

SUPPLEMENTARY MATERIALS

Allostatic load scoring using item response theory

Shelley H. Liu¹, Robert-Paul Juster², Kristen Dams-O'Connor³, & Julie Spicer⁴

¹Department of Population Health Science and Policy, Icahn School of Medicine at Mount Sinai

²Department of Psychiatry and Addiction, University of Montreal

³Department of Rehabilitation Medicine, Department of Neurology, Icahn School of Medicine at Mount Sinai

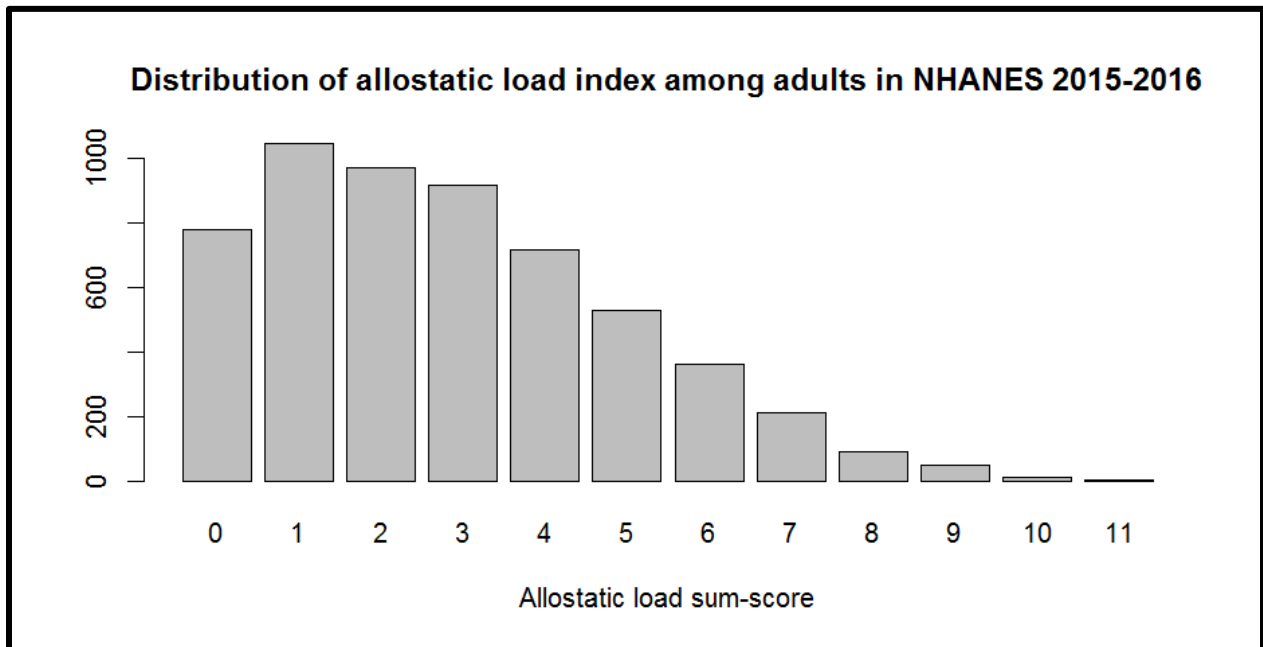
⁴Department of Psychiatry, Icahn School of Medicine at Mount Sinai

Corresponding author:

