

Instructions for adapting the multi-trial version of the Spatial Arrangement Method (SpAM) to suit your personal needs:

First of all, it should be noted that this is a more advanced version of SpAM than the original. There is a fair amount of information that you will need to be familiar with in order to make this version of SpAM work for you. All necessary prior information is in the document (posted above this one on my website) entitled “Spatial Arrangement Method of Multidimensional Scaling, Instructions”. I recommend that you get comfortable with the basic SpAM method first, before attempting this one. And, of course, please feel free to contact me if you need help. For brevity, the instructions below will assume you know how to use SpAM already.

Broadly construed, this experiment is to be used when you want to scale more items than you can fit on the screen at one time. Perhaps you have more than 30 items to scale. Or perhaps you wish to display items very large, and so can only fit a few onscreen at a time. No matter the reason, this method will show you a technique you can use to scale large sets of stimuli, across several trials.

Ideally, you want to pair each item with every other item once, and only once. However, as you will come to find out, depending on the parameters of your experiment (i.e., how many total stimuli you have, how many you are displaying at once), that may or may not be possible. The general method I suggest is to employ a Steiner System.

Here are a few links to familiarize yourself with Steiner Systems:

- A general definition/explanation: <http://mathworld.wolfram.com/SteinerSystem.html>
- An index of known Steiner sets: <http://www.ccrwest.org/cover/steiner.html>
- A repository for looking up Steiner sets given user-defined parameters: <http://www.ccrwest.org/cover.html>

A Steiner System is a mathematical tool. You can think of it as a way to control which items are shown on which trials. It is often denoted $S(v, k, t)$, though sometimes the order of letters is mixed up. Basically, “ v ” is the number of stimuli you wish to scale. “ k ” is the number of items in a set (so, the number of items displayed on each trial). And “ t ” is the number of items being compared in any given set. For the purposes of MDS, t will always be 2, denoting a pairwise rating system for the output data matrices.

For some combinations of v and k , there may be a Steiner set that does not repeat pairwise comparisons. That is, a set of trials that will show each item in comparison with every other once and only once. For other combinations, that is not possible, and some stimuli will have to be shown with others more than once. It’s an imperfect system, leading to (for each subject) multiple observations per “cell” (i.e., per pairwise comparison). But as you’ll see in the rest of this document, we can roughly account for this issue by assuring that, across subjects, the particular pairings that are repeated get randomized. With enough subjects, that would give the user an overall matrix with equal observations per cell. I encourage you to play around with the third website I’ve listed above, so you can get used to locating Steiner Systems for yourself.

In the sample experiment I have provided, I show how you can scale 35 images in one experiment, sampling 15 items on each trial. This takes a total of 7 trials to complete. Some items will be paired with others more than once, but the vast majority of pairings are shown only once. Here's what you'll need to change to get this working for yourself:

1) First, you'll need to set up the experiment to display however many items you wish on each trial. You can learn how to do that by using the basic version of this experiment, and the instructions sheet I mention above.

2) You'll need to obtain the Steiner System that you plan to employ. For our experiment, the Steiner System looks like this (below). Each row corresponds to a trial, and each number (placed across columns) points to a particular stimulus item.

1	2	3	8	9	10	15	16	17	22	23	24	29	30	31
1	4	5	8	11	12	15	18	19	22	25	26	29	32	33
1	6	7	8	13	14	15	20	21	22	27	28	29	34	35
2	4	6	9	11	13	16	18	20	23	25	27	30	32	34
2	5	7	9	12	14	16	19	21	23	26	28	30	33	35
3	4	7	10	11	14	17	18	21	24	25	28	31	32	35
3	5	6	10	12	13	17	19	20	24	26	27	31	33	34

You'll notice right away that some pairings are shown more than once. For instance, items 2 and 9 are shown together on the fourth series, and also the fifth. We'll try to control for this issue in two ways. One, the order in which the series are presented will be randomized for each subject. And two, for each subject, the "Steiner Index" will be randomly assigned to different stimuli. That way, unequal pairings should even out, given a sufficiently large number of subjects. You don't need to do anything to accomplish these two features. I have built them into the program provided.

4) You need to tell the experiment the names of the stimuli you plan to use. You can do this by entering the filenames, widths, and heights of your images into the StimList List object. Use the "FN", "nWidth", and "nHeight" attributes, respectively. You'll notice two other attributes as well. The "strIndex" is basically a shorthand version of your filenames. This is useful for creating less complex data matrices and easier to interpret output (as will become clear below). You can leave that column alone (or add to it if you plan to use more than 35 items). You'll also notice the "nSteinerIndex" column, and that it has "?"s for values. The Steiner Index will be randomly assigned to each item when the experiment runs, to ensure randomized sampling across subjects. You do not need to enter anything into that column.

4) You need to tell the program how many trials to run. You can do this by setting the Weight parameter of the TrialList List object.

5) You need to input your Steiner System into the SteinerList List object. Make sure there are as many rows (corresponding to trials) as you need. And, you'll need a "C" attribute for each image that will be shown per trial. So if you are showing 15 items per trial, you will need attributes "C1".."C15". If you are showing 10 per trial, you will need "C1".."C10", and so on. Copy the Steiner System you obtained into this list.

6) You will need to set two variables, to tell the algorithms how many stimuli you have, and how many items per trial you are going to run. You can do this by opening the SetupExp Inline object, and adjusting the “nStimuli” and “nItems” variables, respectively. You’ll notice for our purposes that they are set to 35 and 15.

