::gghistostats(
  data = pap.long %>% filter(time !=0),
  x = avgpapuse,
  xlab = "CPAP usage (hours)",
  bar.fill = "lightblue")
```

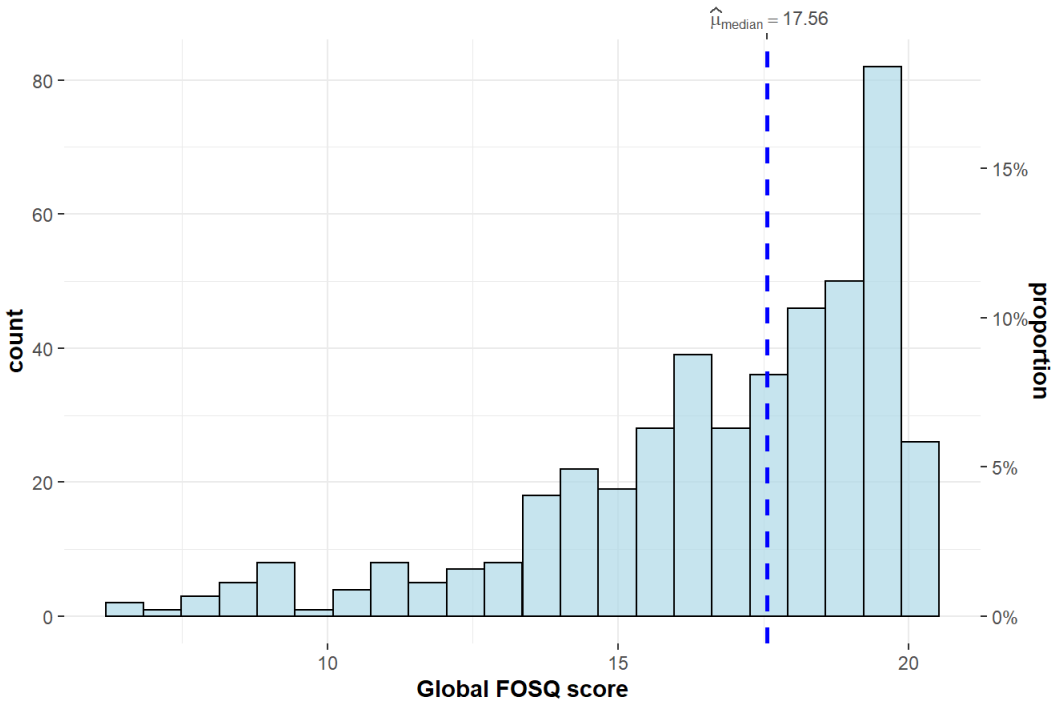
$t_{Student}(280) = 30.27, p = 2.78e-90, \hat{g}_{Hedges} = 1.80, CI_{95\%} [1.61, 1.99], n_{obs} = 281$



distribution of fosq\_global

```
ggstatsplot::gghistostats(
  data = pap.long,
  x = fosq_global,
  type = "np",
  xlab = "Global FOSQ score",
  bar.fill = "lightblue")
```

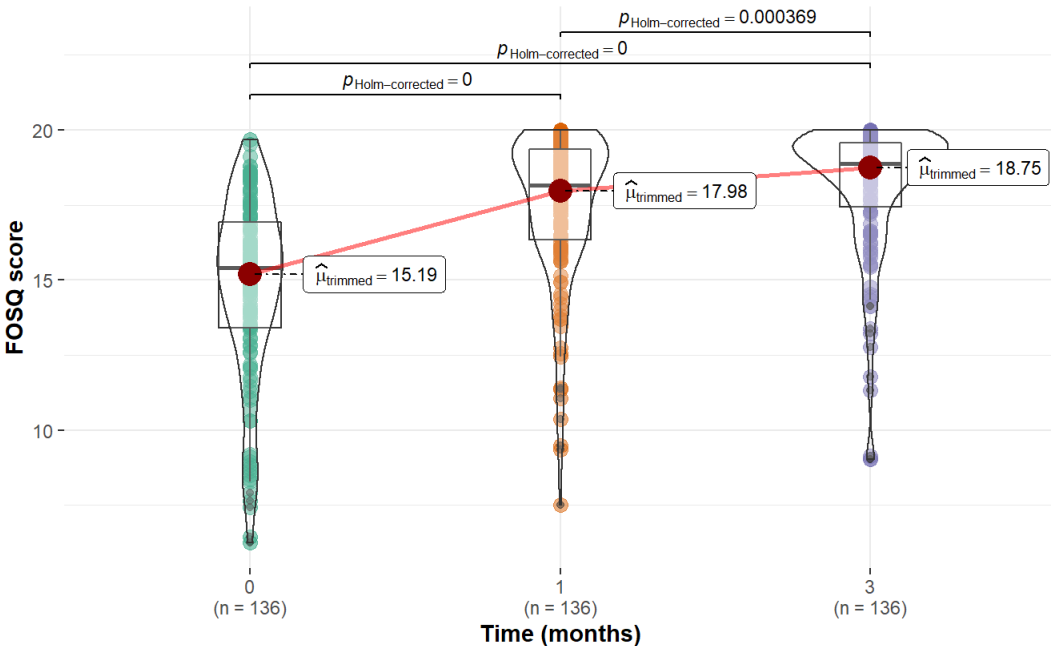
$\log_e(V_{Wilcoxon}) = 11.51, p = 8.34e-75, \hat{r}_{biserial}^{rank} = 1.00, CI_{95\%} [1.00, 1.00], n_{obs} = 446$



What about difference between times

```
ggstatsplot::ggwithinstats(
  data = pap.long,
  x = time,
  y = fosq_global,
  type = "r",
  ylab = "FOSQ score",
  xlab = "Time (months)")
```

$F_{trimmed-means}(1.59, 128.74) = 141.50, p = 0e+00, \hat{\rho}_{R-avg}^{AKP} = 0.10, CI_{95\%} [-0.11, 0.34], n_{pairs} = 136$

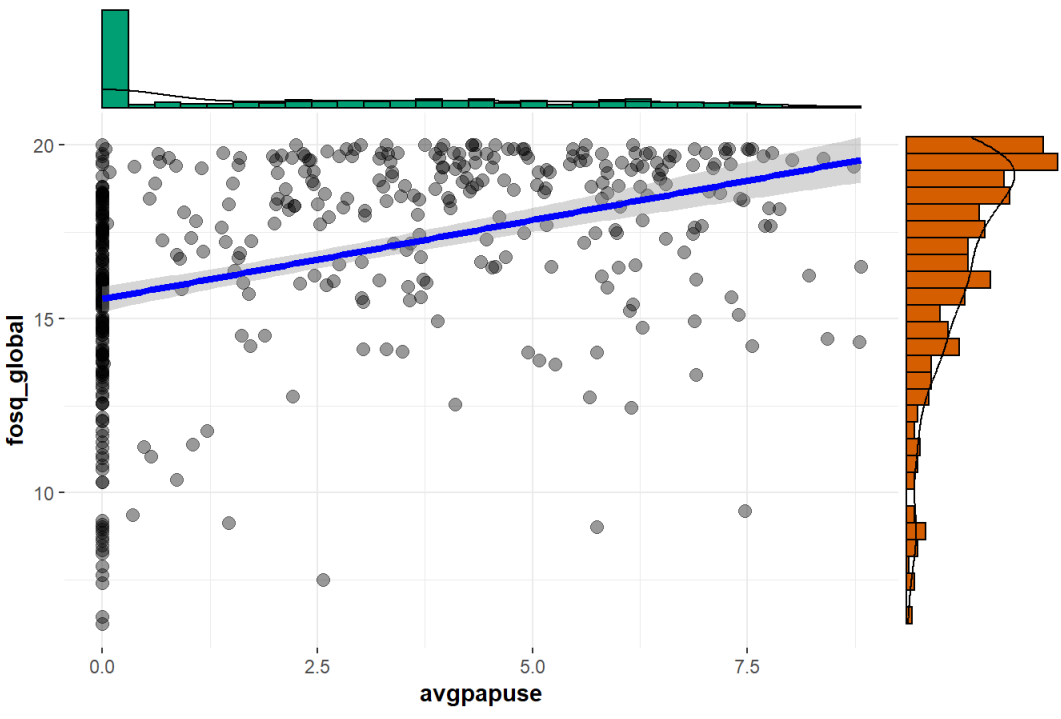


Pairwise test: Yuen's trimmed means test; Comparisons shown: only significant



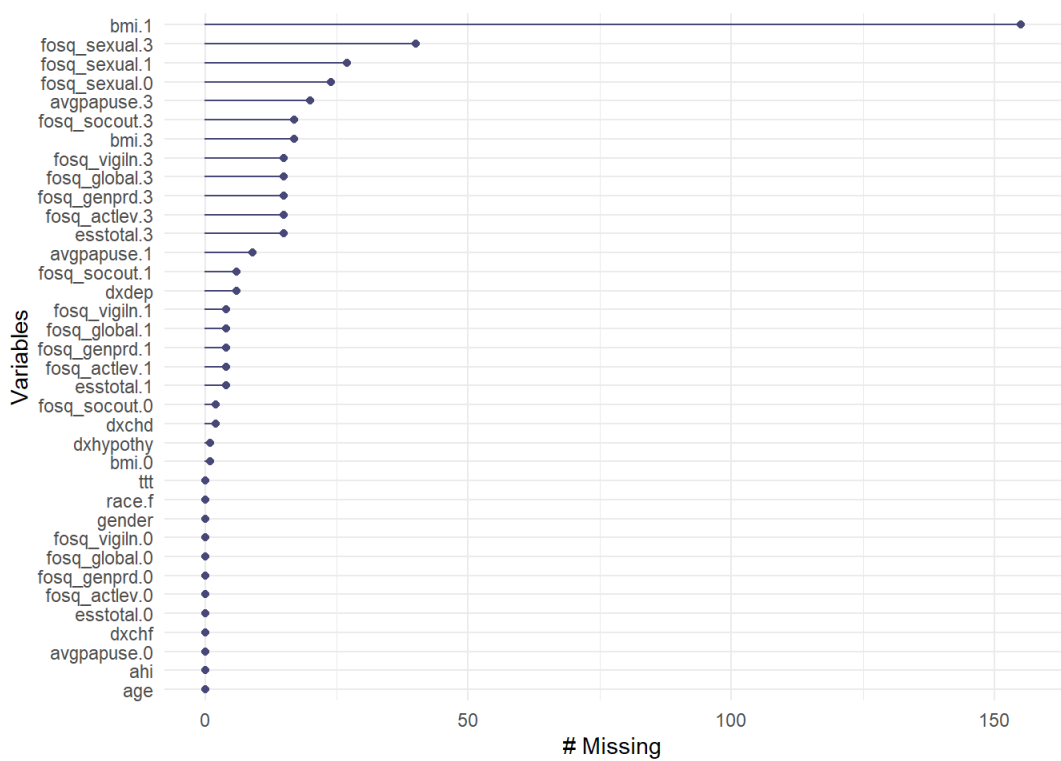
```
ggstatsplot::ggscatterstats(
  data = pap.long,
  x = avgpapuse,
  y = fosq_global,
  type = "np"
)
```

$\log_e(S) = 15.78$ ,  $p = 9.51e-27$ ,  $\hat{\rho}_{\text{Spearman}} = 0.48$ ,  $CI_{95\%} [0.40, 0.55]$ ,  $n_{\text{pairs}} = 435$

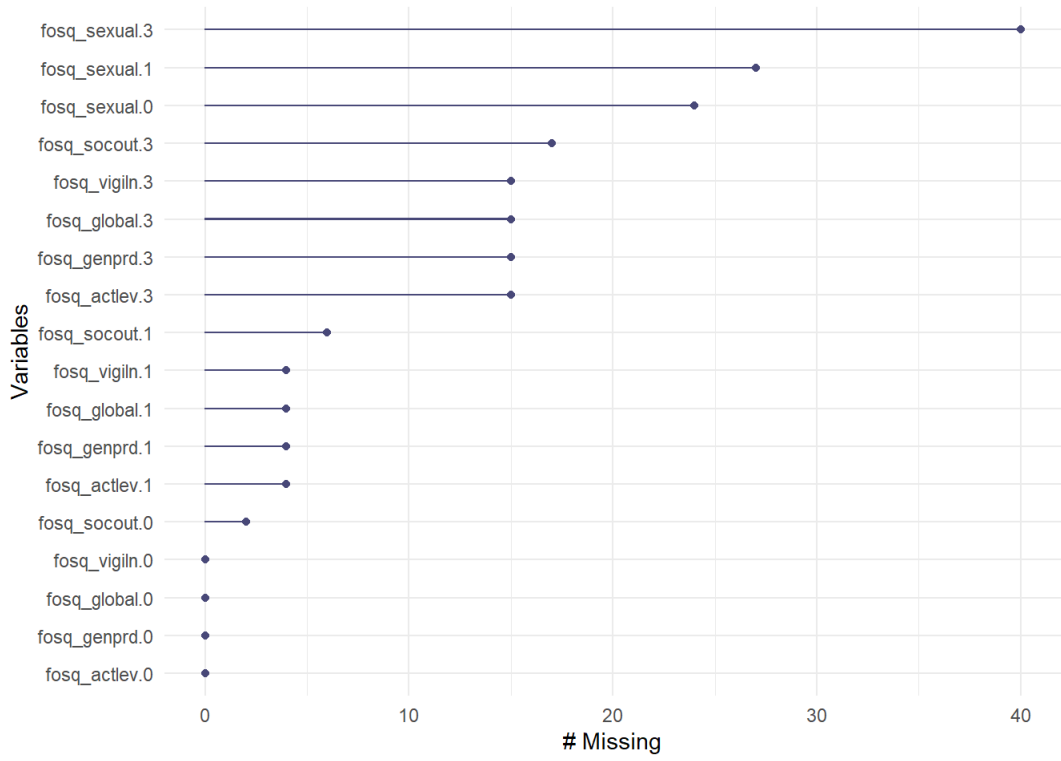


## 4 Missingness

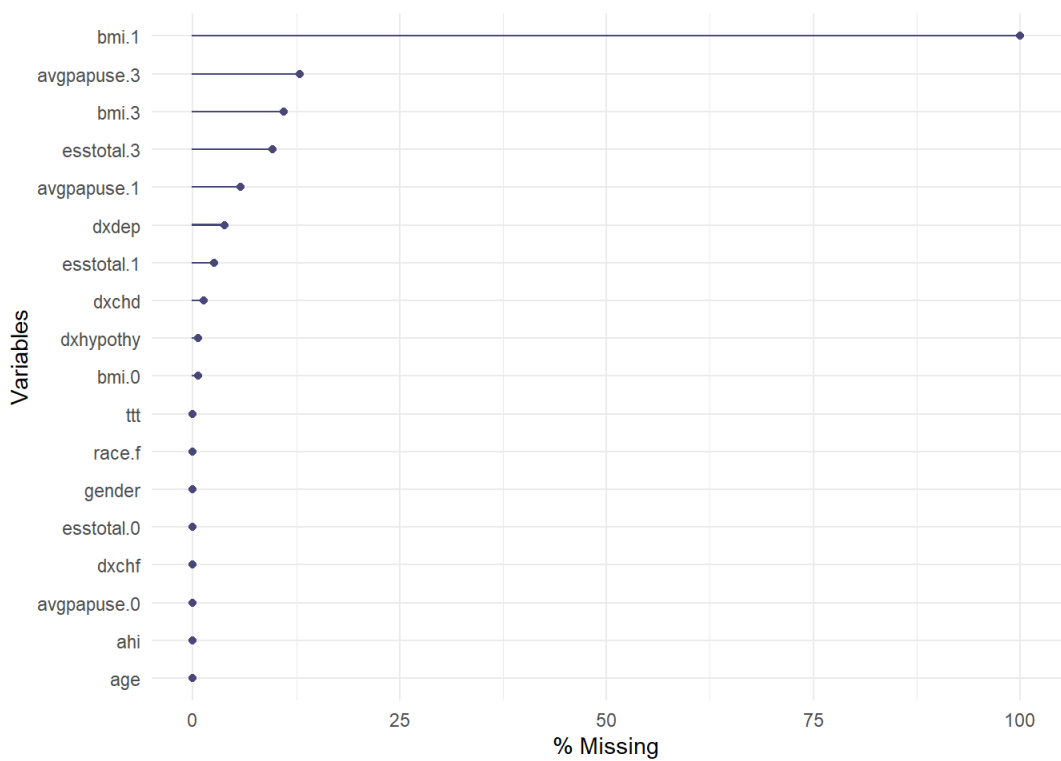
```
#Missingness of original wide dataset
naniar::gg_miss_var(pap %>% select(contains("fosq"), contains("avgpapuse"), contains("dx"), ahi,
  contains("bmi"), age, gender, race.f, ttt, ahi, contains("esstotal")))
```



```
naniar::gg_miss_var(pap %>% select(contains("fosq")))
```



```
naniar::gg_miss_var(pap %>% select(contains("avgpapuse"), contains("dx"), ahi, contains("bmi"), age, gender, race.f, ttt, ahi, contains("esstotal")), show_pct = TRUE)
```



```
#determine if MCAR. I ran it once nad that was more than enough for me.
# b = BaylorEdPsych::LittleMCAR(pap.long)
# #Chi-square
# b[1:3]
# round(b$amount.missing,2)
```

Definitely not MCAR.

But is it MAR? Or maybe some of it is MCAR?

```
RBtest::RBtest(pap.long)$type
```

```
##          nsrrid      treat.f.x          time      systolic      diastolic
##           -1          -1          -1          0          0
##      avgpapuse      esstotal          bmi      fosq_genprd      fosq_socout
##           1          1          0          1          0
##      fosq_actlev      fosq_vigiln      fosq_sexual      fosq_global      sf36_pcs
##           1          1          0          1          1
##      sf36_mcs      sc.fosq_genprd      sc.fosq_socout      sc.fosq_actlev      sc.fosq_vigiln
##           0          1          0          1          1
##      sc.fosq_sexual      sc.fosq_global      treat.f.y          age          gender
##           0          1          -1          -1          -1
##           race.f          ttt          ahi          dxchf          dxchd
##           -1          -1          -1          -1          0
##           dxdep      dxhypothy          desat      pressure
##           0          0          1          -1
```

Zero is MCAR variables, 1 is for MAR variables and -1 is for complete variables.

So, esstotal, average PAP use, FOSQ general productivity, FOSQ activity level, FOSQ global (= FOSQ vigilance, SF36 physical, desaturation) are all not MCAR. They may be MAR (hopefully) or NMAR (hopefully not).

5 mice

Multiply imputed chained equations for the win. The wide dataset doesn't have baseline adherence (since it wasn't a thing at baseline).

First I fit a dummy dataset to get the matrix on which we impute. I want to make sure that we don't use the outcomes in imputation (i.e. don't use the outcomes as a predictor for imputation purposes). I imputed outcomes using only outcomes earlier in time (and the same time) as possible predictors for the imputation.

```
impMeth = make.method(pap, defaultMethod = c("cart", "logreg", "polyreg", "polr"))
# impMeth[pap %>% select(contains(level1)) %>% names] = "pmm"
# impMeth[pap %>% select(contains(level2)) %>% names] = "pmm"
# impMeth[pap %>% select(contains(outcome)) %>% names] = "pmm"
impMeth[pap %>% select(age, race.f, ttt, pressure, ahi) %>% names] = "pmm"

pred = make.predictorMatrix(pap)
predMatrix.old = as.tibble(pred)
pred[, "nsrrid"] = 1

#random slopes
pred[select(predMatrix.old, contains("fosq")) %>% names(),
      select(predMatrix.old, contains("avgpapuse")) %>% names()] = 4
pred[select(predMatrix.old, contains("sf36")) %>% names(),
      select(pap, contains("avgpapuse")) %>% names()] = 4
pred[select(pap, contains("avgpapuse")) %>% names(),
      select(pap, contains("fosq")) %>% names()] = 4
pred[select(pap, contains("avgpapuse")) %>% names(),
      select(pap, contains("sf36")) %>% names()] = 4

baseline = predMatrix.old %>% select(contains(".0")) %>% names()
mo1 = predMatrix.old %>% select(contains(".1")) %>% names()
mo3 = predMatrix.old %>% select(contains(".3")) %>% names()
# predMatrix.old = matrix(1, nrow = 31, ncol = 31, dimnames = list(names(pap)))
# colnames(predMatrix.old) = names(pap)
diag(pred) <- 0

pred[1,] <- 0 # don't impute nsrrid
pred[which(colnames(pap)=="bmi.1"),] <- "~I((bmi.0 + bmi.3)/2)"

#timing
pred[2:19,20:31] <- 0 # don't impute predictors based on outcomes or things that happened later
pred[which(colnames(pred) %in% baseline),c(mo1, mo3)] <- 0 #for all baseline don't use month 1 &
  3 to impute
pred[which(colnames(pred) %in% mo1),mo3] <- 0 #for all month 1 don't use month 3 to impute
# don't use baseline adherence for anything; it's already 0
```

```
#imputin'
iter = 10
imp = mice(data = pap,
           m = iter,
           method = impMeth,
           predictorMatrix = pred,
           seed = 2021,
           print = FALSE
          )
```

## 5.0.1 wide

Complete in wide format.

```

mylist = as.list(1:iter)
complete.wide = map(mylist, function(x) {
  complete(imp, action = x) %>%
    as.tibble() %>%
    mutate(
      across(
        contains(recurrent),
        ~((.x-min(.x, na.rm = TRUE))/(max(.x, na.rm = TRUE)-min(.x, na.rm = TRUE))),
        .names = "sc_{.col}"),
      across(contains("sc_"),
        ~case_when(.x ==1 ~.x - 0.001,
                   .x == 0 ~.x + 0.001,
                   TRUE ~ .x)),
      bmi.1 = (bmi.0 + bmi.3)/2,
      sc_avgpapuse.0 = NULL,
      sc_bmi.1 = (bmi.1 - min(bmi.1))/(max(bmi.1) - min(bmi.1))
    )%>%
  select(nsrrid, treat.f, age, gender, race.f, ttt, starts_with("dx"), desat, pressure, ahi, en
ds_with(".0"), ends_with(".1"),
        everything())
}
)

map(complete.wide,md.pattern)

```

```

## /\      /\
## { `---' }
## { O   O }
## ==> V <== No need for mice. This data set is completely observed.
## \  \|\ / /
## `-----'

```

```

## /\      /\
## { `---' }
## { O   O }
## ==> V <== No need for mice. This data set is completely observed.
## \  \|\ / /
## `-----'

```

#####  
#####

```
## /\      /\  
## { '----' }  
## { O O }  
## ==> V <== No need for mice. This data set is completely observed.  
## \  \|\ / /  
##  '-----'
```

```
## /\      /\  
## { '----' }  
## { O O }  
## ==> V <== No need for mice. This data set is completely observed.  
## \  \|\ / /  
##  '-----'
```

```
## /\      /\  
## { '----' }  
## { O O }  
## ==> V <== No need for mice. This data set is completely observed.  
## \  \|\ / /  
##  '-----'
```

```
## /\      /\  
## { '----' }  
## { O O }  
## ==> V <== No need for mice. This data set is completely observed.  
## \  \|\ / /  
##  '-----'
```

```
## /\      /\
## { '----' }
## { 0 0 }
## ==> V <== No need for mice. This data set is completely observed.
## \  \|\ / /
## '-----'
```

```
## /\      /\
## { '----' }
## { 0 0 }
## ==> V <== No need for mice. This data set is completely observed.
## \  \|\ / /
## '-----'
```

```
## /\      /\
## { '----' }
## { 0 0 }
## ==> V <== No need for mice. This data set is completely observed.
## \  \|\ / /
## '-----'
```

```
## /\      /\
## { '----' }
## { 0 0 }
## ==> V <== No need for mice. This data set is completely observed.
## \  \|\ / /
## '-----'
```

```

## [[1]]
##      nsrrid treat.f age gender race.f ttt dxchf dxchd dxhypothy dxdep desat
## 155      1      1  1  1      1      1  1      1      1      1      1      1
##      0      0  0  0      0      0  0      0      0      0      0      0
##      pressure ahi esstotal.0 bmi.0 avgpapuse.0 fosq_genprd.0 fosq_socout.0
## 155      1  1      1  1      1      1      1      1      1      1
##      0  0      0  0      0      0      0      0      0      0
##      fosq_actlev.0 fosq_vigiln.0 fosq_sexual.0 fosq_global.0 sf36_pcs.0
## 155      1      1      1      1      1      1
##      0      0      0      0      0      0
##      sf36_mcs.0 sc_esstotal.0 sc_bmi.0 sc_fosq_genprd.0 sc_fosq_socout.0
## 155      1      1      1      1      1      1
##      0      0      0      0      0      0
##      sc_fosq_actlev.0 sc_fosq_vigiln.0 sc_fosq_sexual.0 sc_fosq_global.0
## 155      1      1      1      1      1
##      0      0      0      0      0
##      sc_sf36_pcs.0 sc_sf36_mcs.0 esstotal.1 bmi.1 avgpapuse.1 fosq_genprd.1
## 155      1      1      1  1      1      1      1
##      0      0      0  0      0      0      0
##      fosq_socout.1 fosq_actlev.1 fosq_vigiln.1 fosq_sexual.1 fosq_global.1
## 155      1      1      1      1      1      1
##      0      0      0      0      0      0
##      sf36_pcs.1 sf36_mcs.1 sc_esstotal.1 sc_bmi.1 sc_avgpapuse.1
## 155      1      1      1      1      1
##      0      0      0      0      0
##      sc_fosq_genprd.1 sc_fosq_socout.1 sc_fosq_actlev.1 sc_fosq_vigiln.1
## 155      1      1      1      1      1
##      0      0      0      0      0
##      sc_fosq_sexual.1 sc_fosq_global.1 sc_sf36_pcs.1 sc_sf36_mcs.1 esstotal.3
## 155      1      1      1      1      1      1
##      0      0      0      0      0      0
##      bmi.3 avgpapuse.3 fosq_genprd.3 fosq_socout.3 fosq_actlev.3 fosq_vigiln.3
## 155      1      1      1      1      1      1
##      0      0      0      0      0      0
##      fosq_sexual.3 fosq_global.3 sf36_pcs.3 sf36_mcs.3 sc_esstotal.3 sc_bmi.3
## 155      1      1      1      1      1      1
##      0      0      0      0      0      0
##      sc_avgpapuse.3 sc_fosq_genprd.3 sc_fosq_socout.3 sc_fosq_actlev.3
## 155      1      1      1      1
##      0      0      0      0
##      sc_fosq_vigiln.3 sc_fosq_sexual.3 sc_fosq_global.3 sc_sf36_pcs.3
## 155      1      1      1      1
##      0      0      0      0
##      sc_sf36_mcs.3
## 155      1 0
##      0 0
##
## [[2]]
##      nsrrid treat.f age gender race.f ttt dxchf dxchd dxhypothy dxdep desat
## 155      1      1  1  1      1  1  1      1      1      1      1      1
##      0      0  0  0      0      0  0      0      0      0      0      0
##      pressure ahi esstotal.0 bmi.0 avgpapuse.0 fosq_genprd.0 fosq_socout.0
## 155      1  1      1  1      1      1      1      1      1
##      0  0      0  0      0      0      0      0      0
##      fosq_actlev.0 fosq_vigiln.0 fosq_sexual.0 fosq_global.0 sf36_pcs.0
## 155      1      1      1      1      1
##      0      0      0      0      0
##      sf36_mcs.0 sc_esstotal.0 sc_bmi.0 sc_fosq_genprd.0 sc_fosq_socout.0
## 155      1      1      1      1      1
##      0      0      0      0      0

```



```

##      sc_fosq_actlev.0 sc_fosq_vigiln.0 sc_fosq_sexual.0 sc_fosq_global.0
## 155          1          1          1          1
##          0          0          0          0
##      sc_sf36_pcs.0 sc_sf36_mcs.0 esstotal.1 bmi.1 avgpapuse.1 fosq_genprd.1
## 155          1          1          1          1          1          1
##          0          0          0          0          0          0
##      fosq_socout.1 fosq_actlev.1 fosq_vigiln.1 fosq_sexual.1 fosq_global.1
## 155          1          1          1          1          1          1
##          0          0          0          0          0          0
##      sf36_pcs.1 sf36_mcs.1 sc_esstotal.1 sc_bmi.1 sc_avgpapuse.1
## 155          1          1          1          1          1          1
##          0          0          0          0          0          0
##      sc_fosq_genprd.1 sc_fosq_socout.1 sc_fosq_actlev.1 sc_fosq_vigiln.1
## 155          1          1          1          1          1          1
##          0          0          0          0          0          0
##      sc_fosq_sexual.1 sc_fosq_global.1 sc_sf36_pcs.1 sc_sf36_mcs.1 esstotal.3
## 155          1          1          1          1          1          1
##          0          0          0          0          0          0
##      bmi.3 avgpapuse.3 fosq_genprd.3 fosq_socout.3 fosq_actlev.3 fosq_vigiln.3
## 155          1          1          1          1          1          1
##          0          0          0          0          0          0
##      fosq_sexual.3 fosq_global.3 sf36_pcs.3 sf36_mcs.3 sc_esstotal.3 sc_bmi.3
## 155          1          1          1          1          1          1
##          0          0          0          0          0          0
##      sc_avgpapuse.3 sc_fosq_genprd.3 sc_fosq_socout.3 sc_fosq_actlev.3
## 155          1          1          1          1          1          1
##          0          0          0          0          0          0
##      sc_fosq_vigiln.3 sc_fosq_sexual.3 sc_fosq_global.3 sc_sf36_pcs.3
## 155          1          1          1          1          1          1
##          0          0          0          0          0          0
##      sc_sf36_mcs.3
## 155          1 0
##          0 0
##
## [[3]]
##      nsrrid treat.f age gender race.f ttt dxchf dxchd dxhypothy dxdep desat
## 155          1          1 1          1          1 1          1          1          1          1          1
##          0          0 0          0          0 0          0          0          0          0          0
##      pressure ahi esstotal.0 bmi.0 avgpapuse.0 fosq_genprd.0 fosq_socout.0
## 155          1 1          1          1          1          1          1          1
##          0 0          0          0          0          0          0          0
##      fosq_actlev.0 fosq_vigiln.0 fosq_sexual.0 fosq_global.0 sf36_pcs.0
## 155          1          1          1          1          1          1          1
##          0          0          0          0          0          0          0
##      sf36_mcs.0 sc_esstotal.0 sc_bmi.0 sc_fosq_genprd.0 sc_fosq_socout.0
## 155          1          1          1          1          1          1          1
##          0          0          0          0          0          0          0
##      sc_fosq_actlev.0 sc_fosq_vigiln.0 sc_fosq_sexual.0 sc_fosq_global.0
## 155          1          1          1          1          1          1          1
##          0          0          0          0          0          0          0
##      sc_sf36_pcs.0 sc_sf36_mcs.0 esstotal.1 bmi.1 avgpapuse.1 fosq_genprd.1
## 155          1          1          1          1          1          1          1
##          0          0          0          0          0          0          0
##      fosq_socout.1 fosq_actlev.1 fosq_vigiln.1 fosq_sexual.1 fosq_global.1
## 155          1          1          1          1          1          1          1
##          0          0          0          0          0          0          0
##      sf36_pcs.1 sf36_mcs.1 sc_esstotal.1 sc_bmi.1 sc_avgpapuse.1
## 155          1          1          1          1          1          1          1
##          0          0          0          0          0          0          0
##      sc_fosq_genprd.1 sc_fosq_socout.1 sc_fosq_actlev.1 sc_fosq_vigiln.1
## 155          1          1          1          1          1          1          1

```

```

##          0          0          0          0
##   sc_fosq_sexual.1 sc_fosq_global.1 sc_sf36_pcs.1 sc_sf36_mcs.1 esstotal.3
## 155      1          1          1          1          1          1
##          0          0          0          0          0          0
##   bmi.3 avgpapuse.3 fosq_genprd.3 fosq_socout.3 fosq_actlev.3 fosq_vigiln.3
## 155      1          1          1          1          1          1
##          0          0          0          0          0          0
##   fosq_sexual.3 fosq_global.3 sf36_pcs.3 sf36_mcs.3 sc_esstotal.3 sc_bmi.3
## 155      1          1          1          1          1          1
##          0          0          0          0          0          0
##   sc_avgpapuse.3 sc_fosq_genprd.3 sc_fosq_socout.3 sc_fosq_actlev.3
## 155      1          1          1          1          1          1
##          0          0          0          0          0          0
##   sc_fosq_vigiln.3 sc_fosq_sexual.3 sc_fosq_global.3 sc_sf36_pcs.3
## 155      1          1          1          1          1          1
##          0          0          0          0          0          0
##   sc_sf36_mcs.3
## 155      1 0
##          0 0
##
## [[4]]
##   nsrrid treat.f age gender race.f ttt dxCHF dxChd dxHypothy dxDep desat
## 155      1      1 1      1      1 1      1      1      1      1      1
##          0      0 0      0      0 0      0      0      0      0      0
##   pressure ahi esstotal.0 bmi.0 avgpapuse.0 fosq_genprd.0 fosq_socout.0
## 155      1 1      1 1      1 1      1 1      1 1      1 1
##          0 0      0 0      0 0      0 0      0 0      0 0
##   fosq_actlev.0 fosq_vigiln.0 fosq_sexual.0 fosq_global.0 sf36_pcs.0
## 155      1      1      1      1      1      1      1      1
##          0      0      0      0      0      0      0      0
##   sf36_mcs.0 sc_esstotal.0 sc_bmi.0 sc_fosq_genprd.0 sc_fosq_socout.0
## 155      1      1      1      1      1      1      1      1
##          0      0      0      0      0      0      0      0
##   sc_fosq_actlev.0 sc_fosq_vigiln.0 sc_fosq_sexual.0 sc_fosq_global.0
## 155      1      1      1      1      1      1      1      1
##          0      0      0      0      0      0      0      0
##   sc_sf36_pcs.0 sc_sf36_mcs.0 esstotal.1 bmi.1 avgpapuse.1 fosq_genprd.1
## 155      1      1      1      1      1      1      1      1
##          0      0      0      0      0      0      0      0
##   fosq_socout.1 fosq_actlev.1 fosq_vigiln.1 fosq_sexual.1 fosq_global.1
## 155      1      1      1      1      1      1      1      1
##          0      0      0      0      0      0      0      0
##   sf36_pcs.1 sf36_mcs.1 sc_esstotal.1 sc_bmi.1 sc_avgpapuse.1
## 155      1      1      1      1      1      1      1      1
##          0      0      0      0      0      0      0      0
##   sc_fosq_genprd.1 sc_fosq_socout.1 sc_fosq_actlev.1 sc_fosq_vigiln.1
## 155      1      1      1      1      1      1      1      1
##          0      0      0      0      0      0      0      0
##   sc_fosq_sexual.1 sc_fosq_global.1 sc_sf36_pcs.1 sc_sf36_mcs.1 esstotal.3
## 155      1      1      1      1      1      1      1      1
##          0      0      0      0      0      0      0      0
##   bmi.3 avgpapuse.3 fosq_genprd.3 fosq_socout.3 fosq_actlev.3 fosq_vigiln.3
## 155      1      1      1      1      1      1      1      1
##          0      0      0      0      0      0      0      0
##   fosq_sexual.3 fosq_global.3 sf36_pcs.3 sf36_mcs.3 sc_esstotal.3 sc_bmi.3
## 155      1      1      1      1      1      1      1      1
##          0      0      0      0      0      0      0      0
##   sc_avgpapuse.3 sc_fosq_genprd.3 sc_fosq_socout.3 sc_fosq_actlev.3
## 155      1      1      1      1      1      1      1      1
##          0      0      0      0      0      0      0      0
##   sc_fosq_vigiln.3 sc_fosq_sexual.3 sc_fosq_global.3 sc_sf36_pcs.3

```

```

## 155          1          1          1          1
##           0          0          0          0
##      sc_sf36_mcs.3
## 155          1 0
##           0 0
##
## [[5]]
##      nsrrid treat.f age gender race.f ttt dxchf dxchd dxhypothy dxdep desat
## 155      1      1 1      1      1 1      1      1      1      1 1
##           0      0 0      0      0 0      0      0      0      0 0
##      pressure ahi esstotal.0 bmi.0 avgpapuse.0 fosq_genprd.0 fosq_socout.0
## 155      1 1      1      1      1      1      1      1
##           0 0      0      0      0      0      0      0
##      fosq_actlev.0 fosq_vigiln.0 fosq_sexual.0 fosq_global.0 sf36_pcs.0
## 155      1      1      1      1      1      1
##           0      0      0      0      0      0
##      sf36_mcs.0 sc_esstotal.0 sc_bmi.0 sc_fosq_genprd.0 sc_fosq_socout.0
## 155      1      1      1      1      1      1
##           0      0      0      0      0      0
##      sc_fosq_actlev.0 sc_fosq_vigiln.0 sc_fosq_sexual.0 sc_fosq_global.0
## 155      1      1      1      1      1      1
##           0      0      0      0      0      0
##      sc_sf36_pcs.0 sc_sf36_mcs.0 esstotal.1 bmi.1 avgpapuse.1 fosq_genprd.1
## 155      1      1      1      1      1      1
##           0      0      0      0      0      0
##      fosq_socout.1 fosq_actlev.1 fosq_vigiln.1 fosq_sexual.1 fosq_global.1
## 155      1      1      1      1      1      1
##           0      0      0      0      0      0
##      sf36_pcs.1 sf36_mcs.1 sc_esstotal.1 sc_bmi.1 sc_avgpapuse.1
## 155      1      1      1      1      1      1
##           0      0      0      0      0      0
##      sc_fosq_genprd.1 sc_fosq_socout.1 sc_fosq_actlev.1 sc_fosq_vigiln.1
## 155      1      1      1      1      1      1
##           0      0      0      0      0      0
##      sc_fosq_sexual.1 sc_fosq_global.1 sc_sf36_pcs.1 sc_sf36_mcs.1 esstotal.3
## 155      1      1      1      1      1      1
##           0      0      0      0      0      0
##      bmi.3 avgpapuse.3 fosq_genprd.3 fosq_socout.3 fosq_actlev.3 fosq_vigiln.3
## 155      1      1      1      1      1      1
##           0      0      0      0      0      0
##      fosq_sexual.3 fosq_global.3 sf36_pcs.3 sf36_mcs.3 sc_esstotal.3 sc_bmi.3
## 155      1      1      1      1      1      1
##           0      0      0      0      0      0
##      sc_avgpapuse.3 sc_fosq_genprd.3 sc_fosq_socout.3 sc_fosq_actlev.3
## 155      1      1      1      1      1      1
##           0      0      0      0      0      0
##      sc_fosq_vigiln.3 sc_fosq_sexual.3 sc_fosq_global.3 sc_sf36_pcs.3
## 155      1      1      1      1      1      1
##           0      0      0      0      0      0
##      sc_sf36_mcs.3
## 155      1 0
##           0 0
##
## [[6]]
##      nsrrid treat.f age gender race.f ttt dxchf dxchd dxhypothy dxdep desat
## 155      1      1 1      1      1 1      1      1      1      1 1
##           0      0 0      0      0 0      0      0      0      0 0
##      pressure ahi esstotal.0 bmi.0 avgpapuse.0 fosq_genprd.0 fosq_socout.0
## 155      1 1      1      1      1      1      1      1
##           0 0      0      0      0      0      0      0
##      fosq_actlev.0 fosq_vigiln.0 fosq_sexual.0 fosq_global.0 sf36_pcs.0

```

```

## 155      1      1      1      1      1
##          0      0      0      0      0
##      sf36_mcs.0 sc_esstotal.0 sc_bmi.0 sc_fosq_genprd.0 sc_fosq_socout.0
## 155      1      1      1      1      1
##          0      0      0      0      0
##      sc_fosq_actlev.0 sc_fosq_vigiln.0 sc_fosq_sexual.0 sc_fosq_global.0
## 155      1      1      1      1      1
##          0      0      0      0      0
##      sc_sf36_pcs.0 sc_sf36_mcs.0 esstotal.1 bmi.1 avgpapuse.1 fosq_genprd.1
## 155      1      1      1      1      1      1
##          0      0      0      0      0      0
##      fosq_socout.1 fosq_actlev.1 fosq_vigiln.1 fosq_sexual.1 fosq_global.1
## 155      1      1      1      1      1
##          0      0      0      0      0
##      sf36_pcs.1 sf36_mcs.1 sc_esstotal.1 sc_bmi.1 sc_avgpapuse.1
## 155      1      1      1      1      1
##          0      0      0      0      0
##      sc_fosq_genprd.1 sc_fosq_socout.1 sc_fosq_actlev.1 sc_fosq_vigiln.1
## 155      1      1      1      1      1
##          0      0      0      0      0
##      sc_fosq_sexual.1 sc_fosq_global.1 sc_sf36_pcs.1 sc_sf36_mcs.1 esstotal.3
## 155      1      1      1      1      1      1
##          0      0      0      0      0      0
##      bmi.3 avgpapuse.3 fosq_genprd.3 fosq_socout.3 fosq_actlev.3 fosq_vigiln.3
## 155      1      1      1      1      1      1
##          0      0      0      0      0      0
##      fosq_sexual.3 fosq_global.3 sf36_pcs.3 sf36_mcs.3 sc_esstotal.3 sc_bmi.3
## 155      1      1      1      1      1      1
##          0      0      0      0      0      0
##      sc_avgpapuse.3 sc_fosq_genprd.3 sc_fosq_socout.3 sc_fosq_actlev.3
## 155      1      1      1      1      1
##          0      0      0      0      0
##      sc_fosq_vigiln.3 sc_fosq_sexual.3 sc_fosq_global.3 sc_sf36_pcs.3
## 155      1      1      1      1      1
##          0      0      0      0      0
##      sc_sf36_mcs.3
## 155      1 0
##          0 0
##
## [[7]]
##      nsrrid treat.f age gender race.f ttt dxchf dxchd dxhypothy dxdep desat
## 155      1      1      1      1      1      1      1      1      1      1      1
##          0      0      0      0      0      0      0      0      0      0      0
##      pressure ahi esstotal.0 bmi.0 avgpapuse.0 fosq_genprd.0 fosq_socout.0
## 155      1      1      1      1      1      1      1      1
##          0      0      0      0      0      0      0      0
##      fosq_actlev.0 fosq_vigiln.0 fosq_sexual.0 fosq_global.0 sf36_pcs.0
## 155      1      1      1      1      1      1
##          0      0      0      0      0      0
##      sf36_mcs.0 sc_esstotal.0 sc_bmi.0 sc_fosq_genprd.0 sc_fosq_socout.0
## 155      1      1      1      1      1      1
##          0      0      0      0      0      0
##      sc_fosq_actlev.0 sc_fosq_vigiln.0 sc_fosq_sexual.0 sc_fosq_global.0
## 155      1      1      1      1      1
##          0      0      0      0      0
##      sc_sf36_pcs.0 sc_sf36_mcs.0 esstotal.1 bmi.1 avgpapuse.1 fosq_genprd.1
## 155      1      1      1      1      1      1
##          0      0      0      0      0      0
##      fosq_socout.1 fosq_actlev.1 fosq_vigiln.1 fosq_sexual.1 fosq_global.1
## 155      1      1      1      1      1
##          0      0      0      0      0

```

```

##      sf36_pcs.1 sf36_mcs.1 sc_esstotal.1 sc_bmi.1 sc_avgpapuse.1
## 155          1          1          1          1          1
##          0          0          0          0          0
##      sc_fosq_genprd.1 sc_fosq_socout.1 sc_fosq_actlev.1 sc_fosq_vigiln.1
## 155          1          1          1          1          1
##          0          0          0          0          0
##      sc_fosq_sexual.1 sc_fosq_global.1 sc_sf36_pcs.1 sc_sf36_mcs.1 esstotal.3
## 155          1          1          1          1          1
##          0          0          0          0          0
##      bmi.3 avgpapuse.3 fosq_genprd.3 fosq_socout.3 fosq_actlev.3 fosq_vigiln.3
## 155          1          1          1          1          1
##          0          0          0          0          0
##      fosq_sexual.3 fosq_global.3 sf36_pcs.3 sf36_mcs.3 sc_esstotal.3 sc_bmi.3
## 155          1          1          1          1          1
##          0          0          0          0          0
##      sc_avgpapuse.3 sc_fosq_genprd.3 sc_fosq_socout.3 sc_fosq_actlev.3
## 155          1          1          1          1
##          0          0          0          0
##      sc_fosq_vigiln.3 sc_fosq_sexual.3 sc_fosq_global.3 sc_sf36_pcs.3
## 155          1          1          1          1
##          0          0          0          0
##      sc_sf36_mcs.3
## 155          1 0
##          0 0
##
## [[8]]
##      nsrrid treat.f age gender race.f ttt dxchf dxchd dxhypothy dxdep desat
## 155          1          1 1          1          1 1          1          1          1          1
##          0          0 0          0          0 0          0          0          0          0
##      pressure ahi esstotal.0 bmi.0 avgpapuse.0 fosq_genprd.0 fosq_socout.0
## 155          1 1          1          1          1          1
##          0 0          0          0          0          0
##      fosq_actlev.0 fosq_vigiln.0 fosq_sexual.0 fosq_global.0 sf36_pcs.0
## 155          1          1          1          1          1
##          0          0          0          0          0
##      sf36_mcs.0 sc_esstotal.0 sc_bmi.0 sc_fosq_genprd.0 sc_fosq_socout.0
## 155          1          1          1          1          1
##          0          0          0          0          0
##      sc_fosq_actlev.0 sc_fosq_vigiln.0 sc_fosq_sexual.0 sc_fosq_global.0
## 155          1          1          1          1
##          0          0          0          0
##      sc_sf36_pcs.0 sc_sf36_mcs.0 esstotal.1 bmi.1 avgpapuse.1 fosq_genprd.1
## 155          1          1          1          1          1
##          0          0          0          0          0
##      fosq_socout.1 fosq_actlev.1 fosq_vigiln.1 fosq_sexual.1 fosq_global.1
## 155          1          1          1          1          1
##          0          0          0          0          0
##      sf36_pcs.1 sf36_mcs.1 sc_esstotal.1 sc_bmi.1 sc_avgpapuse.1
## 155          1          1          1          1          1
##          0          0          0          0          0
##      sc_fosq_genprd.1 sc_fosq_socout.1 sc_fosq_actlev.1 sc_fosq_vigiln.1
## 155          1          1          1          1          1
##          0          0          0          0          0
##      sc_fosq_sexual.1 sc_fosq_global.1 sc_sf36_pcs.1 sc_sf36_mcs.1 esstotal.3
## 155          1          1          1          1          1
##          0          0          0          0          0
##      bmi.3 avgpapuse.3 fosq_genprd.3 fosq_socout.3 fosq_actlev.3 fosq_vigiln.3
## 155          1          1          1          1          1
##          0          0          0          0          0
##      fosq_sexual.3 fosq_global.3 sf36_pcs.3 sf36_mcs.3 sc_esstotal.3 sc_bmi.3
## 155          1          1          1          1          1

```

```

##           0           0           0           0           0           0
##   sc_avgpapuse.3 sc_fosq_genprd.3 sc_fosq_socout.3 sc_fosq_actlev.3
## 155         1           1           1           1           1
##           0           0           0           0           0
##   sc_fosq_vigiln.3 sc_fosq_sexual.3 sc_fosq_global.3 sc_sf36_pcs.3
## 155         1           1           1           1           1
##           0           0           0           0           0
##   sc_sf36_mcs.3
## 155         1 0
##           0 0
##
## [[9]]
##   nsrrid treat.f age gender race.f ttt dxchf dxchd dxhypothy dxdep desat
## 155     1     1  1     1     1  1     1     1     1     1     1
##           0     0  0     0     0  0     0     0     0     0     0
##   pressure ahi esstotal.0 bmi.0 avgpapuse.0 fosq_genprd.0 fosq_socout.0
## 155     1  1     1     1           1           1           1
##           0  0     0     0           0           0           0
##   fosq_actlev.0 fosq_vigiln.0 fosq_sexual.0 fosq_global.0 sf36_pcs.0
## 155     1           1           1           1           1
##           0           0           0           0           0
##   sf36_mcs.0 sc_esstotal.0 sc_bmi.0 sc_fosq_genprd.0 sc_fosq_socout.0
## 155     1           1     1           1           1
##           0           0     0           0           0
##   sc_fosq_actlev.0 sc_fosq_vigiln.0 sc_fosq_sexual.0 sc_fosq_global.0
## 155     1           1           1           1           1
##           0           0           0           0           0
##   sc_sf36_pcs.0 sc_sf36_mcs.0 esstotal.1 bmi.1 avgpapuse.1 fosq_genprd.1
## 155     1           1           1     1     1           1           1
##           0           0           0     0     0           0           0
##   fosq_socout.1 fosq_actlev.1 fosq_vigiln.1 fosq_sexual.1 fosq_global.1
## 155     1           1           1           1           1
##           0           0           0           0           0
##   sf36_pcs.1 sf36_mcs.1 sc_esstotal.1 sc_bmi.1 sc_avgpapuse.1
## 155     1           1           1     1           1
##           0           0           0     0           0
##   sc_fosq_genprd.1 sc_fosq_socout.1 sc_fosq_actlev.1 sc_fosq_vigiln.1
## 155     1           1           1           1           1
##           0           0           0           0           0
##   sc_fosq_sexual.1 sc_fosq_global.1 sc_sf36_pcs.1 sc_sf36_mcs.1 esstotal.3
## 155     1           1           1           1           1
##           0           0           0           0           0
##   bmi.3 avgpapuse.3 fosq_genprd.3 fosq_socout.3 fosq_actlev.3 fosq_vigiln.3
## 155     1           1           1           1           1
##           0           0           0           0           0
##   fosq_sexual.3 fosq_global.3 sf36_pcs.3 sf36_mcs.3 sc_esstotal.3 sc_bmi.3
## 155     1           1           1           1           1
##           0           0           0           0           0
##   sc_avgpapuse.3 sc_fosq_genprd.3 sc_fosq_socout.3 sc_fosq_actlev.3
## 155     1           1           1           1           1
##           0           0           0           0           0
##   sc_fosq_vigiln.3 sc_fosq_sexual.3 sc_fosq_global.3 sc_sf36_pcs.3
## 155     1           1           1           1           1
##           0           0           0           0           0
##   sc_sf36_mcs.3
## 155     1 0
##           0 0
##
## [[10]]
##   nsrrid treat.f age gender race.f ttt dxchf dxchd dxhypothy dxdep desat
## 155     1     1  1     1     1  1     1     1     1     1     1

```

```

##          0          0          0          0          0          0          0          0          0          0          0
## pressure ahi esstotal.0 bmi.0 avgpapuse.0 fosq_genprd.0 fosq_socout.0
## 155      1      1          1      1          1          1          1          1          1          1
##          0      0          0      0          0          0          0          0          0          0          0
## fosq_actlev.0 fosq_vigiln.0 fosq_sexual.0 fosq_global.0 sf36_pcs.0
## 155          1          1          1          1          1          1          1          1          1          1
##          0          0          0          0          0          0          0          0          0          0          0
## sf36_mcs.0 sc_esstotal.0 sc_bmi.0 sc_fosq_genprd.0 sc_fosq_socout.0
## 155          1          1          1          1          1          1          1          1          1          1
##          0          0          0          0          0          0          0          0          0          0          0
## sc_fosq_actlev.0 sc_fosq_vigiln.0 sc_fosq_sexual.0 sc_fosq_global.0
## 155          1          1          1          1          1          1          1          1          1          1
##          0          0          0          0          0          0          0          0          0          0          0
## sc_sf36_pcs.0 sc_sf36_mcs.0 esstotal.1 bmi.1 avgpapuse.1 fosq_genprd.1
## 155          1          1          1          1          1          1          1          1          1          1
##          0          0          0          0          0          0          0          0          0          0          0
## fosq_socout.1 fosq_actlev.1 fosq_vigiln.1 fosq_sexual.1 fosq_global.1
## 155          1          1          1          1          1          1          1          1          1          1
##          0          0          0          0          0          0          0          0          0          0          0
## sf36_pcs.1 sf36_mcs.1 sc_esstotal.1 sc_bmi.1 sc_avgpapuse.1
## 155          1          1          1          1          1          1          1          1          1          1
##          0          0          0          0          0          0          0          0          0          0          0
## sc_fosq_genprd.1 sc_fosq_socout.1 sc_fosq_actlev.1 sc_fosq_vigiln.1
## 155          1          1          1          1          1          1          1          1          1          1
##          0          0          0          0          0          0          0          0          0          0          0
## sc_fosq_sexual.1 sc_fosq_global.1 sc_sf36_pcs.1 sc_sf36_mcs.1 esstotal.3
## 155          1          1          1          1          1          1          1          1          1          1
##          0          0          0          0          0          0          0          0          0          0          0
## bmi.3 avgpapuse.3 fosq_genprd.3 fosq_socout.3 fosq_actlev.3 fosq_vigiln.3
## 155          1          1          1          1          1          1          1          1          1          1
##          0          0          0          0          0          0          0          0          0          0          0
## fosq_sexual.3 fosq_global.3 sf36_pcs.3 sf36_mcs.3 sc_esstotal.3 sc_bmi.3
## 155          1          1          1          1          1          1          1          1          1          1
##          0          0          0          0          0          0          0          0          0          0          0
## sc_avgpapuse.3 sc_fosq_genprd.3 sc_fosq_socout.3 sc_fosq_actlev.3
## 155          1          1          1          1          1          1          1          1          1          1
##          0          0          0          0          0          0          0          0          0          0          0
## sc_fosq_vigiln.3 sc_fosq_sexual.3 sc_fosq_global.3 sc_sf36_pcs.3
## 155          1          1          1          1          1          1          1          1          1          1
##          0          0          0          0          0          0          0          0          0          0          0
## sc_sf36_mcs.3
## 155          1      0
##          0      0

```

## 5.0.2 long

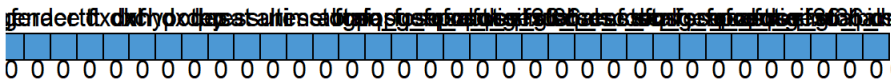
This has to be organized just so to work. It needs the times to be in order in the columns or else there's mass confusion (and NA in the data).

