Using measurementInvariance

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Package overview

measurementInvariance is an R package dedicated to sound measurement invariance (MI) analysis, focusing on issues of establishing partial MI. It subsumes SEM and IRT models by importing from lavaan and mirt respectively.

Imported packages:

- lavaan
- mirt
- Ckmeans.1d.dp
- reshape2
- msm
- plyr
- blavaan (only needed in Bayesian part)
- rstan (only needed in Bayesian part)

Function overview

There are 4 main functions:

- testMI(): Global MI tests
- clusterItems(): Under violations of MI, find clusters (subsets) of items, for which MI holds
- partialMI(): Use a chosen item cluster as anchor
- modelAveraging(): When not choosing an item cluster, apply Bayesian model averaging to reflect information from several competing partial MI models.

All functions deal with unidimensional models only. The typical workflow is intended to be testMI() -> clusterItems() -> either partialMI() or modelAveraging(). However, the functions can also be used independently.

Continuous data (& partial MI)

Here we are taking data from the Holzinger-Swinefort (1939) example on cognitive tests. We will use the "Speed" items with gender as a grouping variable, for which MI is to be tested.

```
suppressMessages(library(MBESS))
data(HS)
Data <- HS[, c("t10_addition", "t11_code", "t12_counting_groups_of_dots", # speed items
               "t13_straight_and_curved_capitals",
               "t20_deduction", "t21_numerical_puzzles", "t22_problem_reasoning", # math items
               "t23_series_completion", "t24_woody_mccall", "sex")]
colnames(Data) <- sub("_.*", "", colnames(Data)) # shorten variable names for convenience
```

```r
str(Data)
#> 'data.frame':	301 obs. of  10 variables:
#>  $ t10: int  78 87 75 69 85 100 108 78 104 95 ...
#>  $ t11: int  74 84 49 65 63 92 65 80 52 74 ...
#>  $ t12: int  115 125 78 106 126 133 124 103 93 91 ...
#>  $ t13: int  229 285 159 175 213 270 175 132 265 157 ...
#>  $ t20: int  3 -3 -3 -2 29 9 18 15 12 33 ...
#>  $ t21: int  14 13 9 10 15 2 10 9 15 8 ...
#>  $ t22: int  34 21 18 22 19 16 19 22 18 25 ...
#>  $ t23: int  5 1 7 6 4 10 3 18 17 8 ...
#>  $ t24: int  24 12 20 19 20 22 15 24 18 16 ...
#>  $ sex: Factor w/ 2 levels "Female","Male": 2 1 1 2 1 1 2 1 1 1 ...
```

Assume, we are interested in establishing strong MI for the purpose of group comparison. The summary function gives an overview over model fit of sequentially tested MI models as well as their comparison.

```r
speed <- c("t10", "t11", "t12", "t13")

testMIspeed <- testMI(items = speed,
                      group = "sex",
                      data = Data,
                      MIlevel = "strong")
summary(testMIspeed)
#> Two group model with:
#>  Female Male total
#>     155  146   301
#>
#>
#> MI level            configural   weak strong
#> chi2                     17.26  26.24  51.09
#> df                           4      7     10
#> p                        0.002  0.000  0.000
#> CFI                      0.950  0.928  0.846
#> RMSEA                    0.148  0.135  0.165
#> RMSEA 90% lower          0.084  0.084  0.122
#> SRMR                     0.038  0.065  0.086
#> diff chi2                       8.796 26.244
#> diff df                             3      3
#> diff p                          0.032      0
#> diff CFI                       -0.022 -0.082
#> diff RMSEA                     -0.013   0.03
#> diff SRMR                       0.027  0.021
#> Effect (DIF range)              0.688  0.565
#>
#> package             lavaan
#> estimator              MLR
#> item type       continuous
#> item missings         none
#> standardized           yes
#>
#> Use getModel() to access parameter estimates or to further process the results.
```

We identify (borderline) issues with weak and definite problems with strong MI (for cut-offs see Chen, 2007).

We proceed to identify item clusters for which MI holds. Most importantly, we need to tell the clusterItem()

