visualizemi: Visualization, Effect Size, and Replication of Measurement

Invariance for Registered Reports

Erin M. Buchanan[1]

[1] Harrisburg University of Science and Technology

Author Note

Correspondence concerning this article should be addressed to Erin M. Buchanan, 326 Market St., Harrisburg, PA, USA. E-mail: ebuchanan@harrisburgu.edu

Abstract

Latent variable modeling as a lens for psychometric theory is a popular tool for social scientists to examine measurement of constructs (Beaujean, 2014). Journals such as *Assessment* regularly publish articles supporting measures of latent constructs wherein a measurement model is established. Confirmatory factor analysis can be used to investigate the replicability and generalizability of the measurement model in new samples, while multi-group confirmatory factor analysis is used to examine the measurement model across groups within samples (Brown, 2015). With the rise of the replication crisis and "psychology's renaissance" (Nelson et al., 2018), interest in divergence in measurement has increased, often focused on small parameter differences within the latent model. This manuscript presents `visualizemi`, an R package that provides functionality to calculate multigroup models, partial invariance, visualizations for (non)-invariance, effect sizes for models and parameters, and potential replication rates compared to random models. Readers will learn how to interpret the impact and size of the proposed non-invariance in models with a focus on potential replication and how to plan for registered reports.

Keywords: multigroup confirmatory factor analysis, measurement invariance, visualization, effect size

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Invariance for Registered Reports

Psychological assessments play a critical role in our ability to measure and analyze constructs to support theories and experimental hypotheses. Defining and creating assessments to validly and reliability measure constructs is often difficult because phenomenon, such as anxiety, are often not directly observable. Instead, we use surveys and questionnaires to indirectly assess the underlying construct (DeVellis & Thorpe, 2022). Latent variable modeling (i.e., structural equation modeling) is a popular tool for the validation of developed survey instruments to verify scale dimensionality, structure, and model fit. A simple search for scale development reveals thousands of articles in psychology that examine new and previously published work, thus, illustrating the interest in both measurement and the use of validation techniques. Unfortunately, except in specialty journals, much of the validity evidence and/or development for measures used in empirical studies is not reported within the journal article (Barry et al., 2014; Weidman et al., 2017). Without this information, it is difficult to interpret individual study conclusions, as validity information allows for judgment of usefulness of the measured values (Flake & Fried, 2020). Further, the current focus on replication (Makel et al., 2012; Makel & Plucker, 2014; Zwaan et al., 2018), reproducibility (Nelson et al., 2018), and the credibility of our results (Vazire et al., 2022) has demonstrated questionable measurement practices - decisions that researchers make like survey selection and scoring that impact the results of the study (Flake & Fried, 2020). Transparent reporting of the use and creation of scales can improve both interpretation and reproducibility when using surveys developed to measure latent constructs (Shadish et al., 2001).

A secondary concern for developed measures is the potential for differential responding and assessment within target populations. For example, Trent et al. (2013) examined for potential variability in the Revised Child Anxiety and Depression Scale in

54 White and Black youths (Chorpita et al., 2000). They found that the scale mostly

55 functioned the same for both White and Black individuals but differences in averages on

56 individual items could potentially affect the scoring and interpretation of the scale results.

57 This comparison of sub-populations is the test of measurement invariance (Meredith,

58 1993). Invariance or equivalence implies that the scale operates in the same fashion for

59 each sub-group, and thus, differences in the final latent variable scores can interpreted as

60 differences in populations. Non-invariance suggests that individuals respond or interpret

61 items differently, and thus, differences in scores may represent different scores on the latent

62 variable in the population or differences in measurement. Non-invariant measurement may

63 lead to misleading results when making group comparisons, and assessing invariance has

64 become a popular technique in scale development (Van De Schoot et al., 2015).

65   Measurement invariance has been explored and implemented for the last fifty years

66 (Jöreskog, 1971; Sörbom, 1978) and implemented in the most popular structural equation

67 modeling programs (Boker et al., 2011; Jöreskog & Sörbom, 2001; Rosseel, 2012). Byrne et

68 al. (1989) extended the ideas of multi-group testing by suggesting partial invariance

69 (followed by Meredith, 1993). Partial invariance occurs when non-invariance is found but

70 can be attributed to only a few parameter estimate differences between groups (i.e., items 1

71 and 2 have different factor loadings but all others are the same). This testing provided an

72 advantage to understand where the potential non-invariance may occur for further study

73 and interpretation guidelines. As the field pushes back against favoring cutoff criteria and

74 rules of thumb (Marsh et al., 2004; Putnick & Bornstein, 2016), an effect size measure for

75 translating "how much" non-invariance was developed d_{MACS} (Nye & Drasgow, 2011). This

76 effect size examines the differences in observed variables between the two groups for both

77 the factor loading and the item intercept; thus, any differences in either or both will

78 increase the effect size for non-invariance (Stark et al., 2006).

79   With d_{MACS} and measurement invariance testing, researchers can begin to quantify

how and where their construct measurement may vary between groups. Yet, given the large

number of studies that show non-invariance, it is clear that equivalence can be hard to

meet. It is difficult to know if non-invariance occurs because of random sampling error,

true population differences, or differences in replication and reproducibility of the construct

in a new sample. The field of psychology is increasingly interested in pre-registration (i.e.,

registering plans for a study before data collection, Nosek et al., 2018) and the promotion

of transparency in study design, implementation, and analysis (Mayo-Wilson et al., 2021),

in addition to supporting replication studies (Zwaan et al., 2018). Registered (replication)

reports provide an advantageous avenue for the pre-registration of measurement tests, as

they allow a researcher the ability to have their study accepted in principle, regardless of

the results of a test of construct validity, reliability, or measurement invariance (Hobson,

2019; Nosek & Lakens, 2014). However, there are few tools that can provide effect size

measures for models, individual parameters, or visualization for researchers to plan for

future studies. d_{MACS} provides the opportunity to begin to think about the smallest effect

size of interest or the smallest meaningful effect size for measurement invariance and

replication (Anvari & Lakens, 2021; i.e., two studies with overlapping confidence intervals

"replicate," even if the test of measurement invariance does not, Lakens, 2017). As

mentioned, d_{MACS} has only really been explored for a combined intercept and loadings,

and while useful, does not necessarily allow a researcher to pinpoint specific issues within

an observed variable.

Therefore, purpose of this manuscript is describe an R package, `visualizemi`, that

provides functionality to calculate multi-group confirmatory factor analysis, partial

invariance tests, visualizations of the size of non-invariance, and potential effect sizes for

overall models and individual parameters. No known visualization techniques have been

proposed for measurement invariance. By creating panel visualizations, we can supplement

a researchers ability to judge the strength of the non-invariance differences and effect size

for each item. The proposed effect sizes demonstrate the likelihood of replication with a

similar sample as compared to a randomly assigned group model, thus, illustrating what

type of measurement one might expect to find, and how different that is from random

chance. Within this technique, the individual parameter effect sizes can calculated: both

the group differences within a model as compared to random and the likelihood of a

parameter replication compared to random groups. Coupled with other indicators (i.e., fit

indices differences, d_{MACS}), we can move toward a better understanding of how much

measurement non-invariance is meaningful. This tutorial and package will help researchers

plan future studies and aid in the ability to estimate a smallest effect of interest for

measurement invariance studies, rather than relying on fit indices and rules of thumb alone.

By the end of this tutorial manuscript, readers will:

1. Learn how to use *visualizemi* to analyze multi-group confirmatory factor analysis,
   examine partial invariance, and create visualizations of parameters.
2. Learn how to estimate the potential replication of multi-group models and their
   parameters using bootstrapping compared to a random group model.
3. Be able to calculate and interpret effect sizes for model and parameter replication, as
   well as parameter group differences.
4. Understand the impact of measurement variability on replication and generalizability.

The tutorial will start with simulated data based on known effect sizes using d_{MACS}

and demonstrating the package functions for 1) running the multigroup analysis, 2) running

a partial invariance analysis, 3) plotting the partial invariance, 4) estimating replication

and effect sizes at the model level, and 5) estimating replication and effect sizes at the

parameter level. Last, data from Aiena et al. (2014) examining the measurement invariance

of the RS-14 (Wagnild, 2009) will be used to demonstrate the application of the package on

real data. The *visualizemi* package vignette includes an additional tutorial walk through.

¹³¹   **Method**

¹³² **Design and Analysis**

¹³³   Data was simulated using the `simulateData` function in the *R* package *lavaan*

¹³⁴ (Rosseel, 2012) assuming multivariate normality using a μ of 0 and σ of 1 for the data.

¹³⁵ This function allows you to write *lavaan* syntax for your model with estimated values to

¹³⁶ generate data for observed variables (see supplemental for examples). The data included

¹³⁷ two groups of individuals ("Group 1", "Group 2") for a multi-group confirmatory factor

¹³⁸ analysis ($n_{group} = 250$, $N = 500$). The latent variables were assumed to be continuous

¹³⁹ normal (the package functions do not require this assumption). The model consisted of five

¹⁴⁰ observed items predicted by one latent variable (`lv =~ q1 + q2 + q3 + q4 + q5`);

¹⁴¹ however, the demonstration in this manuscript extends to multiple latent variables and

¹⁴² other combinations of observed variables. Each item was assumed to be related to the

¹⁴³ latent variable with loadings approximately equal to .40 to .80, except when cases of

¹⁴⁴ non-invariance on the loadings was simulated.

¹⁴⁵   The Brown (2015) steps of testing measurement invariance are demonstrated in this

¹⁴⁶ manuscript for illustration purposes, but in line with Stark et al. (2006) suggestions, the

¹⁴⁷ visualizations show the impact of loadings and intercepts together. A convenience function

¹⁴⁸ `mgcfa` is used for these steps or other measurement invariance test orders and

¹⁴⁹ combinations. Fit indices for the steps for multi-group models are presented in the

¹⁵⁰ appendix for comparison of cutoff rules of thumb (Cheung & Rensvold, 2002) to effect sizes

¹⁵¹ and visualizations presented in this manuscript. Fit indices include Akaike Information

¹⁵² Criterion (AIC, Akaike, 1998), Bayesian Information Criterion (BIC, Schwarz, 1978),

¹⁵³ Comparative Fit Index (CFI, Bentler, 1990), Tucker Lewis Index (TLI, Tucker & Lewis,

¹⁵⁴ 1973), root mean squared error of approximation RMSEA (Steiger, 1990), and

¹⁵⁵ standardized root mean square residual (SRMR, Bentler, 1995).

¹⁵⁶   The data was then simulated to represent invariance across all model steps, small,

¹⁵⁷ medium, and large invariance using d_{MACS} estimated sizes from Nye et al. (2019). While

¹⁵⁸ d_{MACS} is used primarily for an effect size of the (non)-invariance for intercepts and

¹⁵⁹ loadings together, a similar approach was taken for the estimation of small, medium, and

¹⁶⁰ large effects on the residuals. The effect size is presented for all models, calculated from the

¹⁶¹ *dmacs* package (Dueber, 2023; Nye & Drasgow, 2011). Only one item in each model was

¹⁶² manipulated from the invariant model to create the non-invariant models. Given the data

¹⁶³ was simulated with a *z*-score scaling, the loading values were simulated at .30 points apart

¹⁶⁴ (given d_{MACS} suggestions of .2, .4, .7), the intercepts at .25 points apart, and the residuals

¹⁶⁵ at .25 points apart. To plan a simulation for your own study, these values can be used to

¹⁶⁶ simulate small, medium, and large non-invariance effects by first converting data into

¹⁶⁷ *z*-score.

Package Code Examples

¹⁶⁹   The complete code for this manuscript can be found at https://osf.io/wev5f/. This

¹⁷⁰ tutorial was registered at https://osf.io/vwf4d, and the example provided at the end of the

¹⁷¹ manuscript was added after that registration. The *R* package and replication/effect sizes

¹⁷² was added after the original manuscript submission.

Multi-group CFA Caculation

¹⁷⁴   First, we would create our model code in *lavaan* syntax (Rosseel, 2012). The `lv`

¹⁷⁵ latent variable predicts the five measured variables, which are present as columns in our

¹⁷⁶ `df.invariant` data set. The package does generally require raw data for bootstrapping

¹⁷⁷ purposes, and an example of how to simulate data from models and covariance/correlations

¹⁷⁸ tables sometimes provided in manuscripts (rather than the raw data) is provided in the

¹⁷⁹ supplemental documentation.

¹⁸⁰   *lavaan* automatically sets the mean (i.e., the intercept) for latent variables to zero.

¹⁸¹ If we wish to visualize the impact of the changes in parameter estimates across groups on

¹⁸² the latent means, we need to allow the latent mean estimation with `lv ~ 1`. However,

183 adding this estimation into our model will create a non-identified model. To solve this

184 problem, you can set one of the intercepts of another variable to a value to scale the model.

185 Here we will set the scale of the model by using `q1 ~ 0*1`, thus, scaling the expected

186 means to zero. With simulation, this step is easy to know which variable to pick - we set

187 the intercept on the variable we know did not show differences. In real data, you may wish

188 to run the model steps *without* setting this option, examine the results of a configural or

189 separate models, and then add the option for the values most similar. Additionally, you

190 could complete partial invariance steps to determine which value appears most consistent

191 to fix the estimate.

```
# create lavaan model
model.overall <- "
# overall one-factor model
lv =~ q1 + q2 + q3 + q4 + q5
# set the intercept (mean) of q1 to zero
q1 ~ 0*1
# allow the lv intercept to be freely estimated
lv ~ 1"
# look at the data
head(df.invariant)
```

```
192 ##              q1          q2          q3          q4          q5   group
193 ## 1 -0.8903542 -0.81707530  0.06137292 -1.3236407 -1.7916418 Group 1
194 ## 2  1.1054521 -0.03540948 -0.81299606  1.0028340 -0.1909127 Group 1
195 ## 3  1.4555852  1.54083484  1.59084213 -0.3345967 -0.6865496 Group 1
196 ## 4 -1.8745187 -1.27880245 -2.53565792 -1.0024193 -1.6253249 Group 1
197 ## 5 -0.4449517 -0.17782974  1.05507079 -1.2615705  1.7536428 Group 1
198 ## 6  0.2278813  0.71348845  1.63251893  0.6449847 -1.0055700 Group 1
```

₁₉₉   The `mgcfa` function is designed to flexibly allow you to leverage `lavaan`'s package

₂₀₀ functions to calculate multiple measurement steps at once. You would include:

₂₀₁   1) the model syntax in the `model` argument

₂₀₂   2) the dataframe in the `data` argument of our function

₂₀₃   3) the name of the grouping variable in quotes for `group`

₂₀₄   4) and the equality constraints you would like to impose in order in `group.equal`

₂₀₅   5) ... any other *lavaan* arguments you would like to use such as `meanstructure` or

₂₀₆   `estimator`.

₂₀₇   Note: you can also use `sample.cov`, `sample.mean`, `sample.nobs` in this step for

₂₀₈ estimation of multi-group models, but simulated dataframes are needed for bootstrapping

₂₀₉ replication estimates.

```r
# run our mgcfa function to run all models
results.invariant <-
  # name of the saved model syntax
  mgcfa(model = model.overall,
        # name of the dataframe
        data = df.invariant,
        # name of the grouping variable
        group = "group",
        # equality constraints to impose in order
        group.equal = c("loadings", "intercepts", "residuals"),
        # other options to send to lavaan cfa function
        meanstructure = T)

# what is saved for you
names(results.invariant)
```

```
## [1] "model_coef"          "model_fit"          "model_overall"
## [4] "group_models"         "model_configural"  "invariance_models"
```

The following output is saved:

1) `model_coef`: The parameter estimates for each model with the model step included in a *model* column. This set of coefficients can be used for other functions. This dataframe is created with *broom*'s `tidy()` function if you wish to recreate this table without running the `mgcfa()` function (Robinson et al., 2023).

```
results.invariant$model_coef[1:10 , ]
```

```
## # A tibble: 10 x 13
##      term      op   estimate std.error statistic   p.value  std.lv std.all std.nox
##      <chr>    <chr>   <dbl>     <dbl>     <dbl>     <dbl>    <dbl>   <dbl>   <dbl>
##  1 "lv =~ ~ =~      1         0        NA        NA       0.803   0.616   0.616
##  2 "lv =~ ~ =~      0.655     0.0880    7.44      9.77e-14 0.526   0.493   0.493
##  3 "lv =~ ~ =~      0.640     0.0895    7.15      8.83e-13 0.514   0.463   0.463
##  4 "lv =~ ~ =~      0.277     0.0749    3.69      2.24e- 4 0.222   0.209   0.209
##  5 "lv =~ ~ =~      0.955     0.117     8.13      4.44e-16 0.766   0.656   0.656
##  6 "q1 ~1 " ~1      0         0        NA        NA       0       0       0
##  7 "lv ~1 " ~1     -0.0305    0.0582   -0.524     6.00e- 1 -0.0380 -0.0380 -0.0380
##  8 "q1 ~~ ~ ~~      1.05      0.0995   10.6       0        1.05    0.620   0.620
##  9 "q2 ~~ ~ ~~      0.860     0.0653   13.2       0        0.860   0.757   0.757
## 10 "q3 ~~ ~ ~~      0.966     0.0711   13.6       0        0.966   0.785   0.785
## # i 4 more variables: model <chr>, block <int>, group <int>, label <chr>
```

2) `model_fit`: The model fit indices from `fitmeasures()` to review for overall model fit and invariance judgments. The name of the model is included in a *model* column.

```
head(results.invariant$model_fit)
```

233 ## # A tibble: 6 x 18

234 ##   agfi   AIC   BIC   cfi chisq npar rmsea rmsea.conf.high   srmr   tli

235 ##   <dbl> <dbl> <dbl> <dbl> <dbl> <dbl> <dbl>   <dbl>   <dbl> <dbl>

236 ## 1 0.998 7516. 7580. 1   0.650   15 0   0   0.00616 1.04

237 ## 2 0.948 3766. 3819. 0.976 7.79   15 0.0473   0.108   0.0312 0.953

238 ## 3 0.974 3768. 3820. 1   4.48   15 0   0.0831 0.0210 1.01

239 ## 4 0.961 7533. 7660. 0.991 12.3   30 0.0301   0.0785 0.0261 0.982

240 ## 5 0.965 7528. 7638. 0.994 15.4   26 0.0200   0.0660 0.0330 0.992

241 ## 6 0.969 7522. 7615. 1   17.3   22 0   0.0542 0.0352 1.00

242 ## # i 8 more variables: converged <lgl>, estimator <chr>, ngroups <int>,

243 ## #   missing_method <chr>, nobs <int>, norig <int>, nexcluded <int>, model <chr>

244   3) `model_overall`: A saved *lavaan* fitted model of all groups together without any

245   equality constraints or grouping variables. These objects can be used with any

246   function that normally takes a saved model: `parameterEstimates()`,

247   `modificationIndices()`, `semPlot::semPaths()`, and so on (Epskamp, 2022).

248   4) `group_models`: A list of saved fitted models for each group separately.

249   5) `model_configural`: A saved fitted model for the configural model that nests together

250   each group into one model with no other constraints.

251   6) `invariance_models`: A list of saved fitted models that consecutively adds

252   `group.equal` constraints.

253 **Visualization of Invariance**

254 *Package Function*

255   The results from the `model_coef` table can then be used directly in `plot_mi()`.

256 The plot outputs will be described below. First, here are the arguments for the function:

1) `data_coef`: A tidy dataframe of the parameter estimates from the models. This function assumes you have used `broom::tidy()` on the saved model from *lavaan* and added a column called "model" with the name of the model step (Robinson et al., 2023). This function will only run for models that have used the grouping function (i.e., configural, metric, scalar, and strict or other combinations/steps you wish to examine).

2) `model_step`: Which model do you want to plot? You should match this name to the one you want to extract from your model column in the `data_coef`.

3) `item_name`: Which observed variable from your model syntax do you want to plot? Please list this variable name exactly how it appears in the model.

4) `x_limits`: What do you want the x-axis limits to be for your invariance plot? The default option is to assume the latent variable is standardized, and therefore, -1 to 1 is recommended. Use only two numbers, a lower and upper limit. This value also constrains the latent mean diagram to help zoom in on group differences because the scale of latent means is usually centered over zero. You can use this parameter to zoom out to a more traditional histogram using `c(-2, 2)`.

5) `y_limits`: What do you want the y-axis limits to be for your invariance plot? Given that the latent variable is used to predict the observed values in the data, you could use the minimum and maximum values found in the data. If that range is large, consider reducing this value to be able to visualize the results (i.e., otherwise it may be too zoomed out to judge group differences). Use only two numbers, a lower and upper limit.

6) `conf.level`: What confidence limit do you want to plot? Use $1 - \alpha$.

7) `model_results`: In this argument, include the saved *lavaan* output for the model listed in the `model_step` argument.

8) `lv_name`: Include the name of the latent variable, exactly how it is listed in your *lavaan* syntax. You should plot the latent variable that the `item_name` is linked to. If

284   you have items that load onto multiple latent variables, you will need to make

285   multiple plots.

286 9) `plot_groups`: If you include more than two groups in a multi-group model, the

287   automatic assumption is that you want the first two groups for this visualization. If

288   not, include the names of the groups here to plot.

```r
invariant.plot <-
  plot_mi(
    # output from model_coef
    data_coef = results.invariant$model_coef,
    # which model do you want to plot
    model_step = "Configural",
    # name of observed item
    item_name = "q4",
    # latent variable limits to graph
    x_limits = c(-1,1),
    # Y min and max in data
    y_limits = c(min(df.invariant$q4), max(df.invariant$q4)),
    # what ci do you want
    conf.level = .95,
    # what model results do you want
    model_results = results.invariant$model_configural,
    # which latent variable do you want
    lv_name = "lv"
  )


names(invariant.plot)
```

289 `## [1] "complete"  "intercept" "mean"      "variance"`

290   The outputs from this function are several *ggplot2* objects that can be edited or

291 saved directly using *ggplot2* functionality (Wickham, 2016).

292 1) `complete`: The output from this model can be found in Figure 1. On the left hand

293   side, the item invariance is plotted, and on the right hand side, the latent mean

294   distributions for the two groups are plotted. In the item invariance sub-plot, the

295   visualization includes all three components traditionally seen in MGCFA testing

296   steps: loadings, intercepts, and residuals. Each visualization element was designed to

297   match the traditional visualization for that type of output. All parameter estimates

298   are plotted on the unstandardized estimates and their confidence interval based on

299   the standard error of the estimate. All plots are made with *ggplot2* and *cowplot*

300   (Wilke, 2020).

301 2) `intercept`: Only the left hand side of the complete plot designed to represent

302   intercepts and factor loadings. Factor loadings represent the slope of the regression

303   equation for the latent variable predicting the scores on the observed variable

304   ($\hat{Y} \sim b_0 + b_1 X + \epsilon$). The y-axis indicates the observed variable scores, and here, the

305   plot includes the entire range of the scale of the data for item four. The coefficient

306   (b_1) for group 1 was 0.40, while the coefficient for group 2 was 0.21. The ribbon

307   bands around the plotted slopes indicate the confidence interval for that estimate. In

308   this plot, while the coefficients for each group are not literally equal, the overlapping

309   and parallel slope bands indicate they are not different practically.

310   The item intercepts (b_0) are plotted on the middle line where they would cross the

311 y-axis at a latent variable score of zero. These are represented by a dot with a set of

312 confidence error bars around the point. The intercept for group 1 was 0.07, while the

313 coefficient for group 2 was 0.03. In this invariant depiction, the overlap in the intercepts is

314 clear, indicating they are not different. You can use `y_limits` to zoom in on the graph if

315 these are too small to be distinguishable.

316   3) `mean`: The right hand side of the complete plot graphing the latent variable means

317   and density from the data. The latent variable is shown on the x-axis using

318   standardized values (i.e., *z*-scores) where -1 indicates one standard deviation below

319   the mean for the latent variable, 0 indicates the mean for the latent variable and so

320   on. The lines indicate the means of the latent variables from the simulated dataset.

321   Group labels are represented in the figure caption on the bottom. Group 1 is usually

322   the group that is alphabetically first in the data set or whichever group is the first

323   that appears when using the `levels()` command.

324   4) `variance`: A split geom violin plot indicating the variance distribution of the plotted

325   item. Residuals are trickier to plot, as they are the left over error when predicting the

326   observed variables ϵ. It is tempting to plot this value as the confidence band around

327   the slope, however, that defeats the purpose of understanding that the slopes are

328   estimated separately from the residuals, and both have an associated variability

329   around their parameter estimate. Therefore, residuals are represented in the inset

330   picture at the bottom right of the item invariance plot. The black bars represent the

331   estimated residual for each group (group 1: 0.91, group 2: 1.22). The distributions

332   are plotted to represent the normal spread of values using the standard error of the

333   residuals. The violin plot allows for direct comparison of those residuals and their

334   potential distributions. Note that the placement has nothing to do with the x or

335   y-axis and is designed to always show in the same location, regardless of size/value.

336   The plots are included separately so they can be arranged in a different fashion if

337   desired.

Simulated Results

339   The d_{MACS} value for item 4 in the invariant model was 0.16, representing a nil or

340   unimportant difference in this manuscript. It is important to note that while Nye et al.

341   (2019) suggests specific sizes for small, medium, and large, each researcher should

₃₄₂ determine for themselves what effects represent. Figure 2 displays the results from the

₃₄₃ small ($d_{MACS} = 0.27$) difference in loadings, while Figure 3 displays the results from the

₃₄₄ medium ($d_{MACS} = 0.53$) difference in loadings, and Figure 4 shows the large ($d_{MACS} = $

₃₄₅ 0.68) differences. When investigating the slope values, we can clearly see the change in the

₃₄₆ loading for the second group (the only manipulated variable, although random data set

₃₄₇ generation may also change intercepts and residuals slightly). At the medium effect size, we

₃₄₈ see that the confidence bands do not overlap (at the edges), and at the large effect size, we

₃₄₉ can see a clear separation of two lines. Note that the intercepts in this model are estimated

₃₅₀ as equal so the loading representation will not literally separate, but the steepness of the

₃₅₁ lines is the indicator of the difference between the slopes. You can imagine these lines are

₃₅₂ interpreted like a simple slopes analysis for interactions in regression (Cohen et al., 2003).

₃₅₃ When simple slopes for interactions are plotted, if they are parallel, there is no interaction,

₃₅₄ and if they cross, then there is an interaction. Here, we can use this same logic. If they are

₃₅₅ parallel, there is likely invariance (they are the same), and the further from parallel they

₃₅₆ become, the larger the effect size for the differences between group loadings.

₃₅₇   The latent means in Figure 4 do appear to show differences, albeit visually small.

₃₅₈ The latent means diagram shows the impact of any group differences that aren't

₃₅₉ constrained, and this image shows the configural model (as the metric model would force

₃₆₀ them to be equal). In the simulated model, the *only* manipulated parameter is question 4's

₃₆₁ loading. In real models, the differences may be larger due to other variation found in the

₃₆₂ parameter estimates. Therefore, once you discover items you believe would make a model

₃₆₃ "partially" invariant, you may wish to estimate that model and graph the item again using

₃₆₄ the partially invariant model to see only the effect of the non-invariant items. Additionally,

₃₆₅ consider that we set the scaling of the model to 0. The estimate for the lv mean in the

₃₆₆ large loading model was group 1: 0.00, and group 2: -0.06, which results in 0.06 difference

₃₆₇ in group means. The practical implications of this difference will depend on the research

₃₆₈ and interpretations of the researcher.

369   For intercepts, the small (Figure 5), medium (Figure 6), and large (Figure 7)

370 depictions represent d_{MACS} values of 0.26, 0.47, and 0.70, respectively. Intercept differences

371 can be clearly seen represented by the spacing out of the intercept locations (and thus, the

372 overall line as well). While the changes in intercept do not appear to change the latent

373 means, the caveat to this simulation is that only item four was manipulated. An example is

374 provided below that demonstrates large changes in latent means.

375   Last, the effect of the residuals is plotted in small (Figure 8), medium (Figure 9),

376 and large (Figure 10) formats. While d_{MACS} values are not technically available for the

377 residuals, our models showed 0.19, 0.19, and 0.16, respectively. These differences in values

378 are variable due to the random generation of data sets for each measurement invariance

379 manipulation. At first glance, the differences in the small chart may seem large, because

380 the black lines are not touching, but notice that the distributions overlap, indicating a

381 likely small difference. The medium and large differences better illustrate differences in

382 residuals across groups. Further, the impact of the residuals on the shape of the latent

383 mean distribution can also been seen (and unintentionally, in the first figures as well due to

384 random variation). The impact is due to the standard error of the residuals, as smaller

385 standard errors represent lepokurtic distributions (taller), and larger standard errors

386 represent platykurtic distributions (flatter). The effect size difference of the residuals does

387 not appear to change the effects in the latent means.

388 **Partial Invariance Calculation**

389 *Package Function*

390   The results of the simulated models are presented in the appendix, demonstrating

391 that each simulated dataset shows partial invariance if item four is allowed to vary between

392 groups. The function takes the following arguments:

393 1) `saved_model`: The saved *lavaan* model with the equality constraints at the level of

394   measurement invariance you would like to examine for partial invariance.

395   2) `data`: The dataframe where the model was estimated.

396   3) `model`: The model syntax for the overall model.

397   4) `group`: The grouping variable column in the dataframe.

398   5) `group.equal`: The equality constraints including in your original multi-group tests.

399   6) `partial_step`: The level of partial invariance you wish to test.

```r
partial.invariant <-
  partial_mi(
    # saved model output with constraints
    saved_model = results.invariant$invariance_models$model.residuals,
    # dataframe from model
    data = df.invariant,
    # model syntax
    model = model.overall,
    # group column name
    group = "group",
    # group equality constraints from your mgcfa
    group.equal = c("loadings", "intercepts", "residuals"),
    # which step you want to examine for partial invariance
    partial_step = "residuals"
    )

names(partial.invariant)
```

400   `## [1] "models"    "fit_table"`

401   In this function, each parameter with the appropriate *lavaan* syntax is relaxed
402   individually (i.e., `~1` for intercepts, `~~` for residuals, etc.). The fitted models are saved in
403   the `models` output, and the `fit_table` output includes all fit indices for each model to
404   investigate potential areas of partial invariance based on the researcher's desired criterion.

Note: the `partial_step` function is used to determine which types of `op` or operators to freely estimate between groups. If one chooses residuals, you will also freely estimate the residual for the latent variable or any other residuals found in the model. These items may be ignored if they were not meant to be included.

```
head(partial.invariant$fit_table %>%

      dplyr::select(free.parameter, cfi, rmsea))
```

```
## # A tibble: 6 x 3
##    free.parameter cfi        rmsea
##    <chr>          <lvn.vctr> <lvn.vctr>
## 1 q1 ~~ q1        0.9902679  0.02108648
## 2 q2 ~~ q2        0.9868905  0.02447336
## 3 q3 ~~ q3        0.9958241  0.01381266
## 4 q4 ~~ q4        1.0000000  0.00000000
## 5 q5 ~~ q5        0.9868088  0.02454944
## 6 lv ~~ lv        0.9906154  0.02025143
```

Replication and Effect Size: Model

Package Function

The `bootstrap_model` function in *visualizemi* was designed to estimate the likely replication of overall model invariance with the assumption that the data used for the estimation represents the larger population. The following arguments are used:

1) `saved_configural`: a saved fitted model at the configural level with no equality constraints. This model should include all other lavaan settings you would like to use, such as estimator or ordered.

2) `data`: The dataframe where the model was estimated.

3) `model`: The model syntax for the overall model.

428   4) `group`: The grouping variable column in the dataframe.

429   5) `nboot`: The number of bootstraps to run.

430   6) `invariance_index`: The fit index you would like to use to determine invariance.

431   Please use options and labeling from *lavaan* - see `fitmeasures()` for options.

432   7) `invariance_rule`: The invariance difference score you would like to use as your rule.

433   8) `group.equal`: The equality constraints including in your original multi-group tests.

```r
boot.model.invariant <-

  bootstrap_model(

    # saved configural model

    saved_configural = results.invariant$model_configural,

    # dataframe

    data = df.invariant,

    # model syntax

    model = model.overall,

    # group variable column in dataframe

    group = "group",

    # number of bootstraps

    nboot = 1000,

    # which fit index you would like to use

    invariance_index = "cfi",

    # what is your criterion for that fit index

    invariance_rule = .01,

    # what equality constraints are you testing

    group.equal = c("loadings", "intercepts", "residuals")
  )
```

434   The data included in this function will be sampled, with replacement, at the same

435   size as the current dataset, and the included invariance equality constraints are estimated.

436 Each step will be compared to the previous step using the invariance index and comparison

437 rule entered. The output is a dataframe of the proportion of non-invariant bootstraps from

438 the real data and the same bootstrapped dataset with the group labels randomly assigned.

439 The effect size comparison of proportions, h, for non-invariant comparisons:

$$h_{nmi} = 2 \times (asin\sqrt{p_{data}} - asin\sqrt{p_{random}})$$

440 The alternative, h_{mi}, for effect size of measurement invariance replication would

441 simply be the inverse sign of h_{nmi} and is also included in the table. Two additional columns

442 h_{nmi_p} and h_{nmi_p} represent the h values divided by the upper bound of h (i.e., π), to help

443 with interpretation of the effect size (thus, bounding h to -1 to 1).

444 ### *Simulated Results*

445 Figure 11 portrays the h_{nmi_p} values by simulated non-invariance, strength of

446 non-invariance, and type of equality constraint. This image represents 100 simulations of

447 data by 1000 bootstrapped runs (averaged) to explore the expected pattern of results. The

448 bars are arranged to show what a researcher might inspect when thinking about replication

449 possibilities and their effect sizes (i.e., only three bars for each equality constraint would be

450 calculated).

451 In the data that was simulated to be invariant between groups, effect sizes are still

452 non-zero (loadings $h_{nmi_p} = 0.28$, intercepts $= h_{nmi_p} = 0.06$, $h_{nmi_p} = 0.00$). This result

453 mirrors the effects found in the literature - that often, many models fail to show invariance,

454 and potentially not because measurement is poor but because of natural random variation

455 in parameter estimates. This result also indicates the need to be able to identify if specific

456 parameters are driving the differences, which is shown in the next section.