```
complete.long = map(complete.wide, function(x) {
  #z = select(x, nsrrid, treat.f, age, gender, race.f, ttt, ahi, pressure, desat, starts_with("d
  x"), everything())
  pivot_longer(x,
    cols = esstotal.0:sc_sf36_mcs.3,
    names_to = c(".value", "time"),
    names_sep = "\\.") %>%
  arrange(nsrrid, time) %>%
  mutate(id = factor(nsrrid),
    time = as.numeric(time),
    sc_avgpapuse = NULL)
})

#map(complete.long, function(x) {View(x %>% select(nsrrid, time, bmi, avgpapuse))})
map(complete.long, md.pattern)
```

```
## /\      /\
## { `---' }
## {  O  O }
## ==> V <== No need for mice. This data set is completely observed.
## \  \|/ /
## `-----'
```

```
## /\      /\
## { `---' }
## {  O  O }
## ==> V <== No need for mice. This data set is completely observed.
## \  \|/ /
## `-----'
```





```
## /\      /\
## { '----' }
## { 0 0 }
## ==> V <== No need for mice. This data set is completely observed.
## \  \|\ / /
##  '-----'
```

```
## /\      /\
## { '----' }
## { 0 0 }
## ==> V <== No need for mice. This data set is completely observed.
## \  \|\ / /
##  '-----'
```

```
## /\      /\
## { '----' }
## { 0 0 }
## ==> V <== No need for mice. This data set is completely observed.
## \  \|\ / /
##  '-----'
```

```
## /\      /\
## { '----' }
## { 0 0 }
## ==> V <== No need for mice. This data set is completely observed.
## \  \|\ / /
##  '-----'
```

```
## /\      /\
## { '----' }
## { 0 0 }
## ==> V <== No need for mice. This data set is completely observed.
## \  \|\ / /
##  '-----'
```

```
## /\      /\
## { '----' }
## { 0 0 }
## ==> V <== No need for mice. This data set is completely observed.
## \  \|\ / /
##  '-----'
```

```
## /\      /\
## { '----' }
## { 0 0 }
## ==> V <== No need for mice. This data set is completely observed.
## \  \|\ / /
##  '-----'
```

```
## /\      /\
## { '----' }
## { 0 0 }
## ==> V <== No need for mice. This data set is completely observed.
## \  \|\ / /
##  '-----'
```

```

## [[1]]
## nsrrid treat.f age gender race.f ttt dxchf dxchd dxhypothy dxdep desat
## 465 1 1 1 1 1 1 1 1 1 1 1
## 0 0 0 0 0 0 0 0 0 0 0
## pressure ahi time esstotal bmi avgpapuse fosq_genprd fosq_socout
## 465 1 1 1 1 1 1 1 1 1
## 0 0 0 0 0 0 0 0 0
## fosq_actlev fosq_vigiln fosq_sexual fosq_global sf36_pcs sf36_mcs
## 465 1 1 1 1 1 1
## 0 0 0 0 0 0
## sc_esstotal sc_bmi sc_fosq_genprd sc_fosq_socout sc_fosq_actlev
## 465 1 1 1 1 1
## 0 0 0 0 0
## sc_fosq_vigiln sc_fosq_sexual sc_fosq_global sc_sf36_pcs sc_sf36_mcs id
## 465 1 1 1 1 1 1 1 0
## 0 0 0 0 0 0 0 0
##
## [[2]]
## nsrrid treat.f age gender race.f ttt dxchf dxchd dxhypothy dxdep desat
## 465 1 1 1 1 1 1 1 1 1 1 1
## 0 0 0 0 0 0 0 0 0 0 0
## pressure ahi time esstotal bmi avgpapuse fosq_genprd fosq_socout
## 465 1 1 1 1 1 1 1 1 1
## 0 0 0 0 0 0 0 0 0
## fosq_actlev fosq_vigiln fosq_sexual fosq_global sf36_pcs sf36_mcs
## 465 1 1 1 1 1 1
## 0 0 0 0 0 0
## sc_esstotal sc_bmi sc_fosq_genprd sc_fosq_socout sc_fosq_actlev
## 465 1 1 1 1 1
## 0 0 0 0 0
## sc_fosq_vigiln sc_fosq_sexual sc_fosq_global sc_sf36_pcs sc_sf36_mcs id
## 465 1 1 1 1 1 1 1 0
## 0 0 0 0 0 0 0 0
##
## [[3]]
## nsrrid treat.f age gender race.f ttt dxchf dxchd dxhypothy dxdep desat
## 465 1 1 1 1 1 1 1 1 1 1 1
## 0 0 0 0 0 0 0 0 0 0 0
## pressure ahi time esstotal bmi avgpapuse fosq_genprd fosq_socout
## 465 1 1 1 1 1 1 1 1 1
## 0 0 0 0 0 0 0 0 0
## fosq_actlev fosq_vigiln fosq_sexual fosq_global sf36_pcs sf36_mcs
## 465 1 1 1 1 1 1
## 0 0 0 0 0 0
## sc_esstotal sc_bmi sc_fosq_genprd sc_fosq_socout sc_fosq_actlev
## 465 1 1 1 1 1
## 0 0 0 0 0
## sc_fosq_vigiln sc_fosq_sexual sc_fosq_global sc_sf36_pcs sc_sf36_mcs id
## 465 1 1 1 1 1 1 1 0
## 0 0 0 0 0 0 0 0
##
## [[4]]
## nsrrid treat.f age gender race.f ttt dxchf dxchd dxhypothy dxdep desat
## 465 1 1 1 1 1 1 1 1 1 1 1
## 0 0 0 0 0 0 0 0 0 0 0
## pressure ahi time esstotal bmi avgpapuse fosq_genprd fosq_socout
## 465 1 1 1 1 1 1 1 1 1
## 0 0 0 0 0 0 0 0 0
## fosq_actlev fosq_vigiln fosq_sexual fosq_global sf36_pcs sf36_mcs
## 465 1 1 1 1 1 1

```

```

##           0           0           0           0           0           0
##   sc_esstotal sc_bmi sc_fosq_genprd sc_fosq_socout sc_fosq_actlev
## 465         1         1           1           1           1           1
##           0           0           0           0           0           0
##   sc_fosq_vigiln sc_fosq_sexual sc_fosq_global sc_sf36_pcs sc_sf36_mcs id
## 465         1           1           1           1           1           1 1 0
##           0           0           0           0           0           0 0 0
##
## [[5]]
##   nsrrid treat.f age gender race.f ttt dxchf dxchd dxhypothy dxdep desat
## 465     1     1 1 1     1     1 1 1     1     1     1     1     1
##           0     0 0 0     0     0 0 0     0     0     0     0     0
##   pressure ahi time esstotal bmi avgpapuse fosq_genprd fosq_socout
## 465     1 1 1     1 1     1     1     1     1
##           0 0 0     0 0     0     0     0     0
##   fosq_actlev fosq_vigiln fosq_sexual fosq_global sf36_pcs sf36_mcs
## 465     1           1           1           1           1           1
##           0           0           0           0           0           0
##   sc_esstotal sc_bmi sc_fosq_genprd sc_fosq_socout sc_fosq_actlev
## 465     1     1           1           1           1
##           0     0           0           0           0
##   sc_fosq_vigiln sc_fosq_sexual sc_fosq_global sc_sf36_pcs sc_sf36_mcs id
## 465         1           1           1           1           1           1 1 0
##           0           0           0           0           0           0 0 0
##
## [[6]]
##   nsrrid treat.f age gender race.f ttt dxchf dxchd dxhypothy dxdep desat
## 465     1     1 1 1     1     1 1 1     1     1     1     1     1
##           0     0 0 0     0     0 0 0     0     0     0     0     0
##   pressure ahi time esstotal bmi avgpapuse fosq_genprd fosq_socout
## 465     1 1 1     1 1     1     1     1     1
##           0 0 0     0 0     0     0     0     0
##   fosq_actlev fosq_vigiln fosq_sexual fosq_global sf36_pcs sf36_mcs
## 465     1           1           1           1           1           1
##           0           0           0           0           0           0
##   sc_esstotal sc_bmi sc_fosq_genprd sc_fosq_socout sc_fosq_actlev
## 465     1     1           1           1           1
##           0     0           0           0           0
##   sc_fosq_vigiln sc_fosq_sexual sc_fosq_global sc_sf36_pcs sc_sf36_mcs id
## 465         1           1           1           1           1           1 1 0
##           0           0           0           0           0           0 0 0
##
## [[7]]
##   nsrrid treat.f age gender race.f ttt dxchf dxchd dxhypothy dxdep desat
## 465     1     1 1 1     1     1 1 1     1     1     1     1     1
##           0     0 0 0     0     0 0 0     0     0     0     0     0
##   pressure ahi time esstotal bmi avgpapuse fosq_genprd fosq_socout
## 465     1 1 1     1 1     1     1     1     1
##           0 0 0     0 0     0     0     0     0
##   fosq_actlev fosq_vigiln fosq_sexual fosq_global sf36_pcs sf36_mcs
## 465     1           1           1           1           1           1
##           0           0           0           0           0           0
##   sc_esstotal sc_bmi sc_fosq_genprd sc_fosq_socout sc_fosq_actlev
## 465     1     1           1           1           1
##           0     0           0           0           0
##   sc_fosq_vigiln sc_fosq_sexual sc_fosq_global sc_sf36_pcs sc_sf36_mcs id
## 465         1           1           1           1           1           1 1 0
##           0           0           0           0           0           0 0 0
##
## [[8]]
##   nsrrid treat.f age gender race.f ttt dxchf dxchd dxhypothy dxdep desat

```

```

## 465      1      1  1      1      1  1      1      1      1      1      1
##          0      0  0      0      0  0      0      0      0      0      0
##      pressure ahi time esstotal bmi avgpapuse fosq_genprd fosq_socout
## 465          1  1  1      1  1          1          1          1
##          0  0  0      0  0          0          0          0
##      fosq_actlev fosq_vigiln fosq_sexual fosq_global sf36_pcs sf36_mcs
## 465          1          1          1          1          1          1
##          0          0          0          0          0          0
##      sc_esstotal sc_bmi sc_fosq_genprd sc_fosq_socout sc_fosq_actlev
## 465          1      1          1          1          1
##          0      0          0          0          0
##      sc_fosq_vigiln sc_fosq_sexual sc_fosq_global sc_sf36_pcs sc_sf36_mcs id
## 465          1          1          1          1          1      1  1  0
##          0          0          0          0          0          0  0  0
##
## [[9]]
##      nsrrid treat.f age gender race.f ttt dxchf dxchd dxhypothy dxdep desat
## 465      1      1  1      1      1  1      1      1          1      1      1
##          0      0  0      0      0  0      0      0          0      0      0
##      pressure ahi time esstotal bmi avgpapuse fosq_genprd fosq_socout
## 465          1  1  1      1  1          1          1          1
##          0  0  0      0  0          0          0          0
##      fosq_actlev fosq_vigiln fosq_sexual fosq_global sf36_pcs sf36_mcs
## 465          1          1          1          1          1          1
##          0          0          0          0          0          0
##      sc_esstotal sc_bmi sc_fosq_genprd sc_fosq_socout sc_fosq_actlev
## 465          1      1          1          1          1
##          0      0          0          0          0
##      sc_fosq_vigiln sc_fosq_sexual sc_fosq_global sc_sf36_pcs sc_sf36_mcs id
## 465          1          1          1          1          1      1  1  0
##          0          0          0          0          0          0  0  0
##
## [[10]]
##      nsrrid treat.f age gender race.f ttt dxchf dxchd dxhypothy dxdep desat
## 465      1      1  1      1      1  1      1      1          1      1      1
##          0      0  0      0      0  0      0      0          0      0      0
##      pressure ahi time esstotal bmi avgpapuse fosq_genprd fosq_socout
## 465          1  1  1      1  1          1          1          1
##          0  0  0      0  0          0          0          0
##      fosq_actlev fosq_vigiln fosq_sexual fosq_global sf36_pcs sf36_mcs
## 465          1          1          1          1          1          1
##          0          0          0          0          0          0
##      sc_esstotal sc_bmi sc_fosq_genprd sc_fosq_socout sc_fosq_actlev
## 465          1      1          1          1          1
##          0      0          0          0          0
##      sc_fosq_vigiln sc_fosq_sexual sc_fosq_global sc_sf36_pcs sc_sf36_mcs id
## 465          1          1          1          1          1      1  1  0
##          0          0          0          0          0          0  0  0

```

### #Exploring models

Fit to GEE to evaluate whether beta distribution does a good job describing the data. ML-based model. Basically you fit a logistic regression but then the variance is different.

###Using betareg

```
beta.fit = map(complete.long, function(x) {  
  betareg::betareg(sc_fosq_global ~ avgpapuse * time +  
    age + gender + race.f +  
    ttt + ahi + bmi +  
    dxchf + dxchd + dxdep + dxhypothy,  
    data = x,  
    link = "logit"})  
)  
map(beta.fit, summary)
```

```
## [[1]]
##
## Call:
## betareg::betareg(formula = sc_fosq_global ~ avgpapuse * time + age +
##   gender + race.f + ttt + ahi + bmi + dxchf + dxchd + dxdep + dxhypothy,
##   data = x, link = "logit")
##
## Standardized weighted residuals 2:
##   Min      1Q  Median      3Q      Max
## -5.7426 -0.4730 -0.0193  0.4982  3.2742
##
## Coefficients (mean model with logit link):
##           Estimate Std. Error z value      Pr(>|z|)
## (Intercept)  0.2264987  0.3599200   0.629    0.529151
## avgpapuse    0.1334555  0.0320106   4.169 0.000030580264 ***
## time        0.2325283  0.0626522   3.711  0.000206 ***
## age         0.0013292  0.0042036   0.316  0.751843
## gender      0.3174405  0.1134897   2.797  0.005157 **
## race.f2     0.0134861  0.1274972   0.106  0.915760
## race.f3    -0.4485486  0.1723993  -2.602  0.009274 **
## ttt        0.0002984  0.0018915   0.158  0.874632
## ahi        0.0035667  0.0019912   1.791  0.073251 .
## bmi        0.0021847  0.0058063   0.376  0.706721
## dxchf     -0.0198053  0.3174043  -0.062  0.950246
## dxchd      0.1095771  0.1898530   0.577  0.563826
## dxdep     -0.7276683  0.1139829  -6.384 0.000000000173 ***
## dxhypothy  0.2181761  0.1770653   1.232  0.217882
## avgpapuse:time -0.0314911  0.0171430  -1.837  0.066215 .
##
## Phi coefficients (precision model with identity link):
##           Estimate Std. Error z value      Pr(>|z|)
## (phi)    3.2871      0.2065   15.92 <0.0000000000000002 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Type of estimator: ML (maximum likelihood)
## Log-likelihood: 241.8 on 16 Df
## Pseudo R-squared: 0.2426
## Number of iterations: 26 (BFGS) + 2 (Fisher scoring)
##
## [[2]]
##
## Call:
## betareg::betareg(formula = sc_fosq_global ~ avgpapuse * time + age +
##   gender + race.f + ttt + ahi + bmi + dxchf + dxchd + dxdep + dxhypothy,
##   data = x, link = "logit")
##
## Standardized weighted residuals 2:
##   Min      1Q  Median      3Q      Max
## -5.7729 -0.4583 -0.0203  0.4820  3.4124
##
## Coefficients (mean model with logit link):
##           Estimate Std. Error z value      Pr(>|z|)
## (Intercept)  0.2993199  0.3595012   0.833    0.405072
## avgpapuse    0.1356481  0.0319266   4.249 0.000021497070 ***
## time        0.2154807  0.0632191   3.408  0.000653 ***
## age         0.0007219  0.0041989   0.172  0.863487
## gender      0.3303380  0.1136804   2.906  0.003663 **
## race.f2     0.0248707  0.1268403   0.196  0.844549
## race.f3    -0.3895730  0.1719622  -2.265  0.023485 *
```

```

## ttt          0.0001944  0.0018850  0.103      0.917870
## ahi          0.0032372  0.0019821  1.633      0.102422
## bmi          0.0008624  0.0057063  0.151      0.879872
## dxchf       -0.0051743  0.3170076  -0.016     0.986977
## dxchd        0.1097602  0.1892792  0.580      0.561992
## dxdep       -0.7036236  0.1132090  -6.215  0.000000000512 ***
## dxhypoathy   0.2752442  0.1767365  1.557      0.119383
## avgpapuse:time -0.0281456  0.0170354  -1.652     0.098497 .
##
## Phi coefficients (precision model with identity link):
##      Estimate Std. Error z value      Pr(>|z|)
## (phi)  3.3179      0.2086  15.91 <0.0000000000000002 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Type of estimator: ML (maximum likelihood)
## Log-likelihood: 243.3 on 16 Df
## Pseudo R-squared: 0.2483
## Number of iterations: 25 (BFGS) + 1 (Fisher scoring)
##
## [[3]]
##
## Call:
## betareg::betareg(formula = sc_fosq_global ~ avgpapuse * time + age +
##   gender + race.f + ttt + ahi + bmi + dxchf + dxchd + dxdep + dxhypoathy,
##   data = x, link = "logit")
##
## Standardized weighted residuals 2:
##      Min      1Q  Median      3Q      Max
## -5.7729 -0.4557 -0.0269  0.5018  3.3435
##
## Coefficients (mean model with logit link):
##      Estimate Std. Error z value      Pr(>|z|)
## (Intercept)  0.1319757  0.3583788  0.368      0.71268
## avgpapuse    0.1384689  0.0321256  4.310 0.000016308160 ***
## time         0.2603404  0.0594869  4.376 0.000012063883 ***
## age          0.0024563  0.0041973  0.585      0.55841
## gender       0.3577910  0.1130817  3.164      0.00156 **
## race.f2      0.0384898  0.1271316  0.303      0.76208
## race.f3     -0.4508053  0.1718083  -2.624     0.00869 **
## ttt          0.0003135  0.0018861  0.166      0.86800
## ahi          0.0029178  0.0019899  1.466      0.14257
## bmi          0.0029159  0.0057914  0.503      0.61461
## dxchf       -0.0711944  0.3158061  -0.225     0.82164
## dxchd        0.1027929  0.1893521  0.543      0.58722
## dxdep       -0.7322518  0.1153355  -6.349 0.000000000217 ***
## dxhypoathy   0.2411906  0.1766897  1.365      0.17224
## avgpapuse:time -0.0371300  0.0167603  -2.215     0.02674 *
##
## Phi coefficients (precision model with identity link):
##      Estimate Std. Error z value      Pr(>|z|)
## (phi)  3.3253      0.2094  15.88 <0.0000000000000002 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Type of estimator: ML (maximum likelihood)
## Log-likelihood: 248.1 on 16 Df
## Pseudo R-squared: 0.2521
## Number of iterations: 25 (BFGS) + 2 (Fisher scoring)
##
## [[4]]

```

```
##
## Call:
## betareg::betareg(formula = sc_fosq_global ~ avgpapuse * time + age +
##   gender + race.f + ttt + ahi + bmi + dxchf + dxchd + dxdep + dxhypothy,
##   data = x, link = "logit")
##
## Standardized weighted residuals 2:
##   Min      1Q  Median      3Q      Max
## -5.7737 -0.4475 -0.0431  0.4829  3.3776
##
## Coefficients (mean model with logit link):
##              Estimate Std. Error z value      Pr(>|z|)
## (Intercept)  0.2503939  0.3593795   0.697    0.48597
## avgpapuse    0.1393669  0.0319004   4.369 0.000012492016 ***
## time        0.2556312  0.0625205   4.089 0.000043368632 ***
## age         0.0008374  0.0041940   0.200    0.84174
## gender       0.3389659  0.1132434   2.993    0.00276 **
## race.f2     -0.0768792  0.1272090   0.604    0.54561
## race.f3     -0.4526176  0.1720950  -2.630    0.00854 **
## ttt         0.0005025  0.0018939   0.265    0.79075
## ahi         0.0036427  0.0019863   1.834    0.06667 .
## bmi         0.0008769  0.0058178   0.151    0.88019
## dxchf       -0.0319410  0.3169661  -0.101    0.91973
## dxchd       0.0985166  0.1895056   0.520    0.60316
## dxdep       -0.7069127  0.1137008  -6.217 0.000000000506 ***
## dxhypothy   0.2360363  0.1769490   1.334    0.18223
## avgpapuse:time -0.0344509  0.0169044  -2.038    0.04155 *
##
## Phi coefficients (precision model with identity link):
##           Estimate Std. Error z value      Pr(>|z|)
## (phi)      3.315      0.209   15.86 <0.0000000000000002 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Type of estimator: ML (maximum likelihood)
## Log-likelihood: 251.4 on 16 Df
## Pseudo R-squared: 0.252
## Number of iterations: 25 (BFGS) + 2 (Fisher scoring)
##
## [[5]]
##
## Call:
## betareg::betareg(formula = sc_fosq_global ~ avgpapuse * time + age +
##   gender + race.f + ttt + ahi + bmi + dxchf + dxchd + dxdep + dxhypothy,
##   data = x, link = "logit")
##
## Standardized weighted residuals 2:
##   Min      1Q  Median      3Q      Max
## -5.7126 -0.4448 -0.0049  0.4773  3.3506
##
## Coefficients (mean model with logit link):
##              Estimate Std. Error z value      Pr(>|z|)
## (Intercept)  0.2271207  0.3596476   0.632    0.52771
## avgpapuse    0.1399749  0.0325190   4.304 0.000016743555 ***
## time        0.2589746  0.0632240   4.096 0.000042008402 ***
## age         0.0010183  0.0042048   0.242    0.80865
## gender       0.3282720  0.1140808   2.878    0.00401 **
## race.f2     0.0567198  0.1275564   0.445    0.65656
## race.f3     -0.3847692  0.1728908  -2.226    0.02605 *
## ttt         0.0003726  0.0018947   0.197    0.84411
## ahi         0.0033465  0.0019926   1.679    0.09306 .
```



```

## bmi          0.0019559  0.0057373  0.341      0.73317
## dxchf        -0.0452613  0.3184739 -0.142     0.88699
## dxchd         0.1182983  0.1901113  0.622     0.53377
## dxdep        -0.7161585  0.1136301 -6.303 0.000000000293 ***
## dxhypothy     0.1918338  0.1772662  1.082     0.27917
## avgpapuse:time -0.0378544  0.0171040 -2.213     0.02688 *
##
## Phi coefficients (precision model with identity link):
##      Estimate Std. Error z value      Pr(>|z|)
## (phi)   3.2610    0.2051   15.9 <0.0000000000000002 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Type of estimator: ML (maximum likelihood)
## Log-likelihood: 247.2 on 16 Df
## Pseudo R-squared: 0.2505
## Number of iterations: 25 (BFGS) + 2 (Fisher scoring)
##
## [[6]]
##
## Call:
## betareg::betareg(formula = sc_fosq_global ~ avgpapuse * time + age +
##   gender + race.f + ttt + ahi + bmi + dxchf + dxchd + dxdep + dxhypothy,
##   data = x, link = "logit")
##
## Standardized weighted residuals 2:
##      Min      1Q  Median      3Q      Max
## -5.7656 -0.4457 -0.0191  0.4898  3.3925
##
## Coefficients (mean model with logit link):
##      Estimate Std. Error z value      Pr(>|z|)
## (Intercept)  0.2076026  0.3594975  0.577     0.56362
## avgpapuse    0.1287238  0.0320844  4.012 0.00006019613 ***
## time         0.2509838  0.0611804  4.102 0.00004089609 ***
## age          0.0018450  0.0042029  0.439     0.66067
## gender       0.3471414  0.1133804  3.062     0.00220 **
## race.f2      0.0688494  0.1277514  0.539     0.58993
## race.f3     -0.4464758  0.1719894 -2.596     0.00943 **
## ttt          0.0003975  0.0018875  0.211     0.83320
## ahi          0.0029790  0.0019875  1.499     0.13391
## bmi          0.0015298  0.0057976  0.264     0.79188
## dxchf       -0.0703541  0.3166004 -0.222     0.82414
## dxchd        0.1107581  0.1894874  0.585     0.55887
## dxdep       -0.7044619  0.1154412 -6.102 0.00000000105 ***
## dxhypothy    0.1989566  0.1765115  1.127     0.25968
## avgpapuse:time -0.0303446  0.0168184 -1.804     0.07119 .
##
## Phi coefficients (precision model with identity link):
##      Estimate Std. Error z value      Pr(>|z|)
## (phi)   3.3110    0.2084   15.88 <0.0000000000000002 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Type of estimator: ML (maximum likelihood)
## Log-likelihood: 247.3 on 16 Df
## Pseudo R-squared: 0.2518
## Number of iterations: 25 (BFGS) + 1 (Fisher scoring)
##
## [[7]]
##
## Call:

```

```

## betareg::betareg(formula = sc_fosq_global ~ avgpapuse * time + age +
##   gender + race.f + ttt + ahi + bmi + dxchf + dxchd + dxdep + dxhypothy,
##   data = x, link = "logit")
##
## Standardized weighted residuals 2:
##   Min      1Q  Median      3Q      Max
## -5.7212 -0.4613 -0.0114  0.4826  3.3685
##
## Coefficients (mean model with logit link):
##               Estimate Std. Error z value      Pr(>|z|)
## (Intercept)   0.3039739  0.3588973   0.847      0.39701
## avgpapuse     0.1373394  0.0323244   4.249 0.0000214936 ***
## time          0.2499450  0.0616066   4.057 0.0000496828 ***
## age           0.0008663  0.0042093   0.206      0.83694
## gender        0.3419549  0.1138366   3.004      0.00267 **
## race.f2       0.0796233  0.1275733   0.624      0.53254
## race.f3      -0.4123619  0.1725744  -2.389      0.01687 *
## ttt           0.0003982  0.0018966   0.210      0.83370
## ahi           0.0036788  0.0019917   1.847      0.06474 .
## bmi          -0.0009742  0.0057091  -0.171      0.86450
## dxchf        -0.0485805  0.3181971  -0.153      0.87866
## dxchd         0.1034918  0.1898306   0.545      0.58563
## dxdep        -0.6499729  0.1135363  -5.725 0.0000000104 ***
## dxhypothy     0.2712521  0.1774120   1.529      0.12628
## avgpapuse:time -0.0358448  0.0169513  -2.115      0.03447 *
##
## Phi coefficients (precision model with identity link):
##               Estimate Std. Error z value      Pr(>|z|)
## (phi)         3.2714      0.2055   15.92 <0.0000000000000002 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Type of estimator: ML (maximum likelihood)
## Log-likelihood: 242.9 on 16 Df
## Pseudo R-squared: 0.2433
## Number of iterations: 25 (BFGS) + 1 (Fisher scoring)
##
## [[8]]
##
## Call:
## betareg::betareg(formula = sc_fosq_global ~ avgpapuse * time + age +
##   gender + race.f + ttt + ahi + bmi + dxchf + dxchd + dxdep + dxhypothy,
##   data = x, link = "logit")
##
## Standardized weighted residuals 2:
##   Min      1Q  Median      3Q      Max
## -5.5064 -0.4551  0.0087  0.5163  3.0608
##
## Coefficients (mean model with logit link):
##               Estimate Std. Error z value      Pr(>|z|)
## (Intercept)   0.2448301  0.3648560   0.671      0.502200
## avgpapuse     0.1312075  0.0326263   4.022 0.000057822983 ***
## time          0.2241008  0.0631978   3.546      0.000391 ***
## age           0.0016034  0.0042631   0.376      0.706826
## gender        0.3240424  0.1150423   2.817      0.004852 **
## race.f2       0.0216380  0.1286962   0.168      0.866479
## race.f3      -0.5607884  0.1748498  -3.207      0.001340 **
## ttt           -0.0007751  0.0019099  -0.406      0.684848
## ahi           0.0039902  0.0020162   1.979      0.047802 *
## bmi           0.0017601  0.0058845   0.299      0.764863
## dxchf        -0.0043723  0.3224596  -0.014      0.989182

```

```

## dxchd          0.1061353  0.1923164  0.552      0.581031
## dxdep          -0.7431716  0.1160052 -6.406 0.000000000149 ***
## dxhypothy      0.0571375  0.1788383  0.319      0.749353
## avgpapuse:time -0.0311586  0.0172873 -1.802      0.071484 .
##
## Phi coefficients (precision model with identity link):
##      Estimate Std. Error z value      Pr(>|z|)
## (phi)   3.0911    0.1932     16 <0.0000000000000002 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Type of estimator: ML (maximum likelihood)
## Log-likelihood: 235.3 on 16 Df
## Pseudo R-squared: 0.2486
## Number of iterations: 24 (BFGS) + 2 (Fisher scoring)
##
## [[9]]
##
## Call:
## betareg::betareg(formula = sc_fosq_global ~ avgpapuse * time + age +
##   gender + race.f + ttt + ahi + bmi + dxchf + dxchd + dxdep + dxhypothy,
##   data = x, link = "logit")
##
## Standardized weighted residuals 2:
##      Min      1Q  Median      3Q      Max
## -5.7585 -0.4714 -0.0388  0.4943  3.3205
##
## Coefficients (mean model with logit link):
##      Estimate Std. Error z value      Pr(>|z|)
## (Intercept)  0.3315212  0.3580040  0.926    0.35443
## avgpapuse    0.1360988  0.0323639  4.205 0.00002607789 ***
## time        0.2463084  0.0608030  4.051 0.00005101608 ***
## age         0.0006518  0.0041994  0.155    0.87666
## gender      0.3437375  0.1129815  3.042    0.00235 **
## race.f2     0.0048675  0.1270778  0.038    0.96945
## race.f3    -0.4543147  0.1720760 -2.640    0.00829 **
## ttt         0.0003304  0.0018873  0.175    0.86103
## ahi         0.0037363  0.0019861  1.881    0.05993 .
## bmi        -0.0006587  0.0057524 -0.115    0.90884
## dxchf      -0.0417913  0.3164492 -0.132    0.89493
## dxchd       0.0960299  0.1894299  0.507    0.61220
## dxdep      -0.6636324  0.1135716 -5.843 0.00000000512 ***
## dxhypothy   0.2150790  0.1766818  1.217    0.22348
## avgpapuse:time -0.0346483  0.0168557 -2.056    0.03982 *
##
## Phi coefficients (precision model with identity link):
##      Estimate Std. Error z value      Pr(>|z|)
## (phi)   3.3076    0.2079    15.91 <0.0000000000000002 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Type of estimator: ML (maximum likelihood)
## Log-likelihood: 241.6 on 16 Df
## Pseudo R-squared: 0.2407
## Number of iterations: 26 (BFGS) + 1 (Fisher scoring)
##
## [[10]]
##
## Call:
## betareg::betareg(formula = sc_fosq_global ~ avgpapuse * time + age +
##   gender + race.f + ttt + ahi + bmi + dxchf + dxchd + dxdep + dxhypothy,

```

```
##      data = x, link = "logit")
##
## Standardized weighted residuals 2:
##      Min      1Q  Median      3Q      Max
## -5.7892 -0.4606 -0.0070  0.4993  3.3336
##
## Coefficients (mean model with logit link):
##              Estimate Std. Error z value      Pr(>|z|)
## (Intercept)   0.2179337  0.3585455   0.608    0.543302
## avgpapuse     0.1387316  0.0322082  4.307 0.00001652290 ***
## time         0.2234141  0.0598124  3.735   0.000188 ***
## age          0.0015134  0.0041866   0.361   0.717740
## gender       0.3743105  0.1132028  3.307   0.000945 ***
## race.f2      0.0481748  0.1266014   0.381   0.703557
## race.f3     -0.4283462  0.1715552 -2.497   0.012530 *
## ttt         0.0009167  0.0018826   0.487   0.626295
## ahi         0.0035264  0.0019867   1.775   0.075900 .
## bmi         0.0003384  0.0057759   0.059   0.953281
## dxchf      -0.0510851  0.3163256 -0.161   0.871703
## dxchd       0.0994676  0.1890462   0.526   0.598781
## dxdep      -0.6884518  0.1131064 -6.087 0.00000000115 ***
## dxhypothy   0.2737121  0.1764713   1.551   0.120895
## avgpapuse:time -0.0298729  0.0167969 -1.778   0.075325 .
##
## Phi coefficients (precision model with identity link):
##              Estimate Std. Error z value      Pr(>|z|)
## (phi)      3.3412      0.2103   15.89 <0.0000000000000002 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Type of estimator: ML (maximum likelihood)
## Log-likelihood: 246.6 on 16 Df
## Pseudo R-squared: 0.2547
## Number of iterations: 25 (BFGS) + 2 (Fisher scoring)
```

### ###Gamma GEE

```
#GEE with unstructured correlation matrix
gee.fit = map(complete.long, function(x) {
  gee(fosq_global ~ avgpapuse * time +
      age + gender + race.f +
      ttt + ahi + bmi +
      dxchf + dxchd + dxdep + dxhypothy,
      data = x,
      id = nsrrid,
      family = Gamma, #similar in look to beta distribution and can be converted within each oth
er; distribution is 0,+infinity thought rather than [0,1]
      corstr = "unstructured"})
})
```

```

##      (Intercept)      avgpapuse      time      age      gender
## 0.069421883484 -0.001499954531 -0.003225600521 -0.000023847250 -0.003190461072
##      race.f2      race.f3      ttt      ahi      bmi
## 0.000017709136 0.002387222716 -0.000007299965 -0.000024129166 -0.000004005337
##      dxchf      dxchd      dxdep      dxhypothy      avgpapuse:time
## -0.002335101058 0.001129589742 0.006284235296 -0.002926342904 0.000383283655
##      (Intercept)      avgpapuse      time      age      gender
## 0.069232159023 -0.001532296224 -0.003220538309 -0.000018073875 -0.003345261876
##      race.f2      race.f3      ttt      ahi      bmi
## -0.000096328157 0.001982513418 -0.000005486624 -0.000019777921 -0.000005684305
##      dxchf      dxchd      dxdep      dxhypothy      avgpapuse:time
## -0.002318064585 0.001065979128 0.006214851558 -0.003156879740 0.000381785935
##      (Intercept)      avgpapuse      time      age      gender
## 0.07050009557 -0.00156243455 -0.00348029840 -0.00003318335 -0.00358020967
##      race.f2      race.f3      ttt      ahi      bmi
## -0.00023619270 0.00242085525 -0.00000885461 -0.00001938066 -0.00001409918
##      dxchf      dxchd      dxdep      dxhypothy      avgpapuse:time
## -0.00189022681 0.00113031157 0.00649487841 -0.00308428780 0.00044568505
##      (Intercept)      avgpapuse      time      age      gender
## 0.069199337010 -0.001541344924 -0.003517459039 -0.000019401132 -0.003152846301
##      race.f2      race.f3      ttt      ahi      bmi
## -0.000549457311 0.002397055387 -0.000008966888 -0.000025061965 0.000001653271
##      dxchf      dxchd      dxdep      dxhypothy      avgpapuse:time
## -0.002450019325 0.001112493148 0.006693613145 -0.002923272194 0.000435327986
##      (Intercept)      avgpapuse      time      age      gender
## 0.070174625203 -0.001580047433 -0.003516510313 -0.000026642422 -0.003598907932
##      race.f2      race.f3      ttt      ahi      bmi
## -0.000412777401 0.001928386678 -0.000010351482 -0.000024529465 -0.000005284334
##      dxchf      dxchd      dxdep      dxhypothy      avgpapuse:time
## -0.001876484835 0.001025816000 0.006294168232 -0.002903810723 0.000468811086
##      (Intercept)      avgpapuse      time      age      gender
## 0.069993893152 -0.001465963422 -0.003481156262 -0.000028219202 -0.003247729722
##      race.f2      race.f3      ttt      ahi      bmi
## -0.000709067729 0.002285466861 -0.000008749497 -0.000019461678 -0.000010031260
##      dxchf      dxchd      dxdep      dxhypothy      avgpapuse:time
## -0.001944460902 0.000983718325 0.006460079089 -0.002697974837 0.000394024565
##      (Intercept)      avgpapuse      time      age      gender
## 0.069468479413 -0.001542267422 -0.003454253519 -0.000025324199 -0.003331083284
##      race.f2      race.f3      ttt      ahi      bmi
## -0.000493817812 0.002202507883 -0.000007688965 -0.000024682314 0.000007379069
##      dxchf      dxchd      dxdep      dxhypothy      avgpapuse:time
## -0.001942414411 0.001091377590 0.005902081638 -0.003119104056 0.000439200300
##      (Intercept)      avgpapuse      time      age      gender
## 0.069479883106 -0.001524204328 -0.003384124310 -0.000024150665 -0.003174076570
##      race.f2      race.f3      ttt      ahi      bmi
## -0.000163719902 0.003453233673 0.000001147901 -0.000027313797 -0.000011426378
##      dxchf      dxchd      dxdep      dxhypothy      avgpapuse:time
## -0.002359546255 0.001144193536 0.006608961624 -0.001909876539 0.000425504105
##      (Intercept)      avgpapuse      time      age      gender
## 0.069276726695 -0.001530020724 -0.003453367103 -0.000024558794 -0.003351343716
##      race.f2      race.f3      ttt      ahi      bmi
## 0.000024091995 0.002469552575 -0.000008399930 -0.000023844430 0.000003133485
##      dxchf      dxchd      dxdep      dxhypothy      avgpapuse:time
## -0.002147092803 0.001161077153 0.006352349252 -0.002862827810 0.000440555511
##      (Intercept)      avgpapuse      time      age      gender
## 0.069998954544 -0.001560102810 -0.003370573967 -0.000022089283 -0.003573216688
##      race.f2      race.f3      ttt      ahi      bmi
## -0.000431980428 0.002277811486 -0.000013354767 -0.000023842828 -0.000004144128
##      dxchf      dxchd      dxdep      dxhypothy      avgpapuse:time
## -0.001959501299 0.001055391573 0.006120567907 -0.003306977824 0.000419164736

```

```
map(gee.fit, summary)
```

```

## [[1]]
##
## GEE: GENERALIZED LINEAR MODELS FOR DEPENDENT DATA
## gee S-function, version 4.13 modified 98/01/27 (1998)
##
## Model:
## Link: Reciprocal
## Variance to Mean Relation: Gamma
## Correlation Structure: Unstructured
##
## Call:
## gee(formula = fosq_global ~ avgpapuse * time + age + gender +
##      race.f + ttt + ahi + bmi + dxchf + dxchd + dxdep + dxhypothy,
##      id = nsrrid, data = x, family = Gamma, corstr = "unstructured")
##
## Summary of Residuals:
##      Min      1Q   Median      3Q      Max
## -9.4838729 -0.9184774  0.4666252  1.4820567  4.7273972
##
##
## Coefficients:
##              Estimate   Naive S.E.   Naive z   Robust S.E.
## (Intercept)  0.069452057119 0.00454682252 15.27485553 0.00341905036
## avgpapuse    -0.001646605135 0.00021293750 -7.73280964 0.00021597375
## time         -0.002841888426 0.00050944040 -5.57845128 0.00045851008
## age          -0.000018914982 0.00005248344 -0.36039907 0.00003917877
## gender       -0.003166794108 0.00146887654 -2.15592939 0.00134655238
## race.f2      -0.000101500430 0.00162265018 -0.06255226 0.00155138603
## race.f3       0.002482897525 0.00222620798  1.11530349 0.00144770080
## ttt          -0.000009422166 0.00002349166 -0.40108564 0.00001878929
## ahi          -0.000022000081 0.00002499205 -0.88028301 0.00002240296
## bmi          -0.000005431744 0.00007568573 -0.07176708 0.00007420255
## dxchf        -0.002728182709 0.00410998181 -0.66379435 0.00314866760
## dxchd         0.000887200003 0.00236148516  0.37569578 0.00237818016
## dxdep         0.006311229243 0.00153429530  4.11343844 0.00176258532
## dxhypothy    -0.003135299574 0.00223411076 -1.40337696 0.00189051749
## avgpapuse:time 0.000342286719 0.00012138912  2.81974795 0.00009535744
##
##              Robust z
## (Intercept)  20.31325945
## avgpapuse    -7.62409857
## time         -6.19809366
## age          -0.48278656
## gender       -2.35177938
## race.f2      -0.06542564
## race.f3       1.71506262
## ttt          -0.50146465
## ahi          -0.98201678
## bmi          -0.07320157
## dxchf        -0.86645625
## dxchd         0.37305836
## dxdep         3.58066596
## dxhypothy    -1.65843458
## avgpapuse:time 3.58951262
##
## Estimated Scale Parameter: 0.0245543
## Number of Iterations: 5
##
## Working Correlation
##      [,1]      [,2]      [,3]
## [1,] 1.0000000 0.4322326 0.3063084

```

```

## [2,] 0.4322326 1.0000000 0.4780597
## [3,] 0.3063084 0.4780597 1.0000000
##
## [[2]]
##
## GEE: GENERALIZED LINEAR MODELS FOR DEPENDENT DATA
## gee S-function, version 4.13 modified 98/01/27 (1998)
##
## Model:
## Link:                               Reciprocal
## Variance to Mean Relation: Gamma
## Correlation Structure:               Unstructured
##
## Call:
## gee(formula = fosq_global ~ avgpapuse * time + age + gender +
##      race.f + ttt + ahi + bmi + dxchf + dxchd + dxdep + dxhypothy,
##      id = nsrrid, data = x, family = Gamma, corstr = "unstructured")
##
## Summary of Residuals:
##      Min           1Q       Median           3Q          Max
## -9.4519034 -0.8948166  0.4624728  1.4852290  4.7276836
##
##
## Coefficients:
##              Estimate   Naive S.E.   Naive z   Robust S.E.
## (Intercept)  0.069200811218 0.00455552545 15.19052235 0.00346823754
## avgpapuse    -0.001667709355 0.00021538171  -7.74304065 0.00021082265
## time         -0.003037732996 0.00050534320  -6.01122756 0.00044863729
## age          -0.000012196307 0.00005256061  -0.23204271 0.00003891379
## gender       -0.003232327270 0.00147044772  -2.19819259 0.00134988797
## race.f2      -0.000036927248 0.00161220765  -0.02290477 0.00152889945
## race.f3       0.002146308050 0.00222048376   0.96659480 0.00153692902
## ttt          -0.000006691022 0.00002341706  -0.28573278 0.00001827039
## ahi          -0.000019546826 0.00002479133  -0.78845401 0.00002208259
## bmi          -0.000008644675 0.00007426963  -0.11639582 0.00007361663
## dxchf        -0.002653832873 0.00410597704  -0.64633407 0.00311653547
## dxchd         0.000889677916 0.00235573219   0.37766513 0.00232311993
## dxdep         0.006245967856 0.00152638451   4.09200160 0.00174742783
## dxhypothy    -0.003268338392 0.00222519526  -1.46878724 0.00190025163
## avgpapuse:time 0.000382038457 0.00012090824   3.15973875 0.00009852306
##
##              Robust z
## (Intercept)  19.95273115
## avgpapuse    -7.91048475
## time         -6.77102212
## age          -0.31341862
## gender       -2.39451520
## race.f2      -0.02415283
## race.f3       1.39649133
## ttt          -0.36622216
## ahi          -0.88516902
## bmi          -0.11742829
## dxchf        -0.85153302
## dxchd         0.38296685
## dxdep         3.57437815
## dxhypothy    -1.71995031
## avgpapuse:time 3.87765515
##
## Estimated Scale Parameter: 0.0242749
## Number of Iterations: 5
##
## Working Correlation

```



```

##           [,1]      [,2]      [,3]
## [1,] 1.0000000 0.4321329 0.3419714
## [2,] 0.4321329 1.0000000 0.4608691
## [3,] 0.3419714 0.4608691 1.0000000
##
## [[3]]
##
## GEE: GENERALIZED LINEAR MODELS FOR DEPENDENT DATA
## gee S-function, version 4.13 modified 98/01/27 (1998)
##
## Model:
## Link:                               Reciprocal
## Variance to Mean Relation: Gamma
## Correlation Structure:               Unstructured
##
## Call:
## gee(formula = fosq_global ~ avgpapuse * time + age + gender +
##      race.f + ttt + ahi + bmi + dxchf + dxchd + dxdep + dxhypothy,
##      id = nsrrid, data = x, family = Gamma, corstr = "unstructured")
##
## Summary of Residuals:
##           Min           1Q       Median           3Q           Max
## -9.4511962 -0.8773465  0.4303354  1.4731619  4.8090700
##
##
## Coefficients:
##              Estimate   Naive S.E.   Naive z   Robust S.E.   Robust z
## (Intercept)  0.07024116064 0.00451576883 15.5546405 0.00344744633 20.3748380
## avgpapuse    -0.00169495408 0.00021706367 -7.8085572 0.00021391800 -7.9233824
## time         -0.00309521078 0.00046618503 -6.6394470 0.00040530932 -7.6366632
## age          -0.00002492562 0.00005228523 -0.4767239 0.00003863304 -0.6451891
## gender       -0.00343974857 0.00146020250 -2.3556654 0.00136901849 -2.5125655
## race.f2      -0.00036193971 0.00160592678 -0.2253775 0.00150385595 -0.2406745
## race.f3       0.00261494216 0.00221539247  1.1803517 0.00145752729  1.7940948
## ttt          -0.00001332423 0.00002333741 -0.5709384 0.00001847822 -0.7210775
## ahi          -0.00001818745 0.00002485834 -0.7316440 0.00002232425 -0.8146949
## bmi          -0.00001189805 0.00007527053 -0.1580704 0.00007558974 -0.1574029
## dxchf        -0.00233723618 0.00408785288 -0.5717515 0.00308573062 -0.7574336
## dxchd         0.00097462201 0.00235154282  0.4144607 0.00233107314  0.4181001
## dxdep         0.00644552905 0.00155590718  4.1426180 0.00182854185  3.5249557
## dxhypothy    -0.00316811298 0.00222471358 -1.4240543 0.00188047063 -1.6847447
## avgpapuse:time 0.00039047713 0.00011713110  3.3336758 0.00008775479  4.4496391
##
## Estimated Scale Parameter: 0.0240602
## Number of Iterations: 4
##
## Working Correlation
##           [,1]      [,2]      [,3]
## [1,] 1.0000000 0.4277076 0.3598206
## [2,] 0.4277076 1.0000000 0.4628036
## [3,] 0.3598206 0.4628036 1.0000000
##
## [[4]]
##
## GEE: GENERALIZED LINEAR MODELS FOR DEPENDENT DATA
## gee S-function, version 4.13 modified 98/01/27 (1998)
##
## Model:
## Link:                               Reciprocal
## Variance to Mean Relation: Gamma
## Correlation Structure:               Unstructured

```

```

##
## Call:
## gee(formula = fosq_global ~ avgpapuse * time + age + gender +
##      race.f + ttt + ahi + bmi + dxchf + dxchd + dxdep + dxhypothy,
##      id = nsrrid, data = x, family = Gamma, corstr = "unstructured")
##
## Summary of Residuals:
##      Min       1Q   Median       3Q      Max
## -9.4569669 -0.8584714  0.4421521  1.4667605  4.8130093
##
##
## Coefficients:
##              Estimate   Naive S.E.   Naive z   Robust S.E.
## (Intercept)   0.069179733891 0.00447560144 15.4570810 0.00336223865
## avgpapuse     -0.001672964207 0.00021494002 -7.7834002 0.00020742432
## time          -0.003284751584 0.00049440151 -6.6438948 0.00042506202
## age           -0.000014511165 0.00005157966 -0.2813350 0.00003829466
## gender        -0.003093549087 0.00144207998 -2.1451994 0.00132503351
## race.f2       -0.000653666194 0.00157900953 -0.4139723 0.00148369637
## race.f3        0.002527950608 0.00219066428  1.1539653 0.00142549467
## ttt           -0.000010798710 0.00002306147 -0.4682576 0.00001868231
## ahi           -0.000024426372 0.00002460229 -0.9928494 0.00002205395
## bmi           0.000001551333 0.00007475079  0.0207534 0.00007385264
## dxchf         -0.002746870383 0.00405130491 -0.6780211 0.00320801208
## dxchd         0.000946073654 0.00232700448  0.4065629 0.00238733652
## dxdep         0.006671588035 0.00151116503  4.4148640 0.00175926143
## dxhypothy     -0.003081763923 0.00219991126 -1.4008583 0.00186798583
## avgpapuse:time 0.000423731351 0.00011884702  3.5653509 0.00009286132
##
##              Robust z
## (Intercept)  20.57549780
## avgpapuse    -8.06541955
## time         -7.72769948
## age          -0.37893443
## gender       -2.33469499
## race.f2      -0.44056601
## race.f3       1.77338482
## ttt          -0.57801793
## ahi          -1.10757359
## bmi           0.02100579
## dxchf        -0.85625313
## dxchd         0.39628835
## dxdep         3.79226642
## dxhypothy    -1.64977907
## avgpapuse:time 4.56305520
##
## Estimated Scale Parameter: 0.0239395
## Number of Iterations: 5
##
## Working Correlation
##      [,1]      [,2]      [,3]
## [1,] 1.0000000 0.4180023 0.3218412
## [2,] 0.4180023 1.0000000 0.4619553
## [3,] 0.3218412 0.4619553 1.0000000
##
## [[5]]
##
## GEE: GENERALIZED LINEAR MODELS FOR DEPENDENT DATA
## gee S-function, version 4.13 modified 98/01/27 (1998)
##
## Model:
## Link:                      Reciprocal

```

```

## Variance to Mean Relation: Gamma
## Correlation Structure:      Unstructured
##
## Call:
## gee(formula = fosq_global ~ avgpapuse * time + age + gender +
##      race.f + ttt + ahi + bmi + dxchf + dxchd + dxdep + dxhypothy,
##      id = nsrrid, data = x, family = Gamma, corstr = "unstructured")
##
## Summary of Residuals:
##      Min          1Q      Median          3Q          Max
## -9.4777216 -0.8425751  0.4764305  1.4598345  4.8283928
##
##
## Coefficients:
##              Estimate      Naive S.E.      Naive z      Robust S.E.
## (Intercept)   0.070219823778 0.00457725232 15.34104280 0.00371610873
## avgpapuse    -0.001729894533 0.00021497303 -8.04703047 0.00021388113
## time         -0.003132730008 0.00051047145 -6.13693477 0.00044513276
## age          -0.000022691562 0.00005277520 -0.42996642 0.00004018025
## gender       -0.003644644326 0.00147975791 -2.46300040 0.00142357970
## race.f2      -0.000597840337 0.00161244943 -0.37076533 0.00153257183
## race.f3       0.002025295550 0.00223192227  0.90742208 0.00152940424
## ttt          -0.000011864275 0.00002356102 -0.50355530 0.00001849004
## ahi          -0.000023209359 0.00002497752 -0.92920991 0.00002222625
## bmi          -0.000003885453 0.00007496748 -0.05182851 0.00007617172
## dxchf        -0.002246579825 0.00412576473 -0.54452446 0.00317966223
## dxchd         0.000787168561 0.00236908360  0.33226711 0.00234711198
## dxdep         0.006295400648 0.00153598851  4.09859880 0.00176068331
## dxhypothy    -0.003203248558 0.00224818601 -1.42481474 0.00184538522
## avgpapuse:time 0.000431117192 0.00011980232  3.59857126 0.00009433193
##
##              Robust z
## (Intercept)  18.89606274
## avgpapuse    -8.08811182
## time         -7.03774307
## age          -0.56474423
## gender       -2.56019690
## race.f2      -0.39008960
## race.f3       1.32423822
## ttt          -0.64165771
## ahi          -1.04423195
## bmi          -0.05100913
## dxchf        -0.70654669
## dxchd         0.33537751
## dxdep         3.57554401
## dxhypothy    -1.73581566
## avgpapuse:time 4.57021504
##
## Estimated Scale Parameter: 0.0245533
## Number of Iterations: 5
##
## Working Correlation
##      [,1]      [,2]      [,3]
## [1,] 1.0000000 0.4358650 0.3066125
## [2,] 0.4358650 1.0000000 0.4920749
## [3,] 0.3066125 0.4920749 1.0000000
##
## [[6]]
##
## GEE: GENERALIZED LINEAR MODELS FOR DEPENDENT DATA
## gee S-function, version 4.13 modified 98/01/27 (1998)
##

```

```

## Model:
## Link: Reciprocal
## Variance to Mean Relation: Gamma
## Correlation Structure: Unstructured
##
## Call:
## gee(formula = fosq_global ~ avgpapuse * time + age + gender +
##      race.f + ttt + ahi + bmi + dxchf + dxchd + dxdep + dxhypothy,
##      id = nsrrid, data = x, family = Gamma, corstr = "unstructured")
##
## Summary of Residuals:
##      Min      1Q   Median      3Q      Max
## -9.3981562 -0.8594356  0.4229600  1.4645726  4.7786936
##
##
## Coefficients:
##              Estimate   Naive S.E.   Naive z   Robust S.E.
## (Intercept)  0.069794293591 0.00451806116 15.4478417 0.00338053435
## avgpapuse    -0.001602073156 0.00022180756 -7.2228069 0.00022964501
## time        -0.003157808102 0.00048601900 -6.4972935 0.00043735537
## age         -0.000021145895 0.00005220162 -0.4050812 0.00003854492
## gender      -0.003082779510 0.00145659451 -2.1164294 0.00134264507
## race.f2     -0.000861177103 0.00160053892 -0.5380545 0.00151751707
## race.f3     0.002440663338 0.00221031082  1.1042173 0.00145417951
## ttt         -0.000012190468 0.00002325838 -0.5241323 0.00001834895
## ahi         -0.000019141539 0.00002477907 -0.7724881 0.00002231576
## bmi         -0.000007814432 0.00007508201 -0.1040786 0.00007432040
## dxchf      -0.002369056832 0.00408413421 -0.5800634 0.00315325054
## dxchd      0.000862228365 0.00234702192  0.3673712 0.00235732909
## dxdep      0.006397509604 0.00154967438  4.1282928 0.00183254748
## dxhypothy  -0.002821873484 0.00222635759 -1.2674844 0.00181798098
## avgpapuse:time 0.000357256570 0.00011939125  2.9923179 0.00009394192
##              Robust z
## (Intercept)  20.6459354
## avgpapuse    -6.9763030
## time        -7.2202339
## age         -0.5486039
## gender      -2.2960495
## race.f2     -0.5674909
## race.f3     1.6783783
## ttt         -0.6643685
## ahi         -0.8577586
## bmi         -0.1051452
## dxchf      -0.7513062
## dxchd      0.3657650
## dxdep      3.4910471
## dxhypothy  -1.5522019
## avgpapuse:time 3.8029515
##
## Estimated Scale Parameter: 0.0243265
## Number of Iterations: 4
##
## Working Correlation
##      [,1]      [,2]      [,3]
## [1,] 1.0000000 0.4153481 0.3446127
## [2,] 0.4153481 1.0000000 0.4477169
## [3,] 0.3446127 0.4477169 1.0000000
##
## [[7]]
##
## GEE: GENERALIZED LINEAR MODELS FOR DEPENDENT DATA

```

```

## gee S-function, version 4.13 modified 98/01/27 (1998)
##
## Model:
## Link:                      Reciprocal
## Variance to Mean Relation: Gamma
## Correlation Structure:     Unstructured
##
## Call:
## gee(formula = fosq_global ~ avgpapuse * time + age + gender +
##       race.f + ttt + ahi + bmi + dxchf + dxchd + dxdep + dxhypothy,
##       id = nsrrid, data = x, family = Gamma, corstr = "unstructured")
##
## Summary of Residuals:
##           Min           1Q           Median           3Q           Max
## -9.4458266 -0.8386915  0.4771770  1.4704362  4.7120619
##
##
## Coefficients:
##              Estimate      Naive S.E.      Naive z      Robust S.E.      Robust z
## (Intercept)  0.06916796085  0.00451394149  15.3231851  0.00346730322  19.9486334
## avgpapuse    -0.00168232268  0.00021863510  -7.6946597  0.00021694673  -7.7545428
## time         -0.00321272600  0.00049770369  -6.4550979  0.00044112257  -7.2830688
## age          -0.00001863863  0.00005227674  -0.3565378  0.00003937219  -0.4733959
## gender       -0.00318343164  0.00145794947  -2.1834993  0.00134901540  -2.3598186
## race.f2      -0.00058406627  0.00159636989  -0.3658715  0.00149752120  -0.3900220
## race.f3      0.00242898702  0.00222071177  1.0937876  0.00152037939  1.5976190
## ttt          -0.00001022512  0.00002340106  -0.4369514  0.00001893432  -0.5400311
## ahi          -0.00002542832  0.00002468151  -1.0302579  0.00002191529  -1.1603004
## bmi          0.00001381374  0.00007376258  0.1872731  0.00007199533  0.1918700
## dxchf        -0.00236134841  0.00408026536  -0.5787242  0.00315109416  -0.7493741
## dxchd         0.00092877691  0.00234268275  0.3964587  0.00231764564  0.4007416
## dxdep         0.00585734204  0.00151265798  3.8722184  0.00175503244  3.3374551
## dxhypothy    -0.00328654547  0.00221183167  -1.4858931  0.00183330056  -1.7926932
## avgpapuse:time 0.00042255541  0.00012137165  3.4815001  0.00009600633  4.4013287
##
## Estimated Scale Parameter: 0.0244382
## Number of Iterations: 4
##
## Working Correlation
##           [,1]      [,2]      [,3]
## [1,] 1.0000000  0.4394009  0.3158808
## [2,] 0.4394009  1.0000000  0.4340703
## [3,] 0.3158808  0.4340703  1.0000000
##
## [[8]]
##
## GEE: GENERALIZED LINEAR MODELS FOR DEPENDENT DATA
## gee S-function, version 4.13 modified 98/01/27 (1998)
##
## Model:
## Link:                      Reciprocal
## Variance to Mean Relation: Gamma
## Correlation Structure:     Unstructured
##
## Call:
## gee(formula = fosq_global ~ avgpapuse * time + age + gender +
##       race.f + ttt + ahi + bmi + dxchf + dxchd + dxdep + dxhypothy,
##       id = nsrrid, data = x, family = Gamma, corstr = "unstructured")
##
## Summary of Residuals:
##           Min           1Q           Median           3Q           Max

```

```

## -9.5505822 -0.8309815 0.5093538 1.5716772 4.7105476
##
##
## Coefficients:
##              Estimate      Naive S.E.      Naive z      Robust S.E.
## (Intercept)  0.069503564304 0.00451820033 15.3830196 0.00335444206
## avgpapuse    -0.001658031456 0.00022869939 -7.2498290 0.00021722607
## time         -0.003136577847 0.00052439973 -5.9812728 0.00046946217
## age          -0.000020430674 0.00005209313 -0.3921951 0.00003852726
## gender       -0.003020776594 0.00145605045 -2.0746373 0.00132839954
## race.f2      -0.000176103702 0.00159694662 -0.1102753 0.00149867462
## race.f3      0.003739923606 0.00224347511 1.6670226 0.00164298025
## ttt          -0.000001188817 0.00002339983 -0.0508045 0.00001875981
## ahi          -0.000027357202 0.00002473604 -1.1059651 0.00002230578
## bmi          -0.000011353331 0.00007502070 -0.1513360 0.00007262236
## dxchf        -0.002692377355 0.00408573791 -0.6589697 0.00317890040
## dxchd        0.001027881966 0.00234538668 0.4382569 0.00238079217
## dxdep        0.006523648515 0.00152805674 4.2692450 0.00175518408
## dxhypoathy   -0.002171122803 0.00224271016 -0.9680800 0.00179465124
## avgpapuse:time 0.000405593324 0.00012810661 3.1660610 0.00009859610
##              Robust z
## (Intercept)  20.71985831
## avgpapuse    -7.63274635
## time         -6.68121529
## age          -0.53029134
## gender       -2.27399703
## race.f2      -0.11750630
## race.f3      2.27630467
## ttt          -0.06337041
## ahi          -1.22646228
## bmi          -0.15633382
## dxchf        -0.84695241
## dxchd        0.43173948
## dxdep        3.71678878
## dxhypoathy   -1.20977422
## avgpapuse:time 4.11368508
##
## Estimated Scale Parameter: 0.025253
## Number of Iterations: 5
##
## Working Correlation
##           [,1]      [,2]      [,3]
## [1,] 1.0000000 0.4045308 0.2979268
## [2,] 0.4045308 1.0000000 0.4031891
## [3,] 0.2979268 0.4031891 1.0000000
##
## [[9]]
##
## GEE: GENERALIZED LINEAR MODELS FOR DEPENDENT DATA
## gee S-function, version 4.13 modified 98/01/27 (1998)
##
## Model:
## Link:                      Reciprocal
## Variance to Mean Relation: Gamma
## Correlation Structure:     Unstructured
##
## Call:
## gee(formula = fosq_global ~ avgpapuse * time + age + gender +
##      race.f + ttt + ahi + bmi + dxchf + dxchd + dxdep + dxhypoathy,
##      id = nsrrid, data = x, family = Gamma, corstr = "unstructured")
##

```

```

## Summary of Residuals:
##      Min      1Q      Median      3Q      Max
## -9.5107440 -0.8923162  0.4652816  1.5045483  4.7479620
##
##
## Coefficients:
##              Estimate      Naive S.E.      Naive z      Robust S.E.
## (Intercept)  0.06921766657 0.00451368881 15.33505509 0.00348025880
## avgpapuse   -0.00167227521 0.00021777857 -7.67878693 0.00021813213
## time        -0.00300356569 0.00048879287 -6.14486395 0.00042545288
## age         -0.00001877415 0.00005235187 -0.35861461 0.00003900170
## gender      -0.00337535091 0.00145944540 -2.31276272 0.00138523252
## race.f2     -0.00015112948 0.00160874755 -0.09394232 0.00152239485
## race.f3      0.00255178855 0.00221465491  1.15222852 0.00145320749
## ttt         -0.00001075371 0.00002342259 -0.45911690 0.00001871224
## ahi         -0.00002121444 0.00002489076 -0.85230178 0.00002232410
## bmi         0.00000339232 0.00007482238  0.04533830 0.00007462674
## dxchf      -0.00250198455 0.00409156375 -0.61149837 0.00319725352
## dxchd       0.00091507717 0.00235383464  0.38876018 0.00237087317
## dxdep       0.00629131317 0.00152861341  4.11569931 0.00178256689
## dxhypoathy -0.00308402491 0.00223257418 -1.38137624 0.00187942654
## avgpapuse:time 0.00038421617 0.00011762655  3.26640680 0.00009314619
##
##              Robust z
## (Intercept)  19.88865499
## avgpapuse   -7.66634067
## time        -7.05969052
## age         -0.48136733
## gender      -2.43666739
## race.f2     -0.09927088
## race.f3      1.75596986
## ttt         -0.57468835
## ahi         -0.95029297
## bmi         0.04545716
## dxchf      -0.78254181
## dxchd       0.38596631
## dxdep       3.52935600
## dxhypoathy -1.64093933
## avgpapuse:time 4.12487286
##
## Estimated Scale Parameter: 0.0243438
## Number of Iterations: 5
##
## Working Correlation
##      [,1]      [,2]      [,3]
## [1,] 1.0000000 0.4124194 0.3115483
## [2,] 0.4124194 1.0000000 0.4900941
## [3,] 0.3115483 0.4900941 1.0000000
##
## [[10]]
##
## GEE: GENERALIZED LINEAR MODELS FOR DEPENDENT DATA
## gee S-function, version 4.13 modified 98/01/27 (1998)
##
## Model:
## Link:                      Reciprocal
## Variance to Mean Relation: Gamma
## Correlation Structure:     Unstructured
##
## Call:
## gee(formula = fosq_global ~ avgpapuse * time + age + gender +
##      race.f + ttt + ahi + bmi + dxchf + dxchd + dxdep + dxhypoathy,

```

```

##      id = nsrrid, data = x, family = Gamma, corstr = "unstructured")
##
## Summary of Residuals:
##      Min      1Q      Median      3Q      Max
## -9.4317711 -0.8814199  0.4556040  1.4963925  4.7867754
##
##
## Coefficients:
##              Estimate      Naive S.E.      Naive z      Robust S.E.
## (Intercept)  0.069888882447 0.00455193602 15.35366098 0.00351545261
## avgpapuse   -0.001694609053 0.00021430339 -7.90752333 0.00021774070
## time        -0.002999127720 0.00047877805 -6.26412952 0.00041450152
## age         -0.000014702519 0.00005253205 -0.27987713 0.00003929587
## gender      -0.003528667572 0.00146583272 -2.40727849 0.00137198945
## race.f2     -0.000533038912 0.00160434614 -0.33224683 0.00151025675
## race.f3      0.002511712523 0.00223375306  1.12443608 0.00152110077
## ttt         -0.000016917643 0.00002343552 -0.72188031 0.00001829796
## ahi         -0.000022208640 0.00002488419 -0.89247974 0.00002226218
## bmi         -0.000004003218 0.00007568402 -0.05289383 0.00007558653
## dxchf       -0.002337799140 0.00410522473 -0.56946922 0.00307856629
## dxchd        0.000847236237 0.00235718753  0.35942674 0.00229861912
## dxdep        0.006077827393 0.00152757184  3.97875061 0.00177592937
## dxhypoathy  -0.003502276626 0.00223841968 -1.56462019 0.00182629021
## avgpapuse:time 0.000370303690 0.00011752281  3.15090901 0.00009044149
##
##              Robust z
## (Intercept)  19.88047917
## avgpapuse   -7.78269303
## time        -7.23550477
## age         -0.37414923
## gender      -2.57193491
## race.f2     -0.35294589
## race.f3      1.65124664
## ttt         -0.92456465
## ahi         -0.99759495
## bmi         -0.05296205
## dxchf       -0.75937918
## dxchd        0.36858487
## dxdep        3.42233622
## dxhypoathy  -1.91769993
## avgpapuse:time 4.09440076
##
## Estimated Scale Parameter: 0.024201
## Number of Iterations: 4
##
## Working Correlation
##      [,1]      [,2]      [,3]
## [1,] 1.0000000 0.4441127 0.3357410
## [2,] 0.4441127 1.0000000 0.4704698
## [3,] 0.3357410 0.4704698 1.0000000

```

## 6 Linear mixed effects model lme



```
lme.fit1 = map(
  complete.long, function(x) {
    lme(fosq_global~avgpapuse * time +
      age + gender + race.f +
      ttt + ahi + bmi ,
      random = ~1|nsrrid/time,
      data = x,
      #correlation = corSymm(0.7, ~1|nsrrid),
      method = "ML",
      na.action = na.exclude, #trying to choose correlation structure in an overeleborate model
      cor = corAR1() )#can also do corARMA and corCompSymm and corSymm (general correlation ma
      trix)
    }
  )

lme.fit2 = map(
  complete.long, function(x) {
    lme(fosq_global~avgpapuse * time +
      age + gender + race.f +
      ttt + ahi + bmi +
      dxchf + dxchd + dxdep + dxhypothy,
      random = ~1|nsrrid/time,
      data = x,
      #correlation = corAR1(value = 0.7, form = ~time|nsrrid),
      method = "ML",
      na.action = na.exclude,
      cor = corAR1() ) #trying to choose correlation structure in an overeleborate model
    }
  )

#lme.fit1.update <- map(lme.fit1, function(x) {update(x, correlation = corAR1())})

map(lme.fit1, function(x) {
  summary(x)
})
```

```

## [[1]]
## Linear mixed-effects model fit by maximum likelihood
##   Data: x
##       AIC      BIC    logLik
##  2121.29 2183.42 -1045.645
##
## Random effects:
## Formula: ~1 | nsrrid
##          (Intercept)
## StdDev:    1.729706
##
## Formula: ~1 | time %in% nsrrid
##          (Intercept) Residual
## StdDev:    1.699842 0.7303725
##
## Correlation Structure: AR(1)
## Formula: ~1 | nsrrid/time
## Parameter estimate(s):
## Phi
##    0
## Fixed effects: fosq_global ~ avgpapuse * time + age + gender + race.f + ttt +      ahi + bmi
##
##              Value Std.Error   DF   t-value p-value
## (Intercept)  14.338304 1.2325933 306  11.632632  0.0000
## avgpapuse     0.434681 0.0615150 306   7.066252  0.0000
## time          0.771133 0.1314862 306   5.864744  0.0000
## age           0.000832 0.0142043 148   0.058588  0.9534
## gender        1.065225 0.3813125 148   2.793576  0.0059
## race.f2       0.105435 0.4539669 148   0.232252  0.8167
## race.f3      -0.640778 0.6244463 148  -1.026154  0.3065
## ttt           0.004046 0.0066537 148   0.608103  0.5441
## ahi           0.006451 0.0070502 148   0.914968  0.3617
## bmi          -0.009987 0.0200363 306  -0.498453  0.6185
## avgpapuse:time -0.081315 0.0342406 306  -2.374817  0.0182
## Correlation:
##          (Intr) avgpaps time   age   gender rac.f2 rac.f3 ttt   ahi
## avgpapuse -0.047
## time      -0.058  0.103
## age       -0.698 -0.022  0.024
## gender    -0.414 -0.007 -0.022  0.073
## race.f2   -0.061  0.035 -0.077  0.107 -0.126
## race.f3   -0.103 -0.001  0.006  0.141 -0.186  0.183
## ttt       -0.192  0.029 -0.097  0.029  0.120 -0.078  0.053
## ahi       -0.109 -0.023  0.066  0.066 -0.197  0.240  0.123  0.076
## bmi       -0.679  0.006  0.012  0.136  0.352 -0.160 -0.057 -0.066 -0.285
## avgpapuse:time 0.040 -0.613 -0.728 -0.010  0.025  0.054 -0.005  0.076 -0.051
##
##          bmi
## avgpapuse
## time
## age
## gender
## race.f2
## race.f3
## ttt
## ahi
## bmi
## avgpapuse:time -0.011
##
## Standardized Within-Group Residuals:
##          Min           Q1           Med           Q3           Max
## -1.53773717 -0.14320660  0.04699394  0.20321564  0.78348218

```

```

##
## Number of Observations: 465
## Number of Groups:
##          nsrrid time %in% nsrrid
##          155      465
##
## [[2]]
## Linear mixed-effects model fit by maximum likelihood
##   Data: x
##       AIC      BIC    logLik
## 2111.726 2173.856 -1040.863
##
## Random effects:
## Formula: ~1 | nsrrid
##          (Intercept)
## StdDev:    1.730407
##
## Formula: ~1 | time %in% nsrrid
##          (Intercept) Residual
## StdDev:    1.675688 0.7228127
##
## Correlation Structure: AR(1)
## Formula: ~1 | nsrrid/time
## Parameter estimate(s):
## Phi
## 0
## Fixed effects: fosq_global ~ avgpapuse * time + age + gender + race.f + ttt +      ahi + bmi
##              Value Std.Error DF   t-value p-value
## (Intercept)  14.237001 1.2288690 306 11.585451 0.0000
## avgpapuse    0.439832 0.0606831 306  7.248010 0.0000
## time         0.818725 0.1316934 306  6.216901 0.0000
## age          0.000505 0.0141796 148  0.035636 0.9716
## gender       1.117059 0.3802507 148  2.937689 0.0038
## race.f2      0.095211 0.4520340 148  0.210627 0.8335
## race.f3     -0.674541 0.6220411 148 -1.084399 0.2800
## ttt         0.003256 0.0066280 148  0.491271 0.6240
## ahi         0.006066 0.0070095 148  0.865463 0.3882
## bmi        -0.007009 0.0197275 306 -0.355276 0.7226
## avgpapuse:time -0.092002 0.0337047 306 -2.729657 0.0067
## Correlation:
##          (Intr) avgpps time   age   gender rac.f2 rac.f3 ttt   ahi
## avgpapuse -0.046
## time      -0.056  0.099
## age       -0.705 -0.024  0.021
## gender    -0.415 -0.008 -0.023  0.077
## race.f2   -0.057  0.034 -0.062  0.105 -0.129
## race.f3   -0.108 -0.001  0.006  0.142 -0.183  0.182
## ttt       -0.190  0.027 -0.094  0.028  0.118 -0.080  0.052
## ahi       -0.114 -0.024  0.068  0.064 -0.195  0.242  0.121  0.077
## bmi       -0.679  0.007  0.009  0.148  0.353 -0.165 -0.049 -0.069 -0.277
## avgpapuse:time 0.039 -0.612 -0.731 -0.007  0.025  0.040 -0.005  0.073 -0.051
##          bmi
## avgpapuse
## time
## age
## gender
## race.f2
## race.f3
## ttt
## ahi
## bmi

```

