HOW TO RUN CANLAB 2ND LEVEL ANALYSIS TEMPLATE SCRIPTS

walkthrough by Marianne Reddan, 2017 code & videos by tor, 2017

This document (editable version, may be updated):

https://docs.google.com/document/d/1bGpiXUyxxzu6aG0zAU4x8ELNy3bdUMogW TiuoDaH0s/edit?ts=591b73b7#

Videos (see below):

On Youtube and CANIab slack

Example HTML output from these scripts:

https://www.dropbox.com/s/rt8xzf6yq4h0h6e/Example CANIab second level html output.zip?dl=0

What you will need to run:

CANIab core tools, SPM (e.g., SPM12), CANIab second-level analysis scripts For "signature"-based analysis: CANIab signatures (e.g., NPS); some private

If you are sharing data with CANlab, here is a post with details:

https://slack-files.com/T09S4HMUL-F1866CCER-6f7a17803b

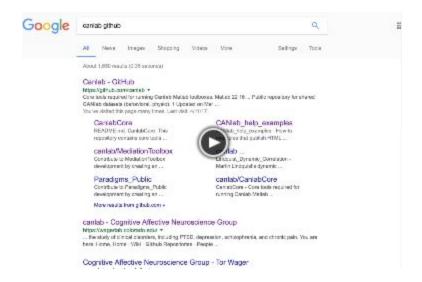
If you are applying the NPS and other "signatures" here are two posts about how to do it, and some notes about image scaling across studies:

https://slack-files.com/T09S4HMUL-F17M8PFS7-09e72ec85b https://slack-files.com/T09S4HMUL-F1J0TF0H5-2885e964cc

1. INSTALL THE CANIAD_help_examples FOLDER FROM GITHUB

Found here https://github.com/canlab

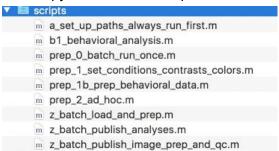
This video provides further instruction.



2. SET UP YOUR DATA ANALYSIS FOLDER

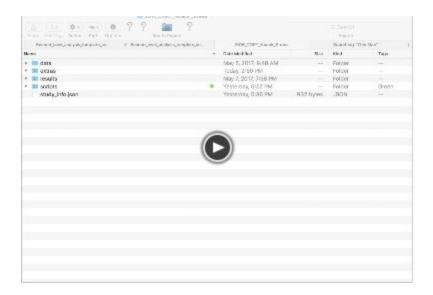
In your **Analysis** folder set up these subfolders:

- data
- extras
- results
- scripts
 - Here copy in a series of scripts from CANLab_help_examples



Copy over to your Analysis folder 'study_info.json'

This video provides further instruction.

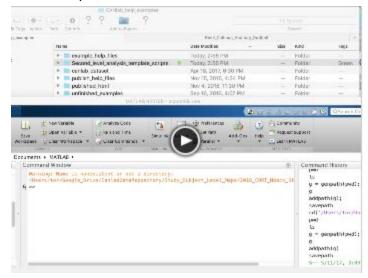


3. ADD ALL THE FOLDERS TO PATH

In MATLAB

- genpath(addpath('/CANLab_help_examples/'))
- genpath(addpath('/YOUR_ANALYSIS_FOLDER/'))

This video provides further instruction.

