

Multidimensional Profile Analysis

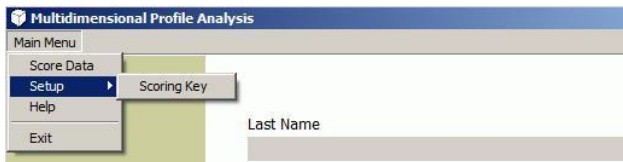
Introduction

This software provides normative scores for the West Haven-Yale Multidimensional Pain Inventory (MPI; Kerns, Turk & Rudy, 1985) based on a sample of 376 respondents diagnosed with fibromyalgia. Output includes MPI subscale scores, summary scale scores, best psychosocial profile fit, and estimated profile stability. Norms and scoring criteria are adapted from McKillop and Nielson (2011).

Scoring Key

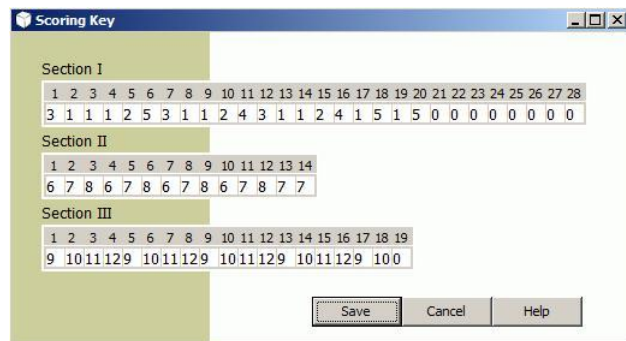
By default, the program provides the scoring key for the MPI-2. Should you wish to score the MPI-1 or should your scoring key become corrupted, the scoring keys for either version of the MPI may be entered directly.

To enter a scoring key for either the MPI-1 or MPI-2, select the *Scoring Key* option from the *Setup* menu.



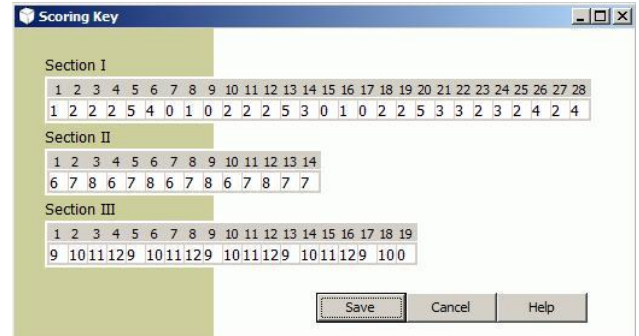
MPI-1

As demonstrated below, in the scoring key for the original version of the MPI, subscale values for items 21 to 28 in Section I and item 19 in Section III should be 0.



MPI-2

The revised version of the MPI contains 61 items. However, only 56 items are used for scoring purposes. As below, in the scoring key for the MPI-2, subscale values for items 7, 9, 15, and 17 in Section I and item 19 in Section III should be 0.



Once you have entered the scoring key for either the MPI-1 or MPI-2, press *Save* and the program will confirm whether your key is correct.

Input Screen

Once you have entered the appropriate key, you can score the MPI. Possible responses to each MPI item range from 0 to 6. If an item response is missing, enter a 9 or leave the item blank.

Once you have entered all items, press *Score Data* to produce a summary report.

Output Screen

The program scores your report and then translates this report into PDF format. The report is then automatically displayed in your PDF viewer. Once displayed, you can take advantage of the printing, saving and viewing functions available in your PDF viewer.

If you wish to save a report for later reference, you must rename the report. This is typically done by using your PDF viewer's *Save As* command or *Save a Copy* command. This is necessary given that the program automatically deletes the scored report

when you exit the program.

Once you have viewed, printed, or saved the report, you can close your PDF viewer to return to the input screen. You can now enter a new set of MPI item scores or press *Exit* to exit and close the program.

Summary Report

The summary report provides general and MPI section information, subscale scores, summary scale scores, and profile information. General information consists of the respondent's name, the date the report was scored, and the specific version of the MPI being used. MPI section information provides a summary of the number of items scored in each of the three MPI questionnaire sections and the number of items not scored or missing. MPI clinical scales and summary scales provide the respondent's raw scores and normative T-scores. Summary scales are unique to this program and are described in detail by McKillop and Nielson (2011).