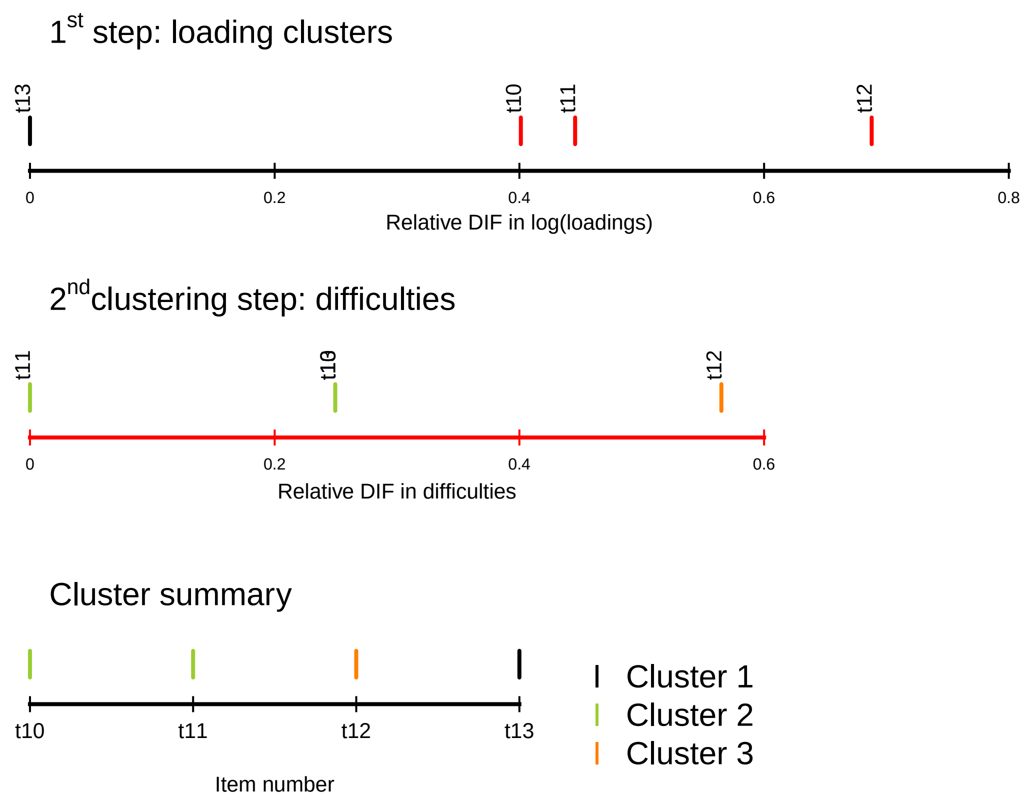
function, for which parameter types there were issues with MI. In this case it's both loadings and difficulties (aka intercepts).

First, item clustering is done by setting a threshold in loading difference that is not to be surpassed by the items of a specific cluster. The smaller the threshold, the more homogeneous the items of a cluster become when compared across groups.

```
clusterItemsSpeed <- clusterItems(res_testMI = testMIspeed,
                                  clusterWhat = c("loadings", "difficulties"),
                                  method = "threshold",
                                  loadThreshold = 0.3,
                                  intThreshold = 0.5)
summary(clusterItemsSpeed,
        order = "clusters")
#> Clustering by threshold criterion with load threshold 0.5 and intercept threshold NA.
#>
#> 3 clusters found after clustering loadings and difficulties
#>     cluster
#> t13       1
#> t10       2
#> t11       2
#> t12       3
```

Three clusters are found. In order to better understand the clustering process, which takes two steps by first clustering item loadings and then item difficulties, a plot can be requested.

```
plotCluster(clusterItemsSpeed,
            showLegend = TRUE)
```



Alternatively to the threshold criterion, a significance test can be used as stopping criterion in the clustering.

```
clusterItemsSpeed_p <- clusterItems(res_testMI = testMIspeed,
                                    clusterWhat = c("loadings", "difficulties"),
                                    method = "sigTest",
                                    alphaValue = 0.05)
summary(clusterItemsSpeed_p,
        order = "clusters")
#> Clustering by sign. test with p of 0.05.
#>
#> 4 clusters found after clustering loadings and difficulties
#>     cluster
#> t13       1
#> t10       2
#> t11       3
#> t12       4
```

Here, four clusters are found. The items differ strong enough that they do not pair up at all according to the significance test.

