

# Utility of Profile Analysis via Multidimensional Scaling in R for the Study of Person Response Profiles in Cross-Sectional and Longitudinal Data

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**Abstract** ■ Profile analysis using multidimensional scaling (PAMS) attempts to identify core profiles, which are the central response patterns from a group of person profiles. From a micro perspective, we can use the core profile information to assess the strengths and weaknesses of individual traits measured by subscales, whereas from a macro perspective, we can use it to understand the average strengths and weaknesses of all responses in the sample. Initially designed for a proprietary purpose, PAMS's use by the general public remains restricted. Here, we introduce a public version of PAMS in R, enhanced with inferential capabilities that enable researchers to assess the statistical significance of core profile coordinates during interpretation. We analyzed the same cross-sectional data using cluster analysis and latent profile analysis and compared the results to amplify the PAMS utility over the other methods because it holds more information. We also demonstrated the utility of PAMS through the analysis of longitudinal data. We extracted three core profiles from both cross-sectional and longitudinal data sets and then described how to interpret core profile coordinates for each data set, in addition to limitations and suggestions for potential PAMS in R users.

**Keywords** ■ Profile Analysis, Multidimensional Scaling, Bootstrap, Cross-sectional and longitudinal data. **Tools** ■ R.

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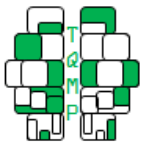
## Introduction

A profile in this article refers to a row vector (or profile) of a person's observed responses to items (or subscales). Most datasets in the social sciences have a rectangular shape where a row can be viewed as person  $i$ 's profile ( $i = 1, \dots, I$ ) consisting of each column subscale  $j$  ( $j = 1, \dots, J$ ), and  $I \gg J$ . The subscores in the data are assumed to be related and continuous.

When a researcher wants to compare group mean differences, univariate or multivariate analysis of variance can be conducted. Or when a researcher wants to investigate linear relationships or latent structures among variables, they conduct univariate/multivariate linear regression or factor analysis. The factor or principal component analysis (e.g., Jolliffe, 2011; Kim & Mueller, 1978) is designed to identify homogenous sets of variables to define

factors/components from a simple structure that is a loading matrix where a set of homogeneous variables loads strongly on one factor but not others, usually after a rotation is applied to an initial factor solution.

The univariate and multivariate statistics addressed above are useful for addressing certain research questions, but they are not designed to study person profiles included in  $I \times J$  rectangular shape data. (Davison, 1996) first introduced profile analysis via multidimensional scaling (PAMS) to study person profiles in the  $I \times J$  data set. PAMS is designed to identify a small number of core profiles from a sample of person profiles to understand central response patterns in a population. Each person profile consists of two features: level and pattern that determine uniqueness of person profiles.



### Level

Person  $i$ 's level is defined as person  $i$ 's numerical mean of the subscores included in her profile:  $\bar{m}_i = (1/J) \sum_{j=1}^J m_{ij}$ , where  $m_{ij}$  represents person  $i$ 's observed score on subscale  $j$  (see details in Kim et al., 2004). The height of person  $i$ 's profile is determined by this level. Person levels are often converted to z-scores to facilitate comparisons between individuals. The level variance in  $I$  individuals is the measure of the between-person variance, which is estimated with

$$(1/(I-1)) \sum_{i=1}^I (\bar{m}_i - \bar{m})^2,$$

where  $\bar{m} = (1/I) \sum_{i=1}^I \bar{m}_i$ .

### Pattern

Person  $i$ 's pattern, on the other hand, is defined as ipsatized subscores around person  $i$ 's mean. Thus,  $(\mathbf{m}_i - \bar{\mathbf{m}}_i)$ , where  $\mathbf{m}_i$  is person  $i$ 's profile:  $\mathbf{m}_i = (m_{i1}, \dots, m_{ij}, \dots, m_{iJ})^T$  and  $\bar{\mathbf{m}}_i = \bar{m}_i \mathbf{1}$ , which is the  $J \times 1$  mean vector of person  $i$ . The pattern of person  $i$ 's profile is uniquely defined by a vector of ipsatized scores,  $(\mathbf{m}_i - \bar{\mathbf{m}}_i)$ . In person  $i$ 's profile of cognitive ability scores ( $i = 1, \dots, I$ ), for instance, peaks represent person  $i$ 's strengths in specific cognitive ability domains, whereas valleys represent person  $i$ 's weaknesses in specific cognitive ability domains. The pattern variance for each individual (e.g., person  $i$ ) is described as within-person variance across  $J$  subscales such as

$$(1/(J-1)) \sum_j (m_{ij} - \bar{m}_i)^2$$

in person  $i$ . Finally, the total within-person variance is defined as

$$\sum_{i=1}^I \left\{ (1/(J-1)) \sum_j (m_{ij} - \bar{m}_i)^2 \right\}.$$

Such patterns contain contextual and qualitative information that cannot be found in any aggregated score, such as the mean of subscores. For example, Person A's profile is (65, 80, 65) with a level of 70, whereas Person B's profile is (35, 50, 35) with a level of 40; the levels are different. However, they share the same response patterns: The pattern of Person A is (65 – 70 = –5, 80 – 70 = 10, 65 – 70 = –5), while the pattern of Person B is (35 – 40 = –5, 50 – 40 = 10, 35 – 40 = –5). In a further instance, two individuals with the same level but distinct patterns: Person C's profile is (45, 60, 45) and Person D's profile is (60, 30, 60); both profiles have a level of 50. However, these individuals' patterns are distinct: Person C's pattern is (45 – 50 = –5, 60 – 50 = 10, 45 –

50 = –5) and Person D's pattern is (60 – 50 = 10, 30 – 50 = –20, 60 – 50 = 10). In this instance, the clinical diagnoses of these persons would differ because their pattern information is distinct, despite the fact that the level information is identical.

The level information is useful to study individuals' differences in terms of person means, which can be used as a global assessment for person mean differences (i.e., the case of Persons A and B in the previous example). Whereas the profile pattern information is clinically useful when clinicians want to diagnose specific individual patients based on their response patterns of symptom indicators (i.e., the case of Persons C and D in the example). Based on the patients' response patterns, clinicians can specify which symptom indicators (included in the patients' profiles) are improved, little changed, or deteriorated after treatment.

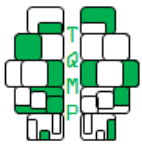
## Different Profile Analysis Methods

### Cluster Profile Analysis (CPA)

In the past, core profiles were identified using cluster analysis (Aldenderfer & Blashfield, 1984; Konald et al., 1999). The goal of a cluster analysis is to group people into meaningful clusters, where individuals within each cluster are more similar to one another than to individuals in other clusters, and each cluster is relatively independent of the others. The mean of each subscale for all people in the cluster is used to describe the cluster's profile characteristics; in other words, a subscale mean profile (or level information defined by PAMS) is considered a core profile for each cluster. There is modal profile analysis, a hybrid method that combines Q-factor and cluster analysis, which was used to extract profile pattern information, but it is obsolete and only applicable to small sample sizes (Kim, 2023; Kim et al., 2007). For instance, Steer (1982) used only 25 males and 25 females out of 700 patients as a test sample for modal profile analysis, indicating its impediment for analysis of large sample data that were ( $n = 1,650$ ) used in the present study.

### Latent Profile Analysis (LPA)

Recently, latent profile analysis (LPA) has been used to identify latent profiles from continuous data sets (e.g., Armour et al., 2011; Parker et al., 2014), using the Mplus statistical software (Muthen & Muthén, 1998). LPA is a subset of Gaussian finite mixture modeling, which is a probabilistic model in which all data points are generated by a mixture of a finite number of Gaussian distributions with unknown parameters (Rosenberg et al., 2018; Scrucca et al., 2016; Shireman et al., 2017). The LPA estimates the likelihood that individuals belong to latent classes. The average of the individ-



uals' subscale scores for each latent class forms a latent profile. Liu et al. (2022) conducted an ANOVA on the average of the participants' subscale means for the latent classes to determine the significant mean differences among the latent classes. This suggests that subscale means within each latent class essentially determine the latent profile. Thus, every latent profile in LPA lacks pattern information but only level information (defined by PAMS), like the cluster profile analysis. Due to a lack of information about response patterns, the latent profiles in LPA cannot replicate the level and pattern information observed in person profiles. For a comparison of the outcomes of LPA, CPA, and PAMS, consult the supplementary materials.

### Necessity of PAMS

Davison (1996) introduced PAMS to compensate for the shortcomings of cluster and latent profile analysis. PAMS explains person profiles with level and pattern parameters estimated by PAMS, assuming that the pattern parameters depict the central response patterns. PAMS is an extension of the Q-factor model in that it focuses on the analysis of person profiles utilizing nonmetric multidimensional scaling (MDS) to identify core profiles. Since nonmetric scaling employed in PAMS analyzes a test  $\times$  test proximity matrix (rather than a person  $\times$  person proximity matrix) to identify core profiles, unlike cluster profile analysis, the matrix to be analyzed does not grow as sample size increases, and PAMS (and PAMS in R) can be performed on samples of any size. While MDS has been employed to visually analyze the relationships between variables on a two-dimensional map (Davison, 1983; Torgerson, 1958), Davison (1996) modeled person profiles across dimensions using dimensional scale values.

### Adopted MDS in PAMS in R for Double Centering

PAMS in R also utilizes MDS with double-centering for data scaling, and the double-centering controls level effects. The double-centering refers to the process of centering of data using both row and column means. Particularly when data contain dominant level effects (as is the case with the current data sets), they are confounded with pattern effects, preventing the identification of meaningful pattern effects. However, the double-centering ensures that there is no level effect in the core profile (for details, see Kim, 2023). Double-centering of data is not required by researchers prior to executing the PAMS in R. This is because the PAMS in R automatically performs the double-centering process when scaling the data.