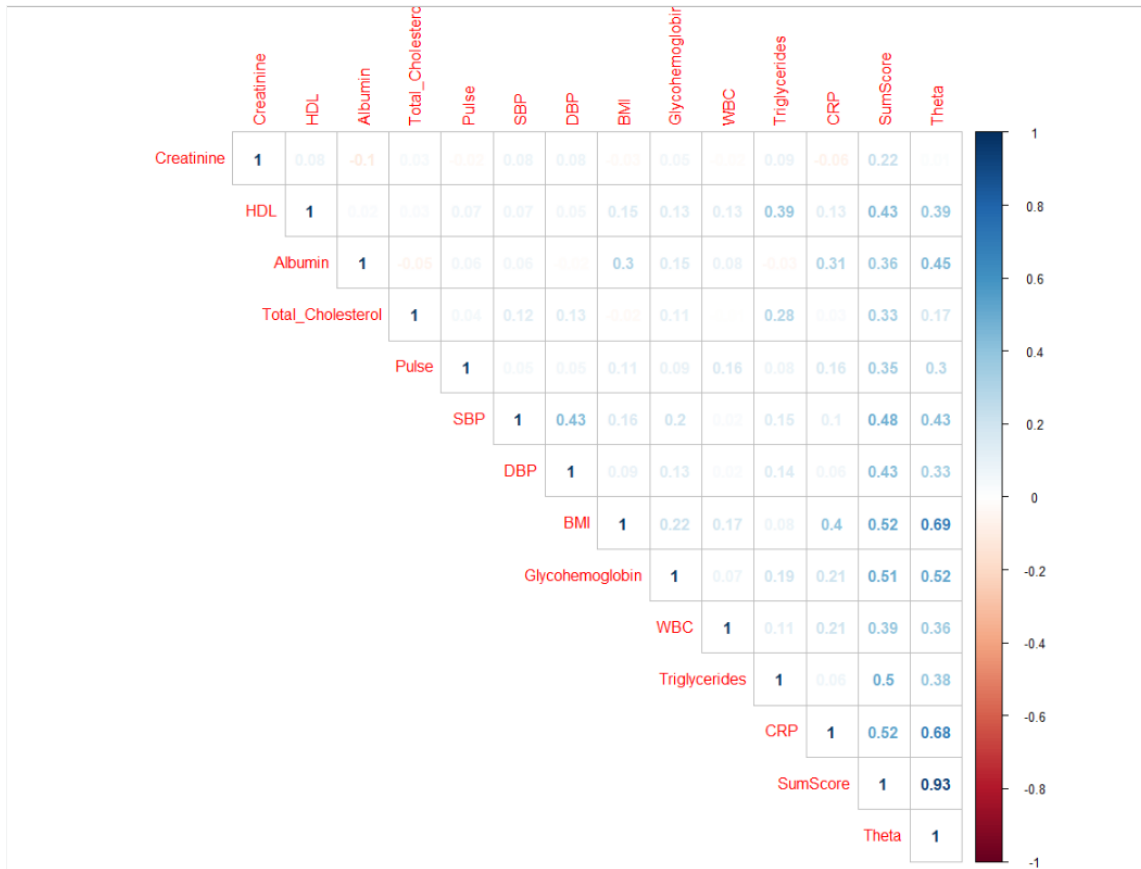
Shelley H. Liu

Email: shelley.liu@mountsinai.org

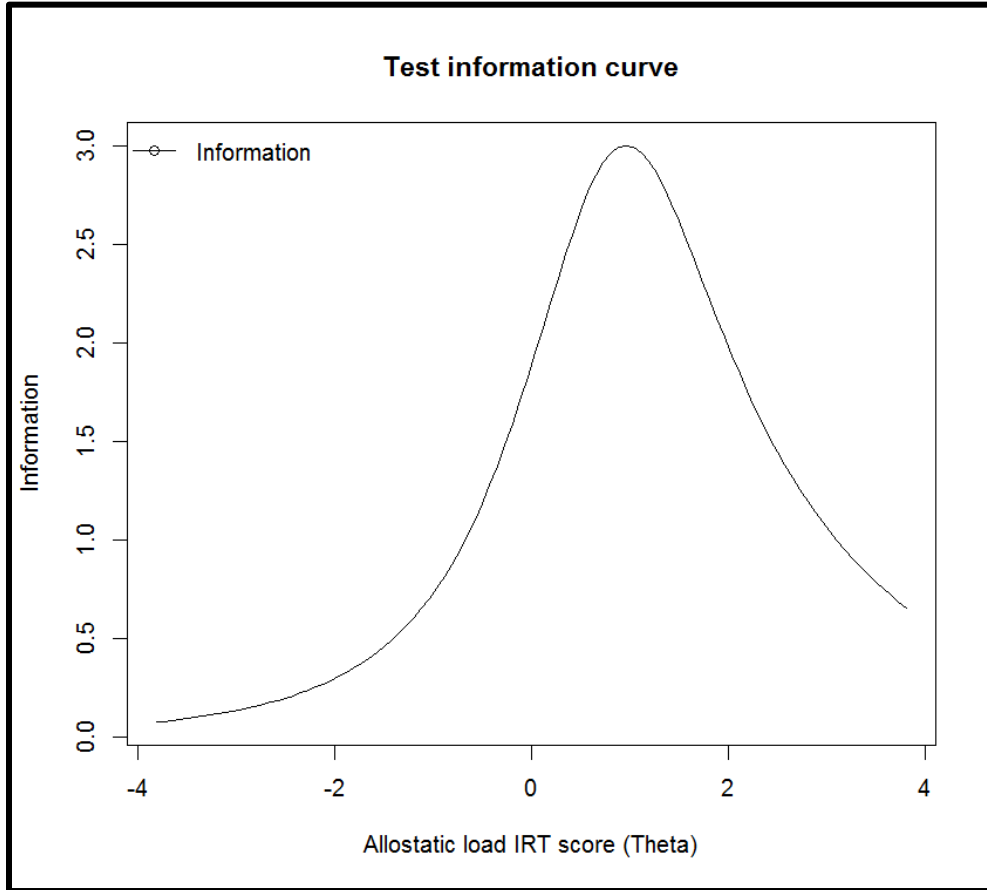
I. Supplementary Figure 1. Distribution of the allostatic load sum-score in adults aged 20-59 in NHANES 2015-2016.