After inspection of the items we might decide for going with cluster 2 of the threshold analysis as anchor items. Hence we call the partialMI() function. It directly displays the model estimates.

```
partialMI(res_clusterItems = clusterItemsSpeed,
          anchor = 2) # cluster number
#> lavaan 0.6-8 ended normally after 32 iterations
#>
#>   Estimator                                         ML
```

```
#>   Optimization method                           NLMINB
#>   Number of model parameters                        26
#>   Number of equality constraints                     4
#>
#>   Number of observations per group:
#>     Male                                           146
#>     Female                                         155
#>
#> Model Test User Model:
#>                                               Standard      Robust
#>   Test Statistic                                22.273      20.489
#>   Degrees of freedom                                 6           6
#>   P-value (Chi-square)                           0.001       0.002
#>   Scaling correction factor                                  1.087
#>        Yuan-Bentler correction (Mplus variant)
#>   Test statistic for each group:
#>     Male                                        12.298      11.313
#>     Female                                       9.975       9.176
#>
#> Model Test Baseline Model:
#>
#>   Test statistic                               293.094     278.690
#>   Degrees of freedom                                12          12
#>   P-value                                        0.000       0.000
#>   Scaling correction factor                                  1.052
#>
#> User Model versus Baseline Model:
#>
#>   Comparative Fit Index (CFI)                    0.942       0.946
#>   Tucker-Lewis Index (TLI)                       0.884       0.891
#>
#>   Robust Comparative Fit Index (CFI)                         0.944
#>   Robust Tucker-Lewis Index (TLI)                            0.888
#>
#> Loglikelihood and Information Criteria:
#>
#>   Loglikelihood user model (H0)              -1551.952   -1551.952
#>   Scaling correction factor                                  0.894
#>       for the MLR correction
#>   Loglikelihood unrestricted model (H1)      -1540.816   -1540.816
#>   Scaling correction factor                                  1.063
#>       for the MLR correction
#>
#>   Akaike (AIC)                                3147.905    3147.905
#>   Bayesian (BIC)                              3229.461    3229.461
#>   Sample-size adjusted Bayesian (BIC)         3159.690    3159.690
#>
#> Root Mean Square Error of Approximation:
#>
#>   RMSEA                                          0.134       0.127
#>   90 Percent confidence interval - lower         0.078       0.072
#>   90 Percent confidence interval - upper         0.196       0.186
#>   P-value RMSEA <= 0.05                          0.010       0.014
```

```
#>
#>   Robust RMSEA                                                0.132
#>   90 Percent confidence interval - lower                      0.072
#>   90 Percent confidence interval - upper                      0.197
#>
#> Standardized Root Mean Square Residual:
#>
#>   SRMR                                           0.045       0.045
#>
#> Parameter Estimates:
#>
#>   Standard errors                             Sandwich
#>   Information bread                           Observed
#>   Observed information based on                Hessian
#>
#>
#> Group 1 [Male]:
#>
#> Latent Variables:
#>                    Estimate  Std.Err  z-value  P(>|z|)
#>   Factor =~
#>     t10     (.p1.)    0.608    0.067    9.015    0.000
#>     t11     (.p2.)    0.666    0.087    7.698    0.000
#>     t12               0.815    0.115    7.086    0.000
#>     t13               0.517    0.078    6.622    0.000
#>
#> Intercepts:
#>                    Estimate  Std.Err  z-value  P(>|z|)
#>    .t10     (.10.)   -0.168    0.070   -2.391    0.017
#>    .t11     (.11.)   -0.200    0.077   -2.588    0.010
#>    .t12               0.043    0.091    0.478    0.633
#>    .t13              -0.047    0.073   -0.642    0.521
#>     Factor            0.000
#>
#> Variances:
#>                    Estimate  Std.Err  z-value  P(>|z|)
#>    .t10               0.469    0.068    6.878    0.000
#>    .t11               0.507    0.090    5.620    0.000
#>    .t12               0.533    0.130    4.090    0.000
#>    .t13               0.521    0.073    7.158    0.000
#>     Factor            1.000
#>
#>
#> Group 2 [Female]:
#>
#> Latent Variables:
#>                    Estimate  Std.Err  z-value  P(>|z|)
#>   Factor =~
#>     t10     (.p1.)    0.608    0.067    9.015    0.000
#>     t11     (.p2.)    0.666    0.087    7.698    0.000
#>     t12               0.635    0.113    5.601    0.000
#>     t13               0.797    0.158    5.056    0.000
#>
```

```
#> Intercepts:
#>                    Estimate  Std.Err  z-value  P(>|z|)
#>    .t10     (.10.)   -0.168    0.070   -2.391    0.017
#>    .t11     (.11.)   -0.200    0.077   -2.588    0.010
#>    .t12              -0.407    0.110   -3.717    0.000
#>    .t13              -0.416    0.145   -2.870    0.004
#>     Factor            0.577    0.167    3.449    0.001
#>
#> Variances:
#>                    Estimate  Std.Err  z-value  P(>|z|)
#>    .t10               0.736    0.092    7.985    0.000
#>    .t11               0.552    0.092    6.020    0.000
#>    .t12               0.427    0.064    6.648    0.000
#>    .t13               0.593    0.105    5.636    0.000
#>     Factor            0.938    0.320    2.930    0.003
#> lavaan 0.6-8 ended normally after 32 iterations
#>
#>   Estimator                                         ML
#>   Optimization method                           NLMINB
#>   Number of model parameters                        26
#>   Number of equality constraints                     4
#>
#>   Number of observations per group:
#>     Male                                           146
#>     Female                                         155
#>
#> Model Test User Model:
#>                                               Standard      Robust
#>   Test Statistic                                22.273      20.489
#>   Degrees of freedom                                 6           6
#>   P-value (Chi-square)                           0.001       0.002
#>   Scaling correction factor                                  1.087
#>        Yuan-Bentler correction (Mplus variant)
#>   Test statistic for each group:
#>     Male                                        12.298      11.313
#>     Female                                       9.975       9.176
```