On the other hand, if factor analytic paradigms such as maximum likelihood estimation-based factor analysis (Kim, 2013) or principal component analysis (Kim & Kim, 2017) are applied to model person profiles, the level effects

cannot be controlled because the core profiles estimated by the factor analytic paradigms are identified from either an intervariable correlation or covariance matrix that is a column centering-based matrix. The numerator of the correlation/covariance matrix between variables  $X$  and  $Y$  is computed by

$$\sum_i^I (X_i - \bar{X}) (Y_i - \bar{Y}),$$

where  $i = 1, \dots, I$ ,  $\bar{X} = (1/I) \sum_i^I X_i$ ,  $\bar{Y} = (1/I) \sum_i^I Y_i$ , and  $I$  is a sample size. This numerator is expressed with a product of the  $X$  and  $Y$  column-centered entities, and the level effects are still present in the column centered covariance/correlation matrix. Therefore, if researchers use factor analytic paradigms to identify core profiles carrying pattern effects, they must remove level effects before analysis, unlike PAMS in R (Kim, 2023). Factor analysis exclusively interprets positive factor loadings, whereas PAMS in R considers both negative (indicating lowered symptoms or achievement) and positive (indicating increased symptoms or achievement) values as equally meaningful. These values are then represented in a core profile with peaks and valleys.

### Modeling Person Profiles with PAMS in R

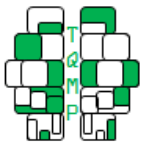
Unlike profile analysis based on clustering or Q-type factoring that analyzes an inter-person  $I \times I$  proximity matrix to identify core profiles, PAMS in R analyzes an inter-variable  $J \times J$  proximity matrix to identify core profiles and then relates the core profiles to person profiles. Thus, in the PAMS in R model, each person profile is expressed with a linear combination of a level parameter, a pattern parameter, and an error term (Kim et al., 2007):

$$\mathbf{m}_i = \bar{m}_i \mathbf{1} + (\mathbf{m}_i - \bar{m}_i \mathbf{1}) = c_i \mathbf{1} + \mathbf{X} \mathbf{w}_i + \mathbf{e}_p \quad (1a)$$

or

$$\hat{\mathbf{m}}_i = c_i \mathbf{1} + \mathbf{X} \hat{\mathbf{w}}_i \quad (1b)$$

The initial portion of Equation 1 represents person level and pattern in raw scores, where  $\mathbf{m}_i$  is person  $i$ 's profile and  $\bar{m}_i$  is a model estimate of  $c_i$ . The second portion in the equation expresses person  $i$ 's profile using the PAMS in R model parameters, where  $\mathbf{X}$  is a  $J \times K$  core profile matrix (e.g., Davison et al., 1996; Frisby & Kim, 2008; McKay et al., 2014, 2018);  $\mathbf{w}_i$  is a  $K \times 1$  vector of person  $i$ 's weights on  $K$  core profiles; and  $\mathbf{e}_p$  is a residual term for person  $i$  that characterizes differences between  $\mathbf{m}_i$  and  $\hat{\mathbf{m}}_i$  ( $= \hat{c}_i \mathbf{1} + \mathbf{X} \hat{\mathbf{w}}_i$ ) which is a model expected person  $i$ 's profile where error is contained, assuming  $\mathbf{X}$  to be fixed. The PAMS in R model, like other scaling methods (Ramsay, 1977; Takane et al., 1977; Kruskal, 1964a, 1964b; Shepard,



1962a, 1962b), assumes homogeneity of variance and normality for the residuals. These assumptions are also required by the regression model, which assumes equal variance and normality for the residuals.

In the PAMS in R model, an individual's pattern effect ( $\hat{\mathbf{m}}_i - \bar{\mathbf{m}}_i \mathbf{1}$ ) is estimated with a product of two model parameters,  $\mathbf{X}\hat{\mathbf{w}}_i$ , as shown in Equation 1, implying that  $\mathbf{X}$  carries only pattern information. Although PAMS in R estimates both level and pattern, since person levels can be easily computed with person means (i.e.,  $c_i = \bar{m}_i = (1/J) \sum_{j=1}^J m_{ij}$ ) without the use of PAMS in R, the main advantage of using PAMS in R is that it allows researchers to identify a small set of core profiles to understand the central response patterns from a large number of person profiles. It would be nearly impossible to grasp the central pattern information by inspecting every ( $\hat{\mathbf{m}}_i - \bar{\mathbf{m}}_i \mathbf{1}$ ) from  $I$  people (e.g.,  $I = 1,650$  in our example data). Since the core profiles carry only pattern information, person  $i$ 's profile of  $J$  ipsatized subscores can be expressed with the PAMS in R model parameters

$$\begin{bmatrix} \hat{m}_{i1} \\ \vdots \\ \hat{m}_{iJ} \end{bmatrix} - \bar{m}_i \mathbf{1} = \hat{w}_{i1} \begin{bmatrix} x_{11} \\ \vdots \\ x_{J1} \end{bmatrix} + \cdots + \hat{w}_{iK} \begin{bmatrix} x_{1K} \\ \vdots \\ x_{JK} \end{bmatrix} \quad (2)$$

In Equation 2, since the sum of the left-hand side is always zero:  $\sum_{j=1}^J (\hat{m}_{ij} - \bar{m}_i) = 0$ , the sum of the right side must be zero as well:  $\hat{w}_{ik} \sum_{j=1}^J x_{jk} = 0$ . Since the person weight is not assumed to be zero,  $\hat{w}_{ik} \neq 0$ , the sum of core profile  $k$ 's coordinates must be zero,  $\sum_{j=1}^J x_{jk} = 0$  ( $k = 1, \dots, K$ ). The coordinates of every core profile are scaled to be ipsative, which is a necessary and sufficient condition for core profiles to carry only pattern information (e.g., Kim, 2013, 2023).

**Modeling Longitudinal Person Profiles with PAMS in R.** PAMS in R can be easily applied to longitudinal data analysis to estimate response pattern trajectories over time. For longitudinal data, that  $\mathbf{m}_{i(T)} = (m_{i1}, \dots, m_{iT})$  is a person profile of observed  $T$  responses over  $T$  time points, where the subscript  $T$  refers to time point  $T$ . Then, as shown in the cross-sectional PAMS in R (Equation 1), person  $i$ 's longitudinal profile of observed responses over time can be modeled with core trajectory profiles such as:  $\mathbf{m}_{i(T)} = c_{i(T)} \mathbf{1} + \mathbf{X}_T \mathbf{w}_{i(T)} + \mathbf{e}_{p(T)}$  or  $\hat{\mathbf{m}}_{i(T)} = c_{i(T)} \mathbf{1} + \mathbf{X}_T \hat{\mathbf{w}}_{i(T)}$ , where  $c_{i(T)}$  is the person  $i$ 's level;  $\mathbf{X}_T$  is a matrix of core trajectory profiles;  $\mathbf{w}_{i(T)}$  is person  $i$ 's weights on the core trajectory profiles; and  $\mathbf{e}_{p(T)}$  is the difference between  $\mathbf{m}_{i(T)}$  and  $\hat{\mathbf{m}}_{i(T)}$ , which is the model's expected person  $i$ 's longitudinal profile where error is contained. All parameter estimates in the longitudinal data are calculated identically to those in cross-sectional PAMS in R.

### Motivation of Making PAMS in R

Despite the fact that PAMS has been demonstrated to be useful for assessment in a variety of substantive domains, no PAMS software is available for public use. ProfileR is the only open-source R software available for profile analysis (<https://www.r-project.org>), but it is Torgerson's scaling in fact (Torgerson, 1958), which is unpopular due to its poor data fitting. PAMS in R incorporates ProfileR as a "classical" scaling option for researchers wishing to implement Torgerson's scaling.

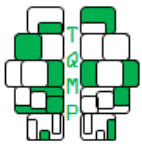
PAMS in R is used with smacof that is based on scaling by majorizing a complicated function. This algorithm seeks an ideal stress value (which is the difference between observed and model estimated dissimilarities) through the optimization process in order to solve local minima problems on the Stress's bumpy surface (Borg & Groenen, 2005; de Leeuw & Mair, 2009). The data transformations "ordinal," "interval," "ratio," and "mspline" built-in in smacof are also included in PAMS in R. However, PAMS in R is unique in that it estimates bootstrap standard errors and confidence intervals for core profile coordinates, which are not available in other scaling methods such as original PAMS, ProfileR, or smacof. In the absence of testing the significance of coordinates, the interpretation of core profile data would be misleading. The recent version of smacof includes the "bootmds" function, which employs bootstrapping to create confidence regions around coordinates in a two-dimensional plot. However, it does not estimate confidence intervals for the coordinates in each core profile. Consequently, researchers using bootmds in smacof are unable to assess the statistical significance of individual coordinates in a core profile.