```

## avgpapuse:time -0.011
##
## Standardized Within-Group Residuals:
##           Min           Q1           Med           Q3           Max
## -1.56266709 -0.14863839  0.04723365  0.20307743  0.80143460
##
## Number of Observations: 465
## Number of Groups:
##           nsrrid time %in% nsrrid
##           155           465
##
## [[3]]
## Linear mixed-effects model fit by maximum likelihood
##   Data: x
##       AIC      BIC    logLik
## 2105.451 2167.582 -1037.726
##
## Random effects:
## Formula: ~1 | nsrrid
##           (Intercept)
## StdDev:    1.741869
##
## Formula: ~1 | time %in% nsrrid
##           (Intercept) Residual
## StdDev:    1.656006 0.7177393
##
## Correlation Structure: AR(1)
## Formula: ~1 | nsrrid/time
## Parameter estimate(s):
## Phi
## 0
## Fixed effects: fosq_global ~ avgpapuse * time + age + gender + race.f + ttt + ahi + bmi
##           Value Std.Error DF  t-value p-value
## (Intercept) 14.220671 1.2287312 306 11.573459 0.0000
## avgpapuse    0.448493 0.0603776 306  7.428137 0.0000
## time         0.827412 0.1212366 306  6.824773 0.0000
## age          0.001535 0.0141873 148  0.108165 0.9140
## gender       1.166269 0.3797845 148  3.070871 0.0025
## race.f2      0.191047 0.4530643 148  0.421677 0.6739
## race.f3     -0.679632 0.6232175 148 -1.090521 0.2773
## ttt          0.004523 0.0066409 148  0.681144 0.4968
## ahi          0.005993 0.0070406 148  0.851253 0.3960
## bmi         -0.010273 0.0199583 306 -0.514716 0.6071
## avgpapuse:time -0.092429 0.0326376 306 -2.831972 0.0049
## Correlation:
##           (Intr) avgpps time  age  gender rac.f2 rac.f3 ttt  ahi
## avgpapuse -0.049
## time      -0.065  0.111
## age       -0.700 -0.021  0.029
## gender    -0.410 -0.005 -0.017  0.072
## race.f2   -0.059  0.034 -0.068  0.107 -0.127
## race.f3   -0.110 -0.001  0.013  0.143 -0.183  0.181
## ttt       -0.191  0.036 -0.088  0.028  0.119 -0.079  0.051
## ahi       -0.112 -0.021  0.073  0.067 -0.195  0.240  0.121  0.076
## bmi       -0.678  0.005  0.009  0.137  0.346 -0.162 -0.047 -0.068 -0.283
## avgpapuse:time 0.048 -0.634 -0.705 -0.016  0.019  0.046 -0.012  0.064 -0.058
##           bmi
## avgpapuse
## time
## age
## gender

```

```

## race.f2
## race.f3
## ttt
## ahi
## bmi
## avgpapuse:time -0.011
##
## Standardized Within-Group Residuals:
##           Min           Q1           Med           Q3           Max
## -1.57382530 -0.14354399  0.04753157  0.20246013  0.81833168
##
## Number of Observations: 465
## Number of Groups:
##           nsrrid time %in% nsrrid
##           155           465
##
## [[4]]
## Linear mixed-effects model fit by maximum likelihood
##   Data: x
##           AIC           BIC           logLik
##   2107.274 2169.405 -1038.637
##
## Random effects:
## Formula: ~1 | nsrrid
##           (Intercept)
## StdDev:           1.727199
##
## Formula: ~1 | time %in% nsrrid
##           (Intercept) Residual
## StdDev:           1.665837 0.7193248
##
## Correlation Structure: AR(1)
## Formula: ~1 | nsrrid/time
## Parameter estimate(s):
## Phi
## 0
## Fixed effects: fosq_global ~ avgpapuse * time + age + gender + race.f + ttt + ahi + bmi
##           Value Std.Error DF t-value p-value
## (Intercept) 14.383964 1.2247158 306 11.744736 0.0000
## avgpapuse 0.442507 0.0603272 306 7.335122 0.0000
## time 0.893573 0.1284515 306 6.956502 0.0000
## age -0.000142 0.0141119 148 -0.010044 0.9920
## gender 1.080410 0.3784442 148 2.854872 0.0049
## race.f2 0.257208 0.4505276 148 0.570904 0.5689
## race.f3 -0.647278 0.6204171 148 -1.043295 0.2985
## ttt 0.003899 0.0066188 148 0.589145 0.5567
## ahi 0.006720 0.0070034 148 0.959501 0.3389
## bmi -0.011785 0.0199648 306 -0.590284 0.5554
## avgpapuse:time -0.104175 0.0331265 306 -3.144762 0.0018
## Correlation:
##           (Intr) avgpps time age gender rac.f2 rac.f3 ttt ahi
## avgpapuse -0.042
## time -0.056 0.104
## age -0.698 -0.026 0.018
## gender -0.412 -0.004 -0.022 0.072
## race.f2 -0.061 0.034 -0.066 0.109 -0.126
## race.f3 -0.105 -0.003 0.009 0.142 -0.185 0.182
## ttt -0.192 0.032 -0.103 0.029 0.120 -0.079 0.052
## ahi -0.108 -0.023 0.061 0.066 -0.196 0.242 0.123 0.076
## bmi -0.679 0.002 0.016 0.135 0.349 -0.161 -0.053 -0.067 -0.285
## avgpapuse:time 0.036 -0.623 -0.722 -0.002 0.024 0.043 -0.007 0.079 -0.045

```

```
##          bmi
## avgpapuse
## time
## age
## gender
## race.f2
## race.f3
## ttt
## ahi
## bmi
## avgpapuse:time -0.013
##
## Standardized Within-Group Residuals:
##          Min          Q1          Med          Q3          Max
## -1.56969152 -0.13789286  0.05013644  0.20027639  0.81595967
##
## Number of Observations: 465
## Number of Groups:
##          nsrrid time %in% nsrrid
##          155          465
##
## [[5]]
## Linear mixed-effects model fit by maximum likelihood
## Data: x
##          AIC          BIC          logLik
## 2116.818 2178.949 -1043.409
##
## Random effects:
## Formula: ~1 | nsrrid
##          (Intercept)
## StdDev: 1.742541
##
## Formula: ~1 | time %in% nsrrid
##          (Intercept) Residual
## StdDev: 1.683933 0.7267456
##
## Correlation Structure: AR(1)
## Formula: ~1 | nsrrid/time
## Parameter estimate(s):
## Phi
## 0
## Fixed effects: fosq_global ~ avgpapuse * time + age + gender + race.f + ttt + ahi + bmi
##          Value Std.Error DF t-value p-value
## (Intercept) 14.087109 1.2327413 306 11.427466 0.0000
## avgpapuse 0.456118 0.0620116 306 7.355371 0.0000
## time 0.868911 0.1318316 306 6.591069 0.0000
## age 0.002055 0.0142530 148 0.144203 0.8855
## gender 1.184469 0.3819494 148 3.101114 0.0023
## race.f2 0.216876 0.4549368 148 0.476718 0.6343
## race.f3 -0.656824 0.6261312 148 -1.049019 0.2959
## ttt 0.004763 0.0066729 148 0.713772 0.4765
## ahi 0.007553 0.0070614 148 1.069613 0.2865
## bmi -0.009768 0.0198932 306 -0.491036 0.6238
## avgpapuse:time -0.109284 0.0338387 306 -3.229561 0.0014
## Correlation:
##          (Intr) avgpaps time age gender rac.f2 rac.f3 ttt ahi
## avgpapuse -0.049
## time -0.051 0.089
## age -0.703 -0.022 0.011
## gender -0.412 -0.001 -0.019 0.074
## race.f2 -0.060 0.033 -0.066 0.108 -0.128
```

```
## race.f3      -0.108 -0.004  0.010  0.142 -0.184  0.182
## ttt         -0.192  0.040 -0.092  0.030  0.119 -0.080  0.052
## ahi         -0.112 -0.023  0.061  0.064 -0.195  0.243  0.122  0.078
## bmi         -0.677  0.006  0.012  0.141  0.349 -0.164 -0.050 -0.069 -0.282
## avgpapuse:time 0.037 -0.613 -0.724  0.002  0.019  0.044 -0.007  0.065 -0.045
##           bmi
## avgpapuse
## time
## age
## gender
## race.f2
## race.f3
## ttt
## ahi
## bmi
## avgpapuse:time -0.012
##
## Standardized Within-Group Residuals:
##           Min           Q1           Med           Q3           Max
## -1.55933490 -0.12370382  0.05083833  0.19837287  0.86413502
##
## Number of Observations: 465
## Number of Groups:
##           nsrrid time %in% nsrrid
##           155           465
##
## [[6]]
## Linear mixed-effects model fit by maximum likelihood
##   Data: x
##           AIC           BIC           logLik
## 2117.747 2179.877 -1043.873
##
## Random effects:
## Formula: ~1 | nsrrid
##           (Intercept)
## StdDev: 1.721076
##
## Formula: ~1 | time %in% nsrrid
##           (Intercept) Residual
## StdDev: 1.694129 0.7276183
##
## Correlation Structure: AR(1)
## Formula: ~1 | nsrrid/time
## Parameter estimate(s):
## Phi
## 0
## Fixed effects: fosq_global ~ avgpapuse * time + age + gender + race.f + ttt + ahi + bmi
##           Value Std.Error DF t-value p-value
## (Intercept) 14.293510 1.2278261 306 11.641315 0.0000
## avgpapuse 0.417419 0.0616378 306 6.772124 0.0000
## time 0.855660 0.1276287 306 6.704296 0.0000
## age 0.000762 0.0141497 148 0.053879 0.9571
## gender 1.096986 0.3792810 148 2.892278 0.0044
## race.f2 0.319407 0.4524735 148 0.705913 0.4814
## race.f3 -0.630492 0.6213282 148 -1.014748 0.3119
## ttt 0.004149 0.0066228 148 0.626459 0.5320
## ahi 0.006210 0.0070165 148 0.885075 0.3776
## bmi -0.010816 0.0199103 306 -0.543237 0.5874
## avgpapuse:time -0.083671 0.0333811 306 -2.506544 0.0127
## Correlation:
##           (Intr) avgpps time age gender rac.f2 rac.f3 ttt ahi
```

```

## avgpapuse      -0.051
## time           -0.059  0.096
## age            -0.700 -0.020  0.027
## gender         -0.413 -0.006 -0.018  0.074
## race.f2        -0.058  0.037 -0.082  0.105 -0.128
## race.f3        -0.109  0.000  0.005  0.142 -0.183  0.181
## ttt           -0.192  0.038 -0.093  0.028  0.119 -0.077  0.052
## ahi            -0.109 -0.022  0.065  0.065 -0.196  0.240  0.121  0.076
## bmi            -0.679  0.006  0.008  0.140  0.350 -0.163 -0.048 -0.065 -0.285
## avgpapuse:time 0.044 -0.622 -0.713 -0.015  0.020  0.057 -0.004  0.067 -0.050
##
##           bmi
## avgpapuse
## time
## age
## gender
## race.f2
## race.f3
## ttt
## ahi
## bmi
## avgpapuse:time -0.010
##
## Standardized Within-Group Residuals:
##           Min           Q1           Med           Q3           Max
## -1.53735865 -0.12778297  0.04900074  0.20416463  0.79446394
##
## Number of Observations: 465
## Number of Groups:
##           nsrrid time %in% nsrrid
##           155           465
##
## [[7]]
## Linear mixed-effects model fit by maximum likelihood
## Data: x
##           AIC           BIC           logLik
## 2121.102 2183.233 -1045.551
##
## Random effects:
## Formula: ~1 | nsrrid
##           (Intercept)
## StdDev: 1.696022
##
## Formula: ~1 | time %in% nsrrid
##           (Intercept) Residual
## StdDev: 1.711784 0.7304466
##
## Correlation Structure: AR(1)
## Formula: ~1 | nsrrid/time
## Parameter estimate(s):
## Phi
## 0
## Fixed effects: fosq_global ~ avgpapuse * time + age + gender + race.f + ttt + ahi + bmi
##
##           Value Std.Error DF t-value p-value
## (Intercept) 14.307880 1.2122156 306 11.803082 0.0000
## avgpapuse    0.438522 0.0625140 306 7.014781 0.0000
## time         0.863409 0.1289987 306 6.693164 0.0000
## age          0.001739 0.0140448 148 0.123799 0.9016
## gender       1.082708 0.3758336 148 2.880819 0.0046
## race.f2      0.225592 0.4484410 148 0.503059 0.6157
## race.f3     -0.725822 0.6166947 148 -1.176955 0.2411
## ttt          0.003972 0.0065801 148 0.603635 0.5470

```



```

## ahi          0.007508 0.0069550 148  1.079537  0.2821
## bmi          -0.012477 0.0195169 306 -0.639273  0.5231
## avgpapuse:time -0.101397 0.0338832 306 -2.992535  0.0030
## Correlation:
##          (Intr) avgpps time   age   gender rac.f2 rac.f3 ttt   ahi
## avgpapuse   -0.050
## time        -0.061  0.103
## age         -0.704 -0.022  0.031
## gender      -0.410 -0.004 -0.023  0.074
## race.f2     -0.055  0.032 -0.064  0.105 -0.129
## race.f3     -0.105 -0.003  0.011  0.141 -0.185  0.182
## ttt         -0.190  0.041 -0.098  0.026  0.119 -0.078  0.052
## ahi         -0.115 -0.023  0.069  0.066 -0.194  0.243  0.123  0.076
## bmi         -0.675  0.004  0.004  0.142  0.347 -0.170 -0.055 -0.070 -0.280
## avgpapuse:time 0.043 -0.628 -0.713 -0.017  0.025  0.042 -0.009  0.070 -0.053
##          bmi
## avgpapuse
## time
## age
## gender
## race.f2
## race.f3
## ttt
## ahi
## bmi
## avgpapuse:time -0.004
##
## Standardized Within-Group Residuals:
##          Min          Q1          Med          Q3          Max
## -1.53369743 -0.14029317  0.05274616  0.20110398  0.77055495
##
## Number of Observations: 465
## Number of Groups:
##          nsrrid time %in% nsrrid
##          155          465
##
## [[8]]
## Linear mixed-effects model fit by maximum likelihood
## Data: x
##          AIC          BIC          logLik
## 2147.645 2209.776 -1058.823
##
## Random effects:
## Formula: ~1 | nsrrid
##          (Intercept)
## StdDev: 1.688403
##
## Formula: ~1 | time %in% nsrrid
##          (Intercept) Residual
## StdDev: 1.782428 0.7518842
##
## Correlation Structure: AR(1)
## Formula: ~1 | nsrrid/time
## Parameter estimate(s):
## Phi
## 0
## Fixed effects: fosq_global ~ avgpapuse * time + age + gender + race.f + ttt + ahi + bmi
##          Value Std.Error DF t-value p-value
## (Intercept) 14.371384 1.2265120 306 11.717279 0.0000
## avgpapuse 0.436362 0.0647078 306 6.743583 0.0000
## time 0.833547 0.1365619 306 6.103801 0.0000

```

```

## age          0.000754 0.0141442 148  0.053291  0.9576
## gender       1.106845 0.3792180 148  2.918757  0.0041
## race.f2      0.172007 0.4507597 148  0.381593  0.7033
## race.f3     -0.911774 0.6216791 148 -1.466632  0.1446
## ttt          0.001352 0.0066225 148  0.204142  0.8385
## ahi          0.007604 0.0070131 148  1.084281  0.2800
## bmi         -0.010719 0.0198947 306 -0.538807  0.5904
## avgpapuse:time -0.096837 0.0356377 306 -2.717267  0.0070
## Correlation:
##          (Intr) avgpps time  age  gender rac.f2 rac.f3 ttt  ahi
## avgpapuse -0.047
## time      -0.072  0.109
## age       -0.699 -0.025  0.021
## gender    -0.412 -0.009 -0.010  0.073
## race.f2   -0.065  0.034 -0.058  0.109 -0.126
## race.f3   -0.106 -0.002  0.004  0.142 -0.184  0.182
## ttt       -0.190  0.031 -0.092  0.029  0.118 -0.082  0.053
## ahi       -0.113 -0.025  0.064  0.067 -0.194  0.240  0.122  0.077
## bmi       -0.678  0.005  0.026  0.136  0.349 -0.156 -0.052 -0.069 -0.281
## avgpapuse:time 0.050 -0.625 -0.723 -0.005  0.016  0.036 -0.003  0.068 -0.048
##          bmi
## avgpapuse
## time
## age
## gender
## race.f2
## race.f3
## ttt
## ahi
## bmi
## avgpapuse:time -0.022
##
## Standardized Within-Group Residuals:
##          Min          Q1          Med          Q3          Max
## -1.47614154 -0.13063779  0.04993646  0.20160662  0.74177399
##
## Number of Observations: 465
## Number of Groups:
##          nsrrid time %in% nsrrid
##          155          465
##
## [[9]]
## Linear mixed-effects model fit by maximum likelihood
## Data: x
##          AIC          BIC          logLik
## 2113.179 2175.31 -1041.59
##
## Random effects:
## Formula: ~1 | nsrrid
##          (Intercept)
## StdDev: 1.731508
##
## Formula: ~1 | time %in% nsrrid
##          (Intercept) Residual
## StdDev: 1.678917 0.7239085
##
## Correlation Structure: AR(1)
## Formula: ~1 | nsrrid/time
## Parameter estimate(s):
## Phi
## 0

```

```

## Fixed effects:  fosq_global ~ avgpapuse * time + age + gender + race.f + ttt +      ahi + bmi
##
##              Value Std.Error   DF   t-value p-value
## (Intercept)  14.471688 1.2239284 306 11.823966  0.0000
## avgpapuse     0.443804 0.0616632 306  7.197225  0.0000
## time          0.822849 0.1261677 306  6.521867  0.0000
## age           0.000503 0.0141744 148  0.035521  0.9717
## gender        1.102337 0.3789819 148  2.908680  0.0042
## race.f2       0.121844 0.4524302 148  0.269310  0.7881
## race.f3      -0.669043 0.6226347 148 -1.074535  0.2843
## ttt           0.004128 0.0066386 148  0.621852  0.5350
## ahi           0.006218 0.0070235 148  0.885314  0.3774
## bmi          -0.013505 0.0198234 306 -0.681280  0.4962
## avgpapuse:time -0.093868 0.0332021 306 -2.827171  0.0050
## Correlation:
##              (Intr) avgpaps time   age   gender rac.f2 rac.f3 ttt   ahi
## avgpapuse    -0.048
## time         -0.063  0.095
## age          -0.701 -0.022  0.029
## gender       -0.408 -0.005 -0.016  0.072
## race.f2      -0.062  0.032 -0.072  0.107 -0.126
## race.f3      -0.110 -0.003  0.008  0.143 -0.183  0.181
## ttt          -0.189  0.039 -0.091  0.027  0.118 -0.078  0.052
## ahi          -0.114 -0.024  0.064  0.067 -0.193  0.240  0.121  0.078
## bmi          -0.675  0.005  0.011  0.137  0.343 -0.159 -0.048 -0.073 -0.281
## avgpapuse:time 0.044 -0.624 -0.710 -0.015  0.019  0.049 -0.007  0.065 -0.049
##
##              bmi
## avgpapuse
## time
## age
## gender
## race.f2
## race.f3
## ttt
## ahi
## bmi
## avgpapuse:time -0.008
##
## Standardized Within-Group Residuals:
##              Min           Q1           Med           Q3           Max
## -1.55935268 -0.13857463  0.05017364  0.19981881  0.79798614
##
## Number of Observations: 465
## Number of Groups:
##              nsrrid time %in% nsrrid
##              155           465
##
## [[10]]
## Linear mixed-effects model fit by maximum likelihood
##   Data: x
##       AIC      BIC    logLik
## 2106.558 2168.688 -1038.279
##
## Random effects:
## Formula: ~1 | nsrrid
##          (Intercept)
## StdDev:    1.73434
##
## Formula: ~1 | time %in% nsrrid
##          (Intercept) Residual
## StdDev:    1.661477 0.7186675
##

```

```

## Correlation Structure: AR(1)
## Formula: ~1 | nsrrid/time
## Parameter estimate(s):
## Phi
## 0
## Fixed effects: fosq_global ~ avgpapuse * time + age + gender + race.f + ttt + ahi + bmi
##
## Value Std.Error DF t-value p-value
## (Intercept) 14.185952 1.2279889 306 11.552183 0.0000
## avgpapuse 0.442934 0.0608244 306 7.282173 0.0000
## time 0.816243 0.1232222 306 6.624158 0.0000
## age 0.001295 0.0141578 148 0.091466 0.9272
## gender 1.178090 0.3791851 148 3.106900 0.0023
## race.f2 0.234344 0.4514212 148 0.519125 0.6044
## race.f3 -0.753944 0.6217421 148 -1.212631 0.2272
## ttt 0.004638 0.0066256 148 0.699992 0.4850
## ahi 0.006875 0.0070238 148 0.978800 0.3293
## bmi -0.010291 0.0199798 306 -0.515093 0.6069
## avgpapuse:time -0.088987 0.0328606 306 -2.708013 0.0071
## Correlation:
## (Intr) avgpps time age gender rac.f2 rac.f3 ttt ahi
## avgpapuse -0.048
## time -0.064 0.103
## age -0.699 -0.022 0.033
## gender -0.411 -0.006 -0.023 0.072
## race.f2 -0.059 0.030 -0.060 0.107 -0.127
## race.f3 -0.109 -0.002 0.009 0.143 -0.183 0.181
## ttt -0.190 0.036 -0.090 0.027 0.120 -0.081 0.052
## ahi -0.110 -0.024 0.069 0.067 -0.196 0.242 0.122 0.076
## bmi -0.079 0.006 0.007 0.137 0.348 -0.161 -0.048 -0.067 -0.284
## avgpapuse:time 0.046 -0.628 -0.708 -0.020 0.026 0.041 -0.008 0.065 -0.053
## bmi
## avgpapuse
## time
## age
## gender
## race.f2
## race.f3
## ttt
## ahi
## bmi
## avgpapuse:time -0.008
##
## Standardized Within-Group Residuals:
## Min Q1 Med Q3 Max
## -1.57068144 -0.14031067 0.04442545 0.20141262 0.81212840
##
## Number of Observations: 465
## Number of Groups:
## nsrrid time %in% nsrrid
## 155 465

```

```

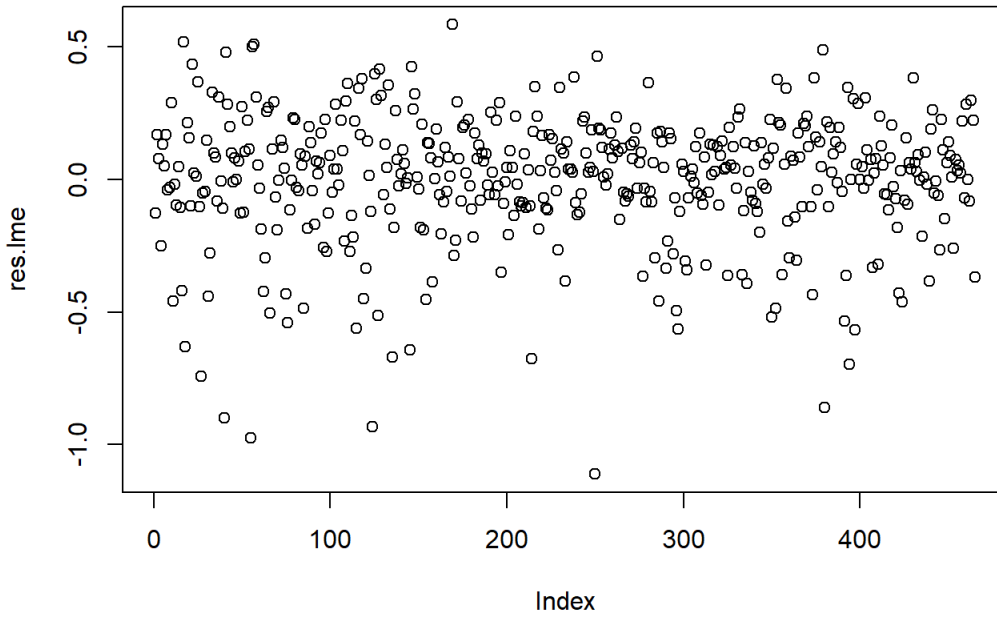
map2(lme.fit1, lme.fit2, function(x,y) {
  anova(x,y)
})

```

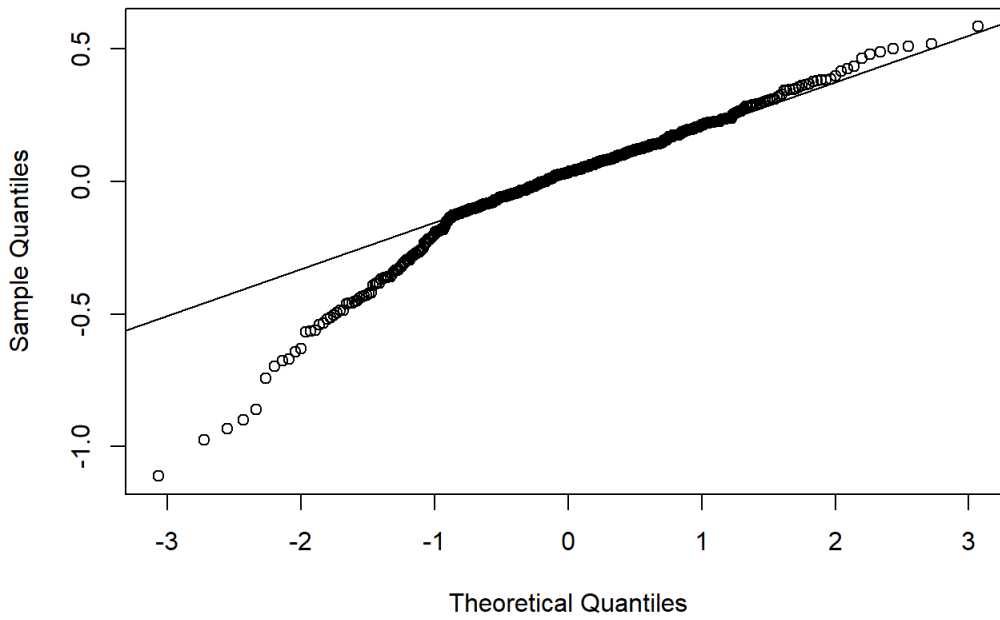
```
## [[1]]
##   Model df      AIC      BIC    logLik  Test  L.Ratio p-value
## x     1  15 2121.290 2183.420 -1045.645
## y     2  19 2109.095 2187.793 -1035.547 1 vs 2 20.19521 0.0005
##
## [[2]]
##   Model df      AIC      BIC    logLik  Test  L.Ratio p-value
## x     1  15 2111.726 2173.856 -1040.863
## y     2  19 2099.435 2178.134 -1030.718 1 vs 2 20.29061 0.0004
##
## [[3]]
##   Model df      AIC      BIC    logLik  Test  L.Ratio p-value
## x     1  15 2105.451 2167.582 -1037.726
## y     2  19 2092.508 2171.206 -1027.254 1 vs 2 20.94354 0.0003
##
## [[4]]
##   Model df      AIC      BIC    logLik  Test  L.Ratio p-value
## x     1  15 2107.274 2169.405 -1038.637
## y     2  19 2092.156 2170.855 -1027.078 1 vs 2 23.11831 0.0001
##
## [[5]]
##   Model df      AIC      BIC    logLik  Test  L.Ratio p-value
## x     1  15 2116.818 2178.949 -1043.409
## y     2  19 2104.778 2183.477 -1033.389 1 vs 2 20.0399 0.0005
##
## [[6]]
##   Model df      AIC      BIC    logLik  Test  L.Ratio p-value
## x     1  15 2117.747 2179.877 -1043.873
## y     2  19 2105.257 2183.956 -1033.629 1 vs 2 20.4892 0.0004
##
## [[7]]
##   Model df      AIC      BIC    logLik  Test  L.Ratio p-value
## x     1  15 2121.102 2183.233 -1045.551
## y     2  19 2110.320 2189.018 -1036.160 1 vs 2 18.7828 0.0009
##
## [[8]]
##   Model df      AIC      BIC    logLik  Test  L.Ratio p-value
## x     1  15 2147.645 2209.776 -1058.823
## y     2  19 2134.532 2213.231 -1048.266 1 vs 2 21.11315 0.0003
##
## [[9]]
##   Model df      AIC      BIC    logLik  Test  L.Ratio p-value
## x     1  15 2113.180 2175.310 -1041.590
## y     2  19 2100.654 2179.352 -1031.327 1 vs 2 20.52572 0.0004
##
## [[10]]
##   Model df      AIC      BIC    logLik  Test  L.Ratio p-value
## x     1  15 2106.557 2168.688 -1038.279
## y     2  19 2095.157 2173.856 -1028.579 1 vs 2 19.40022 0.0007
```

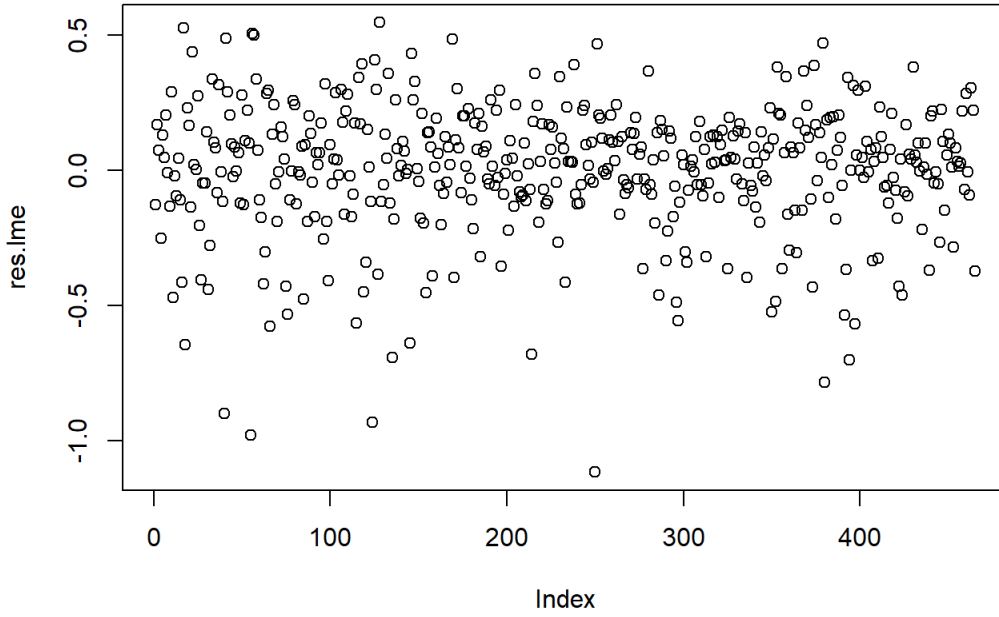
Now the real meat of the operation: residuals

```
map(lme.fit2, function(x) {
  res.lme = residuals(x)
  plot(res.lme)
  qqnorm(res.lme)
  qqline(res.lme)
  plot(x)
})
```

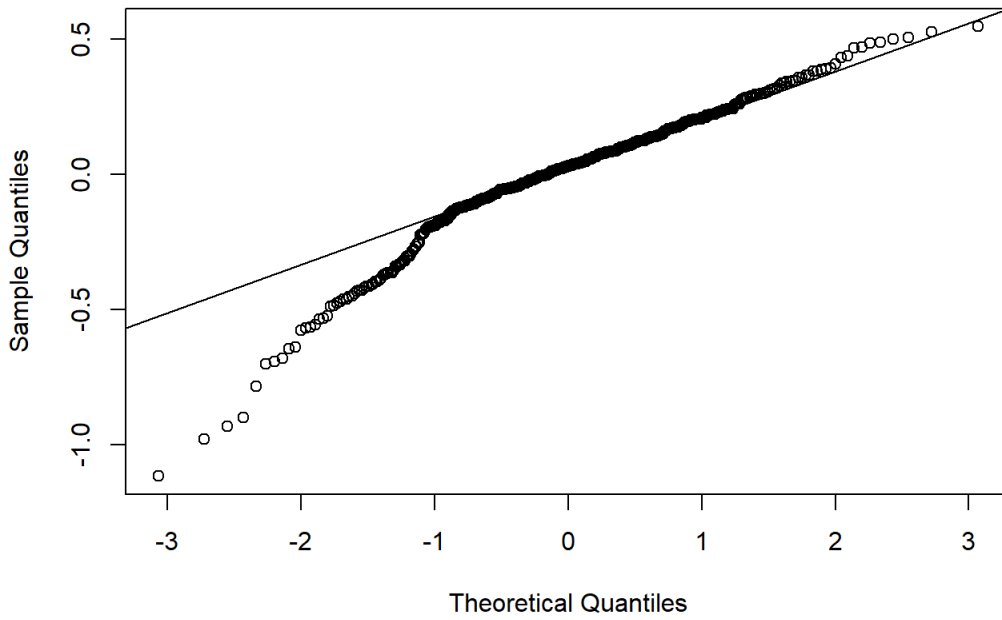


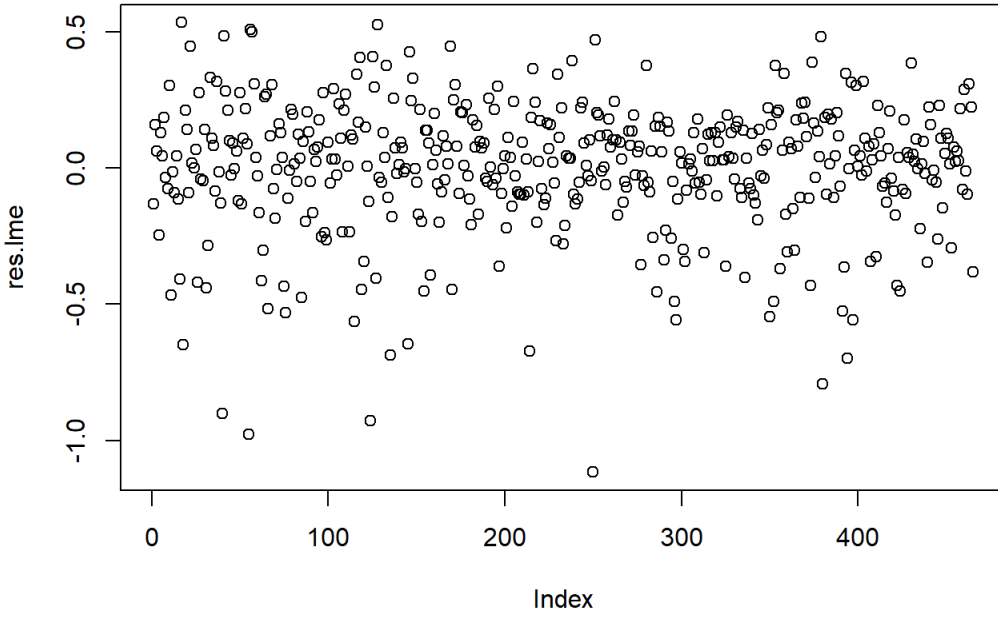
**Normal Q-Q Plot**



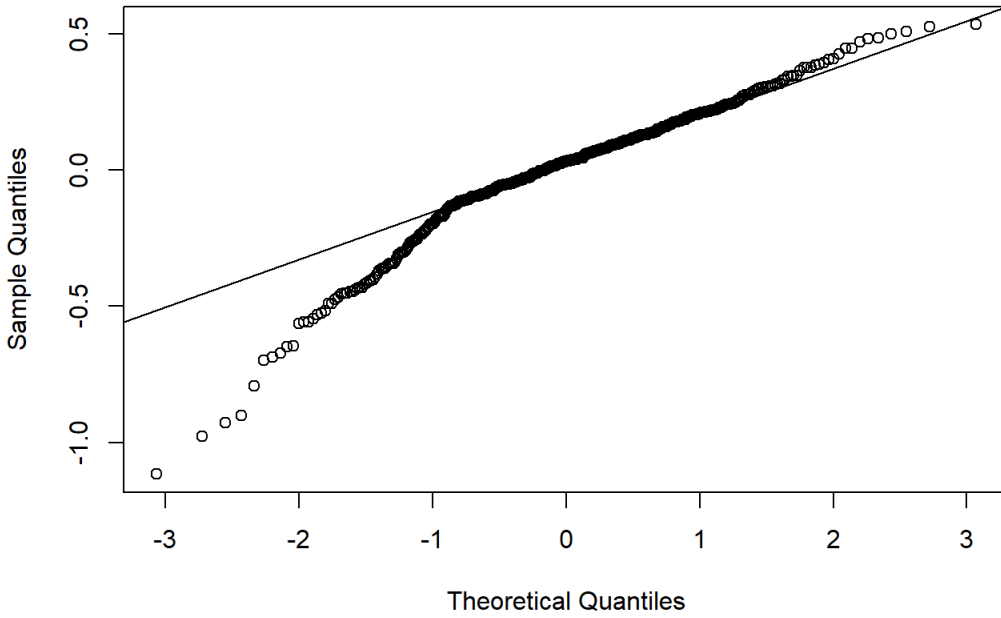


Normal Q-Q Plot

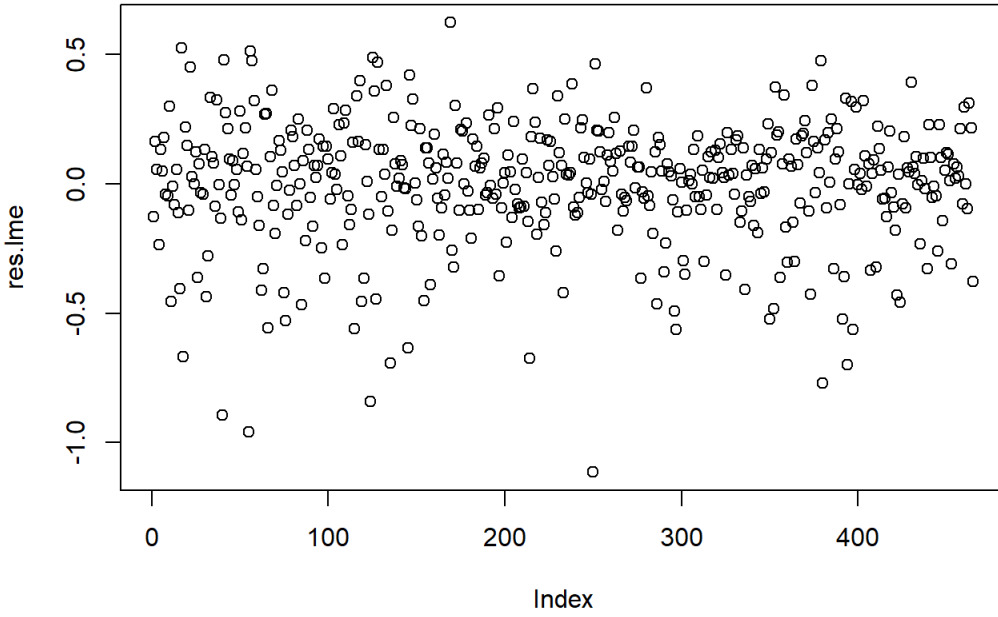




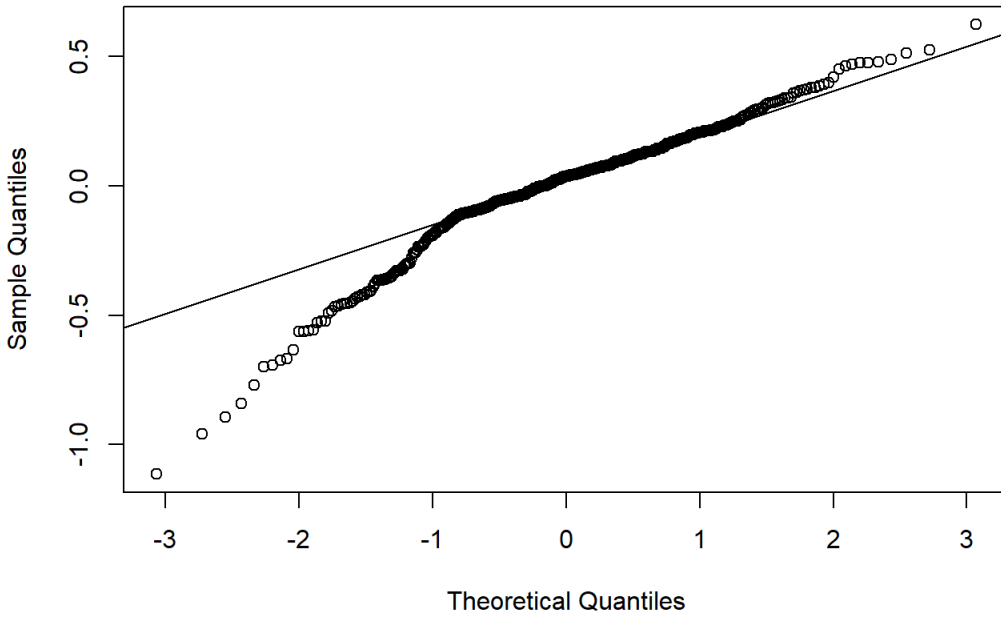
Normal Q-Q Plot

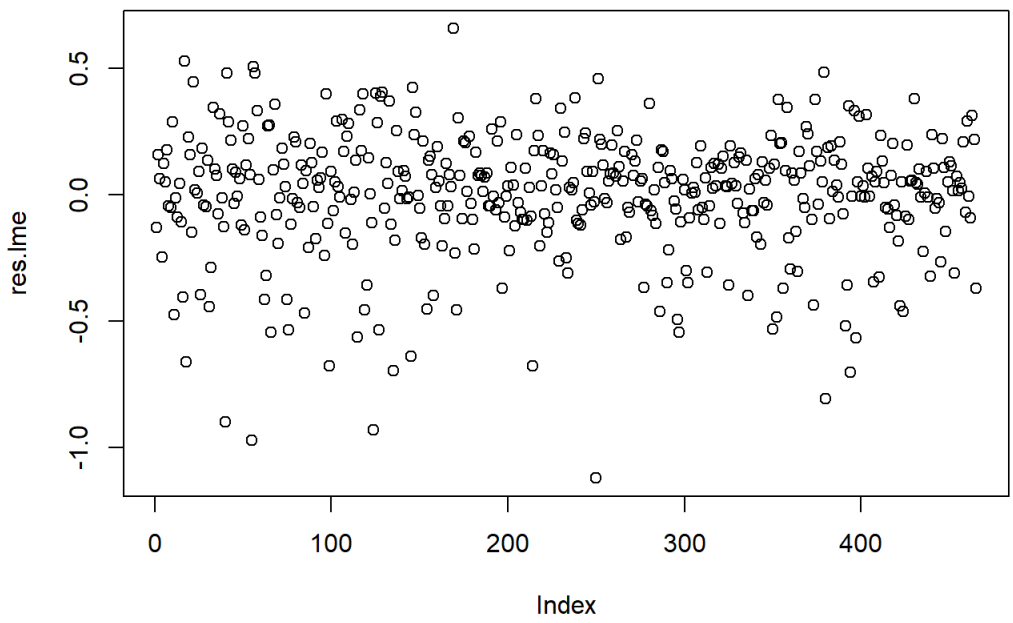




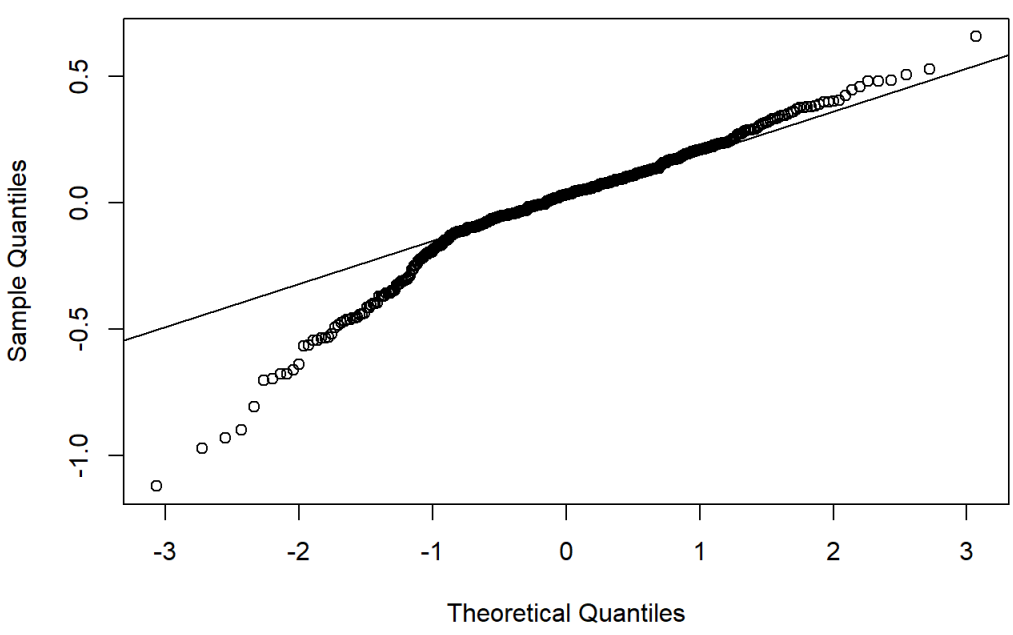


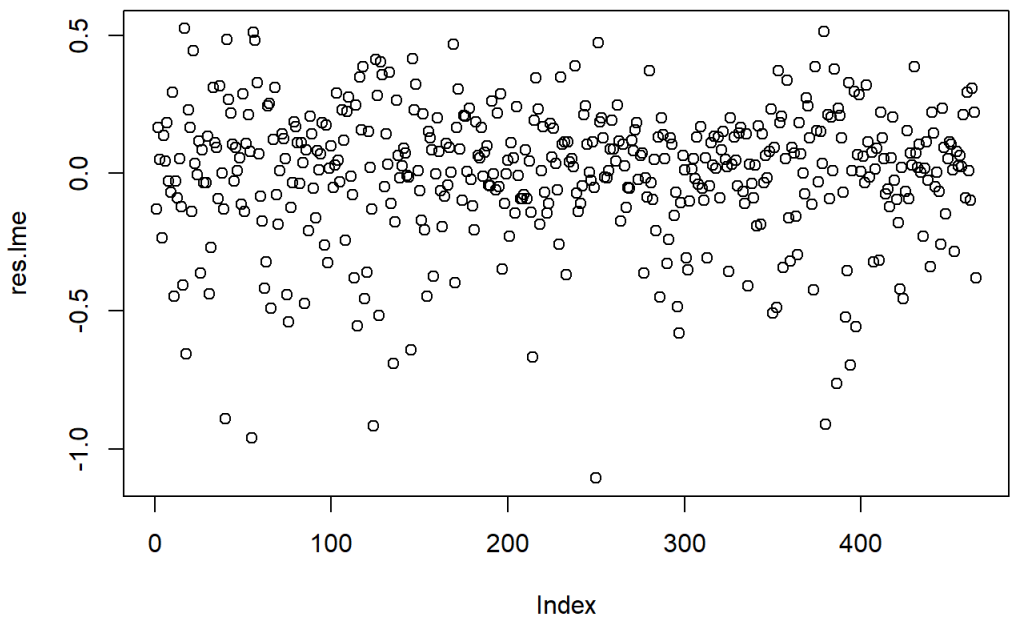
**Normal Q-Q Plot**



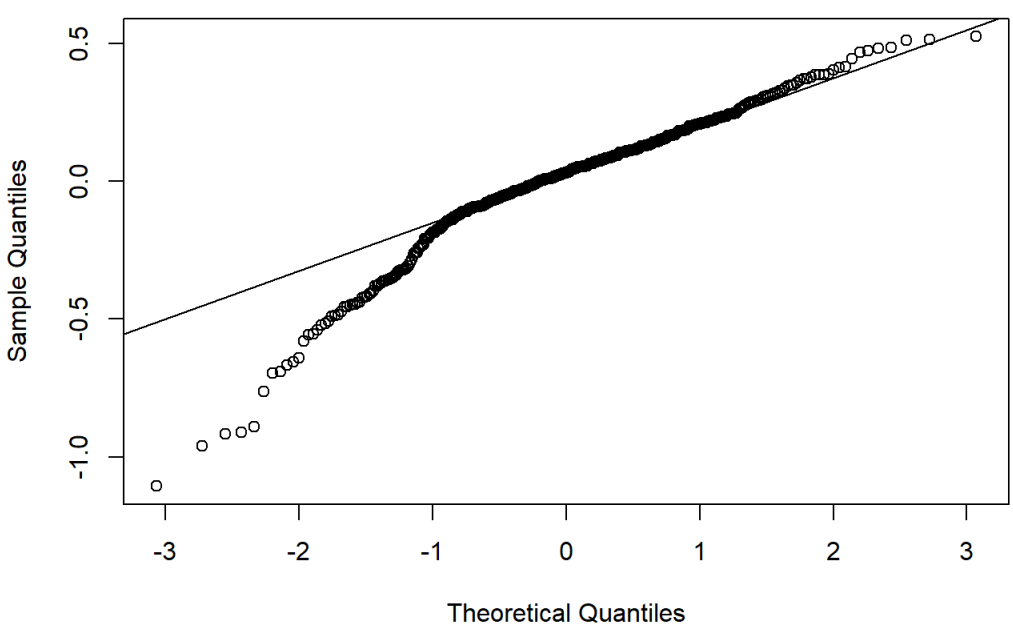


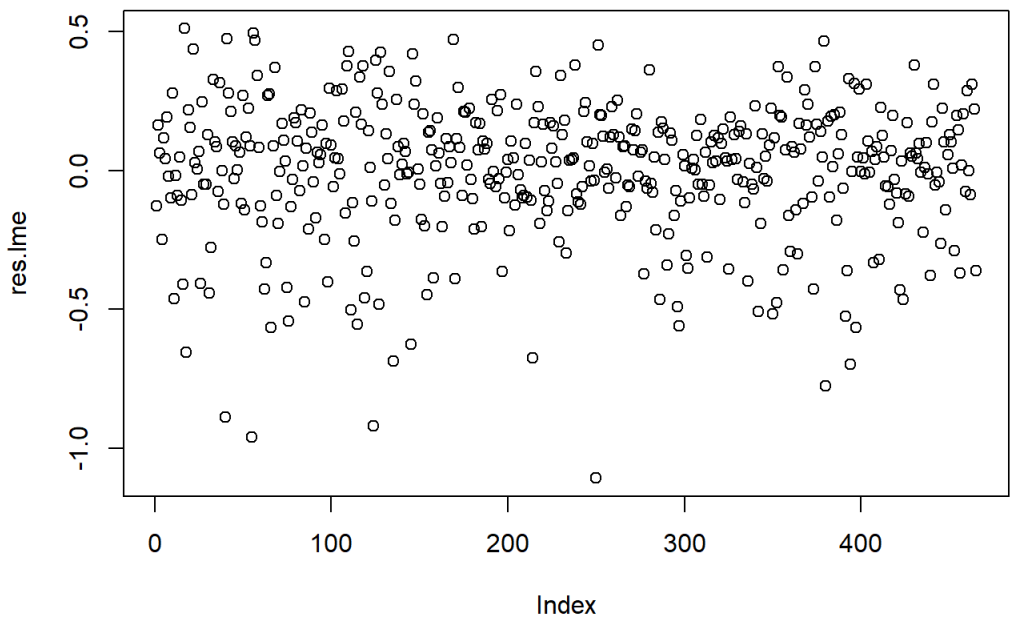
**Normal Q-Q Plot**



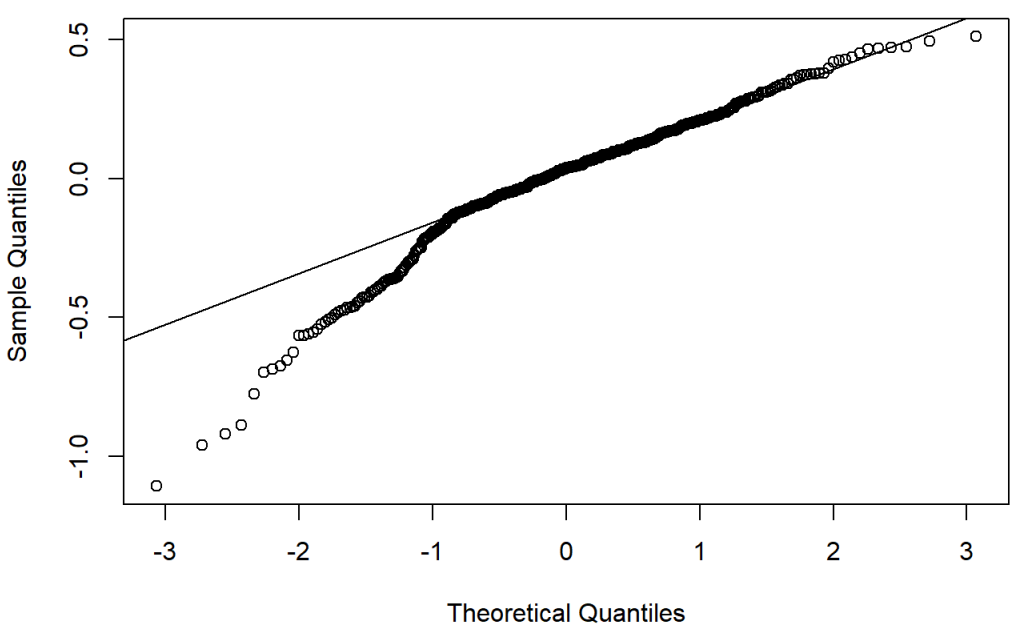


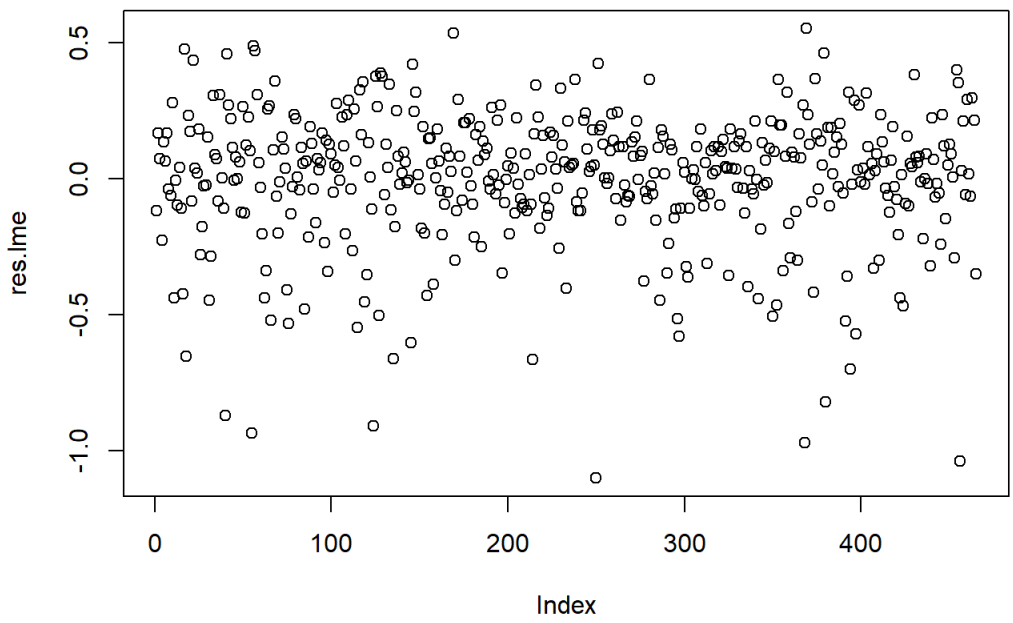
Normal Q-Q Plot



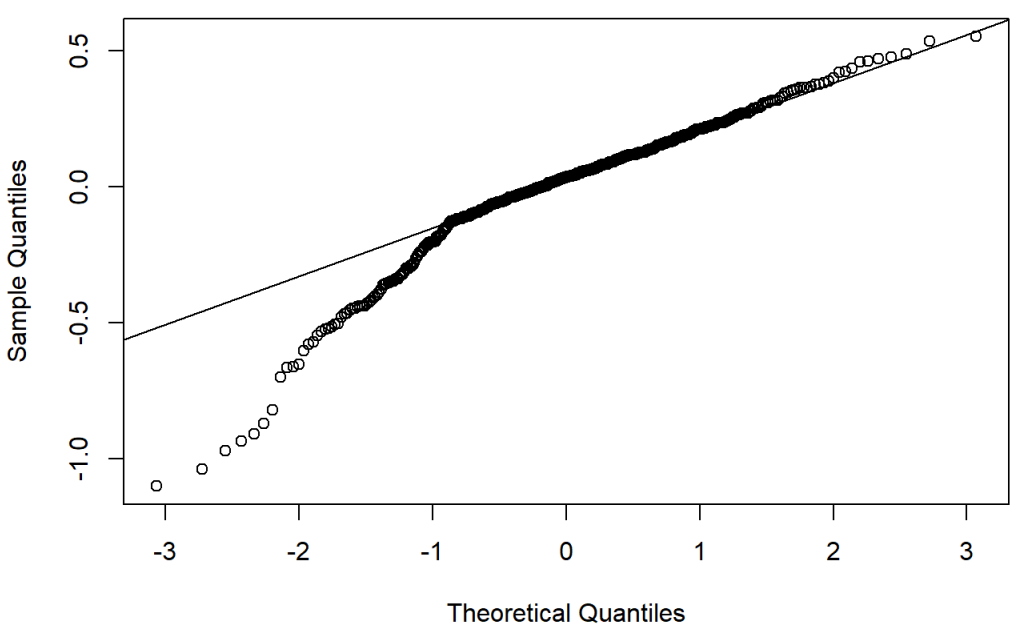


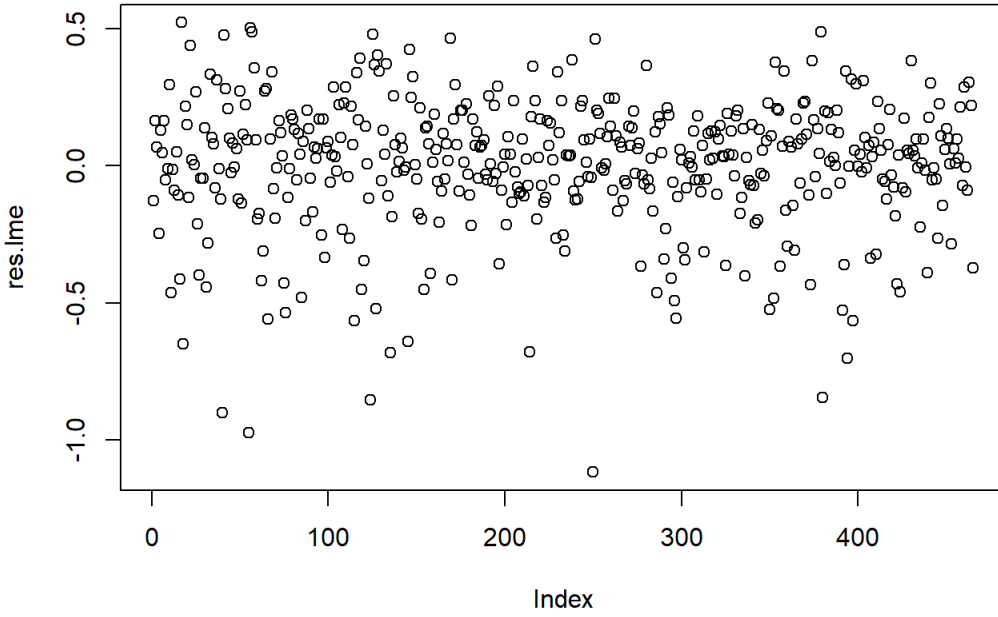
Normal Q-Q Plot



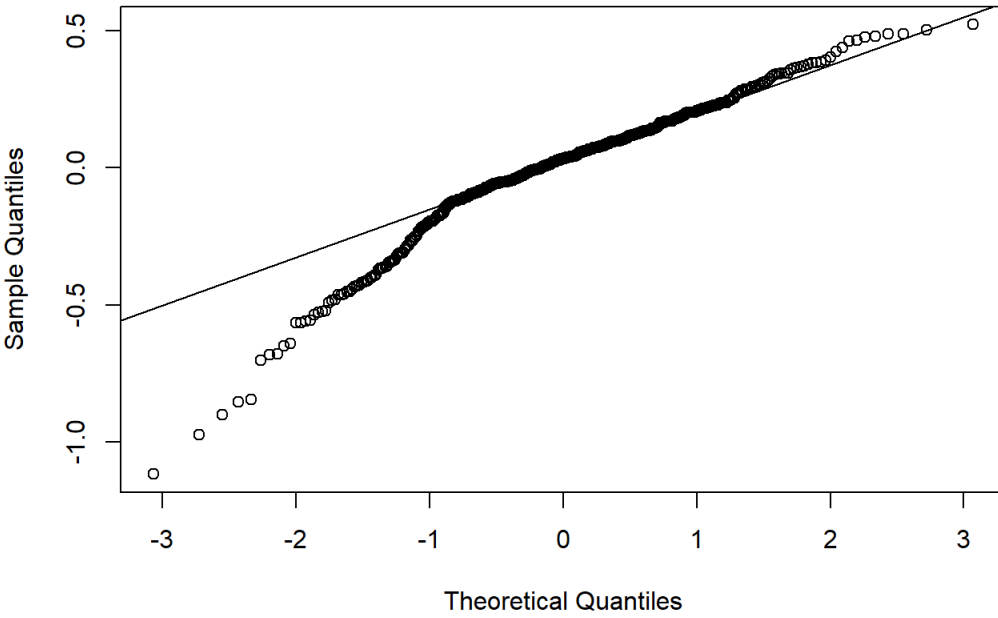


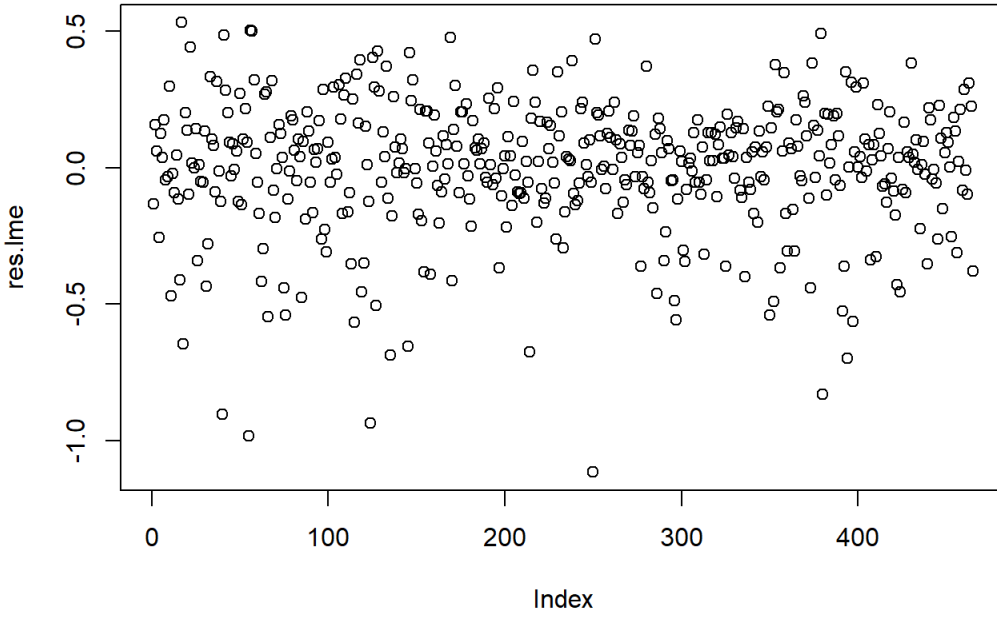
Normal Q-Q Plot



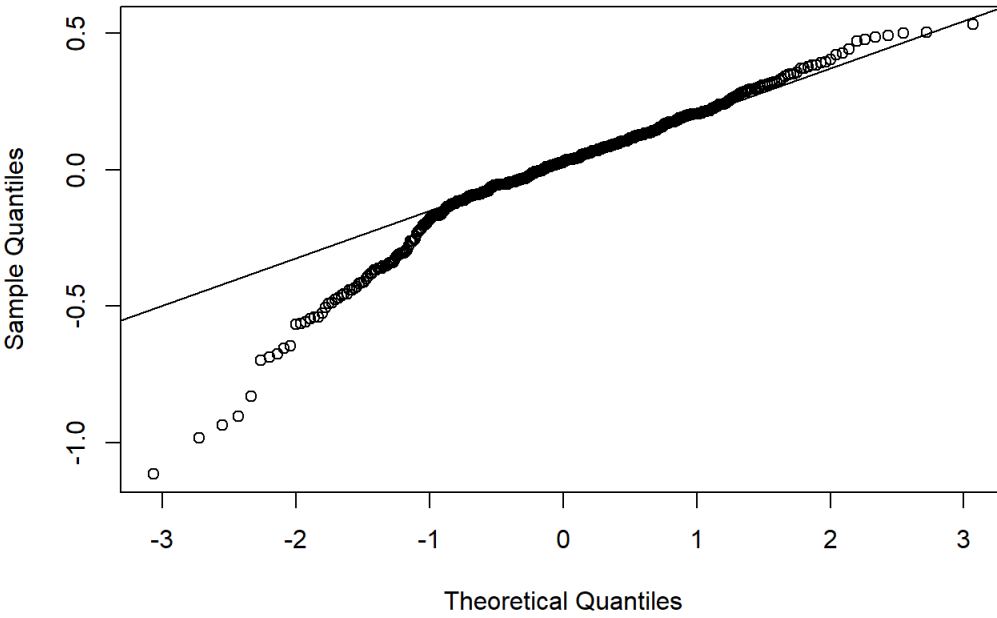


Normal Q-Q Plot

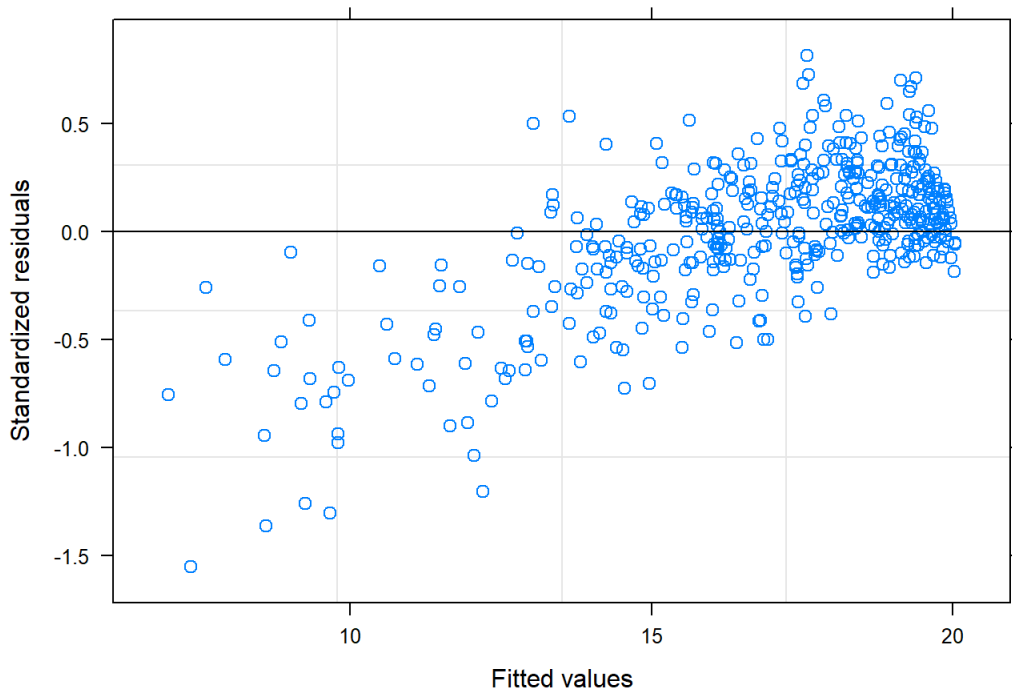




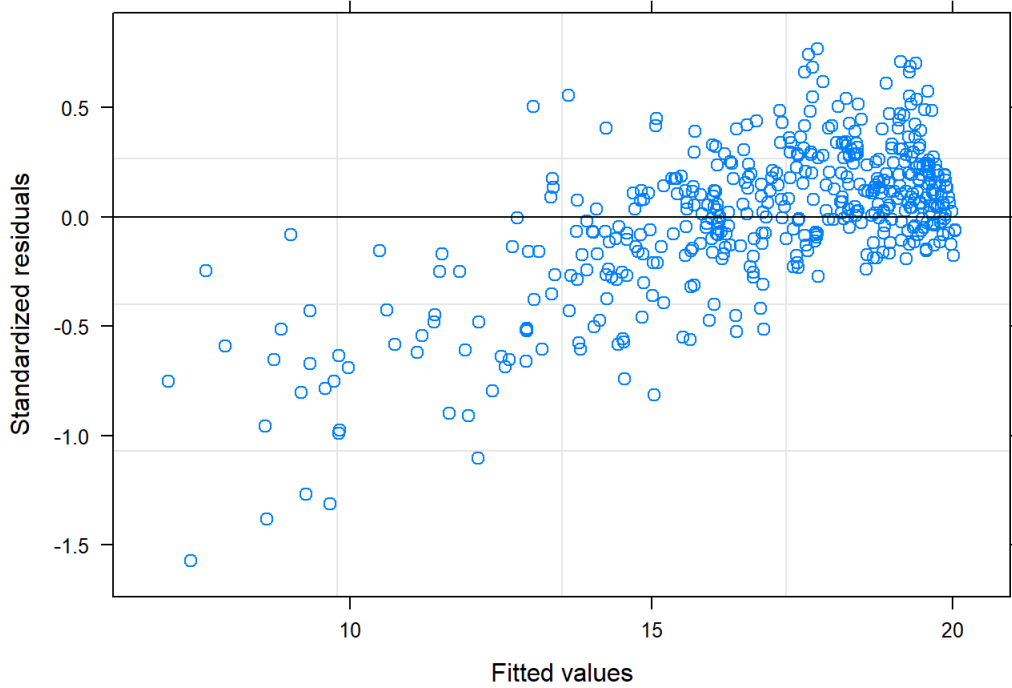
Normal Q-Q Plot