Alternatively, we might have some source other than the clustering for finding anchor candidates. partialMI() also takes item names as anchors and does not only rely on clusterItems(). We can also put in all model information.

```
partialMI(items = speed,
          group = "sex",
          data = Data,
          MIlevel = "strong",
          partialMIwhat = c("loadings", "difficulties"), # equivalent to clusterWhat above
          anchor = c("t10", "t11")) # item names
#> lavaan 0.6-8 ended normally after 32 iterations
#>
#>   Estimator                                         ML
#>   Optimization method                           NLMINB
#>   Number of model parameters                        26
#>   Number of equality constraints                     4
#>
```

```
#>   Number of observations per group:
#>     Male                                           146
#>     Female                                         155
#>
#> Model Test User Model:
#>                                               Standard      Robust
#>   Test Statistic                                22.273      20.489
#>   Degrees of freedom                                 6           6
#>   P-value (Chi-square)                           0.001       0.002
#>   Scaling correction factor                                  1.087
#>        Yuan-Bentler correction (Mplus variant)
#>   Test statistic for each group:
#>     Male                                        12.298      11.313
#>     Female                                       9.975       9.176
#>
#> Model Test Baseline Model:
#>
#>   Test statistic                               293.094     278.690
#>   Degrees of freedom                                12          12
#>   P-value                                        0.000       0.000
#>   Scaling correction factor                                  1.052
#>
#> User Model versus Baseline Model:
#>
#>   Comparative Fit Index (CFI)                    0.942       0.946
#>   Tucker-Lewis Index (TLI)                       0.884       0.891
#>
#>   Robust Comparative Fit Index (CFI)                         0.944
#>   Robust Tucker-Lewis Index (TLI)                            0.888
#>
#> Loglikelihood and Information Criteria:
#>
#>   Loglikelihood user model (H0)              -1551.952   -1551.952
#>   Scaling correction factor                                  0.894
#>       for the MLR correction
#>   Loglikelihood unrestricted model (H1)      -1540.816   -1540.816
#>   Scaling correction factor                                  1.063
#>       for the MLR correction
#>
#>   Akaike (AIC)                                3147.905    3147.905
#>   Bayesian (BIC)                              3229.461    3229.461
#>   Sample-size adjusted Bayesian (BIC)         3159.690    3159.690
#>
#> Root Mean Square Error of Approximation:
#>
#>   RMSEA                                          0.134       0.127
#>   90 Percent confidence interval - lower         0.078       0.072
#>   90 Percent confidence interval - upper         0.196       0.186
#>   P-value RMSEA <= 0.05                          0.010       0.014
#>
#>   Robust RMSEA                                               0.132
#>   90 Percent confidence interval - lower                     0.072
#>   90 Percent confidence interval - upper                     0.197
```

```
#>
#> Standardized Root Mean Square Residual:
#>
#>   SRMR                                           0.045       0.045
#>
#> Parameter Estimates:
#>
#>   Standard errors                             Sandwich
#>   Information bread                           Observed
#>   Observed information based on                Hessian
#>
#>
#> Group 1 [Male]:
#>
#> Latent Variables:
#>                    Estimate  Std.Err  z-value  P(>|z|)
#>   Factor =~
#>     t10     (.p1.)    0.608    0.067    9.015    0.000
#>     t11     (.p2.)    0.666    0.087    7.698    0.000
#>     t12               0.815    0.115    7.086    0.000
#>     t13               0.517    0.078    6.622    0.000
#>
#> Intercepts:
#>                    Estimate  Std.Err  z-value  P(>|z|)
#>    .t10     (.10.)   -0.168    0.070   -2.391    0.017
#>    .t11     (.11.)   -0.200    0.077   -2.588    0.010
#>    .t12               0.043    0.091    0.478    0.633
#>    .t13              -0.047    0.073   -0.642    0.521
#>     Factor            0.000
#>
#> Variances:
#>                    Estimate  Std.Err  z-value  P(>|z|)
#>    .t10               0.469    0.068    6.878    0.000
#>    .t11               0.507    0.090    5.620    0.000
#>    .t12               0.533    0.130    4.090    0.000
#>    .t13               0.521    0.073    7.158    0.000
#>     Factor            1.000
#>
#>
#> Group 2 [Female]:
#>
#> Latent Variables:
#>                    Estimate  Std.Err  z-value  P(>|z|)
#>   Factor =~
#>     t10     (.p1.)    0.608    0.067    9.015    0.000
#>     t11     (.p2.)    0.666    0.087    7.698    0.000
#>     t12               0.635    0.113    5.601    0.000
#>     t13               0.797    0.158    5.056    0.000
#>
#> Intercepts:
#>                    Estimate  Std.Err  z-value  P(>|z|)
#>    .t10     (.10.)   -0.168    0.070   -2.391    0.017
#>    .t11     (.11.)   -0.200    0.077   -2.588    0.010
```

```
#>    .t12              -0.407    0.110   -3.717    0.000
#>    .t13              -0.416    0.145   -2.870    0.004
#>     Factor            0.577    0.167    3.449    0.001
#>
#> Variances:
#>                    Estimate  Std.Err  z-value  P(>|z|)
#>    .t10               0.736    0.092    7.985    0.000
#>    .t11               0.552    0.092    6.020    0.000
#>    .t12               0.427    0.064    6.648    0.000
#>    .t13               0.593    0.105    5.636    0.000
#>     Factor            0.938    0.320    2.930    0.003
#> lavaan 0.6-8 ended normally after 32 iterations
#>
#>   Estimator                                         ML
#>   Optimization method                           NLMINB
#>   Number of model parameters                        26
#>   Number of equality constraints                     4
#>
#>   Number of observations per group:
#>     Male                                           146
#>     Female                                         155
#>
#> Model Test User Model:
#>                                               Standard      Robust
#>   Test Statistic                                22.273      20.489
#>   Degrees of freedom                                 6           6
#>   P-value (Chi-square)                           0.001       0.002
#>   Scaling correction factor                                  1.087
#>        Yuan-Bentler correction (Mplus variant)
#>   Test statistic for each group:
#>     Male                                       12.298      11.313
#>     Female                                      9.975       9.176
```

