

Research Questions 2 and 3 Stopping-Ratio Models for SANE Training Program Data

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Table of contents

1	Purpose	2
2	Research Questions	3
3	Setup	3
3.1	Define Global Options	3
3.2	Load Packages	4
3.3	Declare Path	6
3.4	Load Data	6
4	Overview of Stopping-Ratio Modeling	7
5	Methods	9
5.1	Sample	9
5.2	Measures	10
5.2.1	Attrition (Primary Outcome)	10
5.2.2	Threshold (Structural Predictor)	10
5.2.3	Background Characteristics (Focal Predictor)	10
5.2.4	Motivations (Focal Predictors)	10
5.2.5	Potential Barriers (Focal Predictors)	10
5.2.6	Emotional Readiness (Focal Predictors)	11
5.2.7	Start and Finish Indicators for Didactic Training Modules (Secondary Outcomes)	11
5.3	Planned Statistical Analyses	11
5.3.1	RQ2: What are the attrition rates from enrollment to completion of the CSW, and when (i.e., at which module[s]) did participants commonly attrit?	12
5.3.2	RQ3: Do participants' background characteristics, motivations for seeking training, potential barriers, and emotional readiness for this work predict attrition rates? .	12
5.4	Modeling Software	13
5.5	Model Diagnostics	13
5.5.1	Collinearity	13
5.5.2	Residual Distributions	14
6	Results	14
6.1	Model 1: Thresholds Alone	14
6.1.1	Single Term Deletion Tests	15

6.1.2	Estimated Marginal Means	16
6.1.3	Model Diagnostics	18
6.2	Model 2: Thresholds & Parallel Effects for All Focal Predictors	19
6.2.1	Check for Multicollinearity	20
6.2.2	Compare Models 1 and 2	21
6.2.3	Single Term Deletion Tests	22
6.2.4	Estimated Marginal Means	22
6.2.5	Model Diagnostics	29
6.3	Model 3: Thresholds & Non-Parallel Effects for All Focal Predictors	30
6.3.1	Check for Multicollinearity	32
6.3.2	Compare Models 2 and 3	33
6.3.3	Single Term Deletion Tests	33
6.3.4	Model Diagnostics	34
6.4	Model 4: Thresholds & Parallel Effect for Motivation_NeedSANE	35
6.4.1	Check for Multicollinearity	36
6.4.2	Compare Models 1 and 4	36
6.4.3	Estimated Marginal Means	37
6.4.4	Model Diagnostics	43
6.5	Model 5: Thresholds & Non-Parallel Effect for Motivation_NeedSANE	44
6.5.1	Check for Multicollinearity	45
6.5.2	Compare Models 4 and 5	45
6.5.3	Model Diagnostics	45
6.6	Unconditional Attrition Rates	47
6.7	Start and Finish Rates for DT Modules	48
7	Conclusions	51
7.1	RQ2: What are the attrition rates from enrollment to completion of the CSW, and when (i.e., at which module[s]) did participants commonly attrit?	51
7.2	RQ3: Do participants' background characteristics, motivations for seeking training, potential barriers, and emotional readiness for this work predict attrition rates?	53
8	Recommendations	54
9	References	54
10	Software Information	56
10.1	Versions	56
10.2	Git Details	58

1 Purpose

This file is part of a research compendium (Pierce, 2026) associated with a study about a sexual assault nurse examiner training program (Dontje & Campbell, 07/01/2021–06/30/2025). The study aims to document rates of attrition at three threshold points during the program and understand predictors of attrition at each of those points.

This file reads an R data file created by another script in this compendium, documents some methodology decisions and details, then runs the stopping-ratio (SR) models that comprise the

analyses answering research questions RQ2 and RQ3 for the study. This file also contains some narrative interpretation of the results and supplementary output such as tables and graphs derived from the models.

2 Research Questions

The research questions addressed in this file may be briefly stated as follows:

- **RQ2.** What are the attrition rates from enrollment to completion of the CSW, and when (i.e., at which module[s]) did participants commonly attrit?
- **RQ3.** Do participants' background characteristics, motivations for seeking training, potential barriers, and emotional readiness for this work predict attrition rates?

💡 Tip

This document uses SR models to answer both RQ2 and RQ3.

ℹ Note

The investigators and the program staff have explicitly decided that the following potential predictors are not of substantive interest and should not be pursued in this paper.

- Trainee's learning scores in the didactic training and clinical skills workshop are not of interest.
- Trainee demographics (sex, age, race, etc.) are not of interest because the team wants to focus on analyzing predictors that have more intrinsic meaning and for which there are theoretical reasons to expect effects on attrition.

3 Setup

This section documents some setup tasks that are useful to the statistician on the team. Most readers of this document will probably want skip directly to Section 4.

3.1 Define Global Options

Global R chunk options are defined in the YAML header but local chunk options will over-ride global options. We can temporarily disable an individual chunk by inserting `#| eval: false` on a line at the top of the chunk. The method for creating a `cfsiz` option that controls font size in code chunks and their text output is based on an answer to a question posted on stackoverflow.com.

```
```{r}
#| label: global-options

Create a custom chunk hook/option for controlling font size in chunk & output.
def.chunk.hook <- knitr::knit_hooks$get("chunk")
knitr::knit_hooks$set(chunk = function(x, options) {
 x <- def.chunk.hook(x, options)
 ifelse(options$cfszie != "normalsize",
 paste0("\n \\", options$cfszie, "\n\n", x, "\n\n \\normalsize"),
 x)
})
```

```

3.2 Load Packages

R packages usually add new functions to the base R software, allowing you to do more things. Here, we load the specific R packages required for this script to work.

```
```{r}
#| label: load-packages

library(here) # for here(), i_am(), makes code more portable.
```

```

```
here() starts at P:/Consulting/Cases_1600-1799/C1788/SANETPA/scripts
```

```
```{r}
#| label: load-packages

library(devtools) # for session_info()
```

```

```
Loading required package: usethis
```

```
```{r}
#| label: load-packages

library(rmarkdown) # for pandoc_version()
library(knitr) # for kable()
library(dplyr) # for %>%, filter(), group_by(), mutate(), rename(), etc.
```

```

```
Attaching package: 'dplyr'
```

```
The following objects are masked from 'package:stats':
```

```
filter, lag
```

```
The following objects are masked from 'package:base':
```

```
intersect, setdiff, setequal, union
```

```
```{r}
#| label: load-packages

library(tidyverse) # for map_dfr(), map_chr(), rowid_to_column(),
```

```

```
-- Attaching core tidyverse packages ----- tidyverse 2.0.0 --
v forcats 1.0.1      v readr   2.1.6
v ggplot2  4.0.2      v stringr 1.6.0
v lubridate 1.9.5     v tibble  3.3.1
v purrr    1.2.1      v tidyrr  1.3.2
```

```
-- Conflicts ----- tidyverse_conflicts() --
x dplyr::filter() masks stats::filter()
x dplyr::lag()   masks stats::lag()
i Use the conflicted package (<http://conflicted.r-lib.org/>) to force all conflicts to become errors
```

```
```{r}
#| label: load-packages

 # rownames_to_column()
options(kableExtra.latex.load_packages = FALSE)
library(kableExtra) # for kable_styling(), add_header_above(),
```

```

```
Attaching package: 'kableExtra'

The following object is masked from 'package:dplyr':

  group_rows
```

```
```{r}
#| label: load-packages

 # column_spec(), row_spec() etc.
library(kableExtra) # for add_header_above(), footnote(), kable_styling()
library(broom) # for glance(), tidy()
library(car) # for vif()
```

```

```
Loading required package: carData

Attaching package: 'car'

The following object is masked from 'package:purrr':

  some

The following object is masked from 'package:dplyr':

  recode
```

```
```{r}
#| label: load-packages

library(DHARMa) # for plotQQunif(), plotResiduals(), simulateResiduals(),
```

```

```
This is DHARMa 0.4.7. For overview type '?DHARMa'. For recent changes, type news(package = 'DHARMa')
```

```
```{r}
#| label: load-packages

 # testDispersion()
library(marginaleffects) # for avg_comparisons(), avg_predictions(),
 # plot_predictions()
library(patchwork) # for combining ggplot2 objects, plot_annotation()
library(performance) # for model_performance(), r2()
library(scales) # for label_number()
```

```

```
Attaching package: 'scales'

The following object is masked from 'package:purrr':

  discard

The following object is masked from 'package:readr':

  col_factor
```

```
```{r}
#| label: load-packages

library(piercer) # for brier(), display_num(), file_details(),
 # git_report(), R2Dev()
library(quarto) # for quarto_version()
library(SANETPA) # for version info
```

```

3.3 Declare Path

This next chunk declares the path to this script relative to the project-level root directory. If the file is not in the right location under the project root you'll get a warning message. This helps ensure relative paths are all working as expected. The chunk below uses the `SourceDir` and `SourceFile` parameters set in the YAML header.

```
```{r}
#| label: declare-path

Declare path to this script relative to the project root directory.
here::i_am(path = paste0(params$SourceDir, params$SourceFile))
```

```

`here()` starts at P:/Consulting/Cases_1600-1799/C1788/SANETPA

3.4 Load Data

This subsection loads the data created by rendering `scripts/Import_Data.qmd`. The data is de-identified to preserve participant privacy and protect confidentiality.

```
```{r}
#| label: load-data
#| eval: true

Store path to data file.
DataFile <- here("data/Imported_SANETP_Data.RData")

load(file = DataFile)
```

```

Table 1 shows meta-data about the data file we just loaded and Table 2 shows the sizes of the datasets it contains.

```
```{r}
#| label: tbl-imported-data-file
#| tbl-cap: "Meta-Data About the Data File Loaded"

file_details(DataFile) %>%
 kable(format = "latex", booktabs = TRUE,
 col.names = c("File Name", "Size", "Last Modified")) %>%
 kable_styling()
```

```

Table 1: Meta-Data About the Data File Loaded

| File Name | Size | Last Modified |
|----------------------------|------|---------------------|
| Imported_SANETP_Data.RData | 181K | 2026-02-14 12:56:34 |

```
```{r}
#| label: tbl-datasets
#| tbl-cap: "Sizes of the Datasets"

Compute sample sizes and percent omitted by listwise deletion. These are used
later in the script.

N_All <- nrow(Enrolled_Applicants)
N_CD <- nrow(Enrolled_Applicants_CD)
N_LWD <- N_All - N_CD
P_LWD <- 100*N_LWD/N_All

Create a summary table.
data.frame(Dataset = c("Applicants", "Eligible_Applicants",
 "Enrolled_Applicants", "Enrolled_Applicants_CD",
 "StartedDT_Applicants", "Thresholds"),
```

```

```

N_Rows = c(nrow(Applicants), nrow(Eligible_Applicants),
           nrow(Enrolled_Applicants), nrow(Enrolled_Applicants_CD),
           nrow(StartedDT_Applicants), nrow(Thresholds)),
N_Cols = c(ncol(Applicants), ncol(Eligible_Applicants),
           ncol(Enrolled_Applicants), ncol(Enrolled_Applicants_CD),
           ncol(StartedDT_Applicants), ncol(Thresholds))) %>%
kable(), format = "latex", booktabs = TRUE,
col.names = c("Dataset", "N Rows", "N Columns")) %>%
kable_styling()
```

```

**Table 2: Sizes of the Datasets**

Dataset	N Rows	N Columns
Applicants	497	154
Eligible_Applicants	327	154
Enrolled_Applicants	254	154
Enrolled_Applicants_CD	252	159
StartedDT_Applicants	235	159
Thresholds	661	21

## 4 Overview of Stopping-Ratio Modeling

Attrition from the training program can be conceptualized as a sequential filtering process. There are various threshold points between stages of program participation where a participant may either attrit or continue participating. Each of those thresholds is a filter: participants that attrit at a given threshold are filtered out of the program. That reduces the number of participants who reach the next stage of program participation and encounter the next threshold.

That means an eligible applicant's progress through the training program can be measured by an ordinal stage variable that records the maximum stage reached by the applicant in that sequential filtering process. In this study, the ordinal variable is called **Stage\_Reached**. It is a multinomial ordinal variable with  $J = 4$  possible stages and observed values denoted by stage  $j$ , where  $j \in \{1, 2, 3, 4\}$ .

Figure 1 shows the final set of stages and thresholds (T1 to T3) between them at which attrition from the training program could occur. The arrows associated with each threshold are labeled according to how the outcome variable is coded on the corresponding person-threshold record, depending on whether the person stopped participating at the current stage or moved on to the next stage.

```

```{dot}
/// label: fig-Stages
/// fig-cap: Stages, Thresholds (T1-T3), and Stopping Ratios (SR1-SR3) in the
///          SANE Training Program. CSW, clinical skills workshop; DT, didactic
///          training.
/// fig-width: 5
/// fig-height: 2.5

digraph StagesModeled {
graph [rankdir="LR"];

node [shape = "box", style= "filled", fillcolor = "Gray90", fontsize = "7"];
A1 [label = "Attrited\\nBefore DT\\nSR1"]
A2 [label = "Attrited\\nDuring DT\\nSR2"]
A3 [label = "Attrited\\nBefore/During CSW\\nSR3"]