### Four Estimation Procedures in PAMS in R

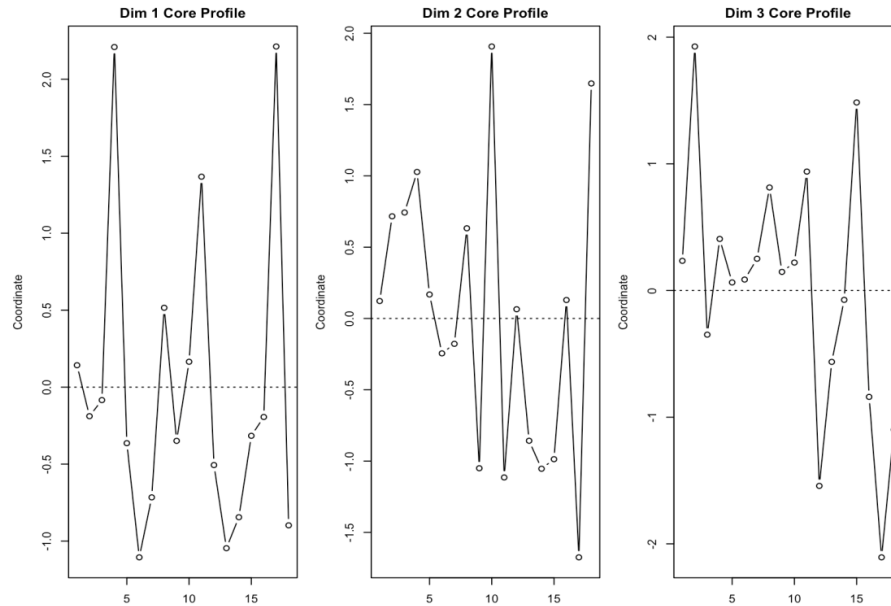
The first part is to install smacof, which is available on the R platform (Borg & Groenen, 2005; de Leeuw & Mair, 2009), identifying the path containing a data file and an R-based PAMS package, BootSmacof.R (included in Supplementary Materials). The first part includes the choice of "ordinal" scaling, the Stress value estimation ( $\leq 0.05$ , as recommended by Kruskal, 1964a), generation of empirical sampling distributions of core profile coordinates (from 2,000 bootstrap samples), and identification of specific individuals of interest for in-depth evaluation. For example, the initial ten participants in this study were included for the purpose of demonstration.

The second part contains estimation of correlations between the subscale mean profile and the core profiles and 95% of the bias-corrected and accelerated (BCa) confidence intervals for individual scale values (or coordinates) of the core profiles along with the scale value confidence bands. Given 2,000 bootstrap samples, for each





**Figure 1 ■** Plotting Dimensions as Core Profiles. The 1st core profile was flipped so that its pattern was the same as the array of 18 subscale means (or a subscale mean profile). Because of the space limit, the figures the horizontal axes were labeled with only 5, 10, and 10, which were [1 = Oral Vocabulary, 2 = Number Series, 3 = Verbal Attention, 4 = Letter-Pattern Matching], 5 = Phonological Processing, [6 = Story Recall, 7 = Visualization, 8 = General Information, 9 = Concept Formation], 10 = Numbers Reversed, [NP11 = Number-Pattern Matching, 12 = Nonword Repetition, 13 = Visual-Auditory Learning, 14 = Picture Recognition], 15 = Analysis-Synthesis, [16 = Object-Number Sequencing, 17 = Pair Cancellation, and 18 = Memory for Words].



$x_{jk}$  that is a coordinate of subscale  $j$  in core profile  $k$ , ( $j = 1, \dots, J$ ;  $k = 1, \dots, K$ ), a sampling distribution is constructed with the 2,000 bootstrapped coordinates such as  $\{\hat{x}_{jk}^1, \dots, \hat{x}_{jk}^{2,000}\}$ . In the coordinate sampling distribution, a 95% of the BCa confidence interval is bounded by the lower 2.5th percentile and the upper 97.5th percentile. If the confidence interval does not contain zero, we consider the coordinate to be significant, indicating that it differs significantly from zero.

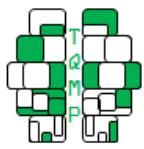
The third part includes the mean R-squared value for all participants, person weights, and person correlations. As explained previously, the person weights in the raw score metric, and to enhance interpretation, we estimate person weights with correlations between person with core profiles.

The fourth part is designed to assess a specific person of interest (Person #9 for our example. To enhance the comparison between the specific person's profile and a certain core profile, we juxtapose the person profile with the core profile to visually inspect the similarity between them. Based on person correlations, every individual's response

pattern can be easily interpreted in terms of core profile patterns. If person  $i$  has a substantial correlation on core profile  $k$  (e.g.,  $r_{ik} = 0.71$  or larger that accounts for at least 50% of shared variance between person  $i$ 's profile and core profile  $k$ ) but trivial ones on other core profiles, person  $i$  would be defined as having of core profile  $k$ 's characteristics. If person  $i$  has a substantial but negative correlation on core profile  $k$  (e.g.,  $r_{ik} = -0.71$ ) but trivial ones on other core profiles, then person  $i$  would be defined as a mirror image of the characteristics of core profile  $k$ .

#### Example 1: PAMS in R of Cross-Sectional Data

The cross-sectional PAMS in R was conducted on the standardization sample of the Woodcock-Johnson IV Cognitive Ability Battery ( $n = 1,650$ ) with ages ranging from 18 to 35 ( $M = 23.79$ ,  $SD = 5.50$ ) (McGrew et al., 2014; Schrank et al., 2014). The sample was assessed using 18 cognitive subscales, including: Oral Vocabulary (OV1;  $M = 524.44$ ,  $SD = 13.58$ ), Number Series (NS2;  $M = 518.31$ ,  $SD = 19.17$ ), Verbal Attention (VA3;  $M = 520.08$ ,  $SD = 15.53$ ), Letter-Pattern Matching (LP4;  $M = 547.64$ ,  $SD = 23.86$ ), Phonological Pro-

**Table 1** ■ The Coordinates of Core Profiles, Standard Errors, and Confidence Intervals

|      | CP1   | se1  | L1    | U1    | CP2   | se2  | L2    | U2    | CP3   | se3  | L3    | U3    |
|------|-------|------|-------|-------|-------|------|-------|-------|-------|------|-------|-------|
| OV1  | 0.09  | 0.02 | 0.07  | 0.13  | 0.02  | 0.05 | −0.06 | 0.12  | 0.04  | 0.07 | −0.10 | 0.14  |
| NS2  | −0.12 | 0.03 | −0.14 | −0.01 | 0.14  | 0.14 | 0.01  | 0.42  | 0.35  | 0.08 | 0.17  | 0.41  |
| VA3  | −0.06 | 0.02 | −0.09 | −0.01 | 0.14  | 0.05 | 0.02  | 0.22  | −0.06 | 0.05 | −0.15 | 0.02  |
| LP4  | 1.45  | 0.02 | 1.41  | 1.49  | 0.20  | 0.05 | 0.08  | 0.27  | 0.07  | 0.09 | −0.13 | 0.22  |
| PP5  | −0.24 | 0.01 | −0.25 | −0.21 | 0.03  | 0.02 | 0.01  | 0.08  | 0.01  | 0.03 | −0.05 | 0.06  |
| SR6  | −0.72 | 0.01 | −0.74 | −0.69 | −0.05 | 0.04 | −0.12 | 0.02  | 0.02  | 0.05 | −0.11 | 0.09  |
| VS7  | −0.47 | 0.01 | −0.49 | −0.44 | −0.03 | 0.02 | −0.06 | 0.04  | 0.05  | 0.03 | 0.01  | 0.09  |
| GI8  | 0.34  | 0.03 | 0.22  | 0.35  | 0.12  | 0.14 | −0.21 | 0.33  | 0.15  | 0.19 | −0.24 | 0.33  |
| CF9  | −0.23 | 0.04 | −0.32 | −0.20 | −0.20 | 0.08 | −0.27 | −0.11 | 0.03  | 0.11 | −0.21 | 0.19  |
| NR10 | 0.11  | 0.04 | 0.05  | 0.19  | 0.37  | 0.12 | 0.34  | 0.44  | 0.04  | 0.17 | −0.27 | 0.26  |
| NP11 | 0.90  | 0.03 | 0.84  | 0.94  | −0.21 | 0.09 | −0.34 | −0.15 | 0.17  | 0.13 | −0.30 | 0.30  |
| NW12 | −0.33 | 0.04 | −0.42 | −0.30 | 0.01  | 0.12 | −0.25 | 0.24  | −0.28 | 0.16 | −0.34 | −0.09 |
| VA13 | −0.69 | 0.02 | −0.73 | −0.67 | −0.16 | 0.04 | −0.24 | −0.10 | −0.10 | 0.07 | −0.20 | −0.02 |
| PR14 | −0.55 | 0.02 | −0.60 | −0.51 | −0.20 | 0.06 | −0.27 | −0.17 | −0.01 | 0.09 | −0.13 | 0.16  |
| AS15 | −0.21 | 0.03 | −0.25 | −0.14 | −0.19 | 0.07 | −0.27 | 0.27  | 0.27  | 0.14 | 0.16  | 0.36  |
| ON16 | −0.13 | 0.02 | −0.19 | −0.09 | 0.02  | 0.08 | −0.18 | 0.12  | −0.15 | 0.08 | −0.21 | 0.02  |
| PC17 | 1.45  | 0.02 | 1.41  | 1.51  | −0.32 | 0.10 | −0.46 | 0.06  | −0.38 | 0.13 | −0.54 | −0.24 |
| MW18 | −0.59 | 0.03 | −0.62 | −0.50 | 0.32  | 0.11 | 0.06  | 0.41  | −0.20 | 0.16 | −0.42 | 0.23  |

*Note.* OV1 = Oral Vocabulary; NS2 = Number Series; VA3 = Verbal Attention; LP4 = Letter-Pattern Matching; PP5 = Phonological Processing; SR6 = Story Recall; VS7 = Visualization; GI8 = General Information; CF9 = Concept Formation; NR10 = Numbers Reversed; NP11 = Number-Pattern Matching; NW12 = Nonword Repetition; VA13 = Visual-Auditory Learning; PR14 = Picture Recognition; AS15 = Analysis-Synthesis; ON16 = Object-Number Sequencing; PC17 = Pair Cancellation; and MW18 = Memory for Words; CP = core profile; se = standard error; L = the lower limit of the 95% BCa CI; U = the upper limit of the 95% BCa CI. The coordinate confidence intervals that do not include zeros are bolded and considered statistically different from zero.

cessing (PP5;  $M = 514.94$ ,  $SD = 12.55$ ), Story Recall (SR6;  $M = 502.43$ ,  $SD = 9.08$ ), Visualization (VS7;  $M = 508.80$ ,  $SD = 12.33$ ), General Information (GI8;  $M = 527.61$ ,  $SD = 17.35$ ), Concept Formation (CF9;  $M = 515.13$ ,  $SD = 17.52$ ), Numbers Reversed (NR10;  $M = 522.59$ ,  $SD = 19.77$ ), Number-Pattern Matching (NP11;  $M = 535.77$ ,  $SD = 21.79$ ), Nonword Repetition (NW12;  $M = 513.66$ ,  $SD = 16.22$ ), Visual-Auditory Learning (VA13;  $M = 503.65$ ,  $SD = 12.68$ ), Picture Recognition (PR14;  $M = 508.09$ ,  $SD = 12.43$ ), Analysis-Synthesis (AS15;  $M = 516.15$ ,  $SD = 18.81$ ), Object-Number Sequencing (ON16;  $M = 517.50$ ,  $SD = 17.97$ ), Pair Cancellation (PC17;  $M = 545.54$ ,  $SD = 28.11$ ), and Memory for Words (MW18;  $M = 508.59$ ,  $SD = 21.15$ ). The grand mean of the 18 subscales is 520.20 ( $SD = 12.24$ ).