Dichotomous data (& Bayesian model averaging)

The package provides good support for dichotomous data models via categorical SEM models in lavaan and IRT models in mirt. Here we have a second example from the FIMS study testing mathematical ability where a 2PL IRT model is applied. Our goal is to compare the latent means of two countries (1 Australia - 2 Japan). We thus need to establish strong MI.

```
suppressMessages(library(TAM))
data("data.fims.Aus.Jpn.scored")
# choosing only a subset of items and a subset of the sample to keep a lid on
# the computation times of Bayesian analyses
dataDich <- data.fims.Aus.Jpn.scored[c(1:500, 5801:6300), c(2, 3, 4, 8, 9, 11, 15, 16)]
str(dataDich)
#> 'data.frame':    1000 obs. of  8 variables:
#>  $ M1PTI1 : num  1 0 1 1 1 1 0 1 0 0 ...
#>  $ M1PTI2 : num  0 1 0 1 1 1 0 1 0 1 ...
#>  $ M1PTI3 : num  1 1 1 1 1 1 1 0 1 1 ...
#>  $ M1PTI12: num  0 0 0 1 0 0 1 0 0 0 ...
#>  $ M1PTI14: num  0 1 0 0 1 0 1 1 1 0 ...
#>  $ M1PTI18: num  0 0 1 0 1 1 0 1 0 1 ...
```

```
#>  $ M1PTI23: num  1 1 1 0 1 0 0 1 0 1 ...
#>  $ country: int  1 1 1 1 1 1 1 1 1 1 ...

testMIfims <- testMI(items = colnames(dataDich[1:7]),
                    group = "country",
                    data = dataDich,
                    MIlevel = "strong",
                    itemType = "dichotomous",
                    dichModel = "2PL")
summary(testMIfims)
#> Two group model with:
#>  group1 group2 total
#>     500    500  1000
#>
#>
#> MI level           configural     weak   strong
#> AIC                  7503.048 7499.910 7593.687
#> SABIC                7551.536 7538.008 7621.394
#> BIC                  7640.466 7607.881 7672.211
#> M2                     44.040   52.092  154.823
#> df                         28       35       42
#> p                       0.028    0.032    0.000
#> RMSEA                   0.024    0.022    0.052
#> RMSEA 90% lower         0.008    0.007    0.043
#> CFI                     0.963    0.961    0.741
#> diff chi2                        8.862  105.776
#> diff df                              6        6
#> diff p                           0.181        0
#> diff RMSEA                      -0.002     0.03
#> diff CFI                        -0.002    -0.22
#> Effect (DIF range)               1.158    2.259
#>
#> package            mirt
#> estimator            EM
#> item type           2PL
#> item missings      none
#>
#> Use getModel() to access parameter estimates or to further process the results.
```

Contrary to the first example, we find no issues with weak MI, but a clear violation of strong MI.