```
## [[1]]
```

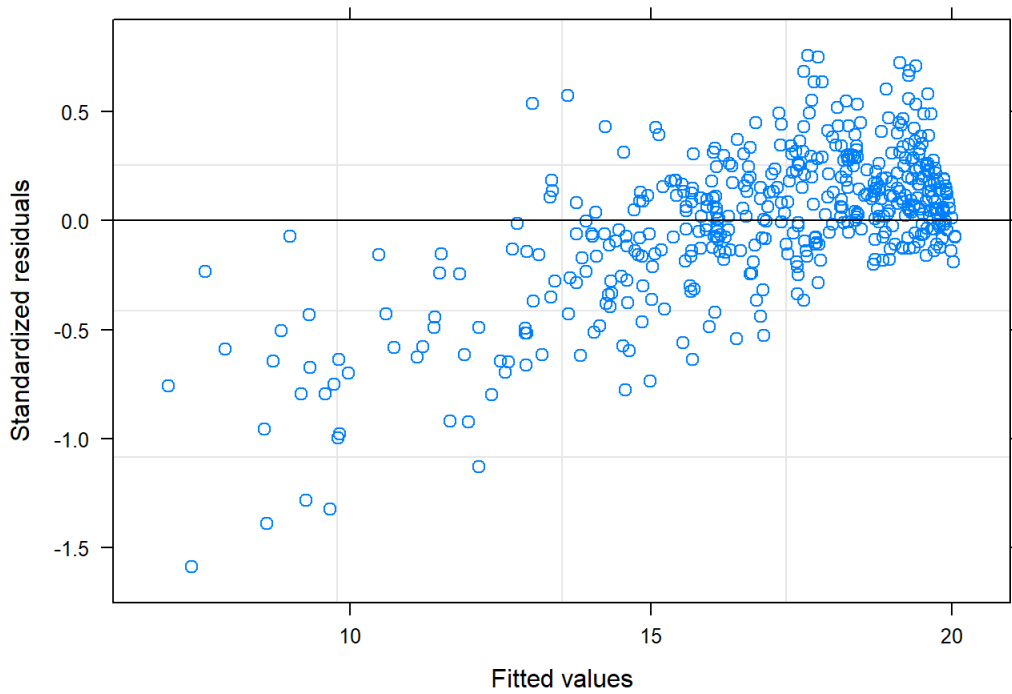


```
##  
## [[2]]
```

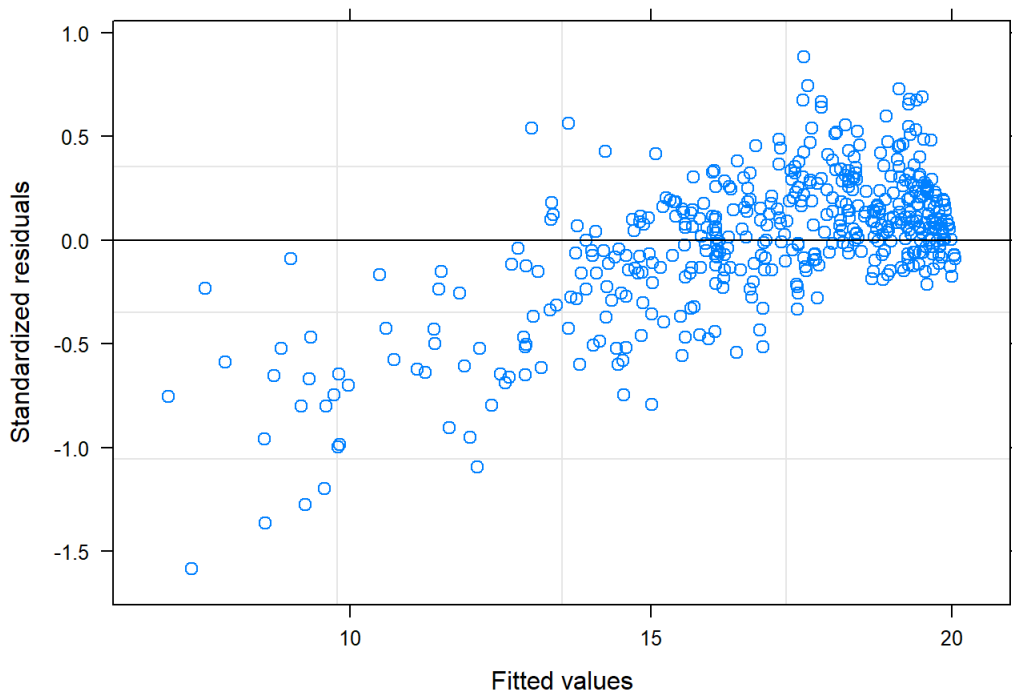


```
##  
## [[3]]
```

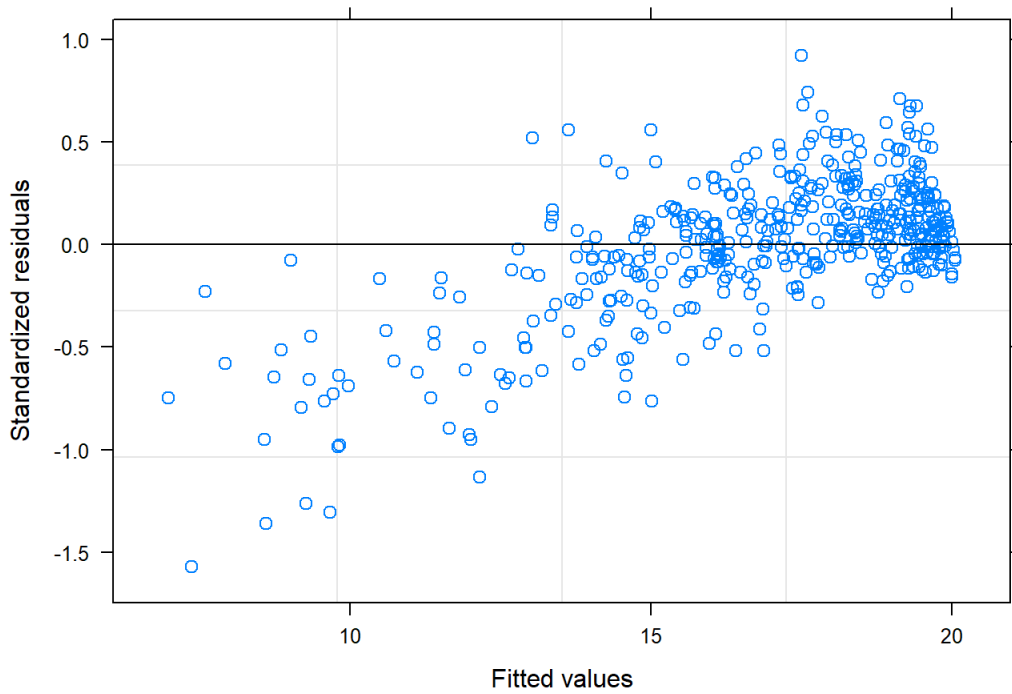




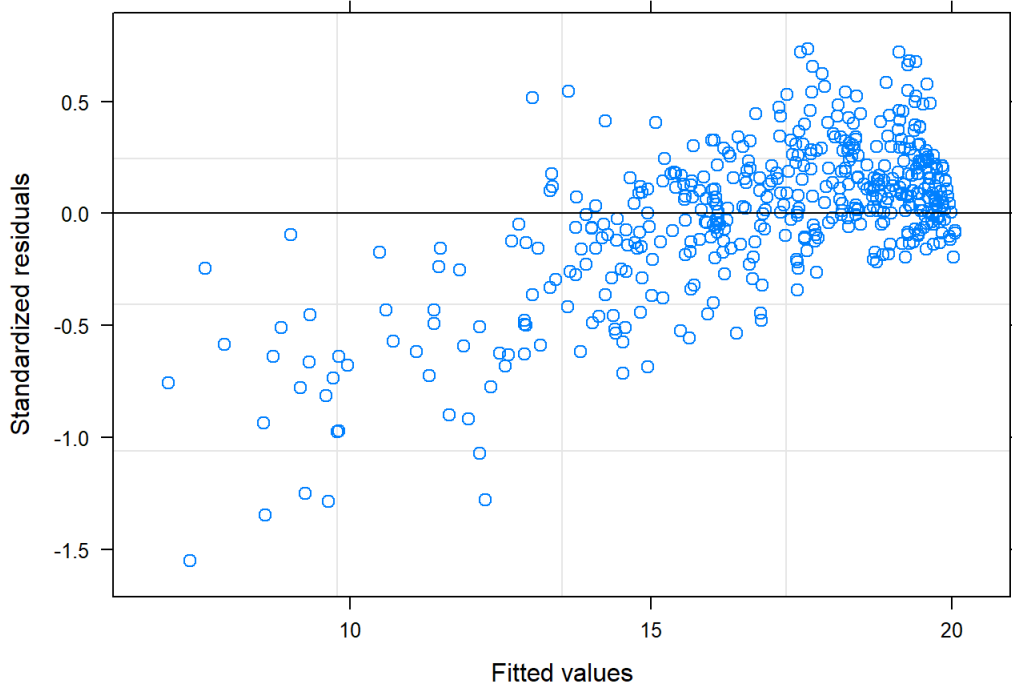
```
##  
## [[4]]
```



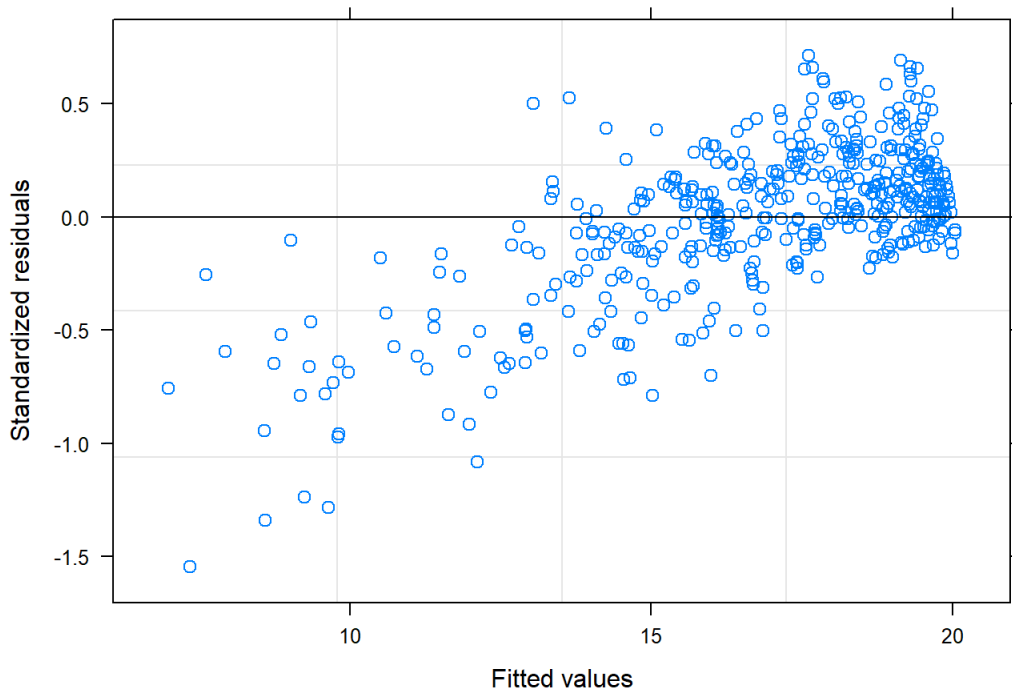
```
##  
## [[5]]
```



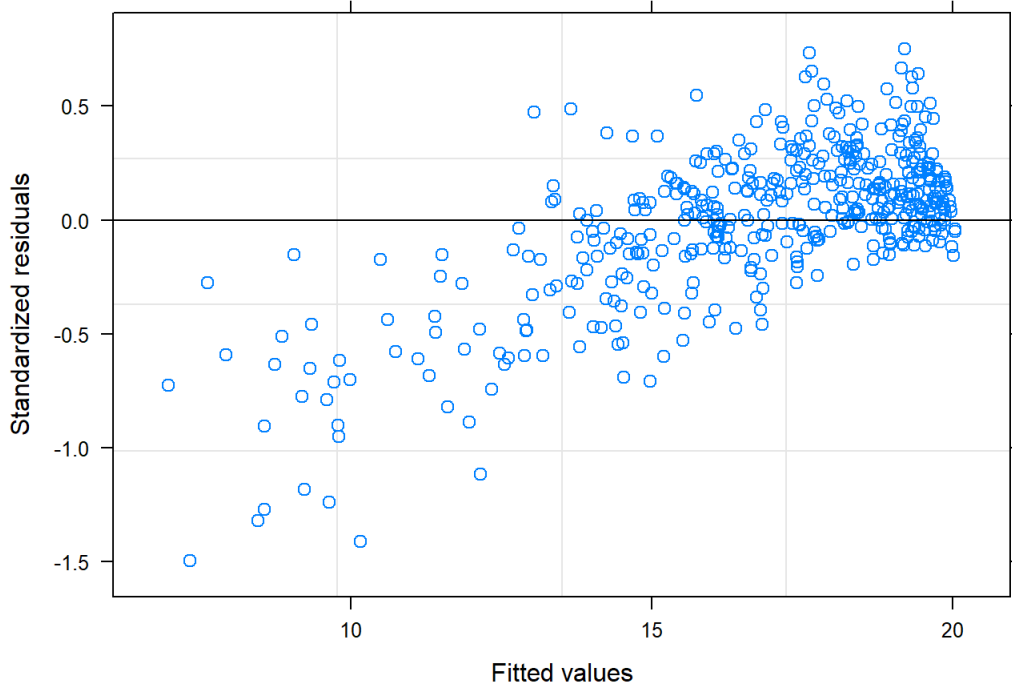
```
##  
## [[6]]
```



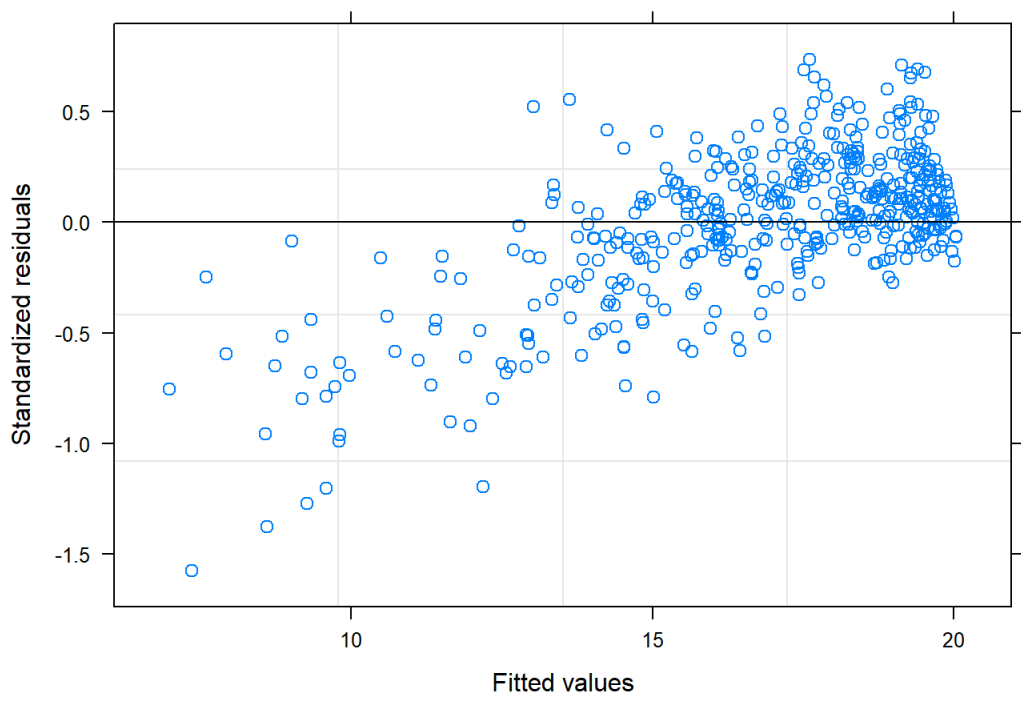
```
##  
## [[7]]
```



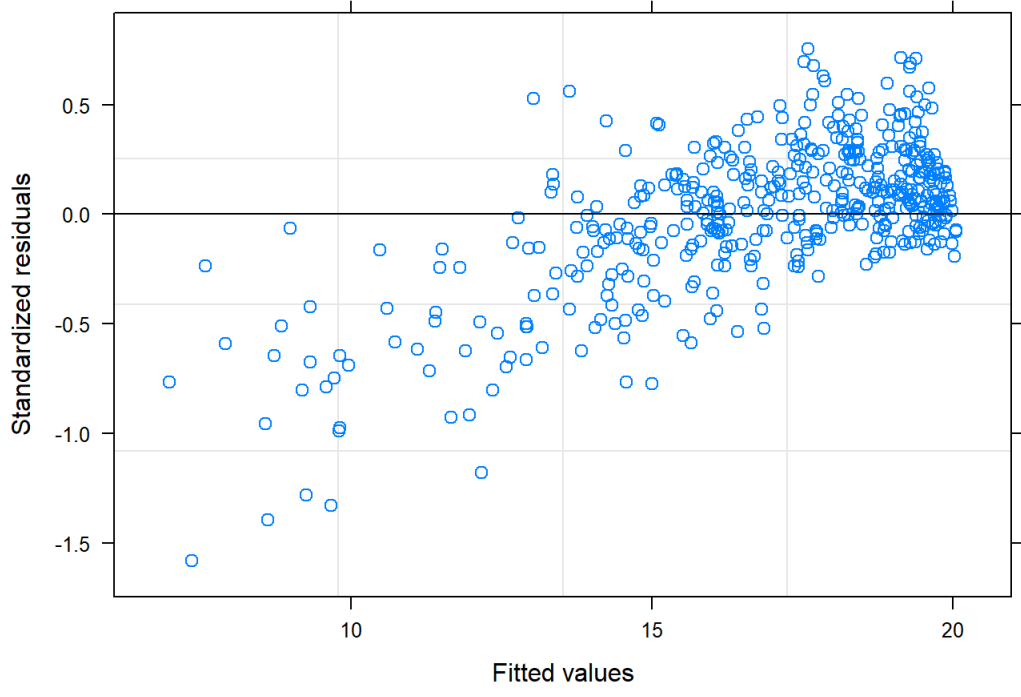
```
##  
## [[8]]
```



```
##  
## [[9]]
```



```
##  
## [[10]]
```



#LME with LMER

```
lmer.fit = map(complete.long, function(x){
  lmer(fosq_global ~avgpapuse * time +
    age + gender + race.f +
    ttt + ahi + bmi +
    dxchf + dxchd + dxdep + dxhypothy +
    (1|nsrrid),
    REML = TRUE,
    na.action = na.exclude,
    data = x)
})

map(lmer.fit, summary)
```

```

## [[1]]
## Linear mixed model fit by REML ['lmerMod']
## Formula: fosq_global ~ avgpapuse * time + age + gender + race.f + ttt +
##      ahi + bmi + dxchf + dxchd + dxdep + dxhypothy + (1 | nsrrid)
##      Data: x
##
## REML criterion at convergence: 2111.3
##
## Scaled residuals:
##      Min       1Q   Median       3Q      Max
## -3.9595 -0.3355  0.1160  0.5179  2.0976
##
## Random effects:
##      Groups   Name                Variance Std.Dev.
## nsrrid      (Intercept) 2.787      1.669
## Residual                    3.454      1.859
## Number of obs: 465, groups: nsrrid, 155
##
## Fixed effects:
##              Estimate Std. Error t value
## (Intercept) 14.132576  1.245108 11.350
## avgpapuse   0.430292  0.061058  7.047
## time        0.771465  0.130304  5.921
## age         0.006771  0.014603  0.464
## gender      0.891646  0.397156  2.245
## race.f2     0.035019  0.442628  0.079
## race.f3    -0.683241  0.606756 -1.126
## ttt         0.002663  0.006528  0.408
## ahi         0.006496  0.006904  0.941
## bmi         0.001828  0.020303  0.090
## dxchf       0.649654  1.113680  0.583
## dxchd      -0.337001  0.656819 -0.513
## dxdep      -1.688287  0.400359 -4.217
## dxhypothy   0.795161  0.618837  1.285
## avgpapuse:time -0.080079  0.033947 -2.359
##
## [[2]]
## Linear mixed model fit by REML ['lmerMod']
## Formula: fosq_global ~ avgpapuse * time + age + gender + race.f + ttt +
##      ahi + bmi + dxchf + dxchd + dxdep + dxhypothy + (1 | nsrrid)
##      Data: x
##
## REML criterion at convergence: 2101.9
##
## Scaled residuals:
##      Min       1Q   Median       3Q      Max
## -4.0015 -0.3450  0.1012  0.5145  1.9719
##
## Random effects:
##      Groups   Name                Variance Std.Dev.
## nsrrid      (Intercept) 2.791      1.671
## Residual                    3.360      1.833
## Number of obs: 465, groups: nsrrid, 155
##
## Fixed effects:
##              Estimate Std. Error t value
## (Intercept) 14.157660  1.242610 11.393
## avgpapuse   0.436737  0.060223  7.252
## time        0.815108  0.130515  6.245
## age         0.005543  0.014580  0.380

```

```

## gender          0.936247   0.397401   2.356
## race.f2         0.041467   0.440613   0.094
## race.f3        -0.570831   0.604729  -0.944
## ttt             0.001784   0.006503   0.274
## ahi             0.005508   0.006861   0.803
## bmi            0.002857   0.019923   0.143
## dxchf          0.608891   1.110988   0.548
## dxchd         -0.317274   0.654198  -0.485
## dxdep         -1.666819   0.397672  -4.191
## dxhypothy      0.861372   0.616351   1.398
## avgpapuse:time -0.090240   0.033414  -2.701
##
## [[3]]
## Linear mixed model fit by REML ['lmerMod']
## Formula: fosq_global ~ avgpapuse * time + age + gender + race.f + ttt +
##       ahi + bmi + dxchf + dxchd + dxdep + dxhypothy + (1 | nsrrid)
## Data: x
##
## REML criterion at convergence: 2095
##
## Scaled residuals:
##      Min       1Q   Median       3Q      Max
## -4.0234 -0.3472  0.1099  0.5206  1.9857
##
## Random effects:
##  Groups   Name                Variance Std.Dev.
## nsrrid   (Intercept)  2.806    1.675
## Residual                   3.289    1.814
## Number of obs: 465, groups: nsrrid, 155
##
## Fixed effects:
##              Estimate Std. Error t value
## (Intercept)  13.904324  1.237221  11.238
## avgpapuse    0.444466  0.059941   7.415
## time         0.835526  0.120128   6.955
## age          0.008963  0.014549   0.616
## gender       0.995388  0.394927   2.520
## race.f2      0.117487  0.440378   0.267
## race.f3     -0.704907  0.603534  -1.168
## ttt          0.003128  0.006496   0.482
## ahi          0.005070  0.006875   0.737
## bmi          0.003574  0.020223   0.177
## dxchf        0.529523  1.106895   0.478
## dxchd       -0.337621  0.653776  -0.516
## dxdep       -1.728050  0.404858  -4.268
## dxhypothy    0.829793  0.616200   1.347
## avgpapuse:time -0.093321  0.032358  -2.884
##
## [[4]]
## Linear mixed model fit by REML ['lmerMod']
## Formula: fosq_global ~ avgpapuse * time + age + gender + race.f + ttt +
##       ahi + bmi + dxchf + dxchd + dxdep + dxhypothy + (1 | nsrrid)
## Data: x
##
## REML criterion at convergence: 2094.9
##
## Scaled residuals:
##      Min       1Q   Median       3Q      Max
## -4.0363 -0.3466  0.1251  0.5134  2.2738
##
## Random effects:

```

```

## Groups Name Variance Std.Dev.
## nsrrid (Intercept) 2.709 1.646
## Residual 3.322 1.823
## Number of obs: 465, groups: nsrrid, 155
##
## Fixed effects:
## Estimate Std. Error t value
## (Intercept) 14.1688122 1.2257921 11.559
## avgpapuse 0.4383338 0.0598622 7.322
## time 0.8981691 0.1271722 7.063
## age 0.0059126 0.0143655 0.412
## gender 0.8879260 0.3905746 2.273
## race.f2 0.1771633 0.4351671 0.407
## race.f3 -0.6915655 0.5971568 -1.158
## ttt 0.0028224 0.0064311 0.439
## ahi 0.0069350 0.0067963 1.020
## bmi 0.0007218 0.0200450 0.036
## dxchf 0.6527151 1.0966676 0.595
## dxchd -0.3380582 0.6466233 -0.523
## dxdep -1.7932240 0.3938725 -4.553
## dxhypothy 0.7898729 0.6094264 1.296
## avgpapuse:time -0.1040150 0.0328230 -3.169
##
## [[5]]
## Linear mixed model fit by REML ['lmerMod']
## Formula: fosq_global ~ avgpapuse * time + age + gender + race.f + ttt +
## ahi + bmi + dxchf + dxchd + dxdep + dxhypothy + (1 | nsrrid)
## Data: x
##
## REML criterion at convergence: 2107
##
## Scaled residuals:
## Min 1Q Median 3Q Max
## -3.9943 -0.3436 0.1096 0.4916 2.3691
##
## Random effects:
## Groups Name Variance Std.Dev.
## nsrrid (Intercept) 2.829 1.682
## Residual 3.396 1.843
## Number of obs: 465, groups: nsrrid, 155
##
## Fixed effects:
## Estimate Std. Error t value
## (Intercept) 14.0115317 1.2459894 11.245
## avgpapuse 0.4528210 0.0615595 7.356
## time 0.8748901 0.1306430 6.697
## age 0.0073620 0.0146405 0.503
## gender 0.9928872 0.3994250 2.486
## race.f2 0.1555708 0.4433379 0.351
## race.f3 -0.5580415 0.6087014 -0.917
## ttt 0.0032944 0.0065467 0.503
## ahi 0.0069790 0.0069145 1.009
## bmi 0.0001535 0.0200690 0.008
## dxchf 0.5285160 1.1184828 0.473
## dxchd -0.3109058 0.6586160 -0.472
## dxdep -1.6739572 0.3996766 -4.188
## dxhypothy 0.7877018 0.6206268 1.269
## avgpapuse:time -0.1097364 0.0335528 -3.271
##
## [[6]]
## Linear mixed model fit by REML ['lmerMod']

```



```

## Formula: fosq_global ~ avgpapuse * time + age + gender + race.f + ttt +
##   ahi + bmi + dxchf + dxchd + dxdep + dxhypothy + (1 | nsrrid)
##   Data: x
##
## REML criterion at convergence: 2107.7
##
## Scaled residuals:
##   Min      1Q  Median      3Q      Max
## -3.9590 -0.3368  0.1077  0.5194  1.9424
##
## Random effects:
##   Groups   Name                Variance Std.Dev.
## nsrrid    (Intercept)  2.751     1.658
## Residual                    3.431     1.852
## Number of obs: 465, groups: nsrrid, 155
##
## Fixed effects:
##              Estimate Std. Error t value
## (Intercept)  13.992446  1.239138  11.292
## avgpapuse    0.413165  0.061178   6.753
## time         0.859300  0.126463   6.795
## age          0.007929  0.014544   0.545
## gender       0.910386  0.395170   2.304
## race.f2      0.241533  0.440760   0.548
## race.f3     -0.658113  0.602943  -1.092
## ttt         0.002900  0.006490   0.447
## ahi          0.005243  0.006865   0.764
## bmi          0.003289  0.020216   0.163
## dxchf        0.537465  1.106761   0.486
## dxchd       -0.299438  0.653085  -0.458
## dxdep       -1.726117  0.404435  -4.268
## dxhypothy    0.730576  0.615415   1.187
## avgpapuse:time -0.083341  0.033095  -2.518
##
## [[7]]
## Linear mixed model fit by REML ['lmerMod']
## Formula: fosq_global ~ avgpapuse * time + age + gender + race.f + ttt +
##   ahi + bmi + dxchf + dxchd + dxdep + dxhypothy + (1 | nsrrid)
##   Data: x
##
## REML criterion at convergence: 2112.8
##
## Scaled residuals:
##   Min      1Q  Median      3Q      Max
## -3.9603 -0.3505  0.1277  0.5295  1.8935
##
## Random effects:
##   Groups   Name                Variance Std.Dev.
## nsrrid    (Intercept)  2.708     1.646
## Residual                    3.496     1.870
## Number of obs: 465, groups: nsrrid, 155
##
## Fixed effects:
##              Estimate Std. Error t value
## (Intercept)  14.235932  1.230258  11.572
## avgpapuse    0.434894  0.062061   7.008
## time         0.860842  0.127921   6.729
## age          0.006715  0.014496   0.463
## gender       0.917148  0.394593   2.324
## race.f2      0.175677  0.438925   0.400
## race.f3     -0.630567  0.602119  -1.047

```

```

## ttt          0.002505   0.006482   0.386
## ahi          0.006990   0.006837   1.022
## bmi         -0.003493   0.019770  -0.177
## dxchf       0.557881   1.105604   0.505
## dxchd      -0.331304   0.651126  -0.509
## dxdep      -1.580513   0.395510  -3.996
## dxhypoathy  0.855833   0.613663   1.395
## avgpapuse:time -0.099689   0.033609  -2.966
##
## [[8]]
## Linear mixed model fit by REML ['lmerMod']
## Formula: fosq_global ~ avgpapuse * time + age + gender + race.f + ttt +
##       ahi + bmi + dxchf + dxchd + dxdep + dxhypoathy + (1 | nsrrid)
## Data: x
##
## REML criterion at convergence: 2136.7
##
## Scaled residuals:
##      Min       1Q   Median       3Q      Max
## -3.8761 -0.3215  0.1243  0.5083  1.9847
##
## Random effects:
##  Groups      Name                Variance Std.Dev.
## nsrrid      (Intercept)  2.624     1.620
## Residual                    3.776     1.943
## Number of obs: 465, groups: nsrrid, 155
##
## Fixed effects:
##              Estimate Std. Error t value
## (Intercept)  14.12712463  1.23567513  11.433
## avgpapuse    0.43075804  0.06422024   6.708
## time         0.83766476  0.13526755   6.193
## age          0.00727300  0.01450079   0.502
## gender       0.88772118  0.39381464   2.254
## race.f2      0.07154779  0.43817369   0.163
## race.f3     -0.97424764  0.60226552  -1.618
## ttt          0.00002253  0.00647781   0.003
## ahi          0.00752336  0.00684638   1.099
## bmi          0.00356422  0.02012563   0.177
## dxchf       0.63386996  1.10569252   0.573
## dxchd      -0.34823496  0.65209720  -0.534
## dxdep      -1.76135607  0.39785528  -4.427
## dxhypoathy  0.51063261  0.61452212   0.831
## avgpapuse:time -0.09609115  0.03531892  -2.721
##
## [[9]]
## Linear mixed model fit by REML ['lmerMod']
## Formula: fosq_global ~ avgpapuse * time + age + gender + race.f + ttt +
##       ahi + bmi + dxchf + dxchd + dxdep + dxhypoathy + (1 | nsrrid)
## Data: x
##
## REML criterion at convergence: 2103.1
##
## Scaled residuals:
##      Min       1Q   Median       3Q      Max
## -4.0060 -0.3460  0.1077  0.5132  1.9373
##
## Random effects:
##  Groups      Name                Variance Std.Dev.
## nsrrid      (Intercept)  2.779     1.667
## Residual                    3.376     1.837

```

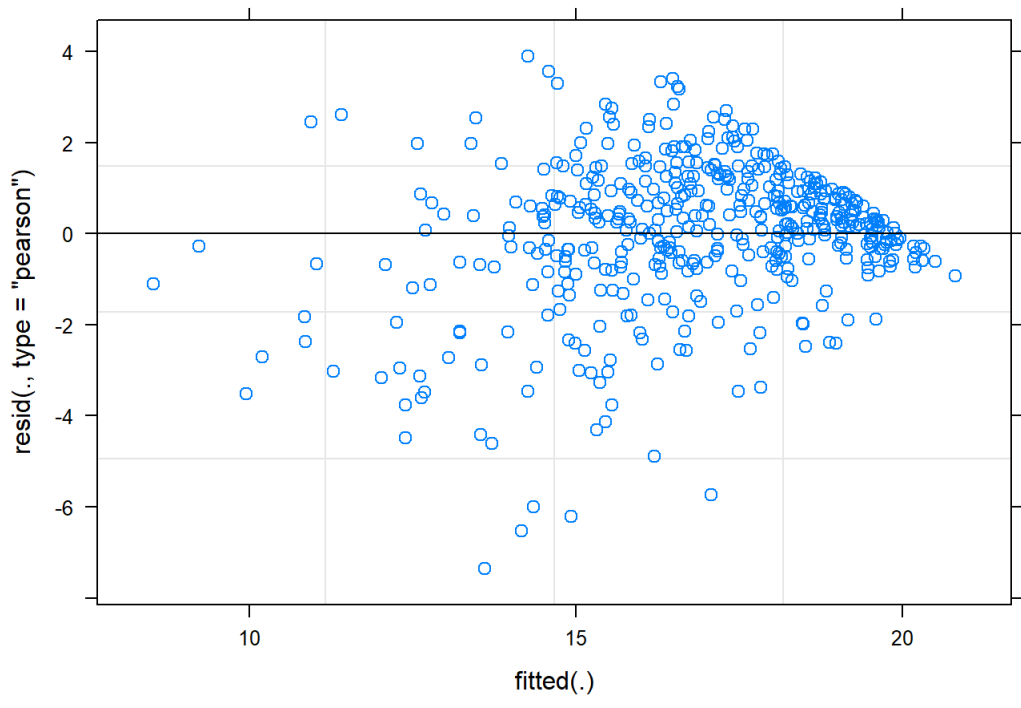
```

## Number of obs: 465, groups: nsrrid, 155
##
## Fixed effects:
##           Estimate Std. Error t value
## (Intercept) 14.259947  1.233844  11.557
## avgpapuse   0.439501  0.061218   7.179
## time        0.830518  0.125037   6.642
## age         0.006442  0.014544   0.443
## gender      0.927239  0.394267   2.352
## race.f2     0.046163  0.440340   0.105
## race.f3    -0.709497  0.603753  -1.175
## ttt         0.003001  0.006500   0.462
## ahi         0.006452  0.006865   0.940
## bmi        -0.001806  0.020035  -0.090
## dxchf       0.613827  1.108123   0.554
## dxchd      -0.344953  0.653850  -0.528
## dxdep      -1.693809  0.398321  -4.252
## dxhypoathy  0.783745  0.616355   1.272
## avgpapuse:time -0.094431  0.032923  -2.868
##
## [[10]]
## Linear mixed model fit by REML ['lmerMod']
## Formula: fosq_global ~ avgpapuse * time + age + gender + race.f + ttt +
##         ahi + bmi + dxchf + dxchd + dxdep + dxhypoathy + (1 | nsrrid)
##      Data: x
##
## REML criterion at convergence: 2097.6
##
## Scaled residuals:
##      Min       1Q   Median       3Q      Max
## -4.0079 -0.3431  0.1036  0.5163  1.9770
##
## Random effects:
##  Groups   Name                Variance Std.Dev.
## nsrrid   (Intercept)  2.824    1.681
## Residual                   3.307    1.819
## Number of obs: 465, groups: nsrrid, 155
##
## Fixed effects:
##           Estimate Std. Error t value
## (Intercept) 14.030610  1.243845  11.280
## avgpapuse   0.440802  0.060373   7.301
## time        0.816763  0.122141   6.687
## age         0.005925  0.014582   0.406
## gender      0.997438  0.397000   2.512
## race.f2     0.158592  0.441261   0.359
## race.f3    -0.656343  0.605958  -1.083
## ttt         0.004193  0.006515   0.644
## ahi         0.006461  0.006895   0.937
## bmi         0.001196  0.020278   0.059
## dxchf       0.545323  1.113417   0.490
## dxchd      -0.313115  0.655771  -0.477
## dxdep      -1.641055  0.398981  -4.113
## dxhypoathy  0.888993  0.618935   1.436
## avgpapuse:time -0.088479  0.032583  -2.715

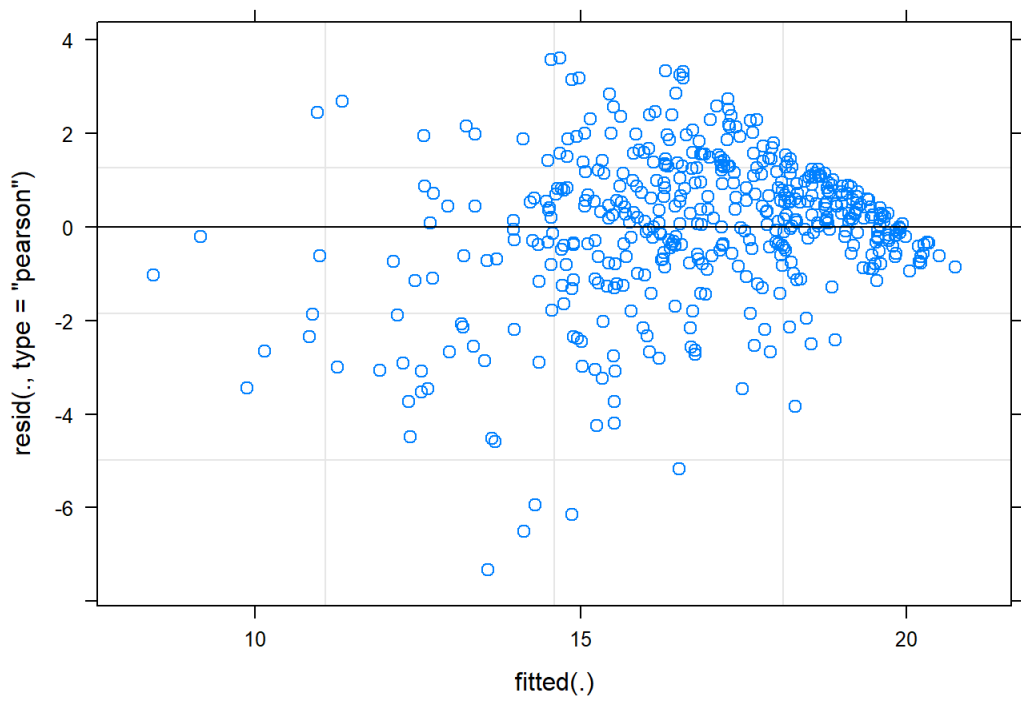
```

```
map(lmer.fit, plot)
```

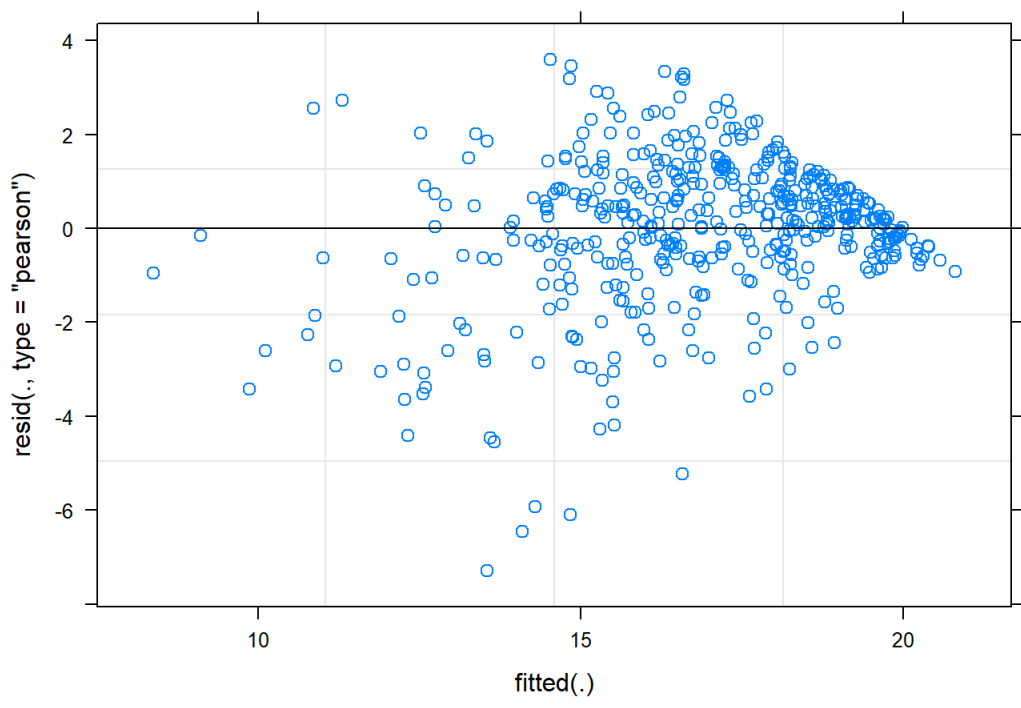
```
## [[1]]
```



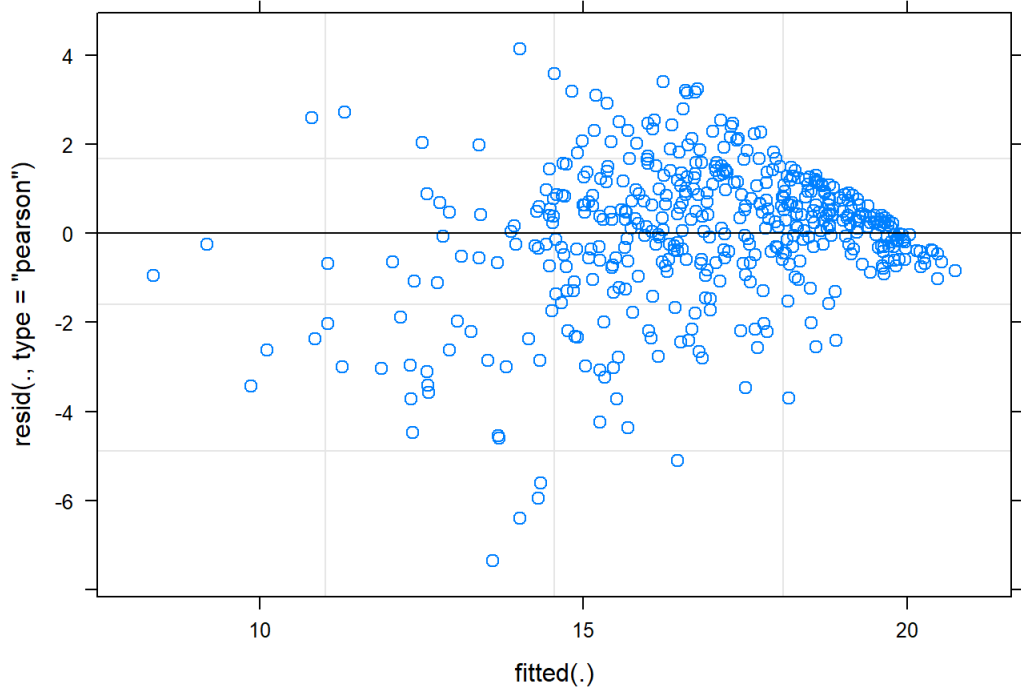
```
##  
## [[2]]
```



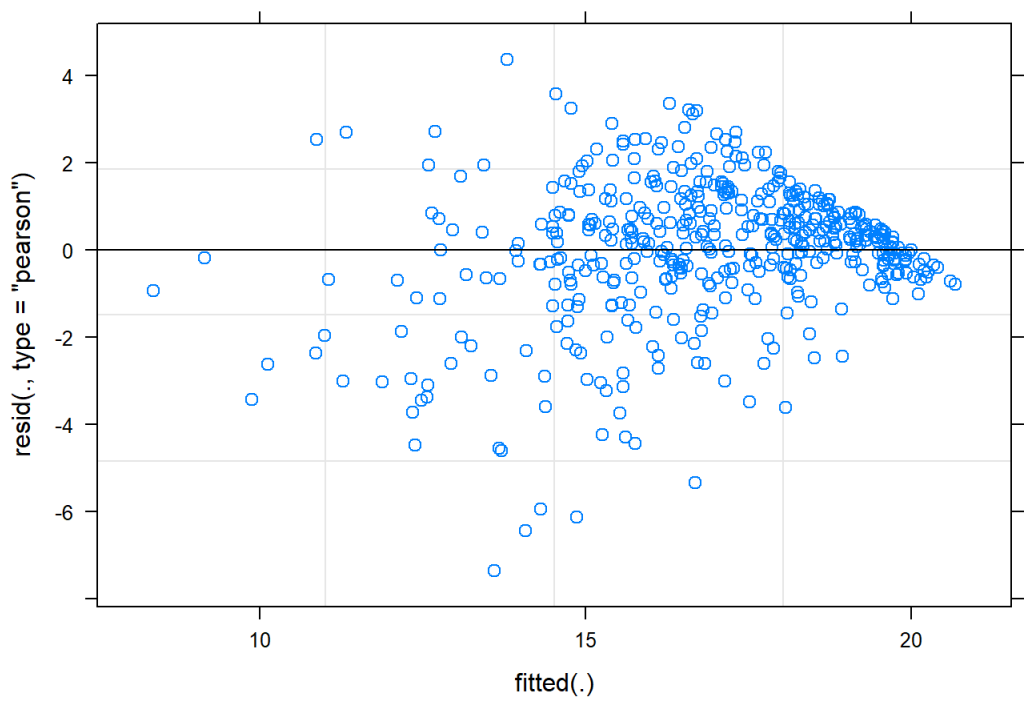
```
##  
## [[3]]
```



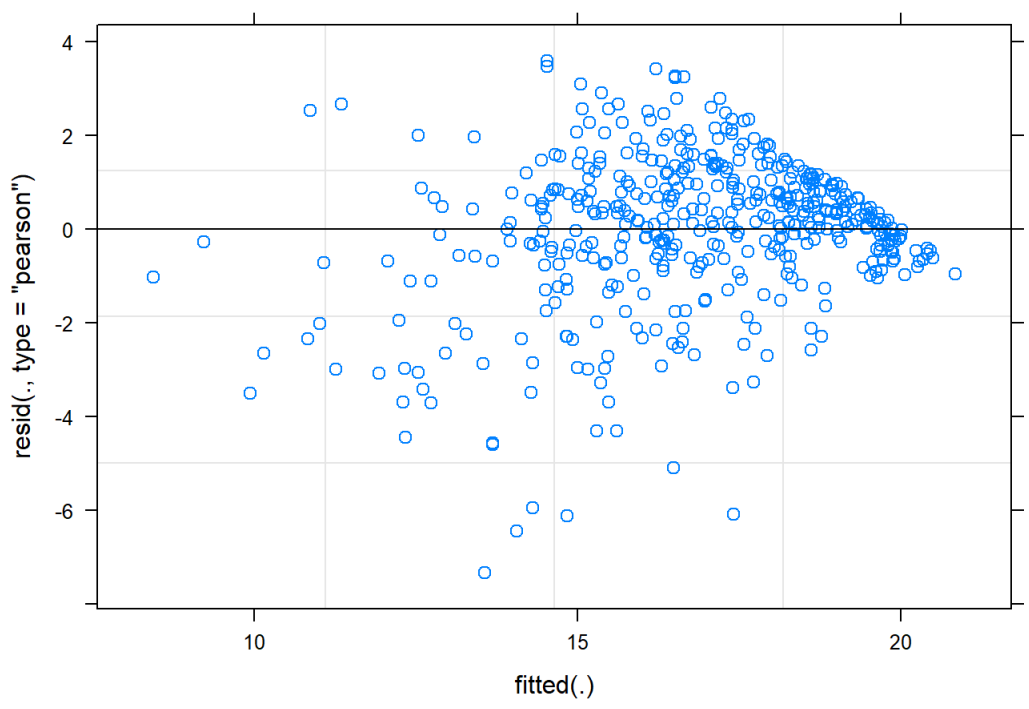
```
##  
## [[4]]
```



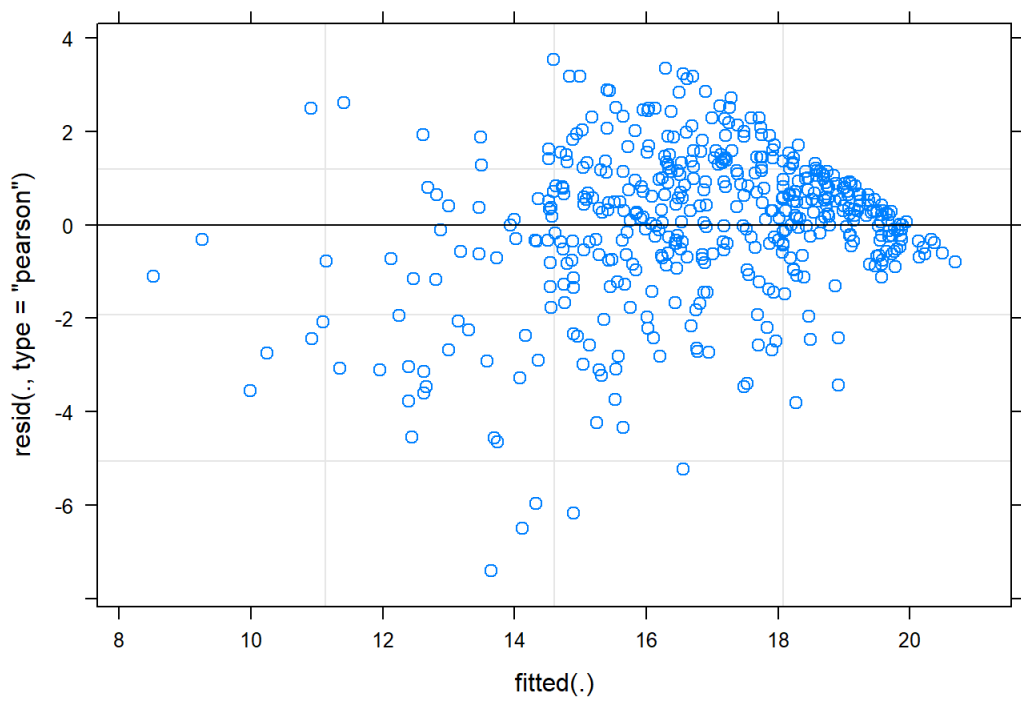
```
##  
## [[5]]
```



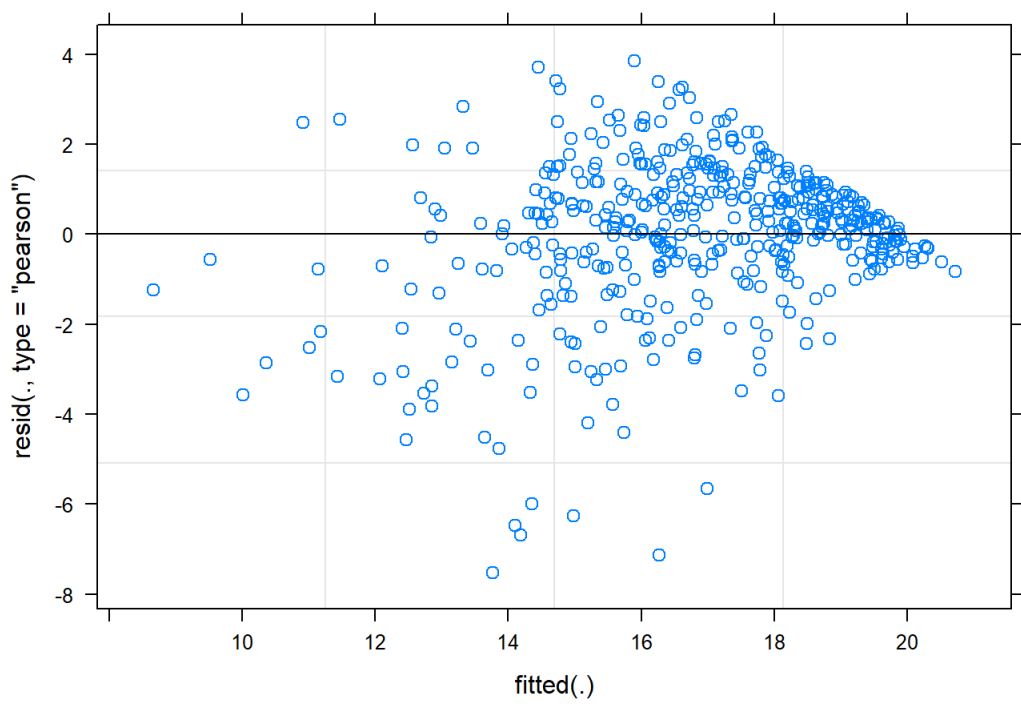
```
##  
## [[6]]
```



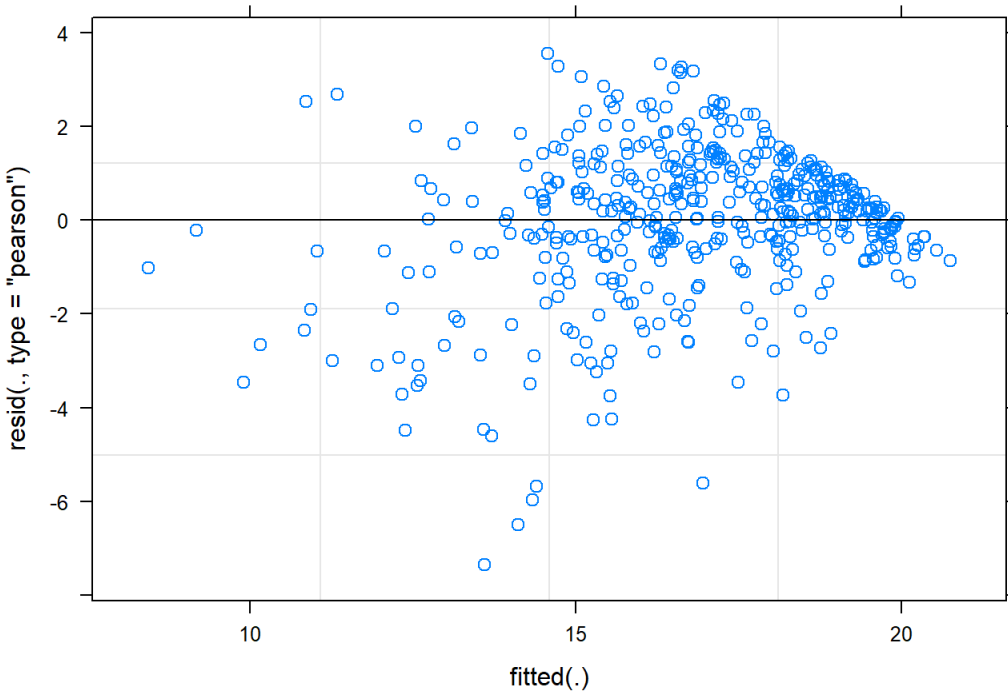
```
##  
## [[7]]
```



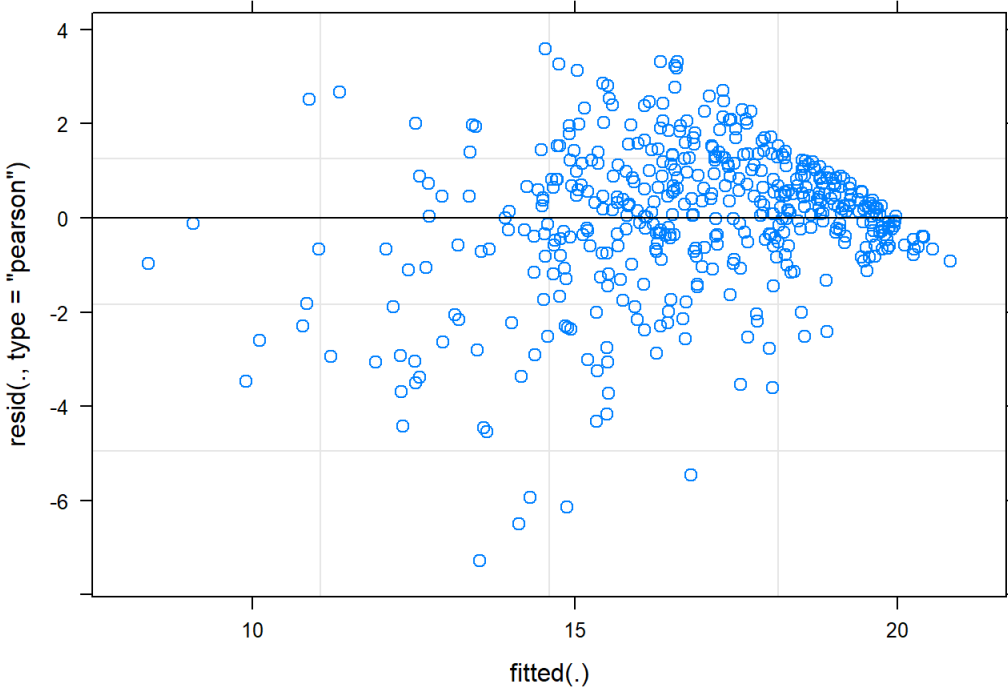
```
##  
## [[8]]
```