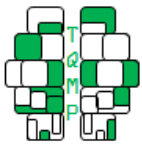
### Part 1: Setting Up

We first ran PAMS in R to determine dimensionality. The stress values for the two-, three-, and four-dimensional solutions, respectively, were 0.069, 0.047, and 0.027. Given the Stress value (less than or equal to 0.05, as recommended by Kruskal, 1964a) and dimension interpretability (as core profiles), the three-dimensional solution was cho-

sen because the four-dimensional solution was redundant in comparison to the three-dimensional one. These selected three dimensions or core profiles correspond to the scale value matrix  $\mathbf{X}$  that characterizes each individual's pattern effect, as described by  $(\mathbf{m}_i - \bar{m}_i \mathbf{1})$  in Equation 1.

Since PAMS in R allows us to flip dimension directions to improve interpretation of them as core profiles; in Figure 1, we flipped the first dimension and depicted the dimensions as core profiles. Dimension 1 had two peaks (LP4 for letter-pattern matching and PC17 for pair cancellation) and two valleys (SR6 for story recall and VA13 for pair cancellation). SR6 and VA13 are Long-Term Retrieval Factors in the CHC (Cattell-Horn-Carroll) factor structure, whereas LP4 and PC17 are parts of the Cognitive Processing Speed Factor. As a result, the first dimension was labeled as High Cognitive Processing Speed with Low Long-Term Retrieval Profile.

Peaks in Dimension 2 included MW18 (auditory memory span factor) and NR10 (numbers reversed, a component of CHC short-term working memory factor), while valleys included PC17 (pair cancellation, a component of CHC cognitive processing speed factor) and NP11 (number-pattern matching, a component of Number Facility in Nar-

**Listing 1** ■ Person's weights W1 to W3 of 10 patients

```
> round(empprofile$Weight[1:10,], 2)
```

|     | w1    | w2     | w3     | level  | R^2  | corDim1 | corDim2 | corDim3 |
|-----|-------|--------|--------|--------|------|---------|---------|---------|
| #1  | 5.23  | -7.62  | 29.11  | 499.91 | 0.22 | 0.27    | -0.12   | 0.40    |
| #2  | 18.44 | 4.85   | -35.18 | 522.52 | 0.59 | 0.72    | 0.08    | -0.48   |
| #3  | 20.13 | 32.34  | 24.13  | 496.48 | 0.70 | 0.80    | 0.53    | 0.41    |
| #4  | 17.63 | 24.18  | 18.16  | 528.80 | 0.57 | 0.72    | 0.39    | 0.29    |
| #5  | 17.33 | -10.75 | 43.94  | 528.42 | 0.69 | 0.77    | -0.22   | 0.65    |
| #6  | 12.03 | 36.26  | 12.11  | 534.54 | 0.38 | 0.50    | 0.46    | 0.16    |
| #7  | 25.58 | 21.22  | 0.06   | 532.92 | 0.83 | 0.91    | 0.47    | 0.00    |
| #8  | 14.98 | 28.23  | -3.87  | 512.12 | 0.31 | 0.51    | 0.31    | -0.04   |
| #9  | 31.14 | 5.53   | -3.28  | 528.17 | 0.86 | 0.93    | 0.13    | -0.07   |
| #10 | 13.93 | -8.35  | 42.34  | 516.88 | 0.67 | 0.74    | -0.19   | 0.68    |

row Ability and Other Clinical Clusters). This dimension was labeled as High Working Memory with Low Cognitive Processing Profile.

Dimension 3 was labeled as High Fluid Reasoning with Low Processing Profile due to its two peaks of NS2 (number series) and AS15 (analysis-synthesis), which are components of the CHC Fluid Reasoning Factor, and two valleys of NW12 (nonword repetition), which is a component of the CHC-Auditory Processing Factor, and PC17 (pair cancellation), which is a component of the CHC Cognitive Processing Speed Factor.

#### *Bootstrapping of the 1,650 × 18 Data Matrix*

Using PAMS in R, we bootstrapped the 1,650 × 18 original data matrix, considering it as a finite population, 2,000 times and ran a 3-dimensional solution for each of the 2,000 bootstrap samples to generate the empirical distribution of every coordinate in given dimension  $k$  (or core profile  $k$ ) with 2,000 bootstrap replications of the coordinate. On dimension  $k$ , a sampling distribution of 2,000 bootstrap coordinate replicates is built for each subscale  $j$   $\hat{x}_{jk}^b$  ( $b = 1, \dots, 2,000$ ). For nonmetric scaling, we selected "ordinal" and chose the Euclidian distance option to compute dissimilarities, but users may choose the squared Euclidean distance if a faster conversion is needed. However, be aware that by squaring, small distances become smaller and large distances become larger, distorting the original differences. Because all subscales were in the same metric, we did not standardize data, but users could standardize them if each subscale included in data has a different measurement unit (e.g., weights versus heights). We used the 95th percentile confidence interval (CI), but (CI = 0.99) or (CI = 0.90) can be chosen. We set the number of bootstrapping to 2,000, but users can choose any number they want; however, at least 1,000 bootstrap (i.e., nboot = 1000) samples are recommended for estimating empirical confidence intervals (Efron & Tibshirani, 1993; Shao & Tu, 1995).

#### **Part 2: Estimating Correlation between Mean and Core Profiles and 95% CIs**

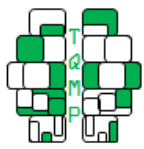
Typically, in cognitive ability or school achievement (math or reading) data, a general or g factor is included to represent general intelligence or overall math/reading ability. Given that WJ-IV cognitive ability data are analyzed in this study, g factor or general intelligence is anticipated. The first core profile in this case usually represents the g factor, which is estimated using an array of the J subscale means, or the subscale mean profile (e.g., Kim, 2010a, 2010b; Kim et al., 2007). Thus, we estimated the correlation between the first core profile and the subscale mean profile to be  $r = 0.994$ , implying that the first core profile pattern coincides with the g factor structure. On the other hand, the correlations between the subscale mean profile and the second and third core profiles were  $r = -0.006$  and  $r = 0.001$ , indicating that the second and third core profiles do not have the g factor structure but response pattern structures.

Then, for the core profile coordinates, we calculated 95% BCa CIs and included them in Table 1. For example, core profile 3 was chosen and Figure 2 includes the 95% BCa CIs surrounding the core profile 3 coordinates. The coordinates would not be statistically significant if their CIs contained zeros.

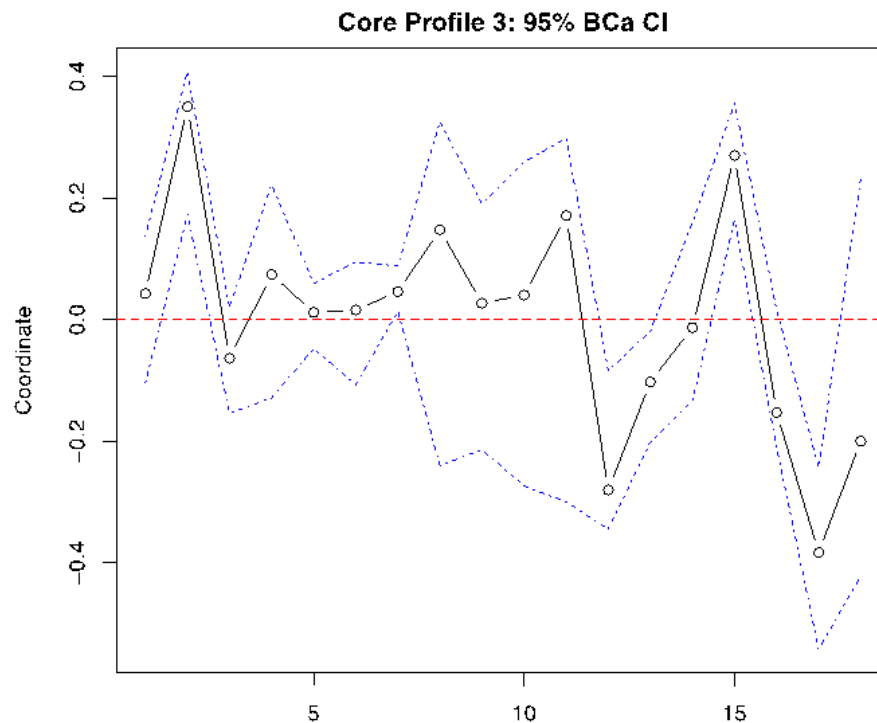
Consistent with the numerical results included in Table 1, the CIs for NS2 (Number Series), NW12 (Nonword Repetition), VA13 (Visual-Auditory Learning), AS15 (Analysis-Synthesis), and PC17 (Pair Cancellation), did not include zeros and were considered statistically significant.

