Supplemental Content

Section 1: MDS Software Algorithm Explanation

At each stage of the sort-and-merge process, the collection of clusters is called a partition step beginning with the initial sort as partition step 1. For each participant k and for each stimulus pair i and j, we compute a proximity value, $p_{ij}^{(k)}$ which is defined as the total number of partition steps (= merge stages + initial sort) in which the i-th and j-th stimuli are grouped together divided by the total number of partition steps (merge stages + initial sort) generated by that participant. For example, suppose eight stimuli are numbered 1, 2, 3, 4, 5, 6, 7, 8 and participant k produces the following partitions:

Initial sort	*1, 3, 5 | 2, 4 | 7, 8 | 6*	(That is, stimuli 1,3, and 5 are sorted into Category 1, stimuli 2 and 4 are in category 2, stimuli 7 and 8 are in Category 3 and stimulus 6 is in the singleton Category 4.)
Merge 1	1, 3, 5, 7, 8 | 2, 4 | 6	(That is, Category 1 and 3 were merged)
Merge 2	1, 3, 5, 7, 8, 6 | 2, 4	(That is, old Cat. 1 & 3 merged with Cat. 4)
Merge 3	all stimuli put together	

The total number of partition steps for this subject is 4 = 1 initial sort + 3 merge steps. For stimuli 3 and 5, the number of sorting partition steps for which these stimuli were grouped together is 4

since they were grouped in the initial sort. Hence, $p_{35}^{(k)}$ = 4/4 = 1. For stimuli 3 and 8, the number of

sorting steps for which they were together is 3 since they were combined at the first merge step.

Hence, $p_{38}^{(k)}$ = 3/4. For stimuli 1 and 2, the number of sorting partitions for which they were together is

1, the final merge. Hence, $p_{12}^{(k)}$ = 1/4. For each participant, an object × object matrix of these proximity

values can be constructed in this manner. To obtain the overall group dissimilarity matrix, we averaged

the entries of all participant proximity matrices and subtracted these cell averages from the total

number of participants. That is, each cell i, j in the final group dissimilarity matrix = $n - \dfrac{\sum\limits_{k} p_{ij}^{k}}{n}$ = where

n = number of participants. Proximities were converted to dissimilarities because the MDS procedure in

SPSS expects the data to be dissimilarities. Any reverse monotonic transformation to the proximities

will work as the scaling procedure only assumes ordinal scale of measurement for the data.

Section 2: Information About the Path Analyses

Table S1. *Covariance matrix for the variables included in the Free Choice condition model.*

	DIM1	DIM2	PATHL	ELIP	PATHN
DIM1	0.006				
DIM2	0.115	62.163			
PATHL	0.002	0.228	0.006		
ELIP	2.378	31.133	0.599	1186.660	
PATHN	0.022	-1.914	-0.015	9.873	1.702

Note: DIM1 = Dimension 1, DIM2 = Dimension 2, ELIP = Elliptical Area, PATHL = Path Length and,
PATHN = Normalized Path Length

Table S2. *The values of the fit indices for the Free Choice condition model.*

Fit Index	Fit Index Value	Fit Indicated
RMSEA	0.000	Excellent Fit
CFI	1.000	Excellent Fit
TLI	1.000	Excellent Fit
SRMR	0.023	Close Fit

Table S3. *Standardized and unstandardized path coefficients and standard errors for the Free Choice condition model.*

Dimension	MP	β (SE)	b (SE)	P Value (β /b)
Dimension 1				
	Path Length	0.213 (0.078)	0.213(0.075)	0.006/0.004
	Normalized Path Length	0.069 (0.067)	0.004 (0.004)	0.303/0.305
	Elliptical Area	0.827 (0.051)	0.002 (0.000)	0.000/0.000
	Error 1 Variance	0.167 (0.047)	0.001 (0.000)	0.000/0.000
Dimension 2				
	Path Length	0.353 (0.159)	-0.012 (0.006)	0.026/0.033
	Normalized Path Length	-0.133 (0.141)	-0.002 (0.001)	0.346/0.393
	Error 2 Variance	0.844 (0.122)	52.447 (21.645)	0.000/0.000

