
Traditional Differential Item Functioning (DIF) using Graded Response Model

Code ▾

2022-10-19

Data Source

Real-world data to demonstrate the implementation of the methods discussed in this workshop were from a population-based Joint Replacement Registry for patients having a total or partial hip or knee replacement.

We selected 1391 individuals who had a total hip replacement and provided complete responses to the SF-12 (version 2) physical and mental components items prior to undergoing surgery (i.e., at the baseline clinic visit).

Objective

To test for DIF by sex on the physical and mental component items of the SF-12

Packages and Functions to Test for DIF in R

We would explore the **lordif**, **multipleGroup** and **DIF** functions in the lordif and mirt packages.

Install the following packages, if not previously installed.

Hide

```
# install.packages(c("tidyverse", "tableone", "lordif", "mirt"))
```

Load the Libraries

Hide

```
library(tidyverse) # For data manipulation
library(tableone) # For creating tables

library(lordif) # For DIF test
library(mirt) # To activate multipleGroup function for DIF test
library(psych)
```


##		
##		Overall
##	n	1391
##	SF1_PH (%)	
##	1	24 (1.7)
##	2	138 (9.9)
##	3	602 (43.3)
##	4	512 (36.8)
##	5	115 (8.3)
##	SF2A_PH (%)	
##	1	960 (69.0)
##	2	354 (25.4)
##	3	77 (5.5)
##	SF2B_PH (%)	
##	1	1014 (72.9)
##	2	308 (22.1)
##	3	69 (5.0)
##	SF3A_PH (%)	
##	1	543 (39.0)
##	2	482 (34.7)
##	3	237 (17.0)
##	4	89 (6.4)
##	5	40 (2.9)
##	SF3B_PH (%)	
##	1	555 (39.9)
##	2	495 (35.6)
##	3	238 (17.1)
##	4	71 (5.1)
##	5	32 (2.3)
##	SF4A_MH (%)	
##	1	145 (10.4)
##	2	248 (17.8)
##	3	325 (23.4)
##	4	283 (20.3)
##	5	390 (28.0)
##	SF4B_MH (%)	
##	1	135 (9.7)
##	2	212 (15.2)
##	3	313 (22.5)

##	4	301 (21.6)
##	5	430 (30.9)
##	SF5_PH (%)	
##	1	385 (27.7)
##	2	632 (45.4)
##	3	261 (18.8)
##	4	95 (6.8)
##	5	18 (1.3)
##	SF6A_MH (%)	
##	1	74 (5.3)
##	2	229 (16.5)
##	3	401 (28.8)
##	4	605 (43.5)
##	5	82 (5.9)
##	SF6B_MH (%)	
##	1	195 (14.0)
##	2	394 (28.3)
##	3	484 (34.8)
##	4	281 (20.2)
##	5	37 (2.7)
##	SF6C_MH (%)	
##	1	35 (2.5)
##	2	94 (6.8)
##	3	389 (28.0)
##	4	466 (33.5)
##	5	407 (29.3)
##	SF7_MH (%)	
##	1	136 (9.8)
##	2	239 (17.2)
##	3	434 (31.2)
##	4	278 (20.0)
##	5	304 (21.9)
##	Sex = Male (%)	674 (48.5)

IRT Assumptions: Unidimensionality, local independence and monotonicity.

Hide

```
#----- IRT-GRM -----  
  
#----Check IRT Assumptions-----  
  
# Scree plot of eigenvalue to assess unidimensionality  
  
polycorrPH <- polychoric(items_PH[,-1],global=FALSE)$rho
```

```
## Warning in polychoric(items_PH[, -1], global = FALSE): The items do not have an  
## equal number of response alternatives, global set to FALSE.
```

```
## Warning in matpLower(x, nvar, gminx, gmaxx, gminy, gmaxy): 1 cells were adjusted  
## for 0 values using the correction for continuity. Examine your data carefully.
```

Hide

```
poly_eigenPH <- eigen(polycorrPH)$values  
round(poly_eigenPH,3)
```

```
## [1] 3.781 0.640 0.328 0.155 0.096
```

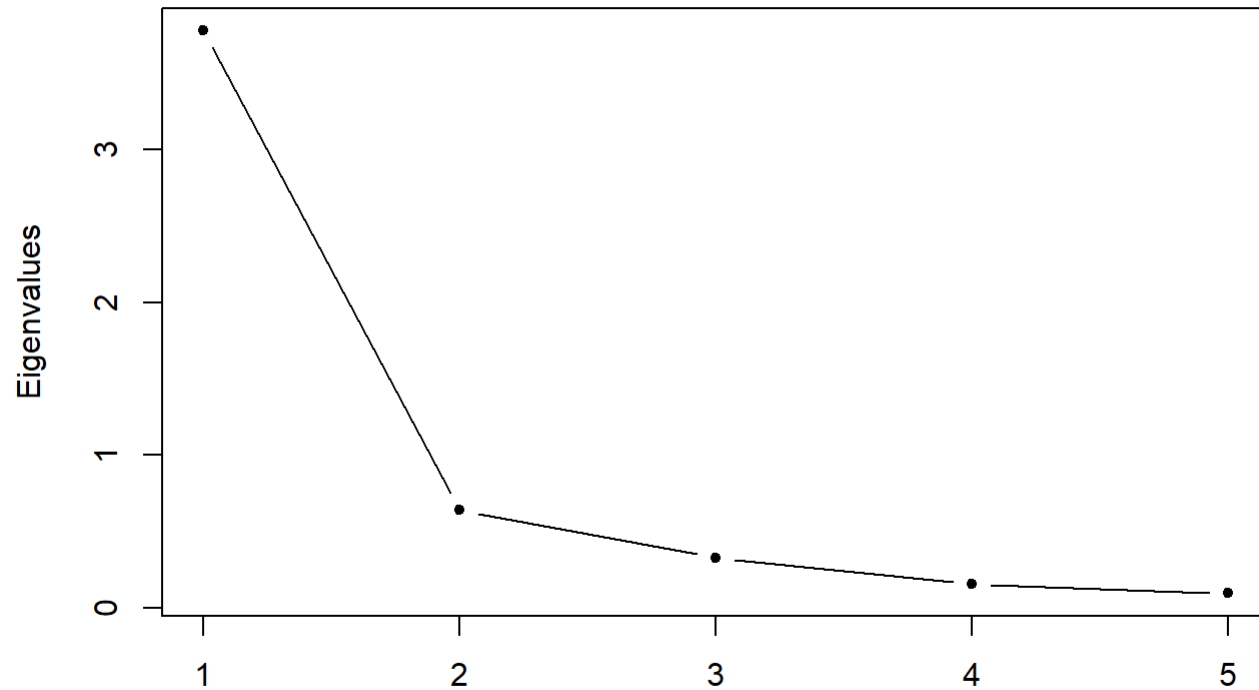
Hide

```
round(round(poly_eigenPH,3)[1]/round(poly_eigenPH,3)[2],3)
```

```
## [1] 5.908
```