```

```

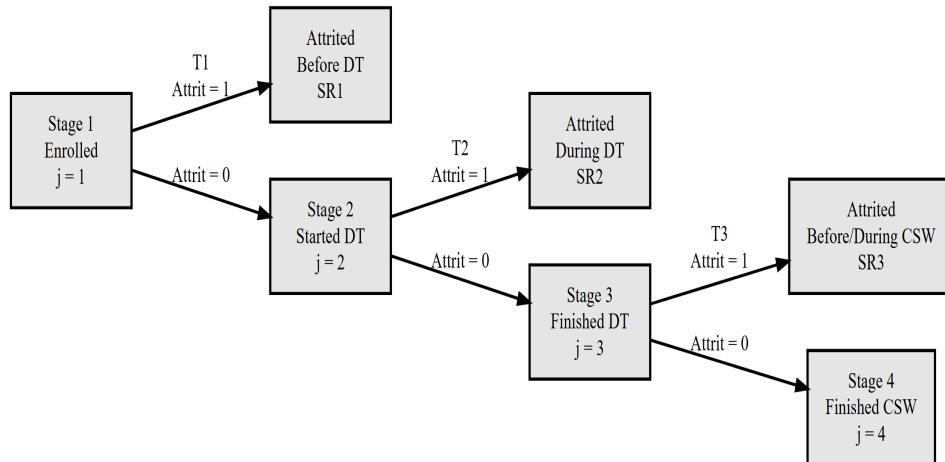
S1 [label = "Stage 1\nEnrolled\nnj = 1"]
S2 [label = "Stage 2\nStarted DT\nnj = 2"]
S3 [label = "Stage 3\nFinished DT\nnj = 3"]
S4 [label = "Stage 4\nFinished CSW\nnj = 4"]

edge [fontsize = "7", arrowsize = 0.5];

S1 -> A1 [label = "T1\nnAttrit = 1"]
S2 -> A2 [label = "T2\nnAttrit = 1"]
S3 -> A3 [label = "T3\nnAttrit = 1"]

S1 -> S2 [label = "Attrit = 0"]
S2 -> S3 [label = "Attrit = 0"]
S3 -> S4 [label = "Attrit = 0"]
}
```

```



**Figure 1: Stages, Thresholds (T1-T3), and Stopping Ratios (SR1-SR3) in the SANE Training Program. CSW, clinical skills workshop; DT, didactic training.**

There are several variations of regression models designed to analyze ordinal outcomes: they test different hypotheses, estimate different parameters, and yield different insights (Fullerton & Xu, 2016). The research questions for this study are best aligned with a broad class of ordinal regression models usually called continuation-ratio (CR) models, though they are also called stopping-ratio (SR) models or stage models (Fullerton & Xu, 2016; Liu & Bai, 2020; Smithson & Merkle, 2014; Yee, 2015). The CR model is ideally suited for ordinal outcome data generated from a sequential selection process where all individuals start from the same initial stage, must pass through earlier stages to reach later ones, and all stage transitions are irreversible (Fullerton & Xu, 2016; O'Connell, 2006). Because our focus is on predicting attrition—which stops a person's progression to the next stage of program participation—we will use the SR nomenclature in most of this document except when referring to broader literature that uses the CR model nomenclature. It should be understood that CR models and SR models are the same statistical method. It mostly doesn't matter which term you use.

Liu & Bai (2020) distinguished between forward and backward types of CR models and emphasized that each type can be expressed in two different sub-models depending on which of the two complementary conditional probabilities for a binary event one wants to emphasize (odds versus inversed odds). Regression coefficients from the two sub-models of the same type of CR model (forward or backward) have the same magnitude but opposite signs. The sub-models for a given type (e.g., forward) will also have the same model fit. However, results and interpretation will differ between types: the forward and backward CR models are not equivalent because they test different

hypotheses. This study uses what Liu & Bai (2020) called a forward CR model of sub-type A. That means we are trying to estimate the conditional probability of stopping at stage  $j$  conditional on being in or above that category given a set of predictors.

One key to understanding SR models is that they divide the analysis of a single ordinal outcome into a series of binary outcomes regarding what happens at each of the thresholds between stages. To run the planned model, we first reorganize the data from one row per person to one row per person per threshold attempted (Cole & Ananth, 2001; Fullerton & Xu, 2016). That reorganization allows us to use standard logistic regression modeling software to fit the model and flexibly choose whether predictor effects are parallel (constrained to equality across thresholds), or non-parallel (unconstrained and allowed to vary across thresholds) by either omitting or including interaction terms. Because the parallel effect model is nested within the non-parallel effect model, we can use likelihood ratio tests to discern whether allowing non-parallel effects improves model fit (Cole & Ananth, 2001).

The SR model is attractive because its parameters can be translated into additional estimates and graphs that are easy to interpret and meaningful for assessing the effects of predictors on program attrition. One prior study compared CR models to other available models (e.g., logistic regression and cumulative odds models for ordinal outcomes) for examining student persistence through the remedial math sequence and successfully passing a college-level credit bearing math course at 2- and 4-year public institutions (Davidson, 2015). Davidson (2015) concluded that CR models provided richer insights, in part because they revealed non-parallel effects of some predictors that could not be discerned with the other kinds of models. Other studies have used CR models to examine predictors of student proficiency in math (Liu et al., 2011), to validate student self-assessments of oral language proficiency in second language learning (Winke et al., 2023), and examine predictors of how far sexual assault kits progressed through several stages of forensic testing (Campbell et al., 2016, 2017, 2019).

## 5 Methods

### 5.1 Sample

The sample consists of the enrolled applicants to the program who had complete data on all the measures used in the SR models. The `Enrolled_Applicants_CD` dataset contains person-level data ( $N = 252$ ) about that sample. Those data were rearranged into the `Thresholds` dataset ( $N = 661$ ) before fitting the SR models (see the data import output for documentation of how that was done and Section 4 for why it was necessary).

We aim to draw conclusions that generalize to the overall population of enrolled applicants to the program. We are using listwise deletion to handle missing data because only 2 of 254 (0.8%) enrolled applicants had incomplete data (see the output from the data import script). These cases would have to be very influential for omitting them to induce substantial bias in the model results. When more than 5% of cases have missing data, more sophisticated approaches may be required (Fernández-García et al., 2018), but this dataset is far below that threshold.

We use the `StartedDT_Applicants` dataset ( $N = 235$ ) to answer the part of RQ2 pertaining to specific training modules because we need to narrow our focus to the subset of `Enrolled_Applicants_CD` containing only applicants with `Stage_Reached`  $\geq 2$  (those who started the didactic training).

## 5.2 Measures

The measures mentioned below include a primary outcome variable, a structural predictor required for SR modeling, eight focal predictors, and 24 secondary outcome variables.

### 5.2.1 Attrition (Primary Outcome)

For measuring conditional attrition rates, we used a binary, threshold-specific transformation of the `Stage_Reached` ordinal variable as the outcome in our SR models. The variable `Attrit` is coded 1 when an applicant attrited at a given threshold, and 0 when they passed the threshold and continued to the next stage of the program. See Figure 1 for a visualization of the coding for `Attrit`.

For unconditional attrition rates, we used a binary indicator of whether the applicant *ever* attrited from the program (`Attrited`). This was coded 1 when an applicant attrited at any threshold, and 0 when they passed all thresholds and completed both DT and CSW components of the program.

### 5.2.2 Threshold (Structural Predictor)

The `Threshold` variable identifies which of three thresholds a participant was attempting on any given record in the `Threshods` dataset. See Figure 1 for an overview of the stages and thresholds.

### 5.2.3 Background Characteristics (Focal Predictor)

The primary setting where the trainee practices nursing was a nominal categorical factor named `Setting`. It originally had four levels, but was recoded to three levels (`Urban`, `Rural/Tribal`, and `Suburban`) due to small sample size in the `Tribal` category (which was then combined with `Rural`). See the descriptive analyses output file for this study for more details. The reference level is `Urban`.

### 5.2.4 Motivations (Focal Predictors)

The two motivation measures are binary (coded 0 = *No*, 1 = *Yes*) and include whether the applicant was motivated to seek the training by (a) a need for SANE services in their community or organization (`Motivation_NeedSANE`), and (b) a personal connection to sexual assault (e.g., someone they know is a survivor) (`Motivation_PersonalConn`). The reference level for each of them is *No*.

### 5.2.5 Potential Barriers (Focal Predictors)

The potential barriers outcome variables are single-item measures of barriers to participation due to family obligations (`Barrier_FO`) and work responsibilities (`Barrier_WR`) as competing demands on applicants' time. While these are technically ordinal items following a 5-point Likert-response format, that should be enough categories to treat them as continuous variables for these analyses. Both measures were mean-centered before use in the model. See the descriptive analyses output file for this study for more details.

### 5.2.6 Emotional Readiness (Focal Predictors)

The emotional readiness measures are all continuous scores measured by ProQOL subscales for burnout (ProQOL\_BO), compassion satisfaction (ProQOL\_CS), and secondary traumatic stress (ProQOL\_STS) (Stamm, 2010). They were all mean-centered prior to use in the model.

### 5.2.7 Start and Finish Indicators for Didactic Training Modules (Secondary Outcomes)

The didactic training consisted of 12 modules. Binary variables coded 0 (*No*), 1 (*Yes*) recorded whether applicants had started each module (`Started_Mod_1` to `Started_Mod_12`) and also whether they had finished it (`Finished_Mod_1` to `Finished_Mod_12`). Unlike the other measures listed above, these variables were not used in the listwise deletion process for selecting enrolled applicants suitable for use in the SR models. The start and finish rates for each module were secondary outcomes. Including them in the listwise deletion process would not have made sense because the models allowed attrition between enrollment and start of the didactic training. Such attrition would have left missing data in these variables. Similarly, if an applicant attrited before a particular module even became available, these variables likely ended up with missing data. We are functionally treating missing values on these variables as *No*.

## 5.3 Planned Statistical Analyses

Research questions RQ2 and RQ3 focus on attrition rates. Our primary interest lies in taking a very granular look at these rates, in particular considering whether attrition rates vary across thresholds between different stages of the the training program. We chose SR models for the bulk of the analyses because they can estimate the conditional attrition rate at each threshold. Both the numerators and denominators for the conditional rates change as we progress from the first threshold to each subsequent threshold. The numerator depends on how many enrolled applicants attrit at the specific threshold in question, while the denominator is the number of enrolled applicants who reached the stage immediately preceding that threshold.

In contrast, the unconditional attrition rate is the total number of enrolled applicants who did not complete the CSW component of the program divided by the number of enrolled applicants. The unconditional rate summarizes the cumulative attrition over the entire set of thresholds, making it a less nuanced summary.

Below we fit and examine a series of SR models by using the `glm()` function to run logistic regression models on a person-threshold dataset called `Thresholds`. This is one way to fit SR models (Cole & Ananth, 2001).

The modeling strategy aims to estimate the minimum number of models required to answer research questions RQ2 and RQ3 and obtain a parsimonious final model. All models use the structural thresholds variable to predict attrition because that lays the foundation for a SR model.

### 5.3.1 RQ2: What are the attrition rates from enrollment to completion of the CSW, and when (i.e., at which module[s]) did participants commonly attrit?

One way to answer the first part of RQ2 is to fit a model that only accounts for the threshold effect, then extract the estimated marginal means (EMMs) representing the attrition rate (i.e., the SR) on the probability scale at each threshold. Thus, our modeling sequence starts by fitting Model 1, which only uses the structural thresholds variable as a predictor. However, we can get a more nuanced answer to RQ2 by examining EMMs extracted from a model that adjusts for covariates. We already plan to fit such models to test the effects of focal predictors relevant to RQ3. Therefore it may make sense to use EMMs from the model that provides the best answer to RQ3 rather than the EMMs from Model 1. Effect sizes are quantified by both odds-ratios and risk differences (absolute difference between attrition rates).

We estimated the overall unconditional attrition rate via the mean of a relevant binary variable (`Attrited`) in the `Enrolled_Applicants_CD` dataset. That mean is the proportion of applicants who ever attrited. In practical terms, the overall unconditional rate corresponds to the cumulative attrition if we ignore the thresholds in SR Model 1. We used a Wilson score confidence interval to quantify the uncertainty in the that rate (Newcombe, 2012; Wilson, 1927).

Next, we used the `StartedDT_Applicants` dataset to examine the proportions of applicants who started and finished each DT module by estimating the means of relevant binary variables (`Started_Mod_*` and `Finished_Mod_*`) for modules 1-12. We used Wilson score confidence intervals to quantify the uncertainty in those rates (Newcombe, 2012; Wilson, 1927).

#### Caution

Missing data for the `Started_Mod_*` and `Finished_Mod_*` variables are currently treated as functionally equivalent to 0 (`No`) in the rate calculations. So, the rate numerator is the number of `Yes` values and the denominator includes all cases (including missing values).

### 5.3.2 RQ3: Do participants' background characteristics, motivations for seeking training, potential barriers, and emotional readiness for this work predict attrition rates?

Answering RQ3 properly requires determining whether the focal predictors have parallel or non-parallel effects on attrition. Model 1 is the baseline model we can compare with models containing the focal predictors mentioned in RQ3. Model 2 adds the set of parallel effects for all eight focal predictors, then Model 3 expands on Model 2 by adding interaction terms to estimate non-parallel effects for all eight focal predictors (Cole & Ananth, 2001).

#### Tip

After testing for non-parallel effects, we have to decide whether to simplify the better model (either Model 2 or Model 3) by omitting focal predictors that do not seem to have any effect at all. Doing so could lead to a more parsimonious model, but sacrifices the ability to claim that our results for retained predictors reflect having controlled for all the omitted focal predictors. Only reporting Models 1-3 would reduce the total amount of output in the manuscript. *That is minimum set of models required to address RQ3.*

As a robustness check, we tried simplifying the models. Models 4 and 5 aim to achieve parsimony by only including the one focal predictor that demonstrated an effect in Model 2. Model 4 builds up from Model 1 by adding a parallel effect for that focal predictor, then Model 5 further extends the analysis to test whether it had a non-parallel effect.

We examined model diagnostics and fit statistics, model comparisons via likelihood ratio tests, single-term deletion tests based on Type II sums of squares, and other supplementary output. Effect sizes are quantified by both odds-ratios and risk differences (absolute difference between attrition rates). EMMs for the attrition rates reported on a probability scale.

We also split `Enrolled_Applicants_CD` dataset to get stratified estimates of the unconditional attrition rates among enrolled applicants at each level of `Motivation_NeedSANE`, with Wilson score confidence intervals (Newcombe, 2012; Wilson, 1927). This is comparable to examining the cumulative attrition implied by SR Model 4.

### Caution

One could estimate unconditional attrition rates that adjust for multiple focal predictors simultaneously (e.g., corollary to SR Model 2) via extracting EMMs from a logistic regression model fitted to the `Enrolled_Applicants_CD` dataset. We skipped that because our main interest was reporting the overall unconditional attrition rate for descriptive purposes. We only added the stratified rates because doing so took little extra effort and space. Fitting and reporting a logistic model with multiple predictors would generate much more output. Interested readers can run such a model themselves using the the data in this research compendium (Pierce, 2026).

## 5.4 Modeling Software

We used the base R (R Development Core Team, 2025) function `glm()` to fit the models because it is a high-quality, reliable, and flexible tool for fitting logistic regression models. We also used several additional R packages. The `broom` package (Robinson et al., 2026) facilitated extracting model parameters, odds-ratios, and associated confidence intervals, while the `performance` package (Lüdecke et al., 2021) extracted model fit statistics. The `DHARMA` (Hartig, 2024) and `car` (Fox & Weisberg, 2019) packages provided tools for examining model diagnostics (see next section) and the `marginalEffects` package (Arel-Bundock et al., 2024) computed EMMs that represent attrition rates.

## 5.5 Model Diagnostics

### 5.5.1 Collinearity

The `car` package (Fox & Weisberg, 2019) provides a function for examining the generalized variance inflation factor (GVIF) for terms in regression models. We checked for multicollinearity problems by examining the GVIF and a transformation of it that adjusts for categorical terms that use multiple degrees of freedom (Fox, 2016). In general, one can compare  $GVIF^{(1/(2*df))}$  to cutoffs defined for  $\sqrt{VIF}$ . Some suggested cutoffs indicating potential problems are  $\sqrt{VIF} \geq 2$  or  $\sqrt{VIF} \geq 3$ . We applied the latter cutoff, so hope to see  $GVIF^{(1/(2*df))} < 3$  in our models.

## 5.5.2 Residual Distributions

The DHARMA package in R uses simulation-based methods to compute scaled residuals that should follow a uniform distribution if the data are consistent with the actual distribution used to model the outcome, making it easier to check for deviations from model assumptions (Hartig, 2024). We used those residuals to run several tests of model assumptions.

First, we conducted a Kolmogorov-Smirnov (K-S) test of overall uniformity of the residual distribution, pairing it with a quantile-quantile (Q-Q) plot of the observed versus expected residual values. As usual with a Q-Q plot, data points should lay close to the reference line for the theoretical distribution.

Second, we split the data by threshold and used both a K-S test of within group deviation from uniformity and a Levene test for homogeneity of variance, pairing the result with a set of box plots showing the residual distribution within a specific level of threshold. That plot should show the upper and lower edges of the boxes laying close to the dashed lines for the 25th and 75th quantiles, and the median bar of the box laying at the 50th quantile. Heterogeneity of variance would be evident if the boxes associated with different thresholds vary substantially in height.

Third, we conducted two-sided binomial tests for outliers on either end of the residual distribution. The accompanying plot is a histogram of the residual distribution, annotated with red lines for any outliers detected.

Finally, we ran a simulation-based a test for over- or under-dispersion in the the scaled residuals. This is paired with a histogram of the distribution of simulated dispersion values, with a red line marking the position of the observed dispersion parameter value.

We applied all of these DHARMA tests to the models below, summarizing the results in figures. For all of the DHARMA tests, good models should produce large  $p$ -values (sometimes displayed on plots as just n.s.) because small values (e.g.,  $p < 0.05$ ) indicate violation of model assumptions.

## 6 Results

### 6.1 Model 1: Thresholds Alone

The modeling starts by first fitting a very simple model (`m1`) containing only a threshold main effect. This should allow us to see whether attrition rate varies across the thresholds. Table 3 shows the model parameters and Table 4 shows its fit statistics.

```
```{r}
#| label: tbl-params-m1
#| tbl-cap: "Model 1 Parameters"

m1 <- glm(Attrit ~ Threshold. + 1,
           data = Thresholds, family = binomial(link = "logit"))

FN <- paste("Values shown are on the link function (logit) scale.")

tidy(m1) %>%
  cbind(confint.default(m1)) %>%
  as_tibble() %>%
  rename(Parameter = term, Est = estimate, SE = std.error, z = statistic,
         p = p.value, LL = `2.5 %`, UL = `97.5 %`) %>%
  mutate(p = display_num(p),
        OR = exp(Est),
        OR.LL = exp(LL),
        OR.UL = exp(UL)) %>%
  relocate(Parameter, Est, SE, LL, UL, OR, OR.LL, OR.UL, z, p) %>%

```

```

kable(format = "latex", booktabs = TRUE, digits = 2) %>%
kable_styling() %>%
add_header_above(header = c(" " = 3, "95% Wald CI" = 2, " " = 1,
                           "OR 95% Wald CI" = 2, "Wald Test" = 2))
```

```

**Table 3: Model 1 Parameters**

| Parameter   | Est   | SE   | 95% Wald CI |       |      | OR 95% Wald CI |       | Wald Test |          |
|-------------|-------|------|-------------|-------|------|----------------|-------|-----------|----------|
|             |       |      | LL          | UL    | OR   | OR.LL          | OR.UL | z         | p        |
| (Intercept) | -2.63 | 0.25 | -3.12       | -2.13 | 0.07 | 0.04           | 0.12  | -10.46    | 1.36e-25 |
| Threshold.2 | 1.58  | 0.29 | 1.01        | 2.15  | 4.85 | 2.73           | 8.59  | 5.41      | 6.44e-08 |
| Threshold.3 | 0.40  | 0.36 | -0.30       | 1.11  | 1.50 | 0.74           | 3.02  | 1.13      | 0.260    |

```

```
#| label: tbl-fit-m1
#|tbl-cap: "Model 1 Fit Statistics"

glance(m1) %>%
  kable(format = "latex", booktabs = TRUE,
        digits = c(2, 0, 2, 2, 2, 0, 0)) %>%
  kable_styling()
```

```

**Table 4: Model 1 Fit Statistics**

| null.deviance | df.null | logLik  | AIC    | BIC    | deviance | df.residual | nobs |
|---------------|---------|---------|--------|--------|----------|-------------|------|
| 544.22        | 660     | -252.49 | 510.99 | 524.47 | 504.99   | 658         | 661  |

### 6.1.1 Single Term Deletion Tests

Table 5 shows the effect of deleting the threshold term from the model to determine whether doing so worsens model fit. A significant effect should be retained in the model because omitting it would damage the model fit.

```

```
#| label: tbl-drop1-m1
#|tbl-cap: "Model 1 Single Term Deletion Tests (Type II SS)"
#| warning: false

m1 %>%
  drop1(., test = "LRT") %>%
  tidy() %>%
  rename(p = p.value) %>%
  mutate(p = display_num(p)) %>%
  kable(format = "latex", booktabs = TRUE,
        digits = c(0, 0, 2, 2, Inf),
        col.names = c("Term Deleted", "df", "Deviance", "AIC", "LRT", "p")) %>%
  kable_styling()
```

```

**Table 5: Model 1 Single Term Deletion Tests (Type II SS)**

| Term Deleted | df | Deviance | AIC    | LRT   | p        |
|--------------|----|----------|--------|-------|----------|
| <none>       | NA | 504.99   | 510.99 | NA    | NA       |
| Threshold.   | 2  | 544.22   | 546.22 | 39.23 | 3.03e-09 |

💡 Tip

The threshold main effect is integral to fitting a SR model. It must remain in the model to properly test for both parallel and non-parallel effects of focal predictors. Removing the threshold main effect would also harm model fit, so we will keep it in all subsequent models.

### 6.1.2 Estimated Marginal Means

The presence of a threshold main effect shows that the attrition rate varies across thresholds. Next we compute estimated marginal means (EMMs) for each threshold and back-transform them to the response (probability) scale to see the attrition rate at each threshold. We expect these rates to agree with the simple descriptive statistics for percent attrition at each threshold because threshold is the sole predictor in Model 1. Table 6 and Figure 2 show the EMMs derived from Model 1, while Table 7 shows the pairwise risk differences between attrition rates at different thresholds.

```
```{r}
#| label: tbl-emmeans-m1
#| tbl-cap: "Model 1 Conditional Attrition Rate by Threshold"

FN <- paste("Values are on the probability scale.",
            "EMM, estimated marginal mean.")

TLabels1 = c("T1 Before DT",
            "T2 During DT",
            "T3 Before/During CSW")

avg_predictions(m1, variables = "Threshold.") %>%
  as_tibble() %>%
  select(Threshold., estimate, std.error, conf.low, conf.high) %>%
  mutate(Threshold. = factor(Threshold., labels = TLabels1)) %>%
  kable(format = "latex", booktabs = TRUE,
        digits = c(0, 3, 3, 3, 3),
        col.names = c("Threshold", "Rate (EMM)", "SE", "LL", "UL")) %>%
  kable_styling() %>%
  add_header_above(header = c(" " = 3, "95% Wald CI" = 2)) %>%
  footnote(kable_input = ., general = FN, footnote_as_chunk = TRUE,
            threeparttable = TRUE)
```

```

**Table 6: Model 1 Conditional Attrition Rate by Threshold**

| Threshold            | Rate (EMM) | SE    | 95% Wald CI |       |
|----------------------|------------|-------|-------------|-------|
|                      |            |       | LL          | UL    |
| T1 Before DT         | 0.067      | 0.016 | 0.036       | 0.098 |
| T2 During DT         | 0.260      | 0.029 | 0.204       | 0.316 |
| T3 Before/During CSW | 0.098      | 0.023 | 0.054       | 0.142 |

*Note:* Values are on the probability scale. EMM, estimated marginal mean.

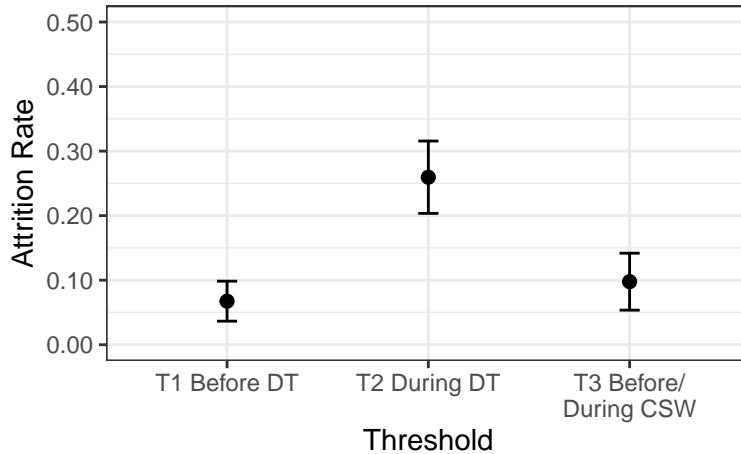
```
```{r}
#| label: fig-emmeans-m1
#| fig-cap: "Model 1 Conditional Attrition Rate by Threshold (Main Effect),
#|           With 95% Confidence Intervals. CSW, clinical skills workshop;
#|           DT, didactic training."
#| fig-width: 4
#| fig-height: 2.5

TLabels2 = c("T1 Before DT",
            "T2 During DT",
            "T3 Before/\nDuring CSW")

avg_predictions(m1, variables = c("Threshold.")) %>%
```

```
as_tibble() %>%
select(Threshold., estimate, conf.low, conf.high) %>%
mutate(Threshold. = factor(Threshold., labels = TLabels2)) %>%
ggplot(data = ., mapping = aes(x = Threshold., y = estimate)) +
geom_errorbar(aes(ymin = conf.low, ymax = conf.high), width = .1) +
geom_point(size = 2) +
ylab("Attrition Rate") +
xlab("Threshold") +
scale_y_continuous(lim = c(0.00, 0.50),
labels = label_number(accuracy = 0.01)) +
theme_bw()
```

```



**Figure 2: Model 1 Conditional Attrition Rate by Threshold (Main Effect), With 95% Confidence Intervals. CSW, clinical skills workshop; DT, didactic training.**

```
```{r}
#| label: tbl-emmc-m1
#| tbl-cap: Model 1 Pairwise Comparisons of Conditional Attrition Rates for the
#| Threshold Main Effect
FN <- paste("Values are on the probability scale.",
            "RD, risk difference between conditional attrition rates.")

avg_comparisons(m1, variables = list(Threshold. = "pairwise"),
                 comparison = "difference") %>%
  as_tibble() %>%
  rename(Contrast = contrast, RD = estimate, SE = std.error, z = statistic,
         p = p.value, LL = conf.low, UL = conf.high) %>%
  select(Contrast, RD, SE, LL, UL, z, p) %>%
  mutate(p = display_num(p)) %>%
  kable(format = "latex", booktabs = TRUE,
        digits = 3) %>%
  kable_styling() %>%
  add_header_above(header = c(" " = 3, "95% CI" = 2, "Wald Test" = 2)) %>%
  footnote(kable_input = ., general = FN, footnote_as_chunk = TRUE,
           threeparttable = TRUE)
```

```

**Table 7: Model 1 Pairwise Comparisons of Conditional Attrition Rates for the Threshold Main Effect**

| Contrast | RD     | SE    | 95% CI |        | Wald Test |          |
|----------|--------|-------|--------|--------|-----------|----------|
|          |        |       | LL     | UL     | z         | p        |
| 2 - 1    | 0.192  | 0.033 | 0.128  | 0.256  | 5.880     | 4.10e-09 |
| 3 - 1    | 0.030  | 0.028 | -0.024 | 0.084  | 1.100     | 0.271    |
| 3 - 2    | -0.162 | 0.036 | -0.233 | -0.091 | -4.448    | 8.67e-06 |

*Note:* Values are on the probability scale. RD, risk difference between conditional attrition rates.

### 6.1.3 Model Diagnostics

Figure 3 shows the plots for diagnostic tests of model assumptions.