If we want to have a look at a specific model estimated by testMI(), we can use getModel(). This prints a model summary. Additionally, any method from the core package (in this case: mirt) can be applied to the resulting object (e.g. coef, itemfit). Here, the weak MI model is requested.

```
resWeak <- getModel(testMIfims,
                    which = "weak")
#> mirt model estimates
#>
#> Full-information item factor analysis with 1 factor(s).
#> Converged within 1e-04 tolerance after 57 EM iterations.
#> mirt version: 1.33.2
#> M-step optimizer: nlminb
#> EM acceleration: Ramsay
```

```
#> Number of rectangular quadrature: 61
#> Latent density type: Gaussian
#>
#> Information matrix estimated with method: Oakes
#> Second-order test: model is a possible local maximum
#> Condition number of information matrix =  17.69478
#>
#> Log-likelihood = -3727.955
#> Estimated parameters: 29
#> AIC = 7499.91; AICc = 7500.946
#> BIC = 7607.881; SABIC = 7538.008
#>                stats
#> M2            52.092
#> df            35.000
#> p              0.032
#> RMSEA          0.022
#> RMSEA_5        0.007
#> RMSEA_95       0.034
#> SRMSR.group1   0.045
#> SRMSR.group2   0.050
#> TLI            0.953
#> CFI            0.961
#>
#>
#> Parameter Estimates:
#>
#> $group1
#> $items
#>            a1      d g u
#> M1PTI1  1.029  0.970 0 1
#> M1PTI2  1.699  1.548 0 1
#> M1PTI3  1.190  1.950 0 1
#> M1PTI12 0.503 -0.787 0 1
#> M1PTI14 0.541  0.353 0 1
#> M1PTI18 1.128  0.487 0 1
#> M1PTI23 1.328  2.049 0 1
#>
#> $means
#> F1
#>  0
#>
#> $cov
#>    F1
#> F1  1
#>
#>
#> $group2
#> $items
#>            a1      d g u
#> M1PTI1  1.029  1.665 0 1
#> M1PTI2  1.699  2.821 0 1
#> M1PTI3  1.190  2.864 0 1
#> M1PTI12 0.503 -0.607 0 1
```

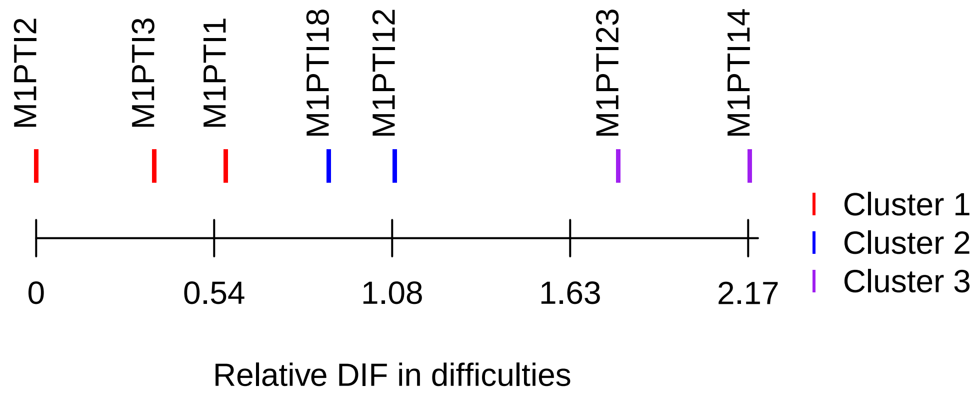
```
#> M1PTI14 0.541 -0.548 0 1
#> M1PTI18 1.128  0.869 0 1
#> M1PTI23 1.328  1.548 0 1
#>
#> $means
#> F1
#>  0
#>
#> $cov
#>       F1
#> F1 0.949
```

Applying clusterItems() with a threshold for difficulties (or thresholds in IRT terms), we find three item clusters.

```
clusterItemsFIMS <- clusterItems(res_testMI = testMIfims,
                                 clusterWhat = "difficulties",
                                 method = "threshold",
                                 intThreshold = 0.6)
summary(clusterItemsFIMS)
#> Clustering by threshold criterion with load threshold NA and intercept threshold NA.
#>
#> 3 clusters found after clustering difficulties
#>         cluster
#> M1PTI1        1
#> M1PTI2        1
#> M1PTI3        1
#> M1PTI12       2
#> M1PTI18       2
#> M1PTI14       3
#> M1PTI23       3
```

Again, the clusters can be plotted. In this case, it is only a single plot as only difficulties were clustered.

```
plotCluster(clusterItemsFIMS,
            showLegend = TRUE)
```