```
##  
## [[9]]
```



```
##
## [[10]]
```

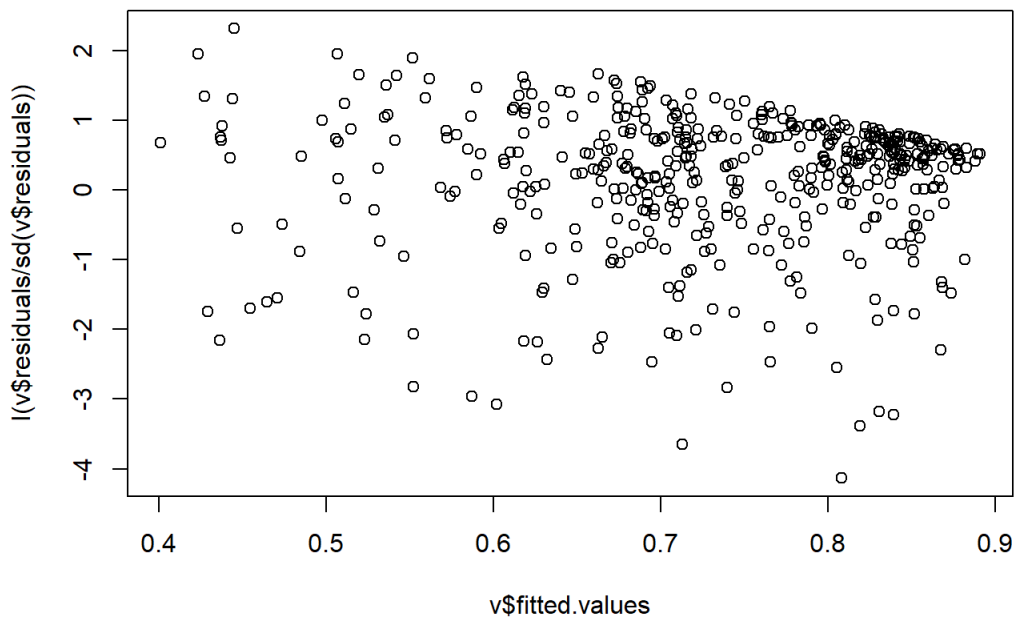


#Comparing models "Draw the damn picture" standardized residuals

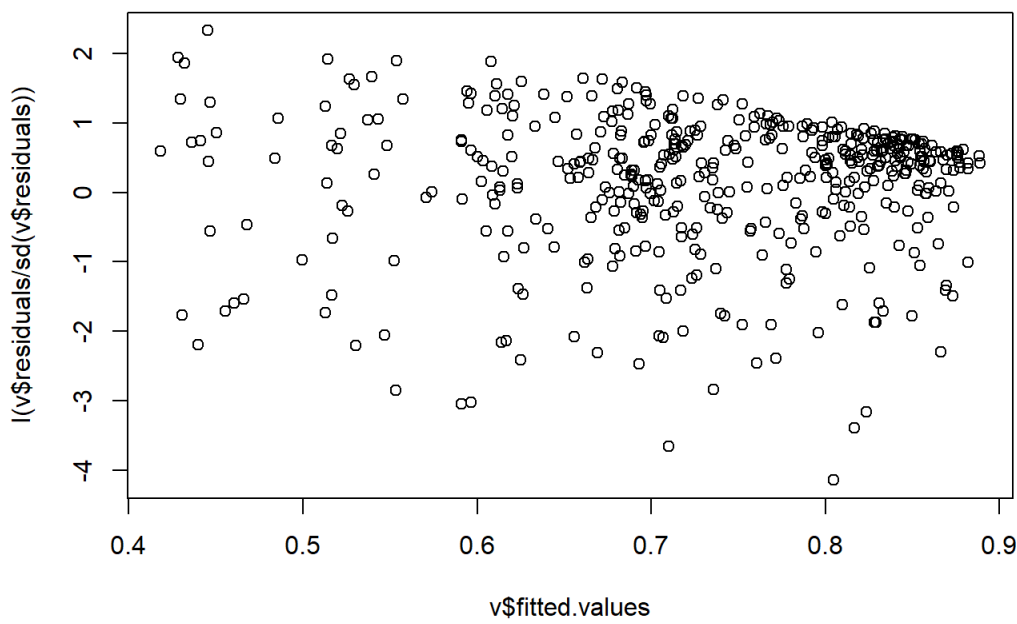
```
map(beta.fit, function(v) {
  plot(I(v$residuals/sd(v$residuals)) ~ v$fitted.values, main = "Beta regression")})
```



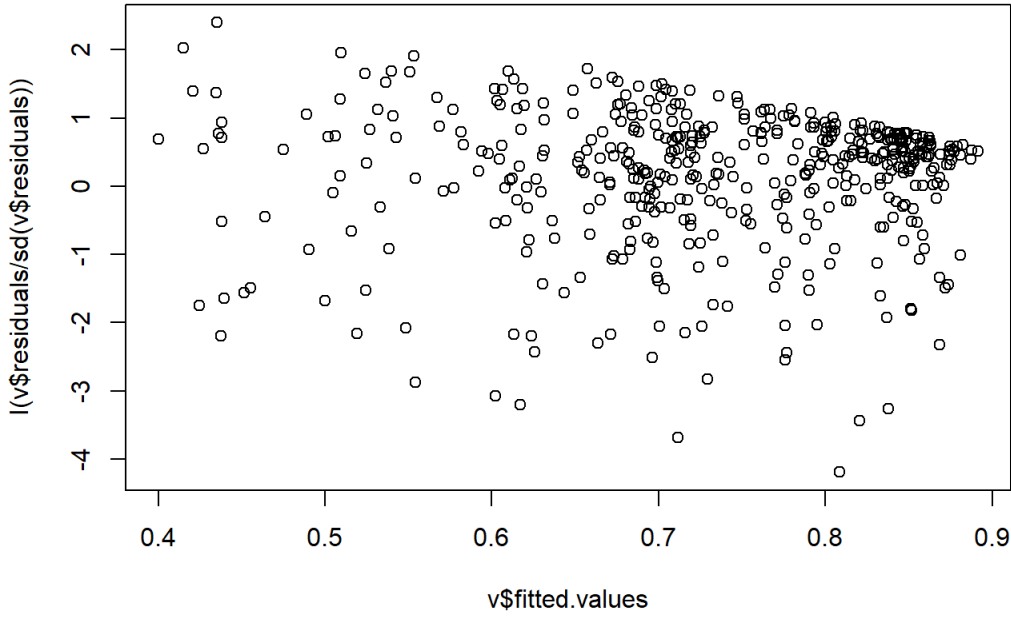
**Beta regression**



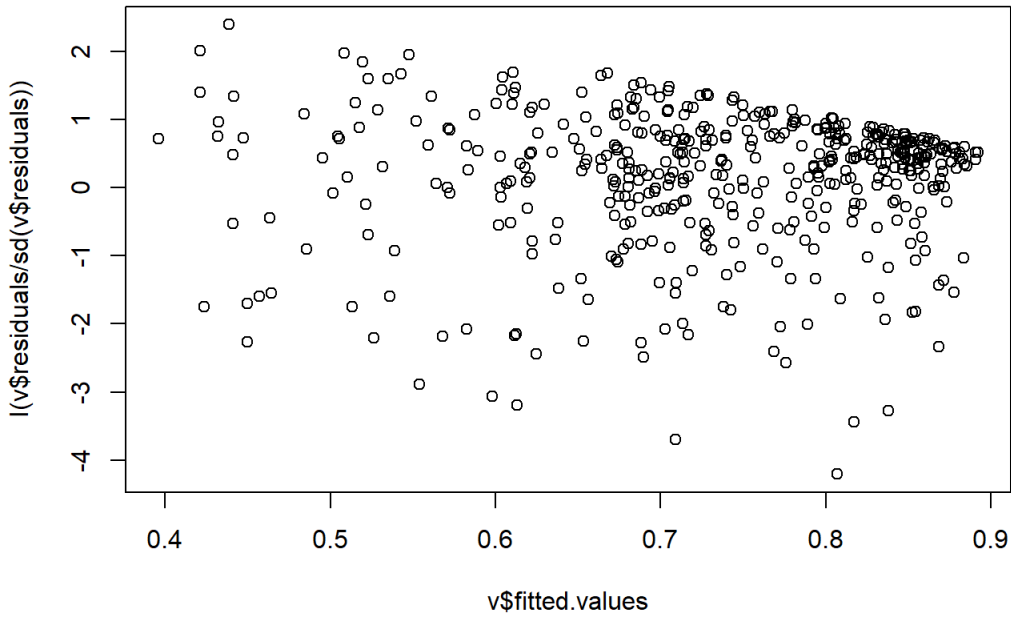
**Beta regression**



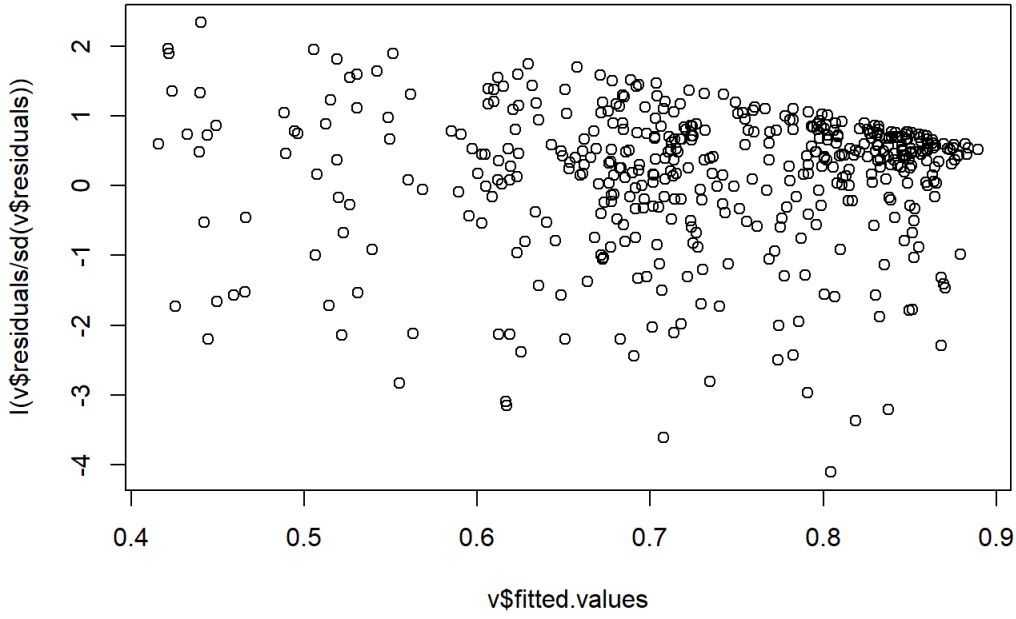
**Beta regression**



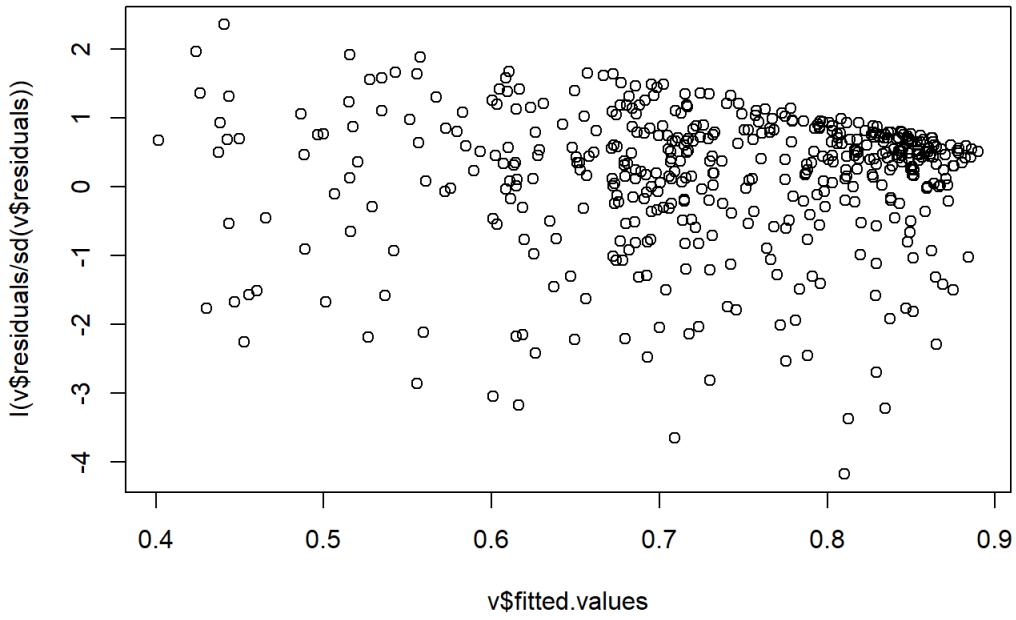
**Beta regression**



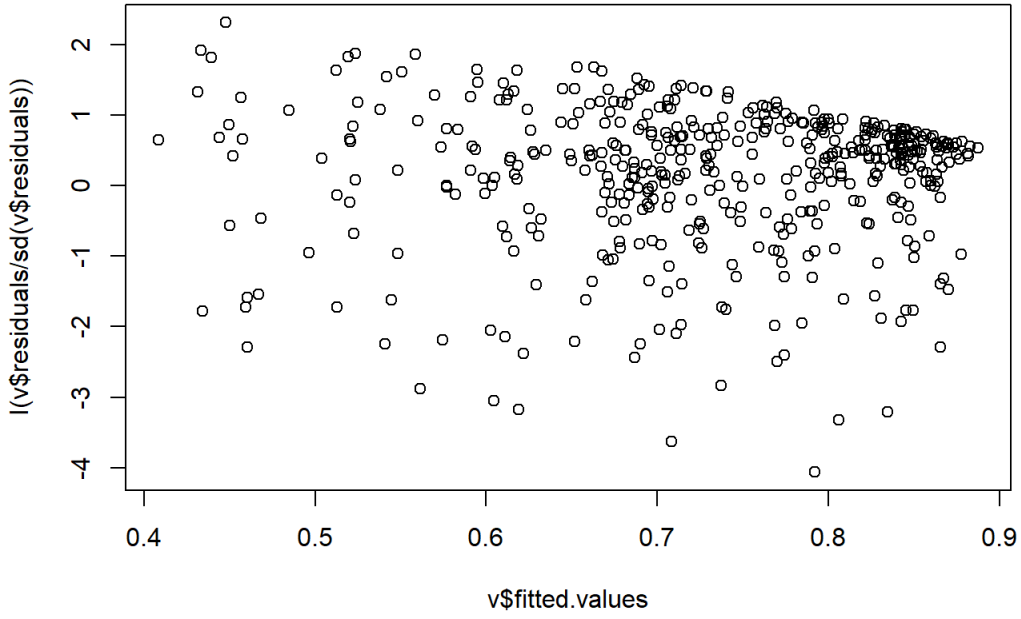
**Beta regression**



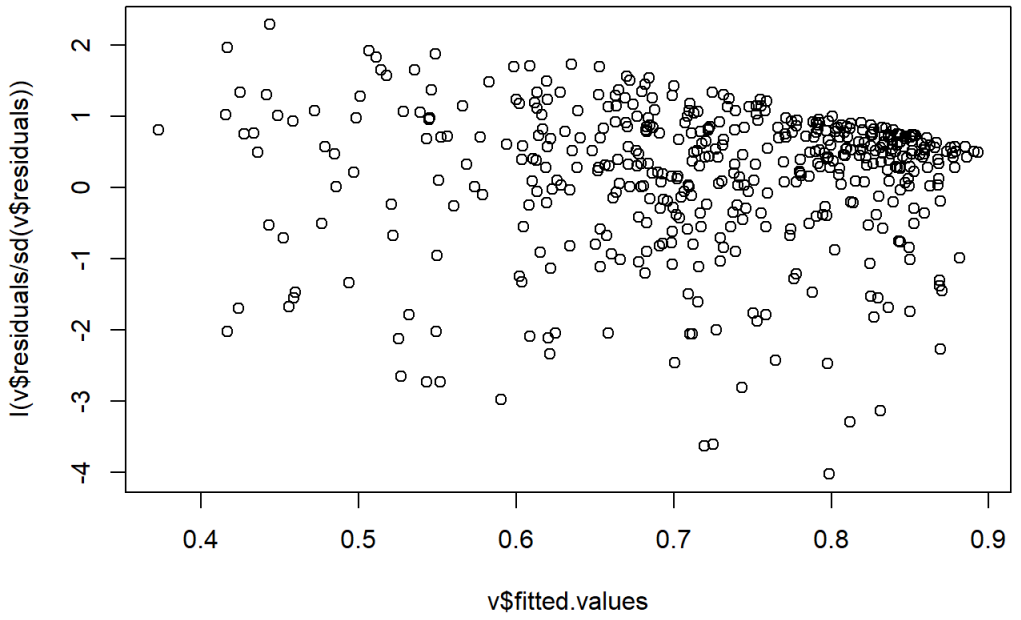
**Beta regression**



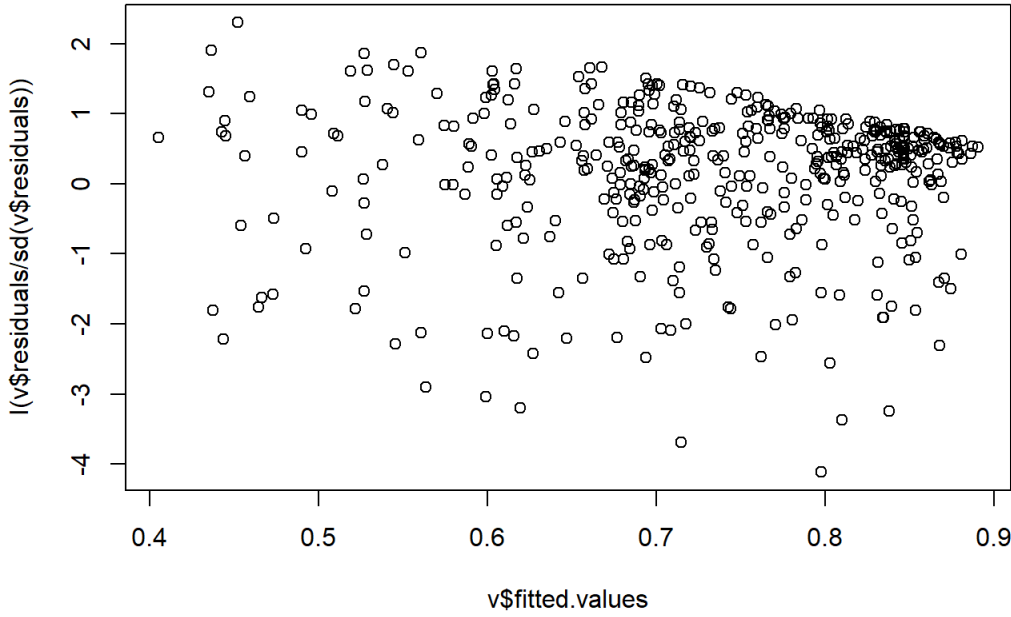
**Beta regression**



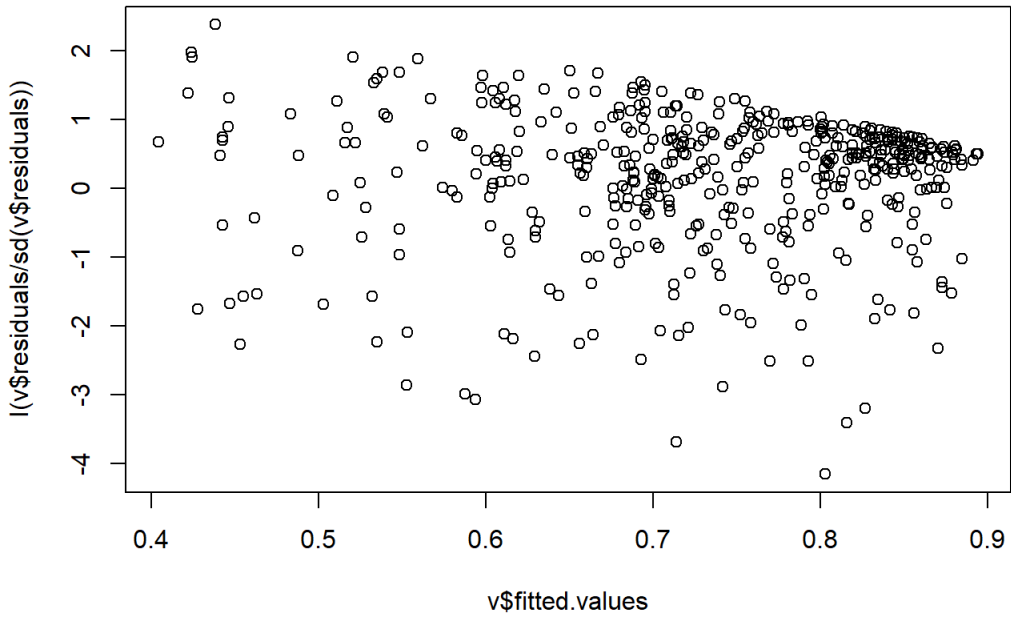
**Beta regression**



**Beta regression**



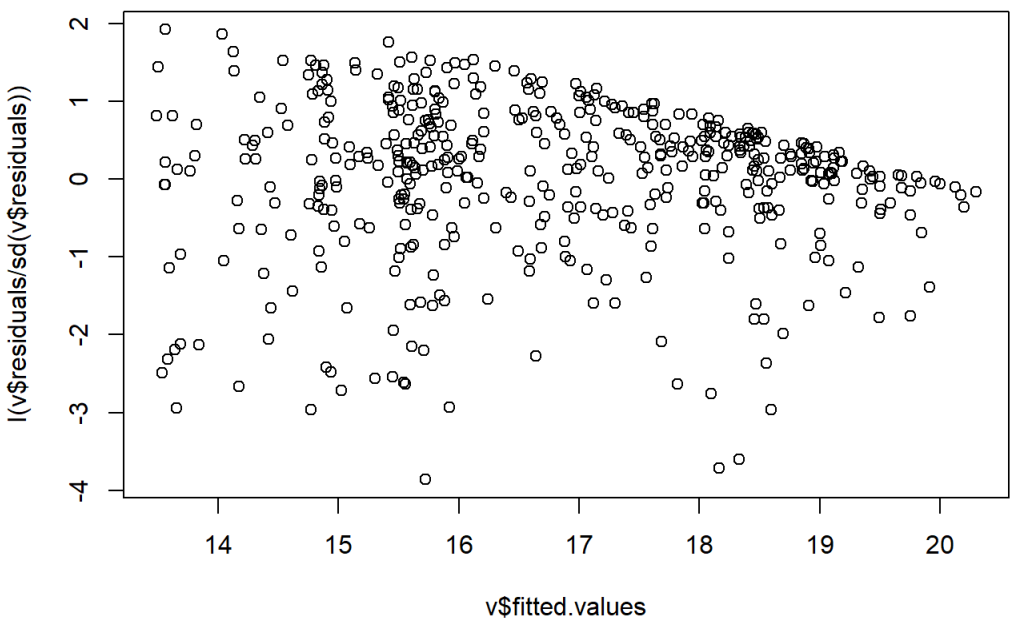
**Beta regression**



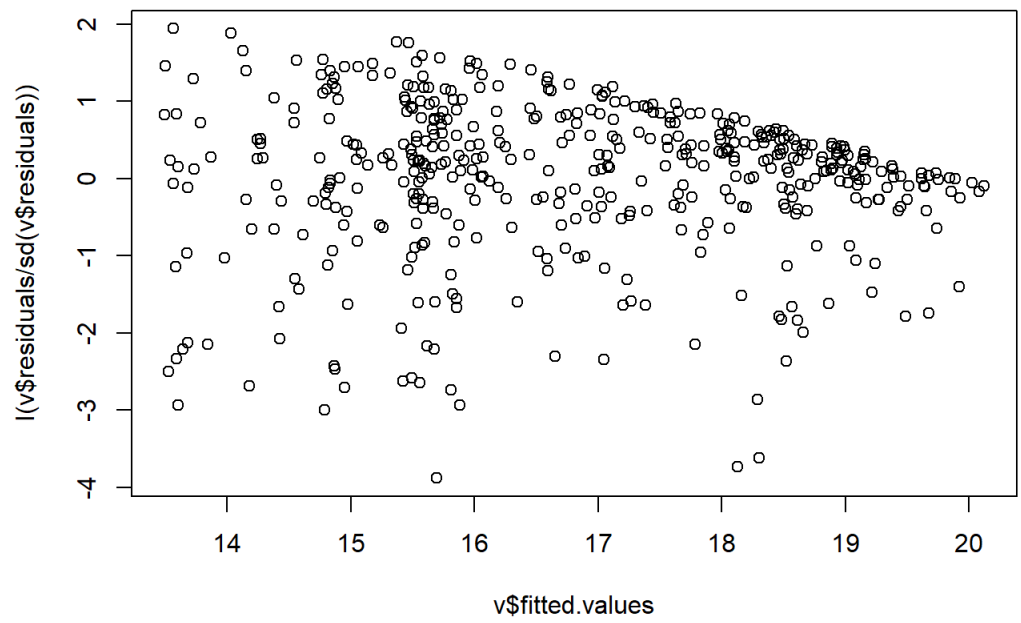
```
## [[1]]
## NULL
##
## [[2]]
## NULL
##
## [[3]]
## NULL
##
## [[4]]
## NULL
##
## [[5]]
## NULL
##
## [[6]]
## NULL
##
## [[7]]
## NULL
##
## [[8]]
## NULL
##
## [[9]]
## NULL
##
## [[10]]
## NULL
```

```
map(gee.fit, function(v) {
  plot(I(v$residuals/sd(v$residuals)) ~ v$fitted.values, main = "GEE Gamma regression")})
```

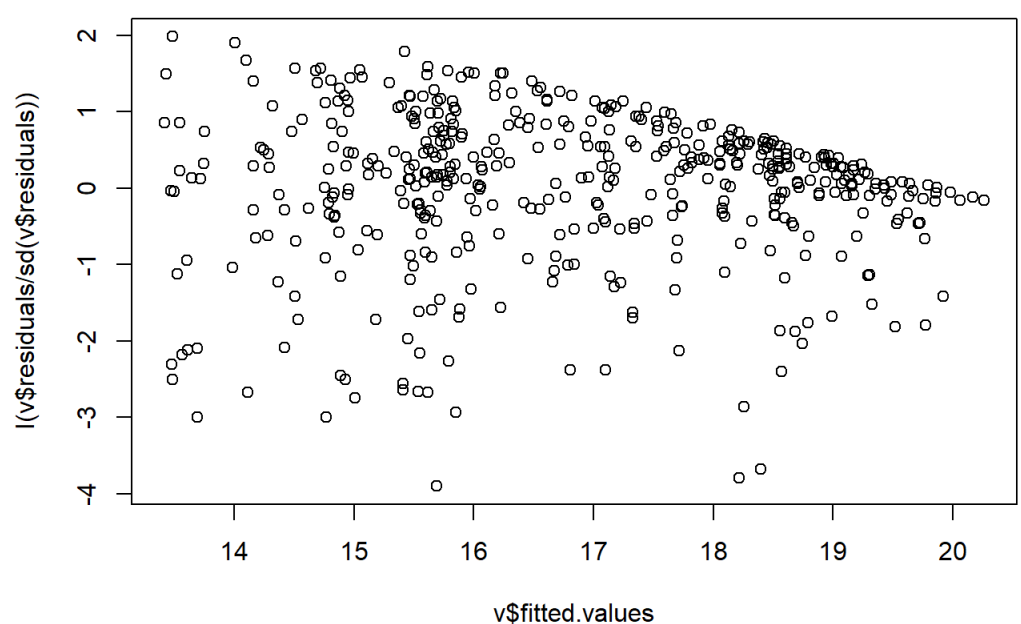
**GEE Gamma regression**



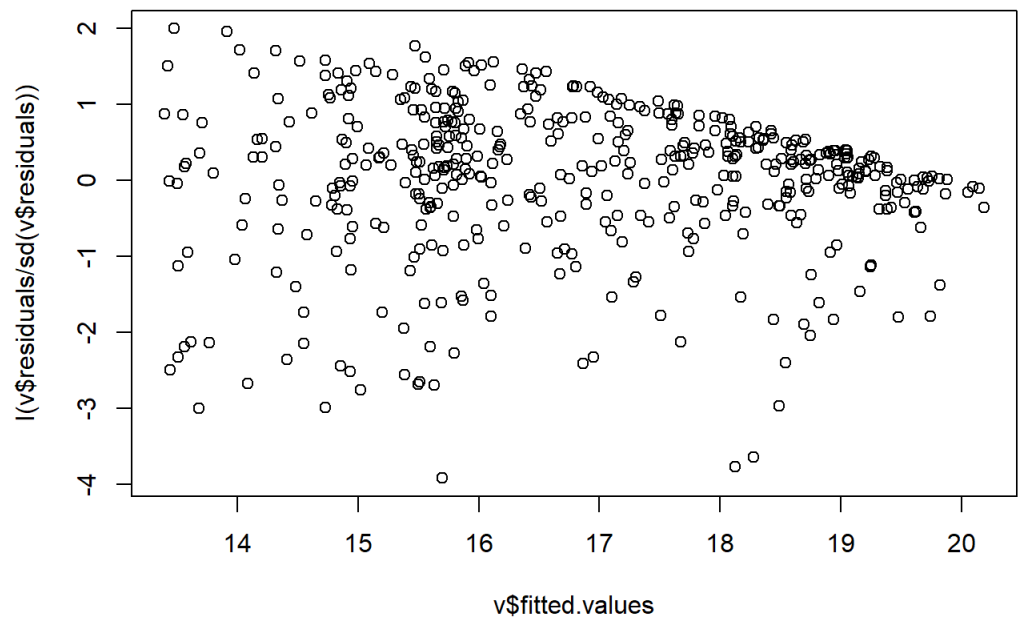
GEE Gamma regression



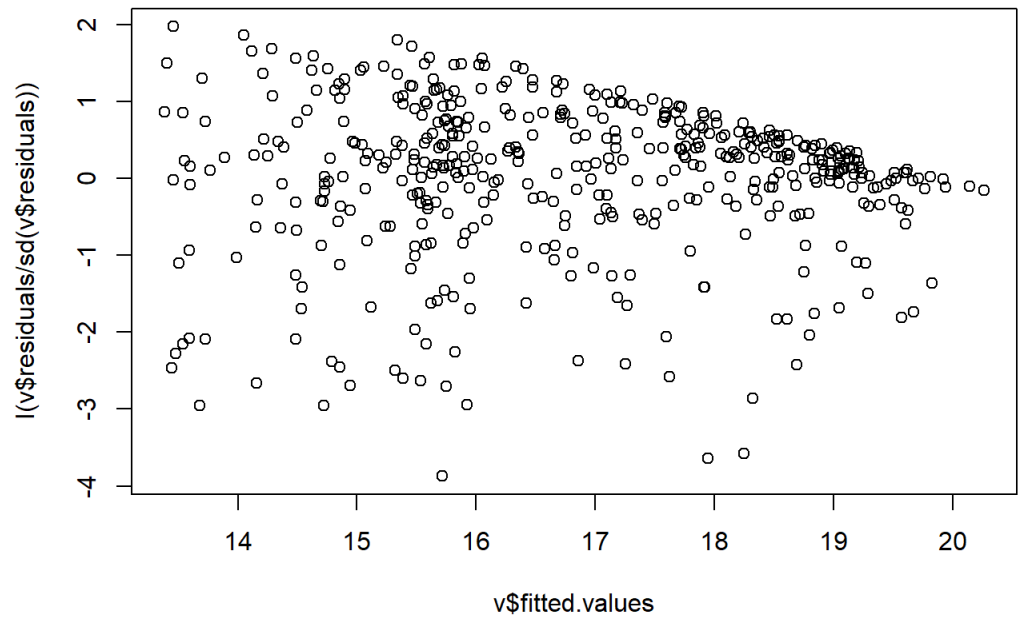
GEE Gamma regression



GEE Gamma regression

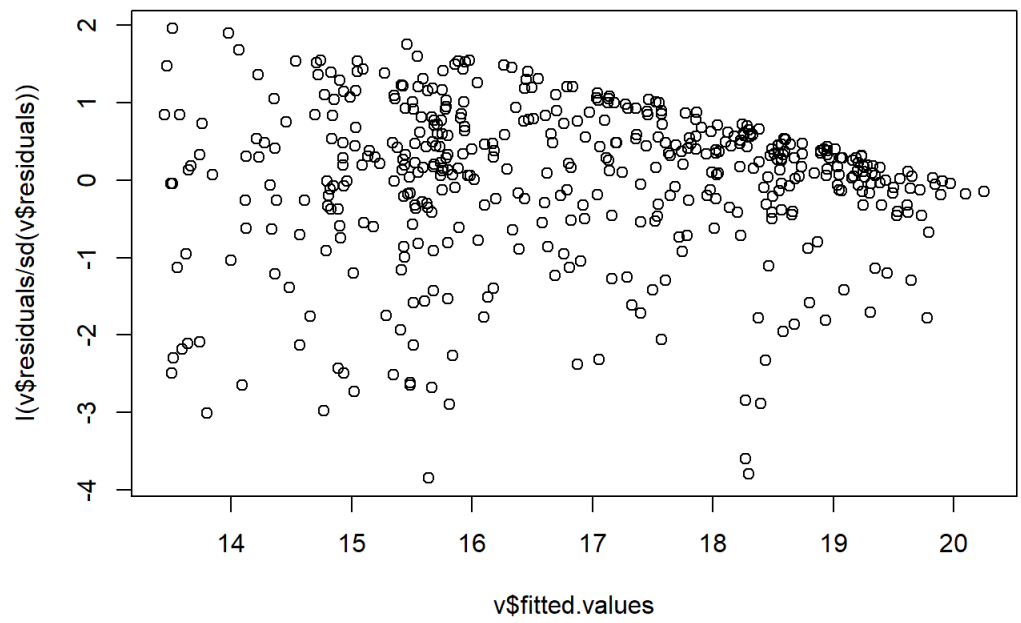


GEE Gamma regression

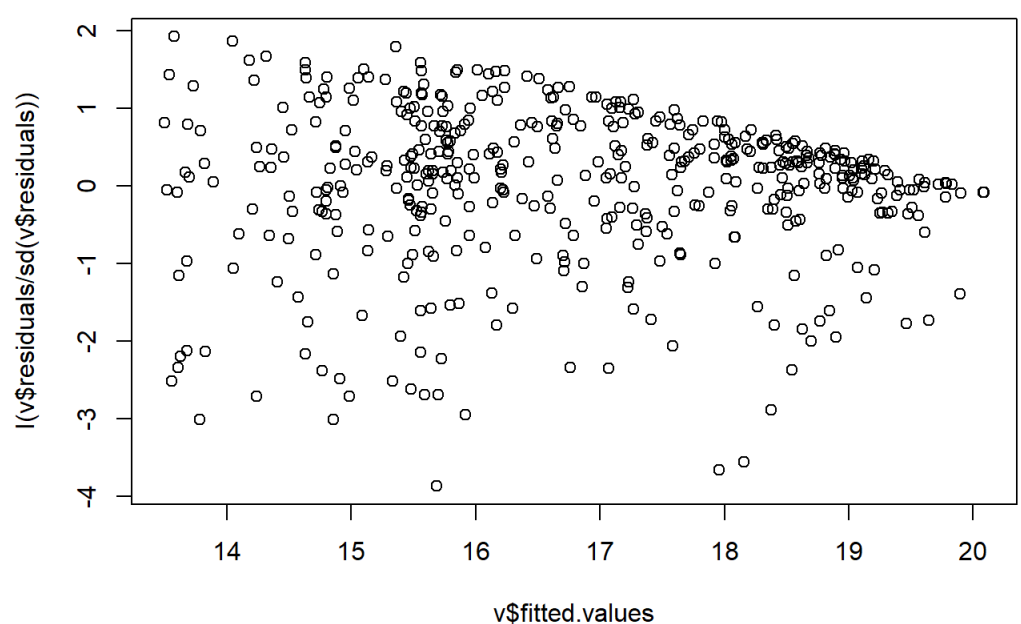




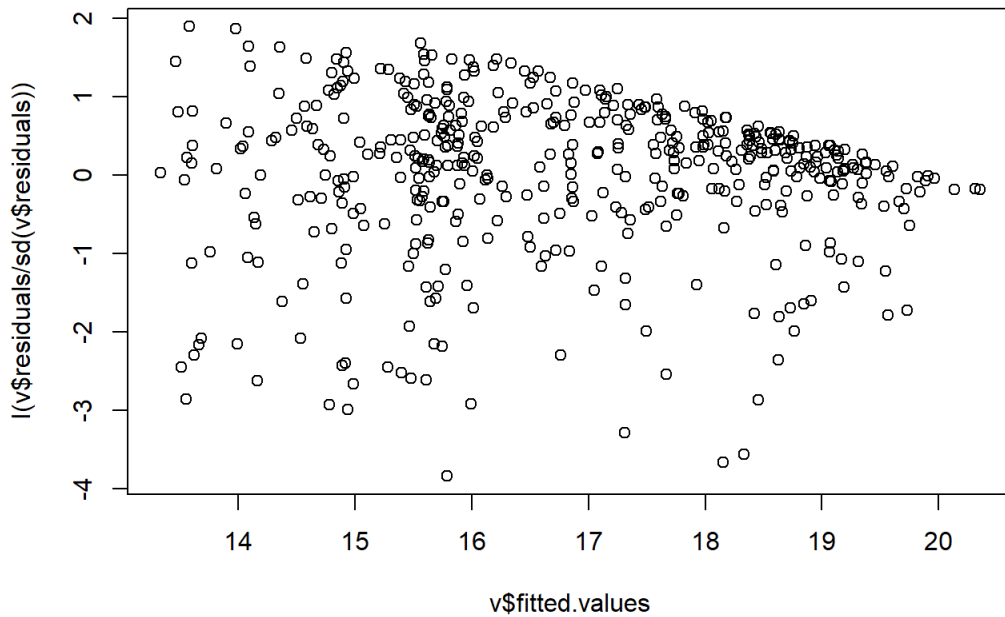
GEE Gamma regression



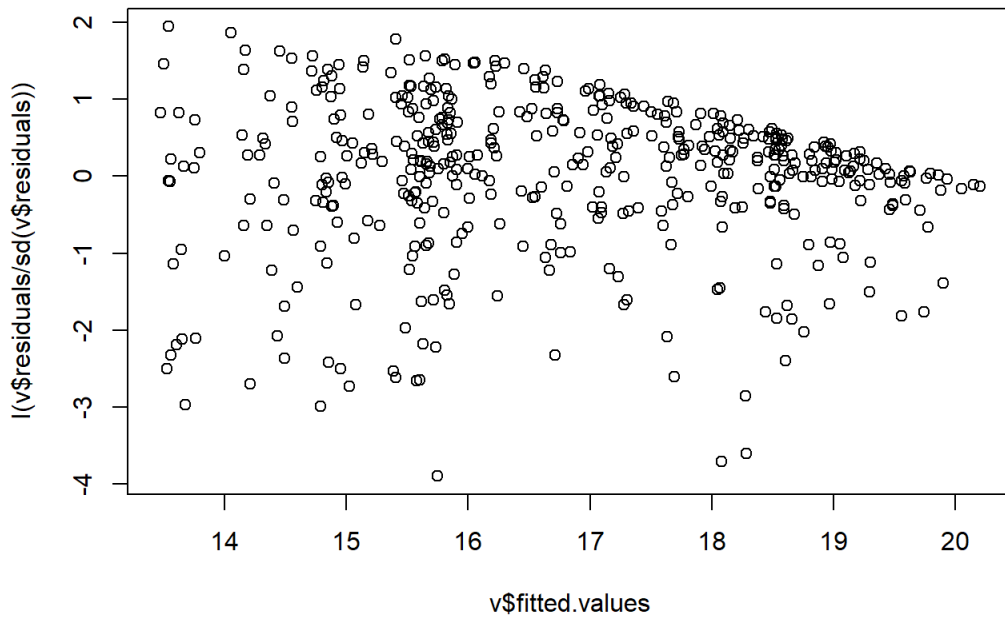
GEE Gamma regression



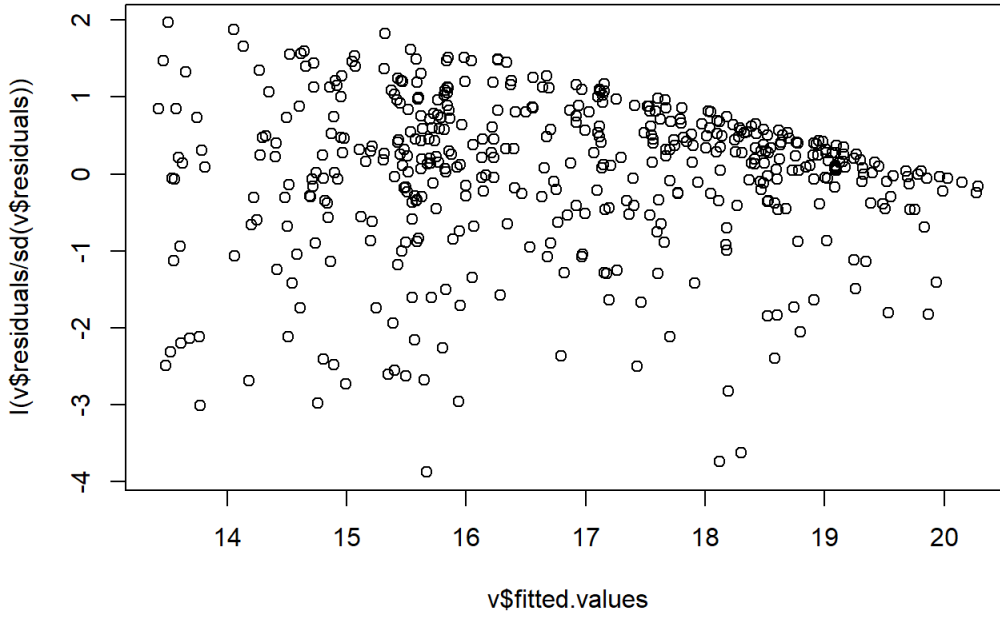
GEE Gamma regression



GEE Gamma regression



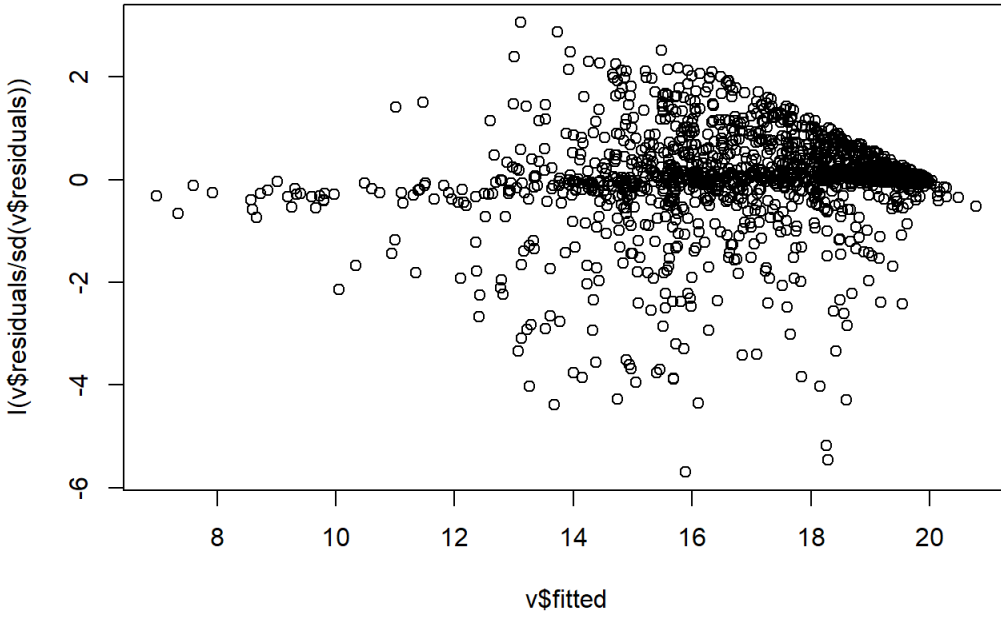
### GEE Gamma regression



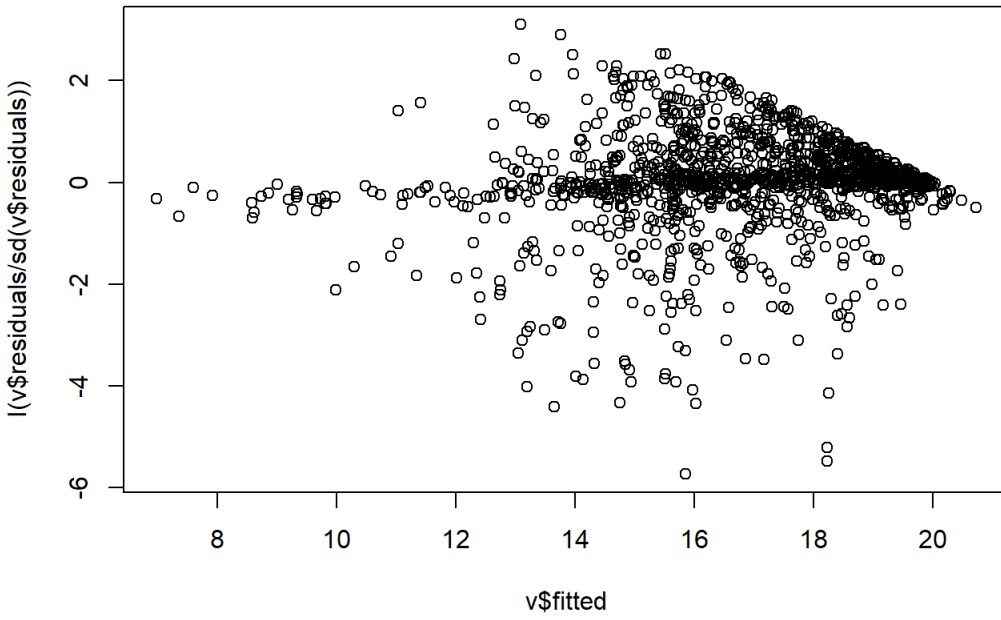
```
## [[1]]
## NULL
##
## [[2]]
## NULL
##
## [[3]]
## NULL
##
## [[4]]
## NULL
##
## [[5]]
## NULL
##
## [[6]]
## NULL
##
## [[7]]
## NULL
##
## [[8]]
## NULL
##
## [[9]]
## NULL
##
## [[10]]
## NULL
```

```
map(lme.fit2, function(v) {
  plot(I(v$residuals/sd(v$residuals)) ~ v$fitted, main = "LME model")})
```

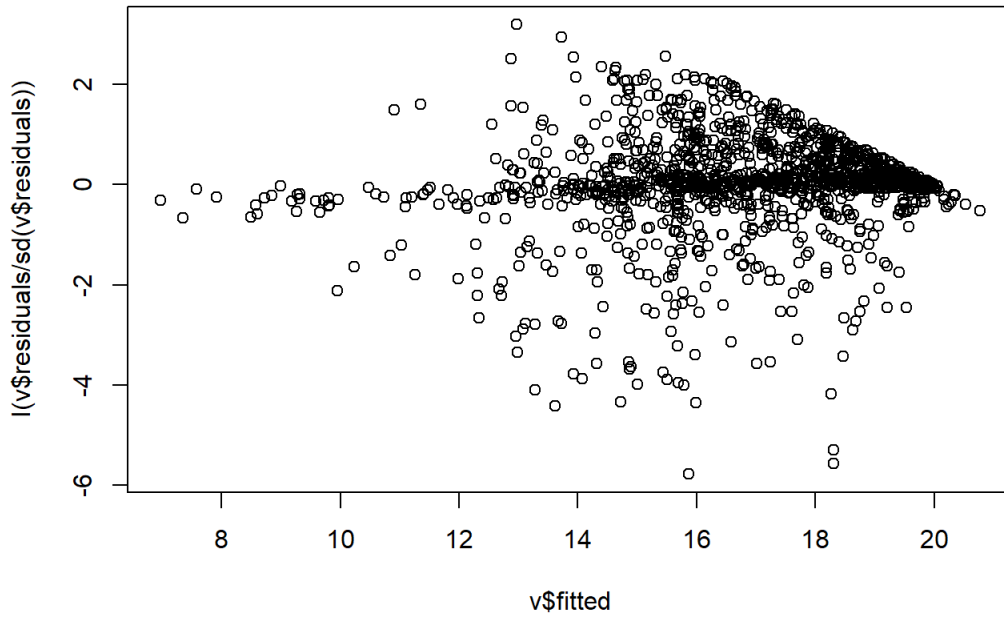
LME model



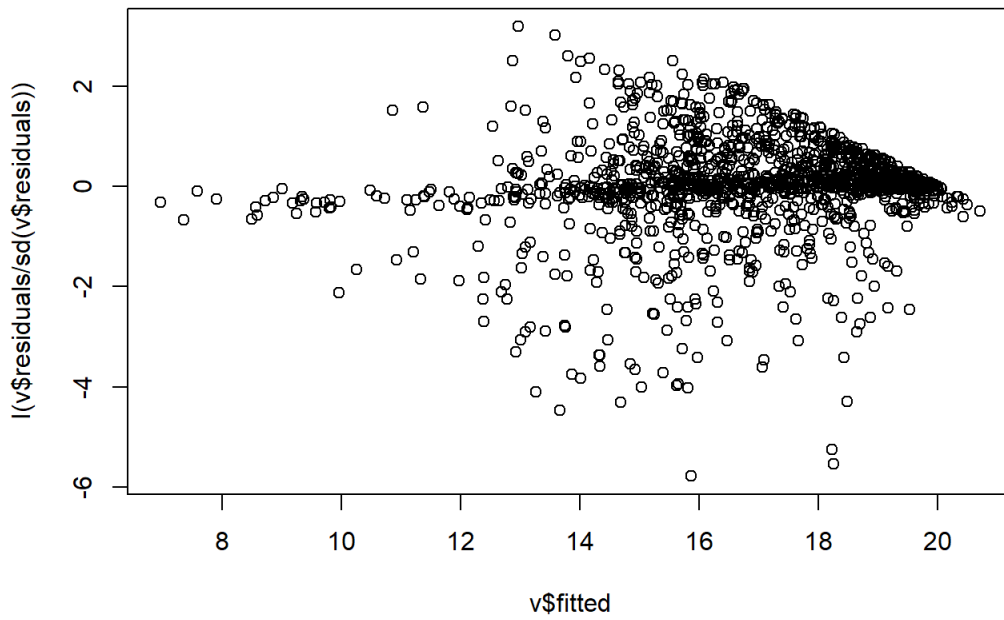
LME model



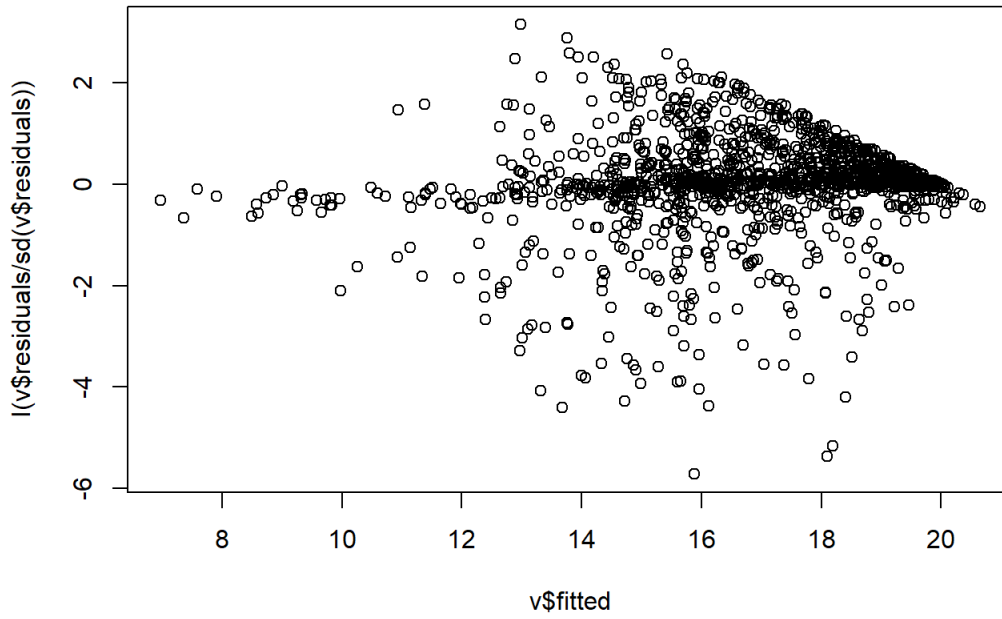
LME model



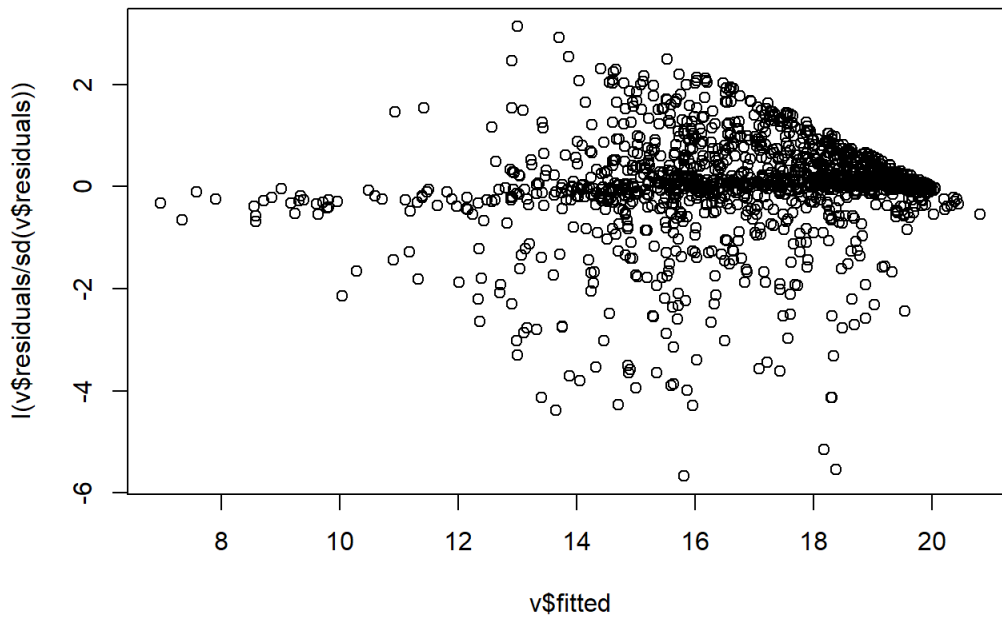
LME model



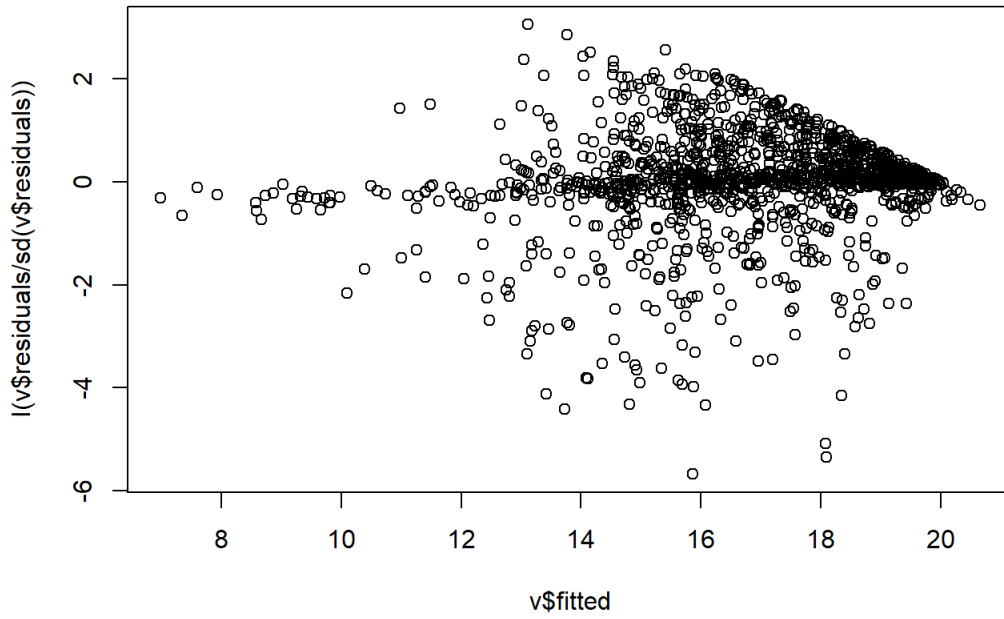
LME model



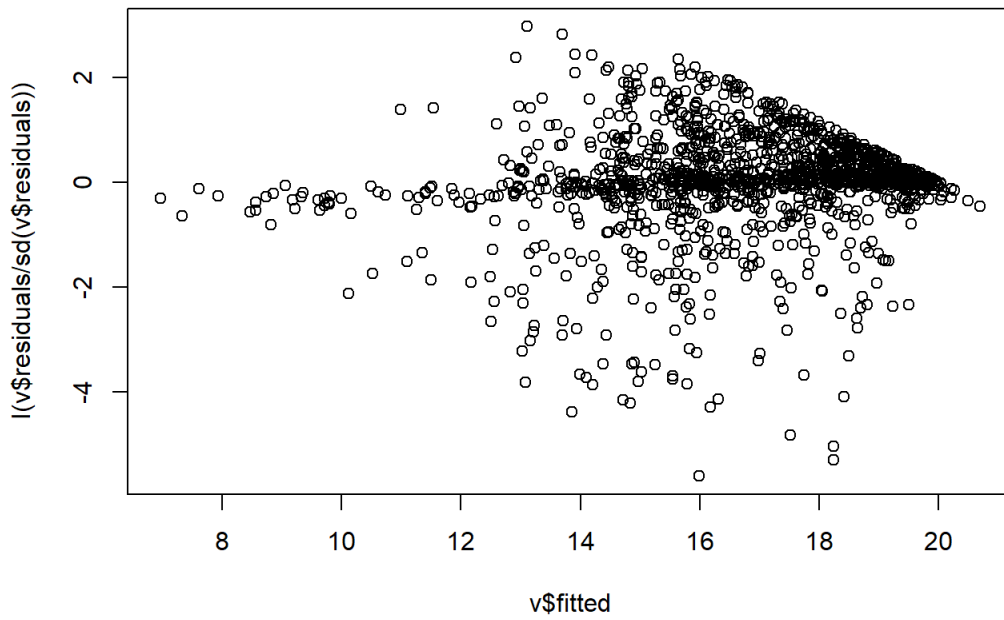
LME model



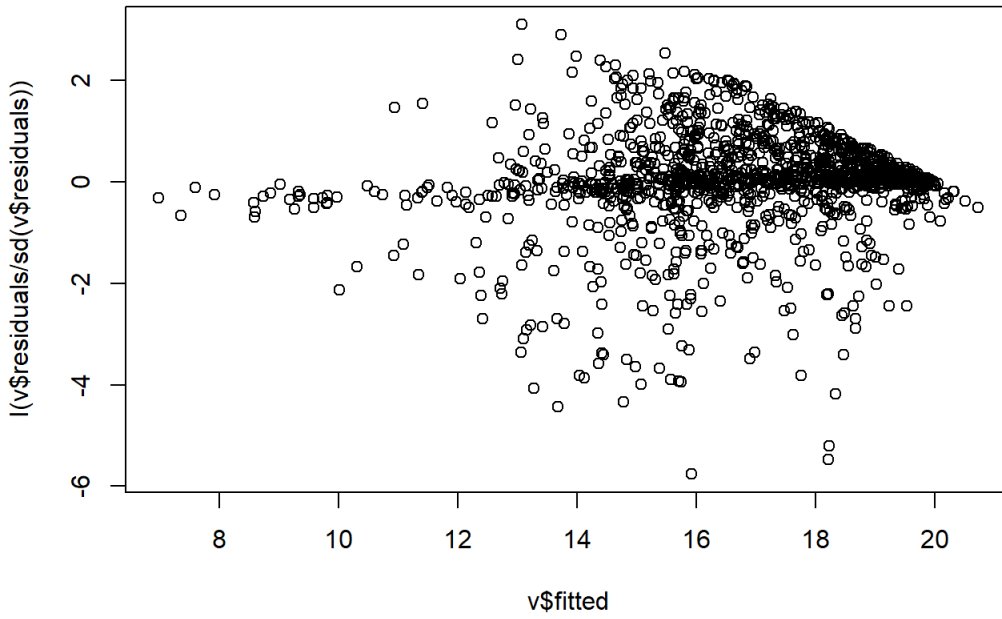
LME model



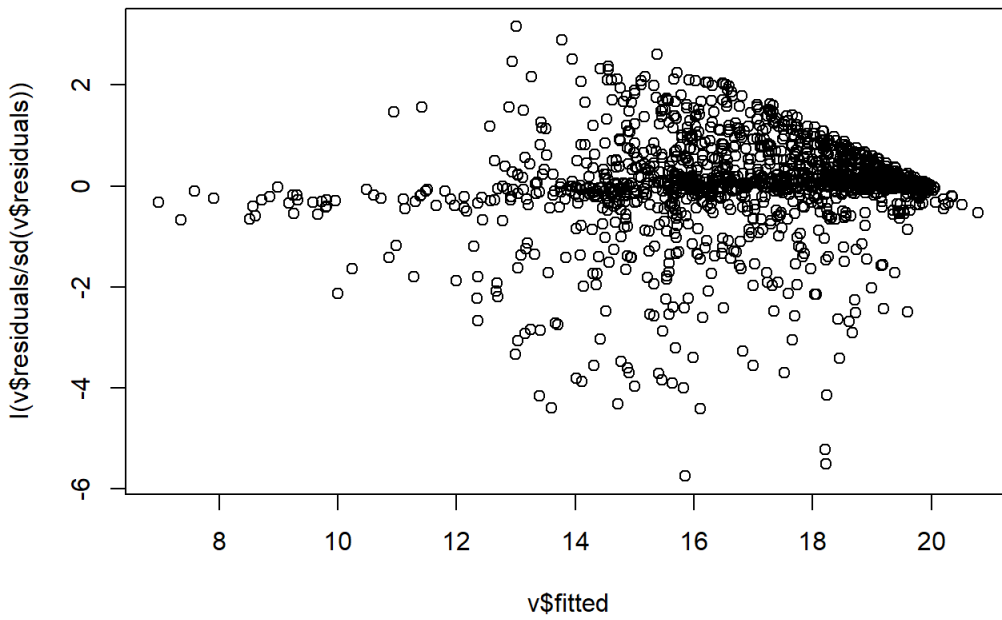
LME model



LME model



LME model

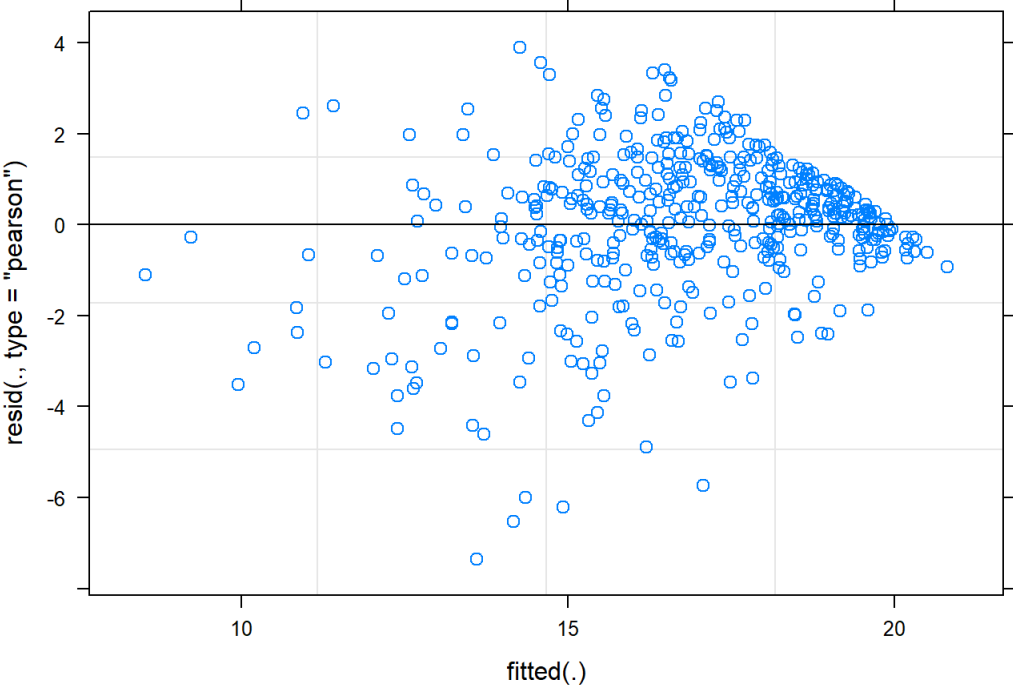




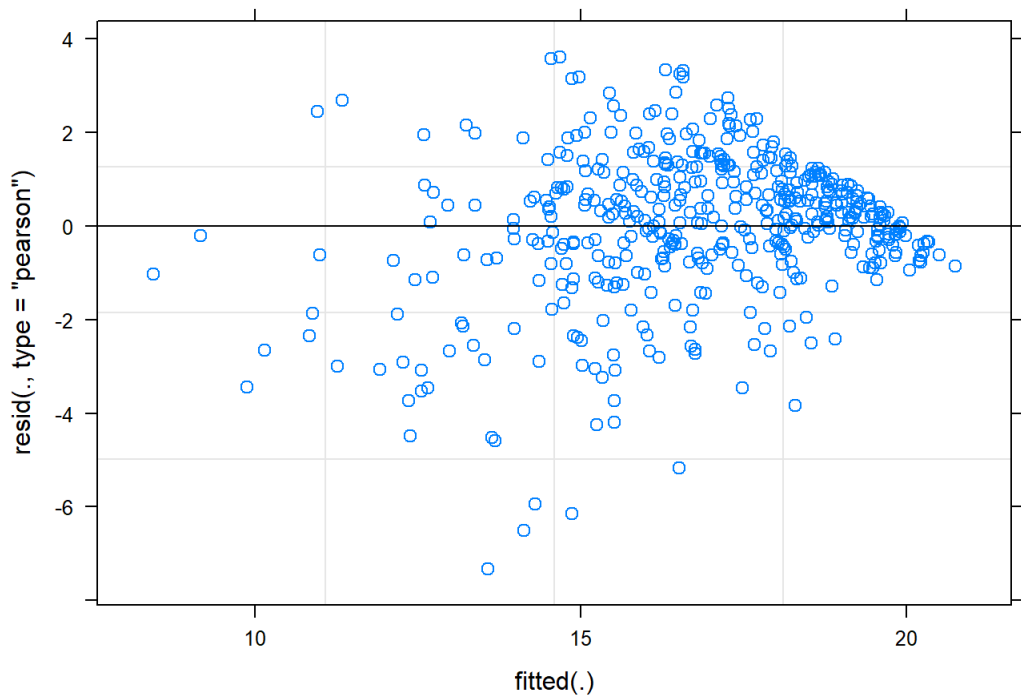
```
## [[1]]  
## NULL  
##  
## [[2]]  
## NULL  
##  
## [[3]]  
## NULL  
##  
## [[4]]  
## NULL  
##  
## [[5]]  
## NULL  
##  
## [[6]]  
## NULL  
##  
## [[7]]  
## NULL  
##  
## [[8]]  
## NULL  
##  
## [[9]]  
## NULL  
##  
## [[10]]  
## NULL
```