```
```{r}
#| label: fig-m1-diagnose
#| fig-cap: "Diagnostic Plots for Model 1"
#| fig-subcap:
#| - "Q-Q Plot and Test for Overall Uniformity"
#| - "Residual Boxplots by Threshold"
#| - "Binomial Outlier Test"
#| - "Nonparametric Dispersion Test"
#| fig.width: 6
#| fig.height: 3
#| layout-ncol: 2
#| layout-nrow: 2

# Save simulated residuals for use in diagnostics using DHARMA.
# Seed uses a parameter defined in YAML header for reproducibility.
m1_sim <- simulateResiduals(fittedModel = m1, n = 1000, method = "PIT",
                             seed = params$DHARMA.seed1)

plotQQunif(simulationOutput = m1_sim, testUniformity = TRUE,
            testDispersion = FALSE, testOutliers = FALSE)

invisible(testCategorical(simulationOutput = m1_sim,
                          catPred = as_factor(Thresholds$Threshold),
                          quantiles = c(0.25, 0.5, 0.75), plot = TRUE))

invisible(testOutliers(simulationOutput = m1_sim, alternative = "two.sided",
                      margin = "both", type = "binomial", plot = TRUE))

invisible(testDispersion(simulationOutput = m1_sim, alternative = "two.sided",
                        plot = TRUE, type = "DHARMA"))
```

```

#### 💡 Tip

Model 1 assumptions are plausible. The scaled residuals appear to be uniform both overall (Figure 3a) and within each threshold with no signs of heterogeneity of variance (Figure 3b). There are no outliers (Figure 3c), and there is no evidence of over- or under-dispersion (Figure 3d).

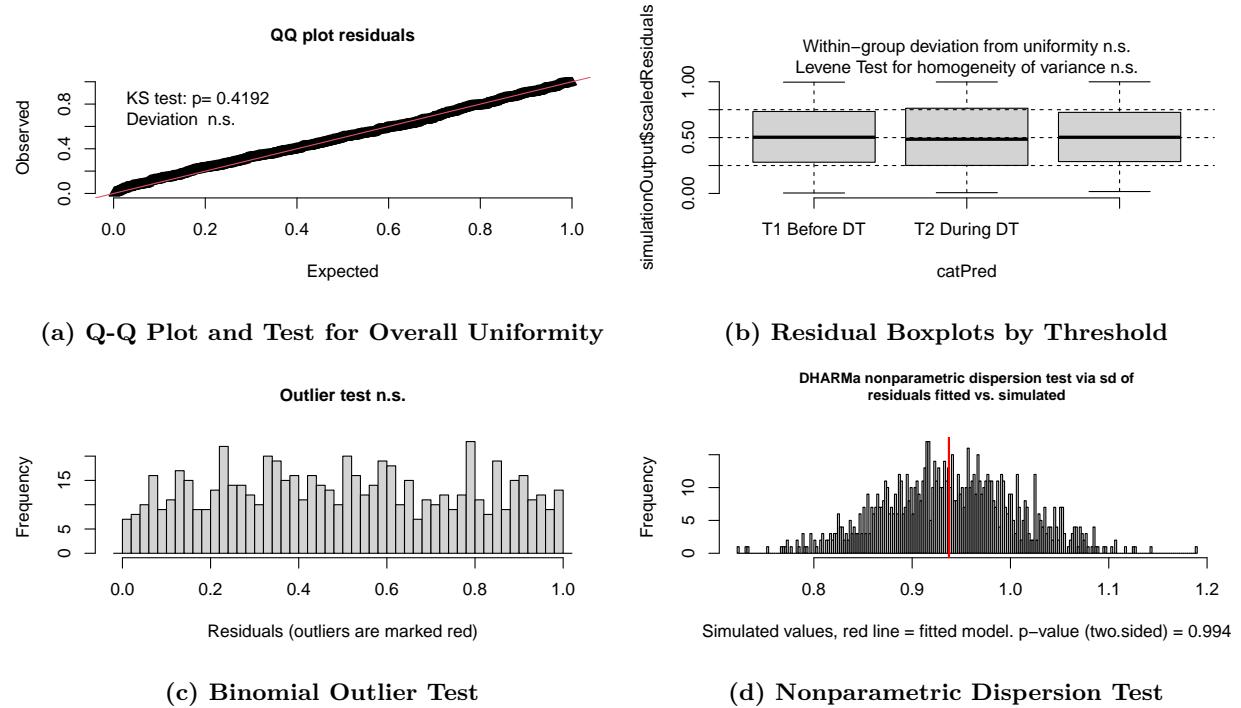


Figure 3: Diagnostic Plots for Model 1

## 6.2 Model 2: Thresholds & Parallel Effects for All Focal Predictors

In SR models, a predictor has a parallel effect when its regression coefficient is constrained equal across all thresholds. This is implemented by estimating only a main effect for the predictor (it cannot interact with the threshold). Model 2 (m2) uses parallel effects for the focal predictors. See Table 8 for parameter estimates and Table 9 for the fit statistics.

```
```{r}
#| label: tbl-params-m2
#| tbl-cap: "Model 2 Parameters"

m2 <- glm(Attrit ~ Threshold. + Setting. + Motivation_NeedSANE. +
           Motivation_PersonalConn. + CBarrier_FO + CBarrier_WR +
           CProQOL_BO + CProQOL_CS + CProQOL_STS + 1,
           data = Thresholds, family = binomial(link = "logit"))

FN <- paste("Values shown are on the link function (logit) scale.")

tidy(m2) %>%
  cbind(confint.default(m2)) %>%
  as_tibble() %>%
  rename(Parameter = term, Est = estimate, SE = std.error, z = statistic,
         p = p.value, LL = `2.5 %`, UL = `97.5 %`) %>%
  mutate(p = display_num(p),
         OR = exp(Est),
         OR.LL = exp(LL),
         OR.UL = exp(UL)) %>%
  relocate(Parameter, Est, SE, LL, UL, OR, OR.LL, OR.UL, z, p) %>%
  kable(format = "latex", booktabs = TRUE, digits = 2) %>%
  kable_styling() %>%
  add_header_above(header = c(" " = 3, "95% Wald CI" = 2, " " = 1,
                             "OR 95% Wald CI" = 2, "Wald Test" = 2))
```

```

```
```{r}
#| label: tbl-fit-m2
#| tbl-cap: "Model 2 Fit Statistics"

glance(m2) %>%
  kable(format = "latex", booktabs = TRUE,

```

Table 8: Model 2 Parameters

Parameter	Est	SE	95% Wald CI		OR	OR 95% Wald CI		Wald Test	
			LL	UL		OR.LL	OR.UL	z	p
(Intercept)	-2.41	0.36	-3.12	-1.70	0.09	0.04	0.18	-6.66	2.76e-11
Threshold.2	1.63	0.30	1.05	2.20	5.08	2.85	9.05	5.51	3.63e-08
Threshold.3	0.46	0.36	-0.25	1.16	1.58	0.78	3.20	1.26	0.207
Setting.Rural/Tribal	0.33	0.29	-0.24	0.89	1.39	0.79	2.44	1.13	0.260
Setting.Suburban	-0.01	0.29	-0.57	0.55	0.99	0.57	1.73	-0.03	0.974
Motivation_NeedSANE.Yes	-0.58	0.27	-1.12	-0.05	0.56	0.33	0.96	-2.13	0.033
Motivation_PersonalConn.Yes	0.15	0.24	-0.32	0.61	1.16	0.73	1.84	0.62	0.533
CBarrier_FO	-0.21	0.14	-0.48	0.06	0.81	0.62	1.06	-1.54	0.125
CBarrier_WR	0.08	0.13	-0.17	0.34	1.09	0.84	1.40	0.63	0.530
CProQOL_BO	-0.03	0.05	-0.14	0.07	0.97	0.87	1.07	-0.61	0.539
CProQOL_CS	-0.01	0.05	-0.10	0.08	0.99	0.90	1.08	-0.31	0.754
CProQOL_STS	-0.04	0.04	-0.12	0.04	0.96	0.88	1.04	-1.01	0.311

```

digits = c(2, 0, 2, 2, 2, 2, 0, 0)) %>%
kable_styling()
```

```

**Table 9: Model 2 Fit Statistics**

| null.deviance | df.null | logLik  | AIC    | BIC    | deviance | df.residual | nobs |
|---------------|---------|---------|--------|--------|----------|-------------|------|
| 544.22        | 660     | -246.86 | 517.72 | 571.64 | 493.72   | 649         | 661  |

### 6.2.1 Check for Multicollinearity

Table 10 shows the generalized variance inflation factors (GVIF) for Model 2.

```

```{r}
#| label: tbl-GVIF-m2
#| tbl-cap: Model 2 Generalized Variance Inflation Factors for Predictors

FN <- paste("Values >= 3 in the last column indicate multicollinearity problems.")

car::vif(m2) %>%
  as.data.frame() %>%
  rownames_to_column(var = "Term") %>%
  kable(format = "latex", booktabs = TRUE, digits = 2) %>%
  kable_styling() %>%
  footnote(kable_input = .., general = FN, footnote_as_chunk = TRUE,
           threeparttable = TRUE)
```

```



We do not appear to have any multicollinearity problems in Model 2.

**Table 10: Model 2 Generalized Variance Inflation Factors for Predictors**

| Term                     | GVIF | Df | GVIF <sup>^(1/(2*Df))</sup> |
|--------------------------|------|----|-----------------------------|
| Threshold.               | 1.01 | 2  | 1.00                        |
| Setting.                 | 1.10 | 2  | 1.03                        |
| Motivation_NeedSANE.     | 1.10 | 1  | 1.05                        |
| Motivation_PersonalConn. | 1.03 | 1  | 1.02                        |
| CBarrier_FO              | 1.21 | 1  | 1.10                        |
| CBarrier_WR              | 1.25 | 1  | 1.12                        |
| CProQOL_BO               | 2.83 | 1  | 1.68                        |
| CProQOL_CS               | 2.03 | 1  | 1.42                        |
| CProQOL_STS              | 1.73 | 1  | 1.31                        |

*Note:* Values  $\geq 3$  in the last column indicate multicollinearity problems.

### 6.2.2 Compare Models 1 and 2

Table 11 shows a likelihood ratio test (LRT) comparing Models 1 and 2.

```
```{r}
#| label: tbl-lrt-m1-m2
#| tbl-cap: "Likelihood Ratio Test Comparing Models 1 and 2"

test_lrt(m1, m2) %>%
  as_tibble() %>%
  mutate(p = display_num(p),
         Model = if_else(Name == "m1",
                           true = "Thresholds",
                           false = "Thresholds + All Parallel Effects")) %>%
  #select(-term) %>%
  kable(format = "latex", booktabs = TRUE, digits = c(0, 0, 0, 0, 2, 3),
        col.names = c("Model", "Terms", "df", "df_diff", "LRT", "p")) %>%
  kable_styling()
```

```

**Table 11: Likelihood Ratio Test Comparing Models 1 and 2**

| Model | Terms                             | df | df_diff | LRT   | p     |
|-------|-----------------------------------|----|---------|-------|-------|
| m1    | Thresholds                        | 3  | NA      | NA    | NA    |
| m2    | Thresholds + All Parallel Effects | 12 | 9       | 11.27 | 0.258 |

#### Caution

This is a simultaneous test of whether adding parallel effects for all of the focal predictors as a block improved the model fit enough to justify adding that many extra parameters. It did not. However, the Wald tests in Table 8 suggest that Motivation\_NeedSANE has an effect while none of the other predictors do. We need to look more closely at the effects of individual predictors via single-term deletion tests.

### 6.2.3 Single Term Deletion Tests

Table 12 shows the effect of deleting specific terms from the model to determine whether doing so worsens model fit. Each main effect term is tested after controlling for all the other main effects. This is a more focused test of individual predictors than the overall LRT comparing Models 1 and 2. Significant effects should be retained in the model because omitting them would damage the model fit. Non-significant effects can potentially be omitted.

```
```{r}
#| label: tbl-drop1-m2
#| tbl-cap: "Model 2 Single Term Deletion Tests (Type II SS)"
#| warning: false

m2 %>%
  drop1(., test = "LRT") %>%
  tidy() %>%
  rename(p = p.value) %>%
  mutate(p = display_num(p)) %>%
  kable(format = "latex", booktabs = TRUE,
        digits = c(0, 0, 2, 2, 2, Inf),
        col.names = c("Term Deleted", "df", "Deviance", "AIC", "LRT", "p")) %>%
  kable_styling()
```

```

**Table 12: Model 2 Single Term Deletion Tests (Type II SS)**

| Term Deleted             | df | Deviance | AIC    | LRT   | p        |
|--------------------------|----|----------|--------|-------|----------|
| <none>                   | NA | 493.72   | 517.72 | NA    | NA       |
| Threshold.               | 2  | 533.85   | 553.85 | 40.13 | 1.93e-09 |
| Setting.                 | 2  | 495.36   | 515.36 | 1.64  | 0.441    |
| Motivation_NeedSANE.     | 1  | 498.08   | 520.08 | 4.37  | 0.037    |
| Motivation_PersonalConn. | 1  | 494.10   | 516.10 | 0.39  | 0.534    |
| CBarrier_FO              | 1  | 496.10   | 518.10 | 2.39  | 0.123    |
| CBarrier_WR              | 1  | 494.11   | 516.11 | 0.39  | 0.530    |
| CProQOL_BO               | 1  | 494.10   | 516.10 | 0.38  | 0.538    |
| CProQOL_CS               | 1  | 493.82   | 515.82 | 0.10  | 0.754    |
| CProQOL_STS              | 1  | 494.75   | 516.75 | 1.04  | 0.309    |

 Tip

Only Threshold and Motivation\_NeedSANE have main effects that need to be retained. We could in theory remove all the other focal predictors.

### 6.2.4 Estimated Marginal Means

Next we compute estimated marginal means (EMMs) for each threshold and back-transform them to the response (probability) scale to see the attrition rate at each threshold. Table 13 and Figure 4 show the EMMs derived from Model 2 for each threshold, while Table 14 shows the pairwise contrasts estimating the risk differences between those EMMs. Table 15 and Figure 5 show the EMMs for each level of Motivation\_NeedSANE, while Table 16 shows the contrast estimating the risk difference between them. Table 17 and Figure 6 show the combined result of the two main effects while averaging over the results of all other predictors. Table 18 shows the contrast of Motivation\_NeedSANE separately by threshold.

```
```{r}
#| label: tbl-emmeans-m2-Threshold
#| tbl-cap: Model 2 Conditional Attrition Rate by Threshold (Main Effect)

FN <- paste("Results are averaged over the levels of all other predictors.",
            "Values are on the probability scale.",
            "EMM, estimated marginal mean.")

avg_predictions(m2, variables = "Threshold.") %>%
  as_tibble() %>%
  select(Threshold., estimate, std.error, conf.low, conf.high) %>%
  mutate(Threshold. = factor(Threshold., labels = TLabels1)) %>%
  kable(format = "latex", booktabs = TRUE,
        digits = c(0, 3, 3, 3),
        col.names = c("Threshold", "Rate (EMM)", "SE", "LL", "UL")) %>%
  kable_styling() %>%
  add_header_above(header = c(" " = 3, "95% Wald CI" = 2)) %>%
  footnote(kable_input = ., general = FN, footnote_as_chunk = TRUE,
            threeparttable = TRUE)
```

```

**Table 13: Model 2 Conditional Attrition Rate by Threshold (Main Effect)**

| Threshold            | Rate (EMM) | SE    | 95% Wald CI |       |
|----------------------|------------|-------|-------------|-------|
|                      |            |       | LL          | UL    |
| T1 Before DT         | 0.066      | 0.015 | 0.036       | 0.097 |
| T2 During DT         | 0.259      | 0.028 | 0.204       | 0.315 |
| T3 Before/During CSW | 0.100      | 0.023 | 0.055       | 0.145 |

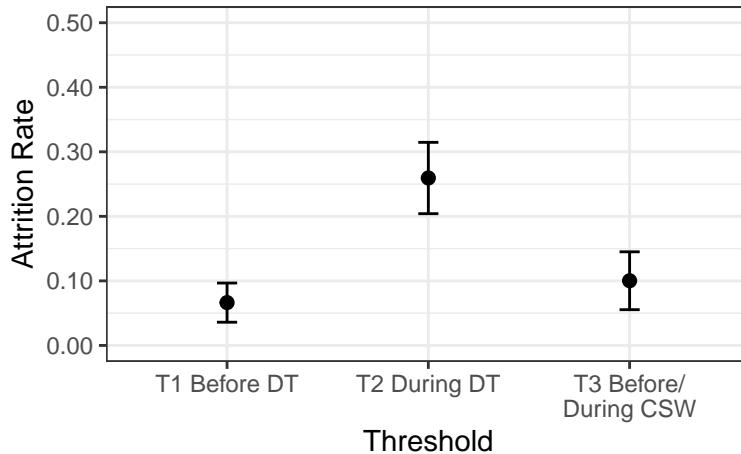
*Note:* Results are averaged over the levels of all other predictors. Values are on the probability scale. EMM, estimated marginal mean.

```
```{r}
#| label: fig-emmeans-m2-Threshold
#| fig-cap: Model 2 Conditional Attrition Rate by Threshold (Main Effect)
#|       Averaged Over All Other Predictors), With 95% Confidence Intervals.
#|       CSW, clinical skills workshop; DT, didactic training.
#| fig-width: 4
#| fig-height: 2.5

p4 <- avg_predictions(m2, variables = c("Threshold.")) %>%
  as_tibble() %>%
  select(Threshold., estimate, conf.low, conf.high) %>%
  mutate(Threshold. = factor(Threshold., labels = TLabels2)) %>%
  ggplot(data = ., mapping = aes(x = Threshold., y = estimate)) +
  geom_errorbar(aes(ymin = conf.low, ymax = conf.high), width = .1) +
  geom_point(size = 2) +
  ylab("Attrition Rate") +
  xlab("Threshold") +
  scale_y_continuous(lim = c(0.00, 0.50),
                     labels = label_number(accuracy = 0.01)) +
  theme_bw()

p4
```

```



**Figure 4: Model 2 Conditional Attrition Rate by Threshold (Main Effect Averaged Over All Other Predictors), With 95% Confidence Intervals. CSW, clinical skills workshop; DT, didactic training.**

```
```{r}
#| label: tbl-emmc-m2-Threshold
#| tbl-cap: Model 2 Pairwise Comparisons of Conditional Attrition Rates for the
#| Threshold Main Effect

FN <- paste("Results are averaged over the levels of all other predictors.",
           "Values are on the probability scale.",
           "RD, risk difference between conditional attrition rates.")

avg_comparisons(m2, variables = list(Threshold. = "pairwise"),
                 comparison = "difference") %>%
  as_tibble() %>%
  rename(Contrast = contrast, RD = estimate, SE = std.error, z = statistic,
         p = p.value, LL = conf.low, UL = conf.high) %>%
  select(Contrast, RD, SE, LL, UL, z, p) %>%
  mutate(p = display_num(p)) %>%
  kable(format = "latex", booktabs = TRUE,
        digits = 3) %>%
  kable_styling() %>%
  add_header_above(header = c(" " = 3, "95% CI" = 2, "Wald Test" = 2)) %>%
  footnote(kable_input = ., general = FN, footnote_as_chunk = TRUE,
            threeparttable = TRUE)
...
```

```

**Table 14: Model 2 Pairwise Comparisons of Conditional Attrition Rates for the Threshold Main Effect**

| Contrast | RD     | SE    | 95% CI |        | Wald Test |          |
|----------|--------|-------|--------|--------|-----------|----------|
|          |        |       | LL     | UL     | z         | p        |
| 2 - 1    | 0.193  | 0.032 | 0.13   | 0.256  | 6.002     | 1.95e-09 |
| 3 - 1    | 0.034  | 0.028 | -0.02  | 0.088  | 1.227     | 0.220    |
| 3 - 2    | -0.159 | 0.036 | -0.23  | -0.088 | -4.384    | 1.17e-05 |

*Note:* Results are averaged over the levels of all other predictors. Values are on the probability scale. RD, risk difference between conditional attrition rates.

```
```{r}
#| label: tbl-emmeans-m2-NeedSANE
#| tbl-cap: Model 2 Conditional Attrition Rate by Motivation_NeedSANE (Main
#| Effect)

FN <- paste("Motivation_NeedSANE has a parallel effect on attrition.",
           "Results are averaged over the levels of all other predictors.",
```

```

"Values are on the probability scale.",
"EMM, estimated marginal mean.")

avg_predictions(m2, variables = "Motivation_NeedSANE.") %>%
  as_tibble() %>%
  select(Motivation_NeedSANE., estimate, std.error, conf.low, conf.high) %>%
  kable(format = "latex", booktabs = TRUE,
    digits = c(0, 3, 3, 3, 3),
    col.names = c("Motivation_NeedSANE", "Rate (EMM)", "SE", "LL", "UL")) %>%
  kable_styling() %>%
  add_header_above(header = c(" " = 3, "95% Wald CI" = 2)) %>%
  footnote(kable_input = ., general = FN, footnote_as_chunk = TRUE,
            threeparttable = TRUE)
...

```

Table 15: Model 2 Conditional Attrition Rate by Motivation_NeedSANE (Main Effect)

Motivation_NeedSANE	Rate (EMM)	95% Wald CI		
		SE	LL	UL
No	0.201	0.034	0.135	0.267
Yes	0.129	0.014	0.101	0.157

Note: Motivation_NeedSANE has a parallel effect on attrition. Results are averaged over the levels of all other predictors. Values are on the probability scale. EMM, estimated marginal mean.

```

```{r}
#| label: fig-emmeans-m2-NeedSANE
#| fig-cap: Model 2 Conditional Attrition Rate by Motivation_NeedSANE (Parallel
#| Main Effect Averaged Over All Other Predictors), With 95% Confidence
#| Intervals
#| fig-width: 2.2
#| fig-height: 2.5

avg_predictions(m2, variables = c("Motivation_NeedSANE")) %>%
 as_tibble() %>%
 select(Motivation_NeedSANE., estimate, conf.low, conf.high) %>%
 ggplot(data = ., mapping = aes(x = Motivation_NeedSANE., y = estimate)) +
 geom_errorbar(aes(ymin = conf.low, ymax = conf.high), width = .1) +
 geom_point(size = 2) +
 ylab("Attrition Rate") +
 xlab("Motivation: Need SANE") +
 scale_y_continuous(lim = c(0.00, 0.50),
 labels = label_number(accuracy = 0.01)) +
 theme_bw()
```

```

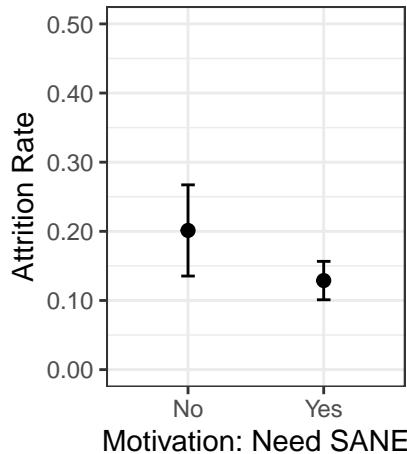


Figure 5: Model 2 Conditional Attrition Rate by Motivation_NeedSANE (Parallel Main Effect Averaged Over All Other Predictors), With 95% Confidence Intervals

```
```{r}
#| label: tbl-emmc-m2-NeedSANE
#| tbl-cap: Model 2 Pairwise Comparisons of Conditional Attrition Rates for
#| Motivation_NeedSANE Main Effect

FN <- paste("Values and confidence limits are on the probability scale.",
 "Results are averaged over the levels of all other predictors.",
 "RD, risk difference between conditional attrition rates.")

avg_comparisons(m2, variables = list(Motivation_NeedSANE. = "pairwise"),
 comparison = "difference") %>%
 as_tibble() %>%
 rename(Contrast = contrast, RD = estimate, SE = std.error, z = statistic,
 p = p.value, LL = conf.low, UL = conf.high) %>%
 select(Contrast, RD, SE, LL, UL, z, p) %>%
 mutate(p = display_num(p)) %>%
 kable(format = "latex", booktabs = TRUE,
 digits = 3) %>%
 kable_styling() %>%
 add_header_above(header = c(" " = 3, "95% CI" = 2, "Wald Test" = 2)) %>%
 footnote(kable_input = ., general = FN, footnote_as_chunk = TRUE,
 threeparttable = TRUE)
```
```

```

**Table 16: Model 2 Pairwise Comparisons of Conditional Attrition Rates for Motivation\_NeedSANE Main Effect**

Contrast	RD	SE	95% CI		Wald Test	
			LL	UL	z	p
Yes - No	-0.072	0.037	-0.145	0	-1.964	0.050

*Note:* Values and confidence limits are on the probability scale. Results are averaged over the levels of all other predictors. RD, risk difference between conditional attrition rates.