457 Next, Figure 11 demonstrates the patterns one might find for small, medium, and

458 large effects at each type of invariance when data is simulated with *one* difference. For

⁴⁵⁹ loadings, the pattern shows a larger effect for loadings with zero or negative effect sizes for

⁴⁶⁰ other effect sizes. The intercept simulations show non-zero effect sizes in the loadings and

⁴⁶¹ intercepts, likely for the same reasons d_{MACS} is interpreted as a combined effect size. When

⁴⁶² intercepts are changed, loadings may naturally shift with those means. Last, the residual

⁴⁶³ results present an unexpected pattern, wherein the effect is primarily seen in the loadings,

⁴⁶⁴ rather than the residuals step. However, when distributions of error variance are different,

⁴⁶⁵ one may expect that those effects are pushed toward the loadings as well (as values can vary

⁴⁶⁶ more, thus potentially weakening the relationship between observed and latent variable).

⁴⁶⁷ An example of interpretation on real data is given in a later section. From a

⁴⁶⁸ research study, only one effect size for each equality constraint would be calculated. The

⁴⁶⁹ interpretation will often be up to the researcher's smallest effect of interest, and this

⁴⁷⁰ simulation gives some guidance that the values should not be interpreted with traditional

⁴⁷¹ rules of thumb. The pattern of effects is potentially the most useful information: 1) positive

⁴⁷² effects on the loadings with negative or very close to zero effects on the other parameters

⁴⁷³ may indicate a non-replication in loadings, 2) equal effects on loadings and intercepts with

⁴⁷⁴ smaller or negative effects may indicate intercepts may be an issue, and 3) residuals may be

⁴⁷⁵ determined by the same pattern as loadings but with a smaller ratio of loadings to

⁴⁷⁶ residuals effect (i.e., loadings h_{nmi} / residuals h_{nmi}. The "size" could be determined by the

⁴⁷⁷ ratio of effect sizes for each constraint. Of course, this represents one simulation study, and

⁴⁷⁸ results from many studies in a meta-analysis would be fruitful for future work.

⁴⁷⁹ **Replication and Effect Size: Parameters**

⁴⁸⁰ *Package Function*

⁴⁸¹ After examining the overall model potential replication effect size, the individual

⁴⁸² parameters within a model can be bootstrapped for partial invariance to with that

⁴⁸³ parameter relaxed (overall partial model statistics) and the difference in group parameter

⁴⁸⁴ estimates (parameter effect size). This function uses arguments seen in other functions, so

485 they will not be repeated here. The general setup consists of using the model you think

486 could be partially invariant in the `saved_model` argument and the fit index for comparison

487 for the model with less constraints in `invariance_compare`. This example examines the

488 loadings in the invariant model, so `saved_model` uses the `mgcfa` output for equality

489 constraints present on the loadings and compares that model to the configural model with

490 no equality constraints on the loadings. The `partial_step` argument will be used to

491 determine which operation syntax (i.e. `=~` for loadings) to relax for modeling.

```r
boot.partial.invariant <-

    bootstrap_partial(

        # saved model you want to examine the partial loadings for

        saved_model = results.invariant$invariance_models$model.loadings,

        # the dataset

        data = df.invariant,

        # the model

        model = model.overall,

        # the group variable in the dataset

        group = "group",

        # number of bootstraps

        nboot = 1000,

        # which fit index you would like to use to determine partial invariance

        invariance_index = "cfi",

        # what is the invariance rule

        invariance_rule = .01,

        # what are we comparing the saved model fit index to

        invariance_compare = fitmeasures(results.invariant$model_configural, "cfi"),

        # what step are we using for invariance

        partial_step = "loadings",

        # what equality constraints should be imposed
```

```
        group.equal = c("loadings")
    )
```

```
names(boot.partial.invariant)
```

```
## [1] "invariance_plot"       "effect_invariance_plot" "density_plot"
## [4] "boot_DF"               "boot_summary"           "boot_effects"
```

The saved output includes several dataframes and plots. The first is the `boot_DF` which the summary of each run in a dataframe for plotting or summarization. This dataframe includes the estimate for each paramter (`term`) separated by group and type (`boot_1`, `boot_2` are the bootstrapped estimates for group 1 and group 2, while the same `random` columns indicate the randomly assigned groups). The fit index used to determine invariance is included for bootstrapped and random estimates, and then the differences between groups and if they were "invariant" or not given the researcher supplied rule.

```
head(boot.partial.invariant$boot_DF)
```

```
##          term    boot_1     boot_2   random_1  random_2   boot_fit random_fit
## 1 lv =~ q1 0.4548783 0.49928877 0.4627486 0.4651391 0.9296990  1.0000000
## 2 lv =~ q2 0.3599017 0.56241016 0.4100874 0.4980215 0.9441125  1.0000000
## 3 lv =~ q3 0.4254283 0.33640233 0.4274329 0.3422124 0.9377130  1.0000000
## 4 lv =~ q4 0.3930716 0.03320619 0.1380833 0.2628802 0.9750274  1.0000000
## 5 lv =~ q5 0.7306414 0.73512673 0.7093891 0.7532471 0.9266587  1.0000000
## 6 lv =~ q1 0.5537083 0.57086815 0.5732166 0.5475714 0.8958929  0.9814658
##   boot_difference random_difference boot_index_difference
## 1     -0.044410454      -0.002390463                  FALSE
## 2     -0.202508484      -0.087934027                  FALSE
## 3      0.089025927       0.085220565                  FALSE
## 4      0.359865463      -0.124796846                  FALSE
```

```
## 5    -0.004485377      -0.043857947                      FALSE

## 6    -0.017159815       0.025645271                      FALSE

##   random_index_difference

## 1                    TRUE

## 2                    TRUE

## 3                    TRUE

## 4                    TRUE

## 5                    TRUE

## 6                    TRUE
```

Next, the `boot_summary` includes a summarized form of the bootstrapped results from separated by bootstrapping versus random and invariant/non-invariant. The d_s for between groups Cohen's d is shown below, and the non-central confidence interval is included. Effect sizes are only calculated when the number of bootstrapped estimates is at least 10% of the data - therefore, you would not receive effect sizes with almost no bootstrapped runs. This dataframe should be used to determine which parameter may be different and at what size between groups in a replication of the study.

```r
boot.partial.invariant$boot_summary %>%
  dplyr::select(term, d_boot, d_random)
```

```
## # A tibble: 10 x 4

## # Groups:   term, invariant [10]

##    invariant term      d_boot d_random

##    <lgl>     <chr>      <dbl>    <dbl>

## 1 FALSE     lv =~ q1 -0.0299   0.0583

## 2 TRUE      lv =~ q1  0.0337   0.0116

## 3 FALSE     lv =~ q2 -0.0326   0.0933

## 4 TRUE      lv =~ q2  0.146    0.0309
```

```
## 5 FALSE      lv =~ q3 -0.0463    0.113

## 6 TRUE       lv =~ q3 -0.148     0.0743

## 7 FALSE      lv =~ q4  0.00785 -0.0668

## 8 TRUE       lv =~ q4 -0.0157    0.0389

## 9 FALSE      lv =~ q5 -0.00129 -0.169

## 10 TRUE      lv =~ q5  0.122    -0.00853
```

The `boot_effects` table creates a summary similar to the overall model replication table based on the proportion of runs that were considered invariant versus not for each parameter. Note that the effects match the overall results, such that simulated invariant data appears to still show the likelihood that loadings may not replicate in a similar dataset.

```
boot.partial.invariant$boot_effects
```

```
## # A tibble: 5 x 7

##    term     non_invariant random_non_invariant h_nmi  h_mi h_nmi_p h_mi_p

##    <chr>         <dbl>           <dbl>          <dbl> <dbl> <dbl>   <dbl>  <dbl>

## 1 lv =~ q1      0.853          0.236           1.34 -1.34  0.427 -0.427

## 2 lv =~ q2      0.858          0.237           1.35 -1.35  0.430 -0.430

## 3 lv =~ q3      0.851          0.23            1.35 -1.35  0.429 -0.429

## 4 lv =~ q4      0.84           0.229           1.32 -1.32  0.420 -0.420

## 5 lv =~ q5      0.819          0.237           1.25 -1.25  0.397 -0.397
```

Plots of the results from dataframes can be found within the `bootstrap_partial()` function. Figure 12 shows the difference between parameters for groups in the bootstrapped and randomly assigned group runs. Figure 13 shows the density plot of the estimates for each group organized by bootstrapped and randomly assigned groups and the invariance decision for each bootstrapped run. Last, Figure 14 indicates the d_s value

561 between groups with an indication of the number of data points in each estimate (i.e., dot

562 size). These visualizations should allow a researcher to understand the likelihood of

563 replication for each parameter, as well as the potential size of the differences. Therefore,

564 one could indicate a specific smallest effect size of interest, rather than a invariance cut-off

565 rule of thumb when planning a replication or registered report.

Simulated Results

567   Figure 15 shows the effect size differences within large loadings simulations. The

568 results demonstrate that most of the loadings were considered non-invariant in the

569 bootstrapped models (while holdings all others equal). This result is partially due to

570 simulating very good data, so small changes in loadings results in a drop in fit for our

571 chosen invariance index. However, we can use this graph to show that question four shows

572 a possible effect size ranging from -0.07 to 0.13. The h_{nmi_p} value for question four was 0.27,

573 representing about a quarter of a possible total effect. Last, the density plot in Figure 16

574 shows the separation of the two different groups loadings in item four, thus, illustrating

575 group differences in the findings for their loadings. Each of the other combination of plots

576 can be found in the supplemental materials.

An Example Analysis

578   Aiena et al. (2014) examined the RS-14 (Wagnild, 2009) exploring the factor

579 structure of the Resiliency Scale in a clinical sample receiving treatment services and a

580 college student sample. Measurement invariance was calculated for differences separately

581 for these samples for gender and race finding a partially invariant models with a few item

582 intercepts or residuals that differed between groups. Aiena et al. (2014) did not compare

583 the clinical to the student sample for measurement invariance, and it is reasonable to

584 expect potential differences in these two populations. This example will demonstrate the

585 procedure for researchers who wish to use partial invariance steps and how to interpret

586 real, messy data.

```r
# load the data, it is called DF

load("manu_data/RS14.Rdata")


# build the one-factor model

model.rs <- "RS =~ RS1+RS2+RS3+RS4+RS5+RS6+RS7+RS8+RS9+RS10+RS11+RS12+RS13+RS14"
# run the multi-group CFA

results.rs <- mgcfa(

  model = model.rs,

  data = DF,

  group = "sample",

  group.equal = c("loadings", "intercepts", "residuals")

  )

# how to get results in table

results.rs$model_fit %>%

        dplyr::select(model, AIC, BIC, cfi, tli, rmsea, srmr)
```

⁵⁸⁷   Table 1 indicates the results after running the one-factor model. There are several

⁵⁸⁸ guidelines for assessing assessing a degradation in model fit (Cao & Liang, 2022; Cheung &

⁵⁸⁹ Rensvold, 2002; Counsell et al., 2020; Jin, 2020; Putnick & Bornstein, 2016) but for the

⁵⁹⁰ purposes of this illustration ΔCFI > .01 will be used. Table 1 indicates that fit was

⁵⁹¹ degraded when the constraint on equal item intercepts was added. The code below

⁵⁹² provides an example of testing each item individually by relaxing the constraints and

⁵⁹³ recalculating the CFI. If these Items bring the CFI value back up to ΔCFI <= .01 from

⁵⁹⁴ the metric model, then the model would be considering partially invariant at the scalar

⁵⁹⁵ level. It seems unlikely that the residuals will show invariance, if partial scalar invariance

⁵⁹⁶ can be found, as the drop in fit is quite large.

```r
partial.rs <-
  partial_mi(
    saved_model = results.rs$invariance_models$model.intercepts,
    data = DF,
    model = model.rs,
    group = "sample",
    # be sure to do only up to the step you are interested in
    group.equal = c("loadings", "intercepts"),
    partial_step = "intercepts")


partial.rs$fit_table %>%
  dplyr::select(free.parameter, cfi)
```

```
## # A tibble: 15 x 2
##     free.parameter cfi
##     <chr>           <lvn.vctr>
##  1 "RS1 ~1 "        0.9116914
##  2 "RS2 ~1 "        0.9129976
##  3 "RS3 ~1 "        0.9117235
##  4 "RS4 ~1 "        0.9111212
##  5 "RS5 ~1 "        0.9126742
##  6 "RS6 ~1 "        0.9133618
##  7 "RS7 ~1 "        0.9139287
##  8 "RS8 ~1 "        0.9111397
##  9 "RS9 ~1 "        0.9119702
## 10 "RS10 ~1 "       0.9118309
## 11 "RS11 ~1 "       0.9110574
## 12 "RS12 ~1 "       0.9112309
```

```
## 13 "RS13 ~1 "       0.9112367

## 14 "RS14 ~1 "       0.9112015

## 15 "RS ~1 "         0.9108805
```

The output indicates that RS6 and RS7 are potential items that could be relaxed to improve model fit and create a partial scalar invariant model (i.e., by picking the largest CFI values). The code below show to check the addition of these items, which are added one at a time. You use the `group.partial` open to "relax" or freely estimate that parameter for each group separately.

```r
# run the partially invariant model with group.partial
partial.rs.1 <- mgcfa(model = model.rs,

                  data = DF,

                  group = "sample",

                  group.equal = c("loadings", "intercepts"),

                  group.partial = c("RS7~1"),

                  meanstructure = TRUE)


# examine the loadings
partial.rs.1$model_coef %>%

  filter(term == "RS7 ~1 ") %>%

  filter(model == "intercepts") %>%

  dplyr::select(term, group, estimate, std.error)
```

```
## # A tibble: 2 x 4

##    term      group estimate std.error

##    <chr>     <int>   <dbl>     <dbl>

## 1 "RS7 ~1 "     1    4.95    0.0580

## 2 "RS7 ~1 "     2    4.49    0.0529
```

```r
# examine the fit indices
partial.rs.1$model_fit %>%
  filter(model == "intercepts") %>%
  dplyr::select(AIC, BIC, cfi, tli, rmsea, srmr)
```

```
## # A tibble: 1 x 6
##       AIC     BIC   cfi   tli rmsea   srmr
##     <dbl>   <dbl> <dbl> <dbl> <dbl>  <dbl>
## 1 122454. 122804. 0.914 0.912 0.102 0.0502
```

```r
# effect size model
lavaan_dmacs(partial.rs.1$invariance_models$model.intercepts, "Clinical")$DMACS[7]
```

```
##       RS7
## 0.282302
```

By examining our estimates, we can see that item seven on the RS-14 is estimated at nearly 5 points for the clinical sample, while the student sample has a lower mean around 4.5 points. Generally, students show higher means on the items of the RS-14, but when all loadings and other intercepts are constrained to be equal, and this one item is relaxed, this pattern flips so that clinical groups show higher item intercepts. Given the scale is a 1-7 Likert type scale, .5 a point represents a potentially sizable change on the scale. Item seven covers perseverance after hardship, and all items can be found in the user manual for the scale at www.resiliencecenter.com. The effect size from d_{MACS} suggests a small to medium effect, 0.28. In this next code section, we repeat this process for the RS6, as the CFI for our model with only RS7 does not achieve the levels of partial invariance for our ΔCFI criterion (i.e., $<=$ .01 downward change in fit: metric CFI = .925, partial scalar CFI = .914). See Figure 17 for the difference between item intercepts and latent means.

```r
# add the second intercept

partial.rs.2 <- mgcfa(model = model.rs,

                      data = DF,

                      group = "sample",

                      group.equal = c("loadings", "intercepts"),

                      group.partial = c("RS7~1", "RS6~1"),

                      meanstructure = TRUE)


# examine the loadings

partial.rs.2$model_coef %>%

  filter(term == "RS6 ~1") %>%

  filter(model == "intercepts") %>%

  dplyr::select(term, group, estimate, std.error)
```

643 ## # A tibble: 0 x 4

644 ## # i 4 variables: term <chr>, group <int>, estimate <dbl>, std.error <dbl>

```r
# examine the fit indices

partial.rs.2$model_fit %>%

  filter(model == "intercepts") %>%

  dplyr::select(AIC, BIC, cfi, tli, rmsea, srmr)
```

645 ## # A tibble: 1 x 6

646 ##   AIC   BIC   cfi   tli rmsea   srmr

647 ##   <dbl>   <dbl> <dbl> <dbl> <dbl>   <dbl>

648 ## 1 122363. 122719. 0.917 0.915 0.100 0.0488

```r
# effect size model

lavaan_dmacs(partial.rs.2$invariance_models$model.intercepts, "Clinical")$DMACS[6]
```

649 ##   RS6

```
## 0.2796334
```

Again, we see about a half-point difference between our clinical and student samples for item 6, which is about drive to achieve. The CFI for this model does meet the requirements for partial invariance, .917. The effect size is approximately the same at $d_{MACS} = 0.28$. See Figure 18 shows the difference between item intercepts and latent means.

```r
# plot the image for RS7
plot_mi(
  data_coef = partial.rs.2$model_coef,
  model_step = "intercepts",
  item_name = "RS7",
  x_limits = c(-1,1),
  y_limits = c(min(DF$RS7), max(DF$RS7)),
  conf.level = .95,
  model_results = partial.rs.2$invariance_models$model.intercepts,
  # which latent variable do you want
  lv_name = "RS"
)$complete
```

```r
# plot the image for RS6
plot_mi(
  data_coef = partial.rs.2$model_coef,
  model_step = "intercepts",
  item_name = "RS6",
  x_limits = c(-1,1),
  y_limits = c(min(DF$RS6), max(DF$RS6)),
  conf.level = .95,
```

```
    model_results = partial.rs.2$invariance_models$model.intercepts,

    # which latent variable do you want

    lv_name = "RS"

)$complete
```

656   Next, we would examine our replication potential for this model. Given our current

657 results, we may not expect our intercepts to replicate. Given the order of `group.equal`,

658 the boot function will select the first non-invariant step in the calculation of the effect size

659 for potential replication. In our output, we do not see a loadings effect size, and this result

660 occurs when *none* of the bootstrapped or random results are non-invariant. Therefore, we

661 would expect the loadings to replicate (and the effect size would be 0 difference between

662 bootstrapped and random, both showing invariance). The intercepts show a large (i.e.,

663 close to the max possible value) non-invariant effect, and therefore, we should not expect

664 this model to show invariance in a replication.

```
boot.model.rs <-
  bootstrap_model(
    saved_configural = results.rs$model_configural,
    data = DF,
    model = model.rs,
    group = "sample",
    nboot = 1000,
    invariance_index = "cfi",
    invariance_rule = .01,
    group.equal = c("loadings", "intercepts", "residuals")
  )
```

```
boot.model.rs
```

```
## # A tibble: 2 x 7
##    model          non_invariant random_non_invariant  h_nmi    h_mi h_nmi_p  h_mi_p
##    <chr>                  <dbl>                <dbl>  <dbl>   <dbl>   <dbl>   <dbl>
## 1 intercepts             0.998                    0   3.05   -3.05   0.972  -0.972
## 2 residuals              0.002                    0 0.0895 -0.0895  0.0285 -0.0285
```

Next, we would examine the strength of the effects of replication on each parameter at the intercept level. By examining Table 2, it is clear that most of the item means are unlikely to replicate, even though two particular items can be used to create partial invariance. Figures 19 and 20 display the three plots provided in the `bootstrap_partial()` function. In general, we should expect $M_D = 0.23$ when items are invariant and $M_D = 0.26$ when items are not invariant. The effect size of non-invariant items ranges from 0.43 to 0.62.

The density plot shown at the bottom of Figure 19 illustrates the likely reasons for the differences found in the top plots. It appears that many items show a bimodal distribution within group 1 (Clinical Sample) and when items are invariant, the intercept averages to the same intercept as group 2 (Student Sample). In non-invariant estimates, the same bimodal distributions are found, but they are more extreme than the student samples, and therefore, item show different averages due to the presence of two separate means of data. Further, some items also appear to show two separate student item averages within the data. This result suggests that it would be fruitful to understand a potential predictor of these differences or other confounding variable that separates these samples, creating differences in item averages.

In summary, if one were planning a replication, the prediction would be that item intercepts would likely not replicate, with a large effect size (i.e., it is easy to judge h_{nmi_p}

close to the max of one as large). While this study found partial invariance by relaxing constraints on two individual items, bootstrapped partial invariance indicates that any item could potentially be problematic with an effect size averaging $d \sim 0.50$ difference in means. While d_{MACS} values represented a "small" effect based on previous publications, this effect may be muted by examining both loadings and intercepts. The results here suggest that the effect is driven by intercepts. The overall average score on items is high: $M_M = 5.04$ (M_{SD} = 1.72). Given the mean standard deviation, a $d \sim 0.50$ represents 0.86 or nearly one whole point on the scale. A researcher could decide that at least $d = 0.33$ or at least a third of a standard deviation would be an important change and set that as their smallest effect size of interest for invariance. Further, a newly planned study should investigate what variables may predict when and why samples separate into bimodal representations for item means.

```r
boot.partial.rs <-

  bootstrap_partial(

    saved_model = results.rs$invariance_models$model.intercepts,

    data = DF,

    model = model.rs,

    group = "sample",

    nboot = 1000,

    invariance_index = "cfi",

    invariance_rule = .01,

    invariance_compare = fitmeasures(results.rs$invariance_models$model.loadings, "cfi")

    partial_step = "intercepts",

    group.equal = c("loadings", "intercepts")

)
```

An Example Extension

One benefit of the open science movement on scale development is the publication of datasets or covariance tables with published articles. We can extend our examination of

703 potential replication on other variables that may effect assessment of underlying

704 phenomena. For example, scale translation across languages is not only impacted by the

705 literal conversion of concepts from one language to another, but also the cultural and

706 societal norms of the target population (Cha et al., 2007; Chang et al., 1999; Yu et al.,

707 2004). The RS14 was tested in Chinese speaking samples in Chen et al. (2020) across five

708 different large samples and determined that the scale showed good psychometric properties

709 for use within Chinese speaking samples as a one-factor model of resiliency. Given these

710 results, another researcher may assume that the models would be comparable between

711 English speaking (i.e., likely United States) and Chinese speaking samples. With the

712 published data, we can use `visualizemi` to determine if the RS14 is invariant across

713 language/culture, and if the results would likely replicate if tested on a new set of samples,

714 and what, if any, effect size differences are found in parameters. The code used for this

715 analysis is presented in Appendix 7.

716   The Aiena et al. (2014) data used in our previous example was first filtered to only

717 college students, as we have already noted that clinical samples show slightly different

718 intercepts for at least two of the items from student samples. The Chen et al. (2020) data

719 also included college students, which allows us to test a comparable sample that varies on

720 translation and culture. The test of measurement invariance indicated that the factor

721 structure and loadings were invariant across groups. Much like our test of clinical versus

722 student samples, the results indicated that the intercepts were not consistent across groups.

723 Within the English clinical/student sample, partial invariance could be achieved by

724 relaxing two item intercept constraints (item 6 and 7). To achieve "partial" invariance

725 between the Chinese and English speaking samples, we would need to relax more than half

726 of the items (specifically, eight items: 1, 2, 3, 4, 10, 11, 12, 14), and it would be difficult to

727 suggest partial invariance given this finding. d_{MACS} values range from 0.26 to 0.32 for the

728 eight items which could be interpreted a small to medium given Nye et al. (2019)'s

729 simulation study. Figure 21 portrays the results from the second item on the RS14 (*life*

₇₃₀ *accomplishments*).

₇₃₁   The results of model bootstrapping indicated that the effect of the loadings was

₇₃₂ likely to replicate (only invariant results were found), but the intercepts were never found

₇₃₃ to be invariant compared to a randomized sample ($h_{nmi_p} = 1$). Therefore, we would expect

₇₃₄ that these differences are persistent, either due to the adaptation or cultural differences in

₇₃₅ resiliency across samples. The bootstrapped partial invariance demonstrates that each item

₇₃₆ intercept has a medium to large difference between the two samples as shown in Figure 22,

₇₃₇ which may explain why full or partial invariance cannot be achieved. This result does not

₇₃₈ invalidate either version of the scale, but informs researchers of potential baseline

₇₃₉ differences in item responding for the two samples. Therefore, careful interpretation should

₇₄₀ be made when comparing these two samples in other instances, as differences in latent

₇₄₁ means may be the default finding, but with these results one may determine if their results

₇₄₂ are different from expectations of general scale responding.

₇₄₃   **Discussion**

₇₄₄   In this tutorial, we examined how to use multiple tools to examine measurement

₇₄₅ invariance and its potential replication. Model fit comparisons and statistics can be paired

₇₄₆ with the proposed effect size measures, and a visualization to examine individual items and

₇₄₇ the overall latent mean scores. The impact of potential replication was estimated on the

₇₄₈ overall model and the individual parameters. Using real data, the effect of two

₇₄₉ non-invariant item intercepts was examined and visualized. This tutorial manuscript has

₇₅₀ provided a concrete way to plan for pre-registration and/or registered reports. Researchers

₇₅₁ could simulate results based on published or previously collected data to determine the

₇₅₂ likelihood and size of potential replication. They could plan and pre-register a smallest

₇₅₃ effect of interest. For example, we may determine that an h_{nmi_p} value above .20 represents

₇₅₄ an important level of non-invariance for our model overall, while $h_{nmi_p} > .30$ for any

₇₅₅ individual parameter warrant caution against invariance for groups. Others have begun to

discuss the importance of focusing on effects in the scale of the data and their practical

importance (Anvari & Lakens, 2021; Cumming, 2012).

From the example, our interpretation may be that the difference between group's latent means is large, as a 0.72 change on a 7 point scale is approximately 10% more resiliency for students when compared to the clinical sample. Practically, 10% in resiliency for an area of the United States (Mississippi) often hit with natural disasters (hurricanes, tornadoes, floods) and high levels of poverty would be very important. Even the smaller difference of .5 point on each individual item could translate into increases in resiliency, and these results may elucidate avenues for further exploration into areas of focus within resiliency, given the items. The secondary example showed that we can extend these results to other samples to examine other potentially impactful variables on assessment. The findings replicate in the sense that the scale shows the same invariant issues with intercepts on a Chinese versus English sample comparison. However, in this analysis, it is clear that the differences in items averages are much larger and across all items, rather than a few.

What do the results of a study on measurement invariance with these results tell us about replication, generalizability, and validity overall? If a researcher decides their effects are large, they should likely caution against suggesting that these scores are directly comparable without weighting or other adjustment. Let's consider a scenario wherein the change metric between models picked (i.e., ΔCFI, ΔRMSEA) indicates a "significant" change in model fit. However, if both the effect size and a visual inspection of the invariance indicates a small difference, we may decide to lessen the practical importance of those results, much like "just significant" p-values with small effect sizes are treated now. The results from our Chinese versus English comparison show us the other scenario: non-invariant results that clearly indicate differences with a large effect size on both replication and item average differences. Given that the goal of measurement invariance is to compare *estimates*, we should expect some differences across samples due to the nature

of sampling and estimation. It may be that many of the published models presented

represent these effects - small variations between groups due to sampling error or other

small crud - but do not represent a fundamental problem with the measurement or

generalizability of the results. The `visualizemi` package is one useful tool to help sort out

if findings are this small sampling error or differences in samples due to other variables.

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Table 1

Model Fit for RS-14 Example

Model	AIC	BIC	CFI	TLI	RMSEA	SRMR
Overall	126,722.491	126,888.707	0.934	0.923	0.094	0.036
Group Clinical	52,961.421	53,099.720	0.919	0.904	0.090	0.044
Group Student	69,100.985	69,254.310	0.928	0.915	0.108	0.035
Configural	122,118.406	122,617.055	0.926	0.912	0.102	0.036
Loadings	122,144.532	122,566.010	0.925	0.918	0.098	0.043
Intercepts	122,544.109	122,888.415	0.911	0.910	0.103	0.052
Residuals	126,466.241	126,727.438	0.780	0.793	0.156	0.086

Table 2

Boot Partial Effects Results for RS-14 Intercepts

Term	Non-Invariant	Random Non-Invariant	h_{nmi}	h_{nmi_p}
RS Intercept	0.991	0.007	2.784	0.886
RS1 Intercept	0.989	0.007	2.764	0.880
RS10 Intercept	0.988	0.007	2.755	0.877
RS11 Intercept	0.991	0.007	2.784	0.886
RS12 Intercept	0.991	0.007	2.784	0.886
RS13 Intercept	0.991	0.007	2.784	0.886
RS14 Intercept	0.990	0.007	2.774	0.883
RS2 Intercept	0.985	0.007	2.728	0.869
RS3 Intercept	0.988	0.007	2.755	0.877
RS4 Intercept	0.990	0.007	2.774	0.883
RS5 Intercept	0.984	0.007	2.720	0.866
RS6 Intercept	0.979	0.007	2.683	0.854
RS7 Intercept	0.974	0.007	2.650	0.844
RS8 Intercept	0.991	0.007	2.784	0.886
RS9 Intercept	0.987	0.007	2.746	0.874
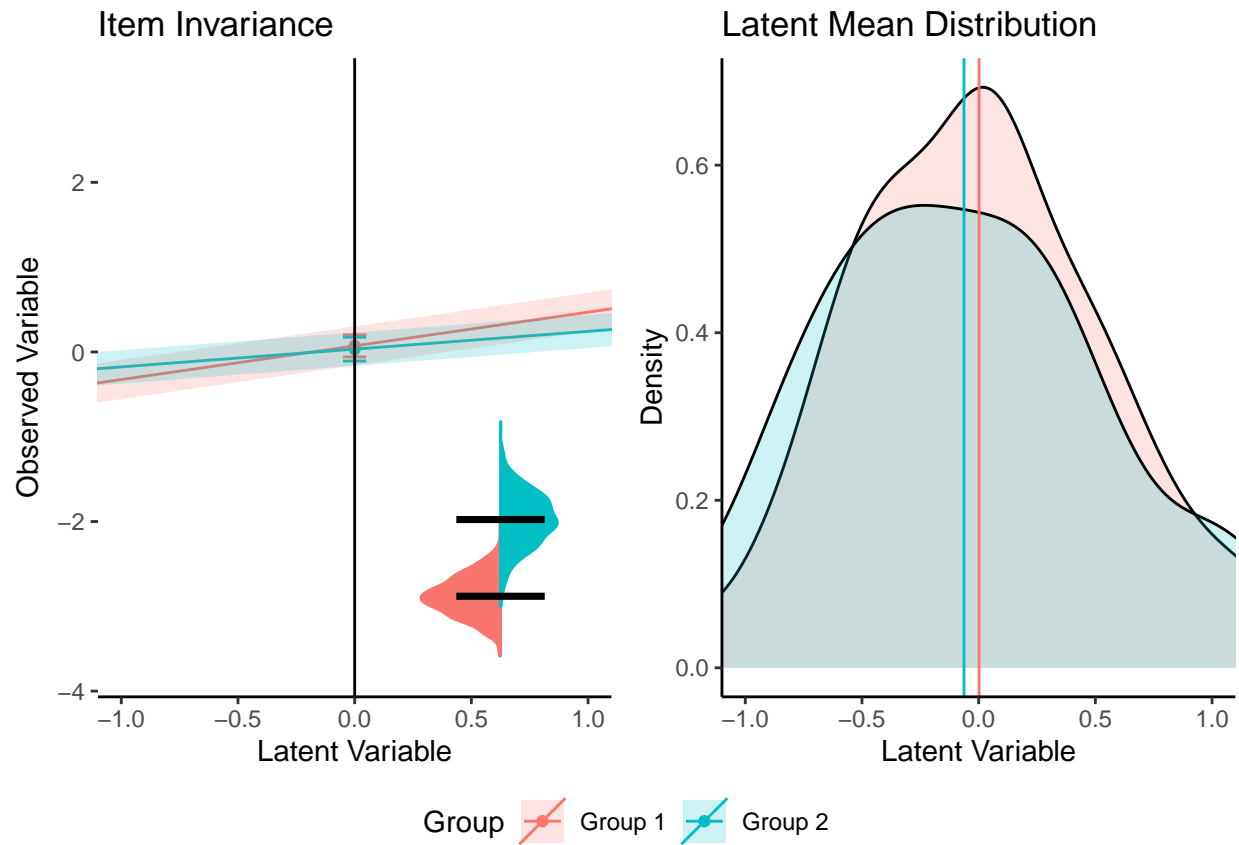
Figure 1