```
map(lmer.fit, plot)
```

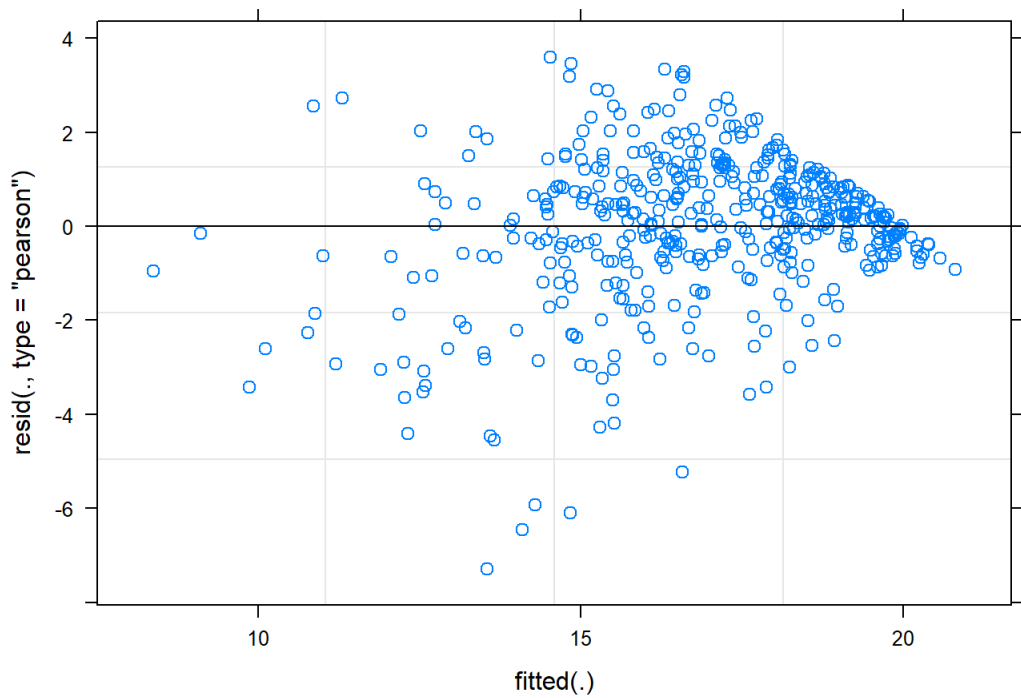
```
## [[1]]
```



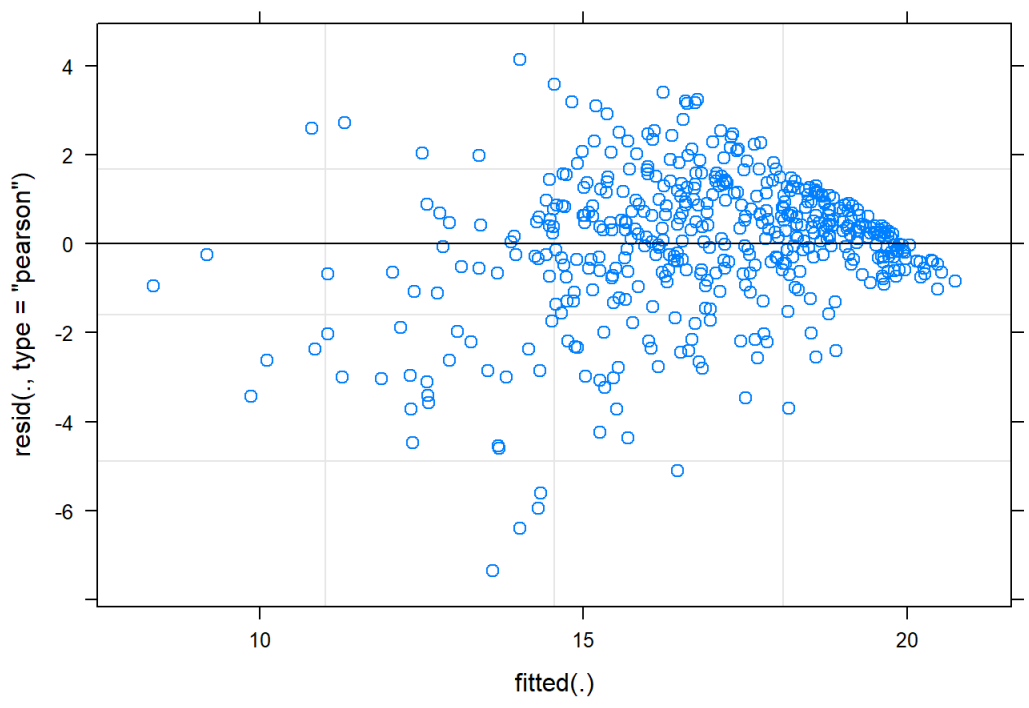
```
##  
## [[2]]
```



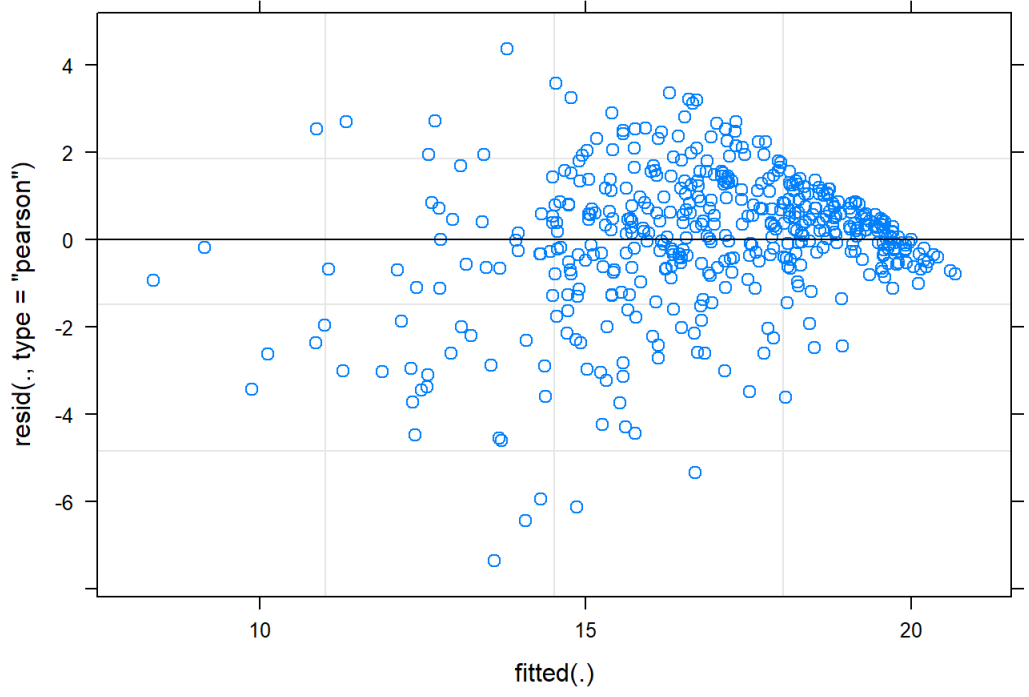
```
##  
## [[3]]
```



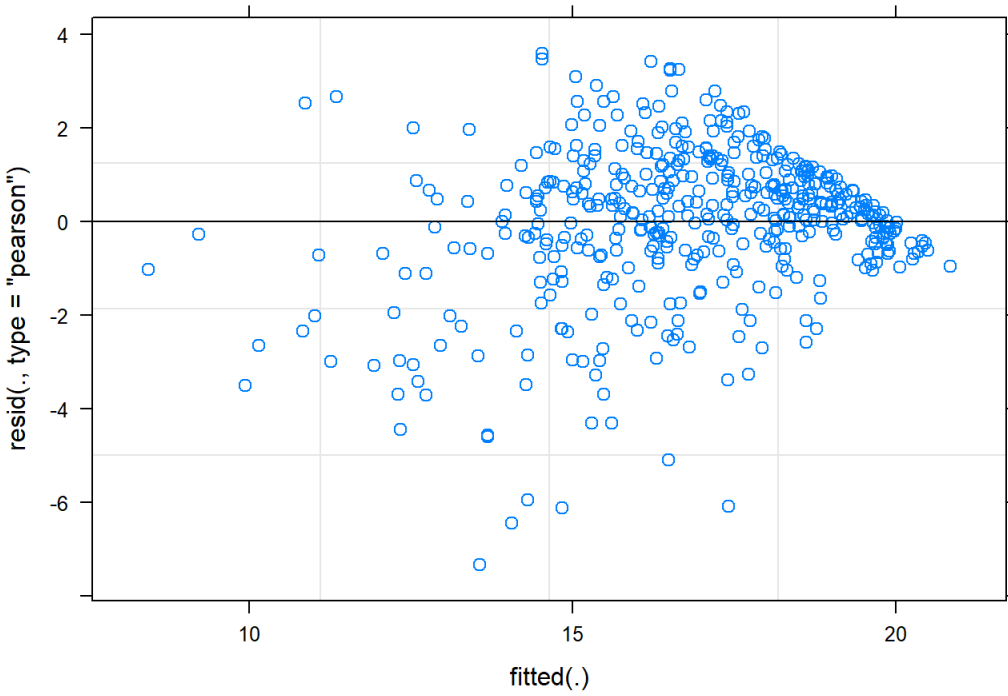
```
##  
## [[4]]
```



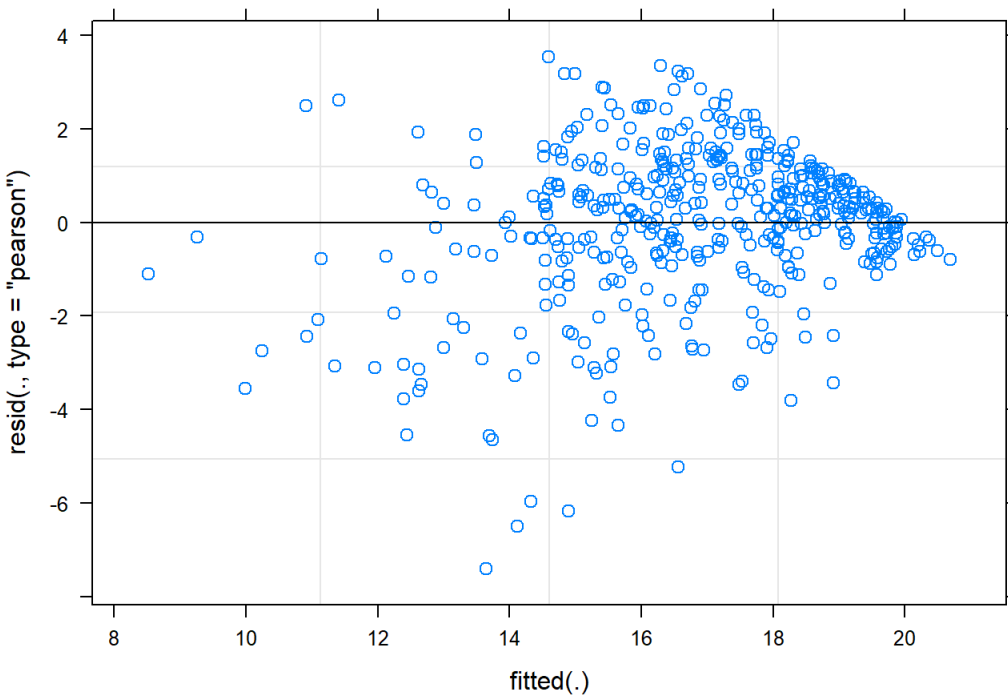
```
##  
## [[5]]
```



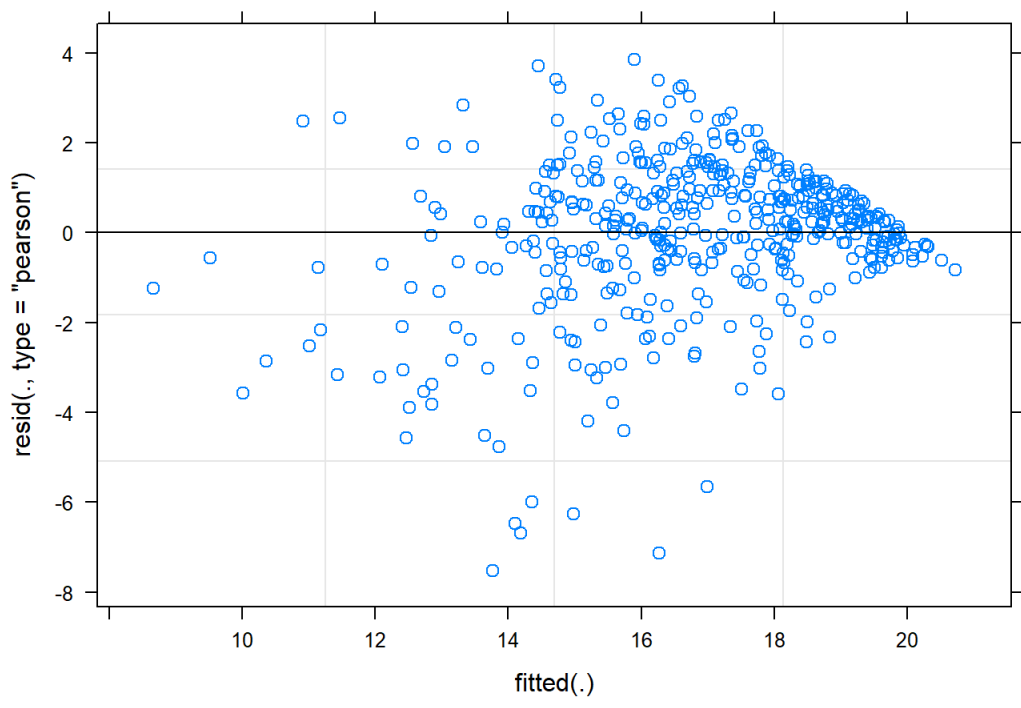
```
##  
## [[6]]
```



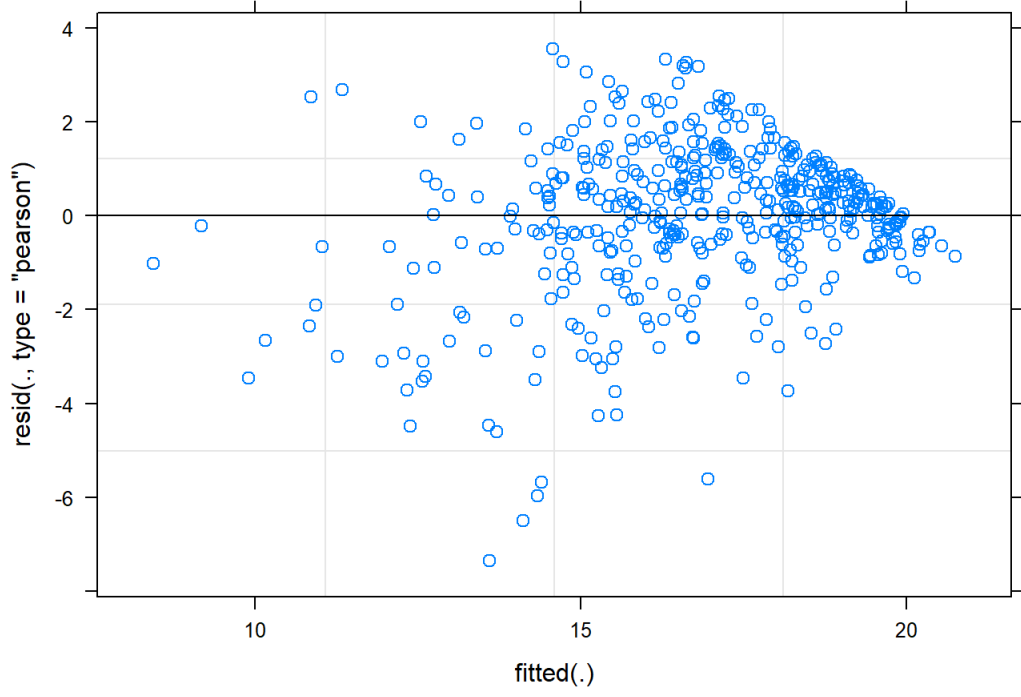
```
##  
## [[7]]
```



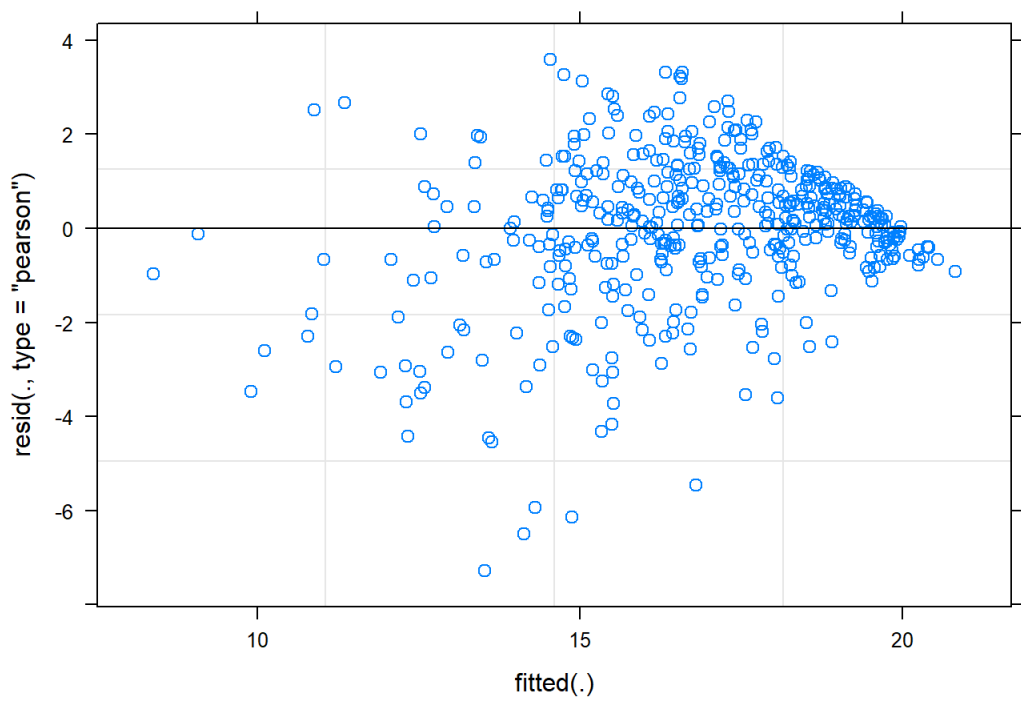
```
##  
## [[8]]
```



```
##  
## [[9]]
```

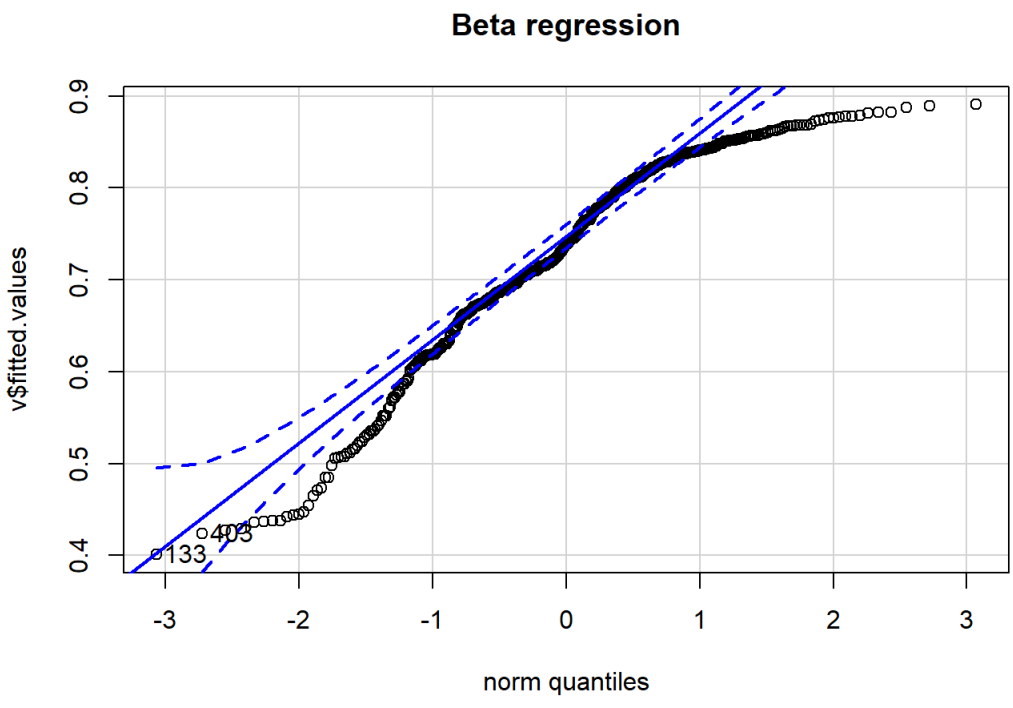


```
##  
## [[10]]
```

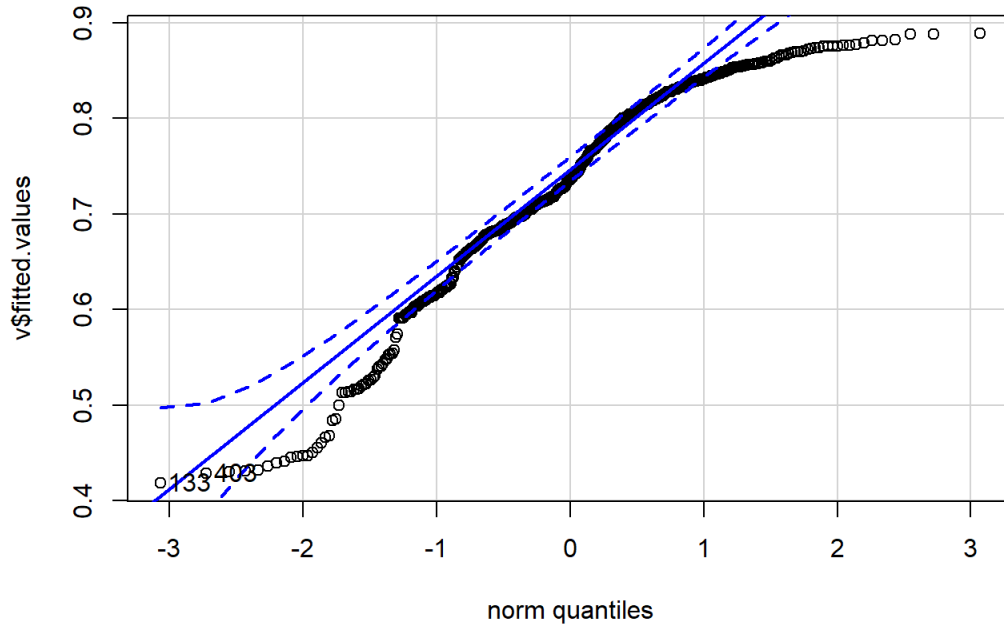


QQ plots

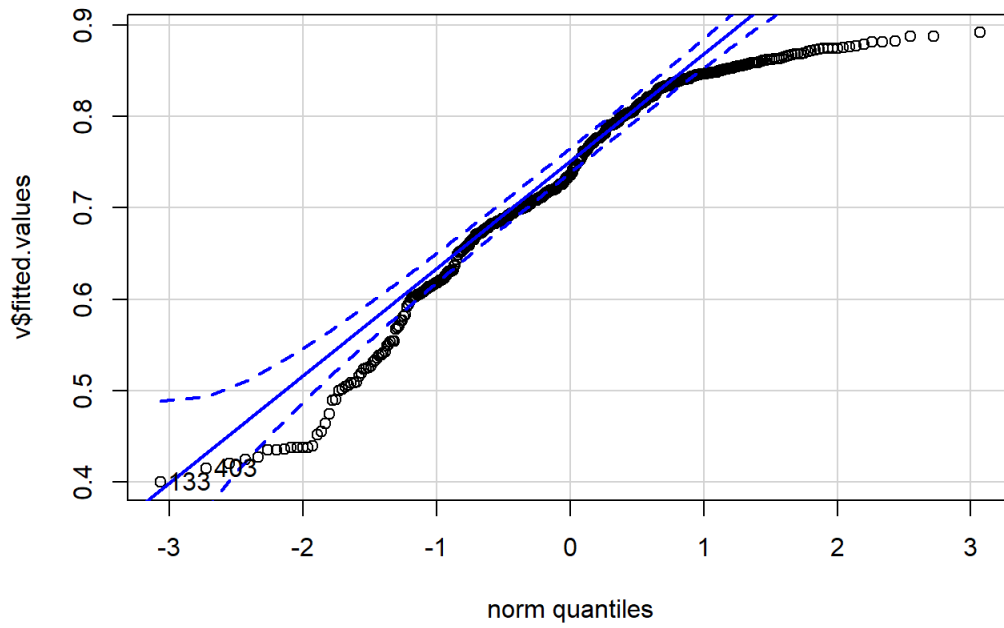
```
map(beta.fit, function(v){car::qqPlot(v$fitted.values,  
  main = "Beta regression")})
```



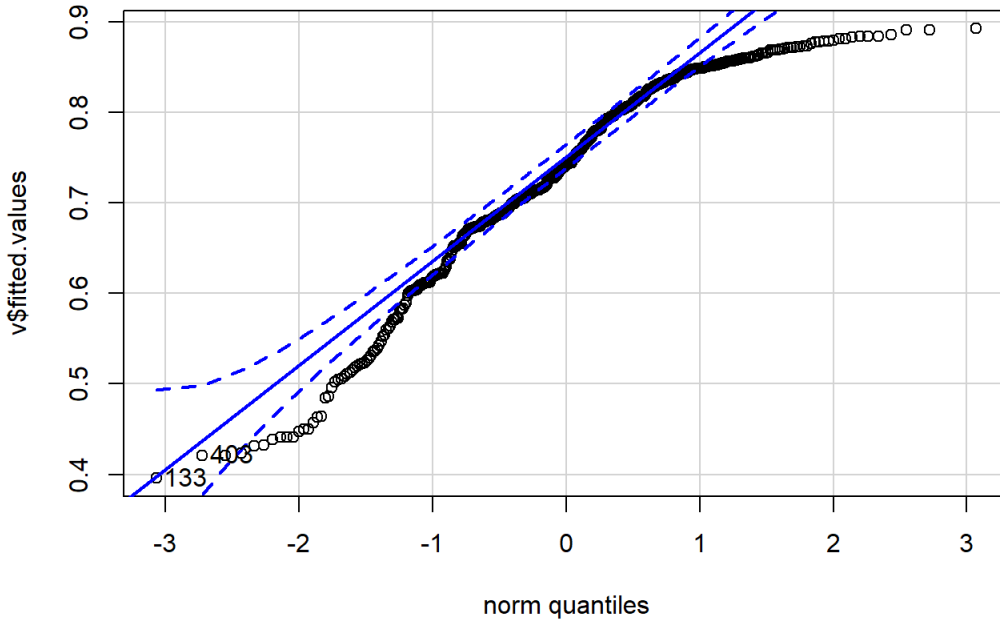
Beta regression



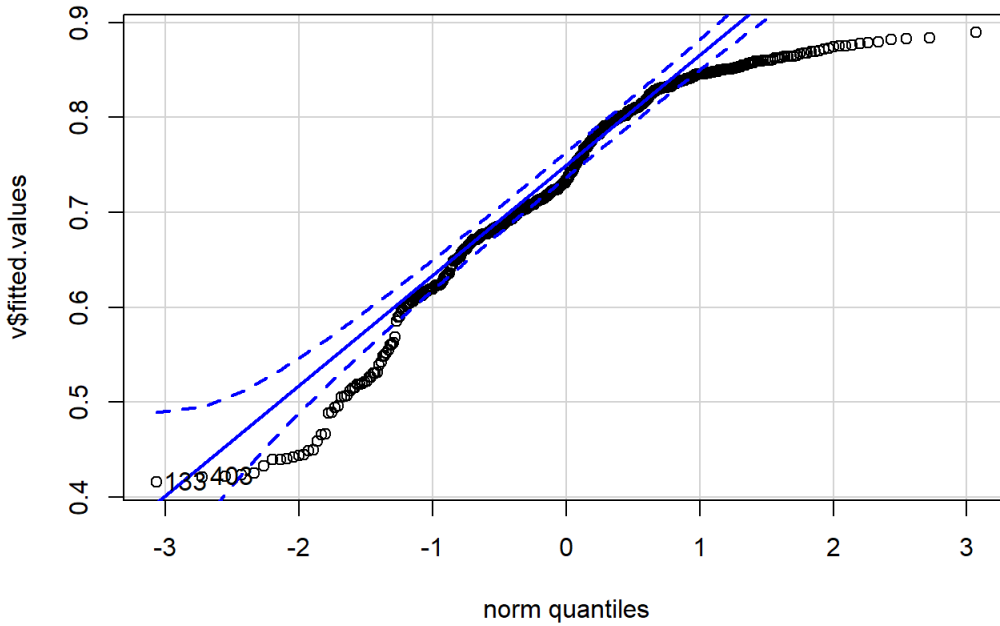
Beta regression



Beta regression

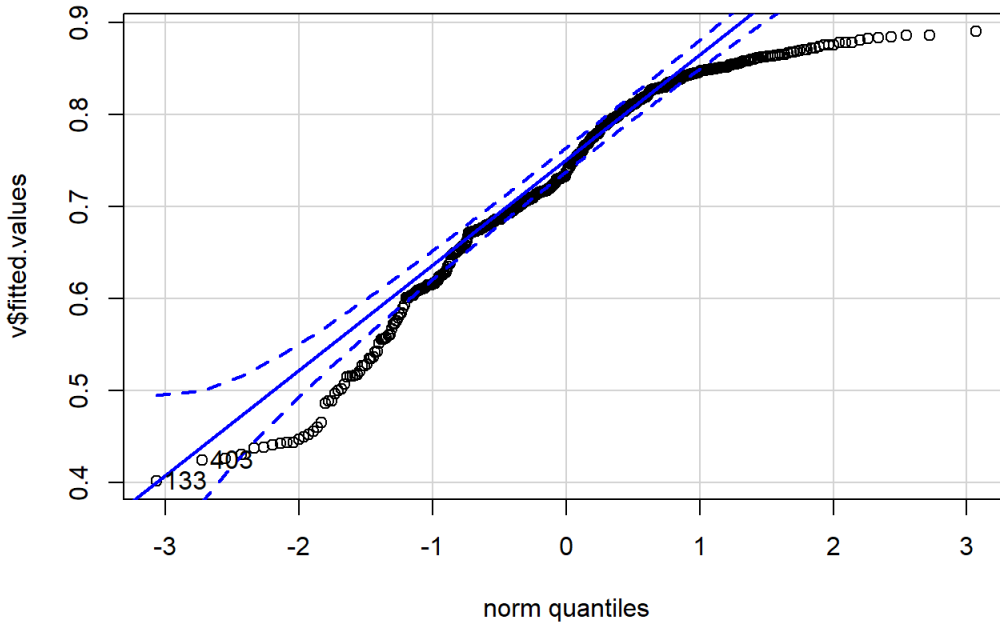


Beta regression

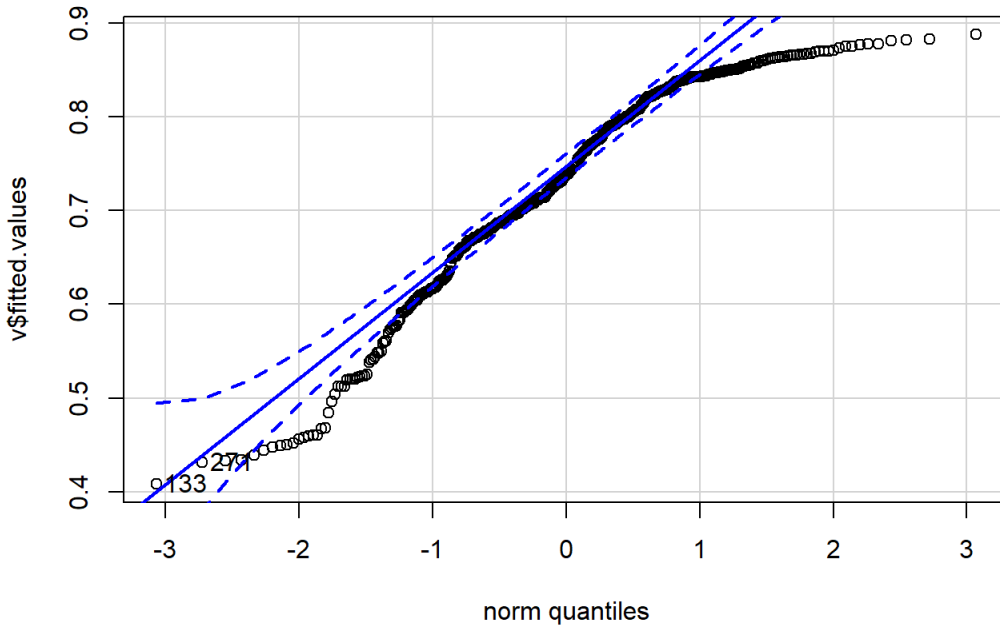




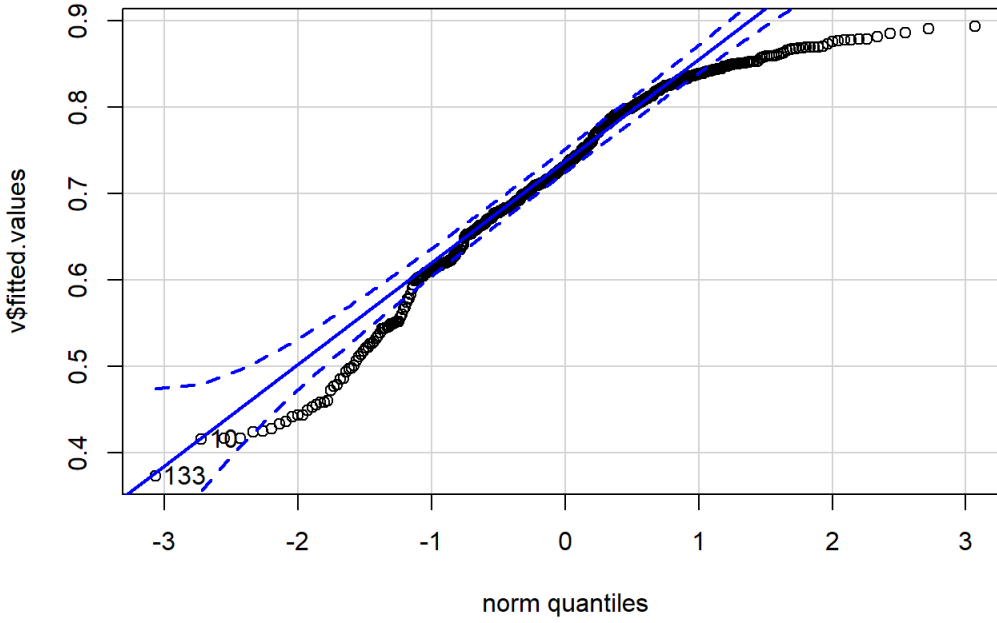
Beta regression



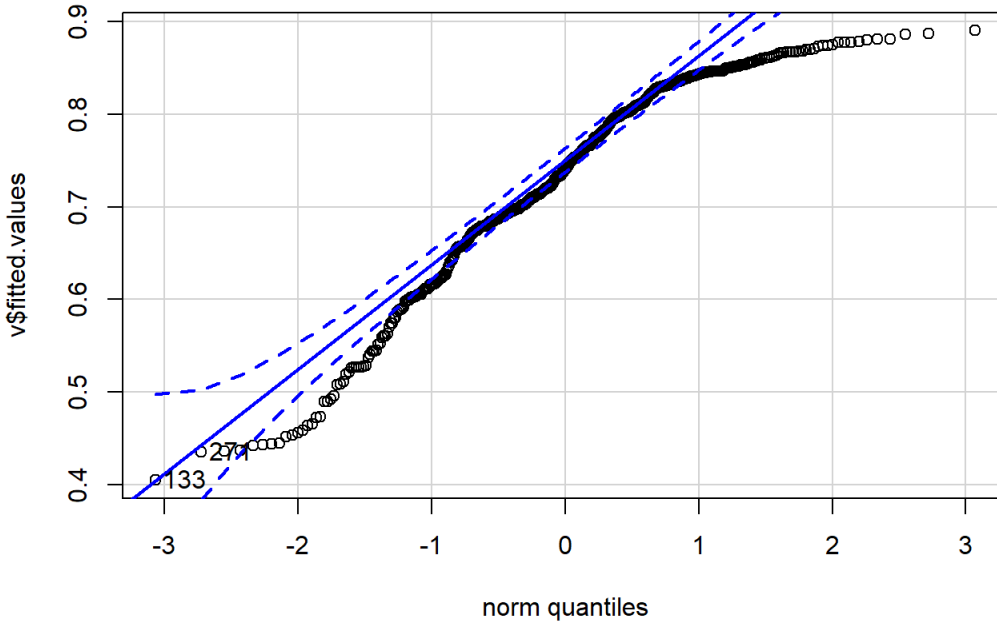
Beta regression



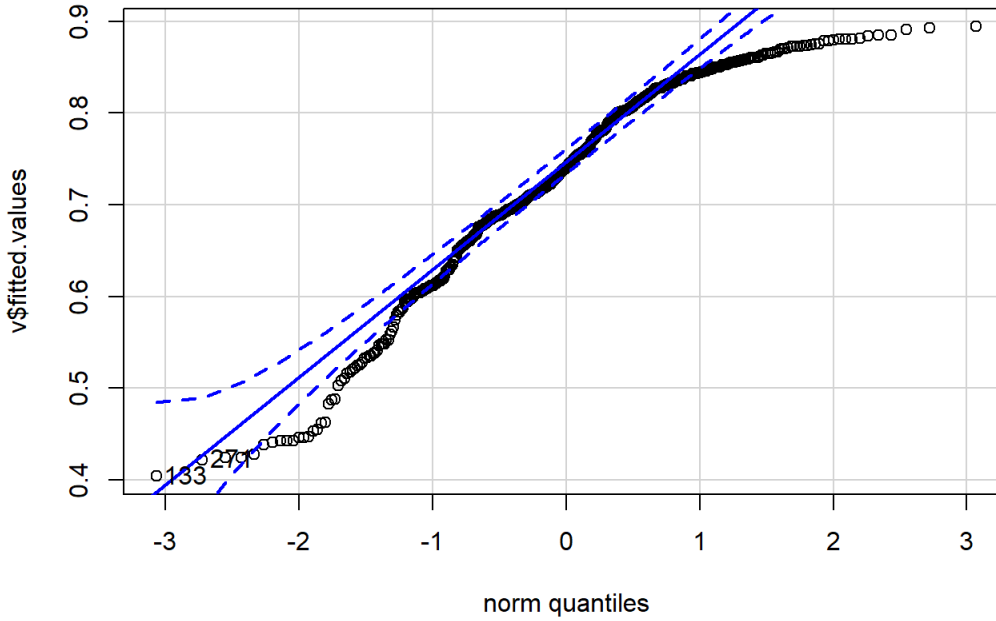
Beta regression



Beta regression



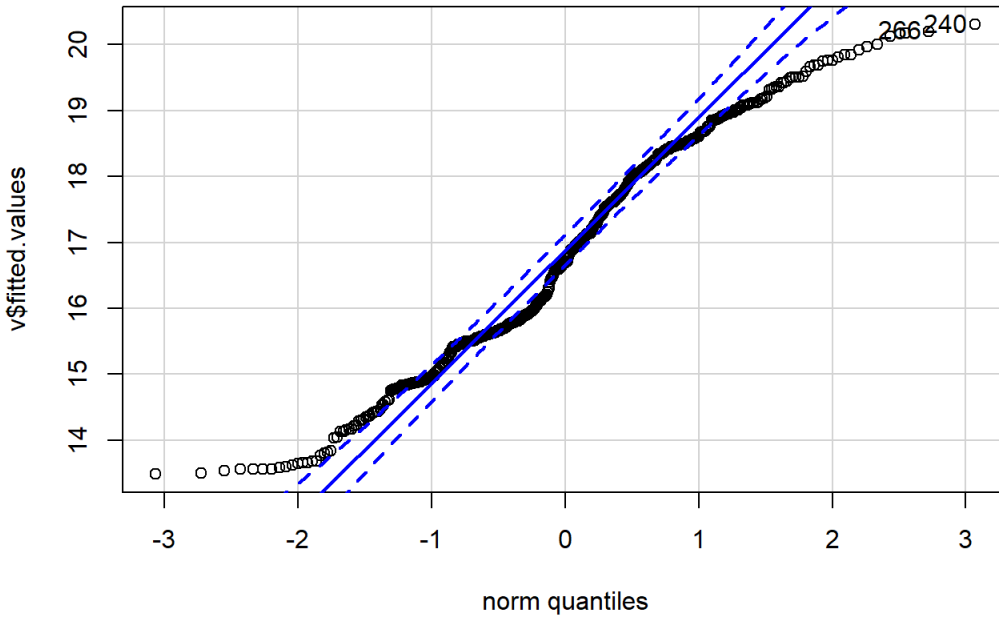
### Beta regression



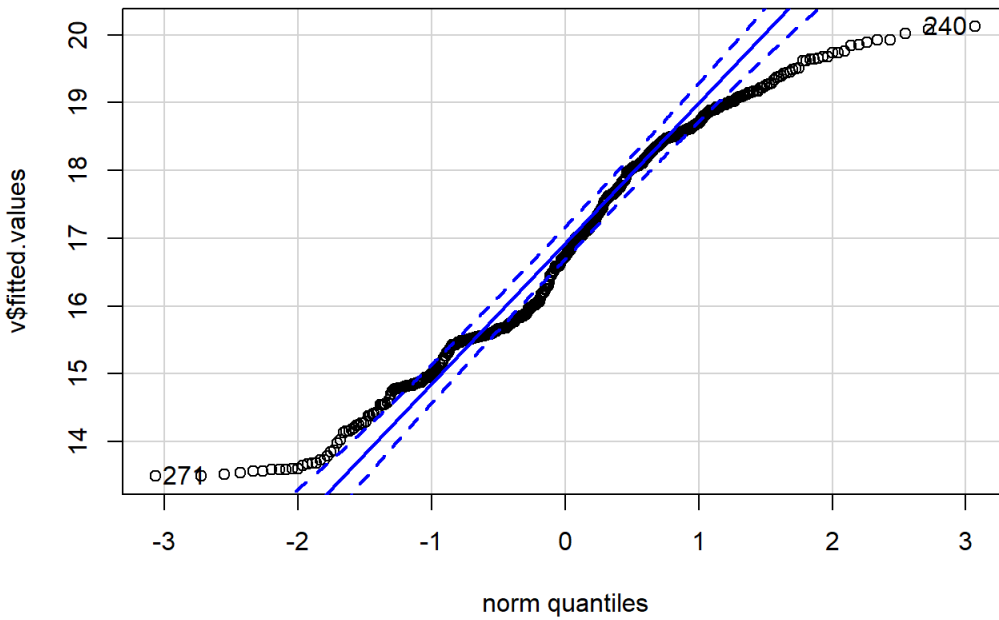
```
## [[1]]
## [1] 133 403
##
## [[2]]
## [1] 133 403
##
## [[3]]
## [1] 133 403
##
## [[4]]
## [1] 133 403
##
## [[5]]
## [1] 133 403
##
## [[6]]
## [1] 133 403
##
## [[7]]
## [1] 133 271
##
## [[8]]
## [1] 133 10
##
## [[9]]
## [1] 133 271
##
## [[10]]
## [1] 133 271
```

```
map(gee.fit, function(v){car::qqPlot(v$fitted.values,
    main = "GEE Gamma regression")})
```

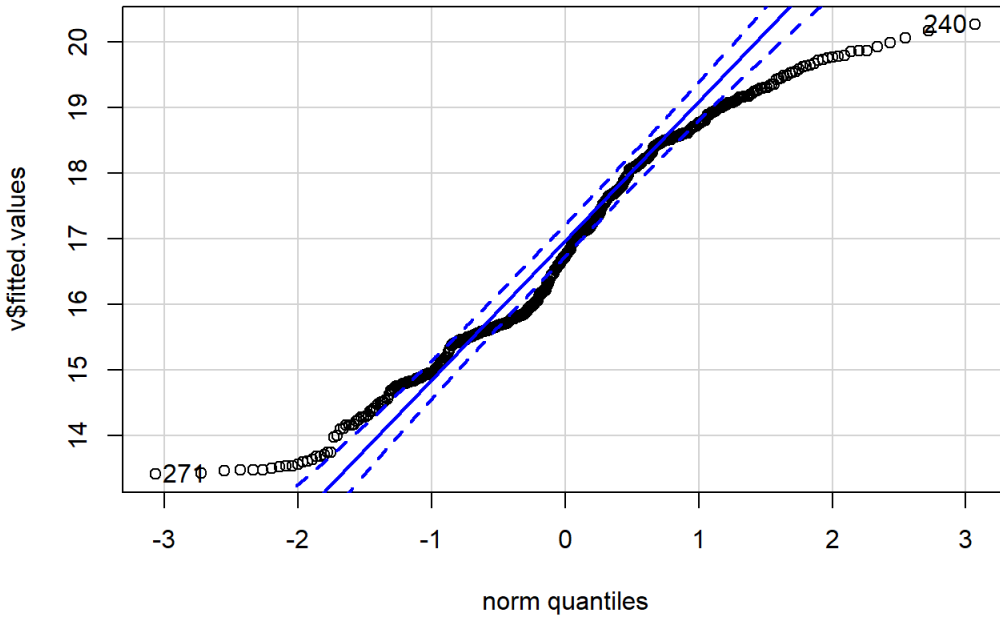
GEE Gamma regression



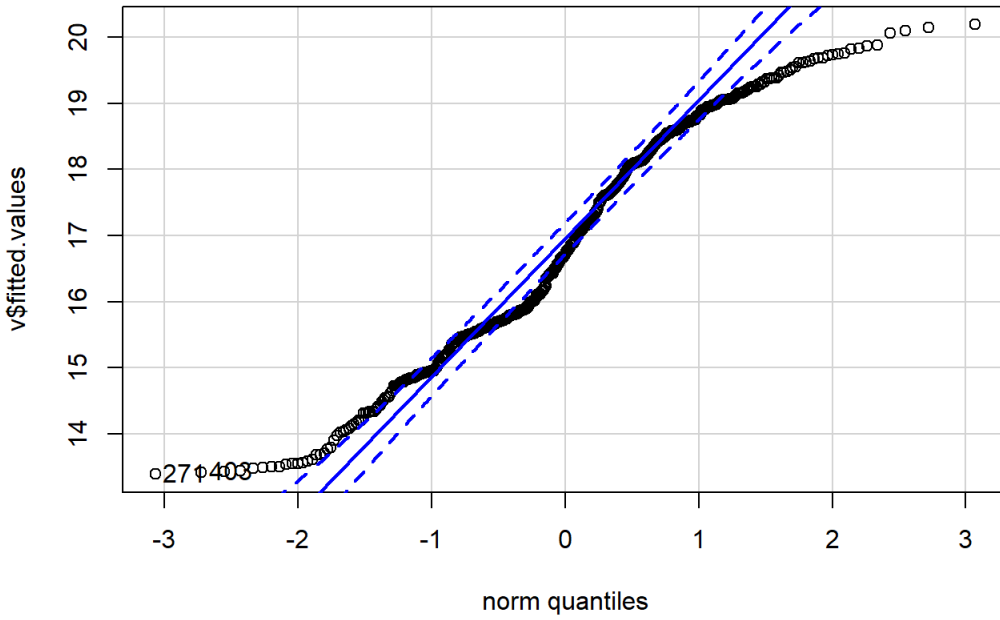
GEE Gamma regression



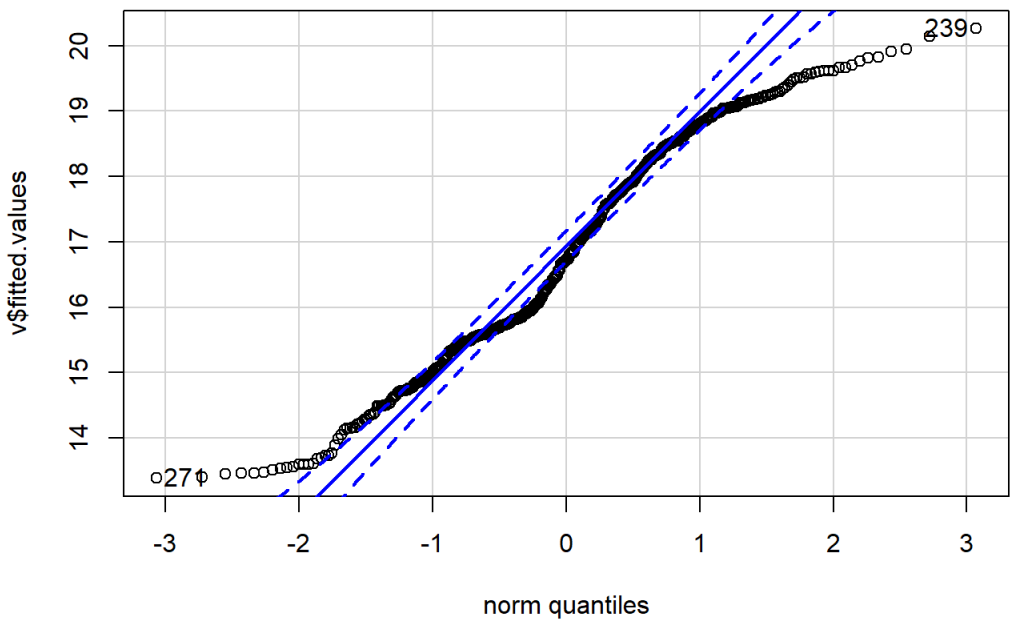
GEE Gamma regression



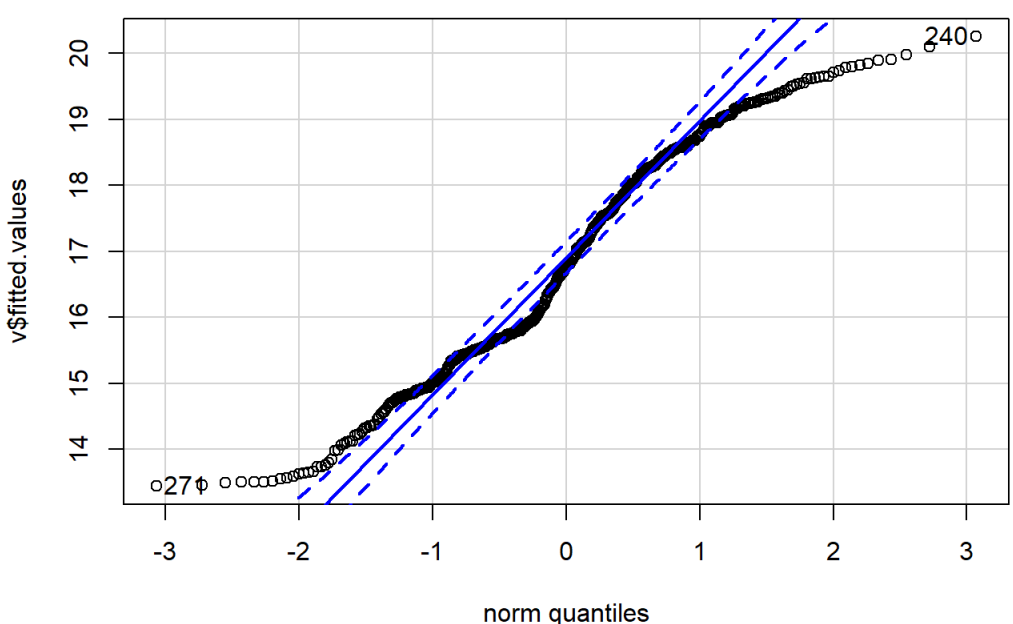
GEE Gamma regression



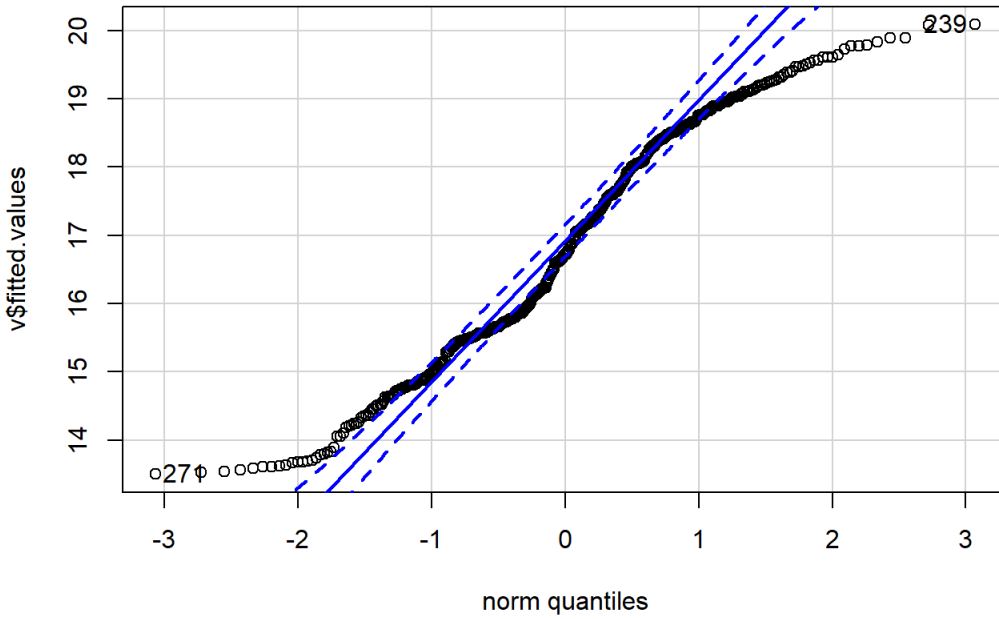
### GEE Gamma regression



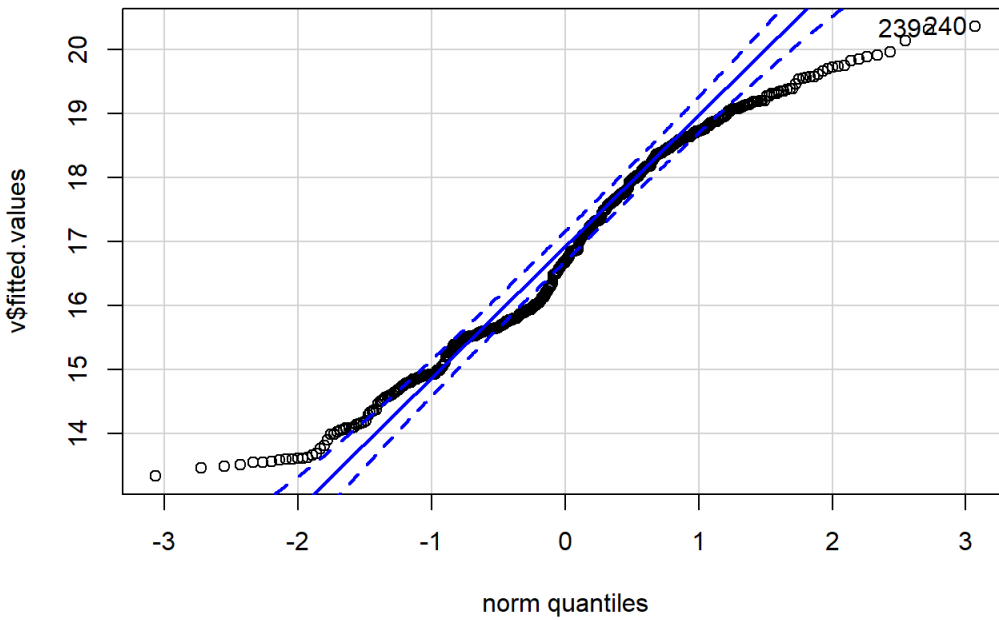
### GEE Gamma regression



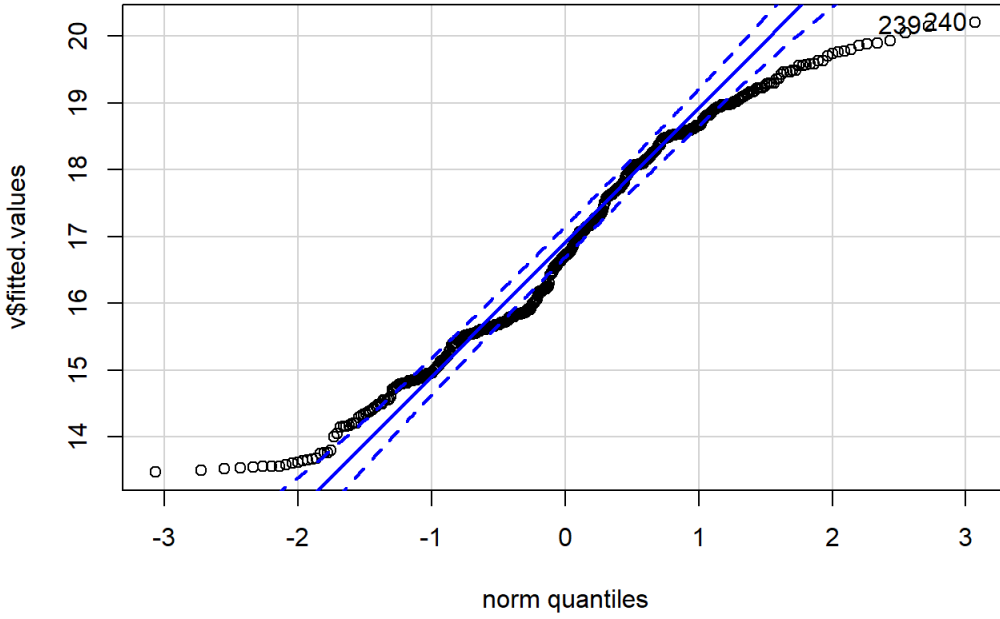
GEE Gamma regression



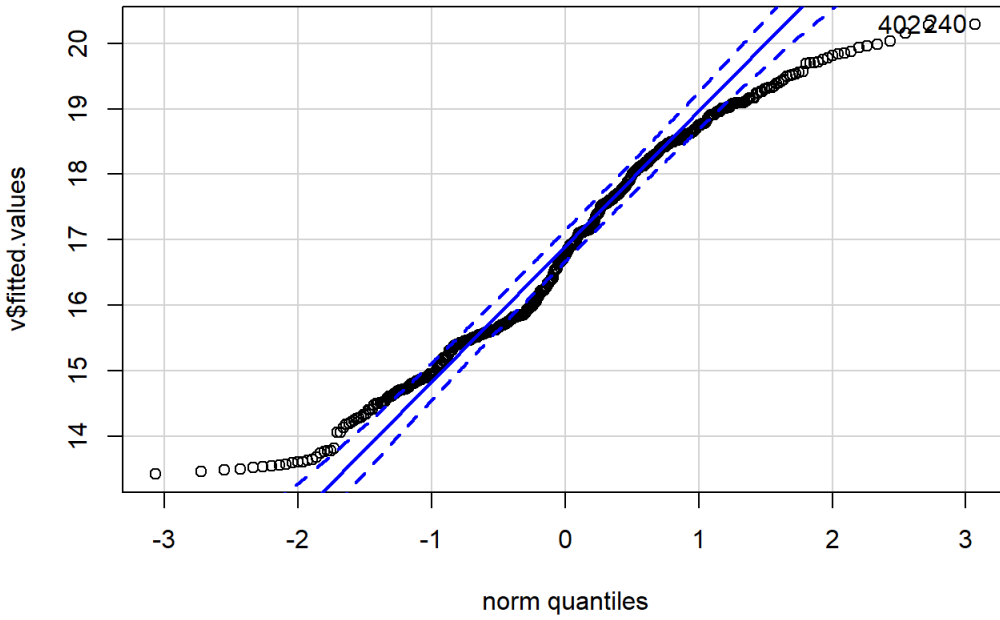
GEE Gamma regression



GEE Gamma regression



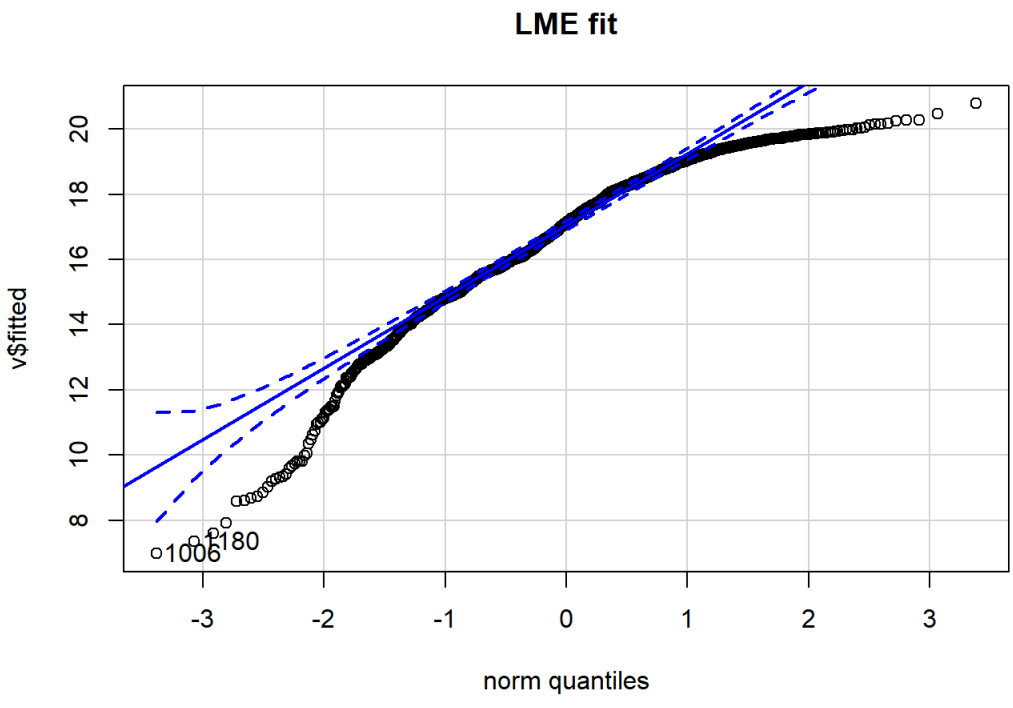
GEE Gamma regression



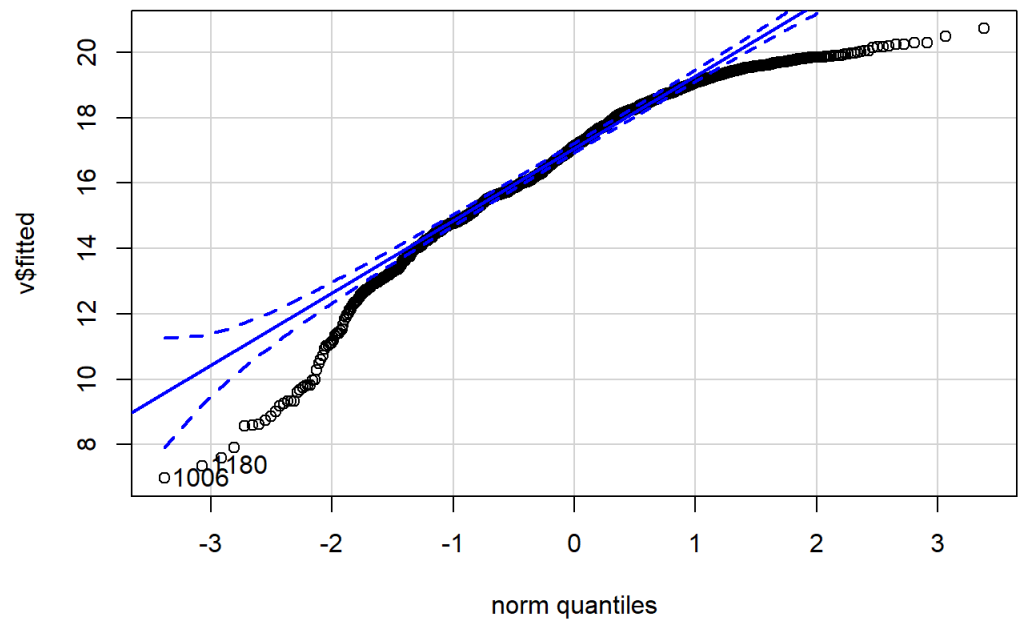