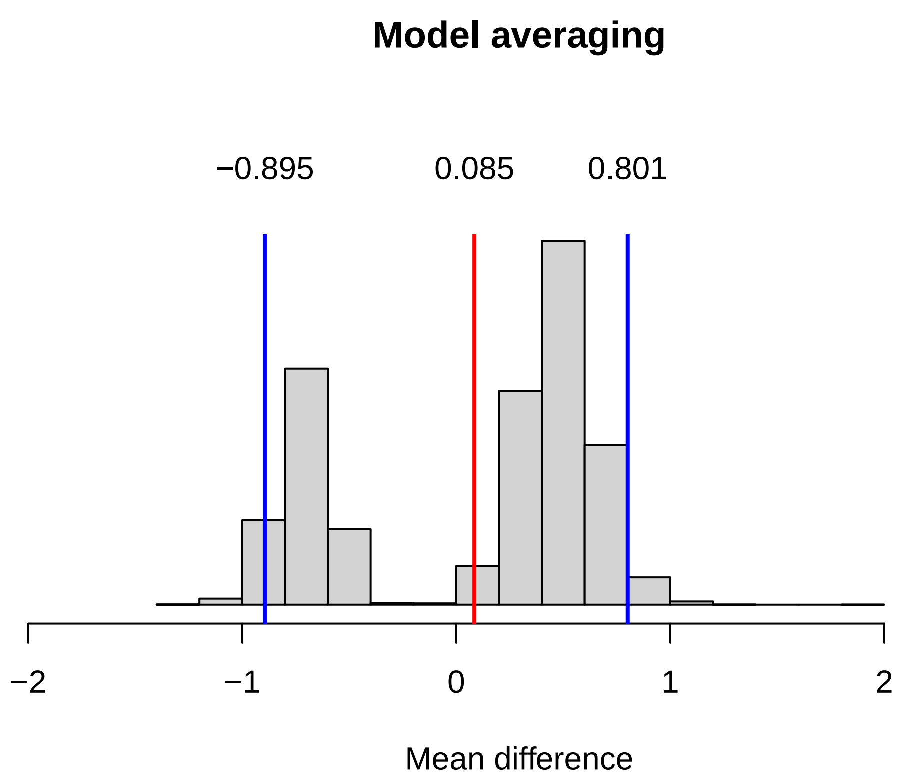


The relative DIF values which form the basis of the plot can be printed as well.

```
printDIF(clusterItemsFIMS)
#> Relative DIF of loadings in configural model, resulting in 1 cluster.
#> NULL
#>
#> Relative DIF of difficulties for loading cluster 1
#>          M1PTI1    M1PTI2     M1PTI3     M1PTI12    M1PTI14    M1PTI18
#> [1,]  0.0000000 0.5774560  0.2179689 -0.5153366 -1.5969640 -0.3141165
#> [2,] -0.5774560 0.0000000 -0.3594871 -1.0927925 -2.1744200 -0.8915725
#> [3,] -0.2179689 0.3594871  0.0000000 -0.7333055 -1.8149329 -0.5320854
#> [4,]  0.5153366 1.0927925  0.7333055  0.0000000 -1.0816274  0.2012201
#> [5,]  1.5969640 2.1744200  1.8149329  1.0816274  0.0000000  1.2828475
#> [6,]  0.3141165 0.8915725  0.5320854 -0.2012201 -1.2828475  0.0000000
#> [7,]  1.1969269 1.7743829  1.4148958  0.6815903 -0.4000371  0.8828104
#>         M1PTI23
#> [1,] -1.1969269
#> [2,] -1.7743829
#> [3,] -1.4148958
#> [4,] -0.6815903
#> [5,]  0.4000371
#> [6,] -0.8828104
#> [7,]  0.0000000
```

The three clusters can be subject to Bayesian model averaging which returns an averaged mean difference of the two countries. Here we will assume a completely naive weighting scheme by equal weights for all clusters. The resulting averaged mean difference is shown in a plot which illustrates the vastly different results depending on the chosen anchor set. One cluster yields an inverse result compared to the other two clusters, leveling out a mean difference on average.

```
bma <- modelAveraging(clusterItemsFIMS,
                      weights = rep(1/3, 3),
                      iter = 40000) # Runs long. Reduce for tests, if needed.
#> ### Model for cluster 1. Total time is estimated...
#>
#> ### Model for cluster 2. Estimated time at finish: 00:09
#>
#> ### Model for cluster 3. Estimated time at finish: 01:55
#>
#> Maximum Rhat (aka PSR): 1 [recommended: < 1.05]
#> Minimum effective sample size (aka N_eff): 447 [recommended: > 400]
#>
#> Mean difference in the latent variable after Bayesian model averaging:
#>
#>  2.5% cred. int. -0.895
#> mean              0.085
#> 97.5% cred. int.  0.801
plotAverage(bma)
```