#### **Part 3: Estimating Individual $R^2$ values and Person Correlations**

We estimated how much pattern variance in 1,650 person profiles were explained by three core profiles, and 1,650  $R^2$  values for all persons are estimated. The mean of these



**Figure 2 ■** The 95% BCa Confidence Intervals Around the Coordinates of Core Profile 3. The CIs for the coordinates of NS2 (Number Series), NW12 (Nonword Repetition); VA13 (Visual-Auditory Learning); AS15 (Analysis-Synthesis), and PC17 (Pair Cancellation) did not include zeros, indicating that these subscale coordinates of core profile 3 were statistically different from zero, but the other subscale coordinates that included zeros were not statistically different from zero.



1,650  $R^2$  values is 0.61 ( $SD = 0.20$ ,  $\min = 0.01$  and  $\max = 0.96$ ).

#### Part 4: Assessment of Specific Persons

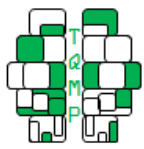
Individual person profiles can be evaluated. This assessment is useful when a psychologist wants to assess individual participants' strengths and weaknesses in their specific cognitive abilities using the interpreted core profile characteristics. In order to facilitate visual comparisons, we specifically selected the first ten patients out of a total of 1,261 and provided the PAMS in R outputs. These outputs include person weights (W1–W3), level estimates (level),  $R$ -squared values ( $R^2$ ), and person correlations with core profiles (corDim1–corDim3). Patient #9 was chosen as an example of a particular person evaluation among ten patients, as seen in Listing 1.

Person #9 was evaluated as a visual illustration of the person's profile juxtaposed with core profiles, but other person profiles can be examined in the same manner. This

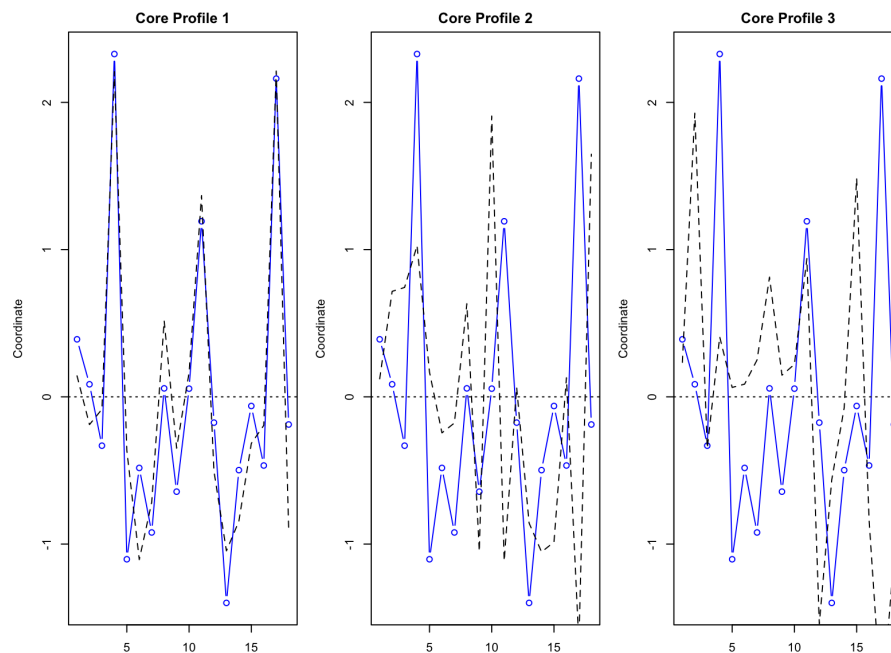
person's level is 528.17, which is slightly higher than the grand mean of  $M = 520.20$  ( $SD = 11.24$ ), implying that this person's average cognitive performance (across 18 cognitive domains) is slightly better than that of 1,650 participants on average. The correlations between Person #9 and the core profiles are  $r = 0.93$  for core profile 1,  $r = 0.13$  for core profile 2, and  $r = -0.07$  for core profile 3.

Because this person's correlation with core profile 1 is substantial but minor with other core profiles, the person profile pattern is similar to core profile 1, as illustrated in Figure 3. As a result, Person #9 is expected to have the cognitive ability of High Cognitive Processing Speed with Low Long-Term Retrieval as part of core profile 1. The squared multiple correlation for Person #9 is  $R^2 = 0.86$ , implying that the three core profiles, but primarily core profile 1, account for 86% of Person #9's profile pattern variance, with core profile 1 accounting for the majority of it due to the person's strongest relationship with core profile 1.





**Figure 3 ■** The Comparison Between Cross-Sectional Core Profiles and Person #9's Profile. The dashed lines depict core profiles, while the solid lines represent the profile of Person #9. Since the person correlation with core profile 1 is considerable,  $r = 0.93$ , but other correlations are negligible, Person #9's profile pattern resembles that of core profile 1.



### Example 2: PAMS in R of Longitudinal Data

Because the detailed procedures for the longitudinal PAMS example are the same as for the cross-sectional data, we demonstrate briefly how longitudinal data are analyzed with PAMS in R and the results are interpreted. The sample consists of 1,261 female anorexic patients who completed the Eating Disorder Inventory-2 (EDI-2; Garner, 1991) at admission (Pre) and discharge (Post). The EDI-2 is made up of 11 subscales that are used to assess 11 ED symptom indicators: 1 = Drive for Thinness; 2 = Bulimia; 3 = Body Dissatisfaction; 4 = Ineffectiveness; 5 = Perfectionism; 6 = Interpersonal Distrust; 7 = Interoceptive Awareness; 8 = Maturity Fears; 9 = Asceticism; 10 = Impulse Regulation; and 11 = Social Insecurity are the 11 subscales. The age range of the sample is 13 to 54 ( $M = 20.42$ ,  $SD = 7.89$ ), and it is 95.2% Caucasian, 2.4% Mixed/Unknown, 0.8% Hispanic, 0.8% Asian, and 0.8% African American. The IRB has approved the data analysis.

Because the data consists of two repeatedly measured subscores (Pre and Post), the input variables total 22 (11 Pre subscales + 11 Post subscales). We ran PAMS in R with the Pre and Post EDI-2 subscores simultaneously to examine which ED symptom indicator improves or deteriorates af-

ter treatment. To assess treatment efficacy for each symptom indicator (measured by the EDI-2 subscales), we examined the coordinates of the subscales in each core profile at Pre and Post. Because the subscales are intended to assess the severity of symptom indicators, high subscores represent deteriorated symptoms and low subscores represent improved symptoms; similarly, in a core profile, coordinates above zero indicate deteriorated symptoms and coordinates below zero indicate improved symptoms.

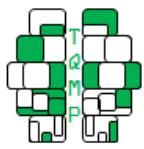
#### Part 1: Setting Up

As with the cross-sectional PAMS in R, we begin by examining the Stress values for the 2-, 3-, and 4-dimensional solutions, which are 0.078, 0.049, and 0.029, respectively. The 3-dimensional solution is chosen with the stress value of 0.049 and dimension interpretability as core profiles.

#### Part 2: Estimating Correlation between Mean and Core Profiles and 95% Coordinate CIs

##### Examine Pre and Post Core Profiles.

For visual inspection, we depicted Pre and Post core profiles along with the 95% BCa confidence intervals (CIs) around their respective coordinates in each dimension.



The purpose of comparing Pre and Post core profiles in each dimension was to examine treatment efficacy for every symptom indicator measured by each subscale. Similarly, the Pre and Post core profiles in each dimension represented particular aspects of the central response patterns observed in a sample of person profiles. We used coordinate CIs in each dimension to evaluate the statistical significance of the coordinates.

**The 1st Core Profile.** Taking two contrasting traits from the 1st Pre core profile depicted in Figure 5, the Pursuit of Slim Body core profile is constituted of the valley of subscale 2 (Bulimia) and the peak of subscale 3 (Body dissatisfaction), as both subscales describe the patient behavior of pursuing a slim body. Although, as shown in the figure, the Pre and Post core profile patterns are comparable, labeling was based on the valleys and peaks of the Pre core profile because the Post core profile pattern could be subject to change after treatment. Except for Bulimia (= 2), all eating disorder symptom indicators improved following treatment. The overlap of the Pre and Post CIs for Bulimia indicates that the disorder did not improve after treatment. Note that although the Post Perfectionism (= 5) was not significantly different from zero because its CI included zero, its Pre CI did not include zero, and we consider Perfectionism to have improved because there is no overlap in Figure 5 between its Pre and Post CIs.

The visual inspection results correspond to the numerical results presented in Table 2, where the overlapping CIs between Pre and Post are highlighted in red and underlined for Bulimia (= 2), indicating no treatment for Bulimia despite the statistical significance of both its Pre and Post coordinates. However, due to Bulimia's significant Pre CI, its Pre coordinate was used when labeling the 1st core profile.

**The Subscale Mean Profile vs. Core Profile 1.** When a general factor of eating disorder appears in the data, it is typically estimated using subscale means (Kim, 2013; Kim et al., 2017). As previously explained, if this is the case, the 1st core profile depicts the general factor pattern (estimated using the subscale mean profile) (e.g., Kim et al., 2007). The correlation between a profile of 22 subscale means and the 1st core profile was  $r = 0.991$ , indicating that the 1st core profile represents the structure of the eating disorder general factor.

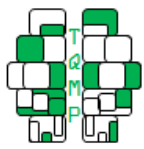
Additionally, we used Bonferroni corrected t-tests to examine the differences in subscale mean scores between Pre and Post. Table 3 is a summary of the results. All mean differences are highly significant, with a range of small to medium effect sizes, indicating that all eleven symptom indicators of eating disorder improved after treatment. However, the results based on the coordinates are somewhat different; the first core profile for Bulimia (= 2) reveals no treatment efficacy. However, the subscales at each time

point are expected to be highly correlated given that they are designed to measure a singular construct, eating disorder. Pre 11 subscale correlations range from  $r = 0.11$  to  $r = 0.76$  ( $p < 0.001$ ), while Post 11 subscale correlations range from  $r = 0.14$  to  $r = 0.81$  ( $p < 0.001$ ). Significant inter-subscale correlations may introduce bias into the paired t-test when comparing the mean differences between Pre and Post for any given subscale.