```
## [[1]]
## [1] 240 266
##
## [[2]]
## [1] 240 271
##
## [[3]]
## [1] 240 271
##
## [[4]]
## [1] 271 403
##
## [[5]]
## [1] 239 271
##
## [[6]]
## [1] 240 271
##
## [[7]]
## [1] 271 239
##
## [[8]]
## [1] 240 239
##
## [[9]]
## [1] 240 239
##
## [[10]]
## [1] 240 402
```

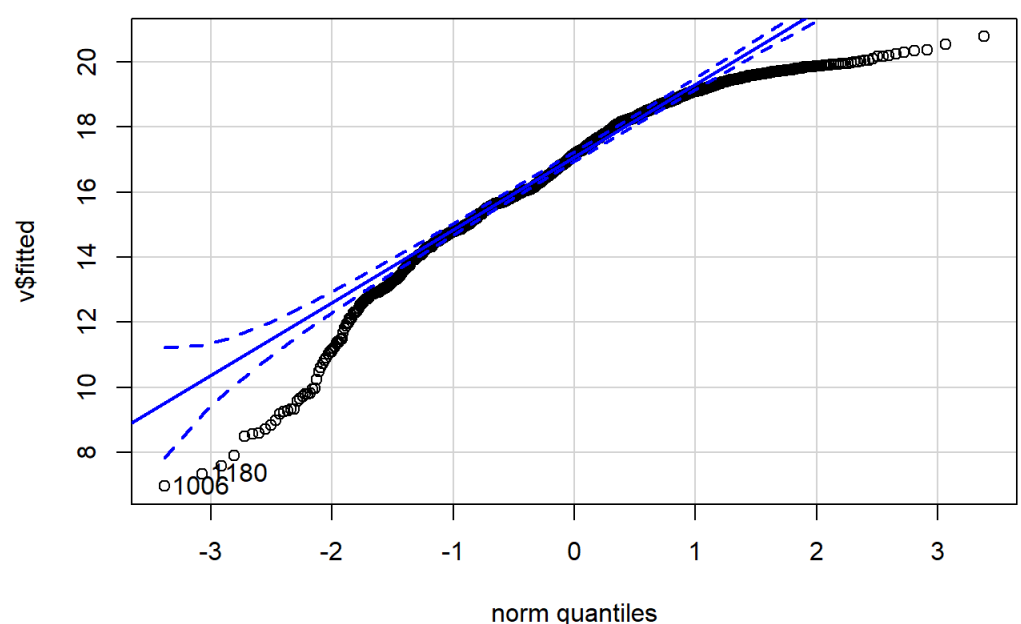
```
map(lme.fit2, function(v){car::qqPlot(v$fitted,
  main = "LME fit")})
```



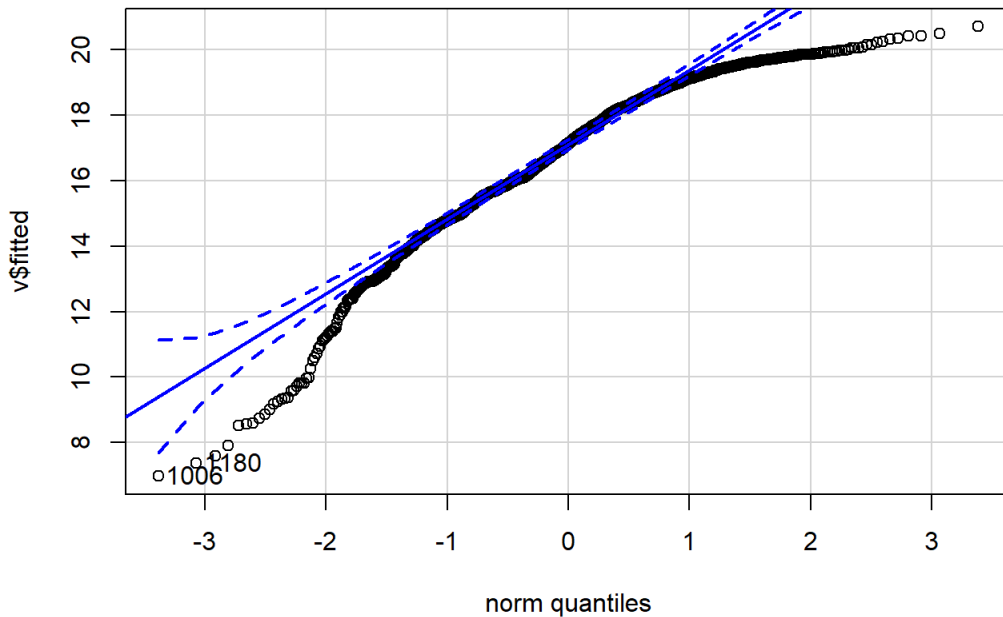
LME fit



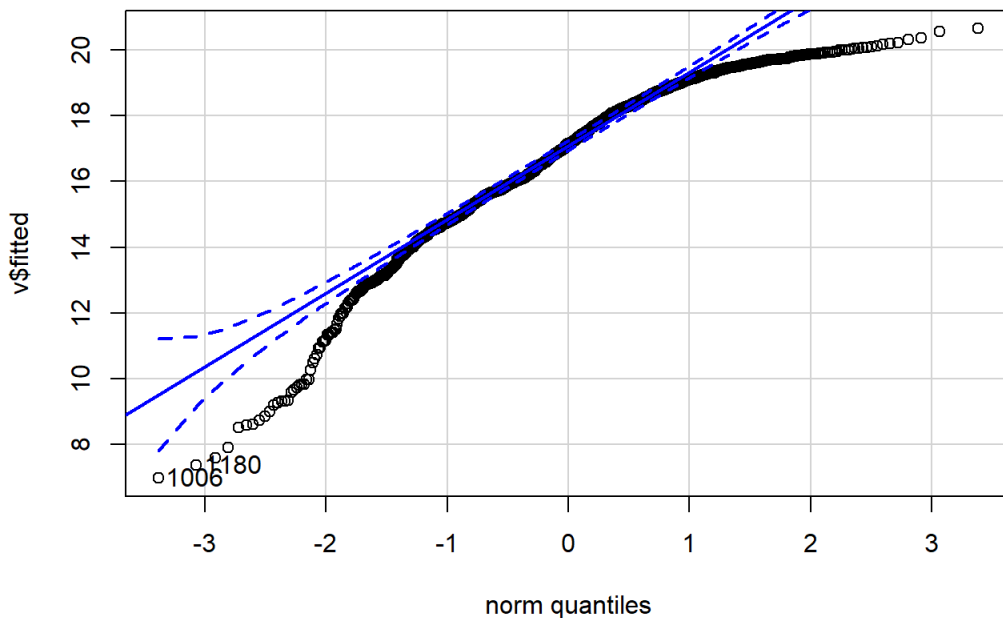
LME fit



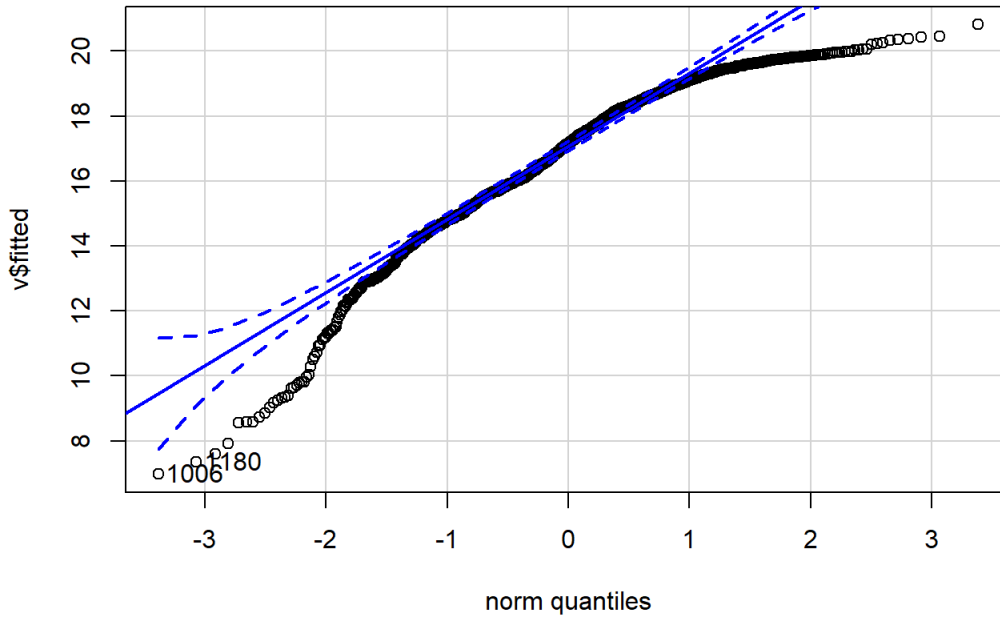
LME fit



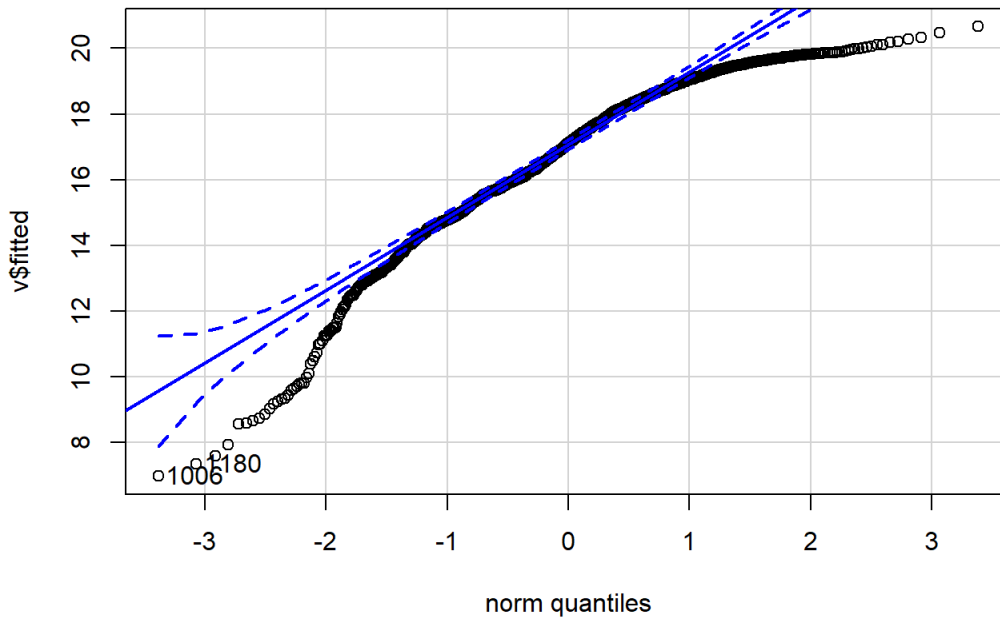
LME fit



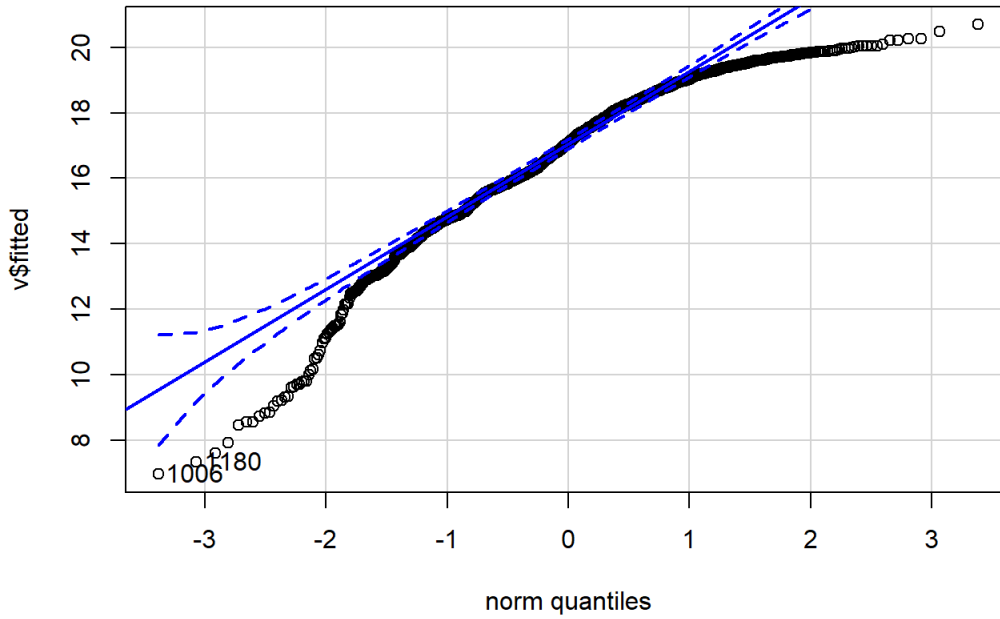
LME fit



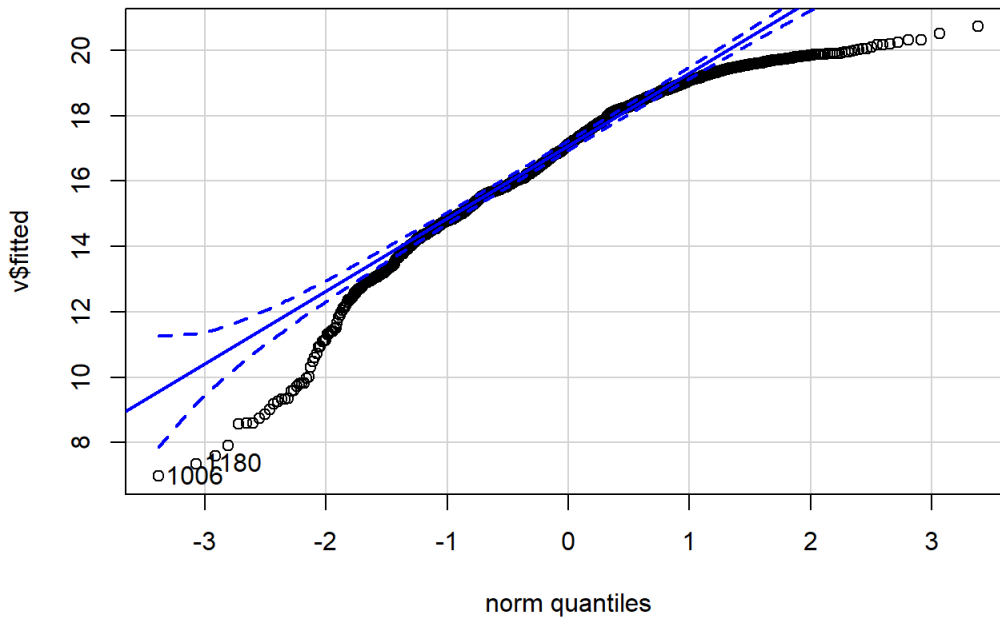
LME fit

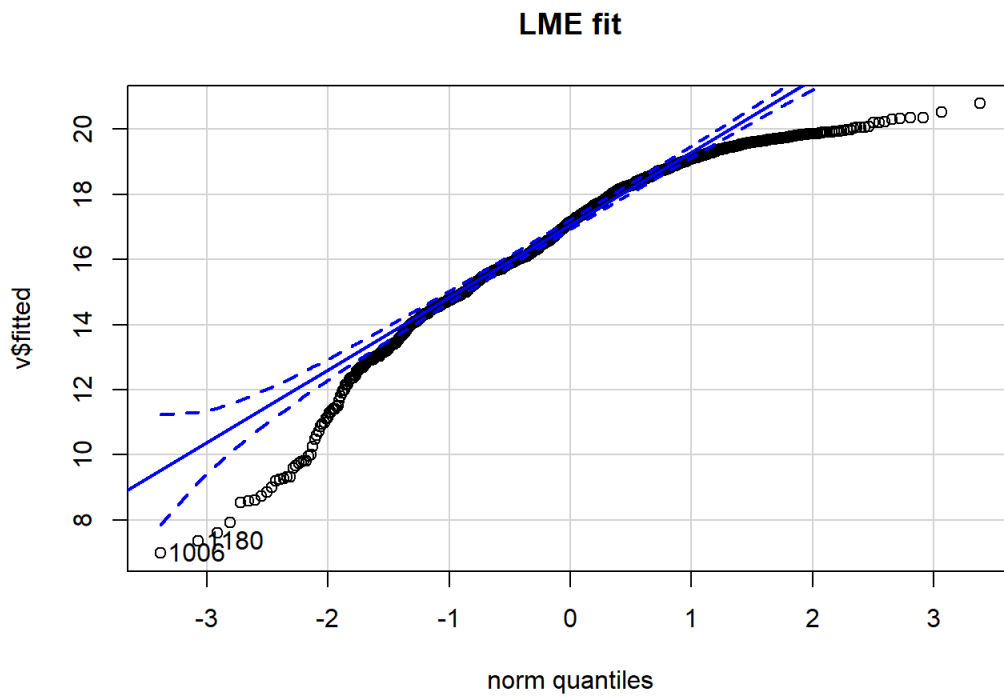


LME fit



LME fit

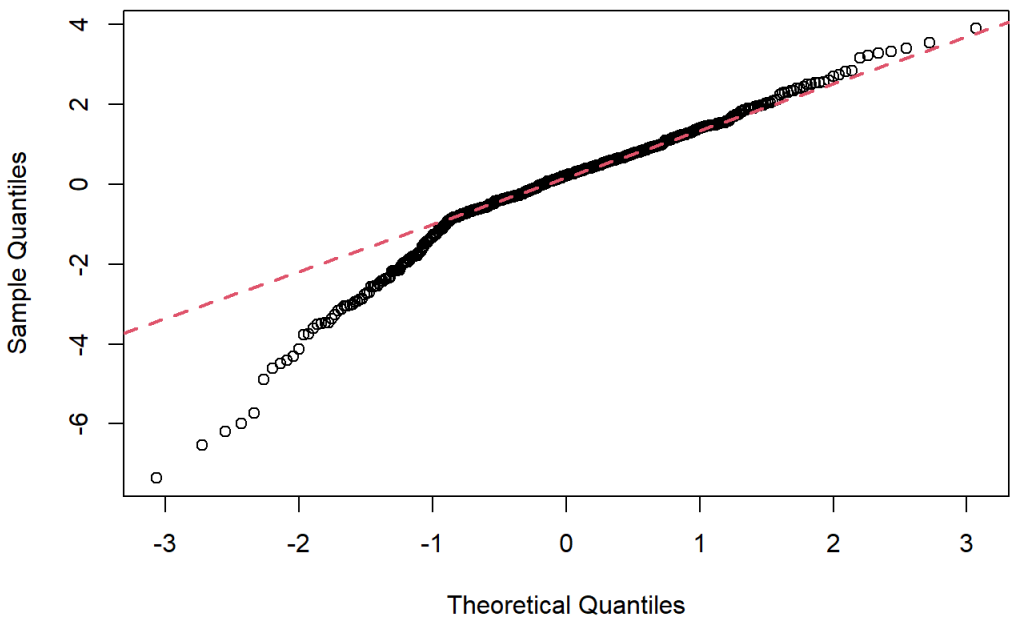




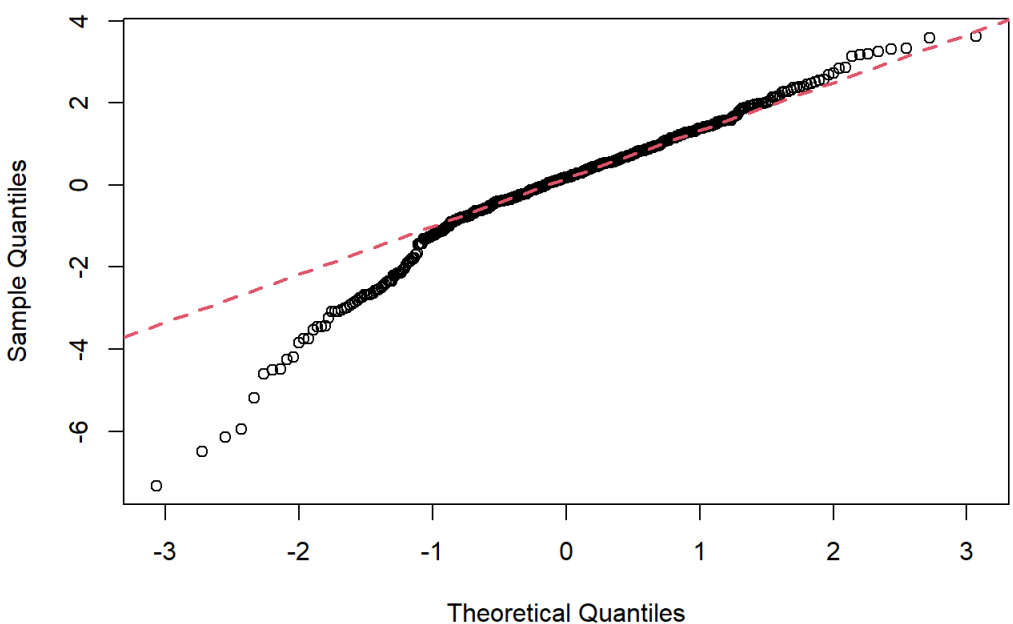
```
## [[1]]
## [1] 1006 1180
##
## [[2]]
## [1] 1006 1180
##
## [[3]]
## [1] 1006 1180
##
## [[4]]
## [1] 1006 1180
##
## [[5]]
## [1] 1006 1180
##
## [[6]]
## [1] 1006 1180
##
## [[7]]
## [1] 1006 1180
##
## [[8]]
## [1] 1006 1180
##
## [[9]]
## [1] 1006 1180
##
## [[10]]
## [1] 1006 1180
```

```
map(lmer.fit, function(v) { qqnorm(resid(v), main = "LMER fit"); qqline(resid(v), col = 2, lwd = 2, lty = 2)})
```

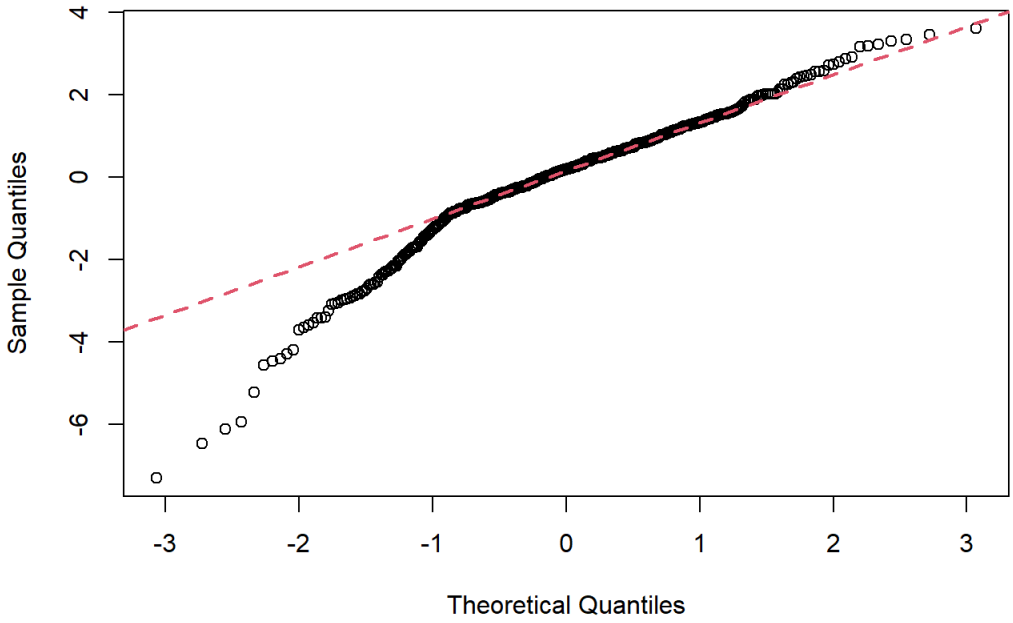
LMER fit



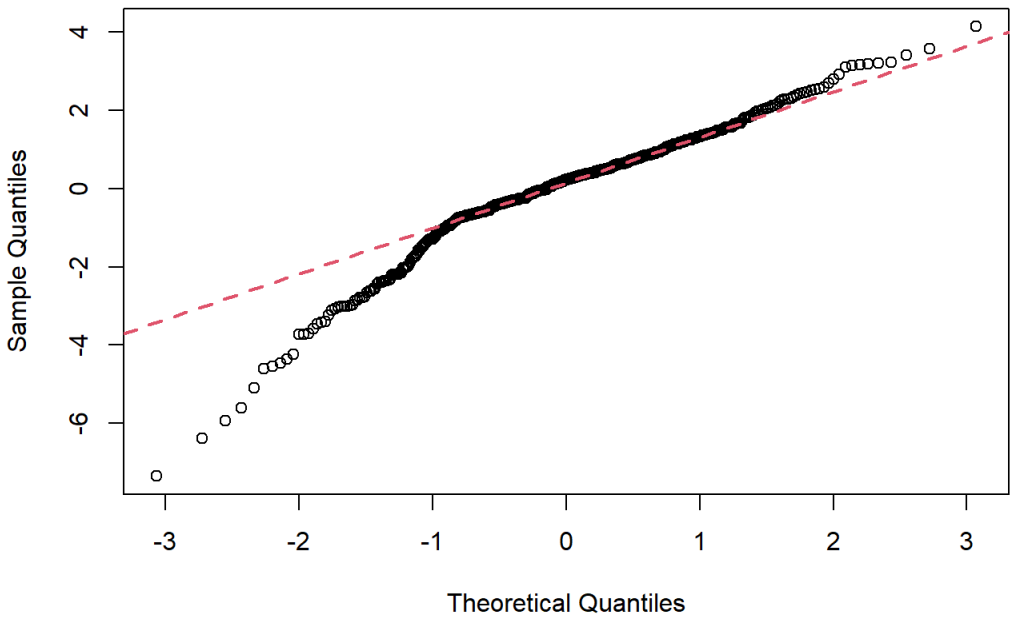
LMER fit



LMER fit

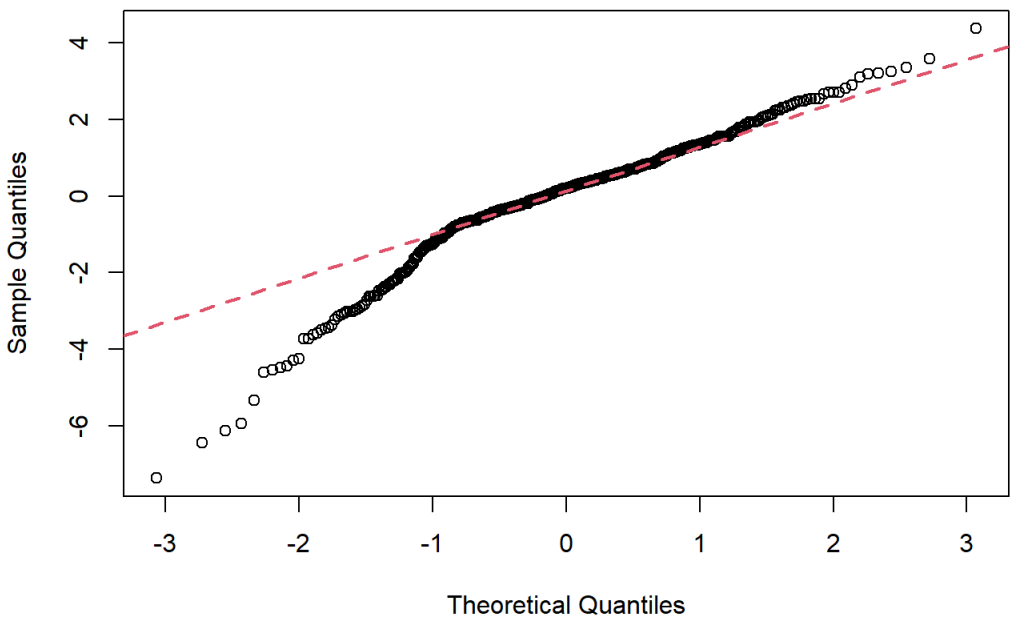


LMER fit

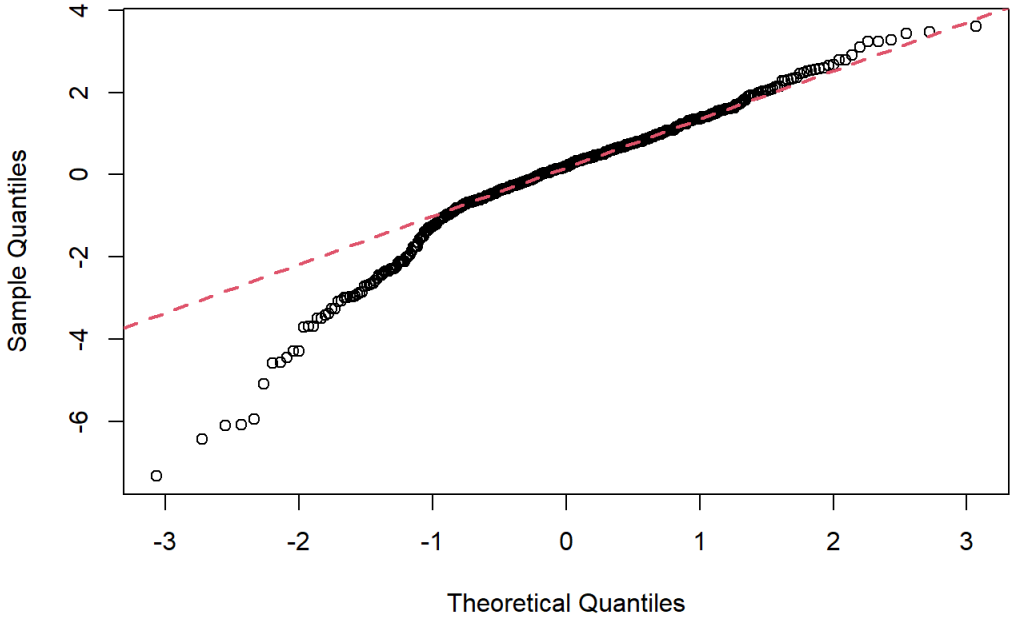




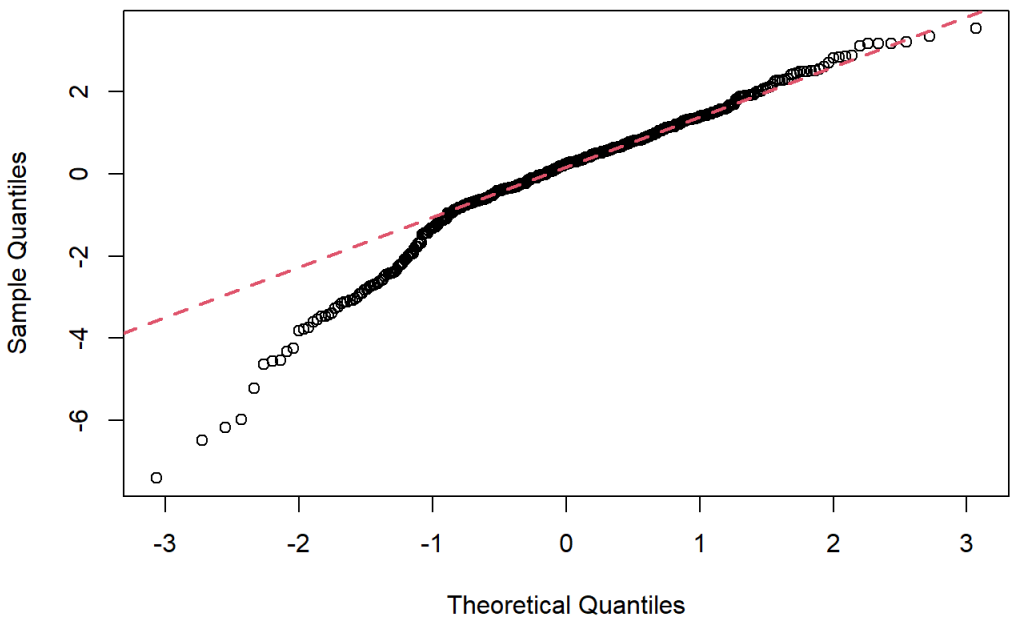
LMER fit



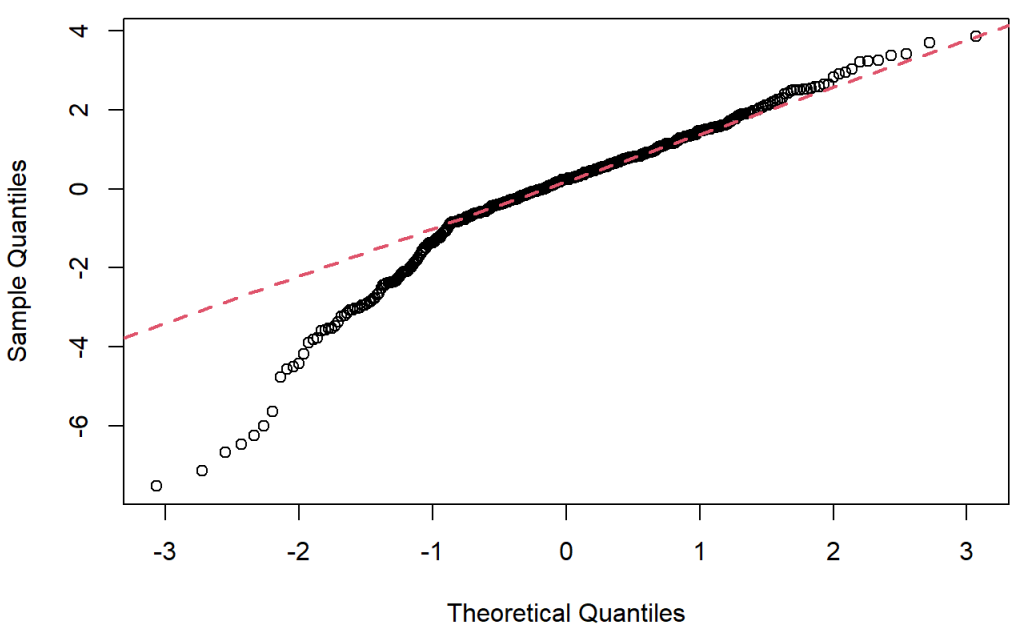
LMER fit



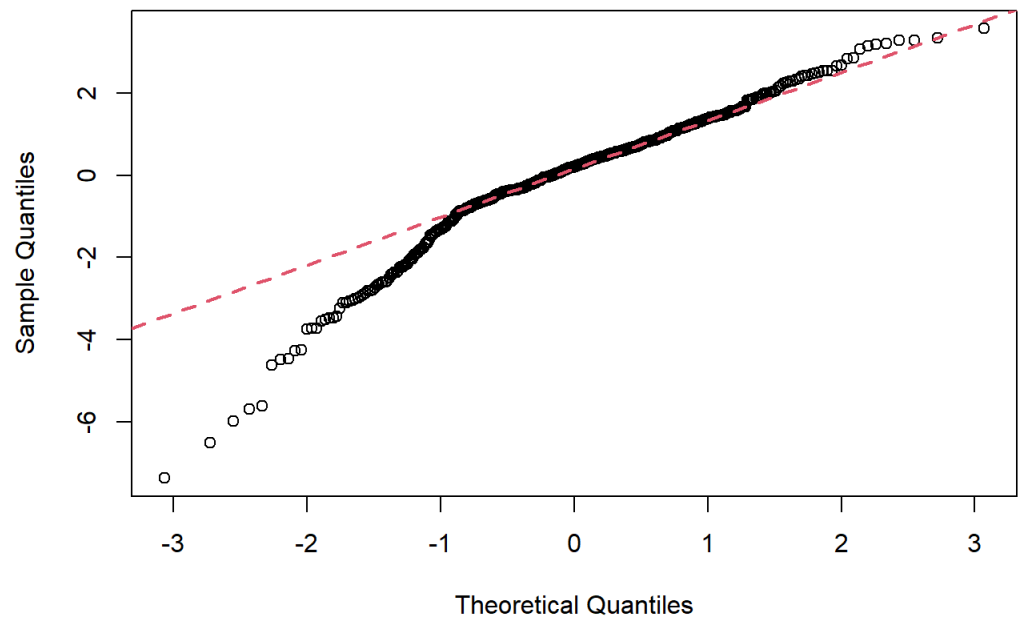
LMER fit



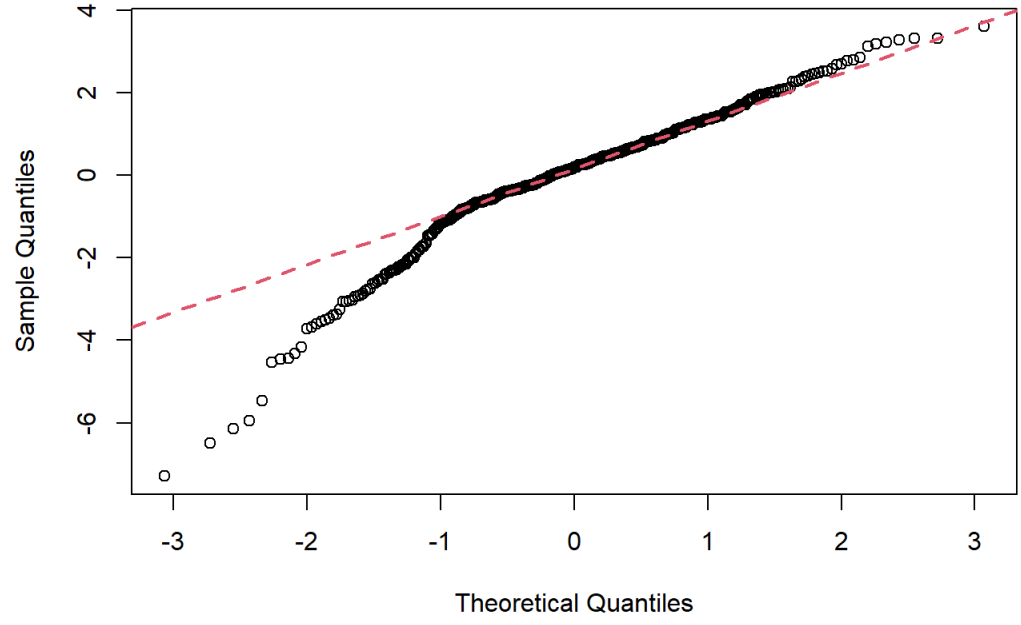
LMER fit



LMER fit



LMER fit



```
## [[1]]
## NULL
##
## [[2]]
## NULL
##
## [[3]]
## NULL
##
## [[4]]
## NULL
##
## [[5]]
## NULL
##
## [[6]]
## NULL
##
## [[7]]
## NULL
##
## [[8]]
## NULL
##
## [[9]]
## NULL
##
## [[10]]
## NULL
```

```
# m.ar1 = with(c.long, lme(fosq_global ~ avgpapuse + time + (1+time|nsrrid),
#   random = ~time|nsrrid,
#   correlation = corAR1(0.67,
#     form =~1+time|nsrrid),
#   method= "REML",
#   na.action = na.exclude))
#
# m.uns = lme(fosq_global ~ avgpapuse * time + (1+time|nsrrid),
#   random = ~1+time|nsrrid,
#   data = c.long[[2]],
#   method= "REML",
#   na.action = na.exclude)
```

## 7 ICC

### ICC

```
performance::icc(lmer(fosq_global ~ avgpapuse * time + (1+time|nsrrid),
  data = pap.long),
  by_group = TRUE)
```

```
## # ICC by Group
##
## Group | ICC
## -----
## nsrrid | 0.676
```

ICC = 0.524 before imputation

#Session info

```
sessionInfo()
```

```
## R version 4.0.2 (2020-06-22)
## Platform: x86_64-w64-mingw32/x64 (64-bit)
## Running under: Windows 10 x64 (build 19042)
##
## Matrix products: default
##
## locale:
## [1] LC_COLLATE=English_United States.1252
## [2] LC_CTYPE=English_United States.1252
## [3] LC_MONETARY=English_United States.1252
## [4] LC_NUMERIC=C
## [5] LC_TIME=English_United States.1252
##
## attached base packages:
## [1] parallel stats graphics grDevices utils datasets methods
## [8] base
##
## other attached packages:
## [1] forcats_0.5.1 stringr_1.4.0 dplyr_1.0.4 purrr_0.3.4
## [5] readr_1.4.0 tidyr_1.1.3 tibble_3.0.6 tidyverse_1.3.1
## [9] magrittr_2.0.1 mitml_0.4-1 nlme_3.1-152 lme4_1.1-26
## [13] glmm_1.4.2 doParallel_1.0.16 iterators_1.0.13 foreach_1.5.1
## [17] Matrix_1.3-2 mvtnorm_1.1-1 trust_0.1-8 Hmisc_4.5-0
## [21] Formula_1.2-4 survival_3.2-11 extrafont_0.17 gee_4.13-20
## [25] miceadds_3.11-6 caret_6.0-86 ggplot2_3.3.3 lattice_0.20-41
## [29] mice_3.13.0 colorspace_2.0-1 tableone_0.12.0
##
## loaded via a namespace (and not attached):
## [1] estimability_1.3 ModelMetrics_1.2.2.2
## [3] coda_0.19-4 visdat_0.5.3
## [5] knitr_1.33 multcomp_1.4-17
## [7] data.table_1.14.0 rpart_4.1-15
## [9] generics_0.1.0 TH.data_1.0-10
## [11] proxy_0.4-25 correlation_0.6.1
## [13] xml2_1.3.2 lubridate_1.7.10
## [15] httpuv_1.6.0 assertthat_0.2.1
## [17] naniar_0.6.0 gower_0.2.2
## [19] WRS2_1.1-1 xfun_0.22
## [21] hms_1.0.0 jquerylib_0.1.4
## [23] evaluate_0.14 promises_1.2.0.1
## [25] DEoptimR_1.0-8 fansi_0.4.2
## [27] dbplyr_2.1.1 readxl_1.3.1
## [29] tmvnsim_1.0-2 DBI_1.1.1
## [31] htmlwidgets_1.5.3 reshape_0.8.8
## [33] kSamples_1.2-9 stats4_4.0.2
## [35] Rmpfr_0.8-4 paletteer_1.3.0
## [37] ellipsis_0.3.1 backports_1.2.1
## [39] insight_0.13.2 survey_4.0
## [41] ggcorrplot_0.1.3 prismatic_1.0.0
## [43] vctrs_0.3.6 here_1.0.1
## [45] abind_1.4-5 cachem_1.0.4
## [47] withr_2.4.2 itertools_0.1-3
## [49] robustbase_0.93-7 checkmate_2.0.0
## [51] emmeans_1.6.0 vcd_1.4-8
## [53] mnormt_2.0.2 cluster_2.1.2
## [55] laeken_0.5.1 crayon_1.4.1
## [57] recipes_0.1.16 pkgconfig_2.0.3
## [59] SuppDists_1.1-9.5 labeling_0.4.2
## [61] statsExpressions_1.0.1 nnet_7.3-15
## [63] rlang_0.4.10 lifecycle_1.0.0
```

```
## [65] miniUI_0.1.1.1           MatrixModels_0.5-0
## [67] sandwich_3.0-0           extrafontdb_1.0
## [69] modelr_0.1.8             cellranger_1.1.0
## [71] rprojroot_2.0.2         lmtest_0.9-38
## [73] mc2d_0.1-19             carData_3.0-4
## [75] boot_1.3-28             zoo_1.8-8
## [77] pan_1.6                 reprex_2.0.0
## [79] base64enc_0.1-3        png_0.1-7
## [81] PMCMRplus_1.9.0        parameters_0.13.0
## [83] pROC_1.17.0.1          ggExtra_0.9
## [85] Rbtest_1.1             multcompView_0.1-8
## [87] jpeg_0.1-8.1          ggsignif_0.6.1
## [89] scales_1.1.1          memoise_2.0.0
## [91] plyr_1.8.6            compiler_4.0.2
## [93] RColorBrewer_1.1-2     cli_2.5.0
## [95] patchwork_1.1.1       pbapply_1.4-3
## [97] htmlTable_2.1.0       MASS_7.3-53.1
## [99] mgcv_1.8-35           tidyselect_1.1.1
## [101] stringi_1.5.3         highr_0.9
## [103] mitools_2.4           yaml_2.2.1
## [105] latticeExtra_0.6-29   ggrepel_0.9.1
## [107] grid_4.0.2           sass_0.3.1
## [109] tools_4.0.2          rio_0.5.26
## [111] rstudioapi_0.13       foreign_0.8-81
## [113] gridExtra_2.3         ipmisc_6.0.0
## [115] prodlim_2019.11.13   pairwiseComparisons_3.1.5
## [117] farver_2.1.0         digest_0.6.27
## [119] shiny_1.6.0          lava_1.6.9
## [121] BWSstest_0.2.2       Rcpp_1.0.6
## [123] car_3.0-10           broom_0.7.6
## [125] BayesFactor_0.9.12-4.2 performance_0.7.1
## [127] later_1.2.0          httr_1.4.2
## [129] psych_2.1.3         effectsize_0.4.4-1
## [131] rvest_1.0.0          fs_1.5.0
## [133] ranger_0.12.1        splines_4.0.2
## [135] statmod_1.4.35       rematch2_2.1.2
## [137] sp_1.4-5             flexmix_2.3-17
## [139] xtable_1.8-4         gmp_0.6-2
## [141] jsonlite_1.7.2       nloptr_1.2.2.2
## [143] timeDate_3043.102    zeallot_0.1.0
## [145] modeltools_0.2-23    ipred_0.9-11
## [147] R6_2.5.0             pillar_1.6.0
## [149] htmltools_0.5.1.1    mime_0.10
## [151] glue_1.4.2           fastmap_1.1.0
## [153] minqa_1.2.4          VIM_6.1.0
## [155] class_7.3-18         codetools_0.2-18
## [157] jomo_2.7-2          utf8_1.1.4
## [159] bslib_0.2.4         curl_4.3.1
## [161] gtools_3.8.2        zip_2.1.1
## [163] openxlsx_4.2.3       Rttf2pt1_1.3.8
## [165] betareg_3.1-4       rmarkdown_2.7
## [167] munsell_0.5.0       e1071_1.7-6
## [169] labelled_2.8.0      ggstatsplot_0.7.2
## [171] haven_2.4.1         reshape2_1.4.4
## [173] gtable_0.3.0        bayestestR_0.9.0
```

- 1 Load data
- 2 Overview
- 3 Table 1
- 4 Imputing with multilevel model
- 5 Imputin'
- 6 LME Models
- 7 Random slope, intercept, or both
- 8 Mean structure
- 9 Mediation analysis
- 10 ICC

# Longitudinal project: evaluating models

Anna M. May & Lindsay Petrenchik

2021-05-07

`/fontfamily{'Calibri'}`

## 0.1 Preliminaries

## 0.2 Functions

`paste(colnames(hiv), collapse = "+")`

```
#paste(colnames(hiv), collapse = "+ ")
anna.qq = function(v){
  # qqnorm(fitted(v), pch = 1, frame = TRUE)
  # qqline(fitted(v), col = "steelblue", lwd = 2)
  car::qqPlot(fitted(v),
              main = v)
}
anna.standardized = function(v){
  res = residuals(v)
  st.res = res/sd(res)
  plot(st.res ~ fitted(v), main = v)
}
```



```

library(ggplot2)

# ***** Base theme *****
base_theme <- theme(
  plot.margin = unit(rep(1, 3), "cm"),
  plot.title = element_text(size = 24,
                             face = "bold",
                             color = "#22292F",
                             margin = margin(b = 8)),
  plot.subtitle = element_text(size = 16,
                                lineheight = 1.1,
                                color = "#22292F",
                                margin = margin(b = 25)),
  plot.caption = element_text(size = 12,
                               margin = margin(t = 25),
                               color = "#3D4852"),
  axis.title.x = element_text(margin = margin(t = 15)),
  axis.title.y = element_text(margin = margin(r = 15)),
  axis.text = element_text(color = "#22292F")
)

set_base_theme <- function() {
  theme_set(theme_minimal(base_size = 18) +
            base_theme)
}

# ***** Set flat theme *****
flat_theme <- theme(
  panel.grid = element_line(color = "#cacfd2", linetype = "dashed"),
  axis.line = element_line(color = "#606F7B")
)

set_flat_theme <- function() {
  theme_set(theme_minimal(base_size = 18,
                          base_family = "Segoe UI") +
            base_theme +
            flat_theme)
}

set_flat_theme()

```

## 1 Load data

```

pap.base = read_csv(here::here("homepap", "datasets", "homepap-baseline-dataset-0.1.0.csv"))
pap.1mo = read_csv(here::here("homepap", "datasets", "homepap-month1-dataset-0.1.0.csv"))
pap.3mo = read_csv(here::here("homepap", "datasets", "homepap-month3-dataset-0.1.0.csv"))

dim(pap.base)

```

```
## [1] 373 104
```

```
dim(pap.1mo)
```

```
## [1] 373 31
```

```
dim(pap.3mo)
```

```
## [1] 373 33
```

Let's check out the variables in each dataset.

```
names(pap.base)
```

```
## [1] "nsrrid"      "clusterid"   "visit"       "treatmentarm"
## [5] "age"         "gender"      "race3"       "ethnicity"
## [9] "heightcm"   "weightkg"    "bmi"         "neckcm"
## [13] "waistcm"    "systolic"    "diastolic"   "cal_total"
## [17] "esstotal"   "fosq_genprd" "fosq_socout" "fosq_actlev"
## [21] "fosq_vigiln" "fosq_sexual" "fosq_global" "pf_norm"
## [25] "rp_norm"    "bp_norm"     "gh_norm"     "vt_norm"
## [29] "sf_norm"    "re_norm"     "mh_norm"     "agg_phys"
## [33] "agg_ment"   "sf36_pcs"    "sf36_mcs"    "dxasth"
## [37] "dxadhd"     "dxca"        "dxcatyp"     "dxchf"
## [41] "dxchd"      "dxdep"       "dxdiab"      "dxemph"
## [45] "dxgerd"     "dxhay"       "dxhich"      "dxhtn"
## [49] "dxhyperthy" "dxhypothy"   "dxkidney"    "dxliver"
## [53] "dxplhtn"    "dxseiz"      "dxstroke"    "slpprdp"
## [57] "slpeffp"    "tmstg1p"     "tmstg2p"     "tmstg34p"
## [61] "tmremp"     "avghr"       "pctsa90h"    "pctstg1_d"
## [65] "pctstg2_d"  "pctstg34_d"  "pctrem_d"    "slpprd_d"
## [69] "slpeff_d"   "pctstg1_t"   "pctstg2_t"   "pctstg34_t"
## [73] "pctrem_t"   "slpprd_t"    "slpeff_t"    "avgsao2_d"
## [77] "avgsao2_t"  "avghr_d"     "avghr_t"     "avgsao2"
## [81] "ahi_full"   "ahi_d"       "ahi_t"       "index_time"
## [85] "aphypi"     "avgsat"      "satlt90p"    "avgbpn"
## [89] "pressure"   "ablation"    "ahi"         "crossover"
## [93] "ttt"        "diagnostic"  "ahige15"     "eligible"
## [97] "titrated"   "acceptance"  "completedm1" "completedm3"
## [101] "completedm1m3" "diagtype"    "pctsa90p_d"  "pctsa90p_t"
```

```
names(pap.1mo)
```

```
## [1] "nsrrid"      "clusterid"   "visit"       "treatmentarm" "age"
## [6] "gender"      "race3"       "ethnicity"    "systolic"     "diastolic"
## [11] "cal_total"   "esstotal"    "fosq_genprd" "fosq_socout"  "fosq_actlev"
## [16] "fosq_vigiln" "fosq_sexual" "fosq_global" "pf_norm"      "rp_norm"
## [21] "bp_norm"     "gh_norm"     "vt_norm"     "sf_norm"      "re_norm"
## [26] "mh_norm"     "agg_phys"    "agg_ment"    "sf36_pcs"     "sf36_mcs"
## [31] "avgpapuse"
```

```
names(pap.3mo)
```

```
## [1] "nsrrid"      "clusterid"   "visit"       "treatmentarm" "age"
## [6] "gender"      "race3"       "ethnicity"    "weightkg"     "bmi"
## [11] "systolic"    "diastolic"   "cal_total"    "esstotal"     "fosq_genprd"
## [16] "fosq_socout" "fosq_actlev" "fosq_vigiln" "fosq_sexual"  "fosq_global"
## [21] "pf_norm"     "rp_norm"     "bp_norm"     "gh_norm"      "vt_norm"
## [26] "sf_norm"     "re_norm"     "mh_norm"     "agg_phys"     "agg_ment"
## [31] "sf36_pcs"    "sf36_mcs"    "avgpapuse"
```

## 1.0.1 Wide dataset

Merge datasets on nsrrid into a wide view. In the wide dataset, I don't include baseline adherence measures at all (because they don't exist).