```
```{r}
#| label: tbl-emmeans-m2-Both
#| tbl-cap: Model 2 Conditional Attrition Rate by Threshold and
#| Motivation_NeedSANE (Main Effects)

FN <- paste("Motivation_NeedSANE has a parallel effect on attrition.",
            "Results are averaged over the levels of all other predictors.",
            "Values are on the probability scale.",
            "CSW, clinical skills workshop; DT, didactic training;",
            " "
```
```

```

```

"EMM, estimated marginal mean.")

avg_predictions(m2, variables = c("Threshold.", "Motivation_NeedSANE.")) %>%
  as_tibble() %>%
  select(Threshold., Motivation_NeedSANE., estimate, std.error, conf.low, conf.high) %>%
  mutate(Threshold. = factor(Threshold., labels = TLLabels1)) %>%
  kable(format = "latex", booktabs = TRUE,
        digits = c(0, 0, 3, 3, 3),
        col.names = c("Threshold", "Motivation_NeedSANE", "Rate (EMM)", "SE",
                     "LL", "UL")) %>%
  kable_styling() %>%
  add_header_above(header = c(" " = 4, "95% Wald CI" = 2)) %>%
  collapse_rows(columns = 1:2, valign = "top", latex_hline = "major",
                 custom_latex_hline = 1, headers_to_remove = 0,
                 row_group_label_position = "stack") %>%
  footnote(kable_input = ., general = FN, footnote_as_chunk = TRUE,
            threeparttable = TRUE)
```

```

**Table 17: Model 2 Conditional Attrition Rate by Threshold and Motivation\_NeedSANE (Main Effects)**

| Threshold                   | Motivation_NeedSANE | Rate (EMM) | 95% Wald CI |       |       |
|-----------------------------|---------------------|------------|-------------|-------|-------|
|                             |                     |            | SE          | LL    | UL    |
| <b>T1 Before DT</b>         |                     |            |             |       |       |
| No                          |                     | 0.099      | 0.028       | 0.044 | 0.154 |
| Yes                         |                     | 0.058      | 0.014       | 0.030 | 0.086 |
| <b>T2 During DT</b>         |                     |            |             |       |       |
| No                          |                     | 0.351      | 0.056       | 0.241 | 0.462 |
| Yes                         |                     | 0.235      | 0.029       | 0.178 | 0.292 |
| <b>T3 Before/During CSW</b> |                     |            |             |       |       |
| No                          |                     | 0.147      | 0.041       | 0.067 | 0.226 |
| Yes                         |                     | 0.088      | 0.021       | 0.047 | 0.130 |

*Note:* Motivation\_NeedSANE has a parallel effect on attrition. Results are averaged over the levels of all other predictors. Values are on the probability scale. CSW, clinical skills workshop; DT, didactic training; EMM, estimated marginal mean.

```

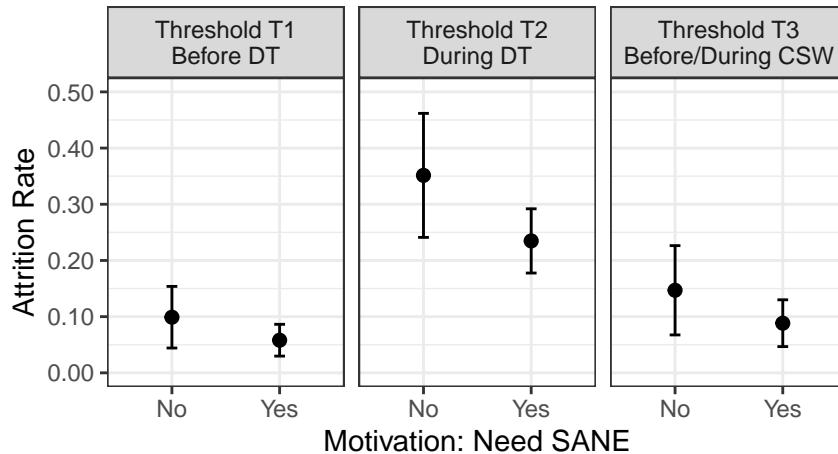
```{r}
#| label: fig-emmeans-m2-Both
#| fig-cap: Model 2 Conditional Attrition Rate by Threshold and
#| Motivation_NeedSANE (Main Effects, Averaged Over All Other
#| Predictors), With 95% Confidence Intervals. CSW, clinical skills
#| workshop; DT, didactic training.
#| fig-width: 4.5
#| fig-height: 2.5

FLabels = c("1" = "Threshold T1\nBefore DT",
           "2" = "Threshold T2\nDuring DT",
           "3" = "Threshold T3\nBefore/During CSW")

p6 <- avg_predictions(m2, variables = c("Threshold.", "Motivation_NeedSANE.")) %>%
  as_tibble() %>%
  select(Threshold., Motivation_NeedSANE., estimate, conf.low, conf.high) %>%
  ggplot(data = ., mapping = aes(x = Motivation_NeedSANE., y = estimate)) +
  facet_grid(cols = vars(Threshold.), labeller = labeller(Threshold. = FLabels)) +
  geom_errorbar(aes(ymin = conf.low, ymax = conf.high), width = .1) +
  geom_point(size = 2) +
  ylab("Attrition Rate") +
  xlab("Motivation: Need SANE") +
  scale_y_continuous(lim = c(0.00, 0.50),
                     labels = label_number(accuracy = 0.01)) +
  theme_bw()

p6
```

```



**Figure 6: Model 2 Conditional Attrition Rate by Threshold and Motivation\_NeedSANE (Main Effects, Averaged Over All Other Predictors), With 95% Confidence Intervals. CSW, clinical skills workshop; DT, didactic training.**

```
```{r}
#| label: tbl-emmc-m2-Both
#| tbl-cap: Model 2 Pairwise Comparisons of Conditional Attrition Rates for
#| Simple Effect of Motivation_NeedSANE at Each Threshold

FN <- paste("Motivation_NeedSANE has a parallel effect on attrition.",
            "Results are averaged over the levels of all other predictors.",
            "Values are on the probability scale.",
            "RD, risk difference between conditional attrition rates.")

avg_comparisons(m2, variables = list(Motivation_NeedSANE. = "pairwise"),
                 comparison = "difference", by = "Threshold.") %>%
  as_tibble() %>%
  rename(Contrast = contrast, RD = estimate, SE = std.error, z = statistic,
         p = p.value, LL = conf.low, UL = conf.high) %>%
  select(Threshold., Contrast, , RD, SE, LL, UL, z, p) %>%
  mutate(Threshold = factor(Threshold., labels = Tlabels1)) %>%
  select(Threshold, Contrast, RD, SE, LL, UL, z, p) %>%
  mutate(p = display_num(p)) %>%
  kable(format = "latex", booktabs = TRUE, digits = 3) %>%
  kable_styling() %>%
  add_header_above(header = c(" " = 4, "95% CI" = 2, "Wald Test" = 2)) %>%
  footnote(kable_input = ., general = FN, footnote_as_chunk = TRUE,
            threeparttable = TRUE)
```

```

**Table 18: Model 2 Pairwise Comparisons of Conditional Attrition Rates for Simple Effect of Motivation\_NeedSANE at Each Threshold**

| Threshold            | Contrast | RD     | SE    | 95% CI |        | Wald Test |       |
|----------------------|----------|--------|-------|--------|--------|-----------|-------|
|                      |          |        |       | LL     | UL     | z         | p     |
| T1 Before DT         | Yes - No | -0.041 | 0.023 | -0.087 | 0.004  | -1.779    | 0.075 |
| T2 During DT         | Yes - No | -0.117 | 0.058 | -0.230 | -0.004 | -2.023    | 0.043 |
| T3 Before/During CSW | Yes - No | -0.058 | 0.032 | -0.121 | 0.005  | -1.792    | 0.073 |

*Note:* Motivation\_NeedSANE has a parallel effect on attrition. Results are averaged over the levels of all other predictors. Values are on the probability scale. RD, risk difference between conditional attrition rates.

## 6.2.5 Model Diagnostics

Figure 7 shows the plots for diagnostic tests of model assumptions.

```
```{r}
#| label: fig-m2-diagnose
#| fig-cap: "Diagnostic Plots for Model 2"
#| fig-subcap:
#| - "Q-Q Plot and Test for Overall Uniformity"
#| - "Residual Boxplots by Threshold"
#| - "Binomial Outlier Test"
#| - "Nonparametric Dispersion Test"
#| fig-width: 6
#| fig-height: 3
#| layout-ncol: 2
#| layout-nrow: 2

# Save simulated residuals for use in diagnostics using DHARMA.
# Seed uses a parameter defined in YAML header for reproducibility.
m2_sim <- simulateResiduals(fittedModel = m2, n = 1000, method = "PIT",
                             seed = params$DHARMA.seed2)

plotQQunif(simulationOutput = m2_sim, testUniformity = TRUE,
            testDispersion = FALSE, testOutliers = FALSE)

invisible(testCategorical(simulationOutput = m2_sim,
                          catPred = as_factor(Thresholds$Threshold),
                          quantiles = c(0.25, 0.5, 0.75), plot = TRUE))

invisible(testOutliers(simulationOutput = m2_sim, alternative = "two.sided",
                      margin = "both", type = "binomial", plot = TRUE))

invisible(testDispersion(simulationOutput = m2_sim, alternative = "two.sided",
                        plot = TRUE, type = "DHARMA"))
```

```

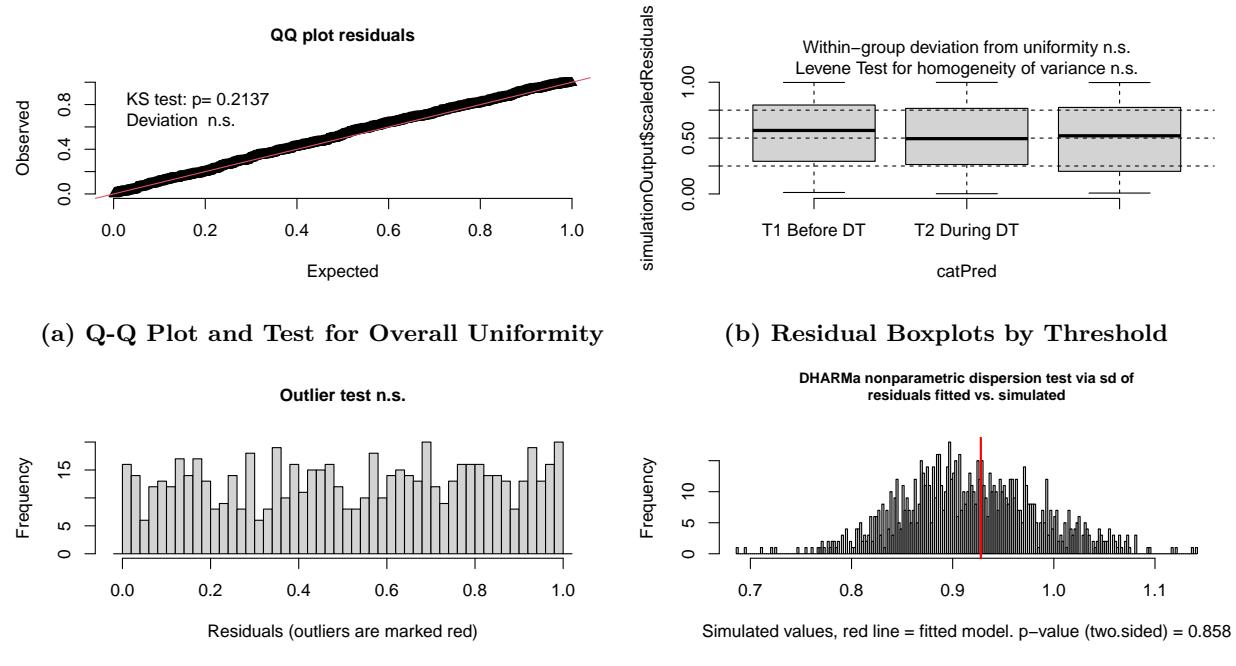


Figure 7: Diagnostic Plots for Model 2

💡 Tip

Model 2 assumptions are plausible. The scaled residuals appear to be uniform both overall (Figure 7a) and within each threshold with no signs of heterogeneity of variance (Figure 7b). There are no outliers (Figure 7c), and there is no evidence of over- or under-dispersion (Figure 7d).

### 6.3 Model 3: Thresholds & Non-Parallel Effects for All Focal Predictors

In SR models, a predictor has a non-parallel effect when its regression coefficient is allowed to vary across all thresholds. That is implemented by allowing the predictor to have both a main effect and an interaction with the threshold. Continuous predictors must be appropriately centered before model fitting as usual when testing interactions (i.e., moderator hypotheses). Model 3 (m3) treats threshold as a moderator of the other predictors' effects. See Table 19 for parameter estimates and Table 20 for fit statistics.

We are continuing to include predictors that did not have significant main effects in Model 2 because it is possible that threshold moderates the effects of other predictors such that there are non-parallel (threshold-specific) effects that get canceled out when averaging across them to estimate a parallel main effect. Thus, our approach maximizes the chance that we detect any unusually nuanced non-parallel effects if they exist.

🔥 Caution

Model 3 is ambitious given the available sample size. Adding eight interaction effects yields many extra parameters. This poses some risk for over-fitting the model, but testing for non-parallel effects either requires fitting this one model, or fitting a set of eight other models where we add only a single non-parallel effect at a time. Fitting this larger model is more efficient and reduces the total amount of output we have to review.

```
```{r}
#| label: tbl-params-m3
#| tbl-cap: "Model 3 Parameters"

m3 <- glm(Attrit ~ Threshold. + Setting. + Motivation_NeedSANE. +
           Motivation_PersonalConn. + CBarrier_FO + CBarrier_WR +
           CProQOL_BO + CProQOL_CS + CProQOL_STS +
           Threshold.:Setting. +
           Threshold.:Motivation_NeedSANE. +
           Threshold.:Motivation_PersonalConn. +
           Threshold.:CBarrier_FO + Threshold.:CBarrier_WR +
           Threshold.:CProQOL_BO + Threshold.:CProQOL_CS +
           Threshold.:CProQOL_STS + 1,
           data = Thresholds, family = binomial(link = "logit"))

FN <- paste("Values shown are on the link function (logit) scale.")

tidy(m3) %>%
  cbind(confint.default(m3)) %>%
  as_tibble() %>%
  rename(Parameter = term, Est = estimate, SE = std.error, z = statistic,
         p = p.value, LL = `2.5 %`, UL = `97.5 %`) %>%
  mutate(Parameter = str_replace(string = Parameter, pattern = ":" ,
                                  replacement = " x "),
         p = display_num(p),
         OR = exp(Est),
         OR_LL = exp(LL),
         OR_UL = exp(UL)) %>%
  relocate(Parameter, Est, SE, LL, UL, OR, OR_LL, OR_UL, z, p) %>%
  kable(format = "latex", booktabs = TRUE, digits = 2) %>%
  kable_styling(font_size = 10) %>%
  add_header_above(header = c(" " = 3, "95% Wald CI" = 2, " " = 1,
```

```
"OR 95% Wald CI" = 2, "Wald Test" = 2) %>%
  column_spec(column = 1, width = "5.5cm")
```

```

**Table 19: Model 3 Parameters**

| Parameter                                 | Est   | SE   | 95% Wald CI |       | OR   | OR 95% Wald CI |       | Wald Test |          |
|-------------------------------------------|-------|------|-------------|-------|------|----------------|-------|-----------|----------|
|                                           |       |      | LL          | UL    |      | OR.LL          | OR.UL | z         | p        |
| (Intercept)                               | -2.80 | 0.67 | -4.10       | -1.49 | 0.06 | 0.02           | 0.22  | -4.21     | 2.58e-05 |
| Threshold.2                               | 2.11  | 0.77 | 0.61        | 3.61  | 8.23 | 1.84           | 36.88 | 2.75      | 0.006    |
| Threshold.3                               | 0.47  | 0.98 | -1.46       | 2.39  | 1.60 | 0.23           | 10.96 | 0.48      | 0.634    |
| Setting.Rural/Tribal                      | 1.15  | 0.69 | -0.21       | 2.51  | 3.16 | 0.81           | 12.31 | 1.66      | 0.098    |
| Setting.Suburban                          | 0.57  | 0.68 | -0.77       | 1.91  | 1.77 | 0.47           | 6.77  | 0.84      | 0.401    |
| Motivation_NeedSANE.Yes                   | -1.24 | 0.58 | -2.38       | -0.11 | 0.29 | 0.09           | 0.90  | -2.15     | 0.032    |
| Motivation_PersonalConn.Yes               | 0.55  | 0.54 | -0.50       | 1.61  | 1.74 | 0.60           | 4.99  | 1.02      | 0.305    |
| CBarrier_FO                               | -0.27 | 0.31 | -0.88       | 0.34  | 0.76 | 0.41           | 1.40  | -0.88     | 0.379    |
| CBarrier_WR                               | 0.05  | 0.29 | -0.52       | 0.62  | 1.05 | 0.60           | 1.86  | 0.17      | 0.862    |
| CProQOL_BO                                | 0.11  | 0.11 | -0.11       | 0.33  | 1.11 | 0.89           | 1.39  | 0.95      | 0.343    |
| CProQOL_CS                                | 0.05  | 0.10 | -0.14       | 0.25  | 1.06 | 0.87           | 1.29  | 0.54      | 0.590    |
| CProQOL_STS                               | -0.18 | 0.10 | -0.38       | 0.02  | 0.83 | 0.68           | 1.02  | -1.79     | 0.074    |
| Threshold.2 x Setting.Rural/Tribal        | -1.25 | 0.79 | -2.80       | 0.30  | 0.29 | 0.06           | 1.35  | -1.58     | 0.115    |
| Threshold.3 x Setting.Rural/Tribal        | -0.40 | 0.95 | -2.26       | 1.46  | 0.67 | 0.10           | 4.29  | -0.43     | 0.670    |
| Threshold.2 x Setting.Suburban            | -0.69 | 0.77 | -2.21       | 0.83  | 0.50 | 0.11           | 2.29  | -0.89     | 0.373    |
| Threshold.3 x Setting.Suburban            | -0.85 | 0.99 | -2.79       | 1.08  | 0.43 | 0.06           | 2.95  | -0.87     | 0.387    |
| Threshold.2 x Motivation_NeedSANE.Yes     | 0.74  | 0.68 | -0.59       | 2.08  | 2.10 | 0.55           | 7.99  | 1.09      | 0.276    |
| Motivation_NeedSANE.Yes                   | 1.09  | 0.93 | -0.72       | 2.91  | 2.99 | 0.49           | 18.36 | 1.18      | 0.238    |
| Threshold.2 x Motivation_PersonalConn.Yes | -0.40 | 0.62 | -1.62       | 0.81  | 0.67 | 0.20           | 2.25  | -0.65     | 0.515    |
| Motivation_PersonalConn.Yes               | -0.77 | 0.76 | -2.27       | 0.73  | 0.46 | 0.10           | 2.07  | -1.01     | 0.313    |
| Threshold.2 x CBarrier_FO                 | 0.13  | 0.36 | -0.57       | 0.83  | 1.14 | 0.56           | 2.29  | 0.36      | 0.717    |
| Threshold.3 x CBarrier_FO                 | 0.00  | 0.44 | -0.87       | 0.86  | 1.00 | 0.42           | 2.37  | -0.01     | 0.994    |
| Threshold.2 x CBarrier_WR                 | -0.05 | 0.34 | -0.71       | 0.61  | 0.95 | 0.49           | 1.84  | -0.15     | 0.877    |
| Threshold.3 x CBarrier_WR                 | 0.35  | 0.42 | -0.48       | 1.17  | 1.42 | 0.62           | 3.23  | 0.83      | 0.408    |
| Threshold.2 x CProQOL_BO                  | -0.23 | 0.13 | -0.49       | 0.03  | 0.80 | 0.61           | 1.04  | -1.70     | 0.089    |
| Threshold.3 x CProQOL_BO                  | -0.03 | 0.16 | -0.35       | 0.29  | 0.97 | 0.71           | 1.34  | -0.17     | 0.867    |
| Threshold.2 x CProQOL_CS                  | -0.14 | 0.12 | -0.37       | 0.10  | 0.87 | 0.69           | 1.10  | -1.15     | 0.252    |
| Threshold.3 x CProQOL_CS                  | 0.07  | 0.15 | -0.23       | 0.36  | 1.07 | 0.80           | 1.43  | 0.44      | 0.656    |
| Threshold.2 x CProQOL_STS                 | 0.20  | 0.11 | -0.03       | 0.42  | 1.22 | 0.97           | 1.52  | 1.72      | 0.086    |
| Threshold.3 x CProQOL_STS                 | 0.09  | 0.14 | -0.18       | 0.36  | 1.09 | 0.83           | 1.44  | 0.65      | 0.516    |

```
```{r}
#| label: tbl-fit-m3
#| tbl-cap: "Model 3 Fit Statistics"

glance(m3) %>%
  kable(format = "latex", booktabs = TRUE,
        digits = c(2, 0, 2, 2, 2, 0, 0)) %>%
  kable_styling()
```

```

**Table 20: Model 3 Fit Statistics**

| null.deviance | df.null | logLik  | AIC    | BIC    | deviance | df.residual | nobs |
|---------------|---------|---------|--------|--------|----------|-------------|------|
| 544.22        | 660     | -239.77 | 539.54 | 674.35 | 479.54   | 631         | 661  |

### 6.3.1 Check for Multicollinearity

Table 21 shows the generalized variance inflation factors (GVIF) for Model 3.