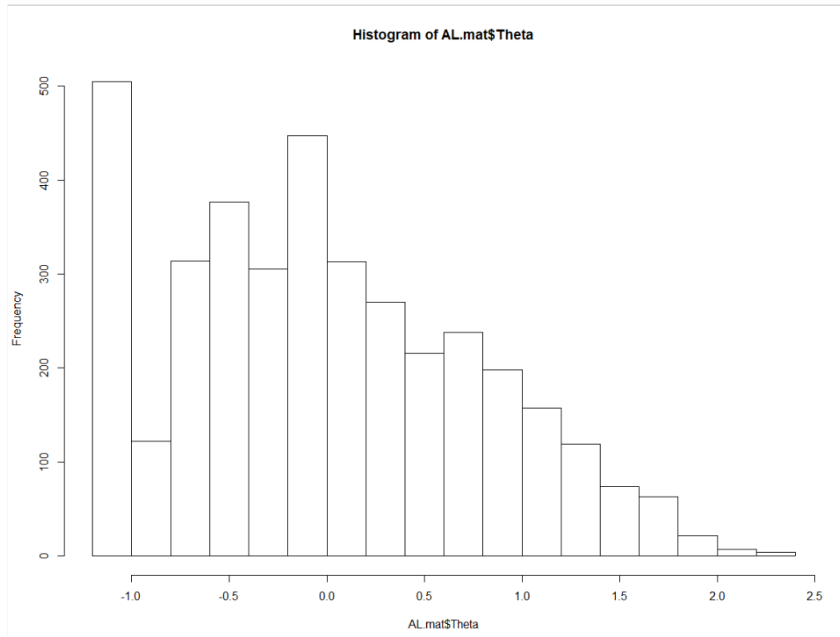
II. Supplementary Figure 2. Correlation between dichotomized (high/low risk) allostatic load biomarkers and the allostatic load sum-score and IRT score.



III. Supplementary Figure 3. Test information curve. The scale for the IRT score in the dataset remains between approximately -1 to 2. However, the test information curve provides a larger range, as it shows the information supplied by the model at different theta scores (but in our dataset, we only have theta scores ranging from -1 to 2).



IV. Supplementary Figure 4. Distribution of the allostatic load IRT score in adults aged 20-59 in NHANES 2015-2016.



V. Supplementary Table 1. Associations of family income to poverty ratio and allostatic load.

| <i>Predictors</i> | AL IRT score | | | AL Sum score | | |
|--------------------------------|---------------------|---------------|------------------|---------------------|---------------|------------------|
| | β | <i>95% CI</i> | <i>p</i> | β | <i>95% CI</i> | <i>p</i> |
| (Intercept) | 0.1 | 0.05 – 0.15 | <0.001 | 3.11 | 2.96 – 3.26 | <0.001 |
| Family income to poverty ratio | -0.04 | -0.05 – -0.02 | <0.001 | -0.07 | -0.12 – -0.02 | 0.008 |
| Observations | 3391 | | | 2835 | | |

Socio-economic status was measured using family income to poverty ratio. The models have different sample sizes, as IRT does not require complete data on all AL biomarkers in order to calculate scores, unlike the sum-score approach.