Hide

```
plot(1:length(poly_eigenPH),poly_eigenPH, type="b", pch=20, xlab="",ylab="Eigenvalues")
```



Hide

```
polycorrMH <- polychoric(items_MH[,-1],global=FALSE)$rho
```

```
## Warning in matpLower(x, nvar, gminx, gmaxx, gminy, gmaxy): 2 cells were adjusted  
## for 0 values using the correction for continuity. Examine your data carefully.
```

Hide

```
poly_eigenMH <- eigen(polycorrMH)$values  
round(poly_eigenMH,3)
```

```
## [1] 3.084 0.672 0.507 0.387 0.350
```

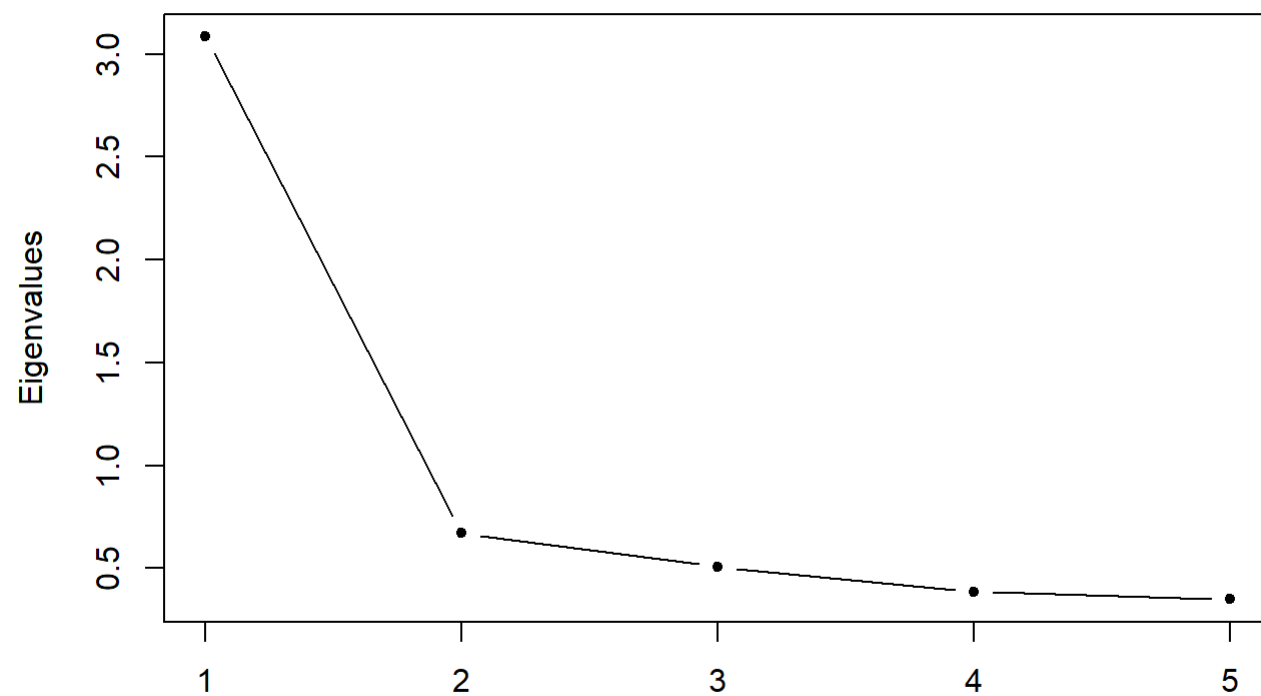
Hide

```
round(round(poly_eigenMH,3)[1]/round(poly_eigenMH,3)[2],3)
```

```
## [1] 4.589
```

Hide

```
plot(1:length(poly_eigenMH),poly_eigenMH, type="b", pch=20, xlab="",ylab="Eigenvalues")
```



Hide

```
# Based on the scree plot, we assume unidimensional
mirtPHgrm <- mirt(data = items_PH,
                 model = 1, # Default is 1, indicating that a unidimensional model will
                 l be fitted
                 itemtype = "graded",
                 verbose = FALSE)

mirtMHgrm <- mirt(data = items_MH,
                 model = 1, # Default is 1, indicating that a unidimensional model will
                 l be fitted
                 itemtype = "graded",
                 verbose = FALSE)

# Residual covariance matrix to assess local independence
round(M2(mirtPHgrm, residmat = TRUE),3)
```

```
##          SF1_PH SF2A_PH SF2B_PH SF3A_PH SF3B_PH SF5_PH
## SF1_PH      NA      NA      NA      NA      NA      NA
## SF2A_PH  0.016      NA      NA      NA      NA      NA
## SF2B_PH  0.090  0.305      NA      NA      NA      NA
## SF3A_PH  0.012 -0.037 -0.047      NA      NA      NA
## SF3B_PH  0.007 -0.042 -0.029  0.011      NA      NA
## SF5_PH   0.002  0.008  0.020 -0.026 -0.045      NA
```