Invariant Model Visualization
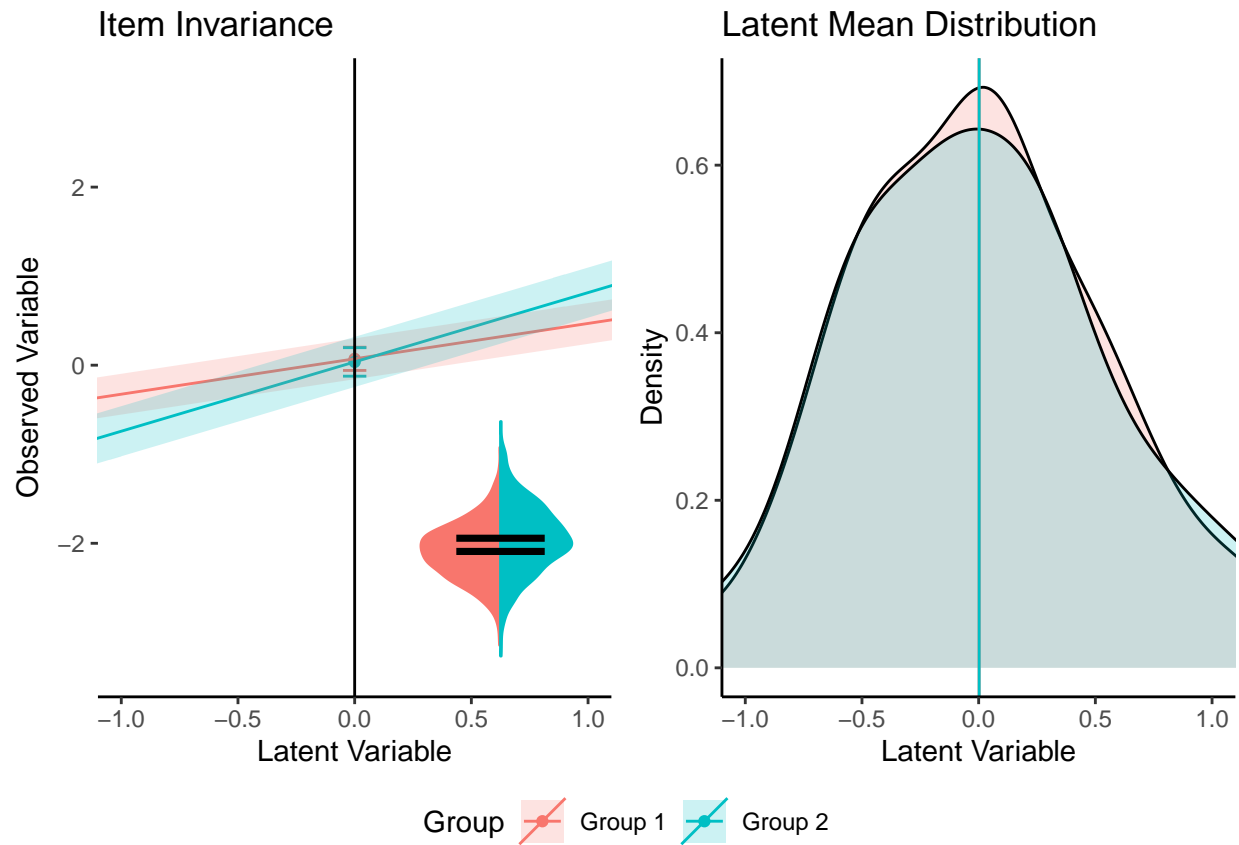
Figure 2

Small Loadings Model Visualization
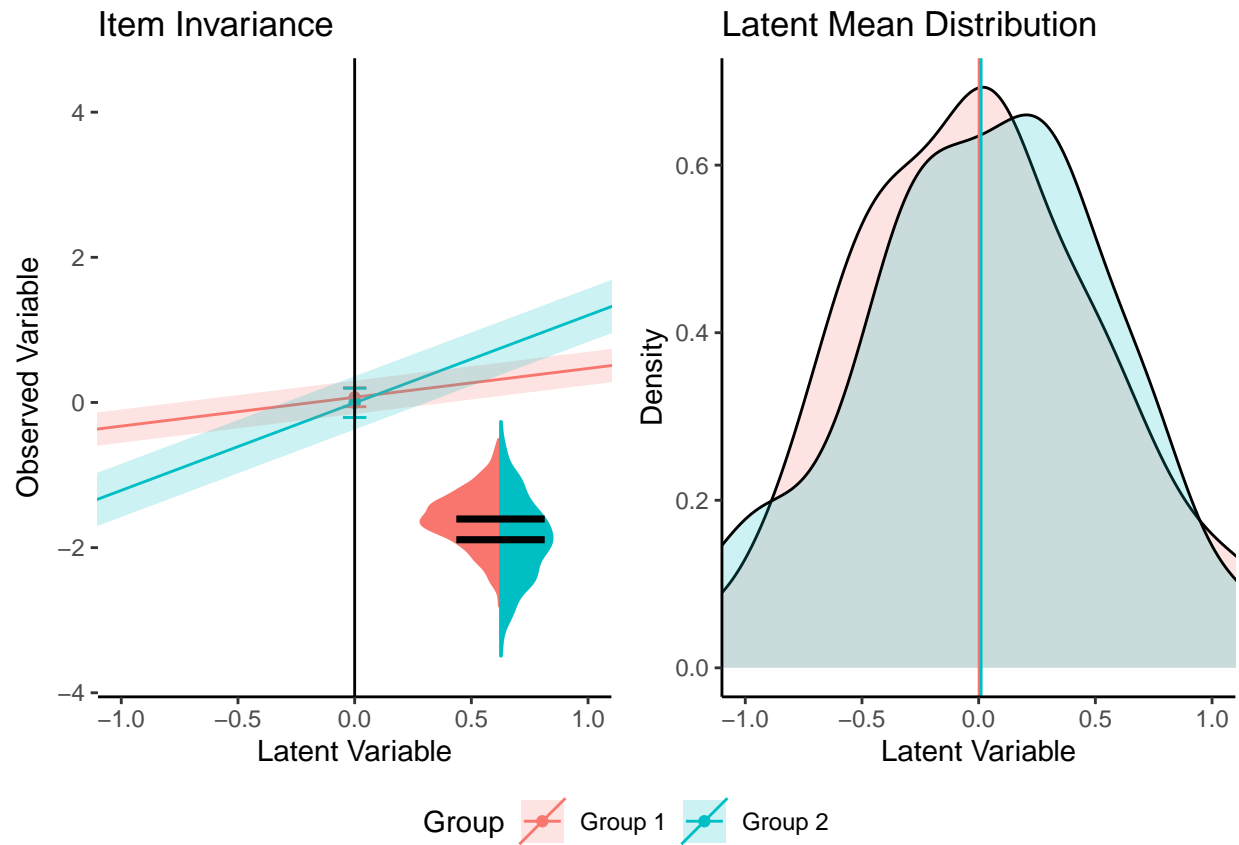
Figure 3

Medium Loadings Model Visualization
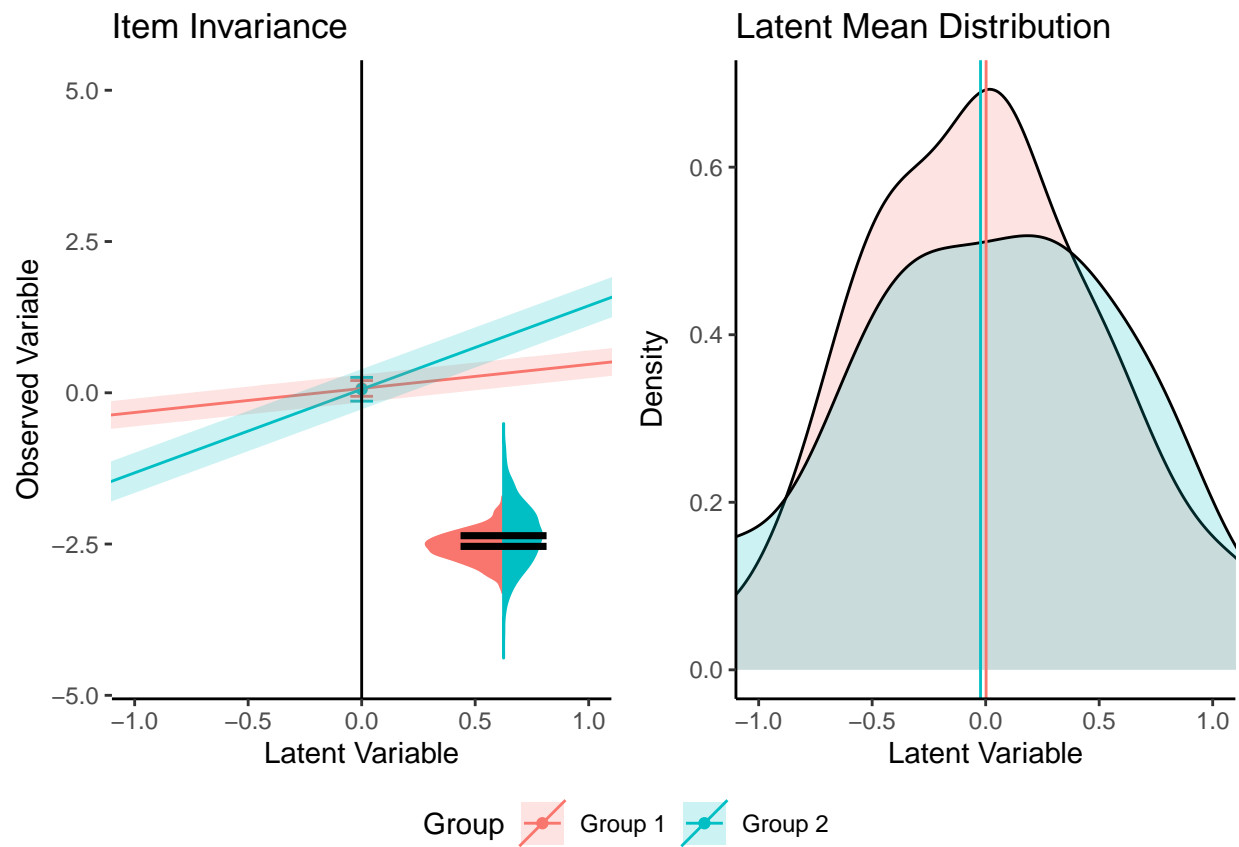
Figure 4

Large Loadings Model Visualization
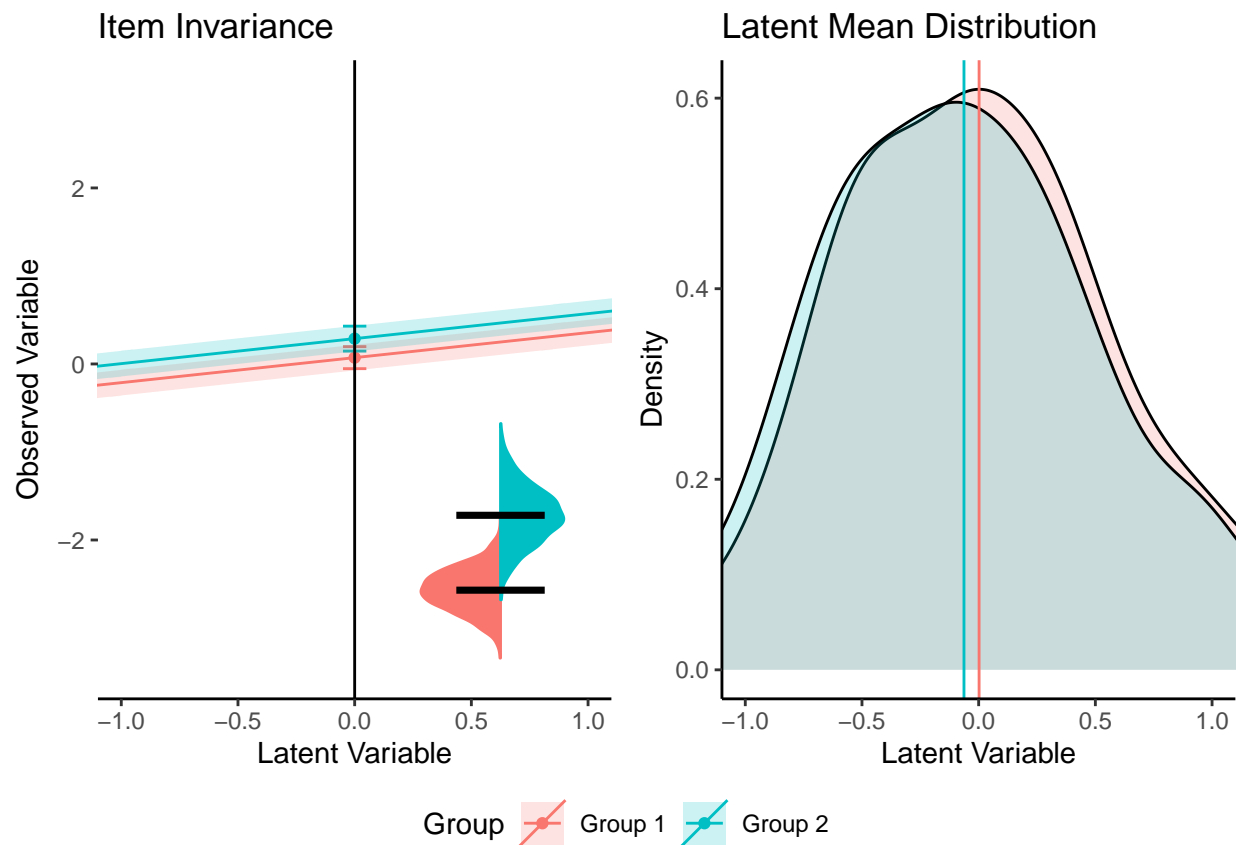
Figure 5

Small Intercepts Model Visualization
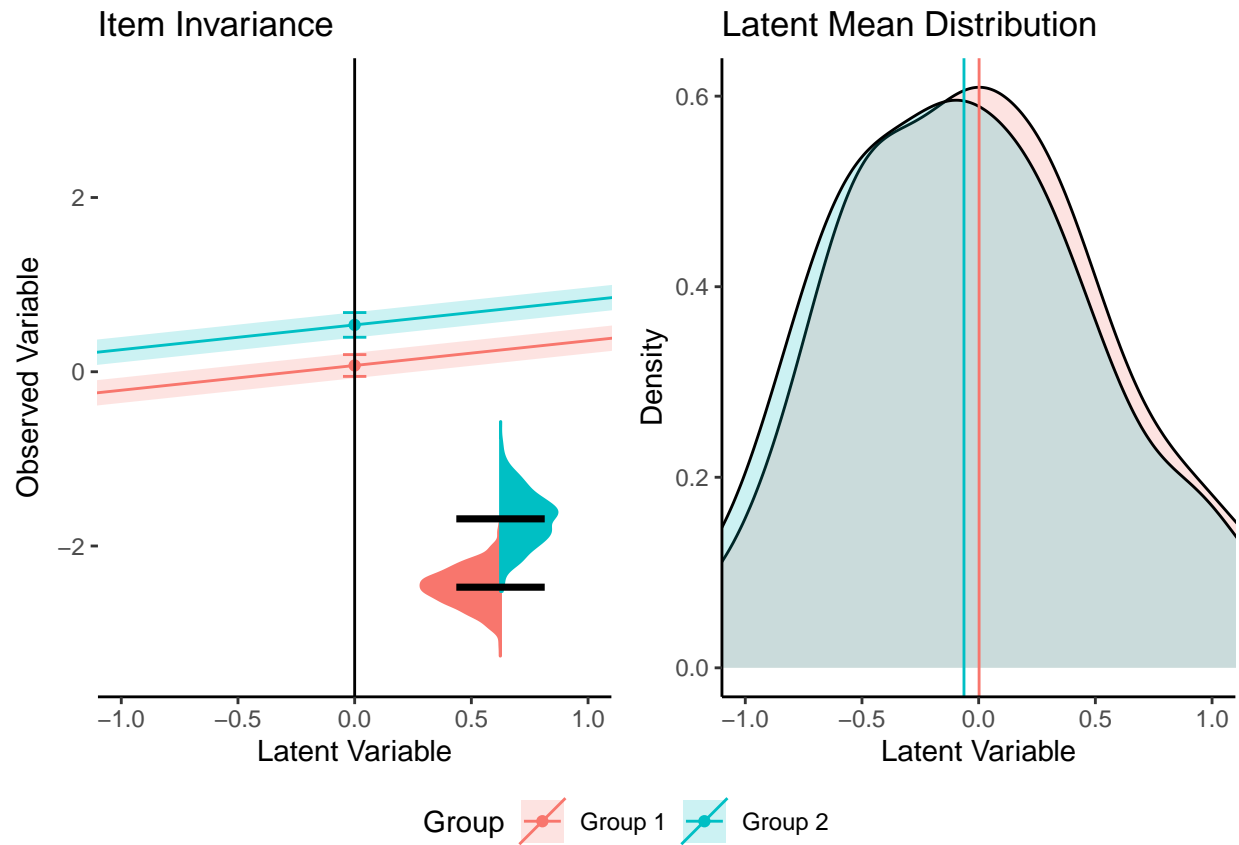
Figure 6

Medium Intercepts Model Visualization
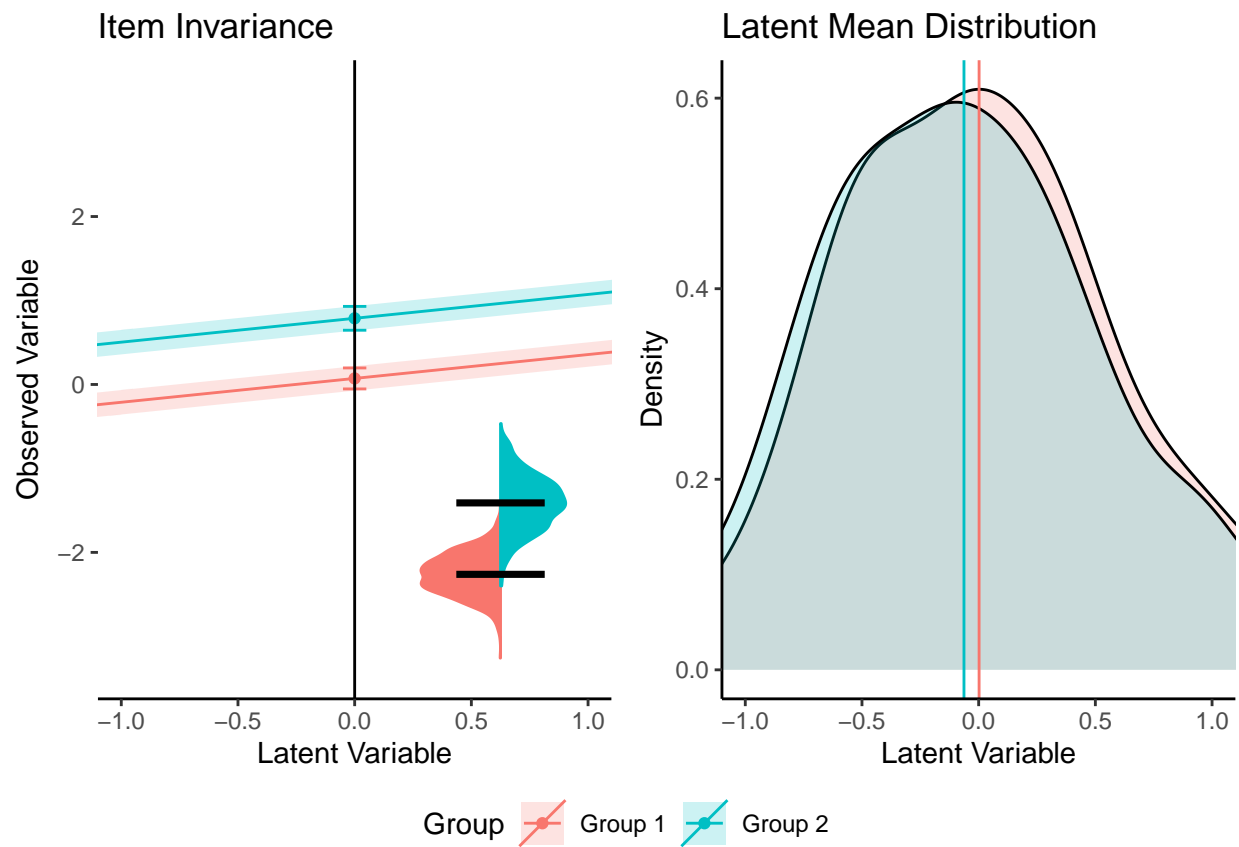
Figure 7

Large Intercepts Model Visualization
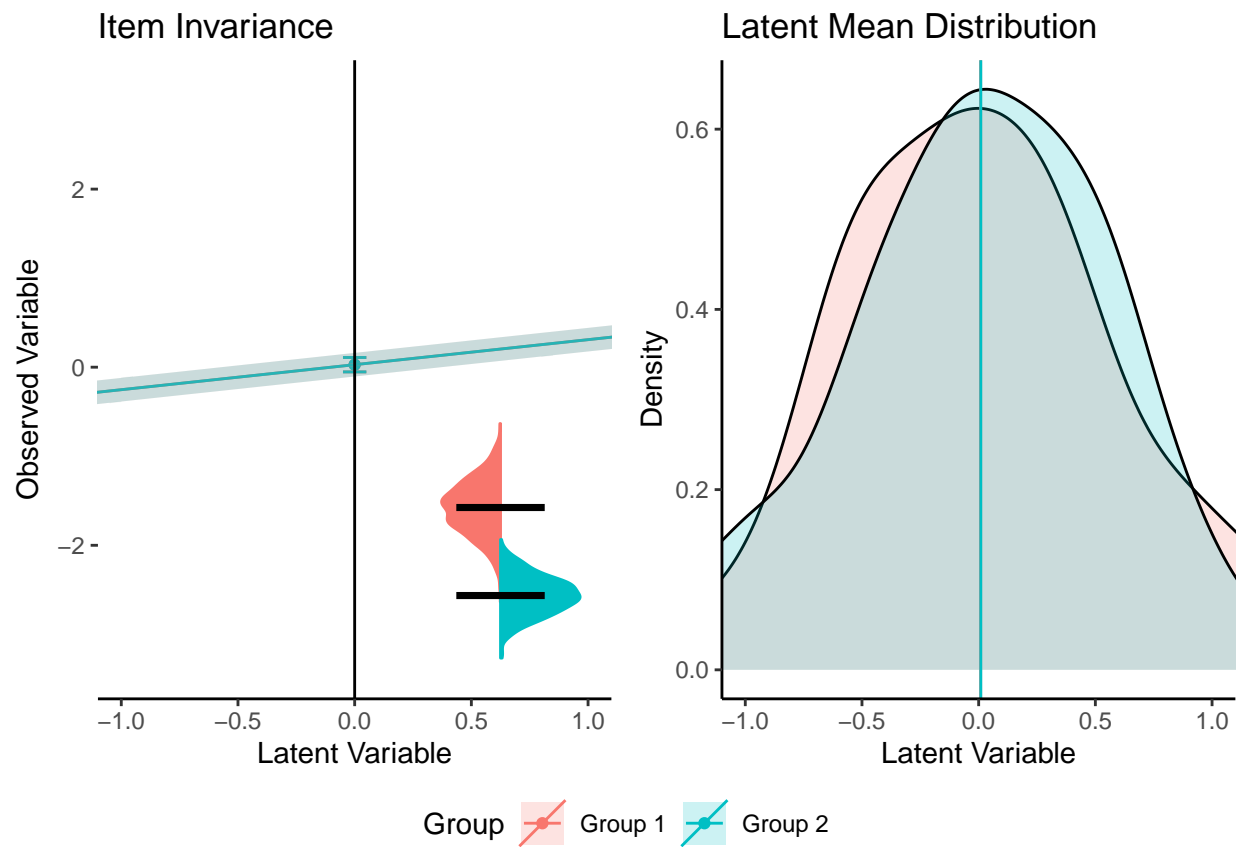
Figure 8

Small Residuals Model Visualization
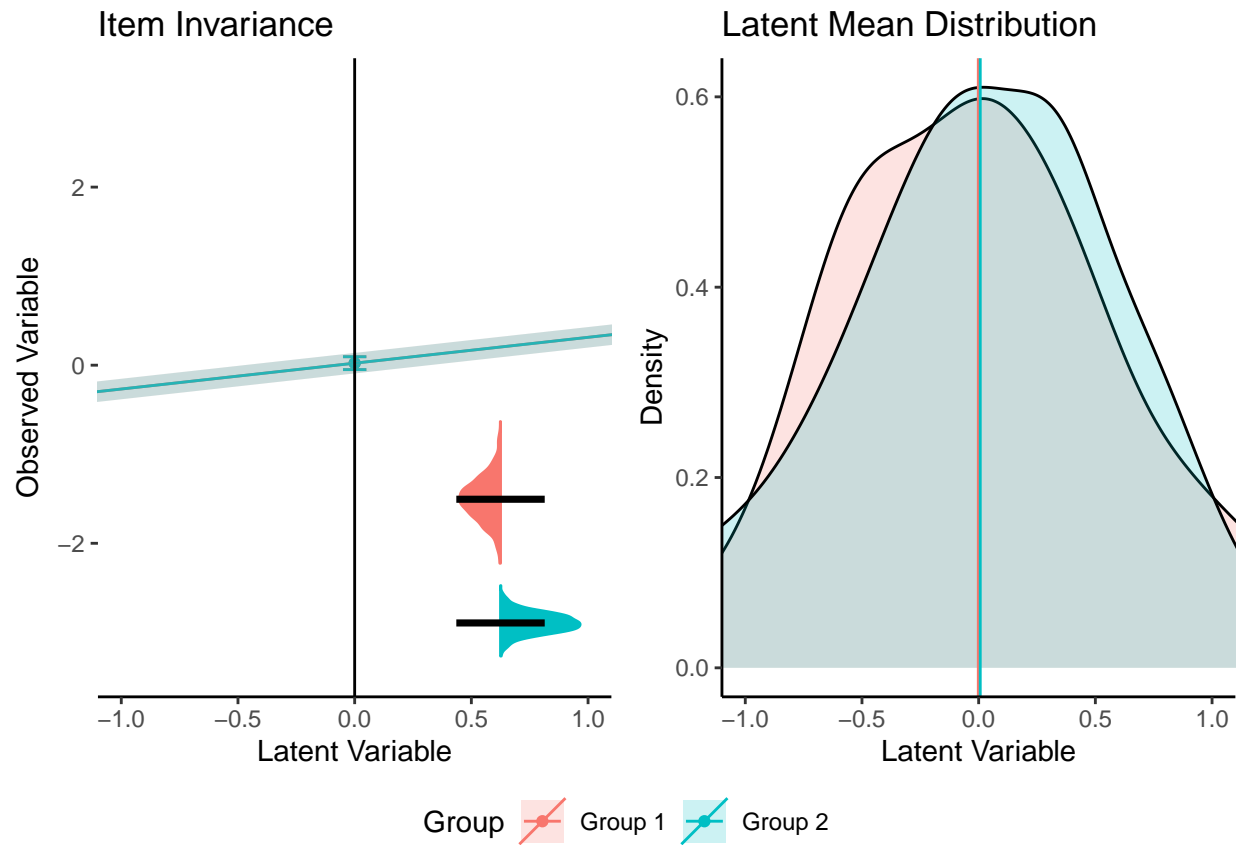
Figure 9

Medium Residuals Model Visualization
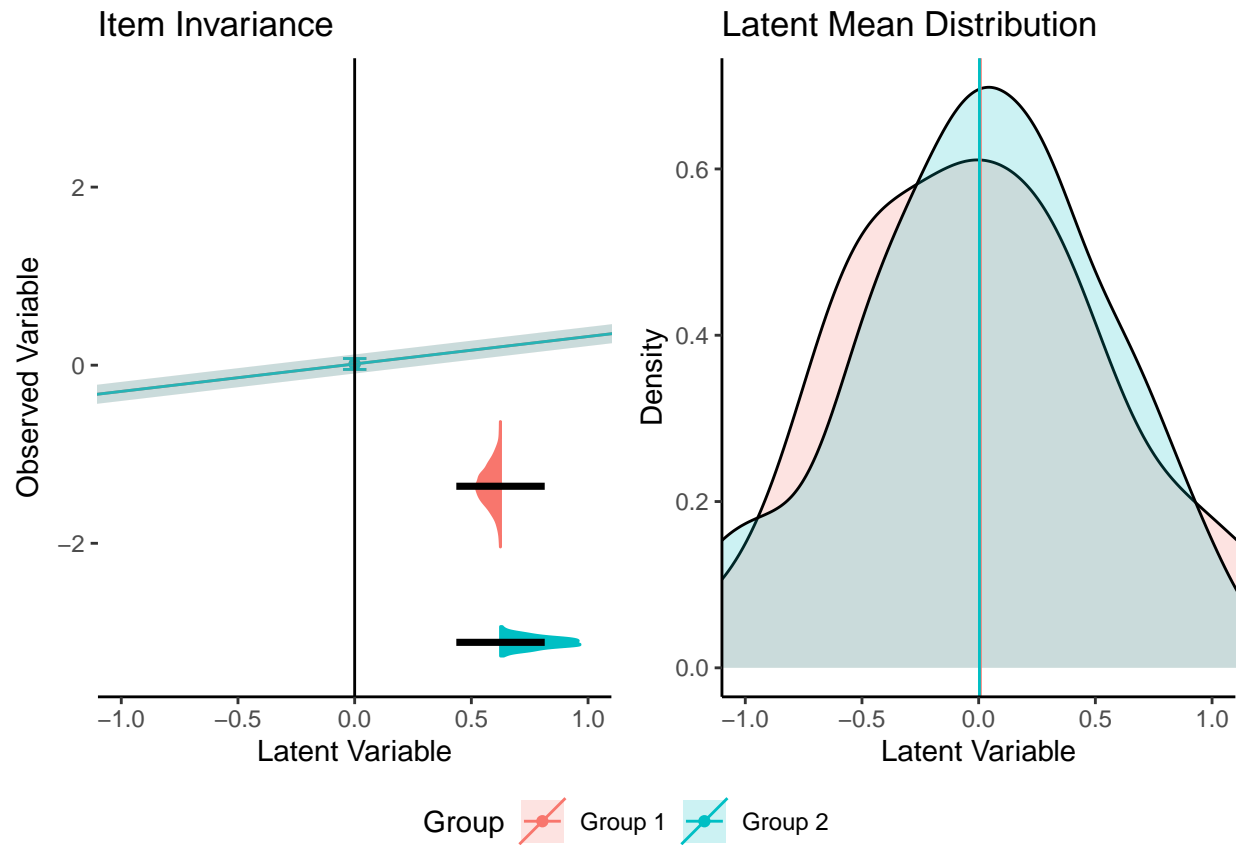
Figure 10

Large Residuals Model Visualization
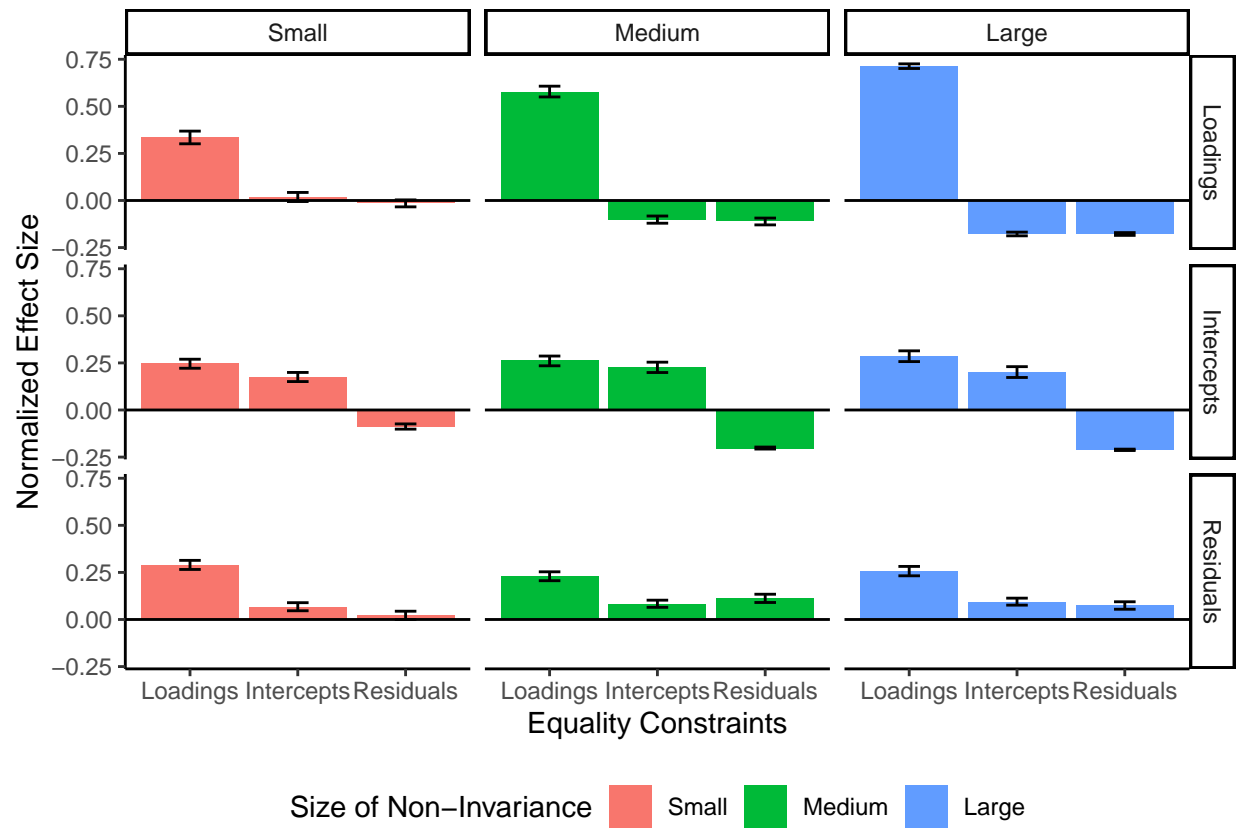
Figure 11