7) You’ll also need to ensure that, on each trial, the appropriate Steiner Index numbers are retrieved. You’ll see that I use a temporary array called “nTemp”, and that it pulls values from the “C” attributes. As such, I place the value of the C1 attribute in the first slot of the array with the following code:

- `nTemp(1) = c.GetAttrib(“C1”)`

You just need to remove lines you aren’t using, or add new ones, depending on how many items you display per trial. So, if you are using only 10 items per trial, remove the last 5 lines from that code. If you are using 20 items per trial, add another five, simply increasing by 1 the slot in the array, and the C value. For instance:

- `nTemp(16) = c.GetAttrib(“C16”)`

That’s pretty much it. You’re ready to collect data. See below for instructions on how to extract and utilize the obtained data!

The data file (EDat):

When the experiment is over, you will have an EDat file, just like any other E-Prime experiment. The Edat file will have 1 line of code for every possible pairwise combination, and the Trial attribute will log which trial each comparison was obtained from. So, in the sample data file provided, there are 7 trials. Each trial has 105 rows, corresponding to each of the 105 pairwise ratings (i.e., Euclidean distances) that are obtained therein. Thus, there are a total of 736 rows (735 pairwise ratings, plus one row with null values, from the SetupExp procedure). Here are the attributes you should pay attention to.

- 1) “Comp1” and “Comp2”: are the filenames of the images that are being considered, per pairwise comparison.
- 2) “Comp1_X”, “Comp1_Y” (same for Comp2): logs the final X/Y coordinates for that image, on any given trial.
- 3) “Distance”: logs the Euclidean distance between the two items being compared, measured in pixels.
- 4) “Index1”, “Index2”: A shortened marker for each image. For instance “F_1”, corresponds to the first image you placed in the StimList object. You can use the “Comp” variables or these

ones for data output; it makes no difference. These are simply a convenience for if you have particularly long filenames.

5) “Steiner1”, “Steiner2”: These are the randomly generated Steiner indexes. The information is NOT particularly informative, as it will be different for each subject. The “F” indexes, however, will remain constant across subjects.

What to do after the experiment:

1) To create the data matrices, you can use the Multidimensional Scaling Matrix Concatenation Excel workbook included in the attached ZIP file, and posted elsewhere on this website. You will need to set the security settings of Excel to allow macros. You can do this via the Windows drop down, Excel Options, Trust Center, Trust Center Settings, Macro Settings... set it to Enable All Macros.

2) To use the sheet, simply copy the Comp1 and Comp2 (or Index1 and Index2; whatever is your preference), and Distance columns of the Edat file into the appropriate locations in the Excel sheet. You can do this with a single subject. Or, you can merge all your Edat files and copy them en masse into the Excel sheet. I encourage you to do this with each individual subject. Although it is more labor-intensive, it has the added advantage of resulting in individual data matrices to which individual differences scaling (e.g., INDSCAL) can be applied. If you concatenate your data across subjects, this will not be possible.

3) Set the properties on the left of the sheet according to your needs. StartRow and StartCol will designate where your data is stored. Then set the number of stimuli you are using. You will also need to tell the sheet the names of your stimuli, by placing them in the “Stimuli” column.

4) Once the data is entered, simply hit the ConcatenateMatrices button on the left side of the sheet, and voila. You can see your matrices being created from the data. There will be three matrices created every time you run the macros. The top-most matrix contains the summed proximities per observation. The middle matrix tells you how many observations there were, per cell. And the bottom-most matrix contains the averaged proximities. This is the matrix that you will copy directly into statistical software packages. The other two are merely for reference.

A few things to pay attention to:

1) Take note of cells that are highlighted in yellow. Those indicate missing data. If your Steiner System was set up appropriately, you will have no yellow cells, other than those on the diagonal of the matrix.

2) The middle matrix is a useful tool for assessing the overall frequency in which observations were recorded. As I mention above, I recommend creating new matrices for each subject, rather than merging all of your subject’s data, and concatenating into a single matrix. The exception is that, if you are concerned about unequal observations, you can merge all of your data, put it into

these macros, and then assess the middle matrix. That will tell you how often each pairwise comparison was made across subjects, therefore giving you an idea of how equal/unequal the sampling ended up.

3) The middle matrix is also a useful tool for quickly figuring out how many times, on average, each pairwise comparison is made per subject. For instance, in the sample I've included (the "Sample_OneSubject" tab of the Excel workbook), you can highlight all the values from the middle matrix. The bottom bar of Excel will tell you the sum of those values, and the average. The sum is 735, which is the total number of pairwise comparisons that were made for a single subject. The average is 1.24. That means that on average, each comparison is made a little more than one time, per subject.

4) Each time you use the macro, make sure to delete the columns containing the old matrices (or just make a copy of the tab and start fresh). The reason for this is that if you try to copy over, it will incorporate values from the prior run and will make your values inaccurate.

Disclaimer

I feel as if I should give a disclaimer here. The software, as it is free, is just my way of giving back to the Psychology community. I cannot assume liability for any problems that a user encounters with the E-Prime files, Excel sheets, etc. I imagine this is assumed from the outset (and I anticipate no problems whatsoever), but of course, I need to cover myself.

Finally, please note that there is always a possibility of bugs, etc. If you have any problems with the software, or if you are having difficulty adjusting it to your future needs, please feel free to contact me. I am quite willing to help anyone get the most out of this software. I hope you find it useful and fun. I also encourage you to visit my website periodically; I will have additional software and macros posted in the future, on the Software page of my site.

Thanks for your interest in this software, and please feel free to let me know how it works for you! I'm very curious to hear how well it works for other researchers, and what kind of purposes it is being used for.

-Mike

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