Hide

```
round(M2(mirtMHgrm, residmat = TRUE),3)
```

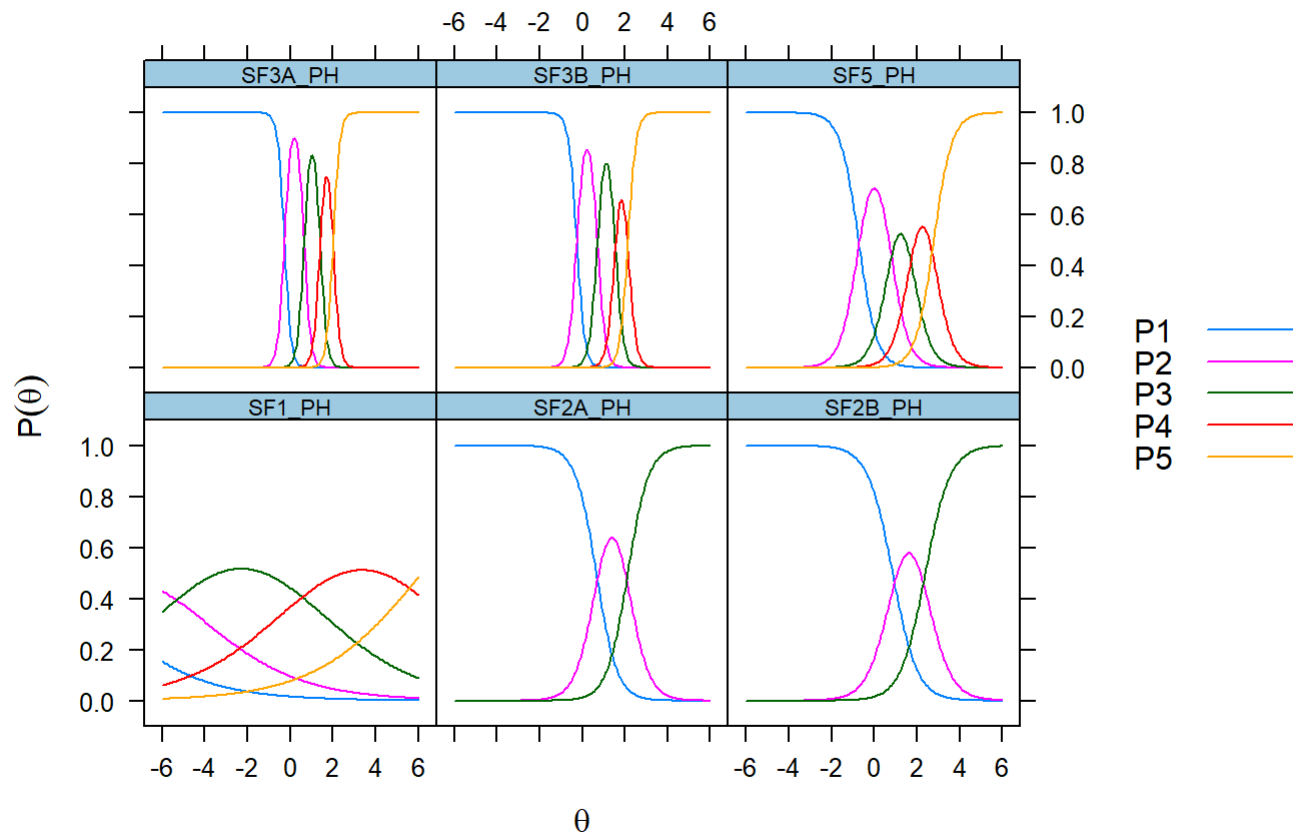


```
##          SF4A_MH SF4B_MH SF6A_MH SF6B_MH SF6C_MH SF7_MH
## SF4A_MH      NA      NA      NA      NA      NA      NA
## SF4B_MH    -0.006      NA      NA      NA      NA      NA
## SF6A_MH    -0.052  -0.091      NA      NA      NA      NA
## SF6B_MH    -0.069  -0.078  0.185      NA      NA      NA
## SF6C_MH    -0.036  -0.079  0.063  0.005      NA      NA
## SF7_MH     -0.057  -0.033  0.084  0.163  0.03      NA
```

Hide

```
# Visualizations to assess monotonicity
plot(mirtPHgrm, type = 'trace') # the category response curves
```