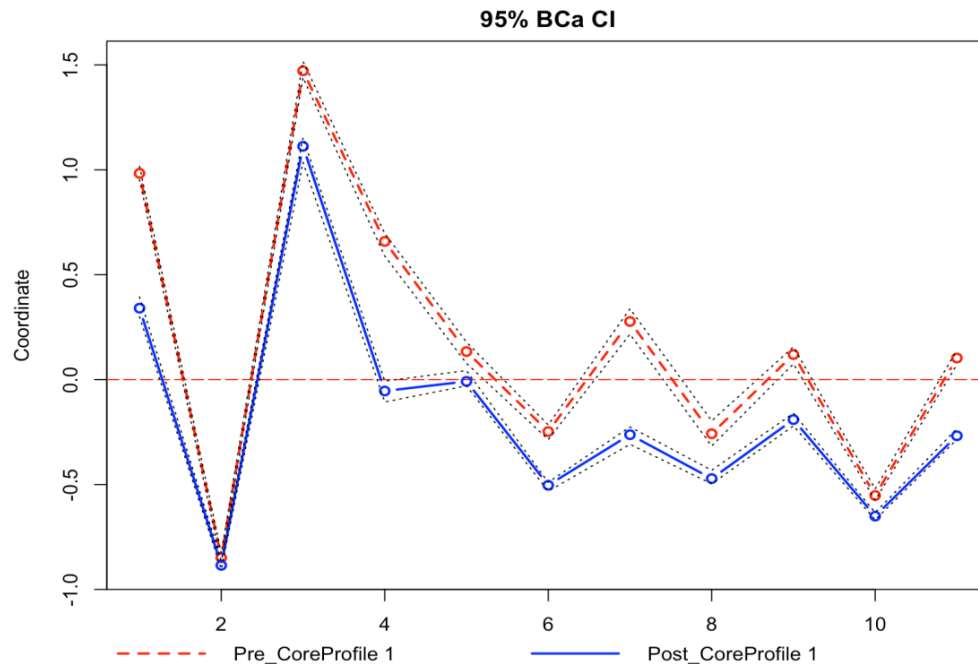
**The 2nd Core Profile.** As previously stated, the 1st core profile contains the same information as the subscale mean profile, and their data are interchangeable. However, the 2nd core profile information is unique and completely absent from the observed scores (e.g., subscale means). The subscale coordinate comparisons in the 2nd core profile are unique information that is only available in PAMS in R and not in any observed score domains (e.g., subscale means).

As shown in Figure 5, since the CI of 2 (= Bulimia) includes zero, we select another valley (5 = Perfectionism) and a peak (8 = Maturity fears) and name the second core profile Pursuit of Perfect Body. The difference between the Pre and Post profiles in the figure indicates that the patients have significantly improved following treatment. In contrast to the distances between the 1st Pre and Post core profiles (in Figure 4), the distances between the 2nd Pre and Post core profiles (in their CIs) are significantly greater, implying that treatment is more effective for patients with a similar pattern of the 2nd core profile. Figure 5 shows that there is no overlap between any Pre and Post CIs, indicating that all eleven symptom indicators have improved following treatment. The numerical results listed in Table 4 agree with those of the visual inspection depicted in Figure 5.

**The 3rd Core Profile.** Figure 6 contrasts the Pre and Post 3rd core profiles with a peak of Pre Ineffectiveness (= 4) and a valley of Pre Perfectionism (= 5); the 3rd profile is labeled as the Ineffective Chase of Perfectionism profile. Similar to the 2nd core profile, none of the 3rd core profile information is available in any observed score domain; however, as shown in Figure 6, seven confidence intervals for the Pre and Post symptom indicators overlap, with the exception of four indicators 1 (= Drive for thinness), 4 (= Ineffectiveness), 6 (= Interpersonal distrust), and 11 (= Social insecurity), indicating that treatment is moderately effective in the 3rd core profile dimension. Patients with the same response pattern as the 3rd core profile would respond less favorably to treatment than those with the same response pattern as the 1st or 2nd core profile. We omit the numerical results on purpose because a visual examination of Figure 6 is sufficient to comprehend ineffective treatment efficacy for the seven symptom indicators (2, 3, 5, and 7–10).



**Figure 4 ■** The 95% BCa Confidence Bands for the 1st Core Profile Coordinates Between Pre and Post. The dotted lines around the coordinates represent the 95% BCa CIs. 1 = Drive for thinness; 2 = Bulimia; 3 = Body dissatisfaction; 4 = Ineffectiveness; 5 = Perfectionism; 6 = Interpersonal distrust; 7 = Interoceptive awareness; 8 = Maturity fears; 9 = Asceticism; 10 = Impulse regulation; and 11 = Social insecurity.



### Part 3: Estimating Individual $R^2$ values and Person Correlations

Person weights, levels, person  $R^2$  values, and person correlations are estimated by PAMS in R for 1,261 individual patients. The average of the 1,261  $R^2$  values is  $R^2 = 0.62$  ( $SD = 0.22$ , min = 0.00 and max = 1.00), meaning that 62% of pattern variance is accounted for by the three core profiles.

### Part 4: Assessment of Specific Persons

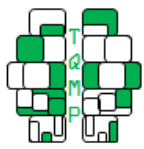
Individual patient profiles can be evaluated. This assessment is useful when a clinician wants to diagnose individual patients' symptom improvement and deterioration after treatment using the interpreted core profile characteristics. In order to facilitate visual comparisons, we specifically selected the first ten patients out of a total of 1,261 and provided the PAMS in R outputs. These outputs include person weights (W1–W3), level estimates (level), R-squared values ( $R^2$ ), and person correlations with core profiles (corDim1–corDim3). Patient #9 was chosen as an example of a particular person evaluation among ten patients.

We juxtaposed the patient's profile with the three (lon-

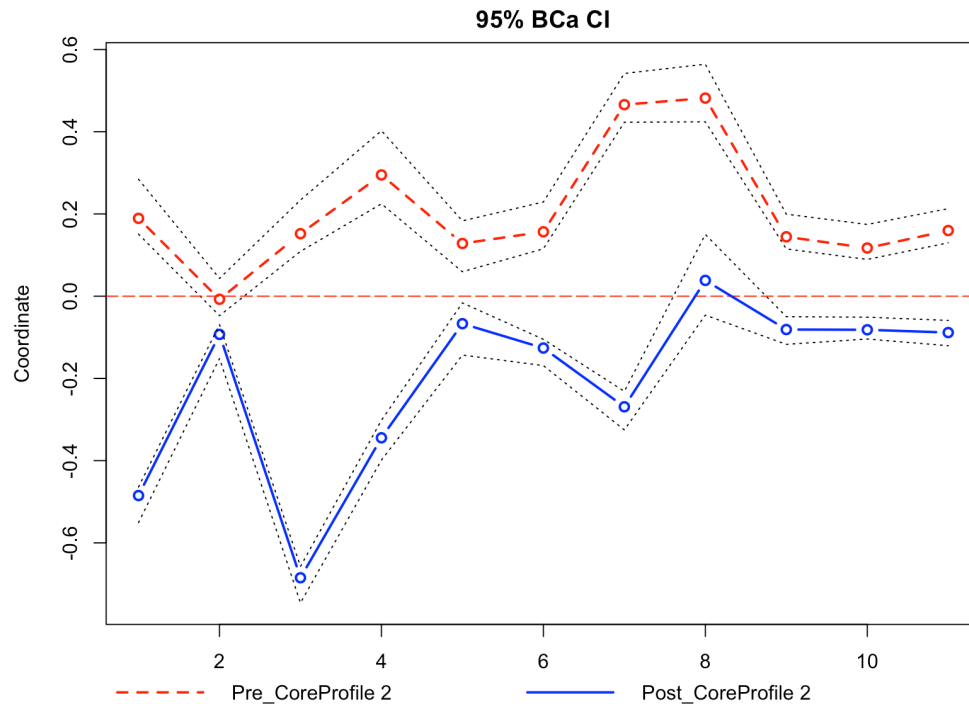
gitudinal) core profiles (see Figure 7). Patient #9's level of 4.77 is lower than the mean level of  $M = 6.46$  ( $SD = 3.18$ ) for 1,261 patients, indicating that this patient's eating disorder has improved as a result of treatment, relative to the mean level. The correlations between Patient #9 and core profiles 1–3 were:  $r = 0.89$ ,  $r = -0.30$ , and  $r = -0.60$ , respectively, and Patient #9's profile would be similar to core profile 1. As illustrated in Figure 7, this patient's profile is similar to core profile 1, and Patient #9's eating disorder symptom is classified as Pursuit of Slim Body, which is a label of core profile 1. ( $R^2 = 0.82$ ) The three core profiles account for 82% ( $R^2 = 0.82$ ) of Patient #9's within-person variance, with core profile 1 accounting for the majority of it due to the person's strongest relationship with core profile 1.

### Discussion

This study demonstrates the efficacy of PAMS in R for comprehending the most typical response patterns of individual profiles in both cross-sectional and longitudinal data. We performed a cross-sectional data analysis using CPA (cluster profile analysis) and LPA (latent profile analysis) to showcase the utility of PAMS in R for identifying the central response patterns. This is essential for evaluating indi-



**Figure 5 ■** The 95% BCa CIs between the Pre and Post Coordinates of Core Profile 2. The dotted lines around the coordinates represent the 95% BCa CIs. 1 = Drive for thinness; 2 = Bulimia; 3 = Body dissatisfaction; 4 = Ineffectiveness; 5 = Perfectionism; 6 = Interpersonal distrust; 7 = Interoceptive awareness; 8 = Maturity fears; 9 = Asceticism; 10 = Impulse regulation; and 11 = Social insecurity.