Visualization of the effect size of bootstrapped replication proportions on simulated data. Each panel indicates the simulated data type, colors represent the differences in the strength of the non-invariance, and the bars on the x-axis represent the effect size for the equality constraint.
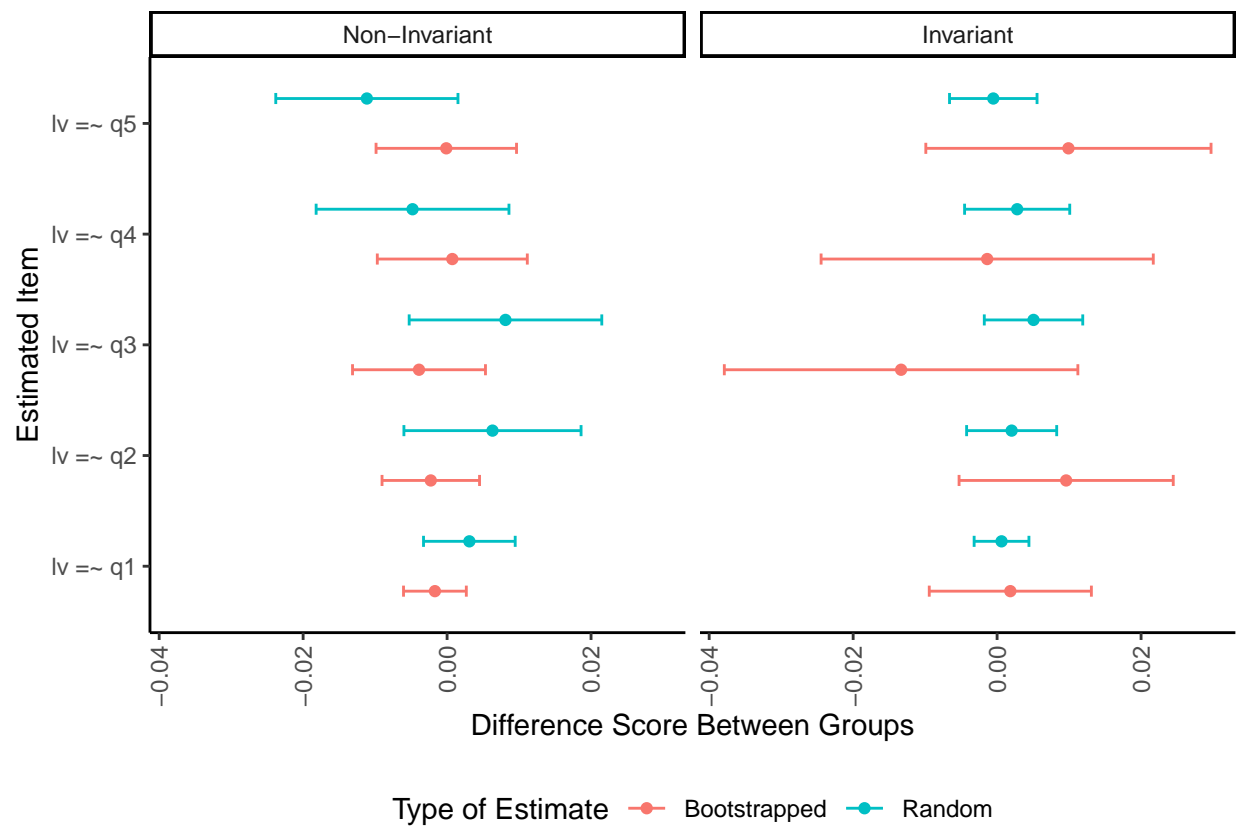
Figure 12

Visualization of the difference score between groups by parameter for invariant and non-invariant bootstrapped and randomly assigned group data.
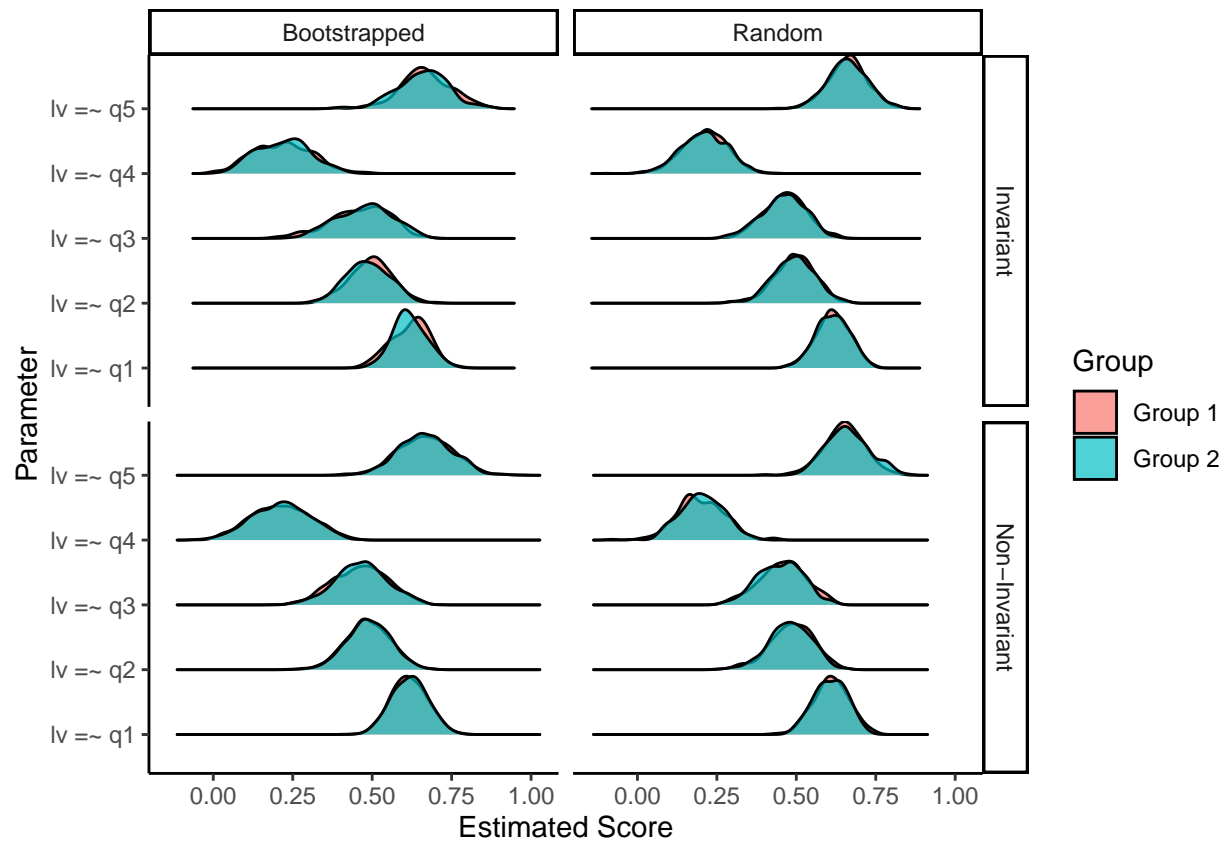
Figure 13

Visualization of the number of estimates for each group by bootstrapped and randomly assigned group runs by their invariance decision.
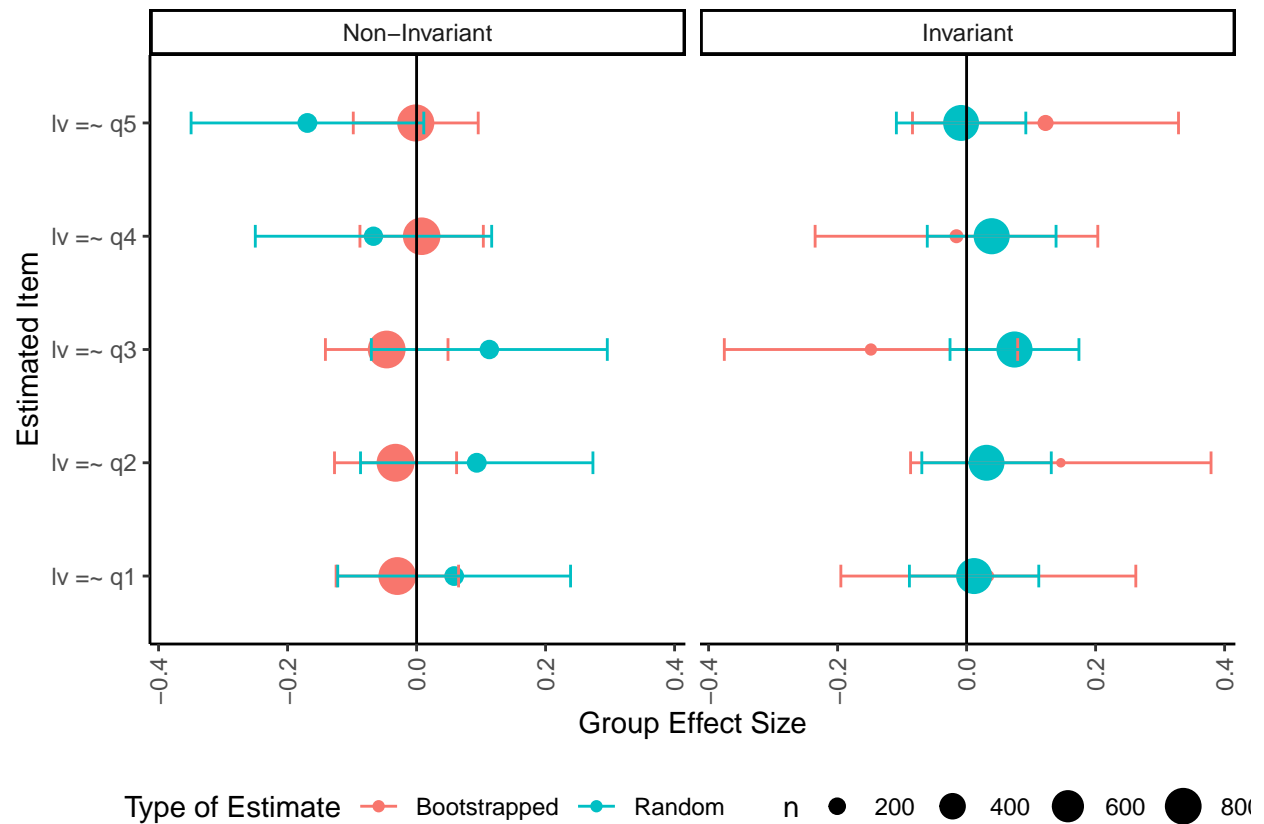
Figure 14

Visualization of effect size between groups by parameter for invariant and non-invariant bootstrapped and randomly assigned group data. The size of the dots indicate the number of data points for that estimate.
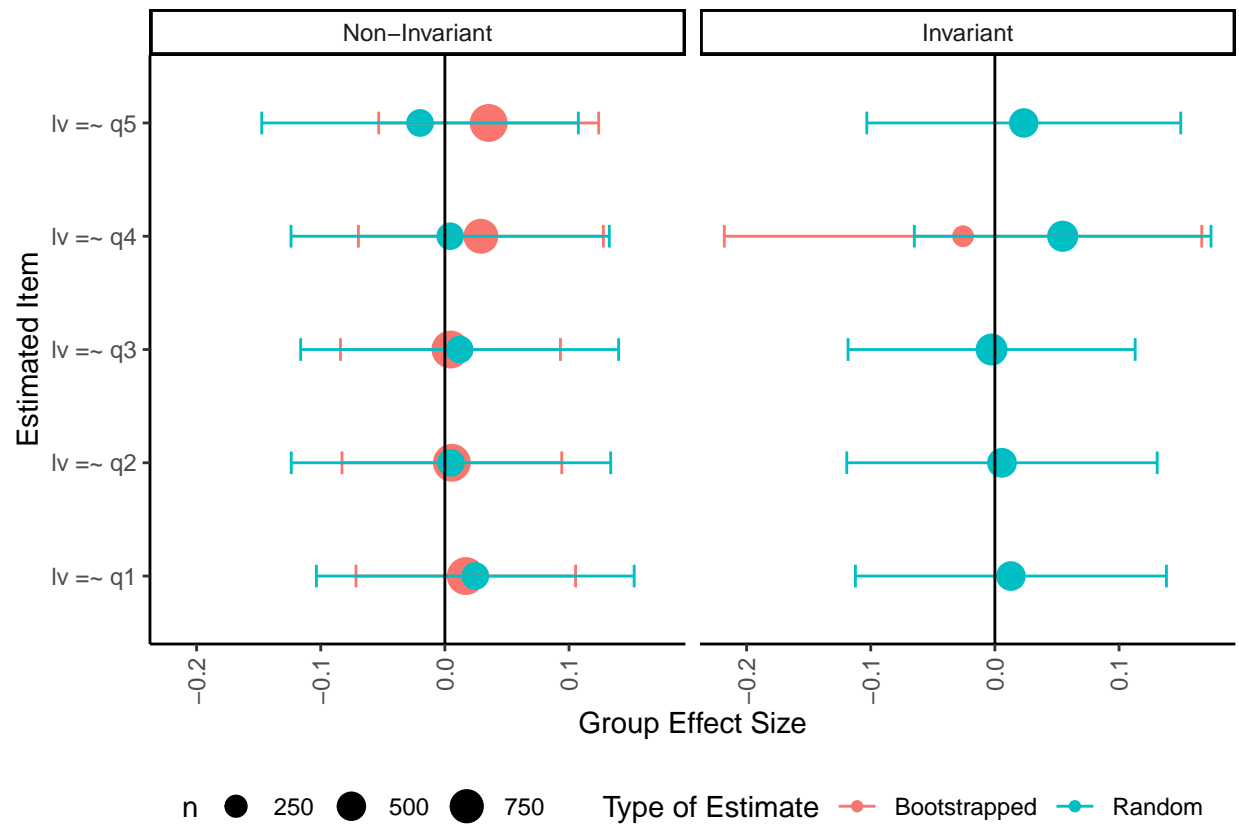
Figure 15

Bootstrapped and Random Group effect size differences in loadings for the Large Loading difference simulation. The size of the point reprensents the number of data points included in that calculation.
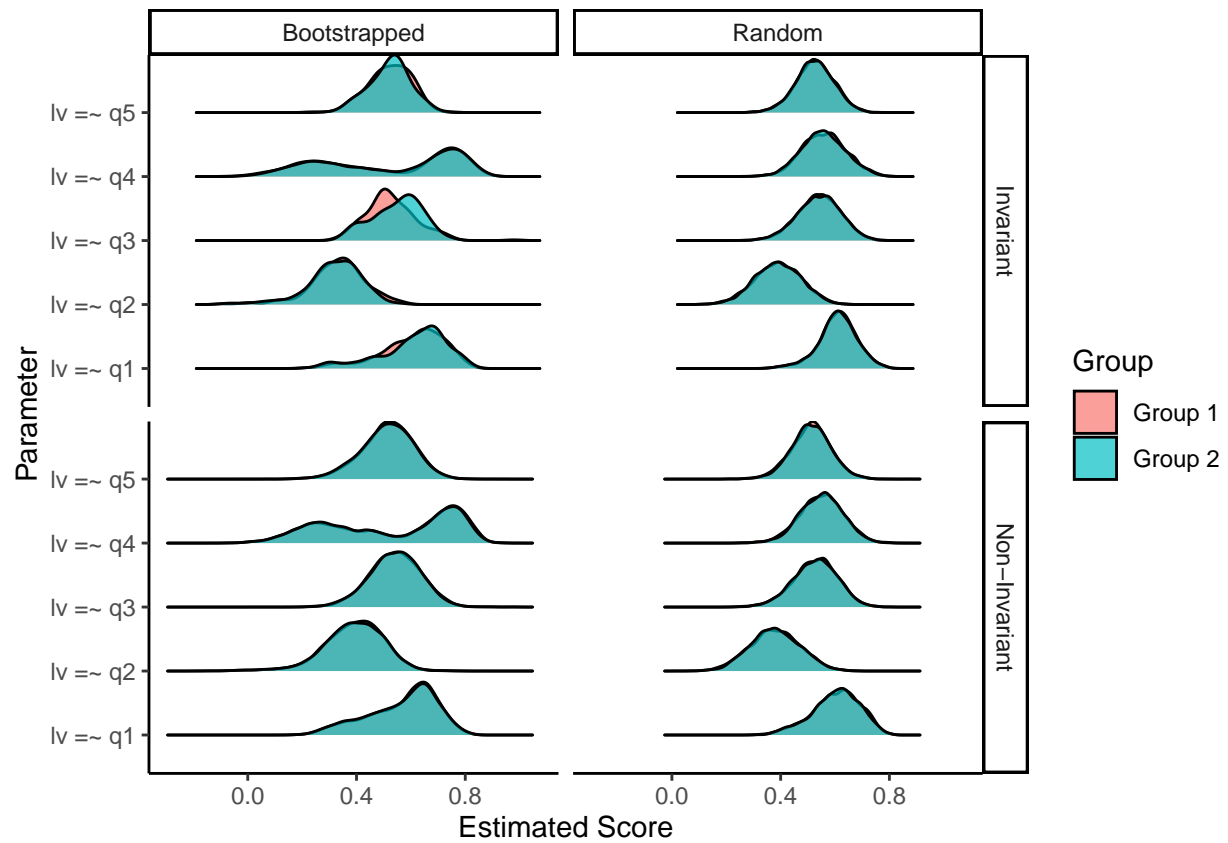
Figure 16

Bootstrapped and Random density plots for invariant and non-invariant bootstrapped partial effects examining only large loadings.
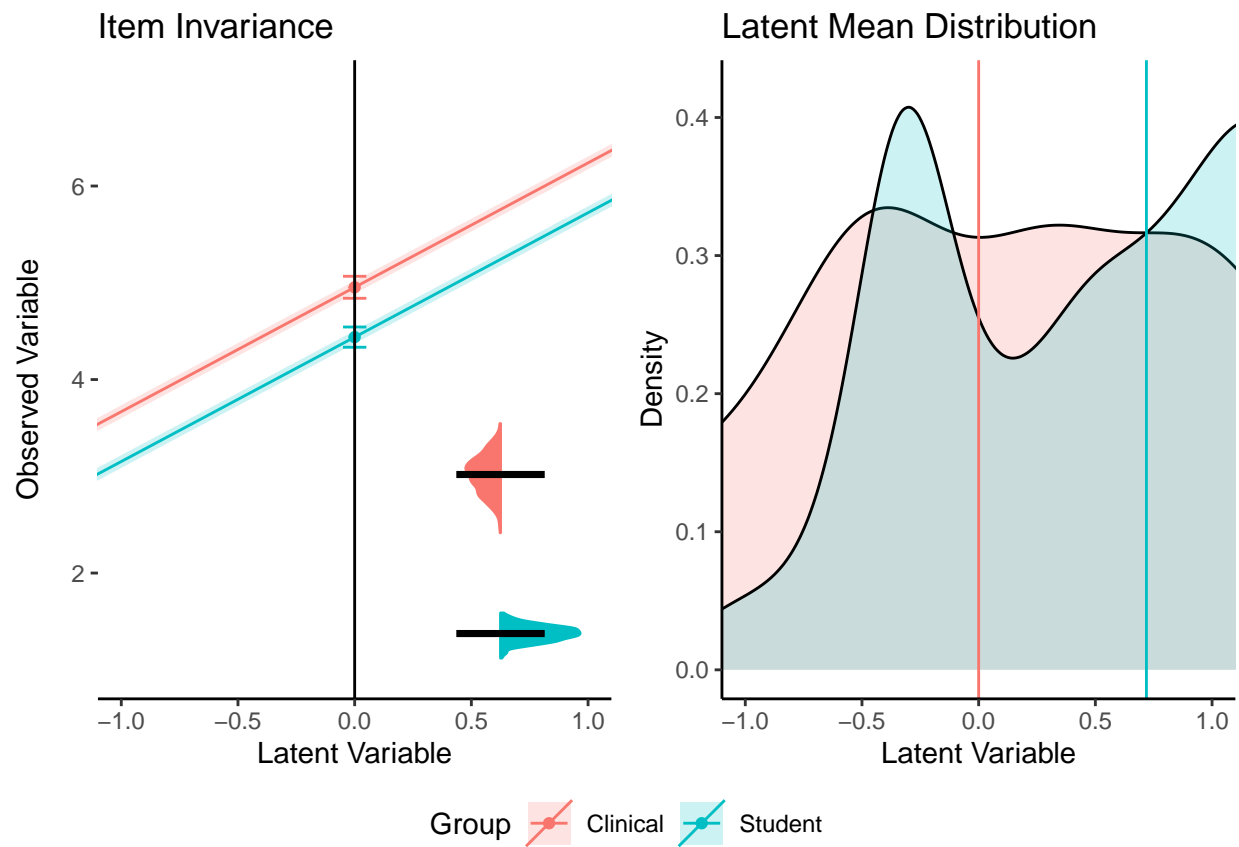
Figure 17

RS7 Item Invariance Visualization
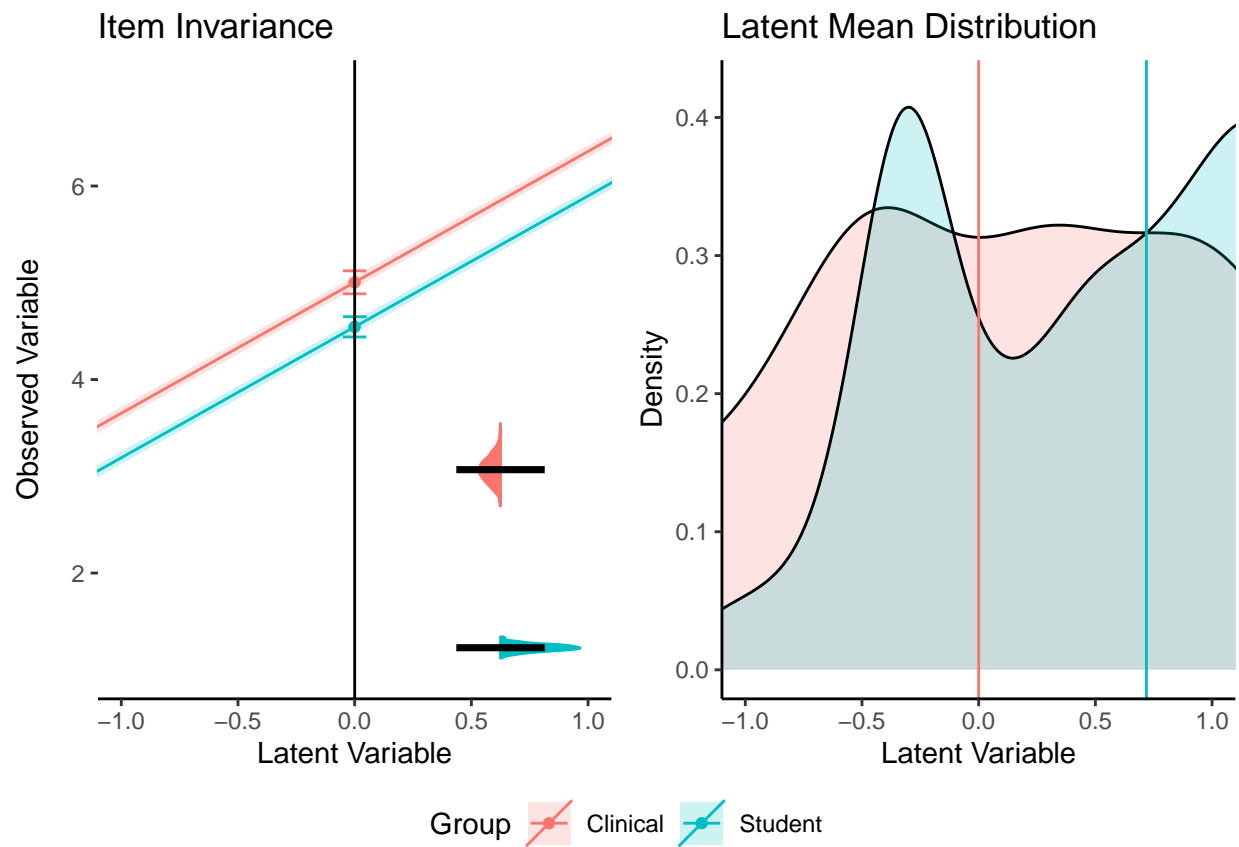
Figure 18

RS6 Item Invariance Visualization
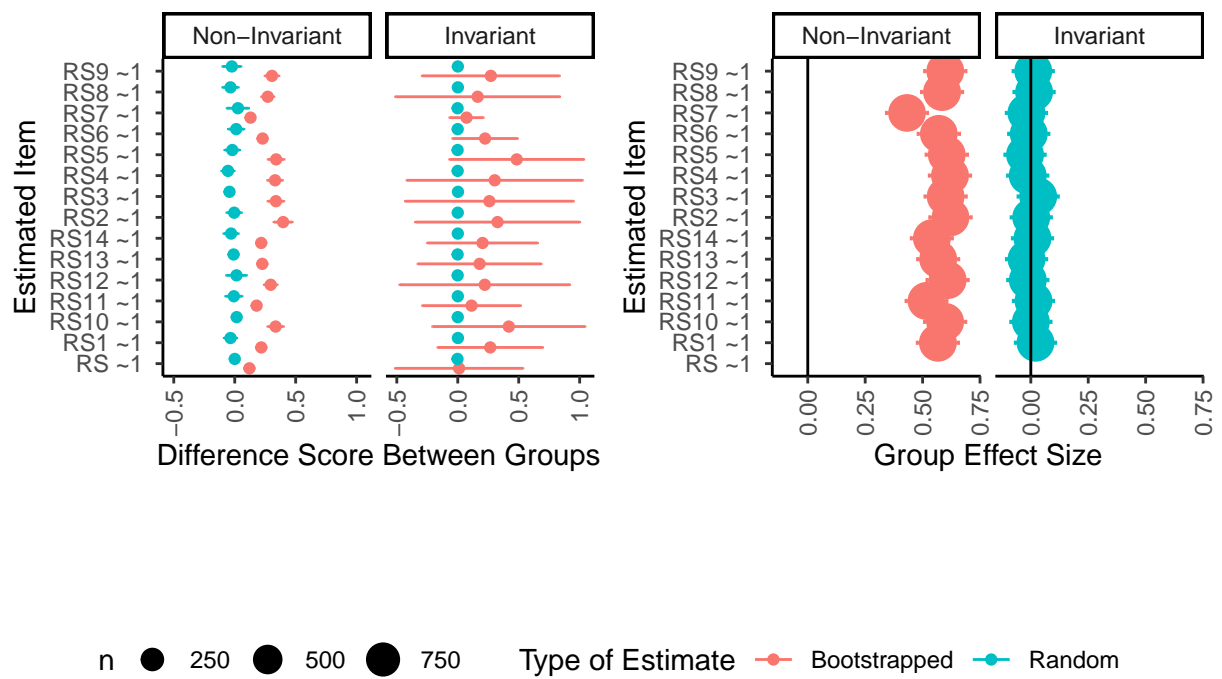
Figure 19

RS-14 scale invariance for item intercepts. The left panel indicates the raw score difference between groups and items, while the right panel indicates the effect size for group differences based on invariance.
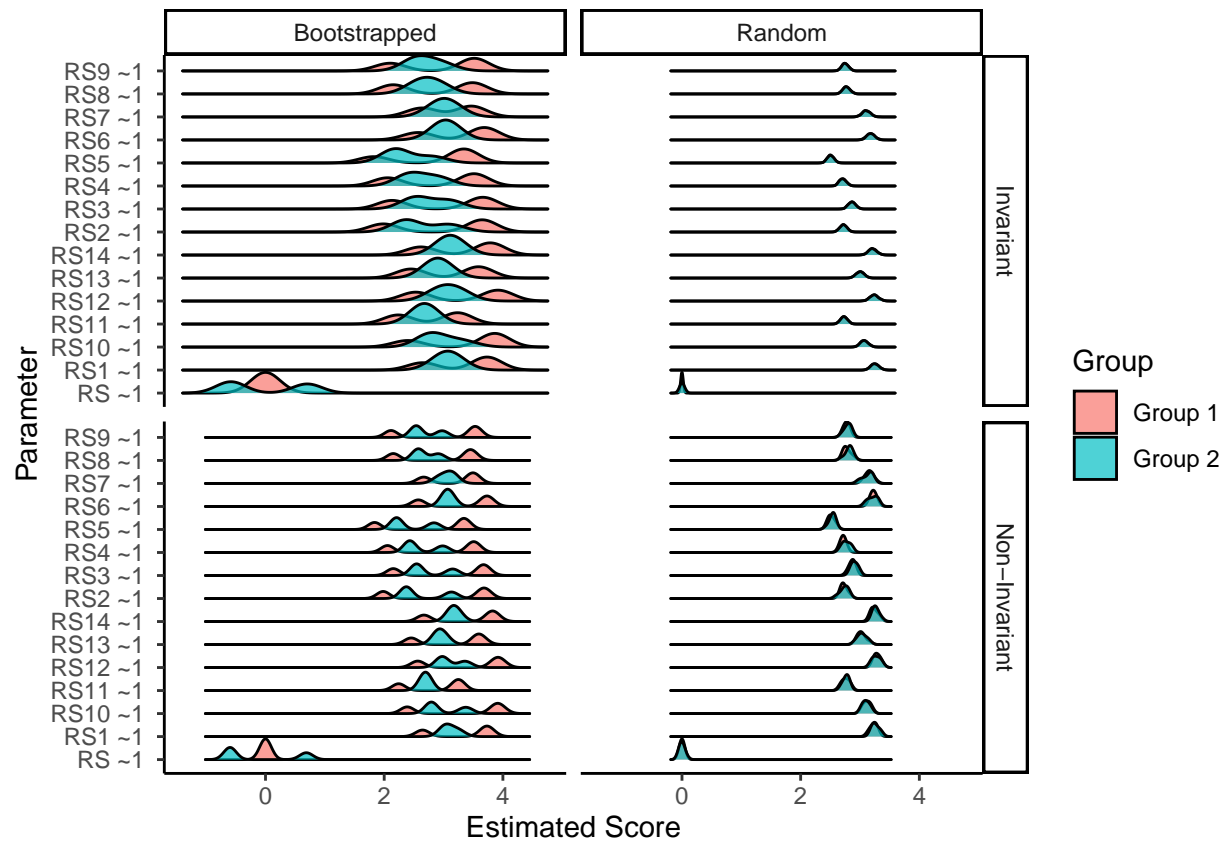
Figure 20

RS-14 scale invariance density plots, illustrating invariant versus non-invariant bootstrapped and random runs for each parameter.
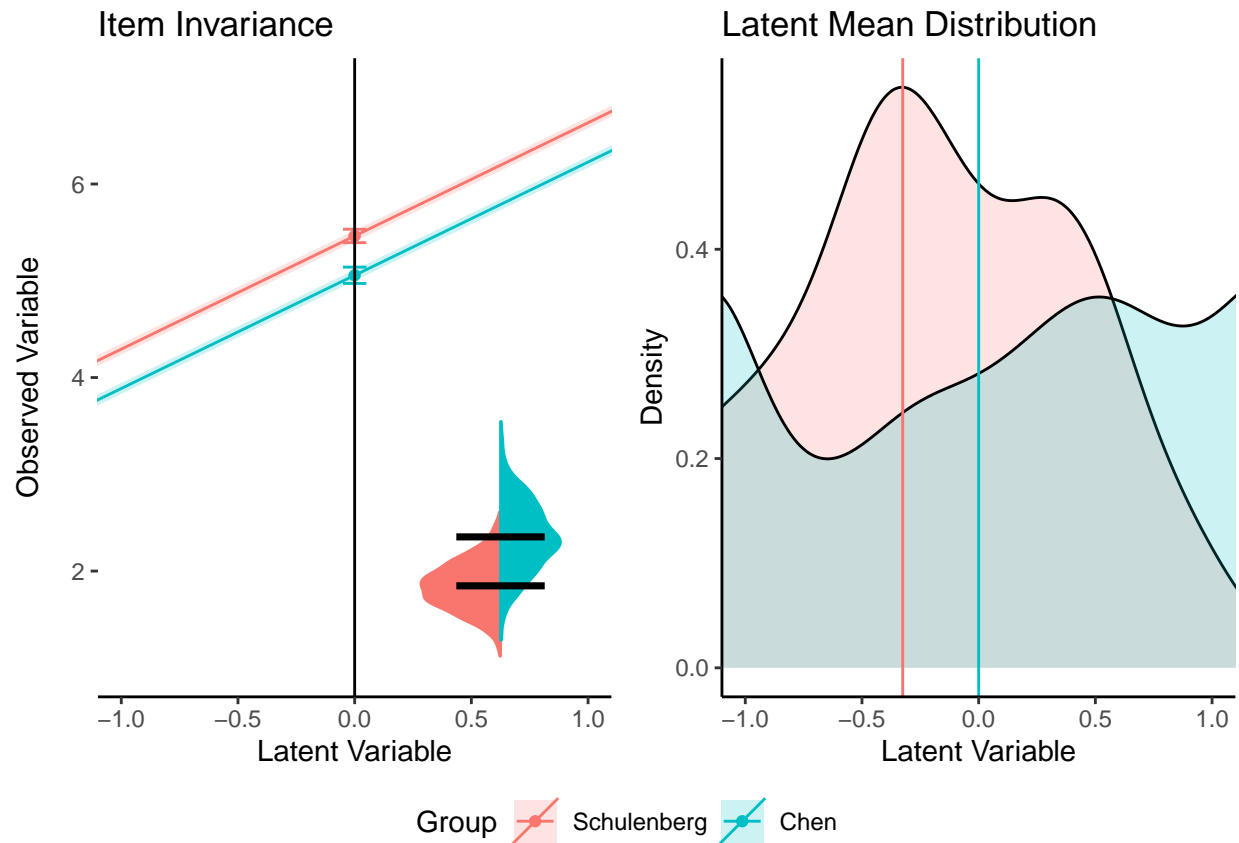
Figure 21

The differences in intercepts for the second item on the RS14 by language sample. The differences between intercepts are shown on the left hand side with a clear separation between lines. The latent means also show a clear difference between groups where the English group appears to have lower scores overall than the Chinese group.
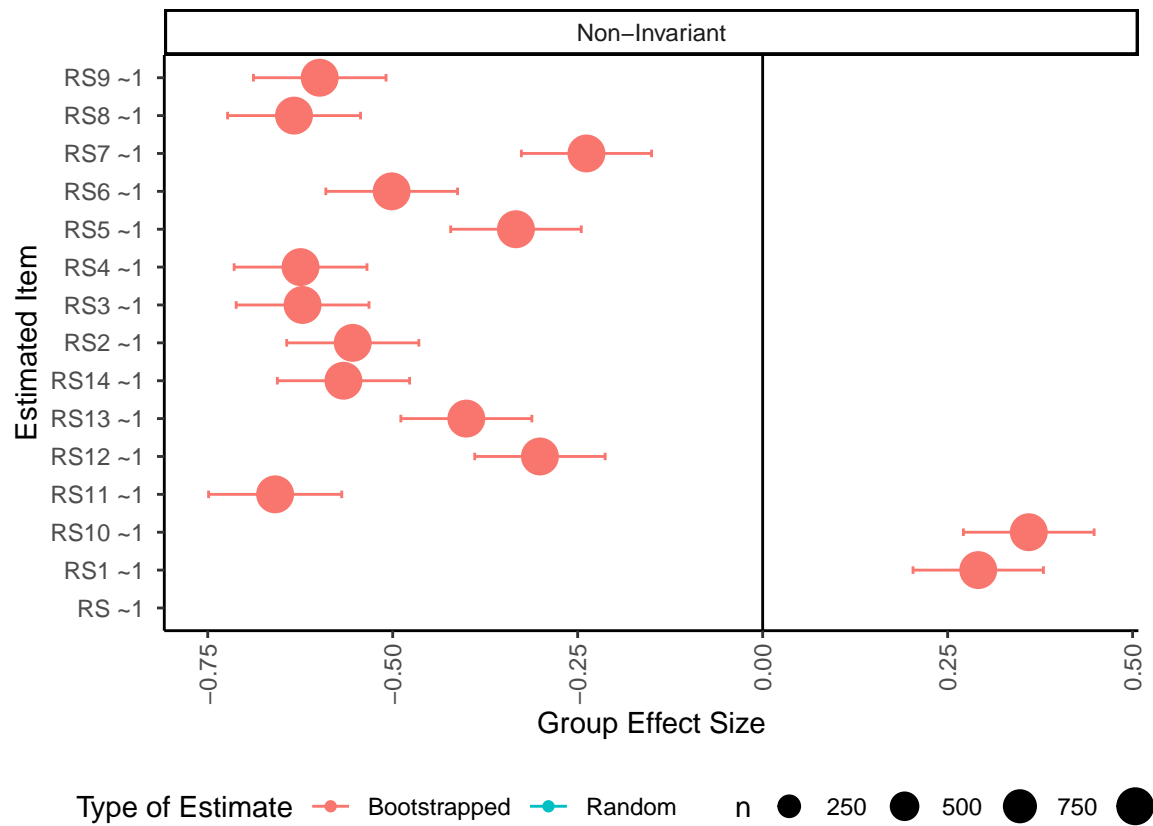
Figure 22

Effect size differences for item intercepts on the English versus Chinese samples for the RS14.

