Manual: SynMap Toolbox for R

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1   Introduction

This is a brief manual on how to use the the functions and scripts provided in the *synMap toolbox for R*
analysis using R. This is a tiny package of scripts and functions for easy analysis of data from *synMap*. The
functions are freely available for re-use and modification by anyone. The software comes with no warranty.

The *synMap* online tool for mapping graphemes to colors in grapheme-color synesthesia is available here:
https://synmap.azurewebsites.net

Note that the instructions are based on data file naming conventions from our own lab. These are simple:
we prefix our data files with `log_ID_`, e.g. `log_ID_subject999.txt`. If you follow this convention, the
instructions should work without modification. If you prefer your own naming scheme, plese edit the
`create_syn_profile_webdata.R` script, so that the inclusion pattern matches the scheme. Below is the line
of code you must change, if you use a different naming scheme. This line of code is found near the top of the
'create_syn_profile_webdata.R' script:

```
allfiles = dir(pattern = 'log_ID_') # <---- change 'log_ID_' to a pattern you prefer
```

Example code, modified to match files with the prefix `my_syn_data_`, rather than `log_ID_`.

```
allfiles = dir(pattern = 'my_syn_data_') #collect only 'my_syn_data_' files into a vector
```

2   Install R

Skip this step if you have a working version of R on your computer.

If you have not yet installed R on your computer, you can download it from here: https://cran.r-project.org.
Follow the installation instructions that match your operating system.

From here, it is wise to intall **Rstudio** to get a nicer user interface https://rstudio.com. If the interface
becomes relevant in this manual, the author will assume that the user is using **Rstudio**.

3 Analyze and visualize the grapheme-color mappings of synesthetes using the `create_syn_profile` script in 8 simple steps.

The `create_syn_profile` script uses all the functions in syn_functions to return: 1) a visualization of grapheme-color associations and their strength and 2) a file with the consistency measures for all graphemes and detailed color information. The visualization gives a quick overview of a synesthete's grapheme-color associations, helps identify incorrect (accidental) color-mappings. The visualization is also very useful for comparing the quality of synesthesia over time.

3.1 Set the working directory

To get started you must first set the working directory to the folder that contains the `create_syn_profile.R` script, and the `syn_functions.R file`. To do this, you type:

setwd('[your target directory]')

into the Console window, where `[target directory]` is the path to the directory containing your script. You can make sure that you have reached the correct destination by typing `dir()` in the Console. This gives you a list of all files and folders in the working directory. Example:

```
dir()
```

```
##  [1] "~$nual_draft.docx"        "colconst_example.MHT"
##  [3] "colconst_example.png"     "create_syn_profile_webdata.R"
##  [5] "dir_prompt.PNG"           "git_check.R"
##  [7] "manual.pdf"               "manual.Rmd"
##  [9] "manual_draft.docx"        "pilot_mini_toobox_edit.Rproj"
## [11] "profile_example.PNG"      "syn_functions_webdata.R"
## [13] "tex2pdf.16024"            "tex2pdf.469688"
## [15] "tex2pdf.518668"           "tex2pdf.590388"
```

3.2 Run the `create_syn_profile_webdata` script

To do a standard analysis of grapheme-color mappings, you run the command: `source('create_syn_profile_webdata')` in the R Console.

3.3 Select the data file directory

The script can analyze data from multiple data files in a single run. Therefore, you start by selecting the directory where you keep all your data files. You will get a chance to select a subset of these files in a later step. A window appears, where you can browse you way to the desired directory.

3.4 Select all data files or a subset

When you have chosen an appropriate folder, a list of data files will be printed in the console window. You are now prompted (in the Console) to confirm that you want to analyze all data files, or a subset. You type `n` and press return, to analyze all files, but `y` if you want to select a subset of these files.

If opt for a subset, you will be prompted to type the index numbers of the desired files. Please separate these numbers by space.

Finally, you will see a list of selected files in the console, and will be asked confirm that the files.

Grapheme	diffScore	hex1	hex2	hex3	hexAvg	R1	G1	B1	R2	G2	B2	R3	G3	B3	R_avg	G_avg	B_avg
0	0.266667	FF0026	FF0015	FF0004	FF0015	255	0	38	255	0	21	255	0	4	255	0	21
1	0.627451	54DAFF	12E7FF	17E8FF	2AE3FF	84	218	255	18	231	255	23	232	255	42	227	255
2	1.121569	FF54B8	FF29FB	FF08E2	FF2CDC	255	84	184	255	41	251	255	8	226	255	44	220
3	5.427451	FF0F23	304CFF	17FF36	6D7373	255	15	35	48	76	255	23	255	54	109	115	115
4	0.376471	FF141C	FF0D00	FF0015	FF0B10	255	20	28	255	13	0	255	0	21	255	11	16
5	4.384314	FF1100	2945FF	0C08FF	671FAA	255	17	0	41	69	255	12	8	255	103	31	170
6	0.454902	1605FF	242FFF	2605FF	2013FF	22	5	255	36	47	255	38	5	255	32	19	255
7	3.694118	34FF30	450DFF	4508FF	3F5CBA	52	255	48	69	13	255	69	8	255	63	92	186
8	5.898039	FF9500	00FF00	9A0DFF	888B55	255	149	0	0	255	0	154	13	255	136	139	85
9	0.650980	D61FFF	9A17FF	AD08FF	B415FF	214	31	255	154	23	255	173	8	255	180	21	255
A	0.713725	FFFF5E	FFDE24	FFDF2B	FFE93A	255	255	94	255	222	36	255	223	43	255	233	58

Figure 1: Example of a Consistency and Color output file in Notepad++

3.5 Select the output

In this step, you select the desired output of the analysis.