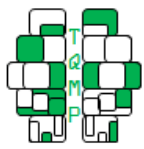
vidual response profiles. In addition, we conducted a comparison between the results obtained using PAMS in R and the findings from CPA and LPA. Both CPA and LPA were primarily designed to estimate level information rather than pattern information. Therefore, they were unsuitable for analyzing individual response profiles that encompassed both level and pattern information, unlike PAMS in R. The Supplementary Materials contained comparison findings.

Since PAMS in R relies on nonmetric scaling, which necessitates a monotone transformation of the input data, meeting the normality assumption for the data is not necessary. However, PAMS in R requires normality and homogeneous variance for the error terms, which we can estimate using residuals ( $m - \hat{m}$ ) from the fitted model. We used both cross-sectional and longitudinal data in this study. To see if their residuals were normal, we performed the Shapiro-Wilks test (Shapiro & Wilk, 1965). To see if the residual variance was homogeneous, we conducted the Breusch-Pagan test (Breusch & Pagan, 1979). The normality and homogeneous variance assumptions were met in PAMS in R, as all test results were statistically not significant at  $\alpha = 0.05$ . The R codes for these tests were included in the supplemen-

tary materials.

### Limitations

PAMS in R is an effective analytical tool for understanding core response patterns in substantive domains. Nevertheless, due to its reliance on nonmetric scaling, it is not feasible to determine the statistical significance of individual core profiles. Instead, we relied on the global measure of stress ( $\leq .05$ ) to ascertain the number of core profiles, as demonstrated in this study. The profile analysis based on factor analysis can test statistical significance of core profiles if parallel analysis is utilized (Horn, 1965), although this nonmetric scaling-based PAMS in R typically fit better to data than a metric version of profile analysis such as factor analysis (e.g., Kim, 2013). To improve data fitting and to enable statistical significance testing for core profiles, principal component analysis and singular value decomposition were introduced to scale individual response profiles (e.g., Kim, 2023; Kim & Kim, 2017). However, these two profile analyses do not include a test function to evaluate statistical significance of the coordinates of a core profile such as bootstrap confidence intervals utilized in PAMS

**Table 2** ■ The 95% BCa CIs for the Coordinates of the 1st Pre and Post Core Profiles

|    |    | Pre core profile |        |        | Post core profile |         |         |
|----|----|------------------|--------|--------|-------------------|---------|---------|
|    |    | Pre CP1          | Pre L1 | Pre U1 | Post CP1          | Post L1 | Post U1 |
| 1  | Dt | 0.98             | 0.95   | 1.02   | 0.34              | 0.30    | 0.39    |
| 2  | Bu | −0.85            | −0.88  | −0.83  | −0.89             | −0.90   | −0.86   |
| 3  | Bd | 1.47             | 1.44   | 1.52   | 1.11              | 1.04    | 1.15    |
| 4  | In | 0.66             | 0.59   | 0.70   | −0.05             | −0.11   | −0.01   |
| 5  | Pf | 0.13             | 0.08   | 0.18   | −0.01             | −0.03   | 0.04    |
| 6  | Id | −0.25            | −0.29  | −0.22  | −0.50             | −0.53   | −0.49   |
| 7  | Ia | 0.28             | 0.22   | 0.34   | −0.26             | −0.31   | −0.23   |
| 8  | Mf | −0.26            | −0.32  | −0.20  | −0.47             | −0.50   | −0.43   |
| 9  | As | 0.12             | 0.08   | 0.16   | −0.19             | −0.22   | −0.16   |
| 10 | Ir | −0.55            | −0.58  | −0.52  | −0.65             | −0.69   | −0.63   |
| 11 | Si | 0.10             | 0.07   | 0.14   | −0.27             | −0.29   | −0.23   |

*Note.* CP1 = the 1st core profiles. L1 = the lower (2.5th %) bound of the 95% BCa CI; U1 = the upper (97.5th %) bound of the 95% BCa CI. Dt = Drive for thinness; Bu = Bulimia; Bd = Body dissatisfaction; In = Ineffectiveness; Pf = Perfectionism; Id = Interpersonal distrust; Ia = Interoceptive awareness; Mf = Maturity fears; As = Asceticism; Ir = Impulse regulation; and Si = Social insecurity. Italicized and red-highlighted confidence intervals were excluded from interpretation because they overlapped or contained zero.

**Listing 2** ■ Person's weights W1 to W3 of 10 patients

```
> round(empprofile2$Weight[1:10,],2)
```

|     | w1          | w2           | w3           | level       | R^2         | corDim1     | corDim2      | corDim3      |
|-----|-------------|--------------|--------------|-------------|-------------|-------------|--------------|--------------|
| #1  | 7.61        | 5.06         | −4.19        | 7.68        | 0.63        | 0.78        | 0.35         | −0.21        |
| #2  | 5.49        | 2.7          | −5.83        | 6.64        | 0.62        | 0.76        | 0.25         | −0.36        |
| #3  | 8.74        | 11.39        | 4.53         | 7.36        | 0.81        | 0.87        | 0.72         | 0.27         |
| #4  | 6.04        | −2.21        | −1.63        | 7.95        | 0.61        | 0.78        | −0.20        | −0.10        |
| #5  | 3.99        | 7.19         | −6.12        | 3.05        | 0.67        | 0.72        | 0.64         | −0.44        |
| #6  | 5.24        | −1.44        | −6.14        | 4.77        | 0.53        | 0.7         | −0.12        | −0.34        |
| #7  | 1.36        | 5.72         | −9.50        | 2.91        | 0.53        | 0.32        | 0.54         | −0.60        |
| #8  | 4.15        | 2.17         | −7.74        | 3.45        | 0.70        | 0.79        | 0.29         | −0.59        |
| #9  | <b>7.06</b> | <b>−2.55</b> | <b>−8.78</b> | <b>4.77</b> | <b>0.82</b> | <b>0.89</b> | <b>−0.30</b> | <b>−0.60</b> |
| #10 | 4.05        | −3.81        | 7.07         | 7.09        | 0.43        | 0.58        | −0.29        | 0.36         |

in R, which remains for future research.

### Suggestions

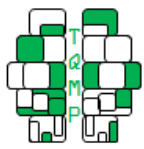
PAMS in R is considered a dimension reduction technique, necessitating at least five input variables for both cross-sectional and longitudinal data. For profile analysis of longitudinal data, if the average or sum of subscores for each time point is analyzed, at least five time point means are required so that each longitudinal core profile (or trajectory) over time consists of at least five coordinates (e.g., Ding et al., 2005; Kim, 2010a).

However, if subscale means are used for this study's longitudinal data, there will be only two data points (Pre and Post) over time, and PAMS in R cannot be performed with only two input variables. Therefore, we used 11 sub-

scale scores at each time point as input variables instead. When there are fewer than five time points in longitudinal data, a researcher may choose to use individual subscale (or item) scores as input variables when conducting longitudinal PAMS in R, rather than using aggregated scores. Using subscale or item scores (as input variables) not only allows PAMS in R to run for scaling them when there are fewer than five time points.

Prior to conducting cross-sectional or longitudinal PAMS in R, if variables are not in the same unit, they must be standardized; otherwise, interpretation of the core profile coordinates would be misleading. It is conceivable for some individuals to have correlations of equal strength with the core profiles. In this instance, none of the core profile patterns resemble the profile patterns of these in-



**Table 3** ■ Comparing 11 Subscale Means Between Pre and Post ( $n = 1, 261$ )

|    |    | Pretest      | Posttest     | Paired t   |                 |                  |
|----|----|--------------|--------------|------------|-----------------|------------------|
|    |    | M (SD)       | M (SD)       | Pre – Post | <i>p</i> -value | Cohen's <i>d</i> |
| 1  | Dt | 12.07 (6.88) | 7.98 (6.85)  | 4.90       | $p < .001$      | 0.64             |
| 2  | Bu | 1.05 (2.13)  | 0.47 (1.34)  | 0.58       | $p < .001$      | 0.29             |
| 3  | Bd | 14.25 (8.18) | 12.87 (8.71) | 1.38       | $p < .001$      | 0.19             |
| 4  | In | 10.26 (7.56) | 6.07 (6.19)  | 4.19       | $p < .001$      | 0.62             |
| 5  | Pf | 7.90 (4.75)  | 6.86 (4.46)  | 1.04       | $p < .001$      | 0.28             |
| 6  | Id | 5.28 (4.25)  | 3.25 (3.48)  | 2.03       | $p < .001$      | 0.53             |
| 7  | Ia | 8.30 (6.34)  | 4.80 (5.03)  | 3.50       | $p < .001$      | 0.60             |
| 8  | Mf | 6.12 (5.34)  | 4.14 (4.29)  | 1.98       | $p < .001$      | 0.45             |
| 9  | As | 7.42 (4.59)  | 5.63 (3.93)  | 1.79       | $p < .001$      | 0.44             |
| 10 | Ir | 2.91 (3.83)  | 2.05 (3.10)  | 0.86       | $p < .001$      | 0.25             |
| 11 | Si | 7.56 (4.62)  | 4.82 (4.00)  | 2.74       | $p < .001$      | 0.66             |

*Note.* Dt = Drive for thinness; Bu = Bulimia; Bd = Body dissatisfaction; In = Ineffectiveness; Pf = Perfectionism; Id = Interpersonal distrust; Ia = Interoceptive awareness; Mf = Maturity fears; As = Asceticism; Ir = Impulse regulation; and Si = Social insecurity. Due to significant correlations between subscales in the Pre or Post condition, the results of the paired t-test would be biased.

dividuals, making it challenging to interpret their profiles in terms of a specific core profile pattern. We suspect that these individuals share common characteristics or traits with all core profiles. Kim et al. (2017) demonstrated that multi-trait person profiles can be replicated using a linear combination of the core profiles weighted by the person correlations. For instance, if a person's correlations with core profiles 1–3 are  $r = 0.6$ ,  $r = 0.5$ , and  $r = 0.6$ , respectively, then this multi-trait person profile can be replicated by a linear combination of  $0.6 \times$  the coordinates of core profile 1,  $0.5 \times$  the coordinates of core profile 2, and  $0.60 \times$  the coordinates of core profile 3 (see details in Kim et al., 2017). Person correlations can also be used as predictor variables if researchers desire to examine the relationships between core profiles and other variables of interest.