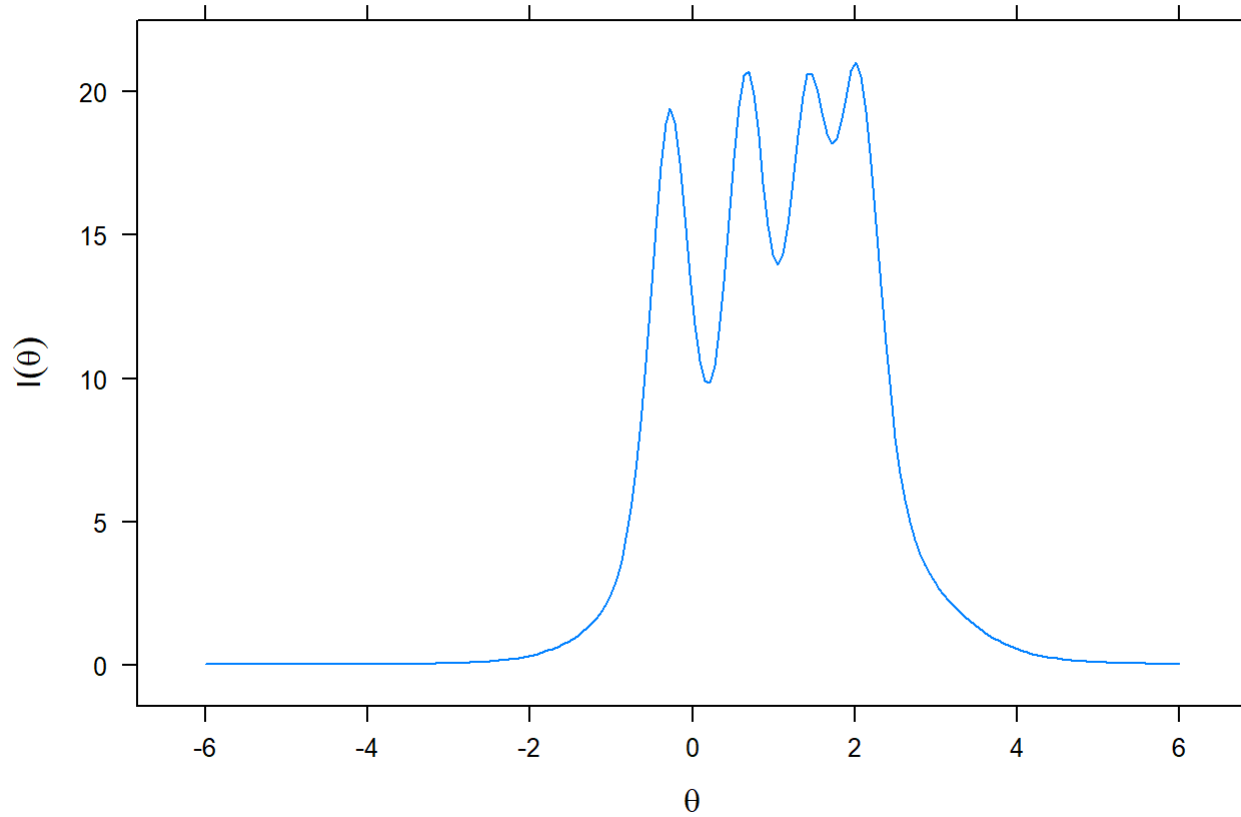
Item Probability Functions



Hide

```
plot(mirtPHgrm, type = 'info') # test information
```

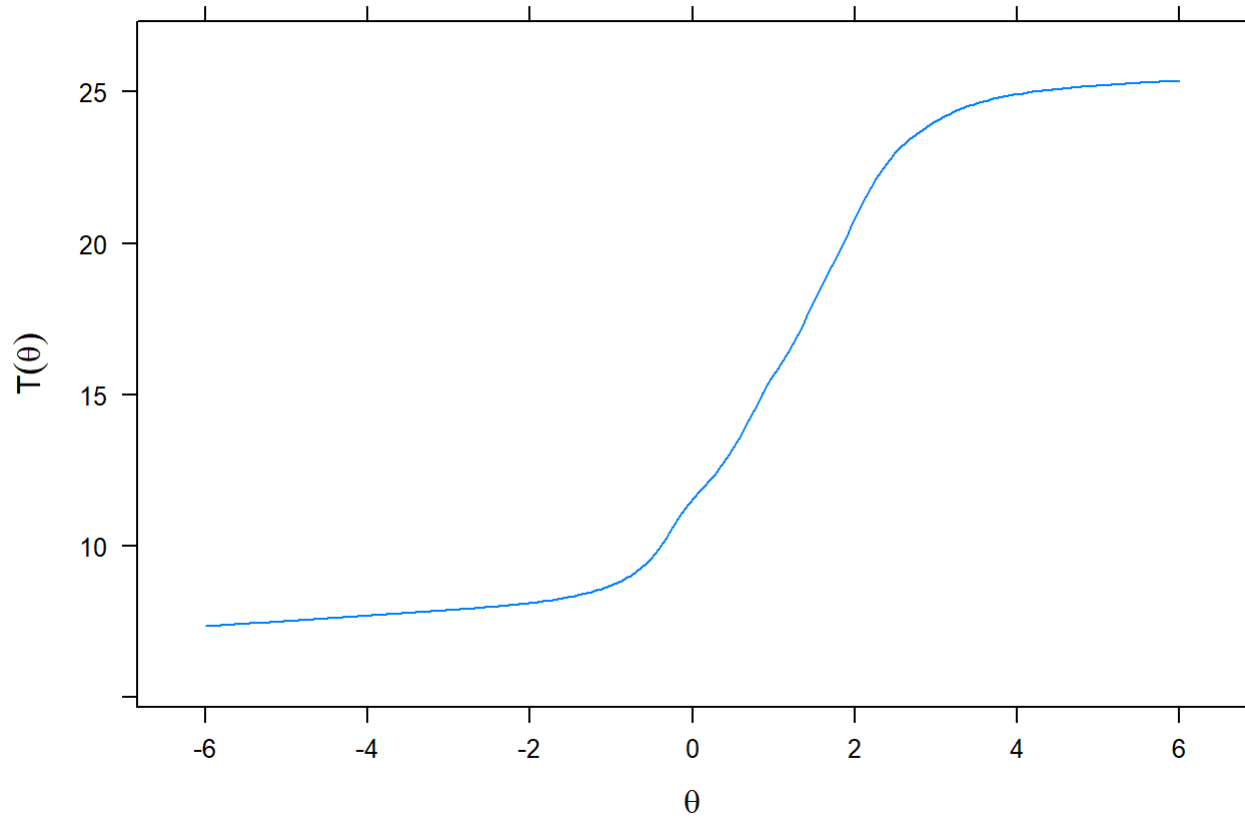
Test Information



Hide

```
plot(mirtPHgrm) # test score function
```

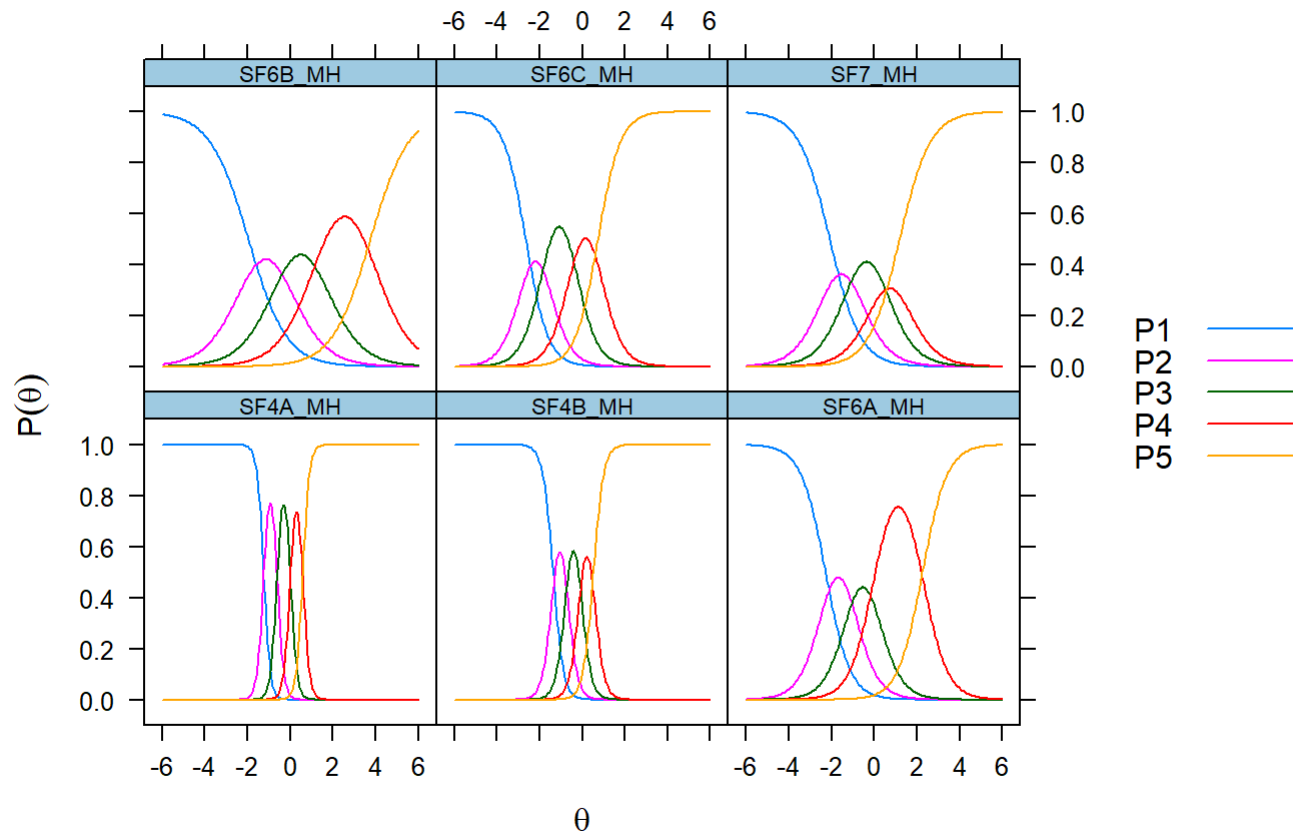
Expected Total Score



Hide

```
plot(mirtMHgrm, type = 'trace') # the category response curves
```

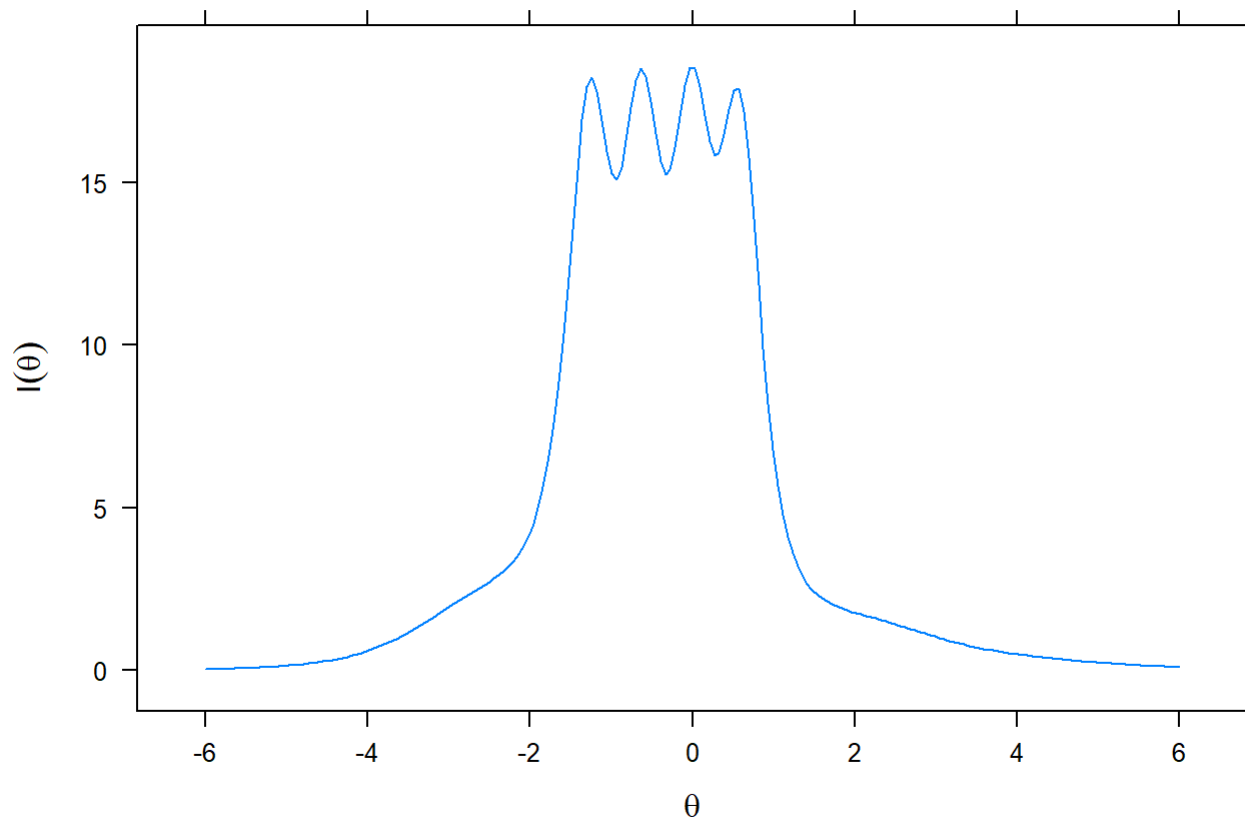
Item Probability Functions



Hide

```
plot(mirtMHgrm, type = 'info') # test information
```

Test Information

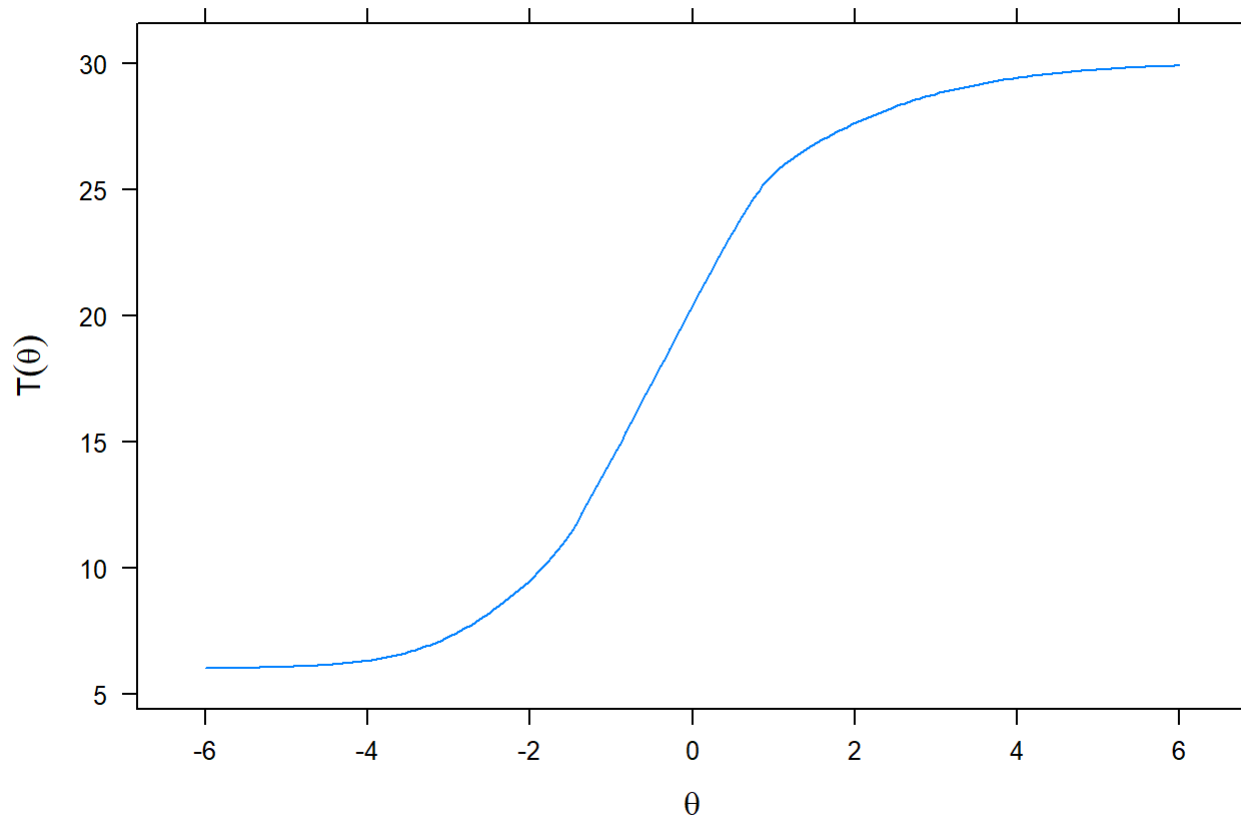


Hide

```
plot(mirtMHgrm)
```

```
# test score function
```

Expected Total Score



Hide

```
#-----
```

To test for DIF, it is important to specify anchor item(s). The functions we used can choose the anchor items and we can as well specify the anchor item(s) ourselves. We will show both.

A. Allowing the R functions to specify the anchor items

Hide

```
#----- Lordif -----#  
# ?Lordif # This line of code call the help function to see the use of Lordif  
# Lordif: performs iterative hybrid ordinal logistic regression/IRT DIF  
  
DIF_PH_sex <- lordif(resp.data = items_PH,  