```
```{r}
#| label: tbl-GVIF-m3
#| tbl-cap: Model 3 Generalized Variance Inflation Factors for Predictors
#| warning: false

FN <- paste("Values >= 3 in the last column indicate multicollinearity problems.")

car::vif(m3) %>%
  as.data.frame() %>%
  rownames_to_column(var = "Term") %>%
  mutate(Term = str_replace(string = Term, pattern = ":" ,
                            replacement = " x ")) %>%
  kable(format = "latex", booktabs = TRUE, digits = 2) %>%
  kable_styling() %>%
  footnote(kable_input = ., general = FN, footnote_as_chunk = TRUE,
           threeparttable = TRUE)
```

```

**Table 21: Model 3 Generalized Variance Inflation Factors for Predictors**

| Term                                  | GVIF   | Df | GVIF <sup>(1/(2*Df))</sup> |
|---------------------------------------|--------|----|----------------------------|
| Threshold.                            | 48.34  | 2  | 2.64                       |
| Setting.                              | 29.89  | 2  | 2.34                       |
| Motivation_NeedSANE.                  | 4.80   | 1  | 2.19                       |
| Motivation_PersonalConn.              | 5.29   | 1  | 2.30                       |
| CBarrier_FO                           | 6.21   | 1  | 2.49                       |
| CBarrier_WR                           | 6.04   | 1  | 2.46                       |
| CProQOL_BO                            | 12.89  | 1  | 3.59                       |
| CProQOL_CS                            | 9.74   | 1  | 3.12                       |
| CProQOL_STS                           | 10.42  | 1  | 3.23                       |
| Threshold. x Setting.                 | 138.13 | 4  | 1.85                       |
| Threshold. x Motivation_NeedSANE.     | 44.06  | 2  | 2.58                       |
| Threshold. x Motivation_PersonalConn. | 10.93  | 2  | 1.82                       |
| Threshold. x CBarrier_FO              | 7.35   | 2  | 1.65                       |
| Threshold. x CBarrier_WR              | 7.72   | 2  | 1.67                       |
| Threshold. x CProQOL_BO               | 35.09  | 2  | 2.43                       |
| Threshold. x CProQOL_CS               | 20.10  | 2  | 2.12                       |
| Threshold. x CProQOL_STS              | 17.57  | 2  | 2.05                       |

*Note:* Values  $\geq 3$  in the last column indicate multicollinearity problems.

🔥 Caution

We may have mild multicollinearity problems in Model 3, but that is not uncommon when adding interactions.

### 6.3.2 Compare Models 2 and 3

Table 22 shows a likelihood ratio test (LRT) comparing Models 2 and 3.

```
```{r}
#| label: tbl-lrt-m2-m3
#| tbl-cap: "Likelihood Ratio Test Comparing Models 2 and 3"

test_lrt(m2, m3) %>%
  as_tibble() %>%
  mutate(p = display_num(p),
         Model = if_else(Name == "m2",
                          true = "Thresholds + All Parallel Effects",
                          false = "Thresholds + All Non-Parallel Effects")) %>%
  #select(-term) %>%
  kable(format = "latex", booktabs = TRUE, digits = c(0, 0, 0, 0, 2, 3),
        col.names = c("Model", "Terms", "df", "df_diff", "LRT", "p"))
  kable_styling()
```

```

**Table 22: Likelihood Ratio Test Comparing Models 2 and 3**

| Model | Terms                                 | df | df_diff | LRT   | p     |
|-------|---------------------------------------|----|---------|-------|-------|
| m2    | Thresholds + All Parallel Effects     | 12 | NA      | NA    | NA    |
| m3    | Thresholds + All Non-Parallel Effects | 30 | 18      | 14.18 | 0.718 |

🔥 Caution

This is a simultaneous test of whether adding non-parallel effects for all of the focal predictors as a block improved the model fit enough to justify adding that many extra parameters. Apparently it did not. We should still look more closely at the effects of individual predictors via single-term deletion tests.

### 6.3.3 Single Term Deletion Tests

Table 23 shows the effect of deleting specific interaction terms from the model to determine whether doing so worsens model fit. Significant effects should be retained in the model because omitting them would damage the model fit. We do not test main effects for predictors involved in interactions because we need to respect the principle of marginality (Fox, 2016; Hector et al., 2010; Langsrud, 2003).

```
```{r}
#| label: tbl-drop1-m3
#| tbl-cap: "Model 3 Single Term Deletion Tests (Type II SS)"
#| warning: false

m3 %>%
  drop1(., test = "LRT") %>%
  tidy() %>%
  rename(p = p.value) %>%
  mutate(term = str_replace(string = term, pattern = ":"),
```

```

replacement = " x "),
p = display_num(p) %>%
kable(format = "latex", booktabs = TRUE,
      digits = c(0, 0, 2, 2, Inf),
      col.names = c("Term Deleted", "df", "Deviance", "AIC", "LRT", "p")) %>%
kable_styling()
```

```

**Table 23: Model 3 Single Term Deletion Tests (Type II SS)**

| Term Deleted                          | df | Deviance | AIC    | LRT  | p     |
|---------------------------------------|----|----------|--------|------|-------|
| <none>                                | NA | 479.54   | 539.54 | NA   | NA    |
| Threshold. x Setting.                 | 4  | 483.54   | 535.54 | 4.00 | 0.406 |
| Threshold. x Motivation_NeedSANE.     | 2  | 481.25   | 537.25 | 1.70 | 0.426 |
| Threshold. x Motivation_PersonalConn. | 2  | 480.57   | 536.57 | 1.03 | 0.597 |
| Threshold. x CBarrier_FO              | 2  | 479.76   | 535.76 | 0.22 | 0.897 |
| Threshold. x CBarrier_WR              | 2  | 480.89   | 536.89 | 1.35 | 0.509 |
| Threshold. x CProQOL_BO               | 2  | 483.52   | 539.52 | 3.97 | 0.137 |
| Threshold. x CProQOL_CS               | 2  | 482.84   | 538.84 | 3.30 | 0.192 |
| Threshold. x CProQOL_STS              | 2  | 483.01   | 539.01 | 3.47 | 0.177 |

### 💡 Tip

We can safely drop all of the interaction effects from the model. None of them improve the model fit. It may be worth trying a final pair of models that are more parsimonious than Models 2 and 3: they should include models with threshold effect and just parallel and non-parallel effects of `Motivation_NeedSANE` without other focal predictors.

### 6.3.4 Model Diagnostics

Figure 8 shows the plots for diagnostic tests of model assumptions.

```

```{r}
#| label: fig-m3-diagnose
#| fig-cap: "Diagnostic Plots for Model 3"
#| fig-subcap:
#| - "Q-Q Plot and Test for Overall Uniformity"
#| - "Residual Boxplots by Threshold"
#| - "Binomial Outlier Test"
#| - "Nonparametric Dispersion Test"
#| fig.width: 6
#| fig.height: 3
#| layout-ncol: 2
#| layout-nrow: 2

# Save simulated residuals for use in diagnostics using DHARMA.
# Seed uses a parameter defined in YAML header for reproducibility.
m3_sim <- simulateResiduals(fittedModel = m3, n = 1000, method = "PIT",
                             seed = params$DHARMA.seed3)

plotQQunif(simulationOutput = m3_sim, testUniformity = TRUE,
           testDispersion = FALSE, testOutliers = FALSE)

invisible(testCategorical(simulationOutput = m3_sim,
                         catPred = as_factor(Thresholds$Threshold),
                         quantiles = c(0.25, 0.5, 0.75), plot = TRUE))

invisible(testOutliers(simulationOutput = m3_sim, alternative = "two.sided",
                      margin = "both", type = "binomial", plot = TRUE))

invisible(testDispersion(simulationOutput = m3_sim, alternative = "two.sided",
                        plot = TRUE, type = "DHARMA"))
```

```

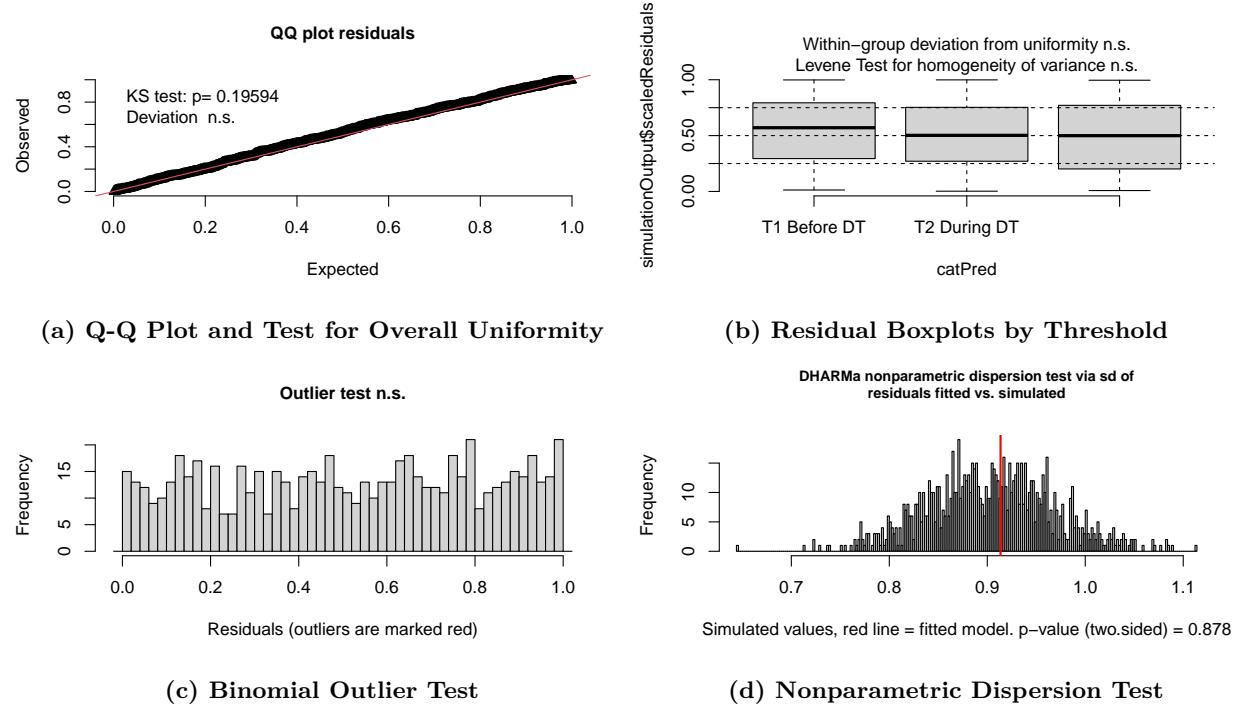


Figure 8: Diagnostic Plots for Model 3

### 💡 Tip

Model 3 assumptions are plausible. The scaled residuals appear to be uniform both overall (Figure 8a) and within each threshold with no signs of heterogeneity of variance (Figure 8b). There are no outliers (Figure 8c), and there is no evidence of over- or under-dispersion (Figure 8d).

## 6.4 Model 4: Thresholds & Parallel Effect for Motivation\_NeedSANE

Model 4 uses a parallel effect for Motivation\_NeedSANE without any of the other focal predictors. Table 24 shows the parameter estimates and Table 25 shows the fit indices.

```
```{r}
#| label: tbl-params-m4
#| tbl-cap: "Model 4 Parameters"

m4 <- glm(Attrit ~ Threshold + Motivation_NeedSANE. + 1,
           data = Thresholds, family = binomial(link = "logit"))

FN <- paste("Values shown are on the link function (logit) scale.")

tidy(m4) %>%
  cbind(confint.default(m4)) %>%
  as_tibble() %>%
  rename(Parameter = term, Est = estimate, SE = std.error, z = statistic,
         p = p.value, LL = `2.5 %`, UL = `97.5 %`) %>%
  mutate(p = display_num(p),
        OR = exp(Est),
        OR.LL = exp(LL),
        OR.UL = exp(UL)) %>%
  relocate(Parameter, Est, SE, LL, UL, OR, OR.LL, OR.UL, z, p) %>%
  kable(format = "latex", booktabs = TRUE, digits = 2) %>%
  kable_styling() %>%
  add_header_above(header = c(" " = 3, "95% Wald CI" = 2, " " = 1,
```

```
```{r}
#| label: tbl-fit-m4
#| tbl-cap: "Model 4 Fit Statistics"

glance(m4) %>%
 kable(format = "latex", booktabs = TRUE,
 digits = c(2, 0, 2, 2, 2, 0)) %>%
 kable_styling()
```

```

Table 24: Model 4 Parameters

| Parameter | Est | SE | 95% Wald CI | | OR | OR 95% Wald CI | | Wald Test | |
|-------------------------|-------|------|-------------|-------|------|----------------|-------|-----------|----------|
| | | | LL | UL | | OR.LL | OR.UL | z | p |
| (Intercept) | -2.31 | 0.31 | -2.91 | -1.70 | 0.10 | 0.05 | 0.18 | -7.47 | 8.26e-14 |
| Threshold.2 | 1.59 | 0.29 | 1.02 | 2.17 | 4.91 | 2.77 | 8.72 | 5.44 | 5.43e-08 |
| Threshold.3 | 0.42 | 0.36 | -0.28 | 1.12 | 1.52 | 0.75 | 3.08 | 1.17 | 0.241 |
| Motivation_NeedSANE.Yes | -0.44 | 0.26 | -0.94 | 0.07 | 0.65 | 0.39 | 1.08 | -1.68 | 0.093 |

```
```{r}
#| label: tbl-lrt-m1-m4
#| tbl-cap: "Likelihood Ratio Test Comparing Models 1 and 4"

test_lrt(m1, m4) %>%
 as_tibble() %>%
 mutate(p = display_num(p),
 Model = if_else(Name == "m1",
 true = "Thresholds",
 false = "Thresholds + Parallel Motivation_NeedSANE Effect")) %>%
 #select(-term) %>%
 kable(format = "latex", booktabs = TRUE, digits = c(0, 0, 0, 0, 2, 3),
 col.names = c("Model", "Terms", "df", "df_diff", "LRT", "p")) %>%
 kable_styling()
```

```

Table 25: Model 4 Fit Statistics

| null.deviance | df.null | logLik | AIC | BIC | deviance | df.residual | nobs |
|---------------|---------|---------|--------|--------|----------|-------------|------|
| 544.22 | 660 | -251.14 | 510.27 | 528.25 | 502.27 | 657 | 661 |

6.4.1 Check for Multicollinearity

Model 4 has only a subset of the predictors that were in Model 3, which had no multicollinearity issues. Therefore we skip checking for it here.

6.4.2 Compare Models 1 and 4

Table 26 shows a likelihood ratio test (LRT) comparing Models 1 and 4.

```
```{r}
#| label: tbl-lrt-m1-m4
#| tbl-cap: "Likelihood Ratio Test Comparing Models 1 and 4"

test_lrt(m1, m4) %>%
 as_tibble() %>%
 mutate(p = display_num(p),
 Model = if_else(Name == "m1",
 true = "Thresholds",
 false = "Thresholds + Parallel Motivation_NeedSANE Effect")) %>%
 #select(-term) %>%
 kable(format = "latex", booktabs = TRUE, digits = c(0, 0, 0, 0, 2, 3),
 col.names = c("Model", "Terms", "df", "df_diff", "LRT", "p")) %>%
 kable_styling()
```

```

Table 26: Likelihood Ratio Test Comparing Models 1 and 4

| Model | Terms | df | df_diff | LRT | p |
|-------|--|----|---------|------|-------|
| m1 | Thresholds | 3 | NA | NA | NA |
| m4 | Thresholds + Parallel Motivation_NeedSANE Effect | 4 | 1 | 2.71 | 0.100 |

🔥 Caution

While we saw an effect of `Motivation_NeedSANE` in Model 2 when controlling for all the other focal predictors, we no longer see one in Model 4 when it is the sole focal predictor. This is evident in both Table 24 and Table 26. That suggests controlling for other focal predictors is important in revealing the effect. Comparing the coefficients and odds-ratios for that predictor between Table 8 and Table 24 shows that sign of the effect is consistent across models but it is stronger and has a narrower confidence interval for the odds-ratio in Model 2 than in Model 4. I think this may be because one or more of the other focal predictors is a confounder or suppressor variable. I'm inclined to rely more on Model 2 than Model 4.

6.4.3 Estimated Marginal Means

Table 27 and Figure 9 show the EMMs derived from Model 4 for each threshold, while Table 28 shows the pairwise contrasts estimating the risk differences between those EMMs. Table 29 and Figure 10 show the EMMs for each level of `Motivation_NeedSANE`, while Table 30 shows the contrast estimating the risk difference between them. Table 31 and Figure 11 show the combined result of the two main effects while averaging over the results of all other predictors. Table 32 shows the contrast of `Motivation_NeedSANE` separately by threshold.

```
```{r}
#| label: tbl-emmeans-m4-Threshold
#| tbl-cap: Model 4 Conditional Attrition Rate by Threshold (Main Effect)

FN <- paste("Results are averaged over the levels of Motivation_NeedSANE.",
 "Values are on the probability scale.",
 "EMM, estimated marginal mean.")

avg_predictions(m4, variables = "Threshold.") %>%
 as_tibble() %>%
 select(Threshold., estimate, std.error, conf.low, conf.high) %>%
 mutate(Threshold. = factor(Threshold., labels = TLabels1)) %>%
 kable(format = "latex", booktabs = TRUE,
 digits = c(0, 3, 3, 3, 3),
 col.names = c("Threshold", "Rate (EMM)", "SE", "LL", "UL")) %>%
 kable_styling() %>%
 add_header_above(header = c(" " = 3, "95% Wald CI" = 2)) %>%
 footnote(kable_input = ., general = FN, footnote_as_chunk = TRUE,
 threeparttable = TRUE)
```

```

```
```{r}
#| label: fig-emmeans-m4-Threshold
#| fig-cap: Model 4 Conditional Attrition Rate by Threshold (Main Effect
#| Averaged Over Motivation_NeedSANE), With 95% Confidence Intervals.
#| CSW, clinical skills workshop; DT, didactic training.
#| fig-width: 4
#| fig-height: 2.5

avg_predictions(m4, variables = c("Threshold.")) %>%
 as_tibble() %>%
 select(Threshold., estimate, conf.low, conf.high) %>%
 mutate(Threshold. = factor(Threshold., labels = TLabels2)) %>%
 ggplot(data = ., mapping = aes(x = Threshold., y = estimate)) +
 geom_errorbar(aes(ymin = conf.low, ymax = conf.high), width = .1) +
 geom_point(size = 2) +

```

**Table 27: Model 4 Conditional Attrition Rate by Threshold (Main Effect)**

Threshold	Rate (EMM)	SE	95% Wald CI	
			LL	UL
T1 Before DT	0.067	0.016	0.036	0.098
T2 During DT	0.260	0.028	0.204	0.315
T3 Before/During CSW	0.099	0.023	0.054	0.143

*Note:*

Results are averaged over the levels of Motivation\_NeedSANE. Values are on the probability scale. EMM, estimated marginal mean.