VI. Simulated data and reproducible IRT code in R.

Here, we simulate data for n=500 participants. There are four correlated binary variables (e.g. four biomarkers, each classified as high/low risk).

```
# Load packages
library(MultiRNG)
library(lavaan)
library(ltm)
```

```
set.seed(123) # For reproducibility of these simulation results
```

```
# Simulate some data for n=500, with 4 correlated binary indicators
```

```
cmat<-matrix(c(1,0.4,0.3,0.25, 0.4,1,0.4,0.4, 0.3,0.4,1,0.2, 0.25,0.4,0.2,1), nrow=4, ncol=4)
propvec=c(0.4,0.4,0.3, 0.2)
```

```
mydata=draw.correlated.binary(no.row=500,d=4,prop.vec=propvec,corr.mat=cmat)
colnames(mydata) = c("V1", "V2", "V3", "V4")
```

```
head(mydata) # print first six rows of mydata
```

```
> head(mydata)
      V1 V2 V3 V4
[1,]  0  0  0  0
[2,]  0  0  0  0
[3,]  0  0  0  0
[4,]  0  0  0  0
[5,]  1  1  1  0
[6,]  0  1  0  1
```

```
# Check for sufficient uni-dimensionality
```

```
CFA.model <- 'Construct =~ V1 + V2 + V3 + V4'
fit <- cfa(CFA.model, data=mydata)
summary(fit, fit.measures=TRUE)
```

```
> summary(fit, fit.measures=TRUE)
lavaan 0.6-5 ended normally after 24 iterations
```

| | |
|---|-----------|
| Estimator | ML |
| Optimization method | NLMINB |
| Number of free parameters | 8 |
| Number of observations | 500 |
| Model Test User Model: | |
| Test statistic | 14.862 |
| Degrees of freedom | 2 |
| P-value (Chi-square) | 0.001 |
| Model Test Baseline Model: | |
| Test statistic | 309.707 |
| Degrees of freedom | 6 |
| P-value | 0.000 |
| User Model versus Baseline Model: | |
| Comparative Fit Index (CFI) | 0.958 |
| Tucker-Lewis Index (TLI) | 0.873 |
| Loglikelihood and Information Criteria: | |
| Loglikelihood user model (H0) | -1073.791 |
| Loglikelihood unrestricted model (H1) | -1066.360 |
| Akaike (AIC) | 2163.582 |
| Bayesian (BIC) | 2197.298 |
| Sample-size adjusted Bayesian (BIC) | 2171.906 |

Root Mean Square Error of Approximation:

| | |
|--|-------|
| RMSEA | 0.113 |
| 90 Percent confidence interval - lower | 0.064 |
| 90 Percent confidence interval - upper | 0.170 |
| P-value RMSEA <= 0.05 | 0.019 |

Standardized Root Mean Square Residual:

| | |
|------|-------|
| SRMR | 0.037 |
|------|-------|

Parameter Estimates:

| | |
|----------------------------------|------------|
| Information | Expected |
| Information saturated (h1) model | Structured |
| Standard errors | Standard |

Latent variables:

| Construct =~ | Estimate | Std.Err | z-value | P(> z) |
|--------------|----------|---------|---------|---------|
| V1 | 1.000 | | | |
| V2 | 1.418 | 0.165 | 8.575 | 0.000 |
| V3 | 0.873 | 0.109 | 8.015 | 0.000 |
| V4 | 0.686 | 0.087 | 7.876 | 0.000 |

Variances:

| | Estimate | Std.Err | z-value | P(> z) |
|-----------|----------|---------|---------|---------|
| .V1 | 0.165 | 0.013 | 12.771 | 0.000 |
| .V2 | 0.093 | 0.015 | 6.159 | 0.000 |
| .V3 | 0.151 | 0.011 | 13.359 | 0.000 |
| .V4 | 0.101 | 0.007 | 13.555 | 0.000 |
| Construct | 0.072 | 0.013 | 5.435 | 0.000 |