Appendix A

Simulating from models

944   Here's an example of how to simulate directly from a `lavaan` model:

```r
# first build your model
# this example is separate for each group
model.invariant.g1 <- "
# loadings
lv =~ .8*q1 + .4*q2 + .6*q3 + .3*q4 + .6*q5
# set the residual for invariance on q4
q4 ~~ 1*q4
# set the intercept for invariance on q4
q4 ~ 0*1
# set the intercept to zero for df purposes
q1 ~ 0*1
# allow the latent mean to be estimated
lv ~ 1"
model.invariant.g2 <- "lv =~ .77*q1 + .43*q2 + .58*q3 + .3*q4 + .61*q5
q4 ~~ 1*q4
q4 ~ 0*1
q1 ~ 0*1
lv ~ 1"

# simulate data invariant separately for each group
df.invariant <- bind_rows(
  # lavaan function
  simulateData(
    # model with estimates
    model = model.invariant.g1,
```

```r
  # how many data points
  sample.nobs = 250,
  # mean structure for mgcfa models
  meanstructure = T,
  # model type
  model.type = "cfa",
  # set seed for reproducibility
  seed = 1234) %>%
  # add a group label to the data
  mutate(group = "Group 1"),
simulateData(
  model = model.invariant.g2,
  sample.nobs = 250,
  meanstructure = T,
  model.type = "cfa",
  seed = 1234) %>%
  mutate(group = "Group 2")
)
```

Appendix B

Simulating from matrices

Here's an example of how to simulate using `MASS` and covariance or correlation matrices.

```r
library(MASS)


# covariance matrix
university.cov <- lav_matrix_lower2full(
    c(169.00,
      73.710, 182.2500,
      73.229, 88.4250, 171.6100,
      63.375, 72.5625, 127.7250, 156.2500,
      42.120, 67.4325, 122.0265, 123.1875, 182.2500,
      57.226, 63.2610, 117.1926, 154.4250, 138.0240, 201.6400,
      30.875, 32.0625, 60.9805, 62.9375, 76.9500, 79.5910, 90.2500,
      36.075, 38.9610, 61.0722, 58.2750, 65.9340, 70.9290, 81.1965, 123.2100,
      18.096, 21.1410, 26.2131, 39.1500, 44.6310, 46.9452, 48.7635, 56.0106, 75.6900))


# give it names
rownames(university.cov) <-
    colnames(university.cov) <-
    c("class", "social", "learn", "chronic", "physical", "sex",
      "depression", "anxiety", "stress")


# means - you need standard deviation if you only have a correlation matrix
university.means <- c(3.4, 4.3, 3.7, 3.2, 4.5, 1.2, 4.0, 3.5, 4.2)


# use mass function
DF <- mvrnorm(n = 200, mu = university.means, Sigma = university.cov)
```

```
head(DF)
```

```
##             class       social      learn    chronic     physical          sex
## [1,] 12.085294 26.83043663 13.895103 20.634374  16.7903295  30.5468832
## [2,]  3.939545 10.93624431  3.093025  8.316128  -7.2199148   9.3579991
## [3,] 15.659627  0.22811723  5.205657  5.224293  -1.4425219  -1.2710662
## [4,] 23.086133 12.43649966  1.891769 -5.913170 -19.4937389 -13.5922410
## [5,] 10.856492 23.30887194 17.124064 11.438840   2.4659294   1.7330709
## [6,] -4.328380  0.07907149 -1.000636 -1.654947  -0.7365838  -0.3958833
##       depression     anxiety      stress
## [1,]  14.174374    8.001766  13.6534279
## [2,]   3.940819   -6.598153  -7.9229552
## [3,]  -8.927508  -10.335571  -2.8100779
## [4,]  -0.149840    6.475669 -15.5300195
## [5,]  -6.492809  -12.524601   0.4924153
## [6,]  11.917631    3.433587   8.1456346
```

Appendix C

MGCFA Model Fit Statistics

960 Model fit statistics are provided for each of the ten model combinations (invariant, three

961 sizes for each loadings, intercepts, and residuals). These tables could be used to examine

962 the traditional change in fit statistics cutoff rules of thumb (Cheung & Rensvold, 2002),

963 such as Δ CFI or Δ RMSEA, to the visualizations presented in the manuscript.

[tbp]

Table C1

Model Fit for Invariant Model

Model	AIC	BIC	CFI	TLI	RMSEA	SRMR
Overall	7,516.454	7,579.673	1.000	1.036	0.000	0.006
Group Group 1	3,765.749	3,818.571	0.976	0.953	0.047	0.031
Group Group 2	3,767.599	3,820.421	1.000	1.008	0.000	0.021
Configural	7,533.348	7,659.786	0.991	0.982	0.030	0.026
Loadings	7,528.476	7,638.056	0.994	0.992	0.020	0.033
Intercepts	7,522.397	7,615.118	1.000	1.003	0.000	0.035
Residuals	7,520.435	7,592.083	0.991	0.992	0.020	0.046

[tbp]

Table C2

Model Fit for Small Differences in Loadings

Model	AIC	BIC	CFI	TLI	RMSEA	SRMR
Overall	7,530.321	7,593.540	0.977	0.955	0.049	0.025
Group Group 1	3,765.749	3,818.571	0.976	0.953	0.047	0.031
Group Group 2	3,785.242	3,838.064	0.979	0.958	0.050	0.029
Configural	7,550.991	7,677.430	0.978	0.956	0.048	0.030
Loadings	7,550.133	7,659.713	0.966	0.952	0.051	0.047
Intercepts	7,542.675	7,635.397	0.979	0.977	0.035	0.047
Residuals	7,534.091	7,605.739	0.993	0.994	0.019	0.054

[tbp]

Table C3

Model Fit for Medium Differences in Loadings

Model	AIC	BIC	CFI	TLI	RMSEA	SRMR
Overall	7,598.681	7,661.900	0.946	0.893	0.078	0.035
Group Group 1	3,765.749	3,818.571	0.976	0.953	0.047	0.031
Group Group 2	3,820.090	3,872.912	0.969	0.938	0.067	0.034
Configural	7,585.839	7,712.277	0.972	0.944	0.058	0.033
Loadings	7,613.434	7,723.014	0.865	0.807	0.107	0.079
Intercepts	7,606.648	7,699.370	0.874	0.860	0.091	0.079
Residuals	7,600.057	7,671.705	0.880	0.895	0.079	0.091

[tbp]

Table C4

Model Fit for Large Differences in Loadings

Model	AIC	BIC	CFI	TLI	RMSEA	SRMR
Overall	7,684.982	7,748.201	0.987	0.973	0.040	0.023
Group Group 1	3,765.749	3,818.571	0.976	0.953	0.047	0.031
Group Group 2	3,857.143	3,909.965	0.992	0.984	0.037	0.029
Configural	7,622.892	7,749.330	0.986	0.972	0.042	0.030
Loadings	7,674.188	7,783.767	0.817	0.738	0.131	0.095
Intercepts	7,667.682	7,760.403	0.824	0.805	0.113	0.096
Residuals	7,683.177	7,754.825	0.762	0.793	0.116	0.138

[tbp]

Table C5

Model Fit for Small Differences in Intercepts

Model	AIC	BIC	CFI	TLI	RMSEA	SRMR
Overall	7,520.471	7,583.690	1.000	1.035	0.000	0.007
Group Group 1	3,765.749	3,818.571	0.976	0.953	0.047	0.031
Group Group 2	3,767.599	3,820.421	1.000	1.008	0.000	0.021
Configural	7,533.348	7,659.786	0.991	0.982	0.030	0.026
Loadings	7,528.476	7,638.056	0.994	0.992	0.020	0.033
Intercepts	7,526.312	7,619.034	0.987	0.986	0.027	0.040
Residuals	7,524.356	7,596.005	0.975	0.978	0.033	0.050

[tbp]

Table C6

Model Fit for Medium Differences in Intercepts

Model	AIC	BIC	CFI	TLI	RMSEA	SRMR
Overall	7,538.375	7,601.594	1.000	1.033	0.000	0.008
Group Group 1	3,765.749	3,818.571	0.976	0.953	0.047	0.031
Group Group 2	3,767.599	3,820.421	1.000	1.008	0.000	0.021
Configural	7,533.348	7,659.786	0.991	0.982	0.030	0.026
Loadings	7,528.476	7,638.056	0.994	0.992	0.020	0.033
Intercepts	7,544.002	7,636.724	0.917	0.907	0.068	0.059
Residuals	7,542.064	7,613.712	0.905	0.917	0.065	0.067

[tbp]

Table C7

Model Fit for Large Differences in Intercepts

Model	AIC	BIC	CFI	TLI	RMSEA	SRMR
Overall	7,568.748	7,631.967	1.000	1.032	0.000	0.008
Group Group 1	3,765.749	3,818.571	0.976	0.953	0.047	0.031
Group Group 2	3,767.599	3,820.421	1.000	1.008	0.000	0.021
Configural	7,533.348	7,659.786	0.991	0.982	0.030	0.026
Loadings	7,528.476	7,638.056	0.994	0.992	0.020	0.033
Intercepts	7,574.054	7,666.776	0.797	0.775	0.106	0.084
Residuals	7,572.174	7,643.823	0.785	0.813	0.097	0.090

[tbp]

Table C8

Model Fit for Small Differences in Residuals

Model	AIC	BIC	CFI	TLI	RMSEA	SRMR
Overall	7,462.007	7,525.226	1.000	1.020	0.000	0.013
Group Group 1	3,765.749	3,818.571	0.976	0.953	0.047	0.031
Group Group 2	3,703.797	3,756.619	0.962	0.924	0.061	0.037
Configural	7,469.546	7,595.984	0.969	0.938	0.054	0.034
Loadings	7,471.637	7,581.217	0.944	0.920	0.062	0.049
Intercepts	7,465.722	7,558.443	0.952	0.946	0.051	0.051
Residuals	7,465.986	7,537.635	0.930	0.939	0.054	0.065

[tbp]

Table C9

Model Fit for Medium Differences in Residuals

Model	AIC	BIC	CFI	TLI	RMSEA	SRMR
Overall	7,382.013	7,445.232	0.997	0.995	0.016	0.018
Group Group 1	3,765.749	3,818.571	0.976	0.953	0.047	0.031
Group Group 2	3,602.905	3,655.727	1.000	1.013	0.000	0.023
Configural	7,368.654	7,495.092	0.992	0.983	0.028	0.027
Loadings	7,364.904	7,474.483	0.990	0.986	0.025	0.036
Intercepts	7,358.503	7,451.224	1.000	1.001	0.000	0.037
Residuals	7,385.958	7,457.607	0.864	0.881	0.075	0.098

[tbp]

Table C10

Model Fit for Large Differences in Residuals

Model	AIC	BIC	CFI	TLI	RMSEA	SRMR
Overall	7,300.856	7,364.075	0.998	0.995	0.015	0.018
Group Group 1	3,765.749	3,818.571	0.976	0.953	0.047	0.031
Group Group 2	3,453.099	3,505.921	0.954	0.908	0.069	0.035
Configural	7,218.848	7,345.287	0.965	0.929	0.059	0.033
Loadings	7,217.332	7,326.912	0.955	0.935	0.056	0.045
Intercepts	7,211.566	7,304.287	0.962	0.958	0.046	0.047
Residuals	7,304.566	7,376.215	0.562	0.619	0.137	0.189

Appendix D

Simulated Partial Invariance Results

[tbp]

Table D1

Fit Estimates for Partial Invariance

Residuals on Invariant Data

Estimated Parameter	CFI	RSMEA
q1 ~~ q1	0.990	0.021
q2 ~~ q2	0.987	0.024
q3 ~~ q3	0.996	0.014
q4 ~~ q4	1.000	0.000
q5 ~~ q5	0.987	0.025
lv ~~ lv	0.991	0.020

[tbp]

Table D2

Fit Estimates for Partial Invariance

Loadings for Small Loading Data

Estimated Parameter	CFI	RSMEA
lv =~ q1	0.993	0.019
lv =~ q2	0.989	0.023
lv =~ q3	0.989	0.023
lv =~ q4	1.000	0.000
lv =~ q5	0.994	0.017

[tbp]

Table D3

Fit Estimates for Partial Invariance

Loadings for Medium Loading Data

Estimated Parameter	CFI	RSMEA
lv =~ q1	0.880	0.079
lv =~ q2	0.898	0.074
lv =~ q3	0.878	0.081
lv =~ q4	0.962	0.045
lv =~ q5	0.907	0.071

[tbp]

Table D4

Fit Estimates for Partial Invariance

Loadings for Large Loading Data

Estimated Parameter	CFI	RSMEA
lv =~ q1	0.762	0.116
lv =~ q2	0.770	0.117
lv =~ q3	0.762	0.119
lv =~ q4	0.971	0.041
lv =~ q5	0.842	0.097

[tbp]

Table D5

Fit Estimates for Partial Invariance

Loadings for Small Intercept Data

Estimated Parameter	CFI	RSMEA
q1 ~1	0.975	0.033
lv ~1	0.975	0.033
q2 ~1	0.972	0.035
q3 ~1	0.972	0.036
q4 ~1	0.988	0.023
q5 ~1	0.971	0.036

[tbp]

Table D6

Fit Estimates for Partial Invariance

Loadings for Medium Intercept Data

Estimated Parameter	CFI	RSMEA
q1 ~1	0.905	0.065
lv ~1	0.905	0.065
q2 ~1	0.901	0.067
q3 ~1	0.901	0.067
q4 ~1	0.988	0.023
q5 ~1	0.902	0.067

[tbp]

Table D7

Fit Estimates for Partial Invariance

Loadings for Large Intercept Data

Estimated Parameter	CFI	RSMEA
q1 ~1	0.785	0.097
lv ~1	0.785	0.097
q2 ~1	0.781	0.100
q3 ~1	0.781	0.100
q4 ~1	0.988	0.023
q5 ~1	0.784	0.099

[tbp]

Table D8

Fit Estimates for Partial Invariance

Loadings for Small Residual Data

Estimated Parameter	CFI	RSMEA
q1 ~~ q1	0.928	0.056
q2 ~~ q2	0.936	0.053
q3 ~~ q3	0.926	0.057
q4 ~~ q4	0.955	0.044
q5 ~~ q5	0.926	0.057
lv ~~ lv	0.930	0.054

[tbp]

Table D9

Fit Estimates for Partial Invariance

Loadings for Medium Residual Data

Estimated Parameter	CFI	RSMEA
q1 ~~ q1	0.869	0.075
q2 ~~ q2	0.860	0.078
q3 ~~ q3	0.870	0.075
q4 ~~ q4	0.994	0.016
q5 ~~ q5	0.862	0.077
lv ~~ lv	0.864	0.075

[tbp]

Table D10

Fit Estimates for Partial Invariance

Loadings for Large Residual Data

Estimated Parameter	CFI	RSMEA
q1 ~~ q1	0.558	0.140
q2 ~~ q2	0.559	0.140
q3 ~~ q3	0.560	0.140
q4 ~~ q4	0.972	0.035
q5 ~~ q5	0.559	0.140
lv ~~ lv	0.562	0.137

Appendix E

Invariance Plots Difference Scores by Condition

Medium Loadings Graph Results

Large Loadings Graph Results

Small Intercepts Graph Results

Medium Intercepts Graph Results

Large Intercepts Graph Results

Small Residuals Graph Results

Medium Residuals Graph Results

972

Large Residuals Graph Results

973
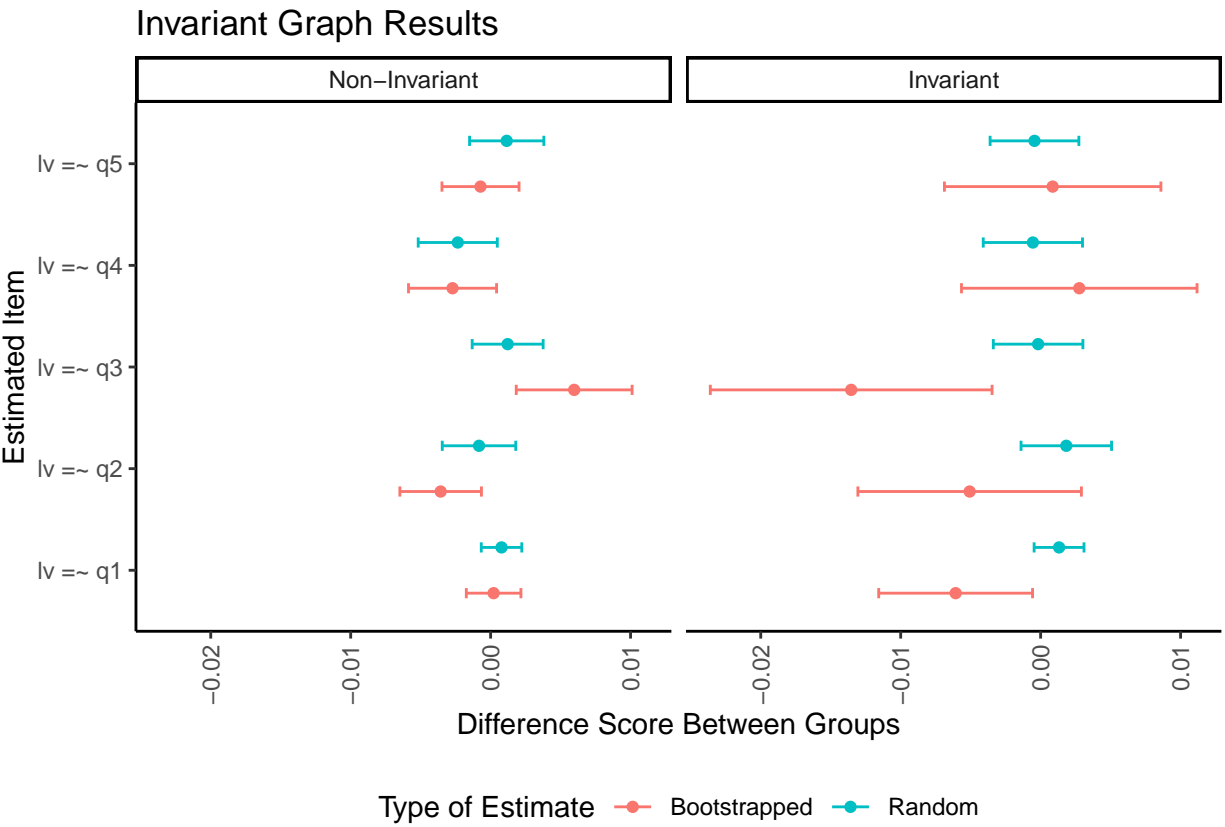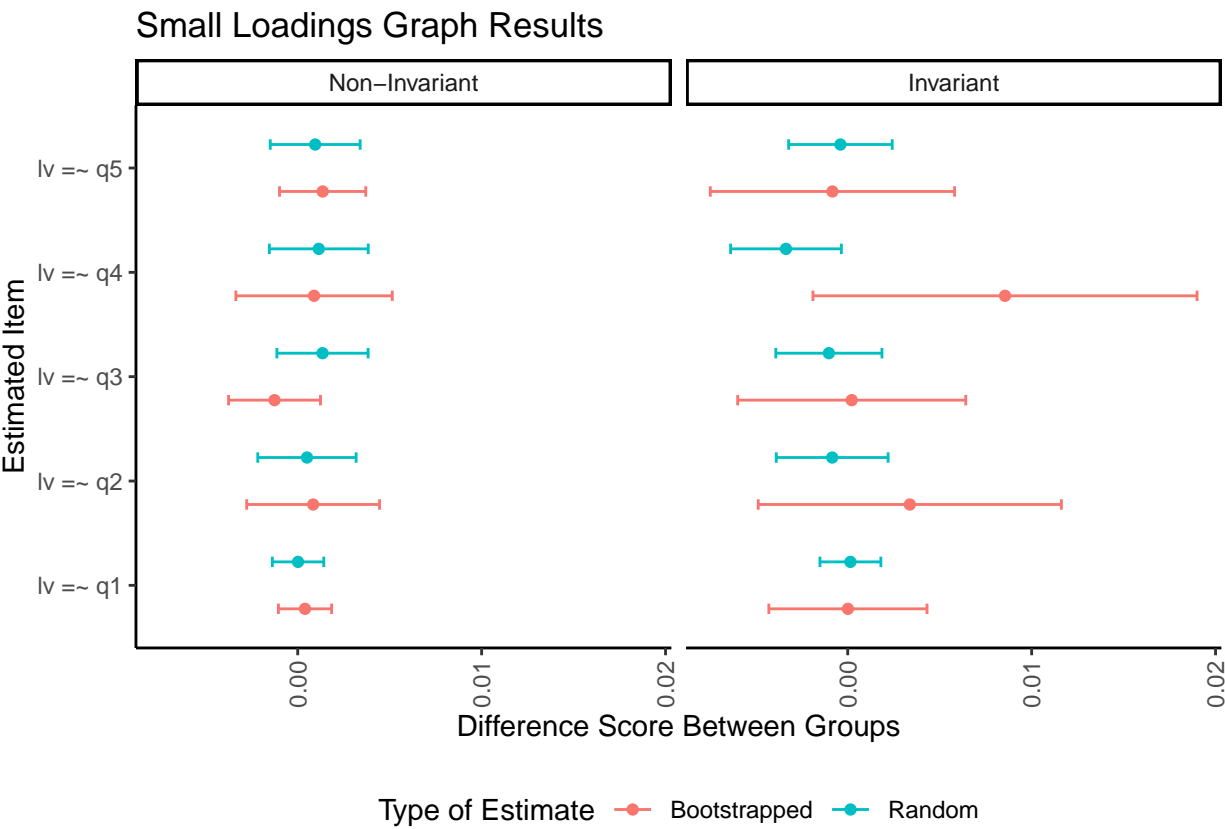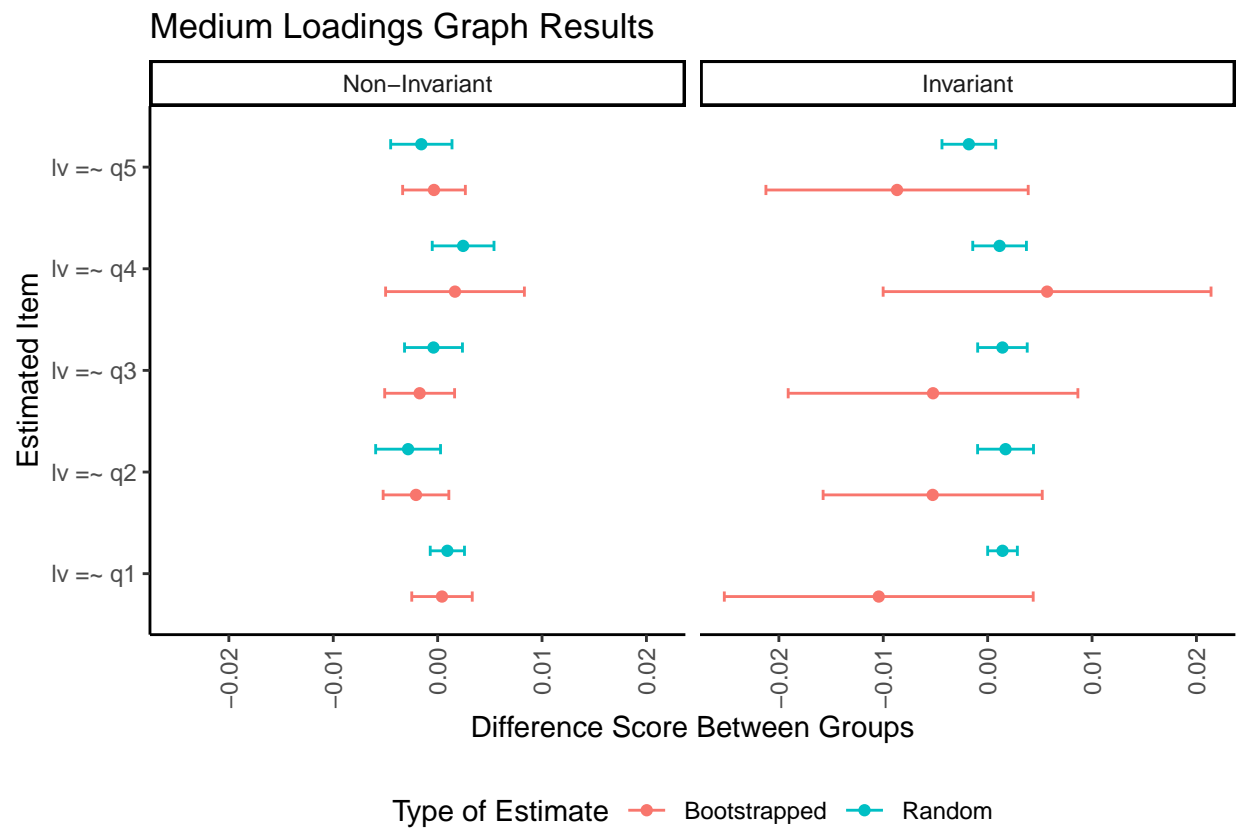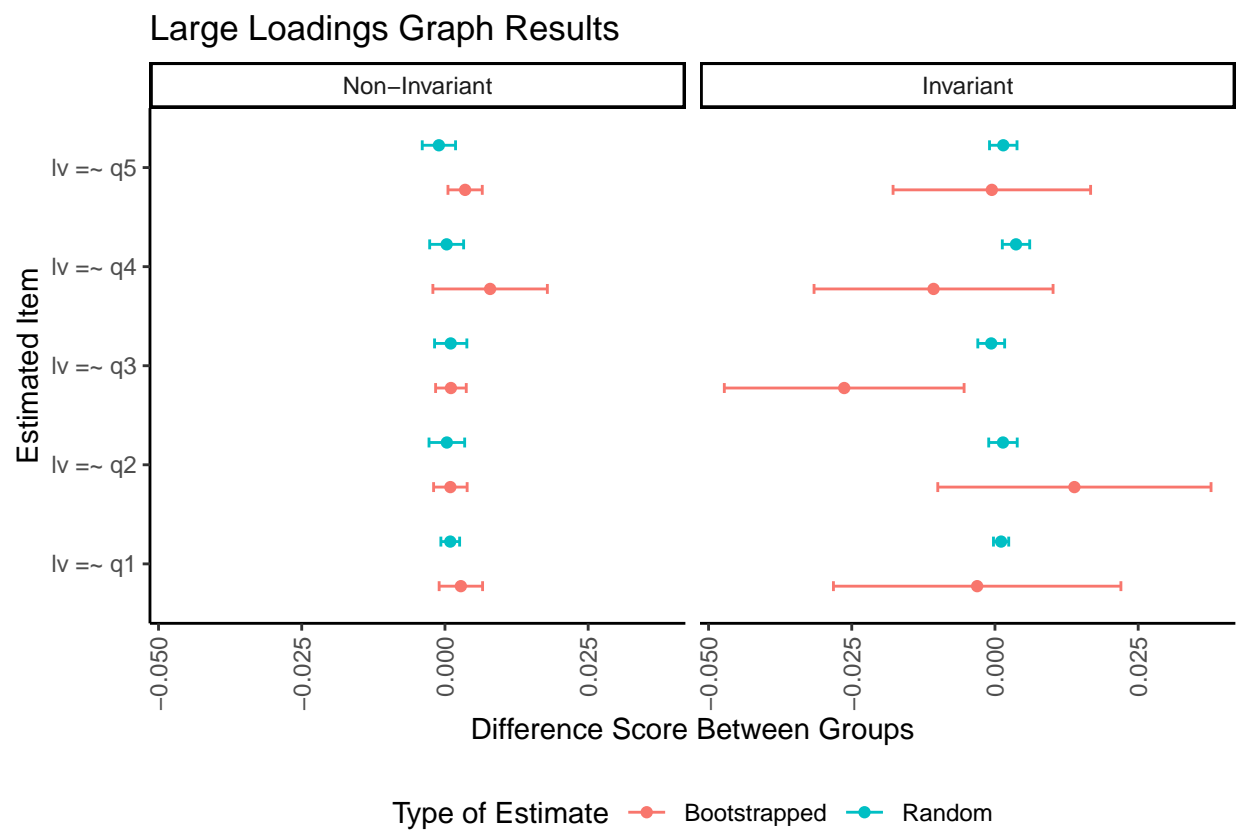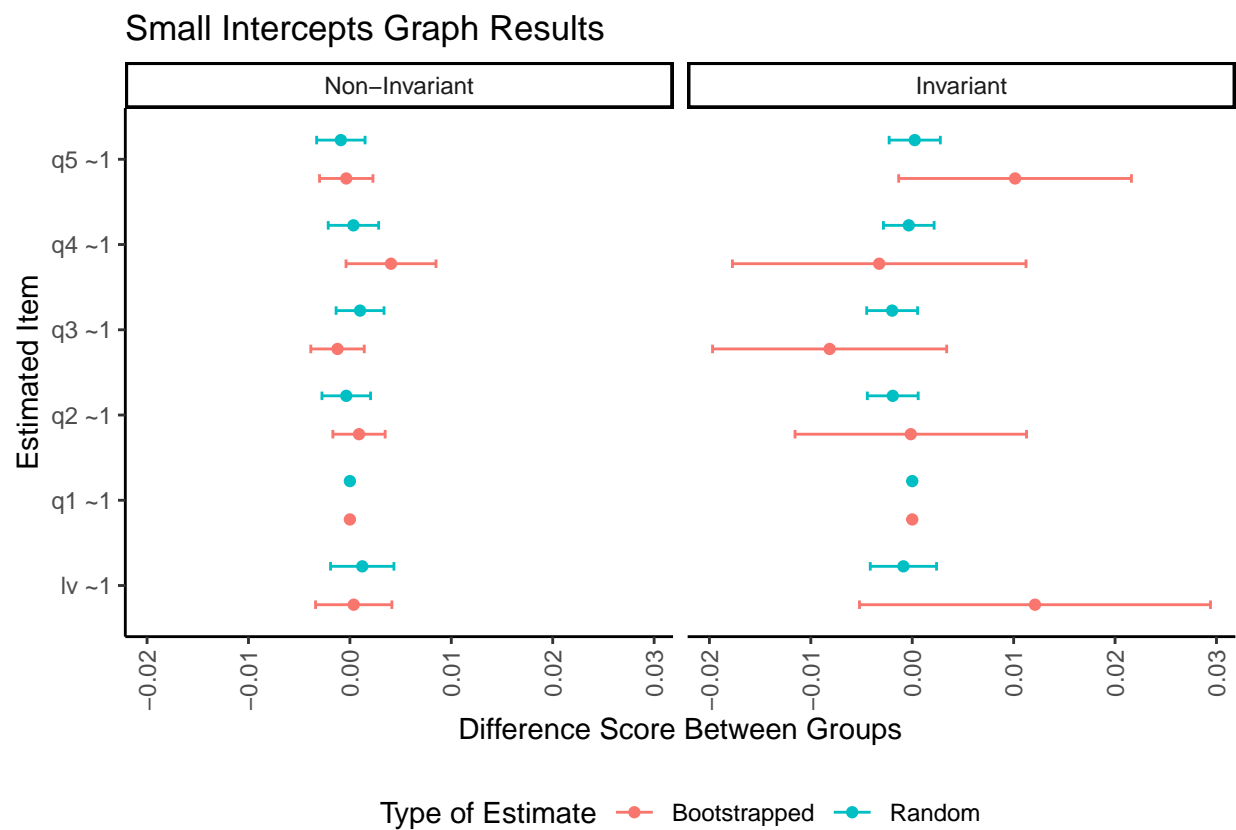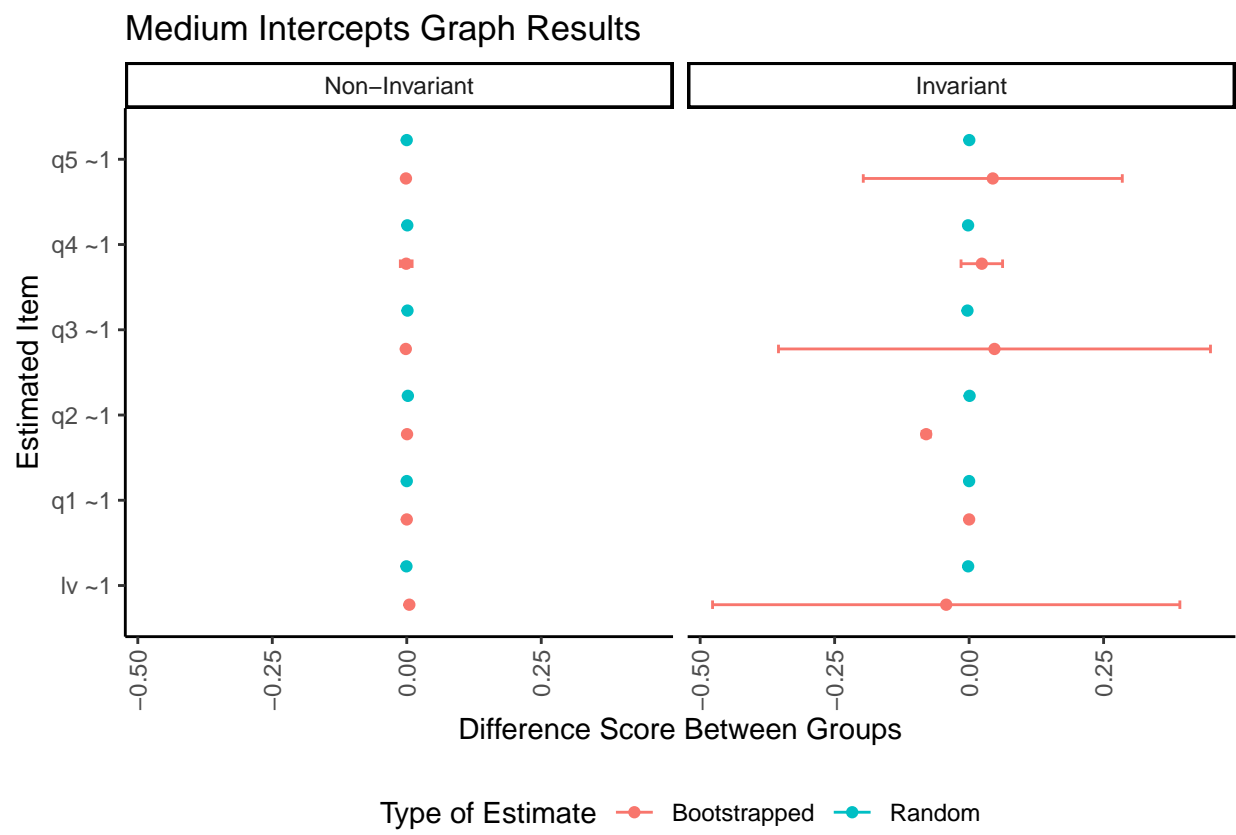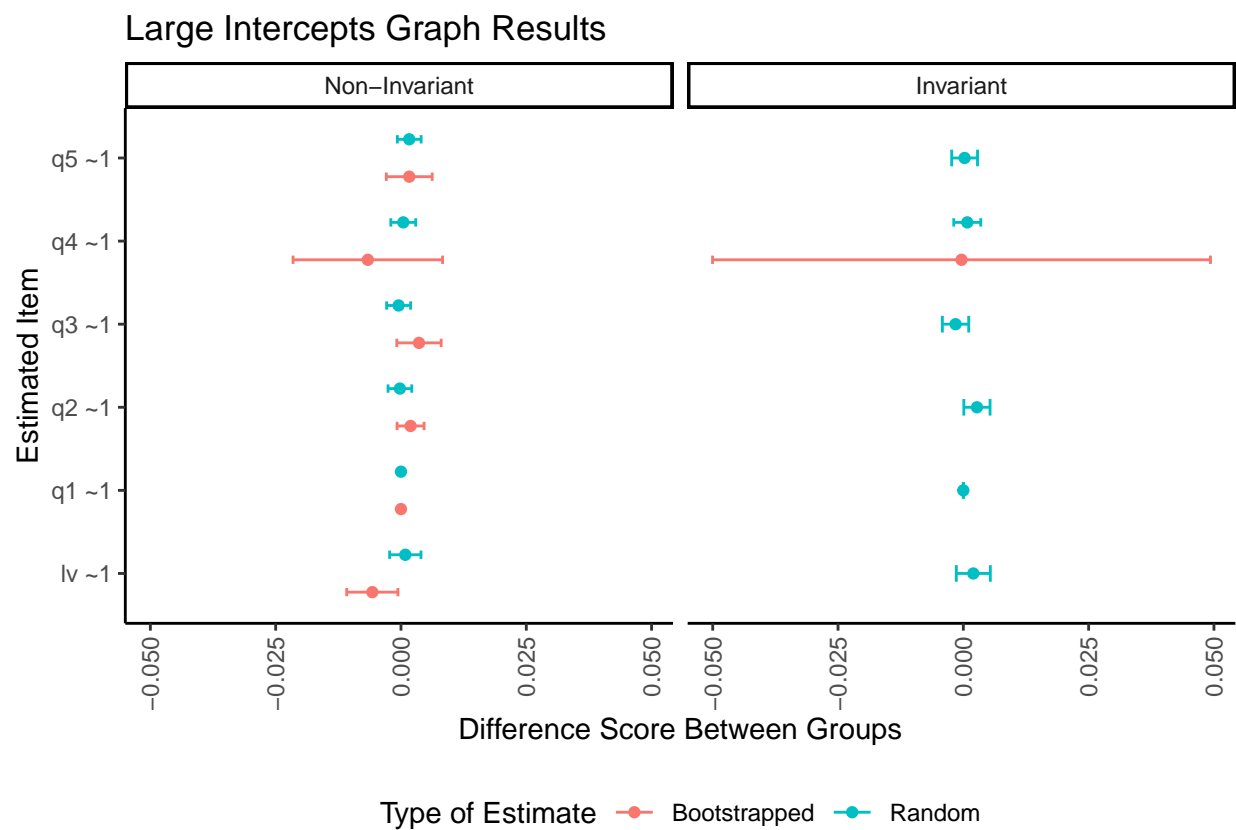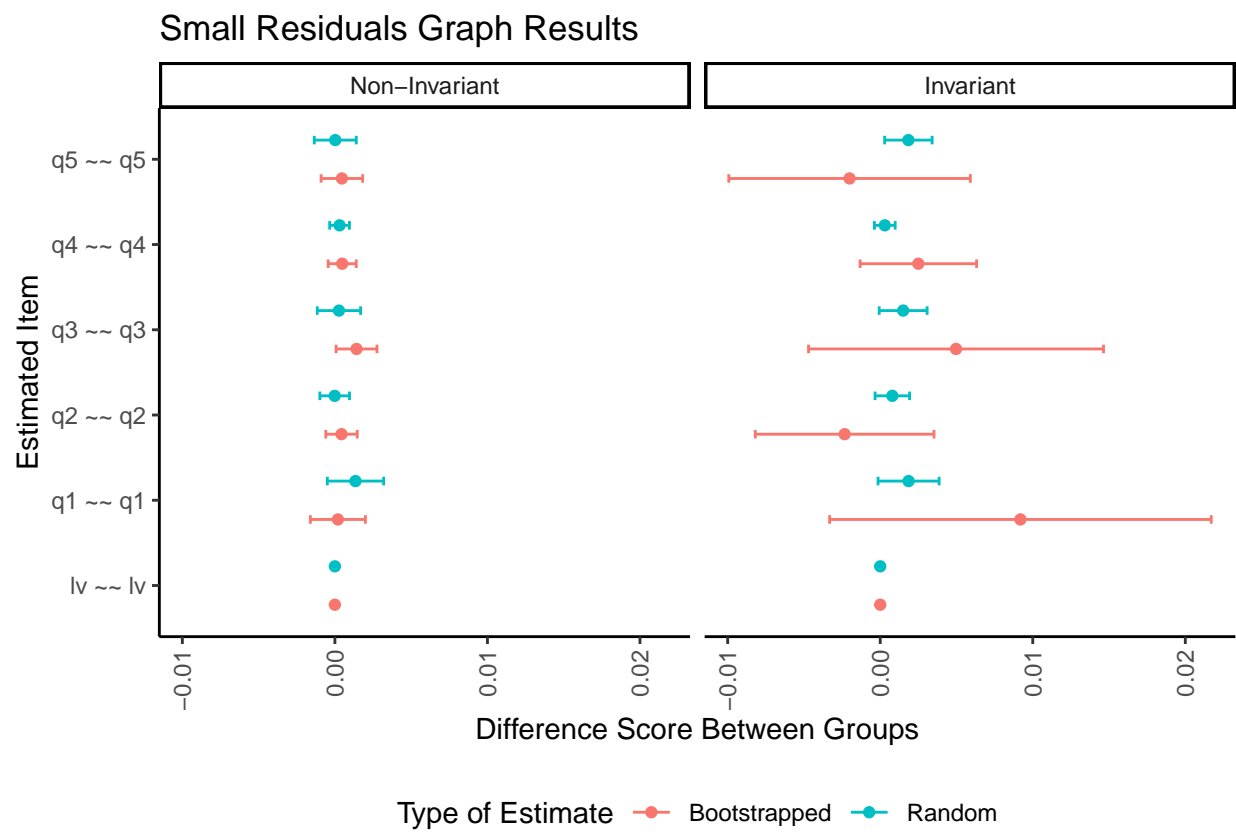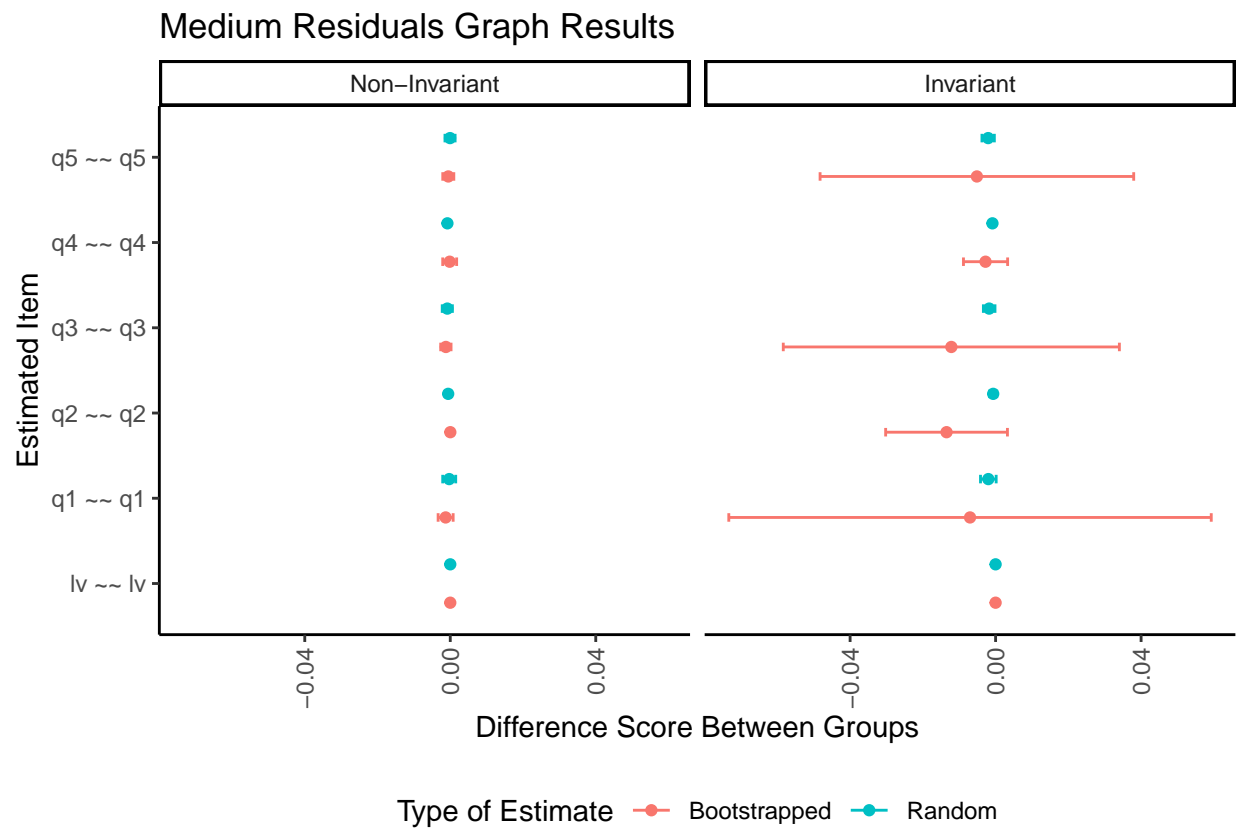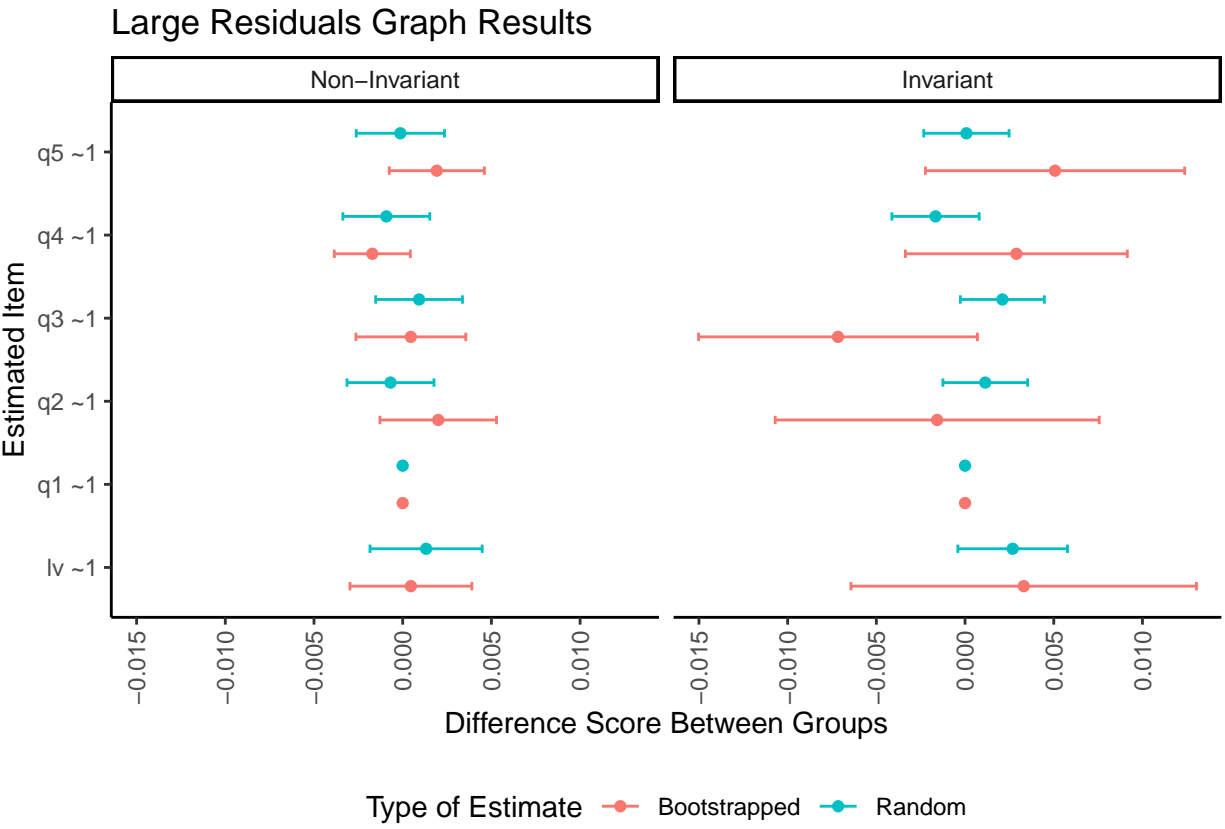
Appendix F