Note: MP = Movement Parameter, b = Unstandardized Estimate, β = Standardized Estimate and SE = Standard Error

Table S4. *Covariance matrix for the variables included in the Forced Scale condition model.*

	DIM1	DIM2	PATHL	ELIP	PATHN
DIM1	1.597				
DIM2	-0.017	0.403			
PATHL	-26.477	11.602	10361.654		
ELIP	-1.735	2.067	1002.730	120.490	
PATHN	-2.143	-5.305	814.388	-0.098	1.00

Note: DIM1 = Dimension 1, DIM2 = Dimension 2, ELIP = Elliptical Area, PATHL = Path Length and, PATHN = Normalized Path Length

Table S5. The values of the fit indices for the Forced Scale condition model.

Fit Index	Fit Index Value	Fit Indicated
RMSEA	0.000	Excellent Fit
CFI	1.000	Excellent Fit
TLI	1.000	Excellent Fit
SRMR	0.008	Close Fit

Table S6. *Standardized and unstandardized path coefficients and standard errors for the Forced Scale condition model.*

Dimension	MP	β (SE)	b (SE)	P Value (β /b)
Dimension 1				
	Path Length	-0.552 (0.443)	-0.011(0.005)	0.046/0.045
	Normalized Path Length	0.234 (0.179)	0.009 (0.007)	0.191/0.189
	Elliptical Area	0.692 (0.460)	0.080 (0.053)	0.132/0.132
	Error 1 Variance	0.917 (0.067)	1.464 (0.192)	0.000/0.000
Dimension 2				
	Path Length	0.353 (0.159)	-0.012 (0.006)	0.026/0.033
	Normalized Path Length	-0.133 (0.141)	-0.002 (0.001)	0.346/0.393
	Error 2 Variance	0.870 (0.068)	0.350 (0.038)	0.000/0.000

Note: MP = Movement Parameter, b = Unstandardized Estimate, β = Standardized Estimate and SE = Standard Error

Table S7. *Covariance matrix for the variables included in the Binary Choice condition model.*

	DIM1	DIM2	PATHL	ELIP	PATHN
DIM1	1.942				
DIM2	0.001	0.058			
PATHL	-26.207	0.889	10361.654		
ELIP	-1.905	0.395	1002.730	120.490	
PATHN	0.480	-2.409	814.388	-34.600	1041.223

Note: DIM1 = Dimension 1, DIM2 = Dimension 2, ELIP = Elliptical Area, PATHL = Path Length and, PATHN = Normalized Path Length

Table S8. *The values of the fit indices for the Binary Choice condition model.*

Fit Index	Fit Index Value	Fit Indicated
RMSEA	0.000	Excellent Fit
CFI	1.000	Excellent Fit
TLI	1.000	Excellent Fit
SRMR	0.037	Close Fit

Note: CFI = Comparative Fit Index, RMSEA = Root Mean Square Error of Approximation, SRMR = Standardized Root Mean Square Residual, TLI = Tucker Lewis Index.

Table S9. *Standardized and unstandardized path coefficients and standard errors for the Binary Choice condition model.*

Dimension	MP	β (SE)	b (SE)	P Value (β /b)
Dimension 1				
	Path Length	-0.896 (0.426)	-0.012 (0.006)	0.035/0.034
	Normalized Path Length	0.302 (0.170)	0.013 (0.007)	0.075/0.071
	Elliptical Area	0.709 (0.440)	0.090 (0.056)	0.108/0.106
	Error 1 Variance	0.920 (0.065)	1.786 (0.199)	0.000/0.000
Dimension 2				
	Path Length	0.121 (0.080)	0.000 (0.000)	0.133/0.139
	Normalized Path Length	-0.340 (0.094)	-0.003 (0.001)	0.000/0.000
	Error 2 Variance	0.890 (0.058)	0.051 (0.007)	0.000/0.000

Note: MP = Movement Parameter, b = Unstandardized Estimate, β = Standardized Estimate and SE = Standard Error