                    group = sex,  
                    model="GRM")  
  
DIF_MH_sex <- lordif(resp.data = items_MH,  
                    group = sex,  
                    model="GRM")  
  
#-----#
```

Hide

```
print(DIF_PH_sex)
```

```
## Call:
## lordif(resp.data = items_PH, group = sex, model = "GRM")
##
##   Number of DIF groups: 2
##
##   Number of items flagged for DIF: 2 of 6
##
##   Items flagged: 2, 3
##
##   Number of iterations for purification: 2 of 10
##
##   Detection criterion: Chisqr
##
##   Threshold: alpha = 0.01
##
##   item ncat  chi12  chi13  chi23
## 1     1     5 0.5844 0.0916 0.0343
## 2     2     3 0.0026 0.0029 0.1056
## 3     3     3 0.0000 0.0001 0.9748
## 4     4     5 0.7057 0.6570 0.4036
## 5     5     5 0.1555 0.2295 0.3358
## 6     6     4 0.1940 0.2121 0.2344
```

Hide

```
print(DIF_MH_sex)
```



```
## Call:
## lordif(resp.data = items_MH, group = sex, model = "GRM")
##
## Number of DIF groups: 2
##
## Number of items flagged for DIF: 4 of 6
##
## Items flagged: 3, 4, 5, 6
##
## Number of iterations for purification: 4 of 10
##
## Detection criterion: Chisqr
##
## Threshold: alpha = 0.01
##
## item ncat chi12 chi13 chi23
## 1 1 5 0.9743 0.9804 0.8442
## 2 2 5 0.7540 0.5983 0.3351
## 3 3 5 0.0004 0.0001 0.0089
## 4 4 5 0.0000 0.0000 0.0911
## 5 5 5 0.0018 0.0071 0.6987
## 6 6 5 0.0002 0.0009 0.8348
```

Hide


```
'free_means', 'free_var'))
```

```
# test uniform DIF
```

```
dropdown_unif_MH <- DIF(model_constrained_MH, c('d1','d2','d3','d4'),  
  scheme = 'drop')
```

```
# test non-uniform DIF
```

```
dropdown_nonunif_MH <- DIF(model_constrained_MH, c('a1'), scheme = 'drop')
```

```
#-----#
```

```
#-----#
```

Hide

```
round(dropdown_unif_PH,3)
```

	converged <dbl>	AIC <dbl>	SABIC <dbl>	HQ <dbl>	BIC <dbl>	X2 <dbl>	df <dbl>	p <dbl>
SF1_PH	1	3.264	11.509	11.099	24.215	4.736	4	0.315
SF2A_PH	1	-2.630	1.492	1.287	7.846	6.630	2	0.036
SF2B_PH	1	-13.708	-9.586	-9.791	-3.232	17.708	2	0.000
SF3A_PH	1	5.502	13.747	13.336	26.453	2.498	4	0.645
SF3B_PH	1	-1.032	7.213	6.803	19.919	9.032	4	0.060
SF5_PH	1	1.979	10.224	9.814	22.930	6.021	4	0.198