3.6 Consistency and color information output file

First, you will be asked whether you want a .txt file wih consistency scores (Eagleman et al, 2007, Equations 1 and 2), as well as color information. The output file will have 18 columns.

Consistency and color information files will be printed in a new folder, within you data folder. The new folder will be named `color-consistency-files`.

3.6.1 Column 1: `Grapheme`

This column displays the graphemes analyzed in your data set.

3.6.2 Column 2: `diffScore`

This column displays the consistency scores.

3.6.3 Column 3-5: `hex1-3`

These columns display the hex color codes for trials 1, 2 and 3, for each grapheme.

3.6.4 Column 6: `hexAvg`

This column displays the averaged hex color code for all 3 trials.

3.6.5 Columns 7-15: `R G B`

These columns display the R, G and B values for trials 1, 2 and 3, for each grapheme.

3.6.6 Columns: 16-19: `R_avg G_avg B_avg`

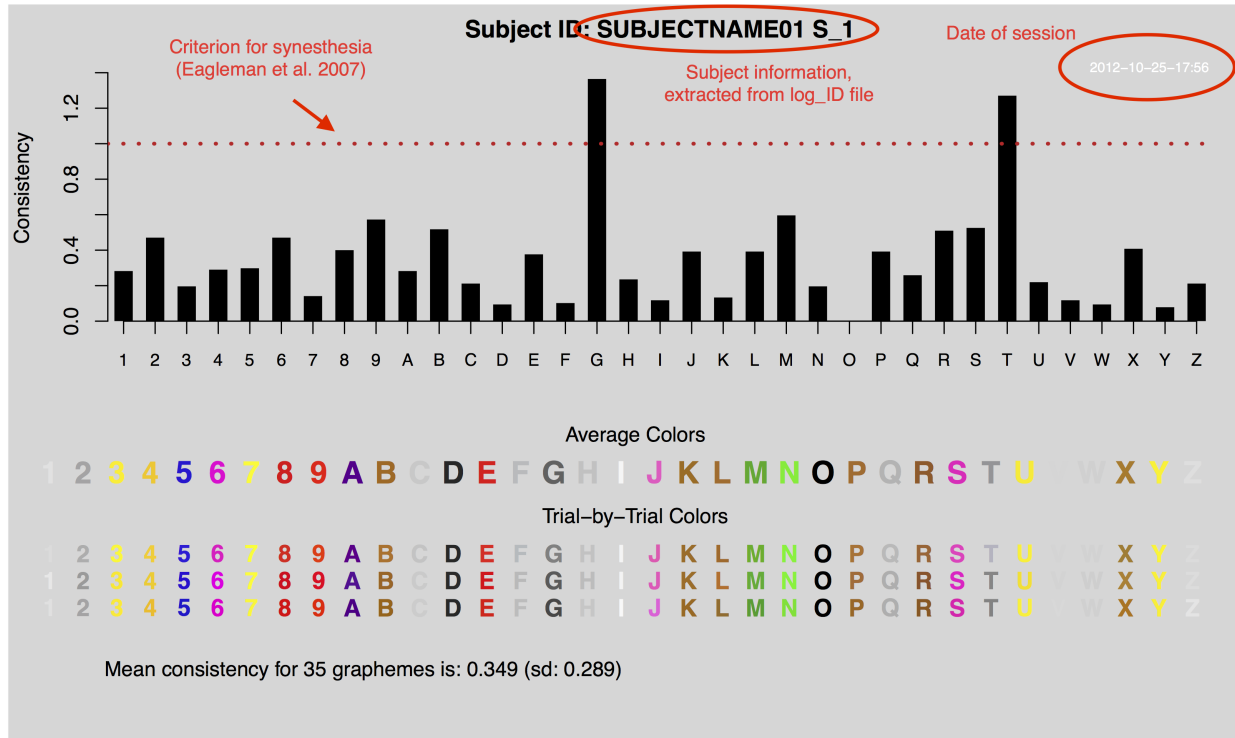These columns display the average R, G and B values for all 3 trials.

Figure 2: Example of a synesthesia profile visualization

3.7 A PDF of consistency scores, and visualized color information.

Second, you will asked whether you want your plots to be printed as .pdf files. If you select **n**, the visualized synesthesia profile of participants will only be displayed in the plot window of R. If you select **y**, PDFs will be rendered in your data folder.