Run IRT

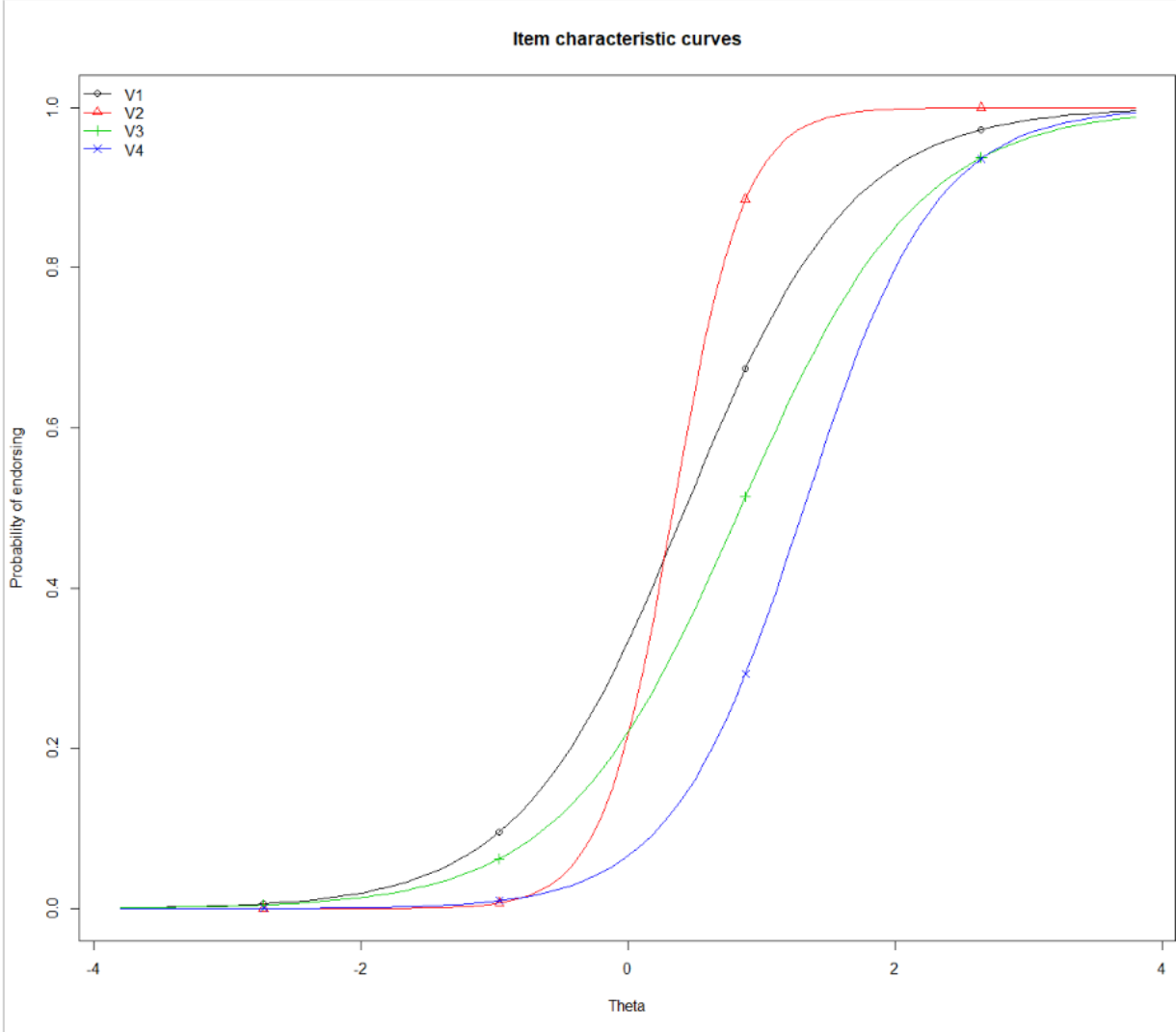
```
irt.dat = ltm(mydata ~ z1, IRT.param = TRUE)
```

```
coef(irt.dat)
```