6 rows

Hide

```
round(dropdown_nonunif_PH,3)
```

	converged <dbl>	AIC <dbl>	SABIC <dbl>	HQ <dbl>	BIC <dbl>	X2 <dbl>	df <dbl>	p <dbl>
--	---------------------------	---------------------	-----------------------	--------------------	---------------------	--------------------	--------------------	-------------------

	converged <dbl>	AIC <dbl>	SABIC <dbl>	HQ <dbl>	BIC <dbl>	X2 <dbl>	df <dbl>	p <dbl>
SF1_PH	1	-2.808	-0.747	-0.850	2.429	4.808	1	0.028
SF2A_PH	1	1.218	3.279	3.177	6.456	0.782	1	0.377
SF2B_PH	1	-6.442	-4.381	-4.483	-1.204	8.442	1	0.004
SF3A_PH	1	0.838	2.899	2.797	6.076	1.162	1	0.281
SF3B_PH	1	1.031	3.092	2.989	6.268	0.969	1	0.325
SF5_PH	1	1.998	4.059	3.956	7.236	0.002	1	0.962

6 rows

Hide

```
round(dropdown_unif_MH,3)
```

	converged <dbl>	AIC <dbl>	SABIC <dbl>	HQ <dbl>	BIC <dbl>	X2 <dbl>	df <dbl>	p <dbl>
SF4A_MH	1	-6.028	2.217	1.807	14.923	14.028	4	0.007
SF4B_MH	1	2.562	10.807	10.397	23.513	5.438	4	0.245
SF6A_MH	1	-3.756	4.489	4.078	17.195	11.756	4	0.019
SF6B_MH	1	-30.255	-22.011	-22.421	-9.304	38.255	4	0.000
SF6C_MH	1	2.691	10.935	10.525	23.642	5.309	4	0.257
SF7_MH	1	-8.025	0.220	-0.190	12.926	16.025	4	0.003

6 rows

Hide

```
round(dropdown_nonunif_MH,3)
```

	converged <dbl>	AIC <dbl>	SABIC <dbl>	HQ <dbl>	BIC <dbl>	X2 <dbl>	df <dbl>	p <dbl>
SF4A_MH	1	1.795	3.856	3.754	7.033	0.205	1	0.651
SF4B_MH	1	1.842	3.903	3.801	7.080	0.158	1	0.691
SF6A_MH	1	0.283	2.344	2.241	5.520	1.717	1	0.190
SF6B_MH	1	-0.053	2.008	1.906	5.185	2.053	1	0.152
SF6C_MH	1	0.220	2.282	2.179	5.458	1.780	1	0.182
SF7_MH	1	0.854	2.916	2.813	6.092	1.146	1	0.284

6 rows

B. Specifying the anchor item(s) using the all-other anchor approach (AOAA) approach

Hide

```
# "SF3A_PH", "SF3B_PH" and "SF5_PH" are not statistically significant for
# uniform and non-uniform DIF from the drop down procedure. Hence, we check the
# slopes of these items and select the item with the maximum slope as the anchor
# item
```

```
coef(model_constrained_PH, simplify=T)
```

```

## $Female
## $items
##      a1      d1      d2      d3      d4
## SF1_PH 0.393  4.039  2.000 -0.289 -2.551
## SF2A_PH 2.034 -1.742 -4.770      NA      NA
## SF2B_PH 1.713 -1.823 -4.469      NA      NA
## SF3A_PH 6.270  0.598 -5.300 -10.071 -13.944
## SF3B_PH 5.167  0.409 -4.690 -9.063 -12.192
## SF5_PH  2.335  1.303 -2.206 -4.541 -7.032
##
## $means
## PH
## 0
##
## $cov
## PH
## PH 1
##
##
## $Male
## $items
##      a1      d1      d2      d3      d4
## SF1_PH 0.393  4.039  2.000 -0.289 -2.551
## SF2A_PH 2.034 -1.742 -4.770      NA      NA
## SF2B_PH 1.713 -1.823 -4.469      NA      NA
## SF3A_PH 6.270  0.598 -5.300 -10.071 -13.944
## SF3B_PH 5.167  0.409 -4.690 -9.063 -12.192
## SF5_PH  2.335  1.303 -2.206 -4.541 -7.032
##
## $means
## PH
## 0.391
##
## $cov
## PH
## PH 0.984

```

Hide

```
# SF3A_PH has the maximum slope, hence we select this item as the anchor item
```

Hide

```
DIF_PH_sex_anch <- lordif(resp.data = items_PH,  
                          group = sex,  
                          model = "GRM",  
                          anchor = c(4))  
  
model_constrained_PH_anch <- multipleGroup(data = items_PH,  
                                           model = model.mgrm_PH,  
                                           group = sex,  
                                           invariance = c('SF3A_PH',  
                                                         'free_means', 'free_var'))  
  
#coef(model_constrained_PH_anch, simplify=T)  
  
# test uniform DIF  
anch_unif_PH <- DIF(model_constrained_PH_anch,  
                   c('d1','d2','d3','d4'),  
                   items2test = c(1:3,5:6))  
  
# test non-uniform DIF  
anch_nonunif_PH <- DIF(model_constrained_PH_anch,  
                       c('a1'),  
                       items2test = c(1:3,5:6))  
  
#-----#
```

Hide

```
print(DIF_PH_sex_anch)
```

```

## Call:
## lordif(resp.data = items_PH, group = sex, model = "GRM", anchor = c(4))
##
## Number of DIF groups: 2
##
## Number of items flagged for DIF: 2 of 6
##
## Items flagged: 2, 3
##
## Number of iterations for purification: 0 of 10
##
## Detection criterion: Chisqr
##
## Threshold: alpha = 0.01
##
## item ncat chi12 chi13 chi23
## 1 1 5 0.6557 0.0481 0.0154
## 2 2 3 0.0011 0.0011 0.0924
## 3 3 3 0.0000 0.0000 0.9918
## 4 4 5 0.2392 0.3243 0.3519
## 5 5 5 0.4493 0.3847 0.2473
## 6 6 4 0.0712 0.0849 0.1951