```
ylab("Attrition Rate") +
xlab("Threshold") +
scale_y_continuous(lim = c(0.00, 0.50),
 labels = label_number(accuracy = 0.01)) +
theme_bw()
```

```

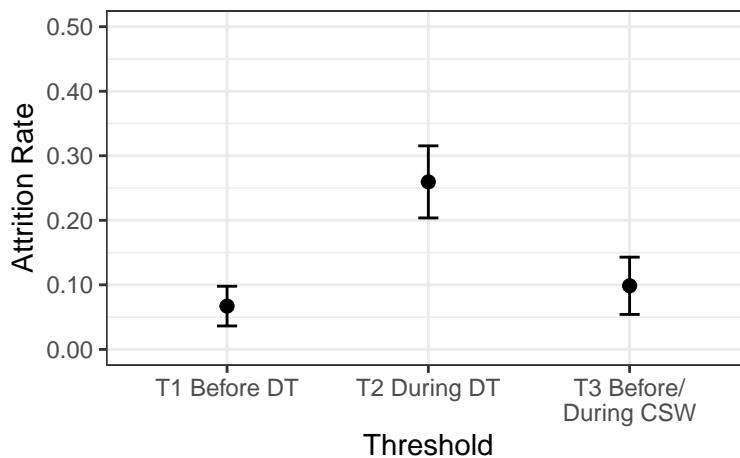


Figure 9: Model 4 Conditional Attrition Rate by Threshold (Main Effect Averaged Over Motivation_NeedSANE), With 95% Confidence Intervals. CSW, clinical skills workshop; DT, didactic training.

```
```{r}
#| label: tbl-emmc-m4-Threshold
#| tbl-cap: Model 4 Pairwise Comparisons of Conditional Attrition Rates for the
#| Threshold Main Effect

FN <- paste("Results are averaged over the levels of Motivation_NeedSANE.",
 "Values are on the probability scale.",
 "RD, risk difference between conditional attrition rates.")

avg_comparisons(m4, variables = list(Threshold. = "pairwise"),
 comparison = "difference") %>%
 as_tibble() %>%
 rename(Contrast = contrast, RD = estimate, SE = std.error, z = statistic,
 p = p.value, LL = conf.low, UL = conf.high) %>%
 select(Contrast, RD, SE, LL, UL, z, p) %>%
 mutate(p = display_num(p)) %>%
 kable(format = "latex", booktabs = TRUE, digits = 3) %>%
 kable_styling() %>%
 add_header_above(header = c(" " = 3, "95% CI" = 2, "Wald Test" = 2)) %>%
 footnote(kable_input = ., general = FN, footnote_as_chunk = TRUE,
 threeparttable = TRUE)
```

```

Table 28: Model 4 Pairwise Comparisons of Conditional Attrition Rates for the Threshold Main Effect

| Contrast | RD | SE | 95% CI | | Wald Test | |
|----------|--------|-------|--------|--------|-----------|----------|
| | | | LL | UL | z | p |
| 2 - 1 | 0.192 | 0.033 | 0.129 | 0.256 | 5.916 | 3.29e-09 |
| 3 - 1 | 0.031 | 0.028 | -0.023 | 0.085 | 1.142 | 0.253 |
| 3 - 2 | -0.161 | 0.036 | -0.232 | -0.090 | -4.423 | 9.72e-06 |

Note: Results are averaged over the levels of Motivation_NeedSANE. Values are on the probability scale. RD, risk difference between conditional attrition rates.

```
```{r}
#| label: tbl-emmeans-m4-NeedSANE
#| tbl-cap: Model 4 Conditional Attrition Rate by Motivation_NeedSANE (Main
#| Effect)

FN <- paste("Motivation_NeedSANE has a parallel effect on attrition.",
 "Results are averaged over the levels of Threshold.",
 "Values are on the probability scale.",
 "EMM, estimated marginal mean.")

avg_predictions(m4, variables = "Motivation_NeedSANE.") %>%
 as_tibble() %>%
 select(Motivation_NeedSANE., estimate, std.error, conf.low, conf.high) %>%
 kable(format = "latex", booktabs = TRUE,
 digits = c(0, 3, 3, 3),
 col.names = c("Motivation_NeedSANE", "Rate (EMM)", "SE", "LL", "UL")) %>%
 kable_styling() %>%
 add_header_above(header = c(" " = 3, "95% Wald CI" = 2)) %>%
 footnote(kable_input = ., general = FN, footnote_as_chunk = TRUE,
 threeparttable = TRUE)
```

```

Table 29: Model 4 Conditional Attrition Rate by Motivation_NeedSANE (Main Effect)

| Motivation_NeedSANE | Rate (EMM) | SE | 95% Wald CI | |
|---------------------|------------|-------|-------------|-------|
| | | | LL | UL |
| No | 0.186 | 0.031 | 0.125 | 0.247 |
| Yes | 0.132 | 0.014 | 0.104 | 0.160 |

Note: Motivation_NeedSANE has a parallel effect on attrition. Results are averaged over the levels of Threshold. Values are on the probability scale. EMM, estimated marginal mean.

```
```{r}
#| label: fig-emmeans-m4-NeedSANE
#| fig-cap: Model 4 Conditional Attrition Rate by Motivation_NeedSANE (Parallel
#| Main Effect Averaged Over Threshold), With 95% Confidence
#| Intervals
#| fig-width: 2.2
#| fig-height: 2.5

avg_predictions(m4, variables = c("Motivation_NeedSANE.")) %>%
 as_tibble() %>%
 select(Motivation_NeedSANE., estimate, conf.low, conf.high) %>%
 ggplot(data = ., mapping = aes(x = Motivation_NeedSANE., y = estimate)) +
 geom_errorbar(aes(ymin = conf.low, ymax = conf.high), width = .1) +
 geom_point(size = 2) +
 ylab("Attrition Rate") +
 xlab("Motivation: Need SANE") +
 scale_y_continuous(lim = c(0.00, 0.50),
 labels = label_number(accuracy = 0.01)) +

```

```
theme_bw()
```

```

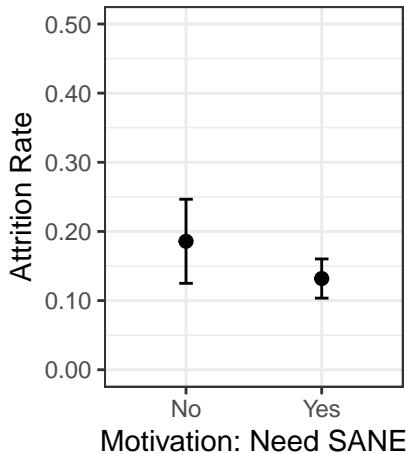


Figure 10: Model 4 Conditional Attrition Rate by Motivation_NeedSANE (Parallel Main Effect Averaged Over Threshold), With 95% Confidence Intervals

```
```{r}
#| label: tbl-emmc-m4-NeedSANE
#| tbl-cap: Model 4 Pairwise Comparisons of Conditional Attrition Rates for
#| Motivation_NeedSANE Main Effect

FN <- paste("Results are averaged over the levels of Threshold.",
 "Values are on the probability scale.",
 "RD, risk difference between conditional attrition rates.")

avg_comparisons(m4, variables = list(Motivation_NeedSANE. = "pairwise"),
 comparison = "difference") %>%
 as_tibble() %>%
 rename(Contrast = contrast, RD = estimate, SE = std.error, z = statistic,
 p = p.value, LL = conf.low, UL = conf.high) %>%
 select(Contrast, RD, SE, LL, UL, z, p) %>%
 mutate(p = display_num(p)) %>%
 kable(format = "latex", booktabs = TRUE, digits = 3) %>%
 kable_styling() %>%
 add_header_above(header = c(" " = 3, "95% CI" = 2, "Wald Test" = 2)) %>%
 footnote(kable_input = ., general = FN, footnote_as_chunk = TRUE,
 threeparttable = TRUE)
```

```

Table 30: Model 4 Pairwise Comparisons of Conditional Attrition Rates for Motivation_NeedSANE Main Effect

| Contrast | RD | SE | 95% CI | | Wald Test | |
|----------|--------|-------|--------|-------|-----------|-------|
| | | | LL | UL | z | p |
| Yes - No | -0.054 | 0.034 | -0.121 | 0.013 | -1.573 | 0.116 |

Note: Results are averaged over the levels of Threshold. Values are on the probability scale. RD, risk difference between conditional attrition rates.

```
```{r}
#| label: tbl-emmeans-m4-Both
#| tbl-cap: Model 4 Conditional Attrition Rate by Threshold and
#| Motivation_NeedSANE (Main Effects)

FN <- paste("Motivation_NeedSANE has a parallel effect on attrition.",
 "Values are on the probability scale.",
```

```

"CSW, clinical skills workshop; DT, didactic training;",
"EMM, estimated marginal mean.")

avg_predictions(m4, variables = c("Threshold.", "Motivation_NeedSANE.")) %>%
 as_tibble() %>%
 select(Threshold., Motivation_NeedSANE., estimate, std.error, conf.low, conf.high) %>%
 mutate(Threshold. = factor(Threshold., labels = TLabels)) %>%
 kable(format = "latex", booktabs = TRUE,
 digits = c(0, 0, 3, 3, 3),
 col.names = c("Threshold.", "Motivation_NeedSANE", "Rate (EMM)", "SE",
 "LL", "UL")) %>%
 kable_styling() %>%
 add_header_above(header = c(" " = 4, "95% Wald CI" = 2)) %>%
 collapse_rows(columns = 1:2, valign = "top", latex_hline = "major",
 custom_latex_hline = 1, headers_to_remove = 0,
 row_group_label_position = "stack") %>%
 footnote(kable_input = ., general = FN, footnote_as_chunk = TRUE,
 threeparttable = TRUE)
...
```

```

Table 31: Model 4 Conditional Attrition Rate by Threshold and Motivation_NeedSANE (Main Effects)

| Threshold | Motivation_NeedSANE | Rate (EMM) | 95% Wald CI | | |
|-----------------------------|---------------------|------------|-------------|-------|-------|
| | | | SE | LL | UL |
| T1 Before DT | | | | | |
| No | | 0.090 | 0.025 | 0.041 | 0.140 |
| Yes | | 0.060 | 0.015 | 0.031 | 0.090 |
| T2 During DT | | | | | |
| No | | 0.328 | 0.054 | 0.223 | 0.434 |
| Yes | | 0.240 | 0.030 | 0.182 | 0.299 |
| T3 Before/During CSW | | | | | |
| No | | 0.131 | 0.036 | 0.060 | 0.203 |
| Yes | | 0.089 | 0.021 | 0.047 | 0.131 |

Note: Motivation_NeedSANE has a parallel effect on attrition. Values are on the probability scale. CSW, clinical skills workshop; DT, didactic training; EMM, estimated marginal mean.

```

```{r}
#| label: fig-emmeans-m4-Both
#| fig-cap: Model 4 Conditional Attrition Rate by Threshold and
#| Motivation_NeedSANE (Main Effects Combined), With 95% Confidence
#| Intervals. CSW, clinical skills workshop; DT, didactic training.
#| fig-width: 4.5
#| fig-height: 2.5

avg_predictions(m4, variables = c("Threshold.", "Motivation_NeedSANE.")) %>%
 as_tibble() %>%
 select(Threshold., Motivation_NeedSANE., estimate, conf.low, conf.high) %>%
 ggplot(data = ., mapping = aes(x = Motivation_NeedSANE., y = estimate)) +
 facet_grid(cols = vars(Threshold.), labeller = labeller(Threshold. = FLabels)) +
 geom_errorbar(aes(ymin = conf.low, ymax = conf.high), width = .1) +
 geom_point(size = 2) +
 ylab("Attrition Rate") +
 xlab("Motivation: Need SANE") +
 scale_y_continuous(lim = c(0.00, 0.50),
 labels = label_number(accuracy = 0.01)) +
 theme_bw()
...
```

```

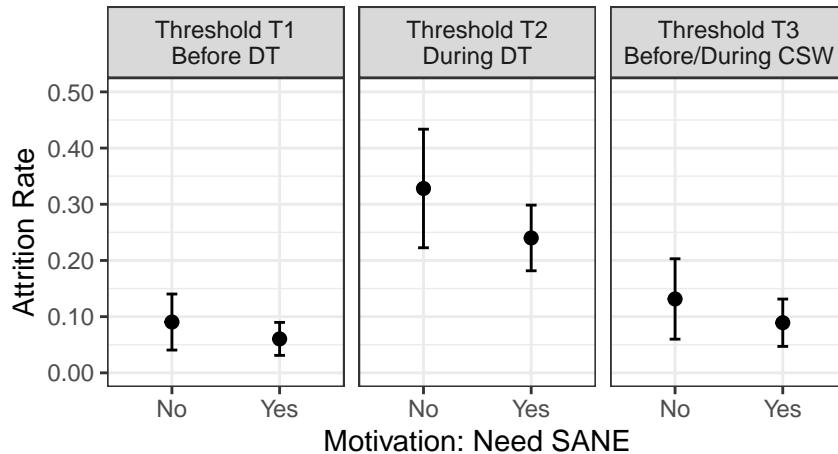


Figure 11: Model 4 Conditional Attrition Rate by Threshold and Motivation_NeedSANE (Main Effects Combined), With 95% Confidence Intervals. CSW, clinical skills workshop; DT, didactic training.

```
```{r}
#| label: tbl-emmc-m4-Both
#| tbl-cap: Model 4 Pairwise Comparisons of Conditional Attrition Rates for
#| Simple Effect of Motivation_NeedSANE at Each Threshold

FN <- paste("Motivation_NeedSANE has a parallel effect on attrition.",
 "Results are averaged over the levels of all other predictors.",
 "Values are on the probability scale.",
 "RD, risk difference between conditional attrition rates.")

avg_comparisons(m4, variables = list(Motivation_NeedSANE. = "pairwise"),
 comparison = "difference", by = "Threshold.") %>%
 as_tibble() %>%
 rename(Contrast = contrast, RD = estimate, SE = std.error, z = statistic,
 p = p.value, LL = conf.low, UL = conf.high) %>%
 select(Threshold., Contrast, , RD, SE, LL, UL, z, p) %>%
 mutate(Threshold = factor(Threshold., labels = Tlabels1)) %>%
 select(Threshold, Contrast, RD, SE, LL, UL, z, p) %>%
 mutate(p = display_num(p)) %>%
 kable(format = "latex", booktabs = TRUE, digits = 3) %>%
 kable_styling() %>%
 add_header_above(header = c(" " = 4, "95% CI" = 2, "Wald Test" = 2)) %>%
 footnote(kable_input = ., general = FN, footnote_as_chunk = TRUE,
 threeparttable = TRUE)
```

```

Table 32: Model 4 Pairwise Comparisons of Conditional Attrition Rates for Simple Effect of Motivation_NeedSANE at Each Threshold

| Threshold | Contrast | RD | SE | 95% CI | | Wald Test | |
|----------------------|----------|--------|-------|--------|-------|-----------|-------|
| | | | | LL | UL | z | p |
| T1 Before DT | Yes - No | -0.030 | 0.020 | -0.070 | 0.010 | -1.474 | 0.140 |
| T2 During DT | Yes - No | -0.088 | 0.055 | -0.196 | 0.020 | -1.601 | 0.109 |
| T3 Before/During CSW | Yes - No | -0.042 | 0.029 | -0.098 | 0.014 | -1.475 | 0.140 |

Note: Motivation_NeedSANE has a parallel effect on attrition. Results are averaged over the levels of all other predictors. Values are on the probability scale. RD, risk difference between conditional attrition rates.

6.4.4 Model Diagnostics

Figure 12 shows the plots for diagnostic tests of model assumptions.

```
```{r}
#| label: fig-m4-diagnose
#| fig-cap: "Diagnostic Plots for Model 4"
#| fig-subcap:
#| - "Q-Q Plot and Test for Overall Uniformity"
#| - "Residual Boxplots by Threshold"
#| - "Binomial Outlier Test"
#| - "Nonparametric Dispersion Test"
#| fig-width: 6
#| fig-height: 3
#| layout-ncol: 2
#| layout-nrow: 2

Save simulated residuals for use in diagnostics using DHARMA.
Seed uses a parameter defined in YAML header for reproducibility.
m4_sim <- simulateResiduals(fittedModel = m4, n = 1000, method = "PIT",
 seed = params$DHARMA.seed4)

plotQQunif(simulationOutput = m4_sim, testUniformity = TRUE,
 testDispersion = FALSE, testOutliers = FALSE)

invisible(testCategorical(simulationOutput = m4_sim,
 catPred = as_factor(Thresholds$Threshold),
 quantiles = c(0.25, 0.5, 0.75), plot = TRUE))

invisible(testOutliers(simulationOutput = m4_sim, alternative = "two.sided",
 margin = "both", type = "binomial", plot = TRUE))

invisible(testDispersion(simulationOutput = m4_sim, alternative = "two.sided",
 plot = TRUE, type = "DHARMA"))
```

```

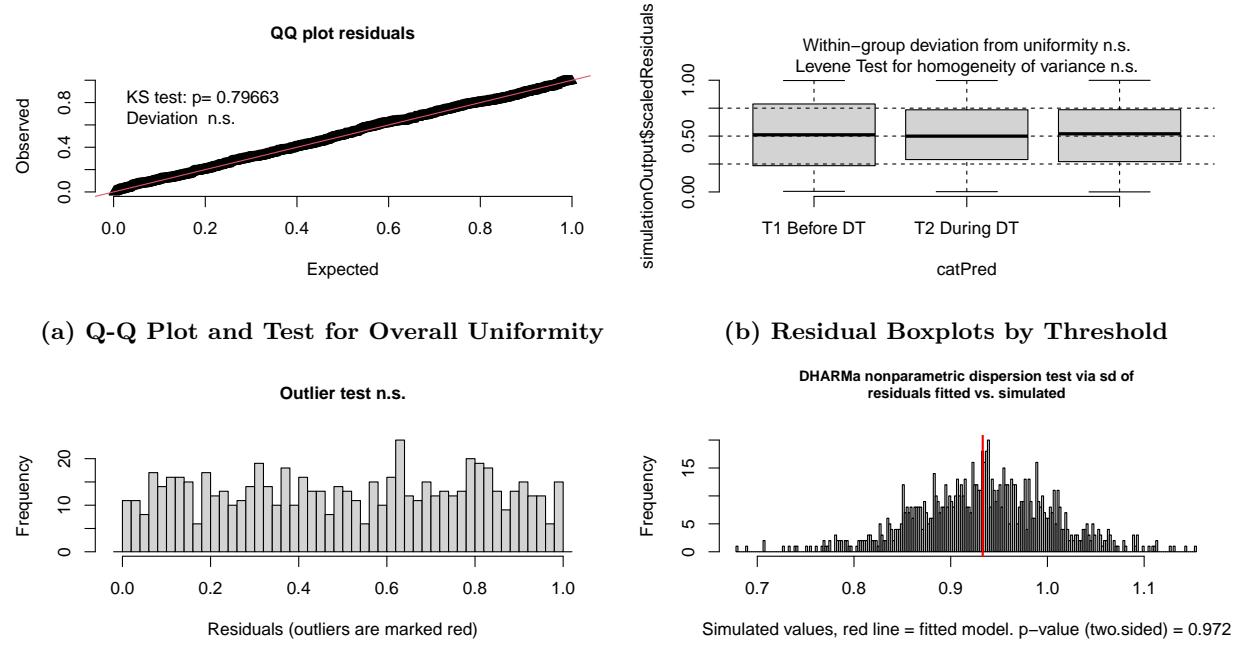


Figure 12: Diagnostic Plots for Model 4

💡 Tip

Model 4 assumptions are plausible. The scaled residuals appear to be uniform both overall (Figure 12a) and within each threshold with no signs of heterogeneity of variance (Figure 12b). There are no outliers (Figure 12c), and there is no evidence of over- or under-dispersion (Figure 12d).

6.5 Model 5: Thresholds & Non-Parallel Effect for Motivation_NeedSANE

Model 5 uses a non-parallel effect for Motivation_NeedSANE without any of the other focal predictors. Table 33 shows the parameter estimates and Table 34 shows the fit indices.

```
```{r}
#| label: tbl-params-m5
#| tbl-cap: "Model 5 Parameters"

m5 <- glm(Attrit ~ Threshold. + Motivation_NeedSANE. +
 Threshold..Motivation_NeedSANE. + 1,
 data = Thresholds, family = binomial(link = "logit"))

FN <- paste("Values shown are on the link function (logit) scale.")

tidy(m5) %>%
 cbind(confint.default(m5)) %>%
 as_tibble() %>%
 rename(Parameter = term, Est = estimate, SE = std.error, z = statistic,
 p = p.value, LL = `2.5 %`, UL = `97.5 %`) %>%
 mutate(Parameter = str_replace(string = Parameter, pattern = ":" ,
 replacement = " x "),
 p = display_num(p),
 OR = exp(Est),
 OR.LL = exp(LL),
 OR.UL = exp(UL)) %>%
 relocate(Parameter, Est, SE, LL, UL, OR, OR.LL, OR.UL, z, p) %>%
 kable(format = "latex", booktabs = TRUE, digits = 2) %>%
 kable_styling(font_size = 10) %>%
 add_header_above(header = c(" " = 3, "95% Wald CI" = 2, " " = 1,
 "OR 95% Wald CI" = 2, "Wald Test" = 2)) %>%
 column_spec(column = 1, width = "5.5cm")
```

```

Table 33: Model 5 Parameters

| Parameter | Est | SE | 95% Wald CI | | OR | OR 95% Wald CI | | Wald Test | |
|-------------------------|-------|------|-------------|-------|------|----------------|-------|-----------|----------|
| | | | LL | UL | | OR.LL | OR.UL | z | p |
| (Intercept) | -2.01 | 0.40 | -2.79 | -1.22 | 0.13 | 0.06 | 0.30 | -4.98 | 6.33e-07 |
| Threshold.2 | 1.28 | 0.50 | 0.30 | 2.26 | 3.61 | 1.36 | 9.60 | 2.57 | 0.010 |
| Threshold.3 | -0.36 | 0.73 | -1.78 | 1.06 | 0.70 | 0.17 | 2.89 | -0.50 | 0.618 |
| Motivation_NeedSANE.Yes | -0.90 | 0.52 | -1.92 | 0.11 | 0.41 | 0.15 | 1.12 | -1.74 | 0.081 |
| Threshold.2 x | 0.47 | 0.62 | -0.74 | 1.69 | 1.61 | 0.48 | 5.42 | 0.76 | 0.445 |
| Motivation_NeedSANE.Yes | | | | | | | | | |
| Threshold.3 x | 1.08 | 0.84 | -0.57 | 2.73 | 2.94 | 0.56 | 15.37 | 1.28 | 0.201 |
| Motivation_NeedSANE.Yes | | | | | | | | | |

```
```{r}
#| label: tbl-fit-m5
#| tbl-cap: "Model 5 Fit Statistics"

glance(m5) %>%
 kable(format = "latex", booktabs = TRUE,
 digits = c(2, 0, 2, 2, 2, 0, 0)) %>%
 kable_styling()
```

```

Table 34: Model 5 Fit Statistics

| null.deviance | df.null | logLik | AIC | BIC | deviance | df.residual | nobs |
|---------------|---------|---------|--------|--------|----------|-------------|------|
| 544.22 | 660 | -250.27 | 512.54 | 539.51 | 500.54 | 655 | 661 |

6.5.1 Check for Multicollinearity

Model 5 has only a subset of the predictors that were in Model 3, which had no multicollinearity issues. Therefore we skip checking for it here.