Invariance Plots Effect Sizes by Condition

Invariant Graph Results

Small Loadings Graph Results

Medium Loadings Graph Results

976

Large Loadings Graph Results

Small Intercepts Graph Results

Medium Intercepts Graph Results

Large Intercepts Graph Results

Small Residuals Graph Results

Medium Residuals Graph Results

Large Residuals Graph Results
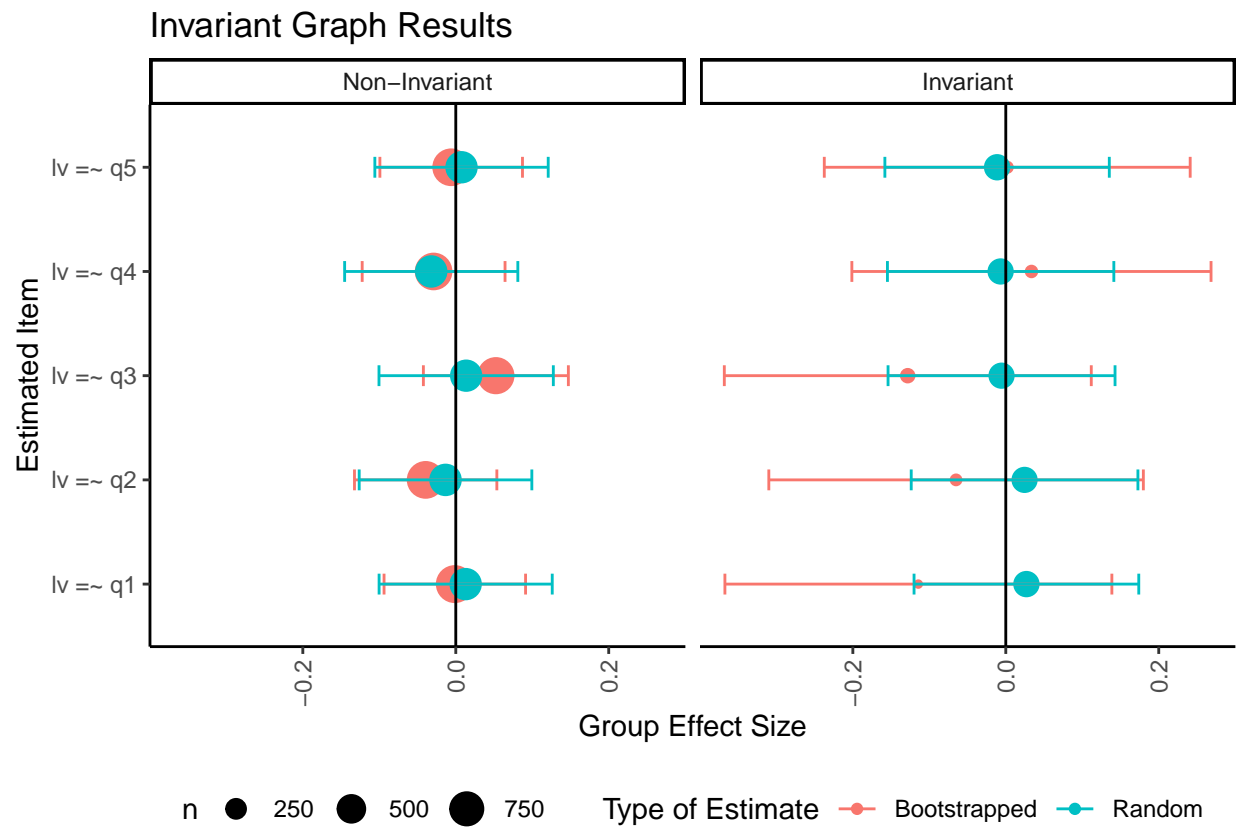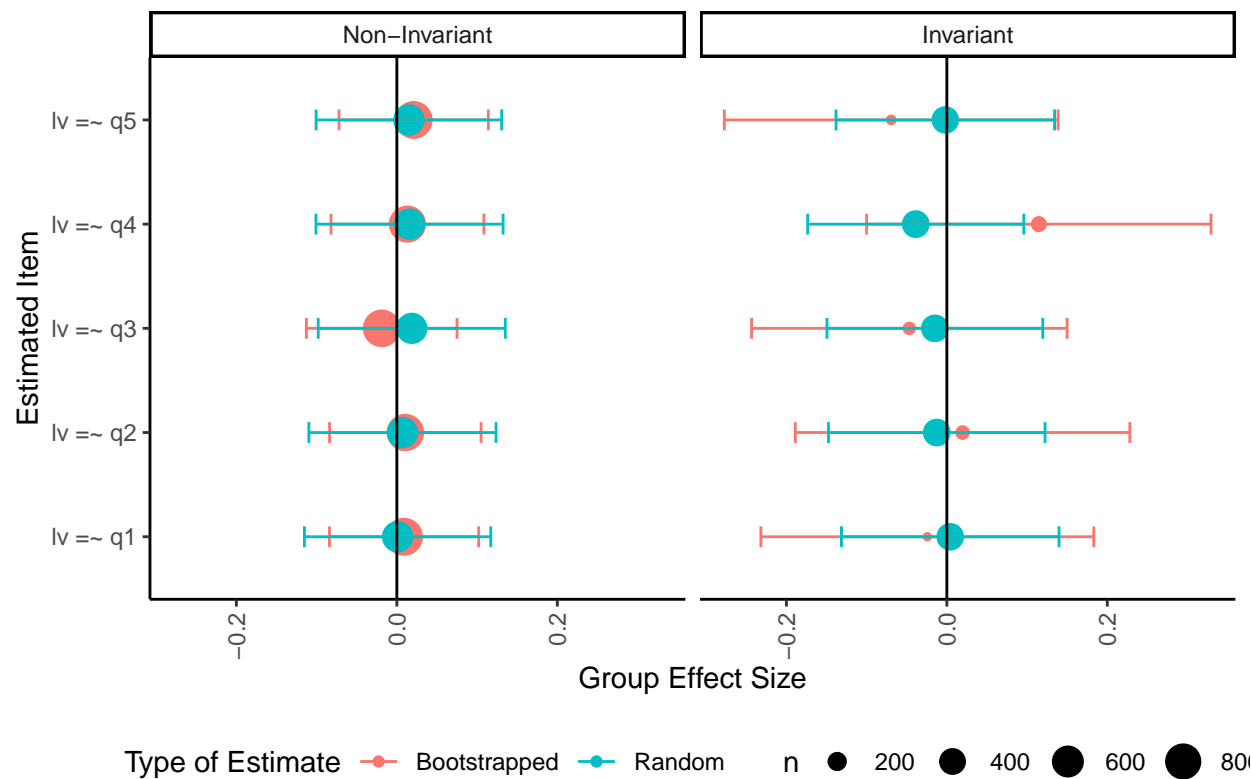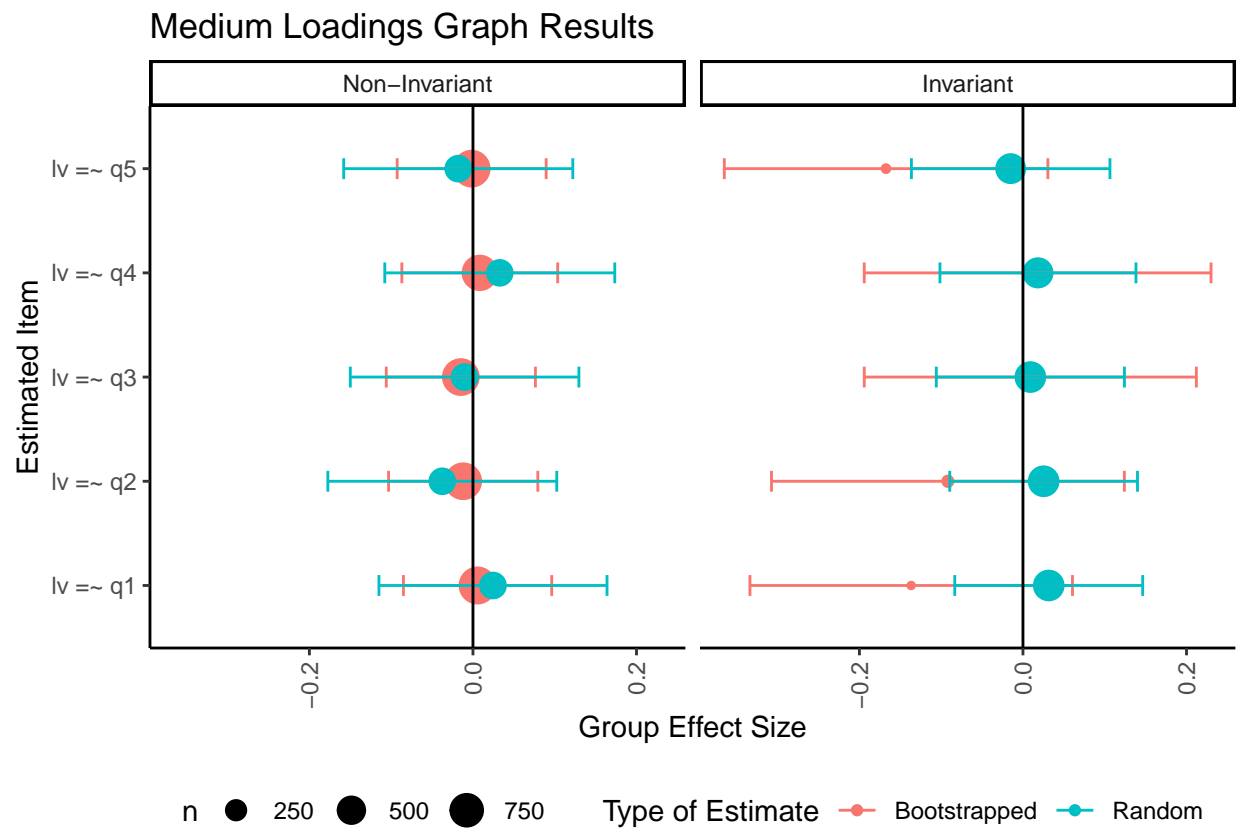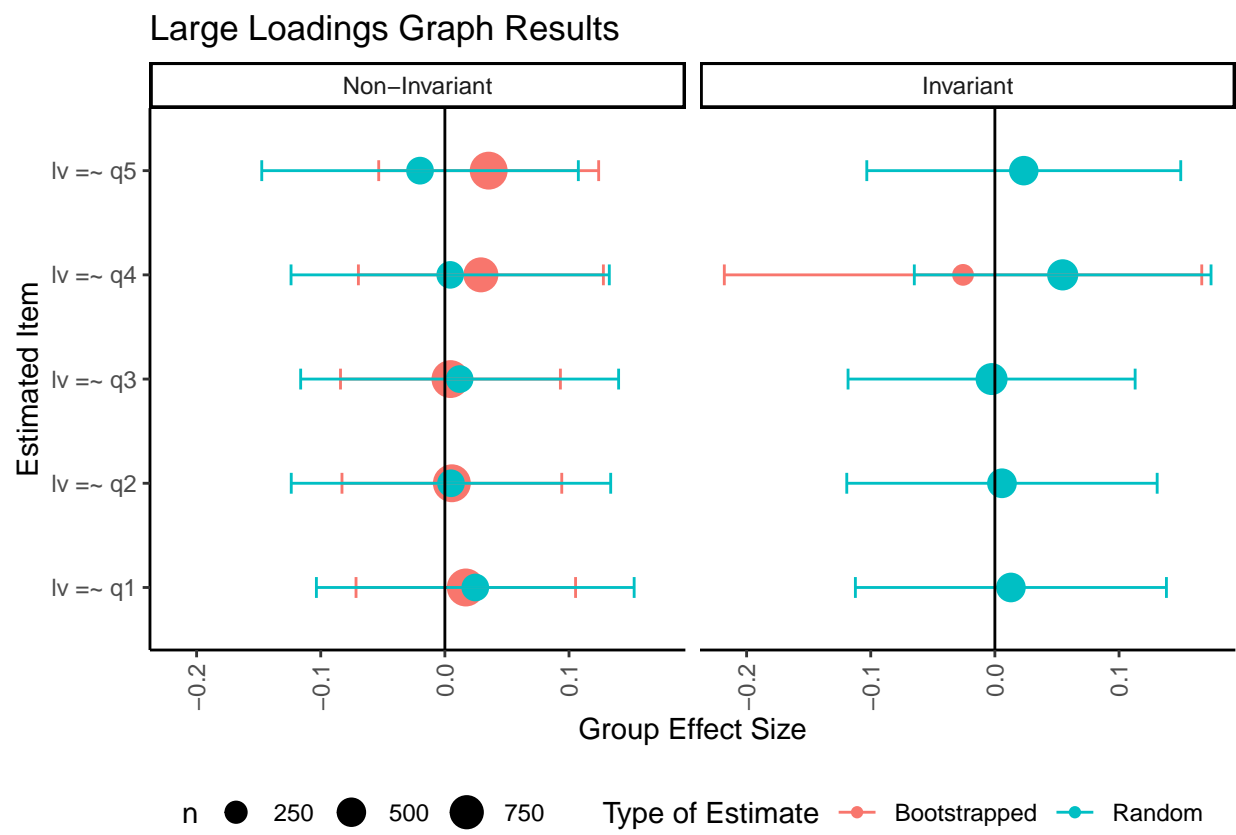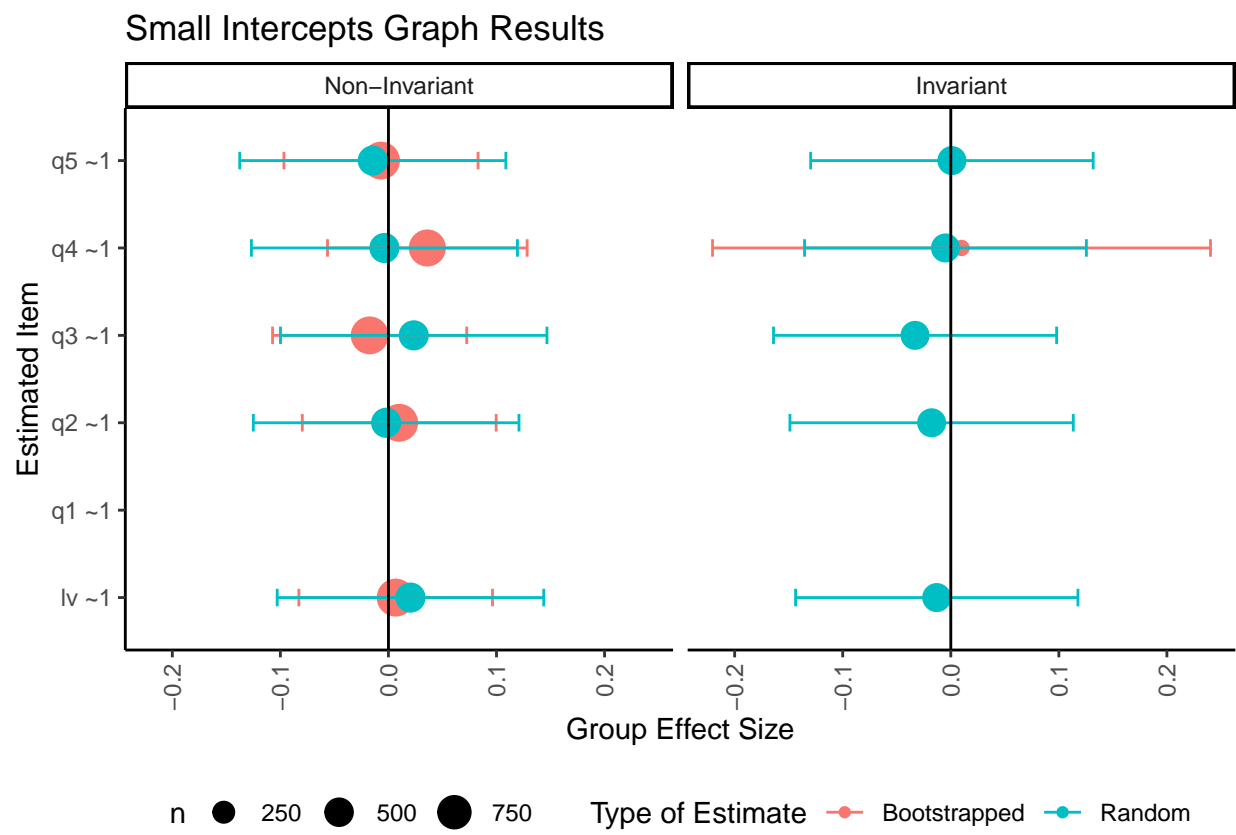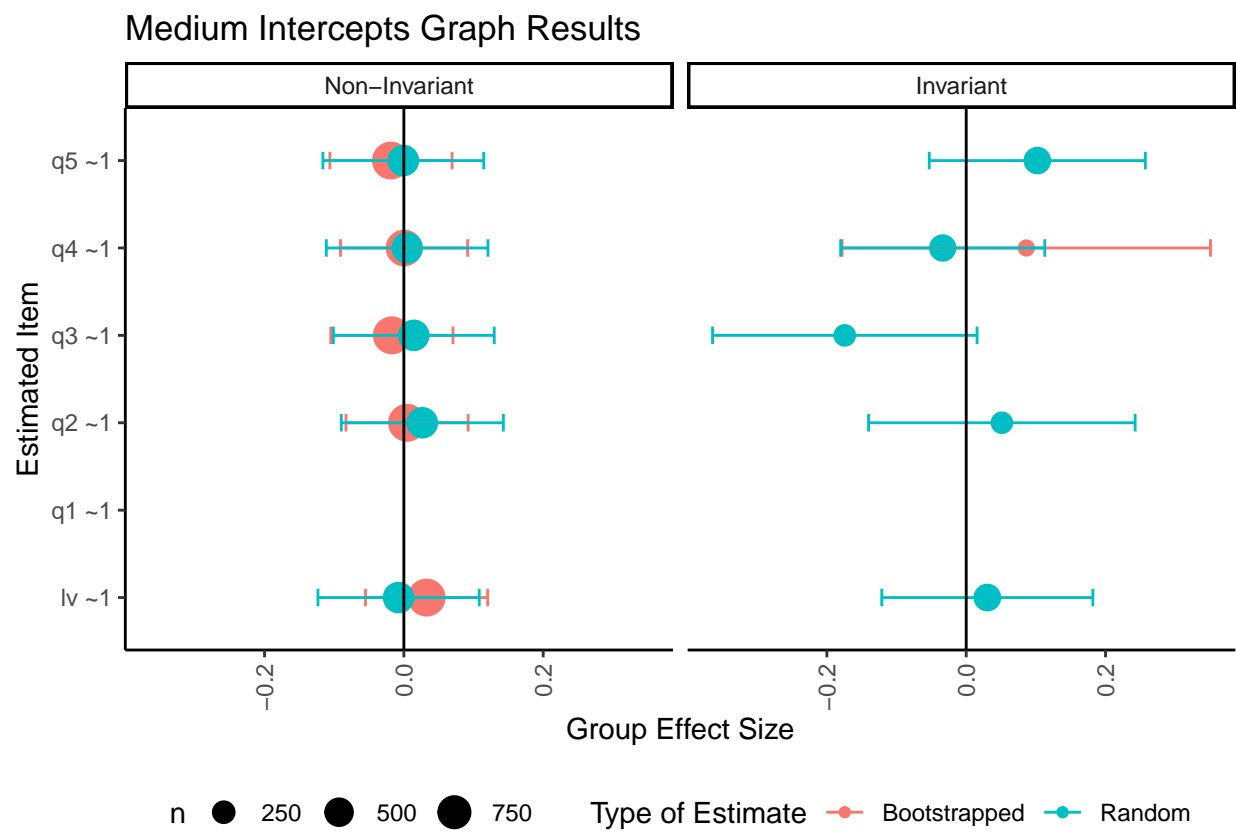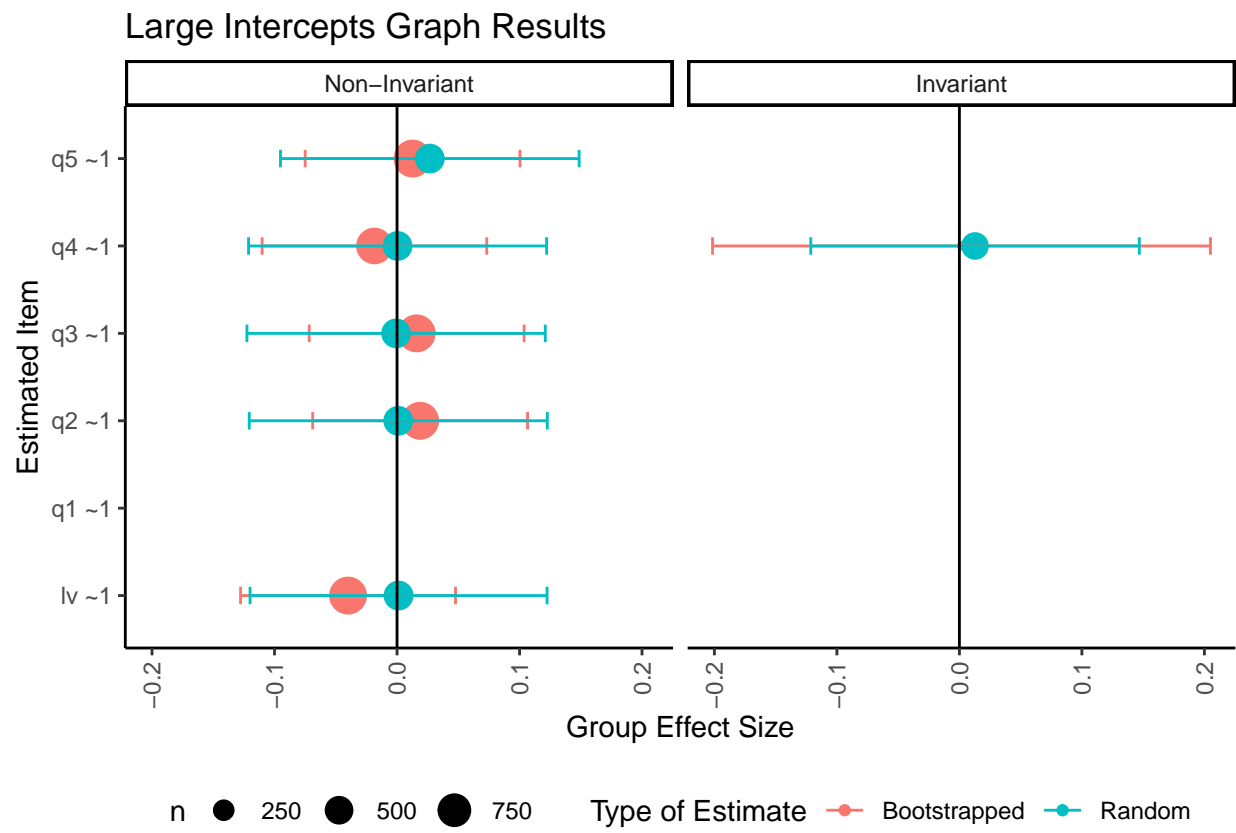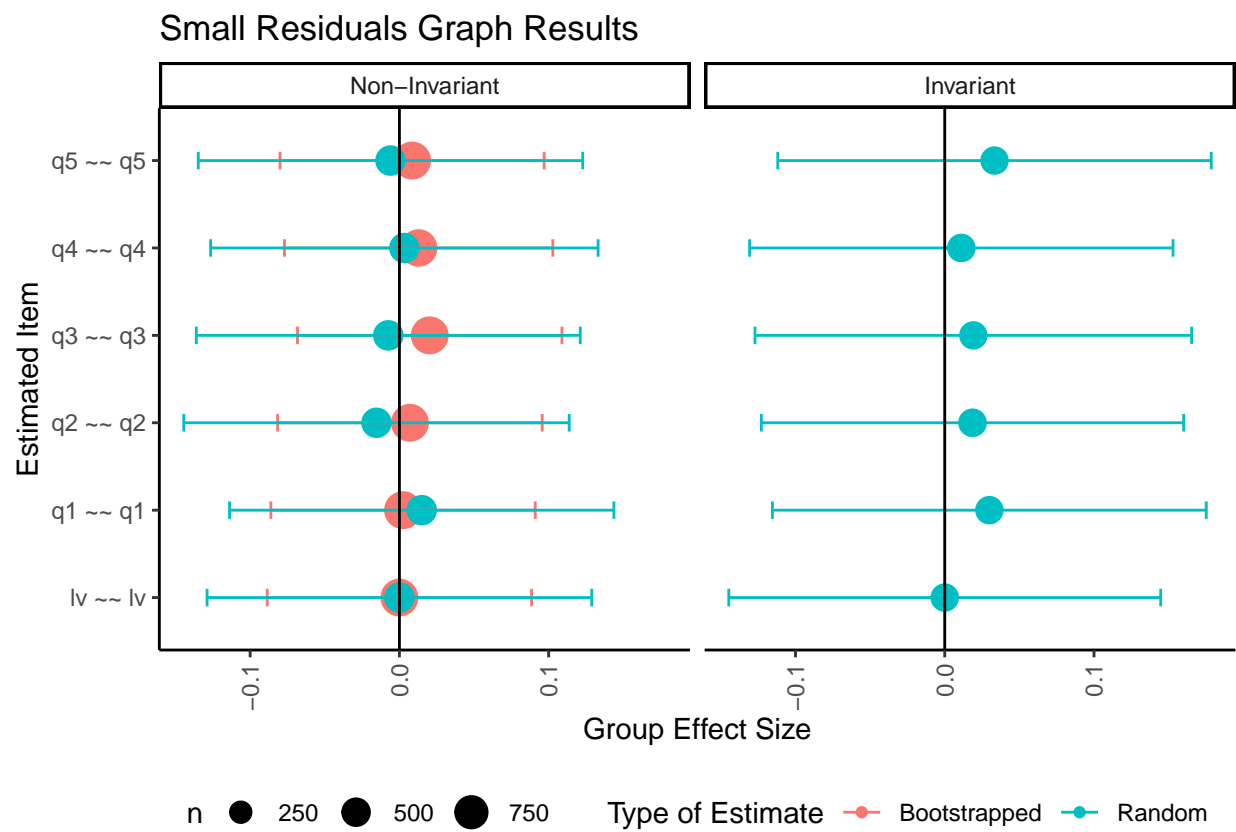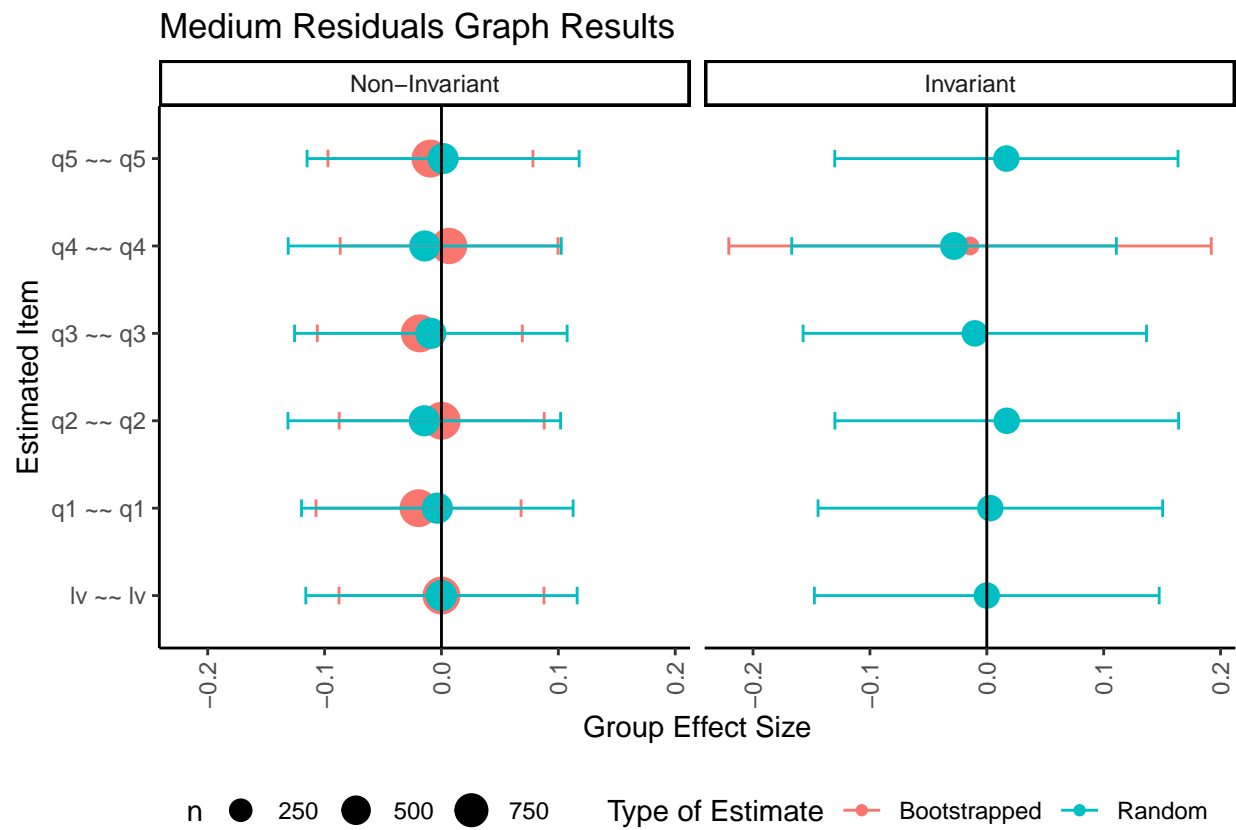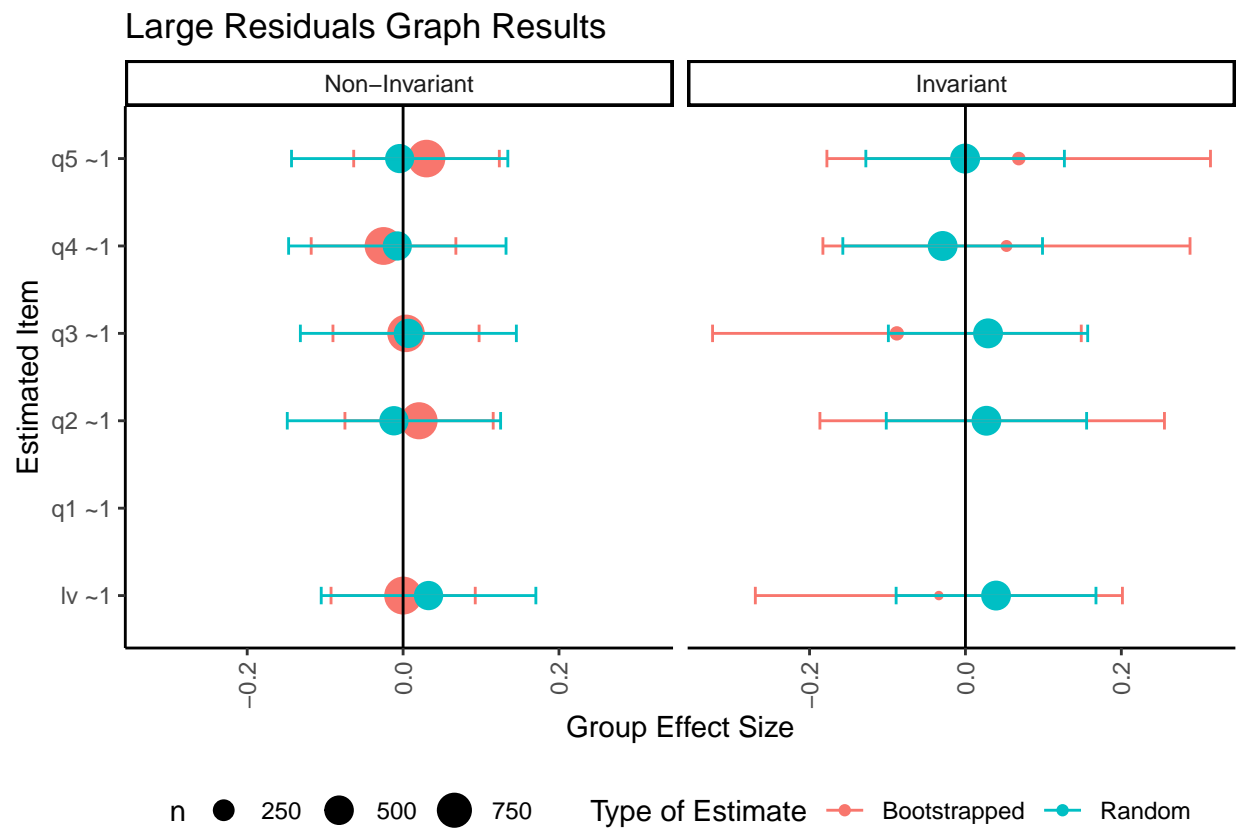
Appendix G

