**Level, Scatter, and Shape—Post-hoc comparisons of two profiles**

* Compare if the difference between levels of two profiles is psychometrically significant?

, where is an average of the elements in , for t=1, 2. Because is a simple linear transformation of the elements in , its standard error is very straightforward to compute.

* Compare if the difference between scatters of two profiles is psychometrically significant?

According to Cronbach & Gleser (1953), scatter is defined as the “square root of the sum of squares of the individual’s deviation scores about his own mean.” In a matrix notation, the scatter of ***θ*** (K-by-1 column vector) can be written as: , where is a K-by-K matrix of all 1’s.

According the known results of the variance of quadratic form of multivariate normal variable[[1]](#footnote-1), assuming ***θ*** follows a multivariate normal distribution (note: this is for an individual theta, so the variance of the multivariate normal is the squared measurement errors), then

.(1)

Because , we have the **variance of the scatter** as

where (3)

Once the variance of the scatter is computed using Eq. (2), we can take the square root to obtain its standard error. Then using a simple Z-test to compare if two scatters are significant different.

* Shape is “the residual information in the score set after equating profiles for both level and scatter” (Cronbach & Gleser,1953). In other words, shape is a standardized version of a profile, i.e., for ***θ*** , its shape is , where .

Given that the shape is also a vector, in order to compare if the shapes of two profiles are psychometrically different, we still need to use the multivariate Z-test in our previous paper (Wang & Weiss, 2018). The difficulty is to figure out the standard error associated with each element in the shape vector.

Take the first element in the shape vector as an example, i.e., , the expectation and variance of (denoted as X hereafter for notational simplicity) are easy to compute.

The variance of *s* is given in (2), and the expectation of *s* is derived as follows.

Because , we have

Once the mean and variance of both the numerator (i.e., X) and denominator (i.e., s) are computed, the variance of the first element in the scatter is computed as:

where is computed from (2) and is computed from (4). Here we can assume X and s are independent, hence the term .

**Group-based approach vs. Individual-based approach**

* If we want to take into account measurement error of *θ* in the group-based approach, we will use the structural equation modeling approach. That is, using IRT model at level 1, and using the latent growth curve model (LGC) at level 2. The LGC model is only recommended when we have 3 or more time points.
  + When T=2, then given the known item parameters, assume *θ* is unidimensional (for simplicity) we can fit a two-dimensional IRT model in the group-based approach. The EM algorithm will output population mean and covariance estimates, denoted as and . Then we will use and to estimate individual and (at both time points).
    - It is expected that in this case, the difference between group and individual based approach will not be large, unless the true and are extreme, in which case using and may have severe “regression toward mean” effect.
    - M*plus* provides factor score estimates, similar to MAP.
  + When T, then given the known item parameters, assume *θ* is unidimensional (for simplicity) we can fit a second-order LGC model (with IRT model at the lower, measurement model level).

Write the model as

. (2)

Again, if assuming a unidimensional is measured per time point, then both and are *T*-by-1 vectors. and are the *T*-by-*p* and *T*-by-*q* design matrices, and ***β*** and are *p*-by-1 and *q*-by-1 vectors denoting fixed and random effects respectively. *T* is the total number of time points. In a more general case, can also differ across individuals (). For simplicity, we assume ***X*** , i.e., random-intercept random-slope model without additional covariates. The random effects, , are typically assumed to follow multivariate normal distribution,

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and it is often assumed in LGC of independent error structure, i.e.,. (, , ) could be estimated using off-the-shelf SEM packages, such as lavaan in R or M*plus*. Then the factor score estimates of in M*plus* (using SAVE = FSCORES) or lavaan (fscore).

A simulation study could be conducted to evaluate the group-level vs. individual-level approach in terms of recovery . The individual-level approach could also be used to evaluate significance of change, whereas the group-level approach usually cannot unless it also provides standard error of factor scores. In this regard, the hypothesis testing methods proposed in our AMC studies will still be used. (Dave, I do not think this step is necessary though because it then becomes a hybrid approach: using group-level approach to estimate individual *θ*’s and their standard errors, and then using our hypothesis testing methods to evaluate significance of change. What do you think?)

1. <https://en.wikipedia.org/wiki/Quadratic_form_(statistics)> [↑](#footnote-ref-1)