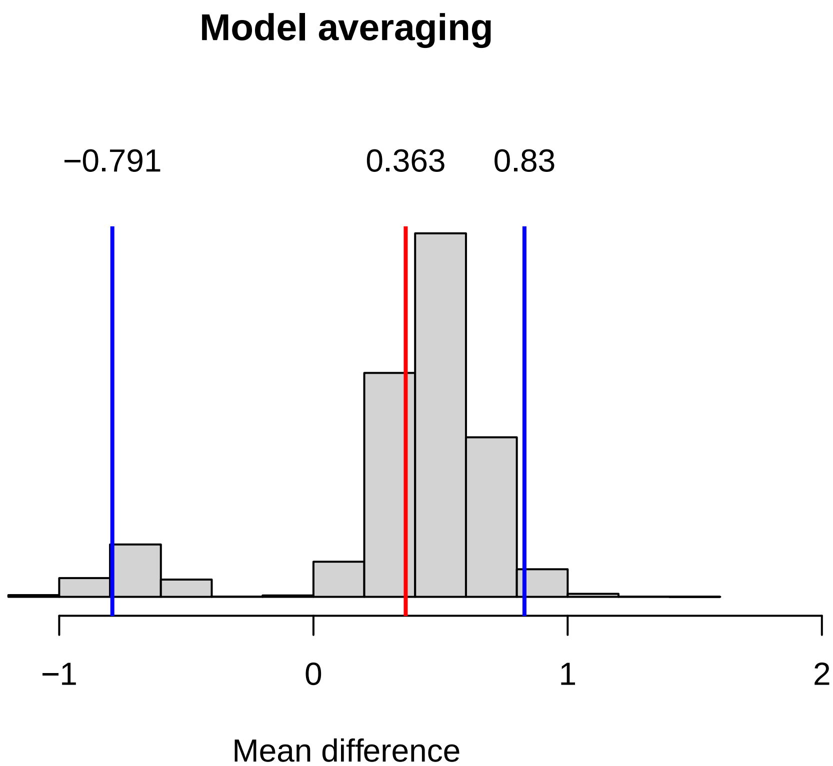


A specific partial model from the Bayesian analysis can be accessed by getModel. We can see that it is cluster three whose items yield a negative mean difference.

```
getModel(bma, which = 3) # e.g. for cluster 3 as anchor
#>                             mean se_mean    sd   2.5%  97.5%     n_eff  Rhat
#> mean_difference           -0.712   0.003 0.123 -0.970 -0.484  1288.732 1.001
#> variance_ratio             0.577   0.005 0.122  0.363  0.842   562.118 1.002
#> item_discrimination[1,1]  1.278   0.002 0.235  0.866  1.793 21018.627 1.000
#> item_discrimination[1,2]  1.367   0.013 0.459  0.639  2.426  1283.929 1.002
#> item_discrimination[2,1]  1.697   0.003 0.351  1.131  2.494 11168.662 1.001
#> item_discrimination[2,2]  3.227   0.029 1.009  1.694  5.628  1237.867 1.001
#> item_discrimination[3,1]  1.316   0.002 0.266  0.847  1.889 16693.808 1.000
#> item_discrimination[3,2]  1.993   0.018 0.668  0.944  3.554  1340.723 1.001
#> item_discrimination[4,1]  0.523   0.001 0.153  0.233  0.833 26319.064 1.000
#> item_discrimination[4,2]  0.761   0.006 0.308  0.230  1.453  3092.492 1.001
#> item_discrimination[5,1]  0.788   0.001 0.123  0.560  1.039  7477.968 1.000
#> item_discrimination[5,2]  0.788   0.001 0.123  0.560  1.039  7477.968 1.000
#> item_discrimination[6,1]  0.860   0.001 0.172  0.543  1.220 27083.300 1.000
#> item_discrimination[6,2]  3.376   0.040 1.222  1.667  6.385   914.668 1.001
#> item_discrimination[7,1]  1.533   0.008 0.304  1.014  2.203  1473.445 1.001
#> item_discrimination[7,2]  1.533   0.008 0.304  1.014  2.203  1473.445 1.001
#> item_difficulty[1,1]     -1.040   0.001 0.146 -1.347 -0.773 26435.299 1.000
#> item_difficulty[1,2]     -2.536   0.009 0.425 -3.509 -1.845  2075.289 1.002
#> item_difficulty[2,1]     -1.539   0.002 0.218 -2.018 -1.168 10998.910 1.000
#> item_difficulty[2,2]     -5.234   0.021 1.073 -7.750 -3.590  2675.669 1.001
#> item_difficulty[3,1]     -2.019   0.001 0.214 -2.481 -1.643 23970.398 1.000
#> item_difficulty[3,2]     -4.254   0.013 0.699 -5.849 -3.118  2738.638 1.001
#> item_difficulty[4,1]      0.796   0.000 0.106  0.595  1.007 59702.421 1.000
#> item_difficulty[4,2]      0.065   0.004 0.239 -0.468  0.471  3273.539 1.001
#> item_difficulty[5,1]     -0.192   0.001 0.095 -0.386 -0.010  4697.145 1.000
#> item_difficulty[5,2]     -0.192   0.001 0.095 -0.386 -0.010  4697.145 1.000
#> item_difficulty[6,1]     -0.447   0.001 0.108 -0.663 -0.238 39561.309 1.000
#> item_difficulty[6,2]     -3.494   0.031 1.067 -6.113 -1.980  1156.826 1.002
#> item_difficulty[7,1]     -2.337   0.004 0.237 -2.860 -1.933  3436.400 1.001
#> item_difficulty[7,2]     -2.337   0.004 0.237 -2.860 -1.933  3436.400 1.001
```

Other weights can be applied fast to an already estimated modelAveraging object:

```
bma2 <- modelAveraging(res_modelAveraging = bma,
                       weights = c(0.45, 0.45, 0.1))
#>
#> Maximum Rhat (aka PSR): 1 [recommended: < 1.05]
#> Minimum effective sample size (aka N_eff): 447 [recommended: > 400]
#>
#> Mean difference in the latent variable after Bayesian model averaging:
#>
#>  2.5% cred. int. -0.791
#> mean              0.363
#> 97.5% cred. int.  0.830
plotAverage(bma2)
```


Model averaging
−0.791
0.363
0.83
−1
0
1
2
Mean difference