6.5.2 Compare Models 4 and 5

Table 35 shows a likelihood ratio test (LRT) comparing Models 4 and 5.

```
```{r}
#| label: tbl-lrt-m4-m5
#| tbl-cap: "Likelihood Ratio Test Comparing Models 4 and 5"

test_lrt(m4, m5) %>%
 as_tibble() %>%
 mutate(p = display_num(p),
 Model = if_else(Name == "m4",
 true = "Thresholds + Parallel Effect of Motivation_NeedSANE",
 false = "Thresholds + Non-Parallel Effect of Motivation_NeedSANE")) %>%
 #select(-term) %>%
 kable(format = "latex", booktabs = TRUE, digits = c(0, 0, 0, 0, 2, 3),
 col.names = c("Model", "Terms", "df", "df_diff", "LRT", "p")) %>%
 kable_styling()
```

```

Table 35: Likelihood Ratio Test Comparing Models 4 and 5

| Model | Terms | df | df_diff | LRT | p |
|-------|---|----|---------|------|-------|
| m4 | Thresholds + Parallel Effect of Motivation_NeedSANE | 4 | NA | NA | NA |
| m5 | Thresholds + Non-Parallel Effect of Motivation_NeedSANE | 6 | 2 | 1.73 | 0.421 |

Tip

This tests whether adding a non-parallel effect for `Motivation_NeedSANE` improved the model fit enough to justify adding that many extra parameters. It did not. We can safely drop the interaction effect from the model. That tells us we that if we're comfortable pursuing a more parsimonious model than Model 2, we should interpret Model 4 instead of Model 5.

6.5.3 Model Diagnostics

Figure 13 shows the plots for diagnostic tests of model assumptions.

```
```{r}
#| label: fig-m5-diagnose
#| fig-cap: "Diagnostic Plots for Model 5"
#| fig-subcap:
#| - "Q-Q Plot and Test for Overall Uniformity"
#| - "Residual Boxplots by Threshold"
#| - "Binomial Outlier Test"
#| - "Nonparametric Dispersion Test"
```

```

```
#| fig.width: 6
#| fig.height: 3
#| layout=ncol: 2
#| layout-nrow: 2

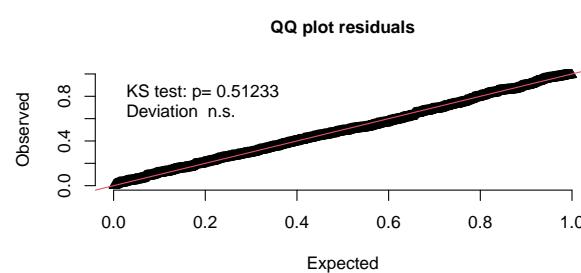
# Save simulated residuals for use in diagnostics using DHARMA.
# Seed uses a parameter defined in YAML header for reproducibility.
m5_sim <- simulateResiduals(fittedModel = m5, n = 1000, method = "PIT",
                             seed = params$DHARMA.seed5)

plotQQunif(simulationOutput = m5_sim, testUniformity = TRUE,
            testDispersion = FALSE, testOutliers = FALSE)

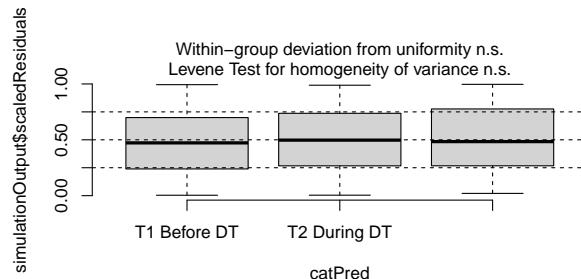
invisible(testCategorical(simulationOutput = m5_sim,
                          catPred = as_factor(Thresholds$Threshold),
                          quantiles = c(0.25, 0.5, 0.75), plot = TRUE))

invisible(testOutliers(simulationOutput = m5_sim, alternative = "two.sided",
                      margin = "both", type = "binomial", plot = TRUE))

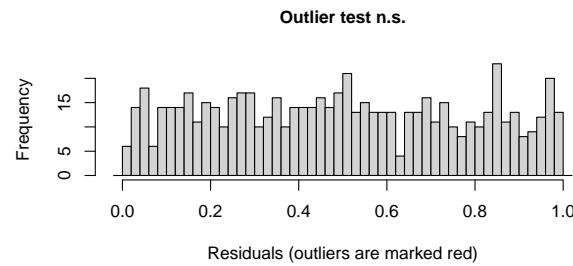
invisible(testDispersion(simulationOutput = m5_sim, alternative = "two.sided",
                        plot = TRUE, type = "DHARMA"))
...
```



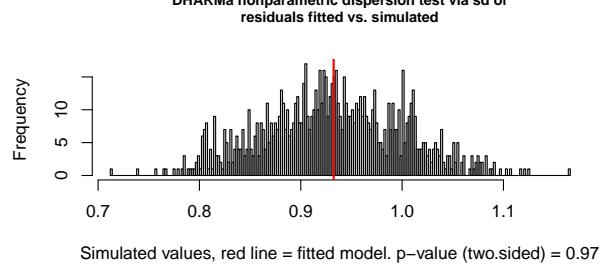
(a) Q-Q Plot and Test for Overall Uniformity



(b) Residual Boxplots by Threshold



(c) Binomial Outlier Test



(d) Nonparametric Dispersion Test

Figure 13: Diagnostic Plots for Model 5

💡 Tip

Model 5 assumptions are plausible. The scaled residuals appear to be uniform both overall (Figure 13a) and within each threshold with no signs of heterogeneity of variance (Figure 13b). There are no outliers (Figure 13c), and there is no evidence of over- or under-dispersion (Figure 13d).

6.6 Unconditional Attrition Rates

Table 36 shows both the overall unconditional attrition rate among all enrolled applicants and the unconditional attrition rate estimated separately for each level of Motivation_NeedSANE. Table 37 shows the corresponding test for a difference between the unconditional rates for the two groups, along with a confidence interval for the difference.

```
```{r}
#| label: tbl-unconditional-attrition-rates
#| tbl-cap: Unconditional Attrition Rate (Overall and Stratified By
#| Motivation_NeedSANE) Among All Eligible Applicants
#| message: false

FN <- paste("CI, Wilson score confidence interval for a proportion.")

bind_rows(dc_summary(data = Enrolled_Applicants_CD,
 vars = "Attrited"),
 dc_summary(data = Enrolled_Applicants_CD %>% filter(Motivation_NeedSANE == 0),
 vars = "Attrited"),
 dc_summary(data = Enrolled_Applicants_CD %>% filter(Motivation_NeedSANE == 1),
 vars = "Attrited")) %>%
bind_cols(Motivation_NeedSANE = c("Overall", "No", "Yes")) %>%
mutate(No = as.character(No),
 Yes = as.character(Yes),
 Total = as.character(Total),
 Motivation_NeedSANE = factor(Motivation_NeedSANE,
 levels = c("Overall", "No", "Yes"))) %>%
relocate(Variable, Motivation_NeedSANE) %>%
arrange(Variable, Motivation_NeedSANE) %>%
kable(format = "latex", booktabs = TRUE, digits = 2, align = "llrrrrrr",
 format.args = list(nsmall = 2)) %>%
kable_styling() %>%
add_header_above(header = c(" " = 2, "Attrited (N)" = 3, " ",
 "95% CI" = 2)) %>%
collapse_rows(columns = 1:2, valign = "top", latex_hline = "major",
 row_group_label_position = "first") %>%
footnote(kable_input = ., general = FN, footnote_as_chunk = TRUE,
 threeparttable = TRUE)
```

```

Table 36: Unconditional Attrition Rate (Overall and Stratified By Motivation_NeedSANE) Among All Eligible Applicants

| Variable | Motivation_NeedSANE | Attrited (N) | | | 95% CI | | |
|----------|---------------------|--------------|-----|-------|--------|------|------|
| | | No | Yes | Total | Rate | LL | UL |
| Attrited | Overall | 157 | 95 | 252 | 0.38 | 0.32 | 0.44 |
| | No | 32 | 27 | 59 | 0.46 | 0.34 | 0.58 |
| | Yes | 125 | 68 | 193 | 0.35 | 0.29 | 0.42 |

Note: CI, Wilson score confidence interval for a proportion.

```
```{r}
#| label: tbl-unconditional-attrition-diff
#| tbl-cap: Test for Difference in Unconditional Attrition Rates Between
#| Enrolled Applicants at Different Values of Motivation_NeedSANE
#| message: false

FN <- paste("CI, score confidence interval for a difference in independent",
 "proportions (Not motivated - Motivated), with continuity correction.")

bind_rows(dc_summary(data = Enrolled_Applicants_CD %>% filter(Motivation_NeedSANE == 0),
 vars = "Attrited"),
 dc_summary(data = Enrolled_Applicants_CD %>% filter(Motivation_NeedSANE == 1),
 vars = "Attrited")) %>%
bind_cols(Motivation_NeedSANE = c("No", "Yes")) %>%
arrange(Variable, desc(Motivation_NeedSANE)) %>%
relocate(Variable, Motivation_NeedSANE) %>%
select(Variable, Motivation_NeedSANE, Yes, Total, Rate) %>%
pivot_wider(id_cols = Variable, names_from = Motivation_NeedSANE,
 values_from = c(Yes, Total, Rate)) %>%
rowwise() %>%
mutate(p.test = tidy(prop.test(x = c(Yes_No, Yes_Yes),
 n = c(Total_No, Total_Yes),
 alternative = "two.sided"))$p.value)
```

```

```

conf.level = 0.95))) %>%
unnest(p.test) %>%
rename(Chisq = statistic, p = p.value, df = parameter, LL = conf.low,
      UL = conf.high) %>%
mutate(Difference = estimate1 - estimate2,
      p = display_num(p)) %>%
select(Variable, Difference, LL, UL, Chisq, df, p) %>%
kable(format = "latex", booktabs = TRUE, digits = 2, align = "lrrrrr",
      format.args = list(nsmall = 2)) %>%
kable_styling() %>%
add_header_above(header = c(" " = 2, "95% CI" = 2,
                           "Test for Diff. in Proportions" = 3)) %>%
collapse_rows(columns = 1:2, valign = "top", latex_hline = "major",
               row_group_label_position = "first") %>%
footnote(kable_input = ., general = FN, footnote_as_chunk = TRUE,
          threeparttable = TRUE)
...

```

Table 37: Test for Difference in Unconditional Attrition Rates Between Enrolled Applicants at Different Values of Motivation_NeedSANE

| Variable | Difference | 95% CI | | Test for Diff. in Proportions | | |
|----------|------------|--------|------|-------------------------------|------|-------|
| | | LL | UL | Chisq | df | p |
| Attrited | 0.11 | -0.05 | 0.26 | 1.71 | 1.00 | 0.191 |

Note: CI, score confidence interval for a difference in independent proportions (Not motivated - Motivated), with continuity correction.

💡 Tip

The comparison of unconditional rates in Table 37 is conceptually similar to SR Model 4 in that it only accounts for one focal predictor (**Motivation_NeedSANE**). Thus it is not surprising that this result is also similar to that of Model 4: it concludes there may be no effect of **Motivation_NeedSANE** on attrition (the difference between the two analyses being that SR Model 4 looks for an effect on conditional attrition rates and this simpler test looks for an effect on the unconditional attrition rates).

Notice however that while the confidence interval for the difference in unconditional rates spans zero, it is not *centered* on zero. Most of it spans positive rather than negative values. The lower bound suggests applicants with **Motivation_NeedSANE** = No could have at best slightly lower attrition, but the upper bound suggests that applicants with **Motivation_NeedSANE** = Yes could have much lower attrition. This asymmetry is worth careful consideration.

6.7 Start and Finish Rates for DT Modules

Table 38 and Figure 14 show the estimated start and finish rates for each DT module among enrolled applicants who started the didactic training.

```

```{r}
#| label: tbl-DT-module-rates
#| tbl-cap: Start and Finish Rates By Didactic Training Module Among Enrolled
#| Applicants Who Started the Didactic Training

FN <- paste("Missing data are included in the total used as the rate",
 "denominator. Only Yes values are included in the numerator.",
 "CI, Wilson score confidence interval for a proportion.")

Module_Content <- c("Overview of Forensic Nursing and Sexual Violence",
 "Victim Responses and Crisis Intervention",

```

```

 "Collaborating with Community Agencies",
 "Medical-Forensic History Taking",
 "Observing and Assessing Physical Examination Findings",
 "Medical-Forensic Specimen Collection",
 "Medical-Forensic Photography",
 "Sexually Transmitted Infection Testing and Prophylaxis",
 "Pregnancy Risk Evaluation and Care",
 "Medical-Forensic Documentation",
 "Discharge and Follow-up Planning",
 "Legal Considerations and Judicial Proceedings")

Module_Rates <- dc_summary(data = StartedDT_Applicants, na.rm = FALSE,
 vars = c(paste0("Started_Mod_", 1:12),
 paste0("Finished_Mod_", 1:12))) %>%
 mutate(Module = str_remove(string = Variable, pattern = "Started_Mod_"),
 Module = str_remove(string = Module, pattern = "Finished_Mod_"),
 Module = factor(Module, levels = 1:12),
 Content = factor(Module, levels = 1:12, labels = Module_Content),
 Rate_Type = if_else(str_starts(string = Variable,
 pattern = "Started_Mod_"),
 true = "Start",
 false = "Finish"),
 Rate_Type = factor(Rate_Type, levels = c("Start", "Finish"))) %>%
 mutate(Missing = as.character(Missing),
 No = as.character(No),
 Yes = as.character(Yes),
 Total = as.character(Total)) %>%
 relocate(Module, Content, Rate_Type) %>%
 arrange(Module, Rate_Type) %>%
 select(-Variable)

Module_Rates %>%
 kable(format = "latex", booktabs = TRUE, digits = 2, align = "rlrrrrrr",
 format.args = list(nsmall = 2)) %>%
 kable_styling(font_size = 8) %>%
 add_header_above(header = c(" " = 3, "Binary Variable (N)" = 4, " ",
 "95% CI" = 2)) %>%
 column_spec(column = 2, width = "6cm") %>%
 collapse_rows(columns = 1:2, valign = "top", latex_hline = "major",
 row_group_label_position = "first", headers_to_remove = 0) %>%
 footnote(kable_input = ., general = FN, footnote_as_chunk = TRUE,
 threeparttable = TRUE)
...
```

```

```

```{r}
#| label: fig-DT-module-rates
#| fig-cap: Start and Finish Rates By Didactic Training Module Among Enrolled
#| Applicants Who Started the Didactic Training, With 95% Confidence
#| Intervals
#| fig-width: 7
#| fig-height: 2.5

Module_Rates %>%
 mutate(CI_Label = paste0(sprintf("%.2f", Rate), " [",
 sprintf("%.2f", LL), ",",
 sprintf("%.2f", UL), "]")) %>%
 ggplot(data = ., mapping = aes(y = fct_rev(Module))) +
 theme_bw() +
 coord_cartesian(xlim = c(0.0, 1.01)) +
 facet_wrap(~ Rate_Type, ncol = 2) +
 geom_point(aes(x=Rate), size = 1.5) +
 geom_linerange(aes(xmin=LL, xmax=UL)) +
 geom_text(x = 0.0, aes(label = CI_Label), hjust = 0, cex = 3) +
 labs(x="Rate", y="Module")
...
```

```

Table 38: Start and Finish Rates By Didactic Training Module Among Enrolled Applicants Who Started the Didactic Training

| Module | Content | Rate_Type | Binary Variable (N) | | | | 95% CI | | |
|--------|--|-----------|---------------------|----|-----|-------|--------|------|------|
| | | | Missing | No | Yes | Total | Rate | LL | UL |
| 1 | Overview of Forensic Nursing and Sexual Violence | Start | 0 | 3 | 232 | 235 | 0.99 | 0.96 | 1.00 |
| | | Finish | 3 | 12 | 220 | 235 | 0.94 | 0.90 | 0.96 |
| 2 | Victim Responses and Crisis Intervention | Start | 14 | 1 | 220 | 235 | 0.94 | 0.90 | 0.96 |
| | | Finish | 15 | 5 | 215 | 235 | 0.91 | 0.87 | 0.94 |
| 3 | Collaborating with Community Agencies | Start | 19 | 2 | 214 | 235 | 0.91 | 0.87 | 0.94 |
| | | Finish | 21 | 2 | 212 | 235 | 0.90 | 0.86 | 0.93 |
| 4 | Medical-Forensic History Taking | Start | 22 | 2 | 211 | 235 | 0.90 | 0.85 | 0.93 |
| | | Finish | 24 | 2 | 209 | 235 | 0.89 | 0.84 | 0.92 |
| 5 | Observing and Assessing Physical Examination Findings | Start | 26 | 1 | 208 | 235 | 0.89 | 0.84 | 0.92 |
| | | Finish | 27 | 8 | 200 | 235 | 0.85 | 0.80 | 0.89 |
| 6 | Medical-Forensic Specimen Collection | Start | 35 | 4 | 196 | 235 | 0.83 | 0.78 | 0.88 |
| | | Finish | 39 | 7 | 189 | 235 | 0.80 | 0.75 | 0.85 |
| 7 | Medical-Forensic Photography | Start | 46 | 3 | 186 | 235 | 0.79 | 0.74 | 0.84 |
| | | Finish | 49 | 2 | 184 | 235 | 0.78 | 0.73 | 0.83 |
| 8 | Sexually Transmitted Infection Testing and Prophylaxis | Start | 51 | 0 | 184 | 235 | 0.78 | 0.73 | 0.83 |
| | | Finish | 51 | 3 | 181 | 235 | 0.77 | 0.71 | 0.82 |
| 9 | Pregnancy Risk Evaluation and Care | Start | 54 | 0 | 181 | 235 | 0.77 | 0.71 | 0.82 |
| | | Finish | 54 | 3 | 178 | 235 | 0.76 | 0.70 | 0.81 |
| 10 | Medical-Forensic Documentation | Start | 57 | 0 | 178 | 235 | 0.76 | 0.70 | 0.81 |
| | | Finish | 57 | 3 | 175 | 235 | 0.74 | 0.69 | 0.80 |
| 11 | Discharge and Follow-up Planning | Start | 60 | 0 | 175 | 235 | 0.74 | 0.69 | 0.80 |
| | | Finish | 60 | 1 | 174 | 235 | 0.74 | 0.68 | 0.79 |
| 12 | Legal Considerations and Judicial Proceedings | Start | 61 | 0 | 174 | 235 | 0.74 | 0.68 | 0.79 |
| | | Finish | 61 | 0 | 174 | 235 | 0.74 | 0.68 | 0.79 |

Note: Missing data are included in the total used as the rate denominator. Only Yes values are included in the numerator.
 CI, Wilson score confidence interval for a proportion.

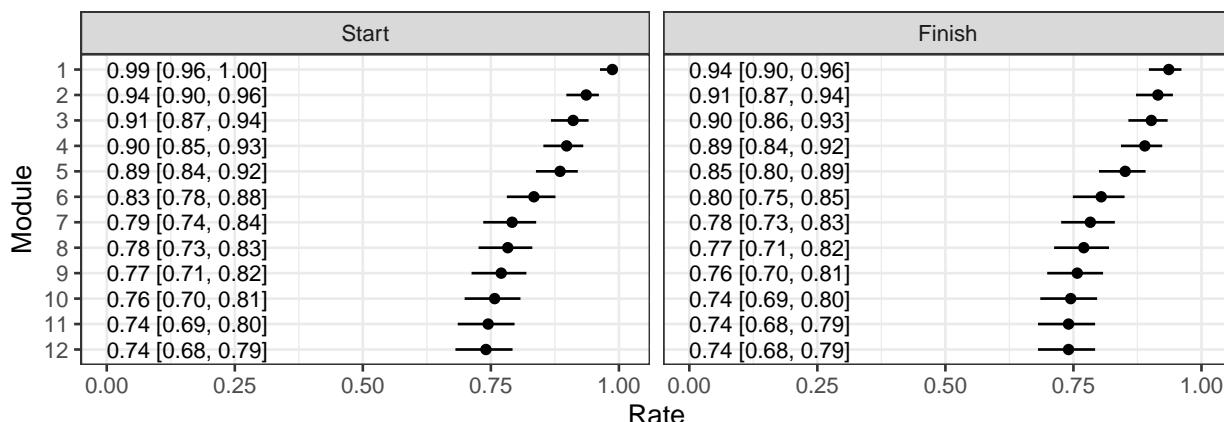


Figure 14: Start and Finish Rates By Didactic Training Module Among Enrolled Applicants Who Started the Didactic Training, With 95% Confidence Intervals

7 Conclusions

7.1 RQ2: What are the attrition rates from enrollment to completion of the CSW, and when (i.e., at which module[s]) did participants commonly attrit?