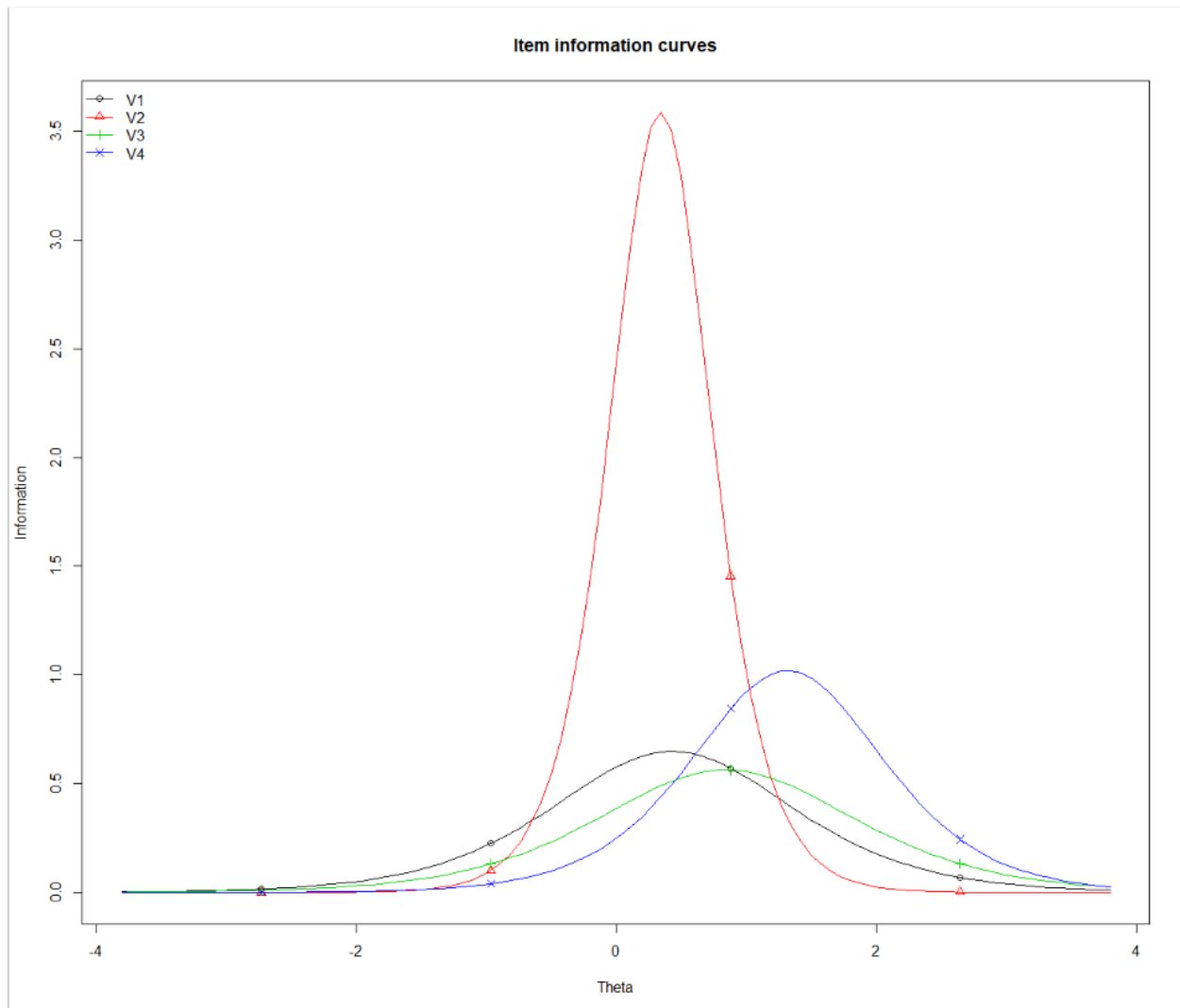
```
> coef(irt.dat)
```

```
      Dffc1t  Dscrmn
V1 0.4328137 1.611859
V2 0.3429488 3.787745
V3 0.8456207 1.501197
V4 1.3186840 2.019666
```