```
# for each adherence that is NA that was taken as 0 adherence; this is a reasonable estimate since
# there is no report if the patient didn't use their machine
recurrent = c("esstotal", "bmi", "avgpapuse", "systolic", "diastolic",
             "fosq_genprd", "fosq_socout", "fosq_genprd",
             "fosq_socout", "fosq_actlev", "fosq_vigiln", "fosq_sexual",
             "fosq_global",
             # "pf_norm", "rp_norm", "bp_norm", "gh_norm", "vt_norm",
             # "sf_norm", "re_norm", "mh_norm", "agg_phys", "agg_ment",
             "sf36_pcs", "sf36_mcs"
            )

recur.base = paste0(recurrent, ".0")
recur.1 = paste0(recurrent, ".1")
recur.3 = paste0(recurrent, ".3")
#the diagnoses we want
diags = c("dxchf", "dxchd", "dxhypothy", "dxdep")
constants = c("nsrrid", "age", "gender", "race.f", "diags", "ttt", "cal_total",
             "desat", "pressure", "ahi")
level2 = c("age", "gender", "race.f", "ttt",
          "desat", "pressure", "ahi", diags)
```

```
pap = pap.base %>%
  mutate(
    race.f = factor(race3),
    female.f = factor(gender, levels = 1:0, labels = c("male", "female")),
    treat.f = factor(treatmentarm, levels = 1:2, labels = c("lab", "home")),
    avgpapuse = 0,
    desat = case_when(!is.na(pctsa90h) ~ pctsa90h,
                     !is.na(pctsa90p_d) ~ pctsa90p_d,
                     TRUE ~ NA_real_)
  ) %>%
  rename_with(~paste0(., ".0"), recurrent) %>%
  filter(acceptance == 1) %>%
  select(nsrrid, treat.f, ttt, age, gender, race.f,
        #systolic, diastolic, cal_total,
        diags, desat,
        pressure, ahi, recur.base) %>%
  left_join(
    pap.1mo %>%
      mutate(bmi = NA) %>%
      rename_with(~paste0(., ".1"), recurrent) %>%
      select(nsrrid, recur.1), by="nsrrid") %>%
  left_join(
    pap.3mo %>%
      rename_with(~paste0(., ".3"), recurrent) %>%
      select(nsrrid, recur.3), by="nsrrid")
```

## 1.0.2 Long dataset

Now do the same thing with a long view. Here we have to make something up for the adherence measures. NA doesn't work well. I think maybe setting everyone to zero (0) may work ok. I thought I needed this but we're imputing on wide...so, don't need it.

```

pap.long = rbind(
  pap.base %>%
    mutate(
      race.f = factor(race3),
      female.f = factor(gender, levels =1:0, labels = c("male", "female")),
      time = 0,
      avgpapuse = 0
    ) %>%
  filter(acceptance == 1) %>%
  select(nsrrid, , time, recurrent),
  pap.lmo %>%
    mutate(
      female.f = factor(gender, levels =1:0, labels = c("male", "female")),
      bmi = NA,
      time = 1) %>%
  select(nsrrid, time, recurrent),
  pap.3mo %>%
    mutate(
      female.f = factor(gender, levels =1:0, labels = c("male", "female")),
      avgpapuse.3 = avgpapuse,
      time = 3) %>%
  select(nsrrid, time, recurrent)) %>%
mutate(
# id = factor(nsrrid),
  across(
    contains(recurrent),
    ~((.x-min(.x, na.rm = TRUE))/(max(.x, na.rm = TRUE)-min(.x, na.rm = TRUE))),
    .names = "sc.{.col}"),
  across(contains("sc."),
    ~case_when(.x ==1 ~.x - 0.0001,
      .x == 0 ~.x + 0.0001,
      TRUE ~ .x))) %>%
group_by(nsrrid) %>%
filter(sum(is.na(fosq_global)) != 3 & sum(is.na(avgpapuse)) !=2) %>% # get rid of everyone tha
t has all fosq or all adherence missing
ungroup() %>%
mutate(across(contains("avgpap"), ~.x/60),
  pap.4 = factor(iffelse(avgpapuse > 4, 1, 0)))%>%
left_join(pap %>% select(nsrrid, treat.f, level2), by = "nsrrid" )

write.csv(pap.long, file = "paplong.csv")
#SASxport::write.xport(pap.long, file = "paplong.xpt")

```

## 2 Overview

The HomePAP study randomized 373 adult patients from 2008-2010 at 7 study sites to either receive diagnosis and therapy titration for sleep apnea at home or in the laboratory (the gold standard). The original study had 3 co-primary outcomes (1) CPAP (the main therapy for sleep apnea) acceptance, (2) therapy adherence and (3) time to treatment initiation. The study manual of procedures is attached, and the most relevant page is 13 which lists all the instruments administered longitudinally (baseline, 1 month, and 3 months). One exciting thing about this randomized controlled trial is that it was coordinated by Cleveland sleep docs.

We plan to evaluate whether *adherence to CPAP* is associated with *functional outcomes* over a 3-month time horizon. We plan to construct a mixed effects model incorporating CPAP adherence as a predictor and functional outcomes as the outcome. The primary analysis will focus on quality of life as measured by the FOSQ. Secondary analyses will evaluate sleepiness, SF-36 subscale scores, and blood pressure measurements. We will also conduct sensitivity analyses including home vs. lab grouping as used in the study as a predictor variable.

Multiple regressions and concern about familywise error rate Consider using the SAQLI for quality of life use general health perception, social functioning, and vitality as outcome or as time-dependent covariate? Albert re: SAS or R

main predictor:avgpapuse (min) main outcomes: FOSQ global secondary outcomes: FOSQ subscales (activity level, general productivity, social outcome, vigilance, sexual activity), aggregate mental score, aggregate physical score SF-36, general health perception, vitality, social functioning, diastolic BP, systolic BP, ESS covariates: time to treatment (ttt), treatment arm (treatmentarm), age, gender, race (race3), ethnicity?, BMI, ahi, past history

### 3 Table 1

```
vars = c( "bmi", "ttt", "age", "gender",
"race.f", "systolic", "diastolic", "cal_total", "ess.base", "dxchf",
"dxchd", "dxhyperthy", "dxdep", "desat", "pressure", "ahi",
"esstotal.base", "fosq_genprd.base", "fosq_socout.base", "fosq_actlev.base",
"fosq_vigiln.base", "fosq_sexual.base", "fosq_global.base", "pf_norm.base",
"rp_norm.base", "bp_norm.base", "gh_norm.base", "vt_norm.base",
"sf_norm.base", "re_norm.base", "mh_norm.base", "agg_phys.base",
"agg_ment.base", "sf36_pcs.base", "sf36_mcs.base")

factorVars = c("gender",
"race.f", "dxchf",
"dxchd", "dxhyperthy", "dxdep")

t1 = CreateTableOne(vars = vars,
                    factorVars = factorVars,
                    strata = c("treat.f"),
                    data = pap,
                    addOverall = TRUE)

t1.print = print(t1,
                 nonnormal = c("ttt", "desat", "pressure", "ahi",
                              "fosq_genprd.base", "fosq_socout.base",
                              "fosq_sexual.base", "fosq_global.base",
                              "pf_norm.base", "rp_norm.base", "bp_norm.base",
                              "vt_norm.base", "gh_norm.base",
                              "sf_norm.base", "re_norm.base", "mh_norm.base",
                              "agg_phys.base", "agg_ment.base", "sf36_mcs.base"
                              ),
                 noSpaces = T, test = TRUE, smd = TRUE)
```

```
##                               Stratified by treat.f
##                               Overall           lab
##   n                           175             80
##   ttt (median [IQR])          26.00 [15.50, 45.00] 29.50 [17.00, 52.50]
##   age (mean (SD))             48.66 (11.87)      49.25 (11.95)
##   gender = 1 (%)              114 (65.1)         56 (70.0)
##   race.f (%)
##     1                          121 (69.1)        59 (73.8)
##     2                           35 (20.0)         13 (16.2)
##     3                           19 (10.9)          8 (10.0)
##   dxchf = 1 (%)                5 (2.9)          4 (5.1)
##   dxchd = 1 (%)                14 (8.2)          8 (10.5)
##   dxdep = 1 (%)               41 (24.6)         13 (16.9)
##   desat (median [IQR])        15.95 [5.27, 41.70] 21.10 [6.63, 47.60]
##   pressure (median [IQR])     10.00 [9.00, 12.00] 10.50 [9.00, 12.00]
##   ahi (median [IQR])          35.50 [22.80, 62.70] 42.90 [25.75, 70.83]
##                               Stratified by treat.f
##                               home           p      test      SMD
##   n                             95
##   ttt (median [IQR])           23.00 [15.00, 37.00] 0.087 nonnorm 0.252
##   age (mean (SD))             48.17 (11.84)      0.550          0.091
##   gender = 1 (%)              58 (61.1)         0.281          0.189
##   race.f (%)                  0.452             0.193
##     1                          62 (65.3)
##     2                          22 (23.2)
##     3                          11 (11.6)
##   dxchf = 1 (%)                1 (1.1)           0.261          0.236
##   dxchd = 1 (%)                6 (6.4)           0.486          0.149
##   dxdep = 1 (%)               28 (31.1)        0.051          0.338
##   desat (median [IQR])        6.50 [2.53, 12.22] 0.002 nonnorm 0.759
##   pressure (median [IQR])     10.00 [9.00, 12.00] 0.705 nonnorm 0.051
##   ahi (median [IQR])          32.90 [21.20, 56.75] 0.036 nonnorm 0.364
```

```
t2 = CreateTableOne(vars = vars,
                    factorVars = factorVars,
                    strata = c("treat.f"),
                    data = pap,
                    addOverall = TRUE,
                    includeNA = TRUE)
t2.print = print(t2, nonnormal = c("ttt", "desat", "pressure", "ahi",
                                   "fosq_genprd.base", "fosq_socout.base",
                                   "fosq_sexual.base", "fosq_global.base",
                                   "pf_norm.base", "rp_norm.base", "bp_norm.base",
                                   "vt_norm.base", "gh_norm.base",
                                   "sf_norm.base", "re_norm.base", "mh_norm.base",
                                   "agg_phys.base", "agg_ment.base", "sf36_mcs.base"),
                  noSpaces = T, test = TRUE, smd = TRUE)
```

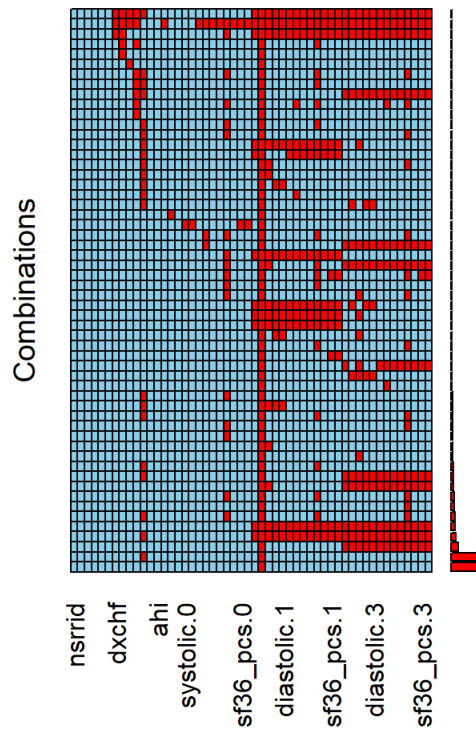
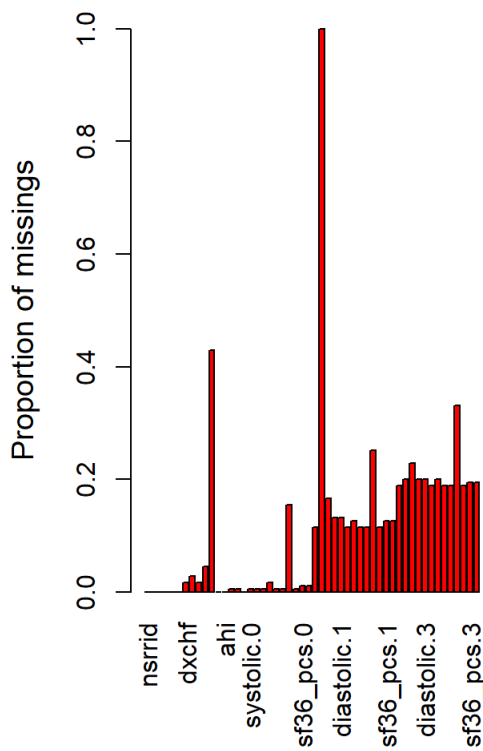
```
##                               Stratified by treat.f
##                               Overall          lab
##   n                          175            80
##   ttt (median [IQR])         26.00 [15.50, 45.00] 29.50 [17.00, 52.50]
##   age (mean (SD))            48.66 (11.87)      49.25 (11.95)
##   gender = 1 (%)             114 (65.1)         56 (70.0)
##   race.f (%)
##     1                         121 (69.1)        59 (73.8)
##     2                         35 (20.0)         13 (16.2)
##     3                         19 (10.9)         8 (10.0)
##   dxchf (%)
##     0                         167 (95.4)        74 (92.5)
##     1                          5 (2.9)          4 (5.0)
##     NA                        3 (1.7)          2 (2.5)
##   dxchd (%)
##     0                         156 (89.1)        68 (85.0)
##     1                         14 (8.0)          8 (10.0)
##     NA                        5 (2.9)          4 (5.0)
##   dxdep (%)
##     0                         126 (72.0)        64 (80.0)
##     1                         41 (23.4)        13 (16.2)
##     NA                        8 (4.6)          3 (3.8)
##   desat (median [IQR])       15.95 [5.27, 41.70] 21.10 [6.63, 47.60]
##   pressure (median [IQR])    10.00 [9.00, 12.00] 10.50 [9.00, 12.00]
##   ahi (median [IQR])         35.50 [22.80, 62.70] 42.90 [25.75, 70.83]
##                               Stratified by treat.f
##                               home           p      test      SMD
##   n                          95
##   ttt (median [IQR])         23.00 [15.00, 37.00] 0.087 nonnorm 0.252
##   age (mean (SD))            48.17 (11.84)      0.550          0.091
##   gender = 1 (%)             58 (61.1)         0.281          0.189
##   race.f (%)                 0.452            0.193
##     1                         62 (65.3)
##     2                         22 (23.2)
##     3                         11 (11.6)
##   dxchf (%)                  0.220            0.260
##     0                         93 (97.9)
##     1                          1 (1.1)
##     NA                        1 (1.1)
##   dxchd (%)                  0.184            0.276
##     0                         88 (92.6)
##     1                          6 (6.3)
##     NA                        1 (1.1)
##   dxdep (%)                  0.092            0.339
##     0                         62 (65.3)
##     1                         28 (29.5)
##     NA                        5 (5.3)
##   desat (median [IQR])       6.50 [2.53, 12.22] 0.002 nonnorm 0.759
##   pressure (median [IQR])    10.00 [9.00, 12.00] 0.705 nonnorm 0.051
##   ahi (median [IQR])         32.90 [21.20, 56.75] 0.036 nonnorm 0.364
```

```
write.csv(tl.print, "WholeTable1.csv")
write.csv(naniar::miss_var_summary(pap, order = FALSE), "missingness.csv")

naniar::miss_var_summary(pap, order = TRUE)
```

```
## # A tibble: 52 x 3
##   variable      n_miss pct_miss
##   <chr>         <int> <dbl>
## 1 bmi.1           175    100
## 2 desat           75    42.9
## 3 fosq_sexual.3   58    33.1
## 4 fosq_sexual.1   44    25.1
## 5 avgpapuse.3    40    22.9
## 6 bmi.3           35    20
## 7 systolic.3     35    20
## 8 diastolic.3    35    20
## 9 fosq_socout.3  35    20
## 10 sf36_pcs.3    34    19.4
## # ... with 42 more rows
```

```
VIM::aggr(pap)
```



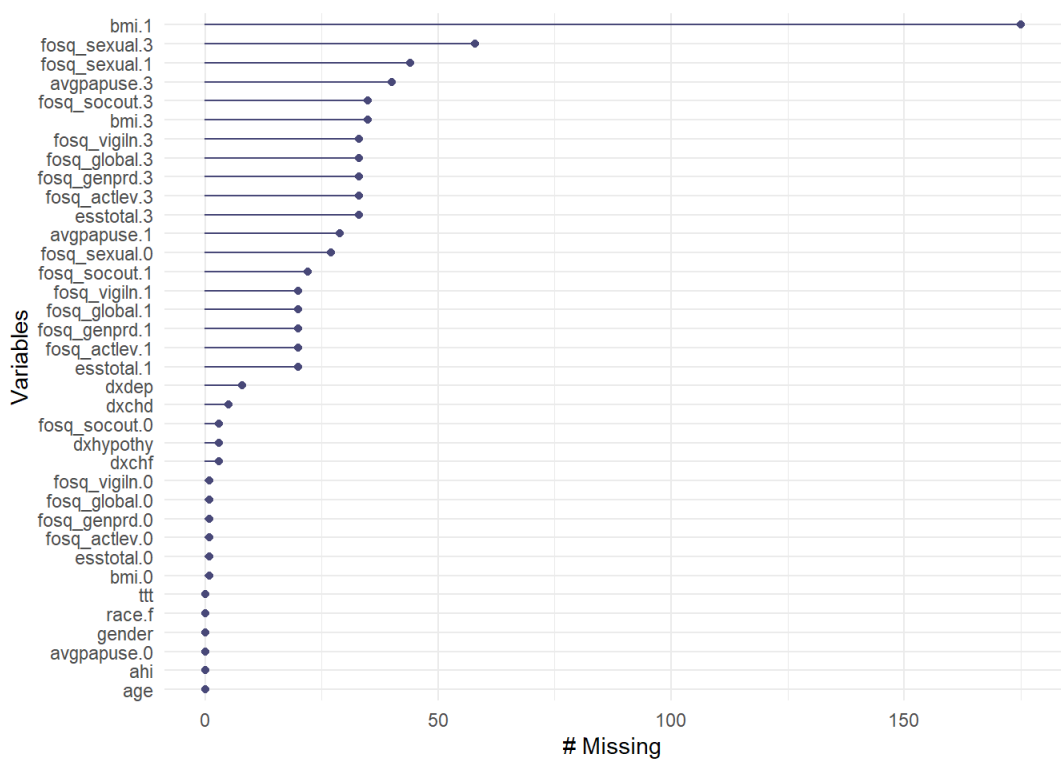
Now the real meat of the operation: residuals

## 4 Imputing with multilevel model

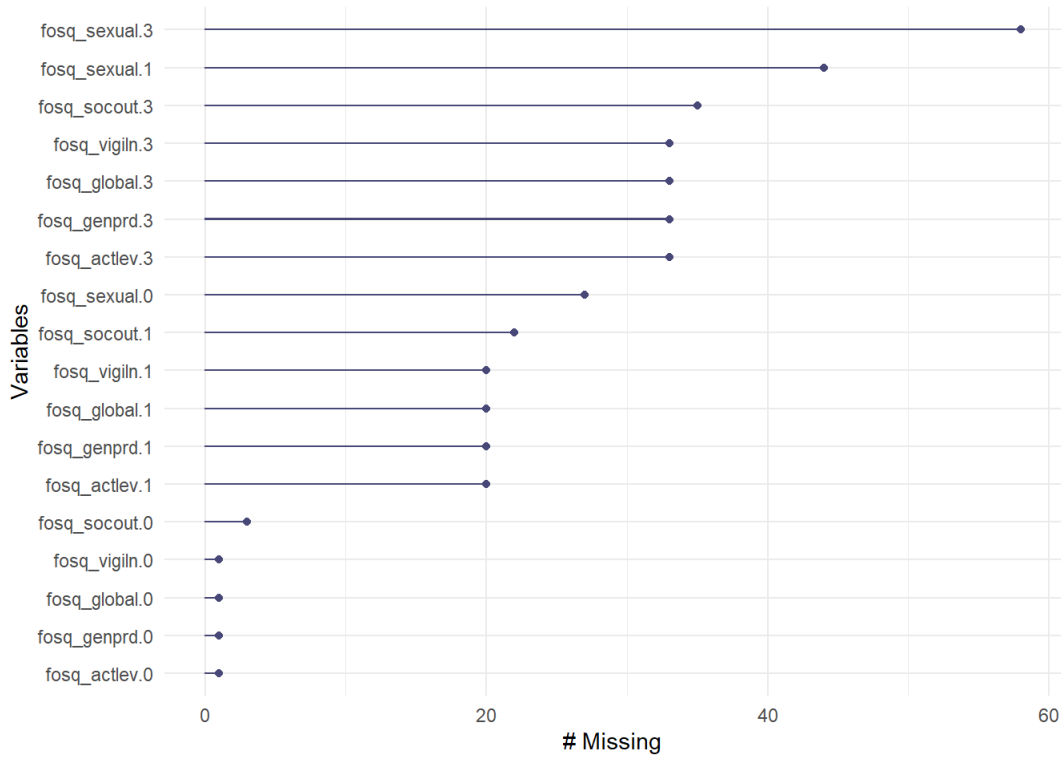
### 4.0.1 missingness

```
#Missingness of original wide dataset
naniar::gg_miss_var(pap %>% select(contains("fosq"), contains("avgpapuse"), contains("dx"), ahi,
  contains("bmi"), age, gender, race.f, ttt, ahi, contains("esstotal")))
```

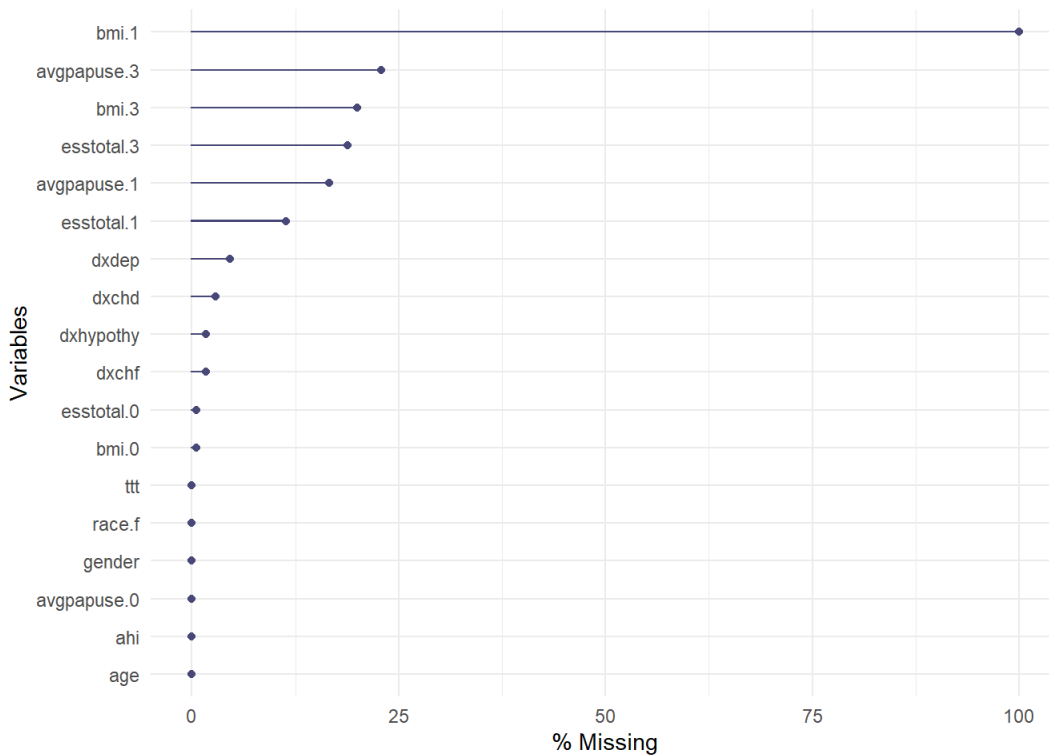




```
naniar::gg_miss_var(pap %>% select(contains("fosq")))
```



```
naniar::gg_miss_var(pap %>% select(contains("avgpapuse"), contains("dx"), ahi, contains("bmi"), age, gender, race.f, ttt, ahi, contains("esstotal")), show_pct = TRUE)
```



### 4.0.2 Is it MCAR?

```
#determine if MCAR. I ran it once and that was more than enough for me. It takes a long time
# b = BaylorEdPsych::LittleMCAR(pap.long)
# #Chi-square
# b[1:3]
# round(b$amount.missing,2)
```

Definitely not MCAR.

```
RBtest::RBtest(pap.long)$type
```

```
##      nsrrid      time      esstotal      bmi      avgpapuse
##      -1        -1        1          0          1
##      systolic  diastolic  fosq_genprd  fosq_socout  fosq_actlev
##      0          0          1          0          1
##      fosq_vigiln  fosq_sexual  fosq_global  sf36_pcs    sf36_mcs
##      1          0          1          1          0
##      sc.esstotal    sc.bmi    sc.avgpapuse  sc.systolic  sc.diastolic
##      1          0          1          0          0
##      sc.fosq_genprd  sc.fosq_socout  sc.fosq_actlev  sc.fosq_vigiln  sc.fosq_sexual
##      1          0          1          1          0
##      sc.fosq_global  sc.sf36_pcs    sc.sf36_mcs    pap.4        treat.f
##      1          1          0          0          -1
##      age          gender      race.f      ttt        desat
##      -1          -1        -1        -1        1
##      pressure    ahi        dxchf      dxchd      dxhypothy
##      -1          -1        -1        0          0
##      dxdep
##      0
```

Zero is MCAR variables, 1 is for MAR variables and -1 is for complete variables.

So, esstotal, average PAP use, FOSQ general productivity, FOSQ activity level, FOSQ global = (FOSQ vigilance, SF36 physical, desaturation) are all not MCAR. They may be MAR (hopefully) or NMAR (hopefully not).

### 4.0.3 levels levels

```

outcome =c("esstotal",
           "fosq_genprd", "fosq_socout", "fosq_genprd",
           "fosq_socout", "fosq_actlev", "fosq_vigiln", "fosq_sexual",
           "fosq_global",
           # "pf_norm", "rp_norm", "bp_norm", "gh_norm", "vt_norm",
           # "sf_norm", "re_norm", "mh_norm", "agg_phys", "agg_ment",
           "sf36_pcs", "sf36_mcs")
level1 = c(recurrent[recurrent %nin% outcome])

level2 = c("treat.f", "age", "gender", "race.f", "ttt", "ahi",
          "dxchf", "dxchd", "dxdep", "dxhypothy",
          "desat", "pressure")

#means and deviations
l1mean = paste0("m", level1[!str_detect(level1, "time")])
l1dev = paste0("d",
              level1[!c(str_detect(level1, "time") |
                       str_detect(level1, str_sub(l1mean[length(l1mean)], start = 2)))]])

#level 1 interactions
f = 1
l1int = c()

for(i in 1:(length(level1)-1)){
  for(j in (i+1):length(level1)){
    if(i != j){
      l1int[f] = paste0(level1[i], ".", level1[j])
      f=f+1
    }
  }
}

#level1:level2 interactions
f = 1
l1l2int = c()
#l1l2int[1] = paste0(level2[1], ".", level1[1])
for(i in 1:(length(level2))){
  for(j in 1:length(level1)){
    l1l2int[f] = paste0(level2[i], ".", level1[j])
    f=f+1
  }
}

#level 2 interactions
f = 1
l2int = c()
l2int[1] = paste0(level2[1], ".", level2[2])
for(i in 1:length(level2)){
  for(j in (i+1):length(level2)){
    if(i != j){
      l2int[f] = paste0(level2[i], ".", level2[j])
      f=f+1
    }
  }
}
}

```

#### 4.0.4 desitgn matrix

Scale things

```
d = pap.long %>% mutate(
  across(level1, ~as.numeric(scale(.x, scale = FALSE)))#do not scale if you want a random slope
)
d[,c(l1mean, l1dev, l1int, l2int, l1l2int)] <- NA
```

### Level 1 variables

```
meth = make.method(d)
meth[level1] = "2l.pmm"

pred = make.predictorMatrix(d)
pred[,] = 0
pred["nsrrid"] = -2
pred[level1, "time"] = 1
for(v in 1:length(level1)){
  pred[level1[v],
    unlist(c(level1[-v], l1int[!str_detect(l1int, level1[v])],
      l1l2int[!str_detect(l1l2int, level1[v])],
      l2int))] = 3
}
#random slopes
pred["fosq_global", "avgpapuse"] = 4
pred["avgpapuse", "fosq_global"] = 4
meth["pap.4"] = "~I(factor(ifelse(avgpapuse>4,1,0)))"
```

### Level 2 variables

```
meth[level2] = "2lonly.pmm"
pred[level2, level1] = 1
pred[level2, l1int] = 1
pred[level2, l1dev] = 1
pred[level2, l2int] = 1
pred[level2, l1l2int] = 1
pred[level2, level2] = 1

#diagonals should be 0
for(v in 1:length(level2)){
  pred[v,v] = 0
}
```

### Derive Group means

```
meth[l1mean] = "2l.groupmean"
pred[which(colnames(pred) == l1mean), level1[1:length(l1mean)]] <- diag(4)
```

### Derive deviations from clusters

```
for(i in 1:(length(level1)-2)){
  meth[l1dev[i]] =
    paste0("~ I(", level1[i], " - ", l1mean[i], ")")
}
```

### Derive interactions

```

#level 1 interactions
f=1
for(i in 1:(length(level1)-1)){
  for(j in (i+1):length(level1)){
    if(i != j){
      meth[l1int[f]] = paste0("~ I(",level1[i],"*",level1[j], ")")
      f=f+1
    }
  }
}

#level1:level2 interactions
f=1
for(i in 1:length(level2)){
  for(j in 1:length(level1)){
    meth[l1l2int[f]] = paste0("~ I(",level2[i],"*",level1[j], ")")
    f=f+1
  }
}

#level 2 interactions
f=1
meth[l2int[1]] = paste0("~ I(",level2[1],"*",level2[2])
for(i in 1:length(level2)){
  for(j in (i+1):length(level2)){
    if(i != j){
      meth[l2int[f]] = paste0("~ I(",level2[i],"*",level2[j], ")")
      f = f+1
    }
  }
}
}

```

Visit sequence to update derived variables

```

#raw level 1
visit = c()
for(a in 1:(length(level1)-1)){
  visit = c(level1[a], l1mean[a], l1dev[a],
            l1int[str_detect(l1int, level1[a])],
            l1l2int[str_detect(l1l2int, level1[a])])
}
for(b in 1:length(level2)){
  visits = append(visit,
                 c(level2[b],
                   l2int[str_detect(l2int, level2[b])],
                   l1l2int[str_detect(l1l2int, level2[b])]))
}

```

```

#outcome imputation
meth[outcome] = "ppm"
pred[outcome,c(level1, level2, outcome)] = 1

```

## 5 Imputin'

```
iter = 10
imps = mice(d,
            predictorMatrix = pred,
            method = meth,
            seed = 100,
            visit = visits,
            m = iter,
            print = FALSE,
            allow.na = FALSE)
imp.mult = imps %>%
  complete("long", include = TRUE) %>%
  group_by(nsrrid) %>%
  mutate(across(levell, ~ .x + mean(.x), na.rm = TRUE)) %>%
  ungroup() %>%
  as.mids()
```

## 6 LME Models

### 7 Random slope, intercept, or both

```

#tried many time many ways to get this to work with the imputed dataset; it would not
m.none = vector()
m.intercept = vector()
m.both = vector()

for(s in 1:iter){
  m.none[s]=fixest::feNmlm(fosq_global ~ avgpapuse * time +
    age + gender + race.f + ttt + ahi +
    dxchf + dxchd + dxdep + dxhypothy,
    panel.id = nsrrid,
    data = complete(imp.mult,s),
    family = 'gaussian') %>% logLik()
}

for(v in 1:iter) {
  m.intercept[v] = lmer(fosq_global ~ avgpapuse * time +
    age + gender + race.f + ttt + ahi +
    dxchf + dxchd + dxdep + dxhypothy + (1|nsrrid),
    data = complete(imp.mult, v),
    REML= FALSE) %>% logLik() %>% as.numeric
}

for(v in 1:iter) {
  m.both[v] = lmer(fosq_global ~ avgpapuse * time +
    age + gender + race.f + ttt + ahi +
    dxchf + dxchd + dxdep + dxhypothy + (1+time|nsrrid),
    data = complete(imp.mult, v),
    REML= FALSE) %>% logLik() %>% as.numeric
}

#compare none to intercept
l.none = mean(m.none)
l.intercept = mean(m.intercept)
l.both = mean(m.both)

#1 deg freedom between none and intercept
l.intercept - l.none

```

```
## [1] 36.71998
```

```
l.both - l.intercept
```

```
## [1] 4.860817
```

The critical value for the intercept is much lower than the 32 we get. So, there's strong evidence that no random effects is insufficient relative to a random intercept. The critical chi-squared value for the intercept and slope is 5.14. Since  $5.28 > 5.14$ , we have evidence that the random intercept is insufficient compared to the random intercept and slope. All models from here on out will have a random intercept and slope.

## 8 Mean structure



```
m.intercept = with(imp.mult,
                  lmer(fosq_global ~ 1 + (1+time|nsrrid), REML= FALSE))
#Pap use and time
m.avgpapuse.time =with(imp.mult,
                      lmer(fosq_global ~ avgpapuse + time+(1+time|nsrrid), REML= FALSE))

m.papint = with(imp.mult,
               lmer(fosq_global ~ avgpapuse * time+(1+time|nsrrid), REML= FALSE))

#demographics
m.demographics = with(imp.mult,
                     lmer(fosq_global ~ avgpapuse * time +
                           age + gender + race.f +(1+time|nsrrid), REML= FALSE))

#pap use, time, depression
m.limit = with(imp.mult,
              lmer(fosq_global ~ avgpapuse * time +
                  dxdep + (1+time|nsrrid), REML= FALSE))

#app use time, depression, sex
m.ladies = with(imp.mult,
               lmer(fosq_global ~ avgpapuse * time +
                   gender +
                   dxdep + (1+time|nsrrid), REML= FALSE))
#pap use, time, depression, age, gender, race, time to treatment, AHI
m.dep = with(imp.mult,
            lmer(fosq_global ~ avgpapuse * time +
                age + gender + race.f + ttt + ahi +
                dxdep + (1+time|nsrrid), REML= FALSE))
#all comorbidities and demographics; no time to treatment or AHI
m.comorbid = with(imp.mult,
                 lmer(fosq_global ~ avgpapuse * time +
                     age + gender + race.f +
                     dxchf + dxchd + dxdep + dxhypo + (1+time|nsrrid), REML= FALSE))

#everything but the kitchen sink
m.full.intercept = with(imp.mult,
                      lmer(fosq_global ~ avgpapuse * time +
                          age + gender + race.f + ttt + ahi +
                          dxchf + dxchd + dxdep + dxhypo + (1+time|nsrrid), REML= FALSE))

m.treat = with(imp.mult,
              lmer(fosq_global ~ treat.f + avgpapuse * time +
                  dxdep + (1+time|nsrrid), REML= FALSE))

models = list(m.intercept,
             m.avgpapuse.time,
             m.demographics,
             m.comorbid,
             m.full.intercept,
             m.dep,
             m.limit,
             m.ladies)

#m.fits = map(models,function(v) {testEstimates(as.mitml.result(v), extra.pars = TRUE)})
```



```
##      test statistic df1      df2 dfcom  p.value riv
## 1  ~ 2  1.013515    5 345.0171   347 0.4095035  0
```

```
D1(m.ladies, m.limit) #no evidence that gender improves fit
```

```
##      test statistic df1      df2 dfcom  p.value riv
## 1  ~ 2  1.65913    1 350.0169   352 0.1985717  0
```

```
D1(m.treat, m.limit) #no evidence that treatment group is important
```

```
##      test statistic df1      df2 dfcom  p.value riv
## 1  ~ 2  1.833507    1 350.0169   352 0.1765875  0
```

Limited model (`mlimit`) for the win!

Very wonky way of indicating that  $p = 0.01$  for intercept + slope being better than intercept alone over 10 datasets and  $p < 0.001$  for intercept + slope being better than slope alone.

## 8.0.2 Pretty graph final model

```
m.fosq = with(imp.mult,
              lmer(fosq_global ~ avgpapuse * time +
                  dxdep + (1+time|nsrrid), REML= TRUE))
pool(m.fosq)
```

```
## Class: mipo      m = 10
##      term m      estimate      ubar b      t dfcom      df riv
## 1  (Intercept) 10 16.40914666 0.0772679517 0 0.0772679517   353 350.9816  0
## 2    avgpapuse 10  0.39426367 0.0031357089 0 0.0031357089   353 350.9816  0
## 3      time    10  0.66140263 0.0085790732 0 0.0085790732   353 350.9816  0
## 4    dxdep    10 -2.06441882 0.1818212461 0 0.1818212461   353 350.9816  0
## 5 avgpapuse:time 10 -0.06897665 0.0005309331 0 0.0005309331   353 350.9816  0
##      lambda      fmi
## 1      0 0.005650011
## 2      0 0.005650011
## 3      0 0.005650011
## 4      0 0.005650011
## 5      0 0.005650011
```

```
testEstimates(as.mitml.result(m.fosq), extra.pars = TRUE)
```

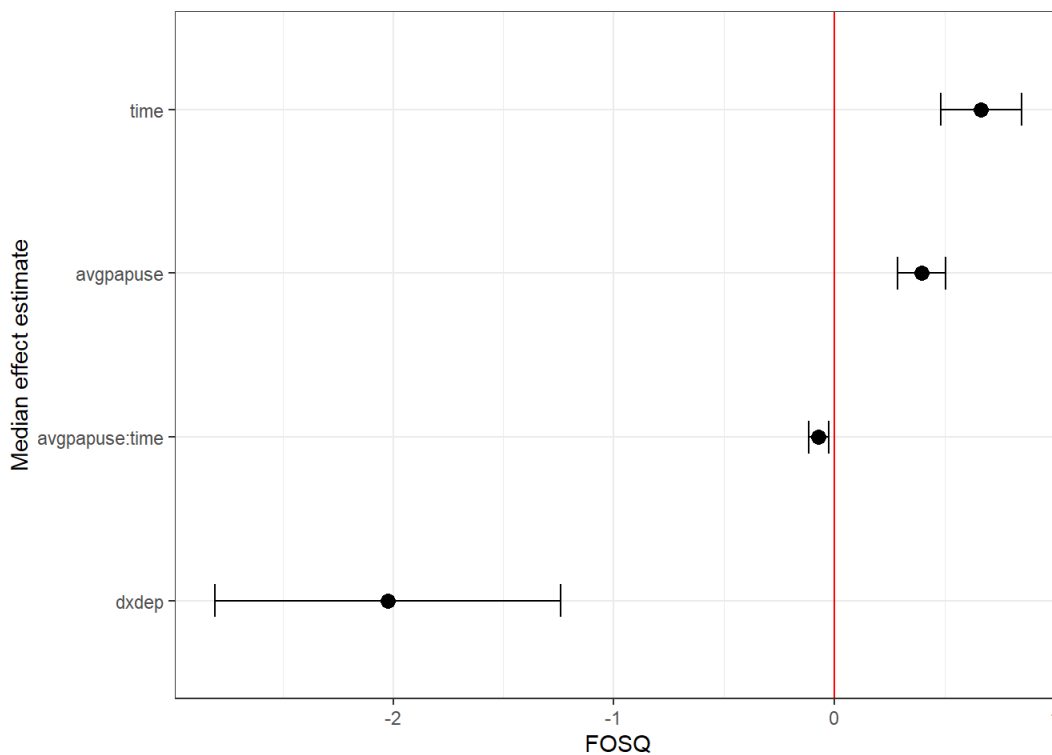
```
##
## Call:
##
## testEstimates(model = as.mitml.result(m.fosq), extra.pars = TRUE)
##
## Final parameter estimates and inferences obtained from 10 imputed data sets.
##
##           Estimate Std.Error   t.value    df    P(>|t|)    RIV    FMI
## (Intercept)   16.409    0.278   59.032   Inf    0.000    0.000  0.000
## avgpapuse      0.394    0.056    7.041   Inf    0.000    0.000  0.000
## time           0.661    0.093    7.141   Inf    0.000    0.000  0.000
## dxdep         -2.064    0.426   -4.841   Inf    0.000    0.000  0.000
## avgpapuse:time -0.069    0.023   -2.994   Inf    0.003    0.000  0.000
##
##                               Estimate
## Intercept~~Intercept|nsrrid    5.091
## time~~time|nsrrid              0.098
## Intercept~~time|nsrrid        -0.625
## Residual~~Residual             3.018
## ICC|nsrrid                     0.628
##
## Unadjusted hypothesis test as appropriate in larger samples.
```

```
#95%CI
confint(testEstimates(as.mitml.result(m.fosq)))
```

```
##           2.5 %    97.5 %
## (Intercept) 15.8643333 16.95396008
## avgpapuse   0.2845108 0.50401655
## time       0.4798643 0.84294094
## dxdep     -2.9001573 -1.22868032
## avgpapuse:time -0.1141381 -0.02381519
```

```
#now you're just showing off
m.1 = lmer(fosq_global ~ avgpapuse * time +
           dxdep + (1+time|nsrrid), data = complete(imp.mult,1), REML= TRUE)
est = FESim(m.1, seed = 25)

plotFESim(est) +
  theme_bw() +
  labs(x = "Median effect estimate", y = "FOSQ")
```



Different ways of displaying the same data. Looks like PAP use is associated with improvements in FOSQ; so is time. Perhaps the influence of PAP use diminishes over time (negative interaction of adherence x time). It's not a huge surprise that depression makes life worse.

## 9 Mediation analysis

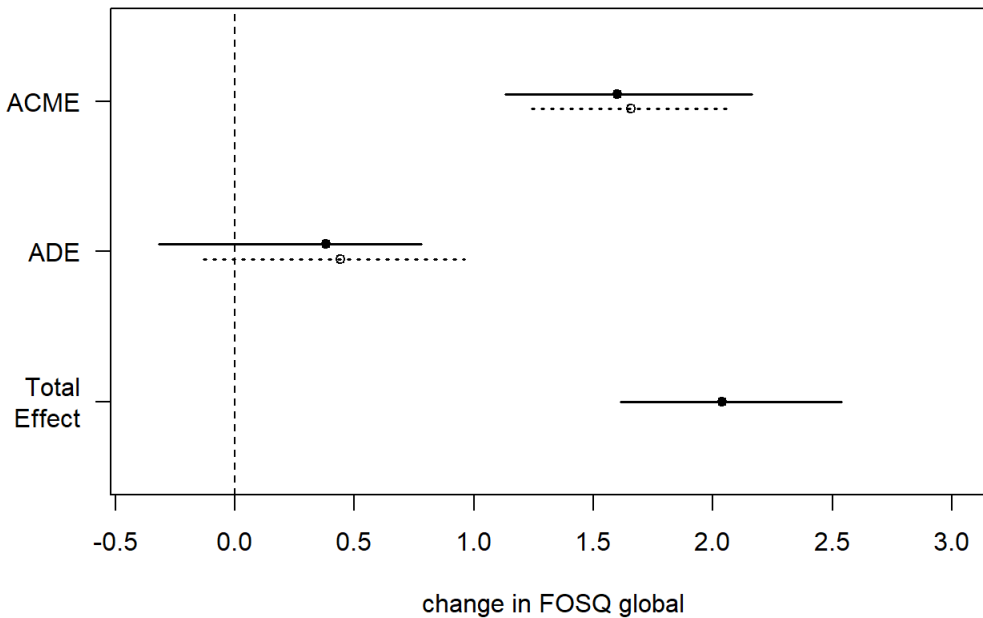
```
#do this with imputed data
#needs a named list of dataframes
dat = list()
for(s in 1:iter){
  dat[s] = complete(imp.mult, s)
}
dat = as.list(imp.mult)

imp.med = mediations(datasets = dat,
  treatment = "pap.4", #split by standard adherence threshold
  mediators = "esstotal",
  outcome = "fosq_global",
  families = c("gaussian", "gaussian"),
  interaction = TRUE,
  sims = 50,
  conf.level = 0.95,
  group.out = "nsrrid") %>%

  amelidiate()
summary(imp.med)
```

```
##
## Causal Mediation Analysis
##
## Quasi-Bayesian Confidence Intervals
##
##           Estimate % CI Lower % CI Upper p-value
## ACME (control)      1.659      1.241      2.06      1
## ACME (treated)      1.600      1.131      2.16      1
## ADE (control)       0.441     -0.132      0.96      1
## ADE (treated)       0.382     -0.318      0.78      1
## Total Effect        2.040      1.613      2.54      1
## Prop. Mediated (control) 0.820      0.665      1.19      1
## Prop. Mediated (treated) 0.791      0.552      1.08      1
## ACME (average)      1.629      1.214      2.02      1
## ADE (average)       0.411     -0.239      0.88      1
## Prop. Mediated (average) 0.795      0.795      0.80      1
##
## Sample Size Used: 435
##
##
## Simulations: 50
```

```
plot(imp.med, xlab = "change in FOSQ global")
```



ACME = average

causal mediation effect (i.e. indirect effect) ADE = average direct effect total = total effect

### 9.0.1 SF-36

```
m.sfmc = with(imp.mult,
  lmer(sf36_mcs ~ avgpapuse * time +
    dxdep + (1+time|nsrrid), REML= TRUE)
  testEstimates(as.mitml.result(m.sfmc), extra.pars = TRUE)
```

```
##
## Call:
##
## testEstimates(model = as.mitml.result(m.sfmc), extra.pars = TRUE)
##
## Final parameter estimates and inferences obtained from 10 imputed data sets.
##
##           Estimate Std.Error  t.value      df  P(>|t|)      RIV      FMI
## (Intercept)   50.198    1.027   48.875     Inf    0.000    0.000    0.000
## avgpapuse      0.874    0.207   4.226     Inf    0.000    0.000    0.000
## time           1.274    0.338   3.766     Inf    0.000    0.000    0.000
## dxdep         -8.415    1.731  -4.861     Inf    0.000    0.000    0.000
## avgpapuse:time -0.136    0.085  -1.601     Inf    0.109    0.000    0.000
##
##                               Estimate
## Intercept~~Intercept|nsrrid   64.576
## time~~time|nsrrid             0.138
## Intercept~~time|nsrrid       -2.989
## Residual~~Residual            41.728
## ICC|nsrrid                    0.607
##
## Unadjusted hypothesis test as appropriate in larger samples.
```

```
confint(testEstimates(as.mitml.result(m.sfmc)))
```

```
##           2.5 %      97.5 %
## (Intercept)  48.1851903 52.21125903
## avgpapuse    0.4687351 1.27974179
## time         0.6111355 1.93727785
## dxdep       -11.8079444 -5.02214644
## avgpapuse:time -0.3023389 0.03046364
```

```
m.sfpc = with(imp.mult,
              lmer(sf36_pcs ~ avgpapuse * time +
                  dxdep + (1+time|nsrrid), REML= TRUE))
testEstimates(as.mitml.result(m.sfpc), extra.pars = TRUE)
```

```
##
## Call:
##
## testEstimates(model = as.mitml.result(m.sfpc), extra.pars = TRUE)
##
## Final parameter estimates and inferences obtained from 10 imputed data sets.
##
##           Estimate Std.Error  t.value    df  P(>|t|)    RIV    FMI
## (Intercept)    45.345    0.994   45.636   Inf  0.000    0.000  0.000
## avgpapuse       0.543    0.167    3.259   Inf  0.001    0.000  0.000
## time            1.023    0.305    3.354   Inf  0.001    0.000  0.000
## dxdep          -5.876    1.770   -3.319   Inf  0.001    0.000  0.000
## avgpapuse:time -0.150    0.074   -2.019   Inf  0.043    0.000  0.000
##
##                               Estimate
## Intercept~~Intercept|nsrrid   69.936
## time~~time|nsrrid             2.095
## Intercept~~time|nsrrid       -3.249
## Residual~~Residual            25.011
## ICC|nsrrid                    0.737
##
## Unadjusted hypothesis test as appropriate in larger samples.
```

```
confint(testEstimates(as.mitml.result(m.sfpc)))
```

```
##           2.5 %    97.5 %
## (Intercept)  43.3976408  47.292613883
## avgpapuse    0.2166207  0.870323012
## time         0.4252606  1.620808272
## dxdep       -9.3453083 -2.406052514
## avgpapuse:time -0.2950066 -0.004410495
```

The minimally clinically important difference (MCID) is thought to be ~9 for SF-36 PFS and MCS. The ESS MCID is 1.5-2.

## 9.1 subscales

```
m.genprd = with(imp.mult,
  lmer(fosq_genprd ~ avgpapuse * time +
    dxdep + (1+time|nsrrid), REML= TRUE))
testEstimates(as.mitml.result(m.genprd), extra.pars = TRUE)
```



```
##
## Call:
##
## testEstimates(model = as.mitml.result(m.genprd), extra.pars = TRUE)
##
## Final parameter estimates and inferences obtained from 10 imputed data sets.
##
##           Estimate Std.Error  t.value    df  P(>|t|)    RIV    FMI
## (Intercept)    3.467    0.054   63.839   Inf  0.000    0.000  0.000
## avgpapuse      0.078    0.011    6.929   Inf  0.000    0.000  0.000
## time           0.100    0.019    5.389   Inf  0.000    0.000  0.000
## dxdep          -0.361    0.078   -4.637   Inf  0.000    0.000  0.000
## avgpapuse:time -0.016    0.005   -3.398   Inf  0.001    0.000  0.000
##
##                               Estimate
## Intercept~~Intercept|nsrrid    0.196
## time~~time|nsrrid              0.005
## Intercept~~time|nsrrid         -0.031
## Residual~~Residual              0.121
## ICC|nsrrid                      0.618
##
## Unadjusted hypothesis test as appropriate in larger samples.
```

```
confint(testEstimates(as.mitml.result(m.genprd)))
```

```
##           2.5 %    97.5 %
## (Intercept)  3.36012610  3.572984258
## avgpapuse    0.05564672  0.099548408
## time         0.06368096  0.136467706
## dxdep        -0.51346812 -0.208384741
## avgpapuse:time -0.02465961 -0.006620074
```

```
m.actlev = with(imp.mult,
                lmer(fosq_actlev ~ avgpapuse * time +
                    dxdep + (1+time|nsrrid), REML= TRUE))
testEstimates(as.mitml.result(m.actlev), extra.pars = TRUE)
```

```
##
## Call:
##
## testEstimates(model = as.mitml.result(m.actlev), extra.pars = TRUE)
##
## Final parameter estimates and inferences obtained from 10 imputed data sets.
##
##           Estimate Std.Error  t.value    df  P(>|t|)    RIV    FMI
## (Intercept)    3.039    0.068   44.800   Inf  0.000    0.000  0.000
## avgpapuse      0.095    0.013    7.015   Inf  0.000    0.000  0.000
## time           0.156    0.023    6.762   Inf  0.000    0.000  0.000
## dxdep          -0.470    0.099   -4.743   Inf  0.000    0.000  0.000
## avgpapuse:time -0.017    0.006   -3.031   Inf  0.002    0.000  0.000
##
##                               Estimate
## Intercept~~Intercept|nsrrid    0.317
## time~~time|nsrrid              0.011
## Intercept~~time|nsrrid        -0.051
## Residual~~Residual             0.173
## ICC|nsrrid                     0.647
##
## Unadjusted hypothesis test as appropriate in larger samples.
```

```
confint(testEstimates(as.mitml.result(m.actlev)))
```

```
##           2.5 %    97.5 %
## (Intercept)  2.90603995  3.17194837
## avgpapuse    0.06821857  0.12112256
## time        0.11074173  0.20113163
## dxdep       -0.66399261 -0.27568325
## avgpapuse:time -0.02818899 -0.00604844
```

```
m.socout = with(imp.mult,
                lmer(fosq_socout ~ avgpapuse * time +
                    dxdep + (1+time|nsrrid), REML= TRUE))
testEstimates(as.mitml.result(m.socout), extra.pars = TRUE)
```

```
##
## Call:
##
## testEstimates(model = as.mitml.result(m.socout), extra.pars = TRUE)
##
## Final parameter estimates and inferences obtained from 10 imputed data sets.
##
##           Estimate Std.Error  t.value    df  P(>|t|)    RIV    FMI
## (Intercept)    3.556    0.067   53.405   Inf  0.000    0.000  0.000
## avgpapuse      0.068    0.014    4.778   Inf  0.000    0.000  0.000
## time           0.088    0.024    3.600   Inf  0.000    0.000  0.000
## dxdep         -0.295    0.088   -3.360   Inf  0.001    0.000  0.000
## avgpapuse:time -0.014    0.006   -2.293   Inf  0.022    0.000  0.000
##
##                               Estimate
## Intercept~~Intercept|nsrrid    0.289
## time~~time|nsrrid              0.013
## Intercept~~time|nsrrid        -0.062
## Residual~~Residual             0.201
## ICC|nsrrid                     0.590
##
## Unadjusted hypothesis test as appropriate in larger samples.
```

```
confint(testEstimates(as.mitml.result(m.socout)))
```

```
##           2.5 %    97.5 %
## (Intercept)  3.42536760  3.68636607
## avgpapuse    0.04033969  0.09646002
## time         0.04018122  0.13620877
## dxdep        -0.46675591 -0.12283390
## avgpapuse:time -0.02567321 -0.00200843
```

```
m.vigiln = with(imp.mult,
                lmer(fosq_vigiln ~ avgpapuse * time +
                    dxdep + (1+time|nsrrid), REML= TRUE))
testEstimates(as.mitml.result(m.vigiln), extra.pars = TRUE)
```

```
##
## Call:
##
## testEstimates(model = as.mitml.result(m.vigiln), extra.pars = TRUE)
##
## Final parameter estimates and inferences obtained from 10 imputed data sets.
##
##           Estimate Std.Error  t.value    df  P(>|t|)    RIV    FMI
## (Intercept)    3.119    0.062   49.982   Inf  0.000    0.000  0.000
## avgpapuse      0.095    0.013    7.298   Inf  0.000    0.000  0.000
## time           0.169    0.022    7.767   Inf  0.000    0.000  0.000
## dxdep          -0.301    0.098   -3.064   Inf  0.002    0.000  0.000
## avgpapuse:time -0.018    0.005   -3.330   Inf  0.001    0.000  0.000
##
##                               Estimate
## Intercept~~Intercept|nsrrid    0.239
## time~~time|nsrrid              0.005
## Intercept~~time|nsrrid        -0.025
## Residual~~Residual             0.169
## ICC|nsrrid                     0.586
##
## Unadjusted hypothesis test as appropriate in larger samples.
```

```
confint(testEstimates(as.mitml.result(m.vigiln)))
```

```
##           2.5 %    97.5 %
## (Intercept)  2.99709300  3.241740109
## avgpapuse    0.06973547  0.120944200
## time         0.12634082  0.211625859
## dxdep        -0.49355398 -0.108484440
## avgpapuse:time -0.02896199 -0.007500099
```

```
m.sexual = with(imp.mult,
                lmer(fosq_sexual ~ avgpapuse * time +
                    dxdep + (1+time|nsrrid), REML= TRUE))
testEstimates(as.mitml.result(m.sexual), extra.pars = TRUE)
```

```
##
## Call:
##
## testEstimates(model = as.mitml.result(m.sexual), extra.pars = TRUE)
##
## Final parameter estimates and inferences obtained from 10 imputed data sets.
##
##           Estimate Std.Error  t.value    df  P(>|t|)    RIV    FMI
## (Intercept)    3.241    0.094   34.550   Inf  0.000    0.000  0.000
## avgpapuse      0.054    0.019    2.815   Inf  0.005    0.000  0.000
## time           0.144    0.031    4.600   Inf  0.000    0.000  0.000
## dxdep          -0.679    0.144   -4.711   Inf  0.000    0.000  0.000
## avgpapuse:time -0.006    0.008   -0.713   Inf  0.476    0.000  0.000
##
##                Estimate
## Intercept~~Intercept|nsrrid    0.510
## time~~time|nsrrid              0.008
## Intercept~~time|nsrrid        -0.063
## Residual~~Residual             0.286
## ICC|nsrrid                     0.641
##
## Unadjusted hypothesis test as appropriate in larger samples.
```

```
confint(testEstimates(as.mitml.result(m.sexual)))
```

```
##           2.5 %    97.5 %
## (Intercept)  3.05722404  3.424949035
## avgpapuse    0.01635070  0.091349324
## time         0.08263667  0.205350226
## dxdep        -0.96180089 -0.396600959
## avgpapuse:time -0.02093892  0.009763064
```

Intercept + slope is better.

```
# m.ar1 = with(imp.mult, lme(fosq_global ~ avgpapuse + time + (1+time|nsrrid),
#   random = ~time|nsrrid,
#   correlation = corAR1(0.67,
#     form =~1+time|nsrrid),
#   method= "REML",
#   na.action = na.exclude))
#
# m.uns = lme(fosq_global ~ avgpapuse * time + (1+time|nsrrid),
#   random = ~1+time|nsrrid,
#   data = imp.mult[[2]],
#   method= "REML",
#   na.action = na.exclude)
```

## 10 ICC

ICC

```
performance::icc(lmer(fosq_global ~ avgpapuse * time + (1+time|nsrrid),
  data = pap.long),
  by_group = TRUE)
```

```
## # ICC by Group
##
## Group | ICC
## -----
## nsrrid | 0.676
```

ICC = 0.524 before imputation

#Session info

```
sessionInfo()
```

```

## R version 4.0.2 (2020-06-22)
## Platform: x86_64-w64-mingw32/x64 (64-bit)
## Running under: Windows 10 x64 (build 19042)
##
## Matrix products: default
##
## locale:
## [1] LC_COLLATE=English_United States.1252
## [2] LC_CTYPE=English_United States.1252
## [3] LC_MONETARY=English_United States.1252
## [4] LC_NUMERIC=C
## [5] LC_TIME=English_United States.1252
##
## attached base packages:
## [1] parallel stats graphics grDevices utils datasets methods
## [8] base
##
## other attached packages:
## [1] forcats_0.5.1 stringr_1.4.0 dplyr_1.0.4 purrr_0.3.4
## [5] readr_1.4.0 tidyr_1.1.3 tibble_3.0.6 tidyverse_1.3.1
## [9] magrittr_2.0.1 broom.mixed_0.2.6 mitml_0.4-1 nlme_3.1-152
## [13] glmm_1.4.2 doParallel_1.0.16 iterators_1.0.13 foreach_1.5.1
## [17] trust_0.1-8 mediation_4.5.0 sandwich_3.0-0 mvtnorm_1.1-1
## [21] merTools_0.5.2 arm_1.11-2 lme4_1.1-26 Matrix_1.3-2
## [25] MASS_7.3-53.1 extrafont_0.17 gee_4.13-20 miceadds_3.11-6
## [29] Hmisc_4.5-0 Formula_1.2-4 survival_3.2-11 caret_6.0-86
## [33] ggplot2_3.3.3 lattice_0.20-41 mice_3.13.0 colorspace_2.0-1
## [37] tableone_0.12.0
##
## loaded via a namespace (and not attached):
## [1] utf8_1.1.4 tidyrselect_1.1.1 htmlwidgets_1.5.3
## [4] grid_4.0.2 ranger_0.12.1 lpSolve_5.6.15
## [7] pROC_1.17.0.1 munsell_0.5.0 codetools_0.2-18
## [10] statmod_1.4.35 withr_2.4.2 highr_0.9
## [13] knitr_1.33 rstudioapi_0.13 stats4_4.0.2
## [16] robustbase_0.93-7 vcd_1.4-8 VIM_6.1.0
## [19] Rttf2pt1_1.3.8 labeling_0.4.2 mnormt_2.0.2
## [22] farver_2.1.0 rprojroot_2.0.2 coda_0.19-4
## [25] vctrs_0.3.6 generics_0.1.0 ipred_0.9-11
## [28] xfun_0.22 itertools_0.1-3 R6_2.5.0
## [31] assertthat_0.2.1 promises_1.2.0.1 scales_1.1.1
## [34] nnet_7.3-15 gtable_0.3.0 timeDate_3043.102
## [37] rlang_0.4.10 splines_4.0.2 extrafontdb_1.0
## [40] TMB_1.7.20 ModelMetrics_1.2.2.2 broom_0.7.6
## [43] checkmate_2.0.0 yaml_2.2.1 reshape2_1.4.4
## [46] abind_1.4-5 modelr_0.1.8 backports_1.2.1
## [49] httpuv_1.6.0 tools_4.0.2 lava_1.6.9
## [52] psych_2.1.3 ellipsis_0.3.1 jquerylib_0.1.4
## [55] RColorBrewer_1.1-2 proxy_0.4-25 Rcpp_1.0.6
## [58] plyr_1.8.6 base64enc_0.1-3 rpart_4.1-15
## [61] dreamer_1.2.3 zoo_1.8-8 haven_2.4.1
## [64] cluster_2.1.2 fs_1.5.0 here_1.0.1
## [67] survey_4.0 data.table_1.14.0 openxlsx_4.2.3
## [70] lmtest_0.9-38 reprex_2.0.0 tmvnsim_1.0-2
## [73] Rbtest_1.1 hms_1.0.0 mime_0.10
## [76] evaluate_0.14 xtable_1.8-4 rio_0.5.26
## [79] jpeg_0.1-8.1 readxl_1.3.1 gridExtra_2.3
## [82] compiler_4.0.2 crayon_1.4.1 minqa_1.2.4
## [85] htmltools_0.5.1.1 later_1.2.0 visdat_0.5.3
## [88] lubridate_1.7.10 DBI_1.1.1 dbplyr_2.1.1

```

```
## [91] boot_1.3-28          car_3.0-10          cli_2.5.0
## [94] mitools_2.4           insight_0.13.2     fixest_0.8.4
## [97] pan_1.6               gower_0.2.2       pkgconfig_2.0.3
## [100] numDeriv_2016.8-1.1  foreign_0.8-81     laeken_0.5.1
## [103] sp_1.4-5              recipes_0.1.16     xml2_1.3.2
## [106] bslib_0.2.4          blme_1.0-5         proclim_2019.11.13
## [109] rvest_1.0.0          digest_0.6.27     naniar_0.6.0
## [112] rmarkdown_2.7        cellranger_1.1.0  htmlTable_2.1.0
## [115] curl_4.3.1           shiny_1.6.0        jomo_2.7-2
## [118] nloptr_1.2.2.2       lifecycle_1.0.0   jsonlite_1.7.2
## [121] carData_3.0-4        fansi_0.4.2        labelled_2.8.0
## [124] pillar_1.6.0         fastmap_1.1.0     httr_1.4.2
## [127] DEoptimR_1.0-8       glue_1.4.2         bayestestR_0.9.0
## [130] zip_2.1.1            png_0.1-7          class_7.3-18
## [133] stringi_1.5.3        sass_0.3.1         performance_0.7.1
## [136] latticeExtra_0.6-29 e1071_1.7-6
```