As per that source, the Impairment summary scale is defined as:

$$\left[\frac{\text{Pain Severity} + \text{Interference} + (6 - \text{Life Control}) + \text{Affective Distress}}{4} \right]$$

The Social Support summary scale is defined as:

$$\left[\frac{\text{Support} + (6 - \text{Negative Responses}) + \text{Solicitous Response} + \text{Distracting Responses}}{4} \right]$$

Finally, the Activity summary scale is defined as:

$$\left[\frac{\text{Household Chores} + \text{Outdoor Work} + \text{Activities Away From Home} + \text{Social Activities}}{4} \right]$$

Profile Matching

Typically, MPI psychosocial profiles are fitted to respondents' clinical subscale scores (e.g., Turk & Rudy, 1988; Rudy, 1989). The current program, however, uses summary scale scores to fit psychosocial profiles (see McKillop & Nielson,

2011). Specifically, profile goodness-of-fit is based on the generalized squared distance from respondents' summary scale profiles to each of the MPI normative psychosocial profiles.

In addition to respondents' goodness-of-fit to MPI psychosocial profiles, the program also provides the generalized distance between respondents' summary scale scores and the overall sample summary scale means. This distance value measures the degree to which a respondent's profile deviates from the overall group average. Should this measure fall outside an acceptable range ($p < .10$), caution should be used when interpreting a respondent's profile fit. The more extreme the deviation, the more likely that profile goodness-of-fit is unreliable and potentially meaningless.

As also demonstrated in McKillop and Nielson (2011), stability of MPI profiles can be assessed by calculating relative distance. Relative distance is the difference between a respondent's distance to the overall group mean and the respondent's distance to any psychosocial profile. As relative distance increases so does the stability of that respondent's profile across time. In general, any relative distance value above 1.00 suggests higher stability or lower likelihood that a respondent's profile will change across time.

The program also provides an estimate of profile stability ranging from 0.00 to 1.00 with 0.00 indicating perfect instability and 1.00 representing perfect stability.

System Requirements

Windows 98 or higher
PDF viewer

Conditions of Use

This software is freeware and can be distributed and shared without permission. It cannot be resold or distributed for profit.

Program Reference

McKillop, J.M. (2010). Multidimensional Profile Analysis: A computer program to score the Multidimensional Pain Inventory. [[Computer software](#)]. London ON.

References

- Kerns, R. D., Turk, D. C., & Rudy, T. E. (1985). The West Haven-Yale Multidimensional Pain Inventory (WHYMPI). *Pain, 23*, 345-356.
- McKillop, J.M., & Nielson, W.R. (2011). Improving the usefulness of the Multidimensional Pain Inventory. *Pain Research and Management, 16*, 239-244.
- Rudy, T.E. (1989). *Multiaxial assessment of pain: Multidimensional Pain Inventory. Computer program users manual. Version 2.1*. Technical report. Pittsburgh: Pain Evaluation and Treatment Institute.
- Turk, D.C., & Rudy, T.E. (1988). Toward an empirically-derived taxonomy of chronic pain patients: Integration of psychological assessment data. *Journal of Consulting and Clinical Psychology, 56*, 233-238.

Appendix

Generalized squared distance is defined as:

$$D^2 = (x_i - x_j)' S^{-1} (x_i - x_j)$$

The terms x_i and x_j represent any two points in multivariate space and S^{-1} is the inverse covariance matrix of the group mean summary scale scores.

In the current program, x_i represents a vector or profile of summary scale scores for any one respondent. For example, let us assume that a respondent's Impairment, Social Support, and Activity summary scale scores are, in order, 2.99 ($T = 37.65$), 3.45 ($T = 51.63$), and 3.86 ($T = 71.04$). Next, let us assume that we wish to compare this respondent's profile to an Adaptive Coper profile. The Impairment, Social Support, and Activity summary scale values for an Adaptive Coper profile are 3.31 ($T = 41.85$), 3.65 ($T = 53.04$), and 2.77 ($T = 56.37$) respectively. Therefore, in matrix format, $(x_i - x_j)'$ is expressed as:

$$\begin{aligned} & [2.99 - 3.31 \quad 3.45 - 3.65 \quad 3.86 - 2.77] \\ & = [-0.32 \quad -0.20 \quad 1.09] \end{aligned}$$

Next, we pre-multiply this vector by the inverse covariance matrix. Specifically:

$$[-0.32 \quad -0.20 \quad 1.09] \times \begin{bmatrix} 1.95 & 0.22 & 0.60 \\ 0.22 & 0.81 & 0.10 \\ 0.60 & 0.10 & 1.99 \end{bmatrix}$$

$$\begin{aligned} & = \begin{bmatrix} -0.32 \times 1.95 & -0.32 \times 0.22 & -0.32 \times 0.60 \\ -0.20 \times 0.22 & -0.20 \times 0.81 & -0.20 \times 0.10 \\ 1.09 \times 0.60 & 1.09 \times 0.10 & 1.09 \times 1.99 \end{bmatrix} \\ & = \begin{bmatrix} -0.62 & -0.07 & -0.19 \\ -0.04 & -0.16 & -0.02 \\ 0.65 & 0.11 & 2.17 \end{bmatrix} \\ & = [-0.02 \quad -0.12 \quad 1.96] \end{aligned}$$