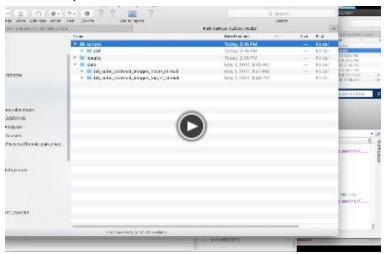


4. MODIFY THE TEMPLATE SCRIPTS

 In a text editor, edit the **study_info.json** file to fit your data For example:

```
"Primary_publication":
"Fill in this JSON-format file and call it study_info.json, in your main study folder. This field would contain the primary publication associated with the study, if any, or null if none.",
6 7 8 9 10 11 12 13 14 15 16 17 18 19 20 21 22 23 24 25 6 27 28 29 31 32 33 34 35 36 37 38 39 40
       "Associated publications":
       "Other publications here. e.g.,
Reddan MC, Wager TD, Schiller D. Imagined Extinction Reduces Learned Threat in Brain and Body. (submitted)",
       "Notes":
"This dataset was shared by Daniela Schiller for Marianne Reddan to analyze the effects of imagined extinction",
       "Publication_URLs": null,
       "Publication_DOIs": null,
       "Paradigm_files_links": null,
       "Data_files_links": null,
       "IRB_number": null,
       "Scanner_site": "New York University",
       "Field_strength": "3.0T",
      "Citing_this_work":
"If you use this dataset in a publication,
please include as authors or acknowledge individuals as specified below.
Please also see information on publications and grants to cite.",
       "Authors_to_include_on_reuse": null,
       "Authors_to_acknowledge_on_reuse": "Tor Wager, Daniela Schiller, Marianne Reddan",
       "Grant_numbers_to_cite": null
```

This video provides further instruction.



- Next, in MATLAB open a_set_up_paths_always_run_first.m and change:
 - a. basedir to the filepath of your analysis folder
- 3. Next, open up **prep_1_set_conditions_constrasts_colors.m** and change the paths and wildcards referring to the contrast images in your data folder:
 - a. Update the conditions to reflect how *your* data are set up
 - i. DAT.subfolders
 - ii. DAT.conditions
 - iii. DAT.structural_wildcard

```
% /Users/maus/Desktop/2017_AuditoryThreatConditioning/data/subj_contrasts/IE101NC/con_0001.hdr
fprintf('Image data should be in /data folder\n');

DAT = struct();
% Names of subfolders in /data
DAT.subfolders = {'subj_contrasts'};
% Names of conditions
DAT.conditions = {'CSp' 'CSm'};

DAT.conditions = format_strings_for_legend(DAT.conditions);

DAT.structural_wildcard = {};
DAT.functional_wildcard = {'IE*/con_0001.img' 'IE*/con_0002.img'};
```

- b. Update the contrasts to reflect what contrasts you are interested in
 - DAT.contrasts
 - ii. DAT.contrastnames

```
% Set Contrasts
% ------
% Vectors across conditions
DAT.contrasts = [1 -1];

DAT.contrastnames = {'CSp_vs_CSm'};

DAT.contrastnames = format_strings_for_legend(DAT.contrastnames);
```

- c. Update the *colors* or leave to default
- d. Update *between-condition contrasts* if you have more than one subject group. If you only one group leave it empty.

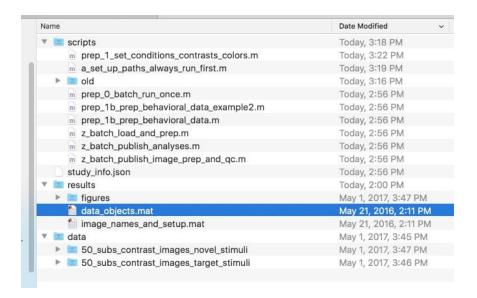
```
% Set BETWEEN-CONDITION contrasts, names, and colors
% ------
% Currently used in c2c_SVM_between_condition_contrasts
%
% Matrix of [n contrasts x k conditions]

DAT.between_condition_cons = [];

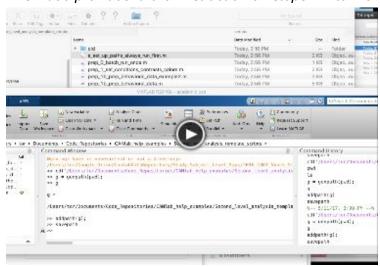
DAT.between_condition_contrastnames = {};

DAT.between_condition_contrastcolors = custom_colors ([.2 .2 .8], [.2 .8 .2], si
```

- 4. Save & run your a_set_up_paths_always_run_first.m and prep_1_set_conditions_constrasts_colors.m in MATLAB
- 5. Run prep_2, 3, and 4
- 6. It will be saved here in data_objects.mat



This video provides further instruction on steps 4.2 to 4.6.



4. RUN THE BATCH AND PUBLISH

1. There are multiple options for what to run. Try z_batch_publish_analyses.m

And you are set. If you have issues with your file structure check out the <u>youtube channel</u> to learn more ways to use the wildcards.