If we just want to know the conditional attrition rate at each threshold, we need to examine the main effect of threshold. Model 1 demonstrated that the attrition rate is not constant throughout the program. Instead, the attrition rates vary across thresholds and all subsequent models continued to demonstrate that fact. *The attrition rate during didactic training is substantially higher than at any other threshold.*

The simplest answer to RQ1 is presented in Table 6 and Figure 2, but Model 2 provides a better answer. Model 2 output reflects controls for all focal predictors regardless of whether their effects were significant. Figure 4 shows the main effect of Threshold while averaging over all focal predictors, while Table 17 and Figure 6 show the combined main effects of Threshold and Motivation_NeedSANE. *In that context, we still see a much higher attrition rate during didactic training than at other thresholds.* For use in the manuscript, we combine those two plots in Figure 15.

```
```{r}
#| label: fig-emmeans-m2-export
#| fig-cap: Model 2 Conditional Attrition Rates With 95% Confidence Intervals By
#| (A) Threshold (Main Effect Averaged Over All Focal Predictors),
#| (B) Threshold and Motivation_NeedSANE (Main Effects Combined,
#| Averaged Over All Other Focal Predictors).
#| CSW, clinical skills workshop; DT, didactic training.
#| fig-width: 4.5
#| fig-height: 5

export_figure <- p4/p6 +
 plot_annotation(tag_levels = "A")
export_figure
```
```

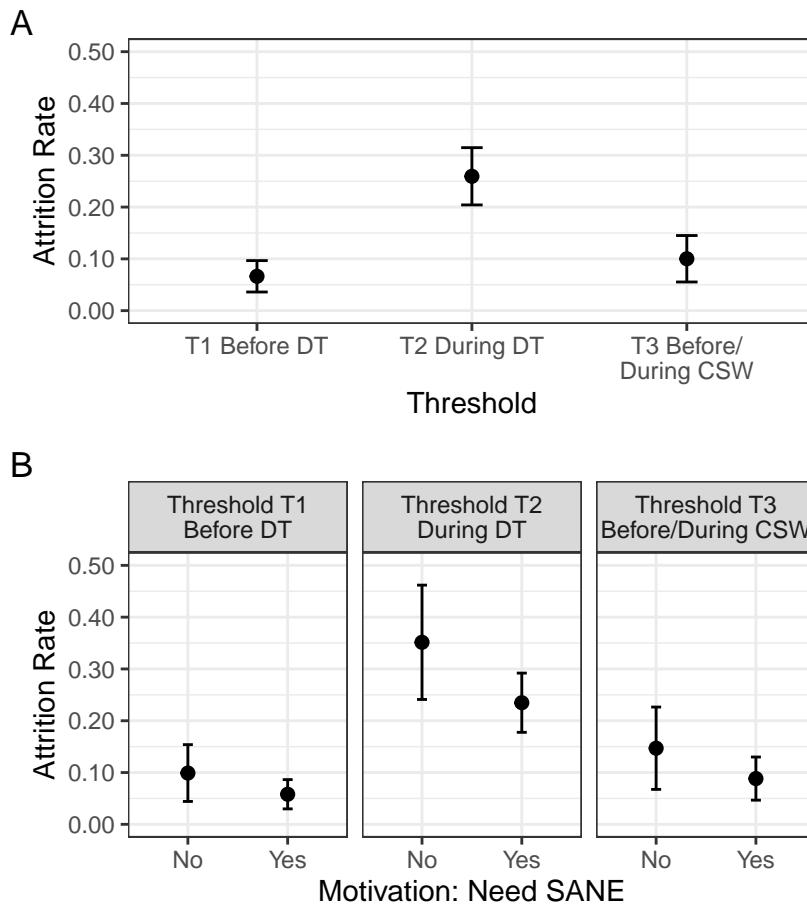


Figure 15: Model 2 Conditional Attrition Rates With 95% Confidence Intervals By (A) Threshold (Main Effect Averaged Over All Focal Predictors), (B) Threshold and Motivation_NeedSANE (Main Effects Combined, Averaged Over All Other Focal Predictors). CSW, clinical skills workshop; DT, didactic training.

Next, we export the combined figure to a TIFF file suitable for use by the intended journal per the instructions for authors.

```
```{r}
#| label: export-figure

tif_file <- paste0("scripts/output/Campbell_Figure_2_", Sys.Date(), ".tif")

ggsave(filename = here(tif_file),
 plot = export_figure,
 width = 4.5, height = 5, units = "in", dpi = 300)

file_details(here(tif_file))
```

```

```
# A tibble: 1 x 3
  File_Name          Size Last_Modified
  <chr>            <fs::bytes> <dttm>
1 Campbell_Figure_2_2026-02-14.tif  5.79M 2026-02-14 13:00:16
```

Meanwhile, the overall unconditional attrition rate corresponding to SR Model 1 is reported in

Table 36. We skipped running a model to estimate the covariate-adjusted unconditional attrition rate that would mirror SR Model 2.

Finally, Figure 14 shows that both start and finish rates for each DT module decrease monotonically when sorted by module number. The largest change was between modules 5 and 6 (6% decrease in start rate, 5% for finish rate), but this was not a sharp discontinuity compared to the changes between successive modules. The lowest observed rates were about 75% for both start and finish of module 12.

7.2 RQ3: Do participants' background characteristics, motivations for seeking training, potential barriers, and emotional readiness for this work predict attrition rates?

Of the eight focal predictors we examined, only whether an applicant was motivated to seek the training by a need for SANE services in their community or organization had a meaningful effect on attrition. The evidence for this lies in the single-term deletion tests from Model 2 (Table 12).

Applicants who reported having that motivation experienced lower attrition than applicants who did not report that motivation. The odds-ratio for this effect in Model 2 (Table 8) controls for all other focal predictors. It is noteworthy that the upper end of that confidence interval spans values very close 1. That means this effect *could* be so small as have no practical implications for practice.

Our analyses showed no evidence that the seven remaining focal predictors listed below exert any influence on attrition from the SANE training program. This is surprising and counter-intuitive, but is nonetheless what our analyses show.

- Primary setting where the trainee practices nursing.
- Family obligations.
- Work responsibilities.
- Motivated to seek the training by a personal connection to sexual assault (e.g., someone they know is a survivor).
- Burnout.
- Compassion satisfaction.
- Secondary traumatic stress.

The comparison of Model 2 and 3 (Table 22), the single-term deletion tests from Model 3 (Table 23) and the comparison of Models 4 and 5 (Table 35) all demonstrated that none of the focal predictors have non-parallel effects on attrition.

As noted above in the conclusions regarding RQ2, whether an applicant was motivated to seek the training by a need for SANE services in their community or organization had a parallel effect on attrition. The evidence for this lies in the single-term deletion tests from Model 2 (Table 12).

Caution

Trimming Model 2 down to produce Model 4 in pursuit of parsimony yields a slightly weaker effect of motivation by a need for SANE services. The shift is just large enough to cause the upper end of the odds-ratio's confidence interval to overlap 1. A really robust effect would be clearly present whether or not the other focal predictors were in the model but that is not what we see here. One or more of the other focal predictors may be a confounder or suppressor

that must be included in the model to see the effect of `Motivation_NeedSANE` even though they don't have discernible direct effects of their own on attrition.

The apparent conflict between Model 2 and Model 4 conclusions about the `Motivation_NeedSANE` effect is an artifact of strict, arbitrary application of a null hypothesis significance testing framework. The confidence intervals for the odds-ratio for that effect from the two models overlap to a large degree. Better statistical thinking and practice would suggest that this latter fact is what is most salient. Model 2 produces a narrower CI for that effect because it controls for other focal predictors. This is not a particularly large effect and both models suggest that it could be either strong enough to matter or so weak as to be of negligible practical importance. The point estimates lean more toward the former possibility, but sampling error leaves room for the latter one too.

Finally, the stratified unconditional attrition rates corresponding to the `Motivation_NeedSANE` effect in SR Model 4 are reported in Table 36. We skipped running a model to estimate the covariate-adjusted unconditional attrition rate that would mirror SR Model 2, but could add that if needed.

8 Recommendations

We should fully report Model 2 in the manuscript. We can perhaps relegate Model 3 to a footnote saying that we tested for non-parallel effects but found no support for them and just refer readers to the online research compendium for full details.

Commenting on the minor conflict between Model 2 and Model 4 could potentially also become a footnote and a referral to the online research compendium. However, we should emphasize thinking about the implications of the range of values spanned by the relevant confidence intervals because that shows there is more similarity between the two results than implied by the overly simplistic interpretation of whether two similar p-values fall above versus below the arbitrary cutoff of 0.05. There is little meaningful difference between a “non-significant” value such as 0.06 and a “significant” one of 0.04 (Gelman & Stern, 2006).

9 References

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10 Software Information

This section documents information that is important for reproducibility. Most users will not need to read it. It is primarily here for use by the statistician on the team if we need to troubleshoot reproducibility issues because someone else is unable to get the same results from the same code. Start by checking for differences in package versions.

We used **R** as our main computing environment and **Quarto** scripts to enhance reproducibility. We used **RStudio** as the editor to interface with R and Quarto.

- Software chain: **qmd file > RStudio > Quarto > R > knitr > md file > Pandoc > tex file > TinyTeX > PDF file.**
- Source file: **RQ2_RQ3_SR_Models.qmd**
- Output file: **RQ2_RQ3_SR_Models_2026-02-14.pdf**
- **Quarto 1.8.27** runs ***.qmd** files through **R** and **knitr** to produce ***.md** markdown files.
- **Pandoc 3.6.3** converts markdown files (***.md**) to other formats, including **LaTeX** (***.tex**) and **HTML** (***.html**) among others.
- **TinyTeX** compiles **LaTeX** files (***.tex**) into **PDF** files. It should be viable to use **MiKTeX** or another **LaTeX** distribution instead.

10.1 Versions

This document was generated using the following computational environment and dependencies:

```
# Check and report whether we used TinyTeX or other LaTeX software.  
which_latex()
```

```
is_tinytex = TRUE. We used TeX Live 2025 (TinyTeX) with tlmgr 2025-11-06.
```

```
tlmgr revision 76773 (2025-11-06 20:43:29 +0100)
tlmgr using installation: C:/Users/pierces1/AppData/Roaming/TinyTeX
TeX Live (https://tug.org/texlive) version 2025
```

```
# Get R and R package version numbers in use.
devtools::session_info()
```

```
Warning in system2("quarto", "-V", stdout = TRUE, env = paste0("TMPDIR=", :
running command "quarto"
TMPDIR=C:/Users/pierces1/AppData/Local/Temp/Rtmp4uh2Ma/file6b1c6ad53d7a -V' had
status 1
```

```
- Session info -----
setting  value
version  R version 4.5.2 (2025-10-31 ucrt)
os       Windows 11 x64 (build 26100)
system   x86_64, mingw32
ui       RTerm
language (EN)
collate English_United States.utf8
ctype    English_United States.utf8
tz       America/New_York
date     2026-02-14
pandoc  3.6.3 @ C:/Program Files/RStudio/resources/app/bin/quarto/bin/tools/ (via rmarkdown)
quarto   NA @ C:\\PROGRA~1\\Quarto\\bin\\quarto.exe

- Packages -----
package      * version date (UTC) lib source
abind        1.4-8   2024-09-12 [1] CRAN (R 4.5.0)
assertthat   0.2.1   2019-03-21 [1] CRAN (R 4.5.0)
backports    1.5.0   2024-05-23 [1] CRAN (R 4.5.0)
boot        1.3-32   2025-08-29 [1] CRAN (R 4.5.1)
broom        * 1.0.12  2026-01-27 [1] CRAN (R 4.5.2)
cachem       1.1.0   2024-05-16 [1] CRAN (R 4.5.0)
car          * 3.1-5   2026-02-03 [1] CRAN (R 4.5.2)
cardata      * 3.0-6   2026-01-30 [1] CRAN (R 4.5.2)
checkmate   2.3.4   2026-02-03 [1] CRAN (R 4.5.2)
cli         3.6.5   2025-04-23 [1] CRAN (R 4.5.0)
data.table  1.18.2.1 2026-01-27 [1] CRAN (R 4.5.2)
devtools    * 2.4.6   2025-10-03 [1] CRAN (R 4.5.1)
DHARMa      * 0.4.7   2024-10-18 [1] CRAN (R 4.5.0)
digest       0.6.39   2025-11-19 [1] CRAN (R 4.5.2)
dplyr        * 1.2.0   2026-02-03 [1] CRAN (R 4.5.2)
ellipsis     0.3.2   2021-04-29 [1] CRAN (R 4.5.0)
evaluate    1.0.5   2025-08-27 [1] CRAN (R 4.5.1)
farver       2.1.2   2024-05-13 [1] CRAN (R 4.5.0)
fastmap      1.2.0   2024-05-15 [1] CRAN (R 4.5.0)
forcats     * 1.0.1   2025-09-25 [1] CRAN (R 4.5.1)
Formula      1.2-5   2023-02-24 [1] CRAN (R 4.5.0)
fs           1.6.6   2025-04-12 [1] CRAN (R 4.5.0)
gap          1.9     2026-02-06 [1] CRAN (R 4.5.2)
gap.datasets 0.0.6   2023-08-25 [1] CRAN (R 4.5.0)
generics     0.1.4   2025-05-09 [1] CRAN (R 4.5.0)
ggplot2     * 4.0.2   2026-02-03 [1] CRAN (R 4.5.2)
git2r        0.36.2   2025-03-29 [1] CRAN (R 4.5.0)
glue         1.8.0   2024-09-30 [1] CRAN (R 4.5.0)
gttable      0.3.6   2024-10-25 [1] CRAN (R 4.5.0)
haven        2.5.5   2025-05-30 [1] CRAN (R 4.5.0)
here         * 1.0.2   2025-09-15 [1] CRAN (R 4.5.1)
hms          1.1.4   2025-10-17 [1] CRAN (R 4.5.1)
htmltools    0.5.9   2025-12-04 [1] CRAN (R 4.5.2)
httr         1.4.8   2026-02-13 [1] CRAN (R 4.5.2)
insight      1.4.6   2026-02-04 [1] CRAN (R 4.5.2)
jsonlite     2.0.0   2025-03-27 [1] CRAN (R 4.5.0)
kableExtra   * 1.4.0   2024-01-24 [1] CRAN (R 4.5.0)
knitr        * 1.51    2025-12-20 [1] CRAN (R 4.5.2)
labeling     0.4.3   2023-08-29 [1] CRAN (R 4.5.0)
later         1.4.5   2026-01-08 [1] CRAN (R 4.5.2)
lattice      0.22-9   2026-02-08 [1] CRAN (R 4.5.2)
lifecycle    1.0.5   2026-01-08 [1] CRAN (R 4.5.2)
lme4         1.1-38   2025-12-02 [1] CRAN (R 4.5.2)
lubridate    * 1.9.5   2026-02-04 [1] CRAN (R 4.5.2)
magrittr     2.0.4   2025-09-12 [1] CRAN (R 4.5.1)
marginaleffects * 0.32.0 2026-02-14 [1] CRAN (R 4.5.2)
MASS         7.3-65   2025-02-28 [1] CRAN (R 4.5.0)
Matrix        1.7-4   2025-08-28 [1] CRAN (R 4.5.1)
MBESS        4.9.42   2026-01-08 [1] CRAN (R 4.5.2)
memoise      2.0.1   2021-11-26 [1] CRAN (R 4.5.0)
minqa        1.2.8   2024-08-17 [1] CRAN (R 4.5.0)
mvtnorm     1.3-3   2025-01-10 [1] CRAN (R 4.5.0)
nlme         3.1-168  2025-03-31 [1] CRAN (R 4.5.0)
nloptr       2.2.1   2025-03-17 [1] CRAN (R 4.5.0)
otel          0.2.0   2025-08-29 [1] CRAN (R 4.5.1)
patchwork   * 1.3.2   2025-08-25 [1] CRAN (R 4.5.1)
```

```

pbivnorm      0.6.0   2015-01-23 [1] CRAN (R 4.5.0)
performance   * 0.16.0  2026-02-04 [1] CRAN (R 4.5.2)
pierce       * 0.23.0  2025-09-07 [1] Github (sjpierce/pierce@7e53e10)
pillar        1.11.1  2025-09-17 [1] CRAN (R 4.5.1)
pkgbuild      1.4.8   2025-05-26 [1] CRAN (R 4.5.0)
pkgconfig     2.0.3   2019-09-22 [1] CRAN (R 4.5.0)
pkgload       1.5.0   2026-02-03 [1] CRAN (R 4.5.2)
prOC          1.19.0.1 2025-07-31 [1] CRAN (R 4.5.1)
processx      3.8.6   2025-02-21 [1] CRAN (R 4.5.0)
PropCIs       0.3-0   2018-02-23 [1] CRAN (R 4.5.0)
ps            1.9.1   2025-04-12 [1] CRAN (R 4.5.0)
purrr        * 1.2.1   2026-01-09 [1] CRAN (R 4.5.2)
quarto       * 1.5.1   2025-09-04 [1] CRAN (R 4.5.1)
R6             2.6.1   2025-02-18 [1] CRAN (R 4.5.0)
ragg           1.5.0   2025-09-02 [1] CRAN (R 4.5.1)
rbibutils     2.4.1   2026-01-21 [1] CRAN (R 4.5.2)
RColorBrewer  1.1-3   2022-04-03 [1] CRAN (R 4.5.0)
Rcpp           1.1.1   2026-01-10 [1] CRAN (R 4.5.2)
Rdpack        2.6.6   2026-02-08 [1] CRAN (R 4.5.2)
readr         * 2.1.6   2025-11-14 [1] CRAN (R 4.5.2)
reformulas    0.4.4   2026-02-02 [1] CRAN (R 4.5.2)
remotes       2.5.0   2024-03-17 [1] CRAN (R 4.5.0)
rlang          1.1.7   2026-01-09 [1] CRAN (R 4.5.2)
rmarkdown     * 2.30    2025-09-28 [1] CRAN (R 4.5.1)
rprojroot     2.1.1   2025-08-26 [1] CRAN (R 4.5.1)
rstudioapi    0.18.0  2026-01-10 [1] CRAN (R 4.5.2)
S7             0.2.1   2025-11-14 [1] CRAN (R 4.5.2)
SANETPA       * 1.0.1   2026-02-14 [1] Github (sjpierce/SANETPA@482345e)
scales        * 1.4.0   2025-04-24 [1] CRAN (R 4.5.0)
sessioninfo   1.2.3   2025-02-05 [1] CRAN (R 4.5.0)
stringi       1.8.7   2025-03-27 [1] CRAN (R 4.5.0)
stringr      * 1.6.0   2025-11-04 [1] CRAN (R 4.5.2)
svglite       2.2.2   2025-10-21 [1] CRAN (R 4.5.1)
systemfonts  1.3.1   2025-10-01 [1] CRAN (R 4.5.1)
texreg        1.39.5  2025-12-22 [1] CRAN (R 4.5.2)
textshaping   1.0.4   2025-10-10 [1] CRAN (R 4.5.1)
tibble        * 3.3.1   2026-01-11 [1] CRAN (R 4.5.2)
tidyverse     * 1.3.2   2025-12-19 [1] CRAN (R 4.5.2)
tidyselect    1.2.1   2024-03-11 [1] CRAN (R 4.5.0)
tidyverse     * 2.0.0   2023-02-22 [1] CRAN (R 4.5.0)
timechange    0.4.0   2026-01-29 [1] CRAN (R 4.5.2)
tinytex       0.58    2025-11-19 [1] CRAN (R 4.5.2)
tzdb           0.5.0   2025-03-15 [1] CRAN (R 4.5.0)
useethis     * 3.2.1   2025-09-08 [1] CRAN (R 4.5.1)
utf8           1.2.6   2025-06-08 [1] CRAN (R 4.5.0)
vctrs          0.7.1   2026-01-23 [1] CRAN (R 4.5.2)
viridisLite   0.4.3   2026-02-04 [1] CRAN (R 4.5.2)
withr          3.0.2   2024-10-28 [1] CRAN (R 4.5.0)
xfun           0.56    2026-01-18 [1] CRAN (R 4.5.2)
xml2          1.5.2   2026-01-17 [1] CRAN (R 4.5.2)
yaml          2.3.12  2025-12-10 [1] CRAN (R 4.5.2)

```

```

[1] C:/Users/pierces1/AppData/Local/R/win-library/4.5
[2] C:/Program Files/R/R-4.5.2/library
* -- Packages attached to the search path.
-----
```

10.2 Git Details

The current Git commit details and status are:

```
git_report()
```

```

Local:  main P:/Consulting/Cases_1600-1799/C1788/SANETPA
Remote: main @ origin (https://github.com/sjpierce/SANETPA.git)
Head:   [482345e] 2026-02-14: Update version number.
```

```

Untracked files:
  Untracked: scripts/Production_Run.rmarkdown
  Untracked: scripts/RQ2_RQ3_SR_Models.rmarkdown
  Untracked: scripts/RQ2_RQ3_SR_Models_files/
  Untracked: scripts/output/Campbell_Figure_2_2026-02-14.tif
```

This is useful because it tells us exactly which commit in the Git history we would need to be using to make sure we are running the exact same code. Sometimes another person is not using the most current code, or has changed the code in some way since it was last committed.

 Tip

- Untracked files are files located in the repository that Git has not been told to entirely ignore, but have also not been committed into the version history.
- Unstaged changes to files indicate that some of the contents have been modified since the last time the file was committed to Git. In production runs, we want the Git output to not show any unstaged changes to key files!