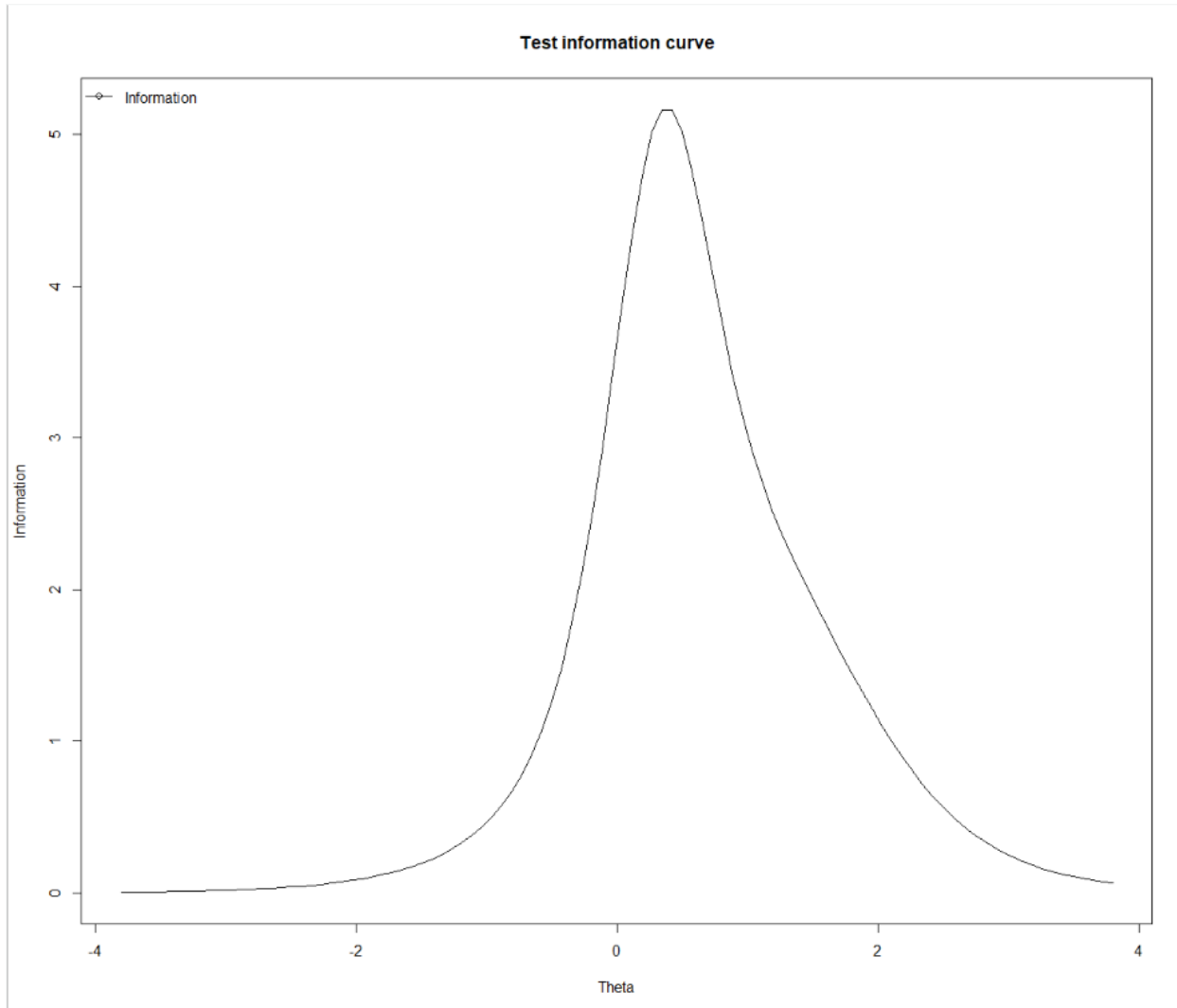
```
plot(irt.dat, pch = c(1:4), lty = 1, type = "ICC", legend = TRUE, xlab = "Theta", main = "Item characteristic curves", ylab = "Probability of endorsing")
```