Density Plots by Condition

Invariant Graph Results

Small Loadings Graph Results

Medium Loadings Graph Results

Large Loadings Graph Results

Small Intercepts Graph Results

988

Medium Intercepts Graph Results

Large Intercepts Graph Results

Small Residuals Graph Results

Medium Residuals Graph Results

992

Large Residuals Graph Results
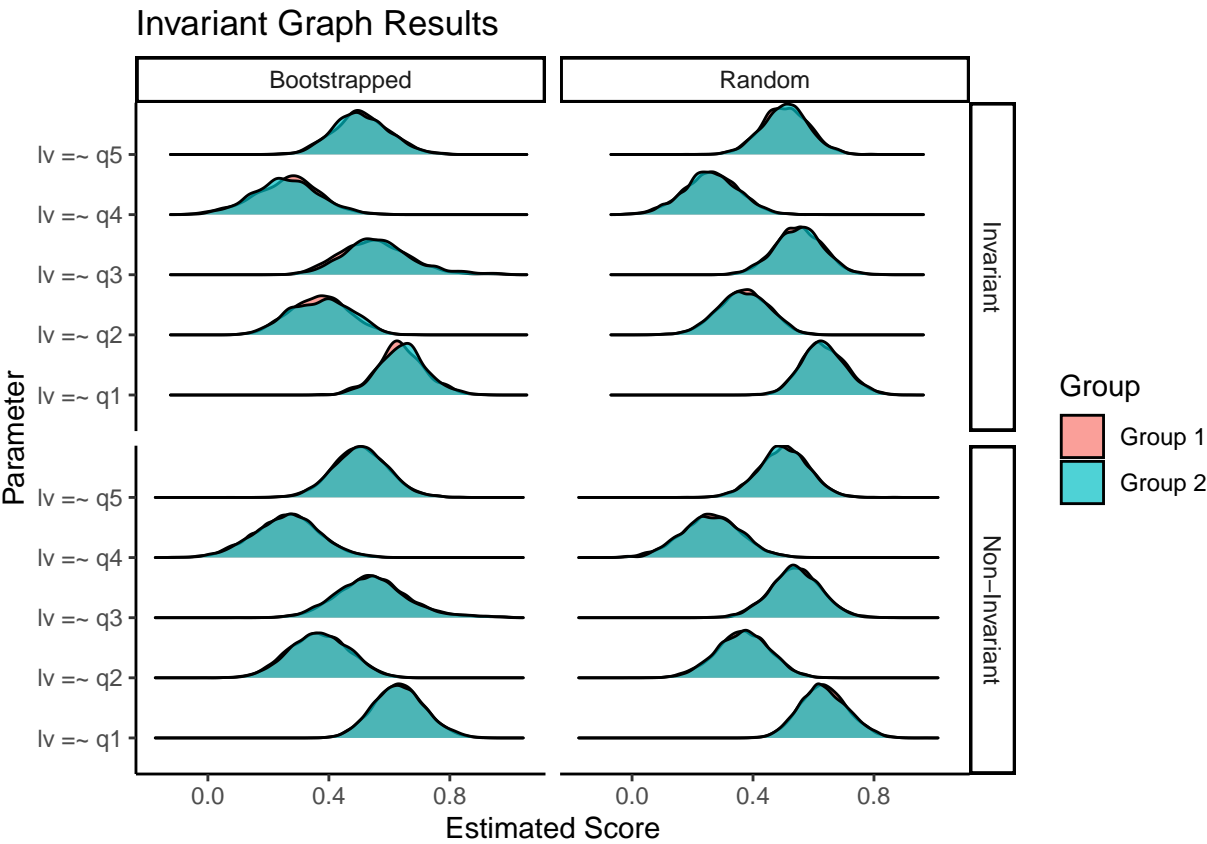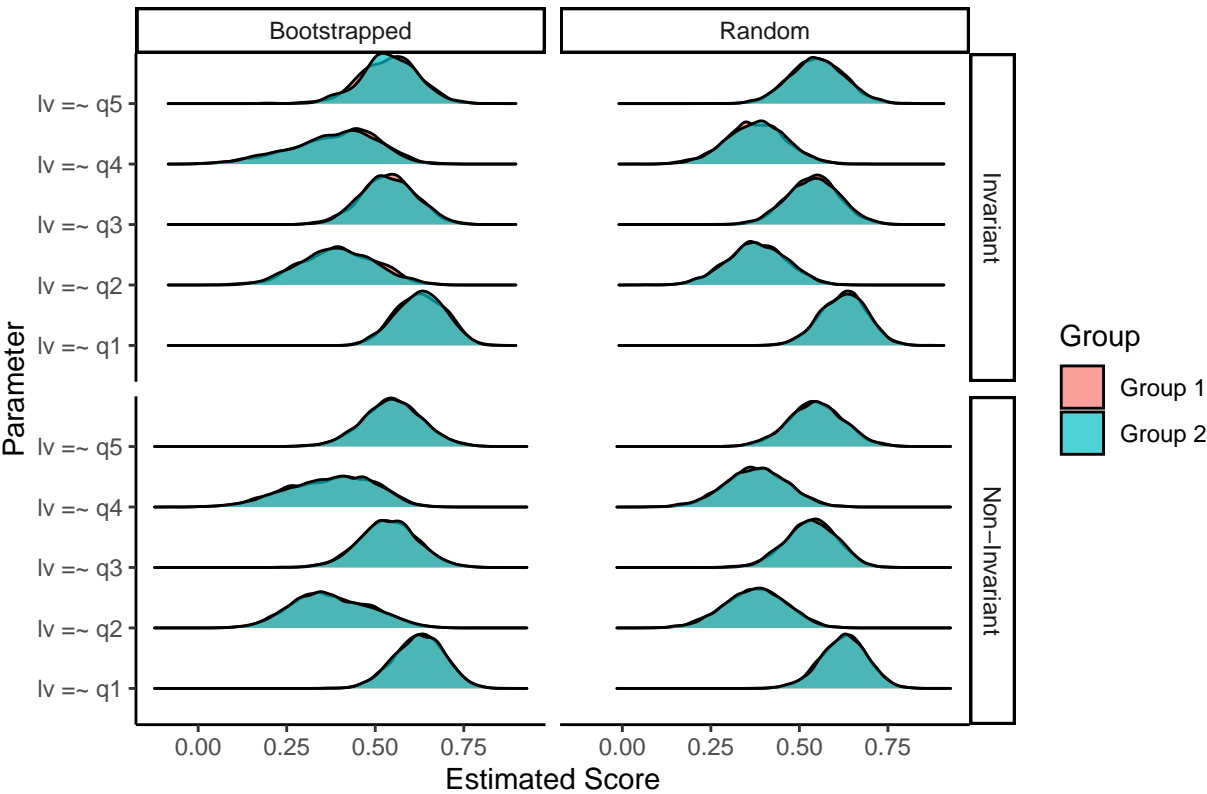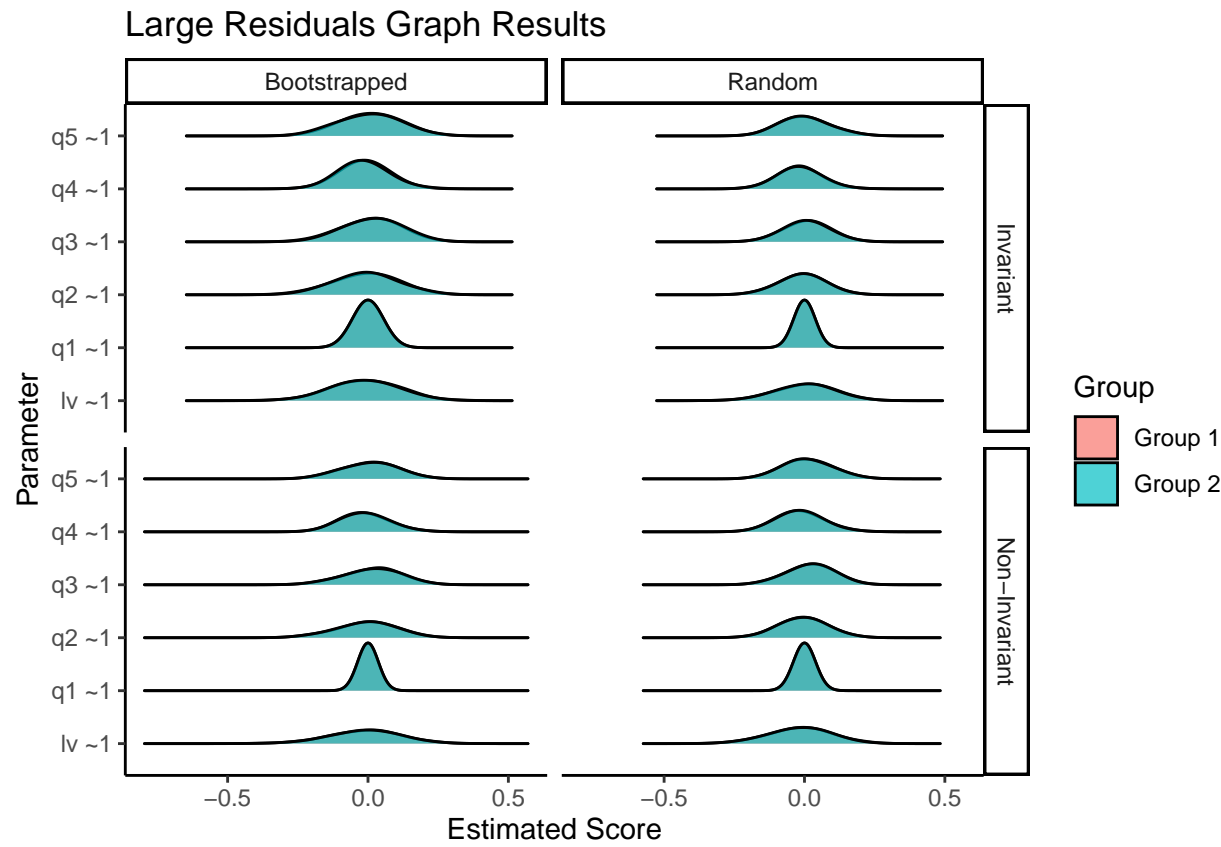
Replication Test

Data

```
## # A tibble: 2 x 2
##   group       sample
##   <chr>        <int>
## 1 Chen          1010
## 2 Schulenberg   1765
```

MGCFA

```
## # A tibble: 7 x 7
##   model              AIC      BIC   cfi   tli  rmsea   srmr
##   <chr>            <dbl>    <dbl> <dbl> <dbl>  <dbl>  <dbl>
## 1 Overall        113442. 113608. 0.939 0.928 0.0890 0.0344
## 2 Group Schulenberg 69101.  69254. 0.928 0.915 0.108  0.0353
```

```
## 3 Group Chen        42603.   42741. 0.929 0.916 0.0766 0.0399
```

```
## 4 Configural       111760. 112258. 0.929 0.916 0.0975 0.0347
```

```
## 5 loadings         111789. 112210. 0.927 0.921 0.0946 0.0427
```

```
## 6 intercepts       112785. 113129. 0.892 0.891 0.111  0.0599
```

```
## 7 residuals        113318. 113579. 0.873 0.880 0.116  0.0661
```

Overall, the one-factor model fits the data well. Each group also shows adequate model fit. If we use ΔCFI $<=$ .01, we find that the loadings would be considered invariant across the English and Chinese samples. The intercepts were not invariant.

Partial Invariance

```
## # A tibble: 15 x 2
```

```
##    free.parameter cfi
```

```
##    <chr>          <lvn.vctr>
```

```
##  1 "RS2 ~1 "      0.8970997
```

```
##  2 "RS11 ~1 "     0.8963948
```

```
##  3 "RS4 ~1 "      0.8961938
```

```
##  4 "RS12 ~1 "     0.8960095
```

```
##  5 "RS14 ~1 "     0.8954496
```

```
##  6 "RS1 ~1 "      0.8954215
```

```
##  7 "RS10 ~1 "     0.8953395
```

```
##  8 "RS3 ~1 "      0.8948455
```

```
##  9 "RS5 ~1 "      0.8945236
```

```
## 10 "RS7 ~1 "      0.8941450
```

```
## 11 "RS8 ~1 "      0.8920022
```

```
## 12 "RS13 ~1 "     0.8919491
```

```
## 13 "RS9 ~1 "      0.8919293
```

```
## 14 "RS ~1 "       0.8917757
```

```
## 15 "RS6 ~1 "        0.8917604
```

Examining partial invariance reveals several potential candidates for partial invariance. In this next section, we relaxed group constraints until we achieved partial invariance (i.e., $\Delta\text{CFI} <= .01$). We will need to find our CFI as at least 0.92. More than half the items are necessary to achieve "partial" invariance (which really implies no invariance is likely possible).

```
## # A tibble: 1 x 6
##       AIC     BIC   cfi   tli  rmsea   srmr
##     <dbl>   <dbl> <dbl> <dbl>  <dbl>  <dbl>
## 1 111935. 112326. 0.922 0.917 0.0966 0.0462
```
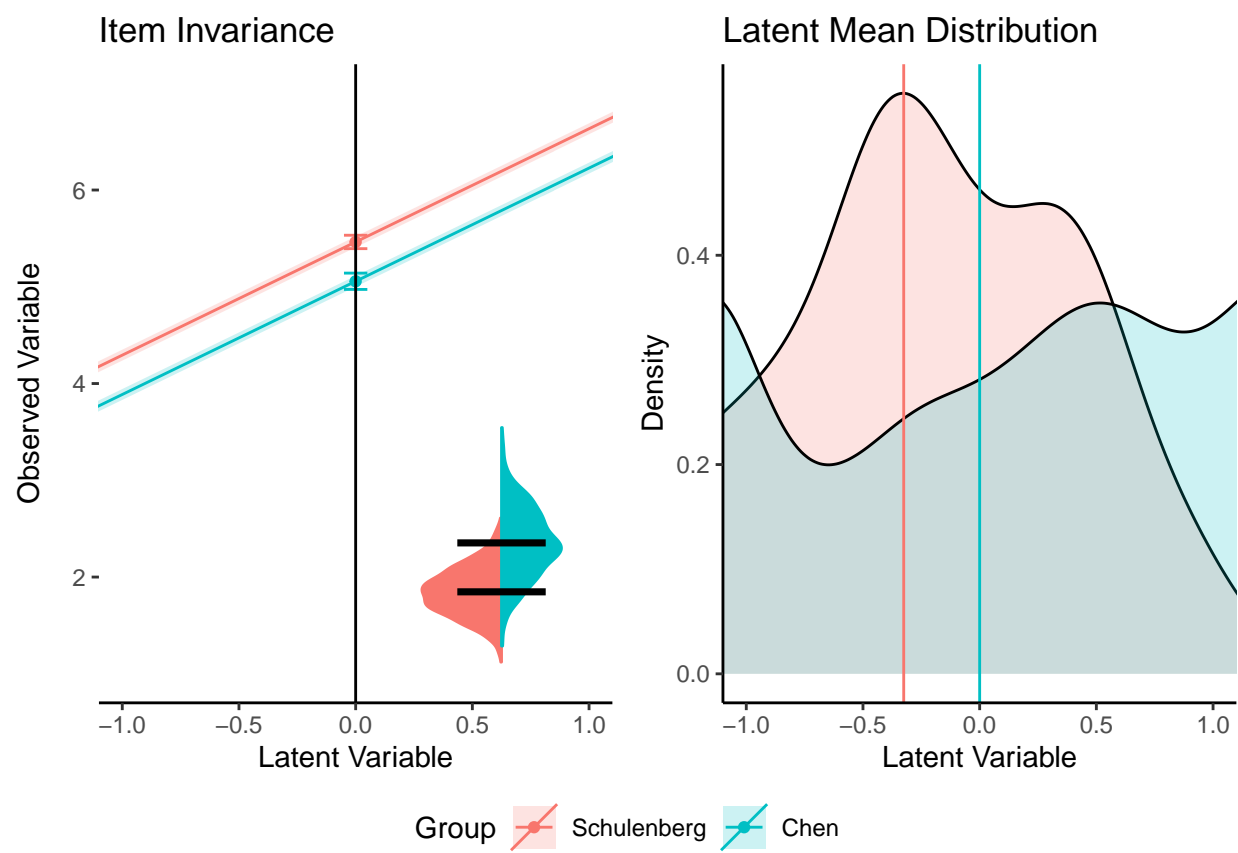
```
## # A tibble: 6 x 3
##   term        English Chinese
##   <chr>         <dbl>   <dbl>
## 1 "RS1 ~1 "      5.24    4.78
## 2 "RS3 ~1 "      5.14    5.46
## 3 "RS4 ~1 "      5.29    5.71
## 4 "RS5 ~1 "      5.13    5.13
## 5 "RS7 ~1 "      5.26    5.26
## 6 "RS12 ~1 "     5.57    5.16
```

```
##  RS1  RS2  RS3  RS4  RS5  RS6  RS7  RS8  RS9 RS10 RS11 RS12 RS13 RS14
## 0.32 0.29 0.23 0.30 0.00 0.00 0.00 0.00 0.00 0.29 0.27 0.29 0.00 0.26
```
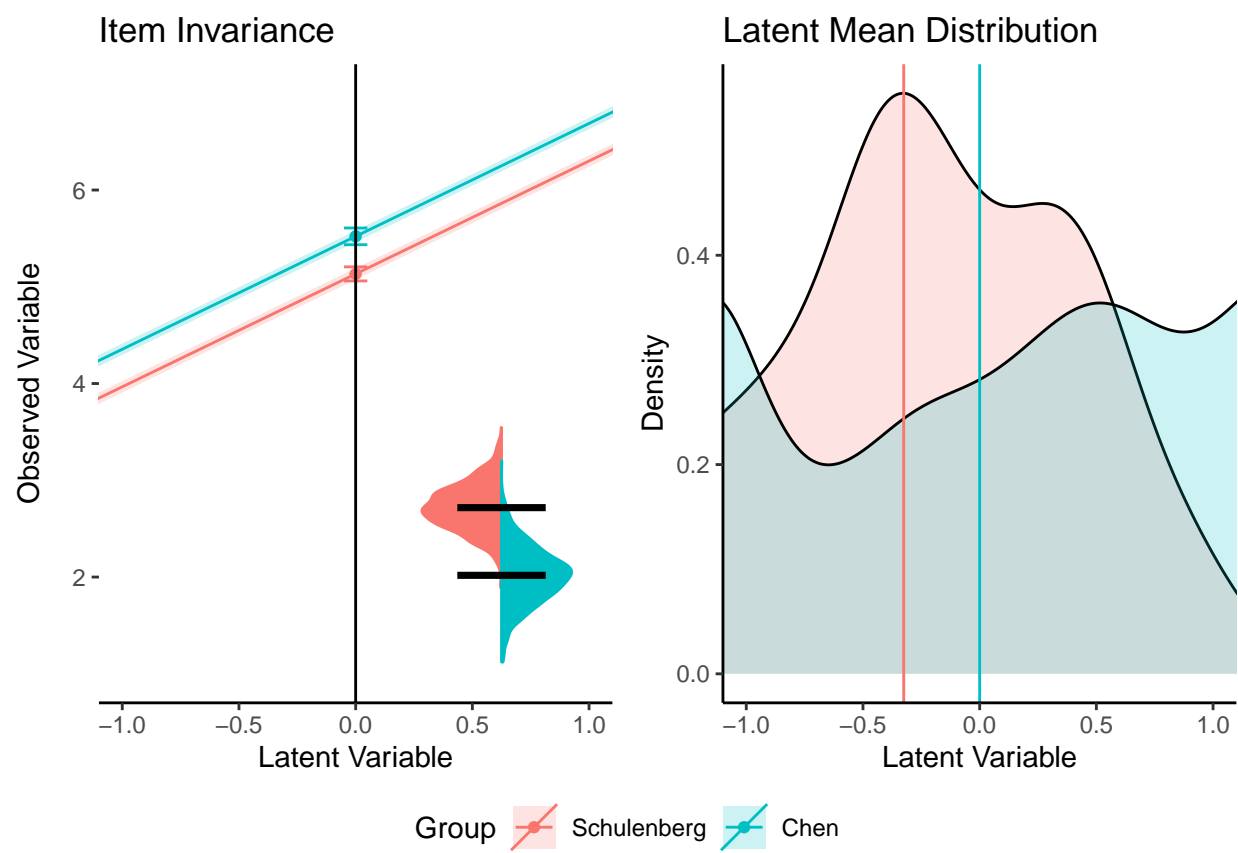
Visualize Invariance

```
## Plot for RS2
```
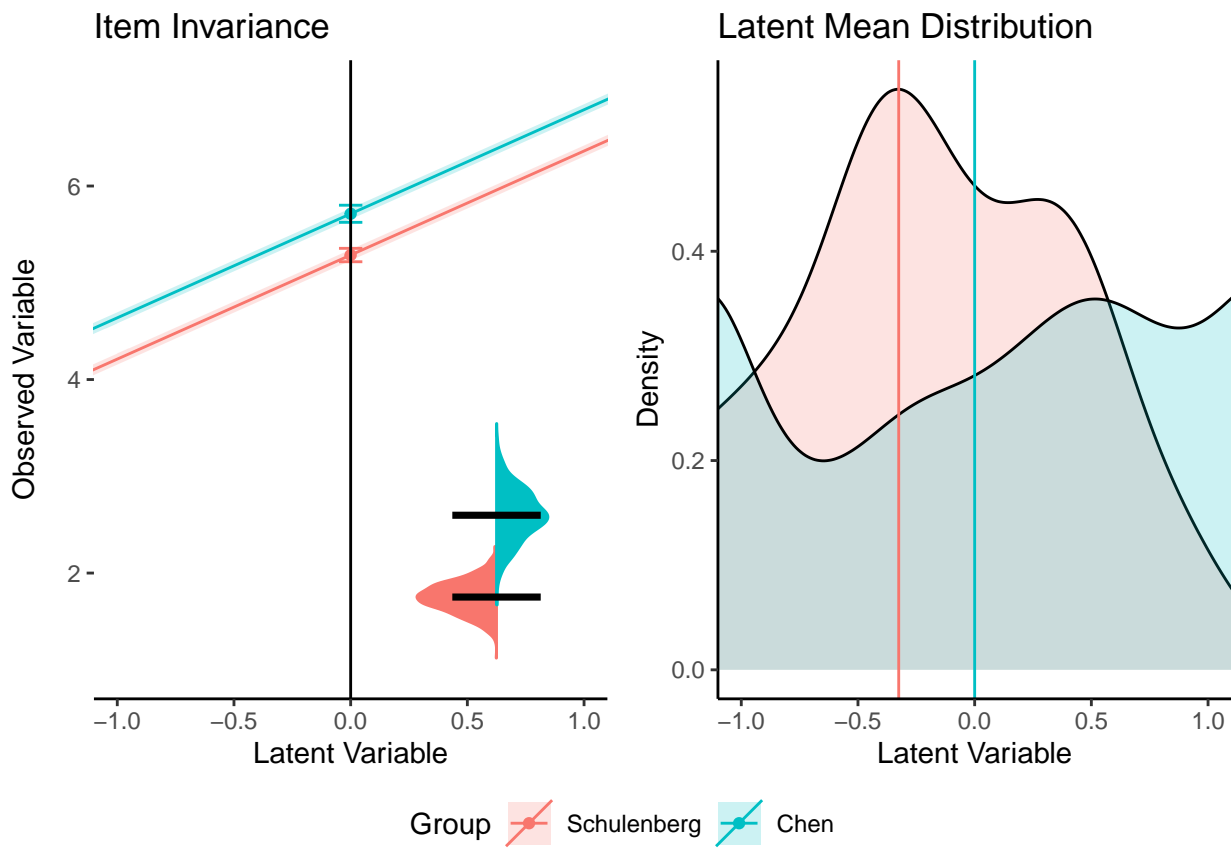
1057 ## -------