```

Hide

```
round(anch_unif_PH,3)
```

	converged <dbl>	AIC <dbl>	SABIC <dbl>	HQ <dbl>	BIC <dbl>	X2 <dbl>	df <dbl>	p <dbl>
SF1_PH	1	2.817	11.062	10.652	23.769	5.183	4	0.269
SF2A_PH	1	-3.260	0.862	0.657	7.215	7.260	2	0.027
SF2B_PH	1	-4.954	-0.832	-1.037	5.522	8.954	2	0.011
SF3B_PH	1	3.518	11.762	11.352	24.469	4.482	4	0.345
SF5_PH	1	2.272	10.516	10.106	23.223	5.728	4	0.220

5 rows

Hide

```
round(anch_nonunif_PH,3)
```

	converged <dbl>	AIC <dbl>	SABIC <dbl>	HQ <dbl>	BIC <dbl>	X2 <dbl>	df <dbl>	p <dbl>
SF1_PH	1	-3.405	-1.344	-1.447	1.833	5.405	1	0.020
SF2A_PH	1	0.348	2.409	2.306	5.585	1.652	1	0.199
SF2B_PH	1	1.708	3.769	3.667	6.946	0.292	1	0.589
SF3B_PH	1	1.374	3.435	3.333	6.612	0.626	1	0.429
SF5_PH	1	1.335	3.396	3.294	6.573	0.665	1	0.415

5 rows

Hide

```
# "SF4B_MH" and "SF6C_MH" are not statistically significant for  
# uniform and non-uniform DIF from the drop down procedure. Hence, we check the  
# slopes of these items and select the item with the maximum slope as the anchor  
# item
```

```
coef(model_constrained_MH, simplify=T)
```

```

## $Female
## $items
##           a1    d1    d2    d3    d4
## SF4A_MH 5.963 7.162 3.124 -0.859 -4.593
## SF4B_MH 3.877 5.125 2.490 -0.186 -2.723
## SF6A_MH 1.628 3.742 1.655 -0.245 -4.218
## SF6B_MH 1.046 2.042 0.243 -1.647 -4.370
## SF6C_MH 1.773 4.779 3.024  0.556 -1.655
## SF7_MH  1.291 2.701 1.180 -0.568 -1.840
##
## $means
## MH
##  0
##
## $cov
##   MH
## MH 1
##
##
## $Male
## $items
##           a1    d1    d2    d3    d4
## SF4A_MH 5.963 7.162 3.124 -0.859 -4.593
## SF4B_MH 3.877 5.125 2.490 -0.186 -2.723
## SF6A_MH 1.628 3.742 1.655 -0.245 -4.218
## SF6B_MH 1.046 2.042 0.243 -1.647 -4.370
## SF6C_MH 1.773 4.779 3.024  0.556 -1.655
## SF7_MH  1.291 2.701 1.180 -0.568 -1.840
##
## $means
##   MH
## 0.304
##
## $cov
##           MH
## MH 1.303

```

Hide

```
# SF4B_MH has the maximum slope, hence we select this item as the anchor item
```

Hide

```
DIF_MH_sex_anch <- lordif(resp.data = items_MH,
                          group = sex,
                          model="GRM",
                          anchor=c(2))

model_constrained_MH_anch <- multipleGroup(data = items_MH,
                                           model = model.mgrm_MH,
                                           group = sex,
                                           invariance = c('SF4B_MH',
                                                         'free_means', 'free_var'))

# test uniform DIF
anch_unif_MH <- DIF(model_constrained_MH_anch,
                   c('d1', 'd2', 'd3', 'd4'),
                   items2test = c(1,3:6))

# test non-uniform DIF
anch_nonunif_MH <- DIF(model_constrained_MH_anch,
                       c('a1'),
                       items2test = c(1,3:6))

#-----#
```

Hide

```
print(DIF_MH_sex_anch)
```

```

## Call:
## lordif(resp.data = items_MH, group = sex, model = "GRM", anchor = c(2))
##
## Number of DIF groups: 2
##
## Number of items flagged for DIF: 4 of 6
##
## Items flagged: 3, 4, 5, 6
##
## Number of iterations for purification: 0 of 10
##
## Detection criterion: Chisqr
##
## Threshold: alpha = 0.01
##
## item ncat chi12 chi13 chi23
## 1 1 5 0.1374 0.1618 0.2306
## 2 2 5 0.2200 0.2130 0.2075
## 3 3 5 0.0001 0.0000 0.0065
## 4 4 5 0.0000 0.0000 0.0822
## 5 5 5 0.0004 0.0017 0.7956
## 6 6 5 0.0000 0.0002 0.8796

```

Hide

```
round(anch_unif_MH,3)
```

	converged <dbl>	AIC <dbl>	SABIC <dbl>	HQ <dbl>	BIC <dbl>	X2 <dbl>	df <dbl>	p <dbl>
SF4A_MH	1	7.133	15.378	14.968	28.084	0.867	4	0.929
SF6A_MH	1	-4.392	3.853	3.443	16.559	12.392	4	0.015
SF6B_MH	1	-30.748	-22.503	-22.913	-9.797	38.748	4	0.000
SF6C_MH	1	1.593	9.838	9.428	22.545	6.407	4	0.171
SF7_MH	1	-9.687	-1.443	-1.853	11.264	17.687	4	0.001

5 rows

Hide

```
round(anch_nonunif_MH, 3)
```

	converged <dbl>	AIC <dbl>	SABIC <dbl>	HQ <dbl>	BIC <dbl>	X2 <dbl>	df <dbl>	p <dbl>
SF4A_MH	1	1.998	4.059	3.956	7.236	0.002	1	0.963
SF6A_MH	1	1.836	3.897	3.795	7.074	0.164	1	0.685
SF6B_MH	1	1.297	3.358	3.255	6.534	0.703	1	0.402
SF6C_MH	1	1.554	3.615	3.513	6.792	0.446	1	0.504
SF7_MH	1	1.621	3.682	3.579	6.858	0.379	1	0.538

5 rows

Hide

```
#----- Visualize the results for items that showed DIF -----#  
# plot(DIF_PH_sex)  
# plot(DIF_MH_sex)  
# plot(DIF_PH_sex_anch, labels = c("Female", "Male"))  
# plot(DIF_MH_sex_anch, labels = c("Female", "Male"))  
#-----#
```