

## Appendix Section 2: Study 1 Expanded Methods and Results

### Simulation Method

To conduct the simulations, we generated 16, 36, or 72 equally-spaced items at angles from 0 to 360 degrees. Items were assumed to load on each of the two true score dimensions with loadings varying as the cosine of the angle for factor 1 and sin of the angle for factor 2. Item communalities were specified by adding random normal error to each item ( $w_{E1}$  and  $w_{E2}$ , respectively). We weighted the error to obtain communalities averaging 0.6. After adding the error, and to further approximate the data collected in typical affect studies, we converted the item scores into a 7-point bipolar ordinal scale, ranging from -3 to +3.

Simulated sample sizes were chosen to represent ones found in the literature, ranging from the more typical samples of several hundreds to the very large sample we report in the following section. Thus, sample sizes of 200, 800 and 3,200 were examined.

Each simulation was conducted twice, once with bipolar items (generated as described above) and once with unipolar items. Following Russell and Carroll's (1999) assumption of how unipolar items are formed, we collapsed all item scores  $< 0$  to zero. Naturally, truncating bipolar items (ranging from negative to positive scores) into a reduced, unipolar range (ranging from zero to positive scores) creates a certain level of skew, and does so for all items. In addition, a major purpose of this simulation was to show that the factor structure of items (though greatly affected by differences or non-uniformity in item skew) could be recovered using exploratory factor analysis. To further increase skew for some (but not all) items, we subtracted a constant (1.0) from the  $T_2$  scores, before adding error and before truncation. This led to greater skew for items with positive loadings on  $T_2$ , and less skew for items with negative loadings on  $T_2$ . It did not affect the degree of skew for items with only  $T_1$  loadings.

### Simulation Results

Using this criterion, we examined all 18 simulated samples, with consistent results. For

brevity, we present only nine of these analyses, but the remaining were identical in their results.

The Very Simple Structure (VSS) algorithm is easily understood by visual inspection of the VSS fit index of different solutions at a particular complexity level (e.g., complexity=2).

Solutions which differ in the number of factors extracted can be compared, and the analyst can determine which solution offers the best fit to the data. The top section of Figure A-1 shows the VSS criterion applied for three sample sizes (N=200, 800, and 3,200) to 72 bipolar items. The middle section of Figure A-1 displays the VSS criterion applied for similar samples to 72 unipolar items. The bottom section of Figure A-1 shows the VSS criterion applied for similar samples to 16 unipolar items in circumplex structure.

Two things are of note. As expected, a two-dimensional circumplex structure fits the bipolar data well. This is evident from the great improvement in fit in the move from complexity=1 to complexity=2, and from the absence of further increase in fit with any further increase in complexity or in the number of factors extracted. This merely means that the simulation produced items as requested. Similar results were obtained with conventional goodness of fit measures (e.g., chi-square tests for goodness of fit or the eigen-value > 1 rule).

More importantly, the VSS algorithm out-performed conventional goodness of fit indices in detecting the appropriate number of factors of the (skewed) unipolar data. While the eigen-value > 1 criterion suggested that these data require five factors, and the chi-square test suggested seven factors, the VSS criterion clearly indicates that a 2 dimensional solution is most interpretable if every item is thought to load on only one or at most two factors (i.e., if complexity equals 1 or 2).

A final demonstration using the simulated data can be seen in the left three panels of Figure 1 in the main text. In each panel, all the simulated items are located according to the strength of their correlations with two target items, ones that lie at 90 degrees (top), 120 degrees (middle) or 180 degrees (bottom) away from each other. Despite the presence of skew and error variance in

all items (as well as in the two target ones in each panel), a clear picture emerges; specifically, it is very easy to distinguish between the pattern of associations (of the entire item pool) found with orthogonal items versus that found with bipolar opposite items. We later return to a similar analysis with non-simulated data.