1058 ## Plot for RS11

Item Invariance

Latent Mean Distribution

Group ── Schulenberg ── Chen

1060 ## -------

1061 ## Plot for RS4

Item Invariance

Latent Mean Distribution

Group ⟋ Schulenberg ⟋ Chen

1063 ## -------

1064 ## Plot for RS12

1066 ## -------

1067 ## Plot for RS14

Item Invariance

Latent Mean Distribution

Group ⟍ Schulenberg ⟍ Chen
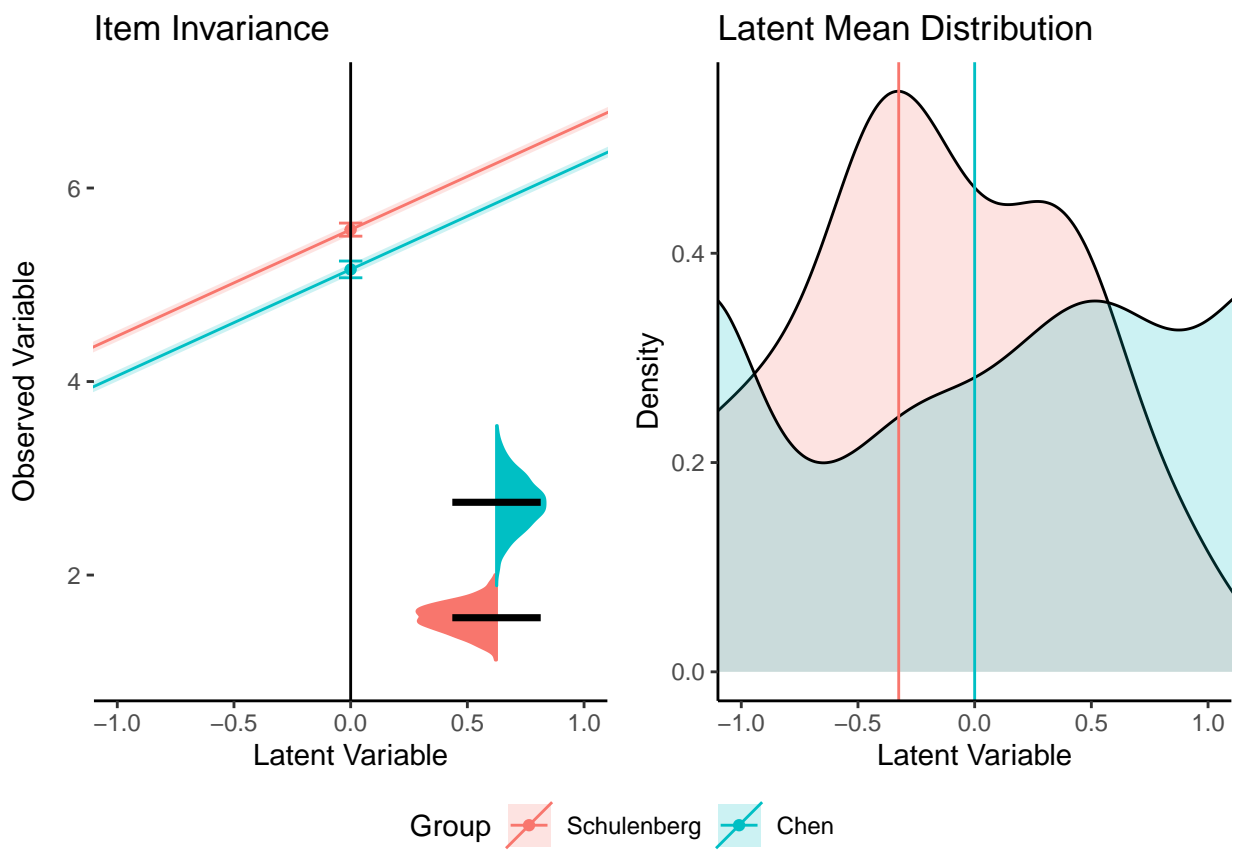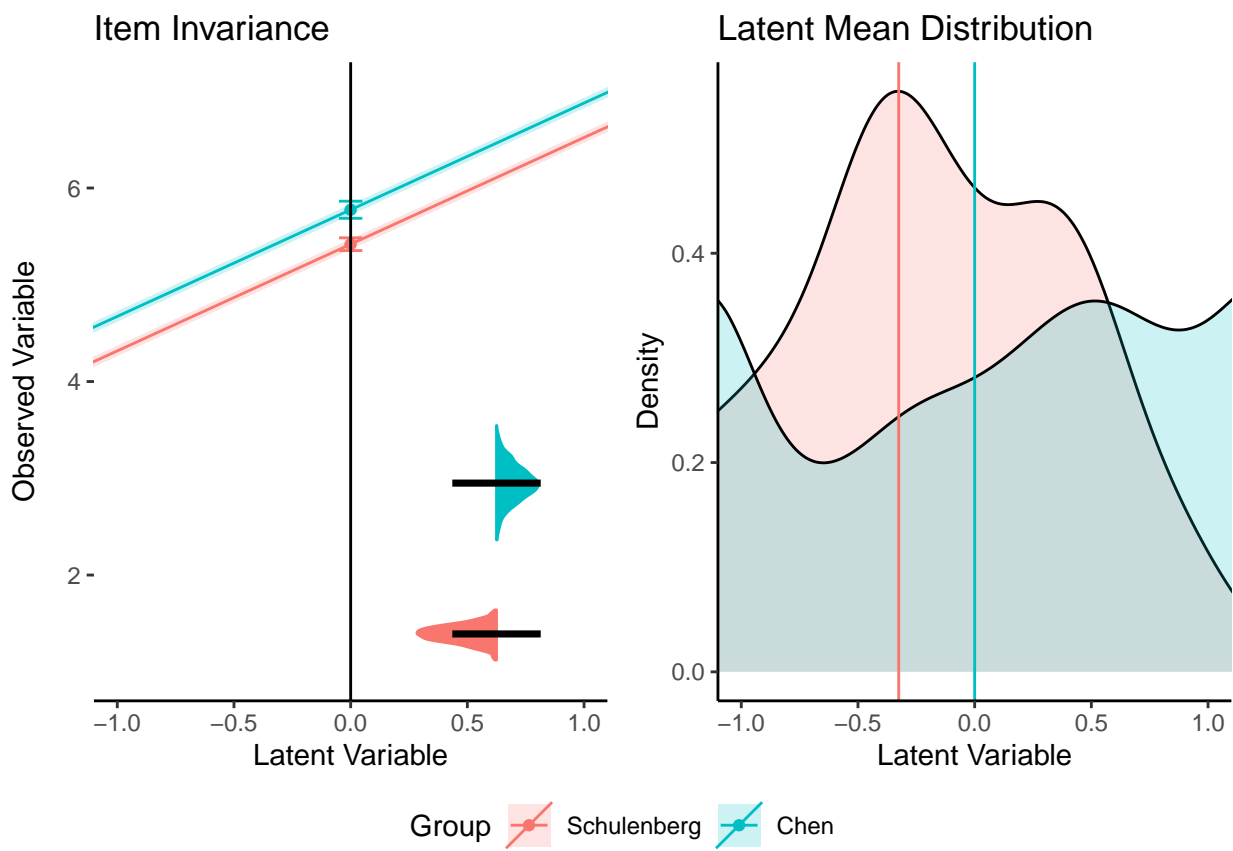
1068

1069   ## -------

1070   ## Plot for RS1

Item Invariance

Latent Mean Distribution

Group   — Schulenberg   — Chen
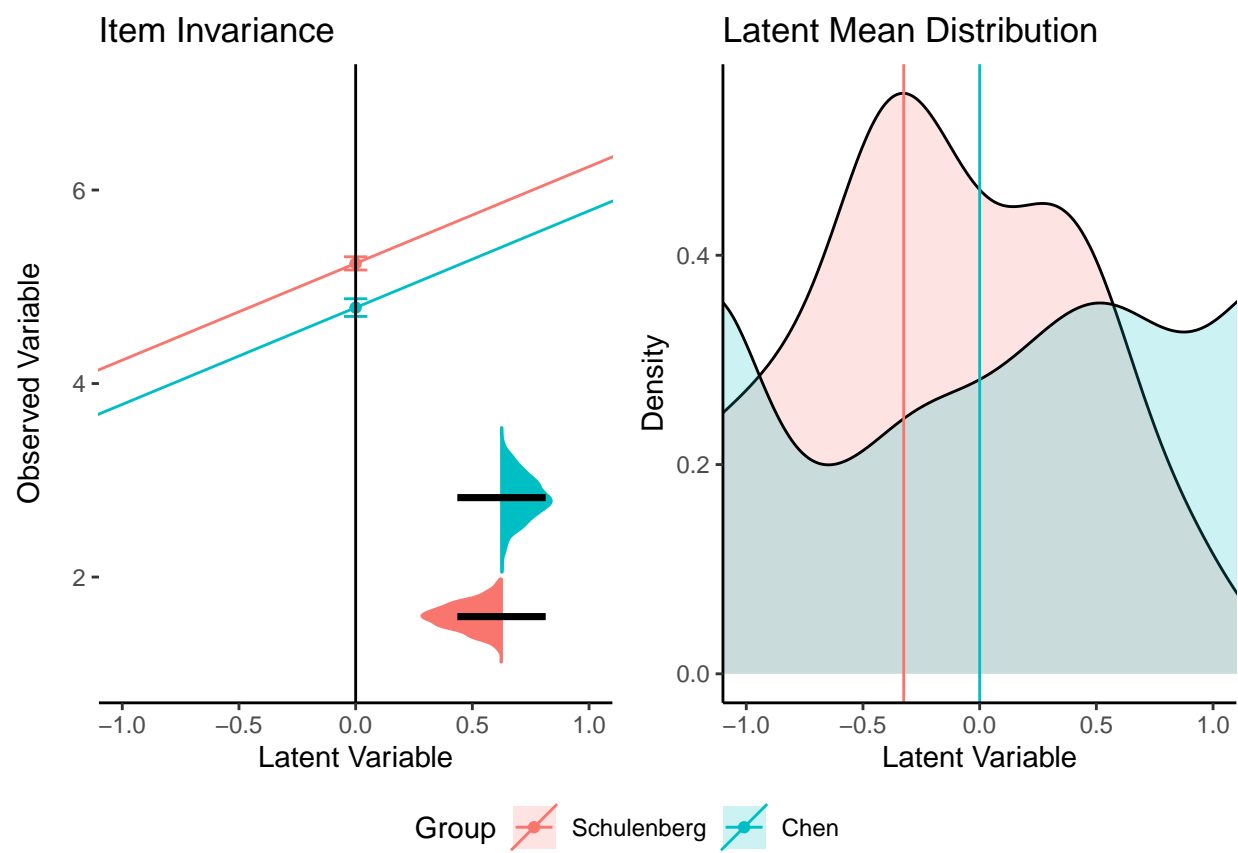
1072 ## -------

1073 ## Plot for RS10
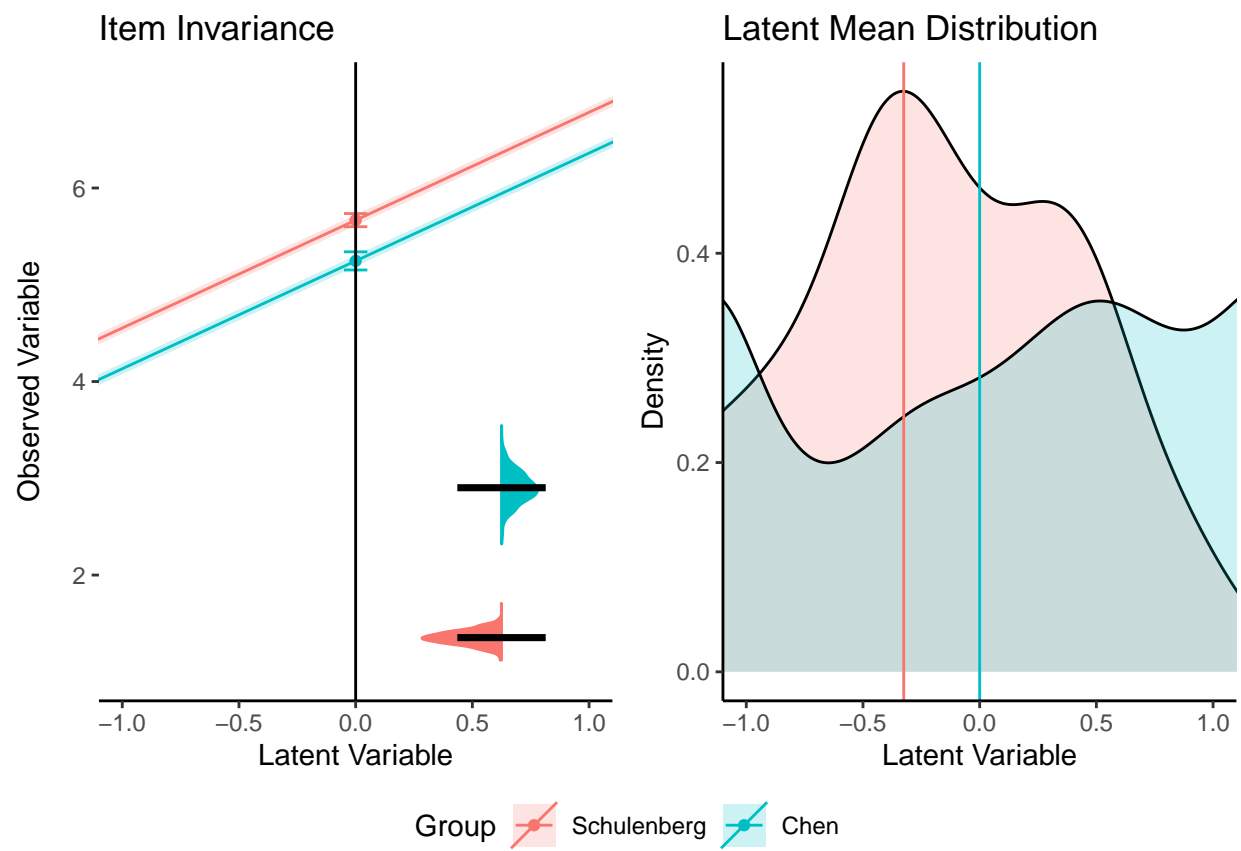
1075   ## -------

1076   ## Plot for RS3

1078   ## -------

1079   **Bootstrap Model**

1080   ##   model non_invariant random_non_invariant   h_nmi h_nmi_p

1081   ## 1 intercepts   1   0 3.141593   1

1082   In this case, we do not see loadings print out. That implies that all models in both

1083   real data and randomized data are invariant because the function only calculates

1084   information for non-invariance. We see that the intercepts are unlikely to ever replicate

1085   across Chinese and English samples. This result is not surprising given the large number of

1086   relaxed parameters required to achieve partial invariance.

1087   **Bootstrap Partial Invariance**

1088   ***Each Parameter on the Overall Model Invariance***

1089   ##   term non_invariant random_non_invariant   h_nmi h_nmi_p

```
## 1     RS ~1              1              0.002 3.052120 0.971520

## 2    RS1 ~1              1              0.001 3.078337 0.979865

## 3   RS10 ~1              1              0.002 3.052120 0.971520

## 4   RS11 ~1              1              0.002 3.052120 0.971520

## 5   RS12 ~1              1              0.002 3.052120 0.971520

## 6   RS13 ~1              1              0.002 3.052120 0.971520

## 7   RS14 ~1              1              0.002 3.052120 0.971520

## 8    RS2 ~1              1              0.002 3.052120 0.971520

## 9    RS3 ~1              1              0.002 3.052120 0.971520

## 10   RS4 ~1              1              0.002 3.052120 0.971520

## 11   RS5 ~1              1              0.002 3.052120 0.971520

## 12   RS6 ~1              1              0.002 3.052120 0.971520

## 13   RS7 ~1              1              0.001 3.078337 0.979865

## 14   RS8 ~1              1              0.002 3.052120 0.971520

## 15   RS9 ~1              1              0.002 3.052120 0.971520
```

In this output, we see that all the bootstrapped runs of the real data are non-invariant, even when each parameter is relaxed individually. A few runs of the random data are *non*-invariant (meaning most are actually invariant when randomized). This indicates that no one parameter is likely the reason for non-invariance, as they all show large non-replication effects. If we use the `boot_summary`, we can see the effect size for each parameter when the two intercepts are compared to each other (as the chart above shows the overall model invariance effect).

Each Parameter's Standardized Difference Score

```
##         term invariant n_boot     d_boot

## 1    RS ~1      FALSE   1000         NA

## 2   RS1 ~1      FALSE   1000  0.2913872
```

```
1116  ## 3   RS10 ~1     FALSE   1000  0.3596961

1117  ## 4   RS11 ~1     FALSE   1000 -0.6589317

1118  ## 5   RS12 ~1     FALSE   1000 -0.3010202

1119  ## 6   RS13 ~1     FALSE   1000 -0.4005088

1120  ## 7   RS14 ~1     FALSE   1000 -0.5665988

1121  ## 8    RS2 ~1     FALSE   1000 -0.5540349

1122  ## 9    RS3 ~1     FALSE   1000 -0.6218628

1123  ## 10   RS4 ~1     FALSE   1000 -0.6245830

1124  ## 11   RS5 ~1     FALSE   1000 -0.3334520

1125  ## 12   RS6 ~1     FALSE   1000 -0.5014247

1126  ## 13   RS7 ~1     FALSE   1000 -0.2381644

1127  ## 14   RS8 ~1     FALSE   1000 -0.6333750

1128  ## 15   RS9 ~1     FALSE   1000 -0.5986866


1129  ##          term invariant n_random d_random

1130  ## 1    RS ~1     FALSE         2       NA

1131  ## 2   RS1 ~1     FALSE         1       NA

1132  ## 3  RS10 ~1     FALSE         2       NA

1133  ## 4  RS11 ~1     FALSE         2       NA

1134  ## 5  RS12 ~1     FALSE         2       NA

1135  ## 6  RS13 ~1     FALSE         2       NA

1136  ## 7  RS14 ~1     FALSE         2       NA

1137  ## 8   RS2 ~1     FALSE         2       NA

1138  ## 9   RS3 ~1     FALSE         2       NA

1139  ## 10  RS4 ~1     FALSE         2       NA

1140  ## 11  RS5 ~1     FALSE         2       NA

1141  ## 12  RS6 ~1     FALSE         2       NA

1142  ## 13  RS7 ~1     FALSE         1       NA
```
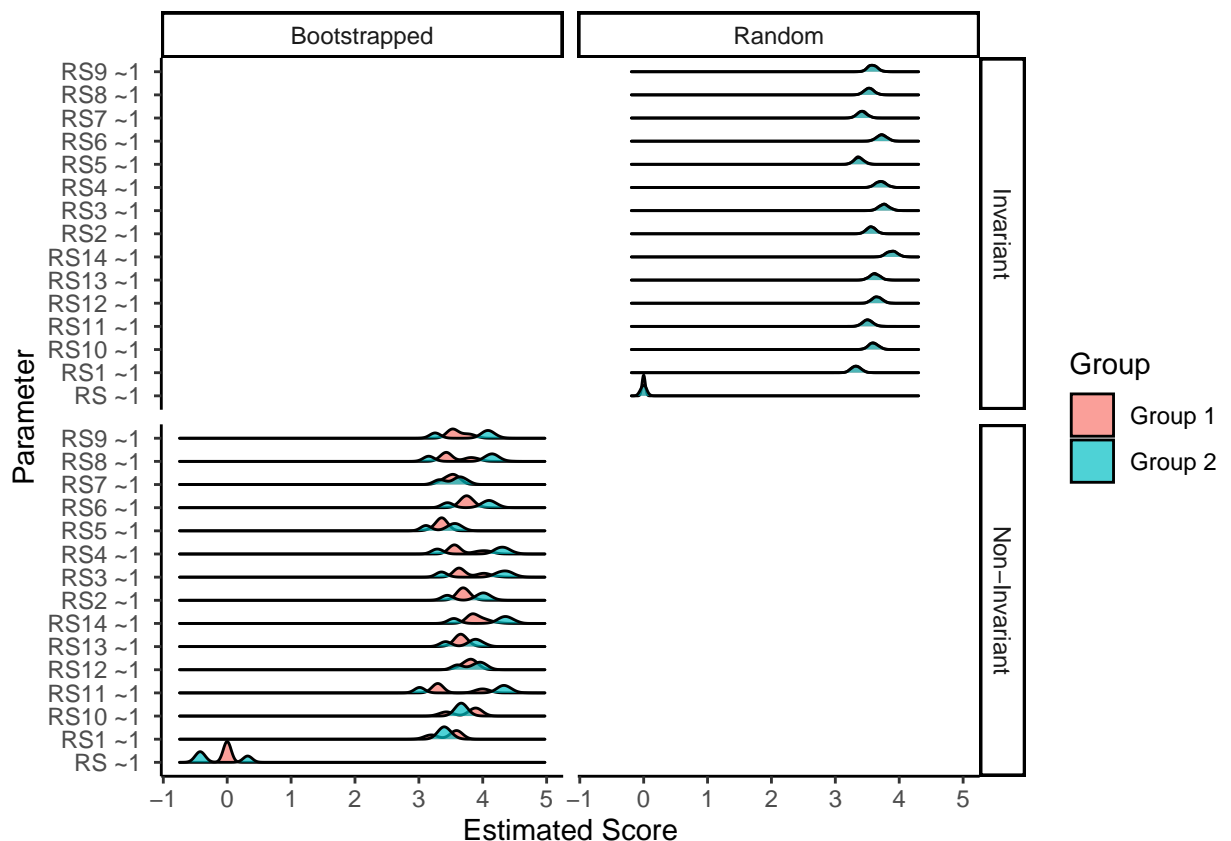
```
1143  ## 14  RS8 ~1        FALSE         2        NA

1144  ## 15  RS9 ~1        FALSE         2        NA
```

With the bootstrap summary, we see that no invariant intercept runs are found (not all columns shown to save space). Note that the `RS~1` does not calculate d because the sd is zero (thus, this would cause an error as sd is part of the denominator). The random runs also do not show a d score because the effect size is only calculated when at least 10% of the runs in `n_boot` or `n_random` are found. Since we only have a few in that column, no effect size is calculated. The differences in the intercepts for the real data (`boot` columns) appear to be medium to large, showing d scores from 0.3 to 0.6. Therefore, we might expect that the English and Chinese samples have different average endorsement levels of the RS14.

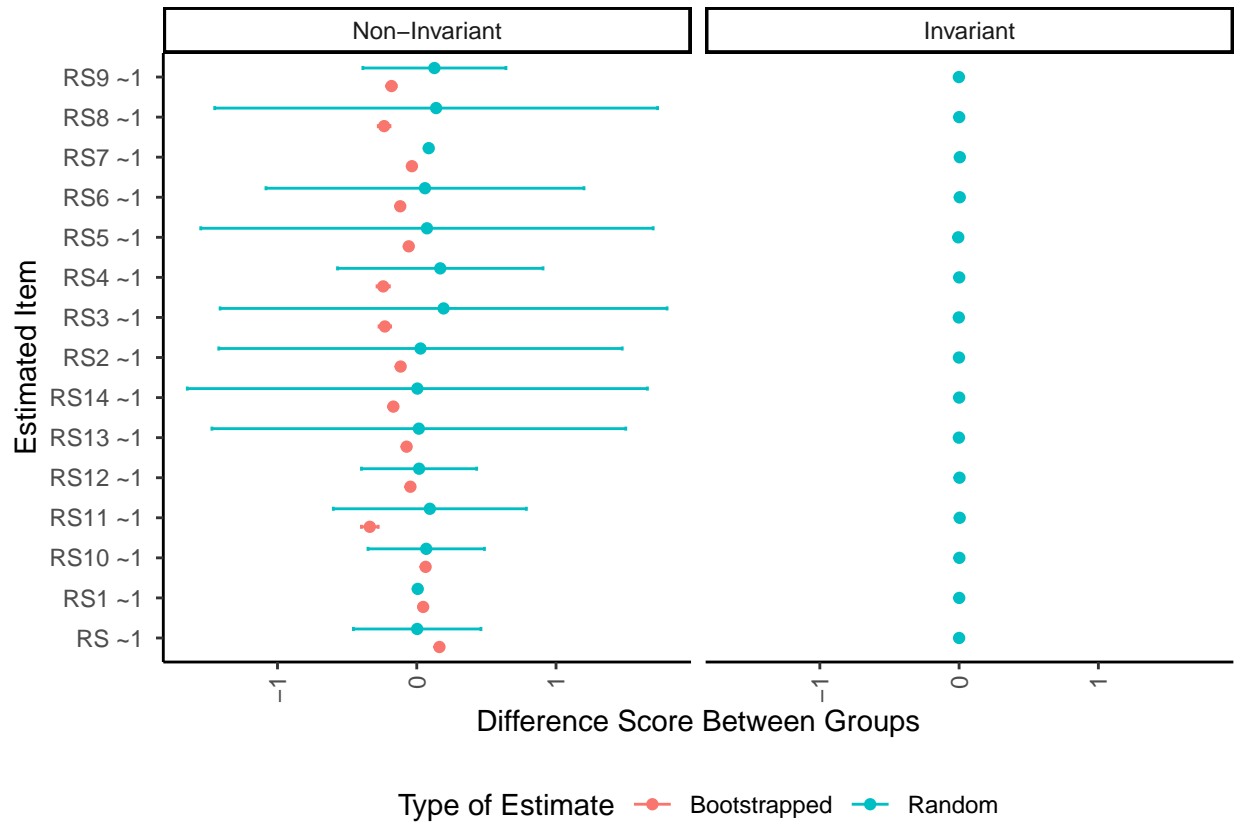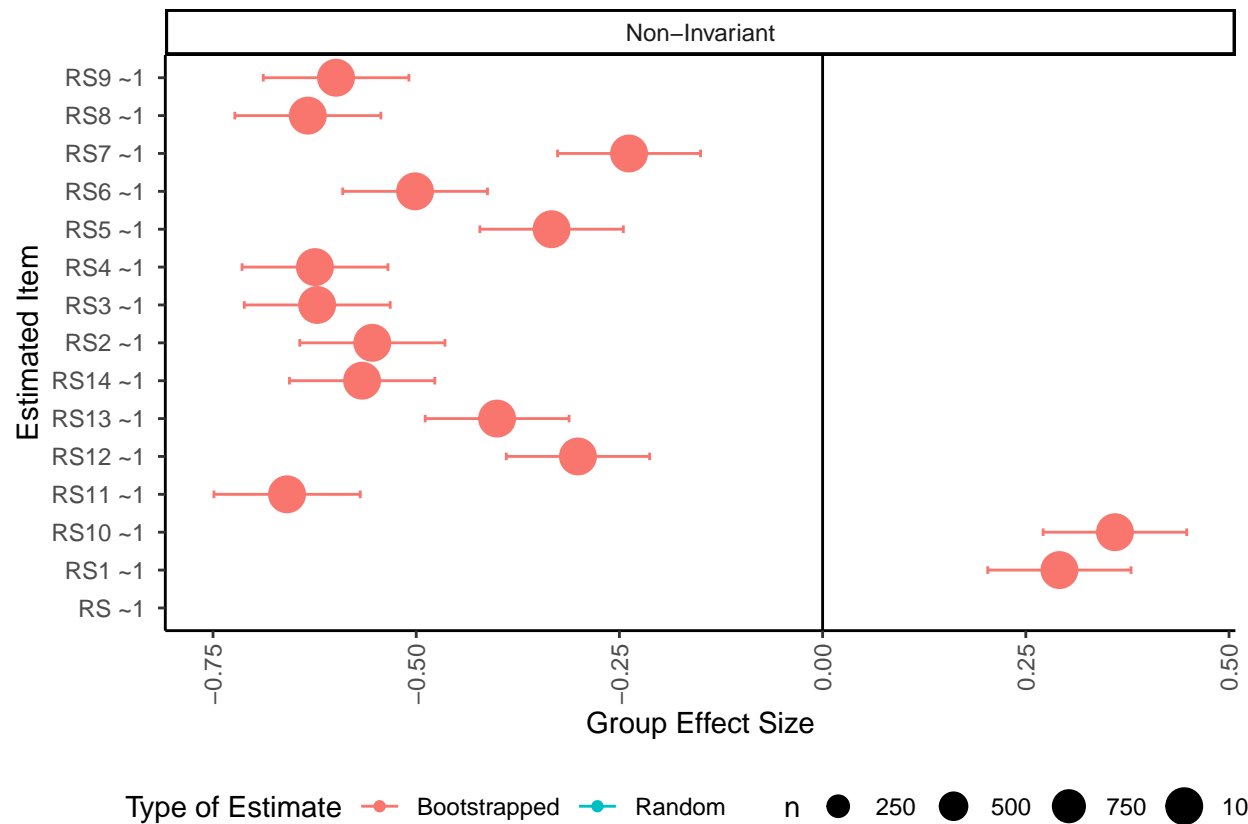The examination of the density plot shows how group 1 (Schulenberg English) tends to show lower average scores than group 2 (Chen Chinese) for most but not all items.

1156   We can view the mean difference or standardized mean difference by using:

When effects are non-invariant in the randomized data, the mean difference is still fairly small, but we see large mean differences in intercepts when the bootstrapped data is non-invariant. In the effect size graph, we can see that this effect is medium to large for all the parameters.