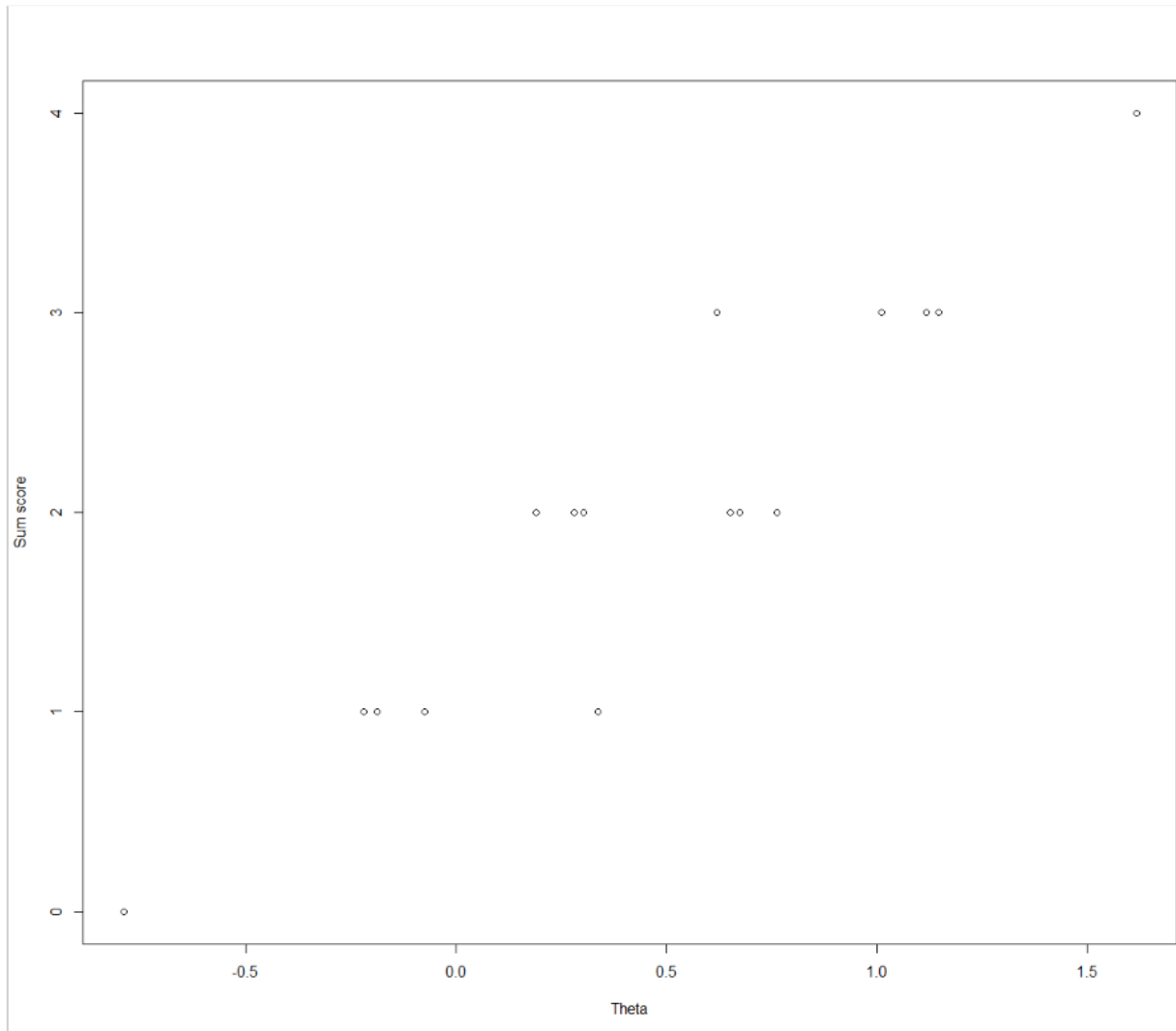
```
plot(irt.dat, pch = c(1:4), item = 1:4, lty = 1, type = "IIC", legend = TRUE, xlab = "Theta", main = "Item information curves", ylab = "Information")
```




```
plot(irt.dat, pch = c(1:4), item = 0, type = "IIC", legend = TRUE, xlab = "Theta", main = "Test information curve", ylab = "Information")
```



```
Theta = factor.scores(irt.dat, method = "EAP", resp.patterns = mydata)$score.dat$z1  
sum.score = apply(mydata, 1, sum)  
plot(sum.score ~ Theta, xlab = "Theta", ylab = "Sum score")
```



```
mydata2 = cbind(mydata, Theta, sum.score)  
cor(sum.score, Theta) # Correlation = 0.98
```