#### *Handling Large Number of Item in PAMS in R*

Interpreting the core profiles in longitudinal PAMS analysis in R can be challenging when the measures consist of a large number of items, such as 50 items, at each time point, and there are no subscales. This is because there are multiple sets (with the same number of time points) of 50 coordinates distributed over multiple time points. In this situation, a researcher may wish to conduct exploratory factor analysis or cluster analysis with 50 items at the initial time point (Time 1) to identify a few distinct clusters within the items. These clusters, which represent different subscales, can then be generated for subsequent time points such as Time 2, Time 3, and so forth, based on the initial exploratory clusters at Time 1. We suggest employing exploratory (clustering) analysis on the item scores from Time 1 instead of other time points, as the treatment or time

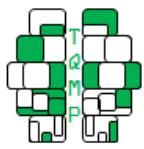
effect (such as maturity) might have influenced the scores after Time 1. As a result, the researcher can use the individual person mean scores from the newly derived clusters or subscales as input variables to implement longitudinal PAMS in R. If this is a single instance of analysis at Time 1, then it is a cross-sectional analysis using the PAMS method in R.

#### **Authors' note**

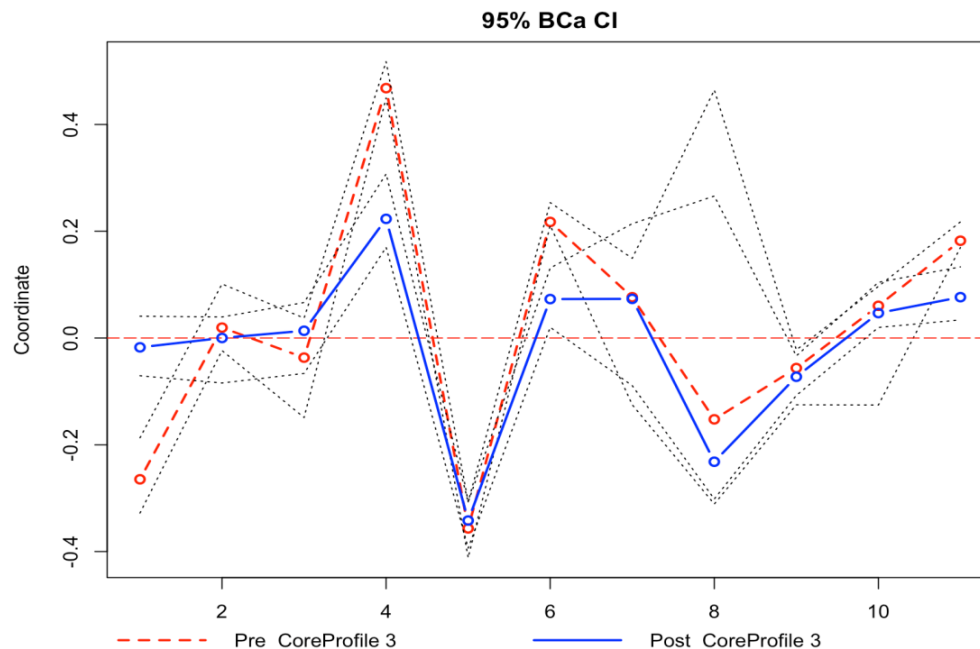
This research was supported by the Basic Science Research Program granted to Donghoh Kim through the National Research Foundation of Korea (NRF) funded by the Ministry of Education (2021R1F1A1047506). The cross-sectional data from Woodcock-Johnson IV Cognitive Ability Battery were never published, but a part of longitudinal data used in the study by Kim et al. (2017) were analyzed. Acknowledgment: We are grateful to Erica LaForte at Northwestern University for the cross-sectional data and to Bunmi Olatunji at Vanderbilt University for the longitudinal data used in this study. Correspondence concerning the manuscript should be addressed to Se-Kang Kim, The Psychology Division in the Department of Pediatrics at Baylor College of Medicine, Houston, TX 77030-2399.

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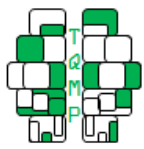
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**Figure 6 ■** The 95% BCa CIs between the Pre and Post Coordinates of the 3rd Core Profiles. The dotted lines around the solid lines represent the 95% BCa CIs. 1 = Drive for thinness; 2 = Bulimia; 3 = Body dissatisfaction; 4 = Ineffectiveness; 5 = Perfectionism; 6 = Interpersonal distrust; 7 = Interceptive awareness; 8 = Maturity fears; 9 = Asceticism; 10 = Impulse regulation; and 11 = Social insecurity.



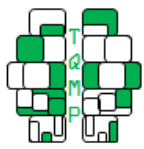
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**Table 4** ■ The 95% BCa Confidence Bands for the Coordinates of the 2nd Pre and Post Core Profiles

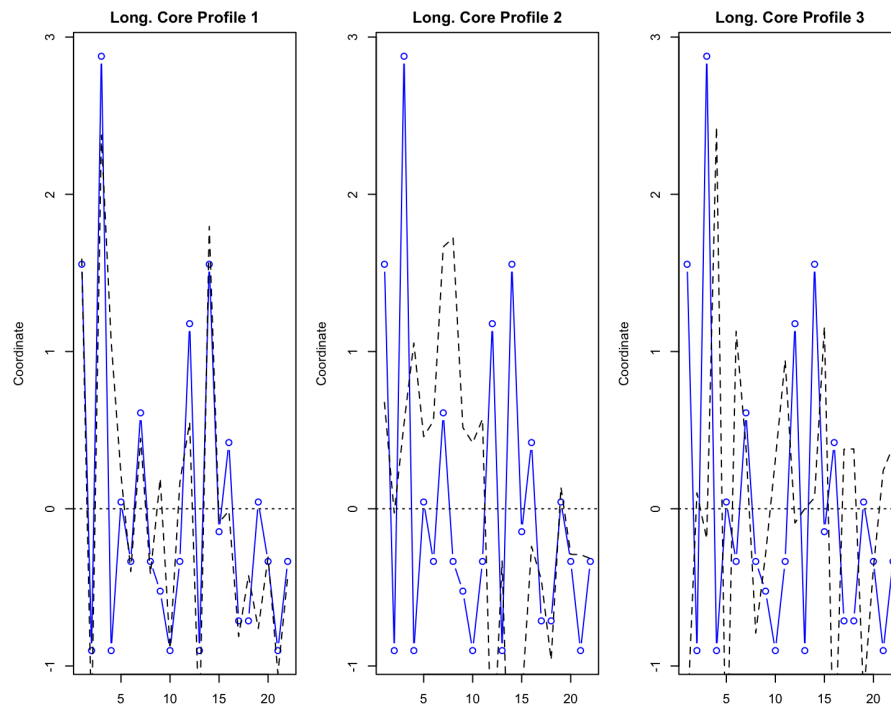
|    |    | Pre core profile |        |        | Post core profile |         |         |
|----|----|------------------|--------|--------|-------------------|---------|---------|
|    |    | Pre CP2          | Pre L2 | Pre U2 | Post CP2          | Post L2 | Post U2 |
| 1  | Dt | 0.19             | 0.15   | 0.28   | −0.48             | −0.55   | −0.46   |
| 2  | Bu | −0.01            | −0.05  | 0.04   | −0.09             | −0.15   | −0.07   |
| 3  | Bd | 0.15             | 0.11   | 0.23   | −0.69             | −0.75   | −0.66   |
| 4  | In | 0.30             | 0.23   | 0.40   | −0.34             | −0.40   | −0.30   |
| 5  | Pf | 0.13             | 0.06   | 0.18   | −0.07             | −0.14   | −0.02   |
| 6  | Id | 0.16             | 0.12   | 0.23   | −0.13             | −0.17   | −0.11   |
| 7  | Ia | 0.47             | 0.42   | 0.54   | −0.27             | −0.33   | −0.23   |
| 8  | Mf | 0.48             | 0.12   | 0.56   | 0.04              | −0.05   | 0.15    |
| 9  | As | 0.14             | 0.12   | 0.20   | −0.08             | −0.12   | −0.05   |
| 10 | Ir | 0.12             | 0.09   | 0.17   | −0.08             | −0.10   | −0.05   |
| 11 | Si | 0.16             | 0.13   | 0.21   | −0.09             | −0.12   | −0.06   |

*Note.* CP2 = the 2nd core profile. L = the lower (2.5th %) bound of the 95% BCa CI; U = the upper (97.5th %) bound of the 95% BCa CI. 1 Dt = Drive for thinness; 2 Bu = Bulimia; 3 Bd = Body dissatisfaction; 4 In = Ineffectiveness; 5 Pf = Perfectionism; 6 Id = Interpersonal distrust; 7 Ia = Interoceptive awareness; 8 Mf = Maturity fears; 9 As = Asceticism; 10 Ir = Impulse regulation; and 11 Si = Social insecurity.

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**Figure 7 ■** The Comparison Between Longitudinal Core Profiles and Person #9's Profile. The dashed lines are longitudinal core profiles, and the solid lines are the profile of Patient #9. The first eleven numbers (1–11) represent Pre subscales, while the last twelve numbers (12–22) represent Post subscales. Patient #9's profile resembles longitudinal core profile 1 because the correlation with core profile 1 is substantial,  $r = 0.89$ , compared to other correlations.



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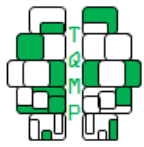
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