We then post-multiply to achieve the distance value between the respondent's profile and an Adaptive Coper profile:

$$\begin{aligned} & [-0.02 \quad -0.12 \quad 1.96] \times \begin{bmatrix} -0.32 \\ -0.20 \\ 1.09 \end{bmatrix} \\ & = \begin{bmatrix} -0.02 \times -0.32 \\ -0.12 \times -0.20 \\ 1.96 \times 1.09 \end{bmatrix} = \begin{bmatrix} 0.01 \\ 0.02 \\ 2.14 \end{bmatrix} = [2.17] \end{aligned}$$

Generalized squared distance approximates a chi-square (χ^2) distribution with degrees of freedom equal to the number of vector or profile variables. Therefore, goodness-of-fit can be expressed as:

$$\chi^2(3) = 2.17, p = .54$$

Relative Distance

McKillop and Nielson (2011) demonstrated that distance values that reside farther away from the overall sample mean tend to be more stable than distance values that reside closer to the sample mean. Therefore, in addition to determining respondents' goodness-of-fit to MPI taxonomy profiles, it is also important to consider how far a respondent's profile deviates from the overall sample mean.

McKillop and Nielson offered a simple formula that yields a relative distance value that may be helpful in determining profile stability.

Specifically, relative distance is defined as:

$$RD = \begin{bmatrix} (x_i - \bar{x}_i)' S^{-1} (x_i - \bar{x}_i) - \\ (x_i - x_j)' S^{-1} (x_i - x_j) \end{bmatrix}$$

As before, the vector $(x_i - x_j)'$ represents the

distance between a respondent and any MPI taxonomy profile. Using the previous example, we know that the distance from the respondent's profile to an Adaptive Coper profile is 2.17. Therefore:

$$RD = \left[\frac{(x_i - \bar{x}_i)' S^{-1} (x_i - \bar{x}_i)}{2.17} \right]$$

The vector $(x_i - \bar{x}_i)'$ represents the distance between a respondent's profile and the overall sample summary scale means. To solve for $(x_i - \bar{x}_i)'$ we use summary scale mean scores. The mean scores for the Impairment, Social Support, and Activity summary scales are, in order, 3.93 ($T = 50$), 3.27 ($T = 50$), and 2.30 ($T = 50$).

Therefore, $(x_i - \bar{x}_i)'$ is:

$$\begin{aligned} & [2.99 - 3.93 \quad 3.45 - 3.27 \quad 3.86 - 2.30] \\ & = [-0.94 \quad 0.18 \quad 1.56] \end{aligned}$$

Pre-multiplying by the inverse covariance matrix yields:

$$\begin{aligned} & [-0.94 \quad 0.18 \quad 1.56] \times \begin{bmatrix} 1.95 & 0.22 & 0.60 \\ 0.22 & 0.81 & 0.10 \\ 0.60 & 0.10 & 1.99 \end{bmatrix} \\ & = \begin{bmatrix} -0.94 \times 1.95 & -0.94 \times 0.22 & -0.94 \times 0.60 \\ 0.18 \times 0.22 & 0.18 \times 0.81 & 0.18 \times 0.10 \\ 1.56 \times 0.60 & 1.56 \times 0.10 & 1.56 \times 1.99 \end{bmatrix} \\ & = \begin{bmatrix} -1.83 & -0.21 & -0.56 \\ 0.04 & 0.15 & 0.02 \\ 0.93 & 0.15 & 3.11 \end{bmatrix} \\ & = [-0.86 \quad 0.09 \quad 2.57] \end{aligned}$$

As previously, we post-multiply these results to find the distance between the respondent's scores and the sample mean:

$$\begin{aligned} & [-0.86 \quad 0.09 \quad 2.57] \times \begin{bmatrix} -0.94 \\ 0.18 \\ 1.56 \end{bmatrix} \\ & = \begin{bmatrix} -0.86 \times -0.94 \\ 0.09 \times 0.18 \\ 2.57 \times 1.56 \end{bmatrix} = \begin{bmatrix} 0.81 \\ 0.02 \\ 4.01 \end{bmatrix} = [4.84] \end{aligned}$$

$$\chi^2(3) = 4.84, p = .18$$

Relative distance, therefore, is:

$$[4.84 - 2.17] = 2.67$$

An approximate estimate of stability can be achieved through the following formula:

$$\begin{aligned} & \frac{(\text{Relative Distance} \times 12.94) + 51.83}{100} \\ & = \frac{(2.67 \times 12.94) + 51.83}{100} = .86 \end{aligned}$$

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