
HOW TO RUN CANLAB 2ND LEVEL ANALYSIS TEMPLATE SCRIPTS

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code & videos by tor, 2017

This document (editable version, may be updated) :

https://docs.google.com/document/d/1bGpiXUyxxzu6aG0zAU4x8ELNy3bdUMogW_TiuoDaH0s/edit?ts=591b73b7#

GENERAL INFORMATION

Videos (see below):

On Youtube [note: youtube video audio not working] and CANlab slack
Or on [Drive](#)

Example HTML output from these scripts:

https://www.dropbox.com/s/rt8xf6yq4h0h6e/Example_CANlab_second_level_html_output.zip?dl=0

What you will need to run:

1. CANlab core tools <https://github.com/canlab/CanlabCore>
2. SPM (e.g., SPM12)
3. CANlab second-level analysis scripts https://github.com/canlab/CANlab_help_examples
4. For “signature”-based analysis: CANlab 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>

To do: add instructions on the behavioral data

1. INSTALL THE CANlab_help_examples FOLDER FROM GITHUB

Found here <https://github.com/canlab>

This video provides further instruction.

3. SET UP YOUR DATA ANALYSIS FOLDER

Are your data set up so that the folders represent conditions and inside those folders are subject data? If not, maybe this bash reorganization [script](#) will help you. Alternatively you can change the way the 2nd Level Scripts look at your folders. However, I recommend you keep their inherent structure the same and just conform. Path of least resistance. Do not apply this advice to your social life.

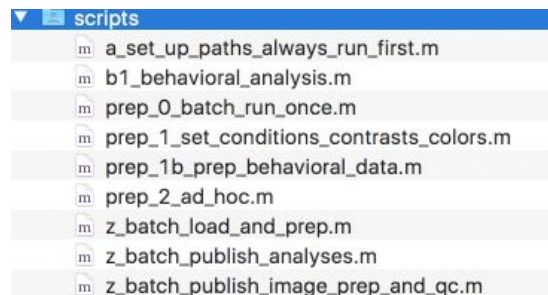
STEP A - SET UP NEW FOLDERS

There is a script you can use which will auto set up your folders to play well with the 2nd level analysis pipeline. Go to your new **Analysis** folder and run this from within it:

- `a_set_up_new_analysis_folder_and_script.m`

If you want to do this by hand you can go to your **Analysis** folder set up these subfolders:

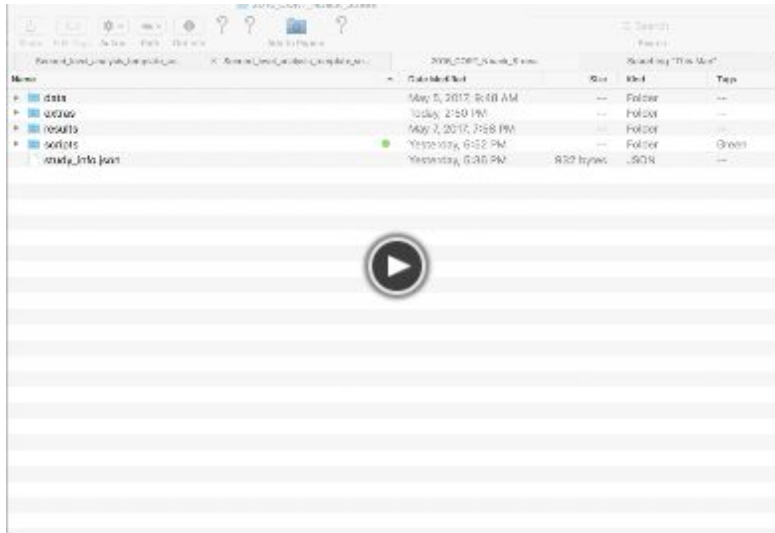
- data
- extras
- results
- scripts
 - Here copy in a series of scripts from CANLab_help_examples



STEP B - SET UP THE STUDY INFO DOCUMENT

- Copy over to your **Analysis** folder 'study_info.json'

This video provides further instruction.



4. MODIFY THE TEMPLATE SCRIPTS

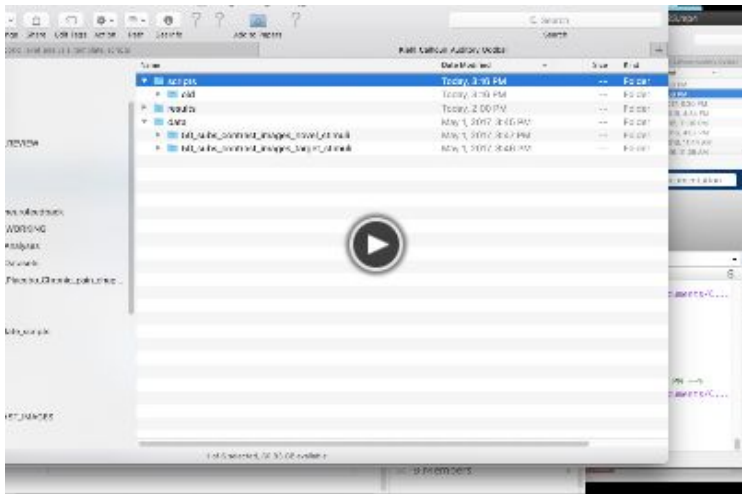
1. In a text editor, edit the **study_info.json** file to fit your data

For example:

```

1  {
2    "Primary_publication":
3    "Fill in this JSON-format file and call it study_info.json, in your main
4    study folder. This field would contain the primary publication associated
5    with the study, if any, or null if none.",
6
7    "Associated_publications":
8    "Other publications here. e.g.,
9    Reddan MC, Wager TD, Schiller D. Imagined Extinction Reduces Learned Threat in Brain and Body. (submitted)",
10
11   "Notes":
12   "This dataset was shared by Daniela Schiller for Marianne Reddan to analyze the effects of imagined extinction",
13
14   "Publication_URLs": null,
15
16   "Publication_DOIs": null,
17
18   "Paradigm_files_links": null,
19
20   "Data_files_links": null,
21
22   "IRB_number": null,
23
24   "Scanner_site": "New York University",
25
26   "Field_strength": "3.0T",
27
28   "Citing_this_work":
29   "If you use this dataset in a publication,
30   please include as authors or acknowledge individuals as specified below.
31   Please also see information on publications and grants to cite.",
32
33   "Authors_to_include_on_reuse": null,
34
35   "Authors_to_acknowledge_on_reuse": "Tor Wager, Daniela Schiller, Marianne Reddan",
36
37   "Grant_numbers_to_cite": null
38
39
40 }
```

This video provides further instruction.



2. 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_contrasts_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
 - i. 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 = [];

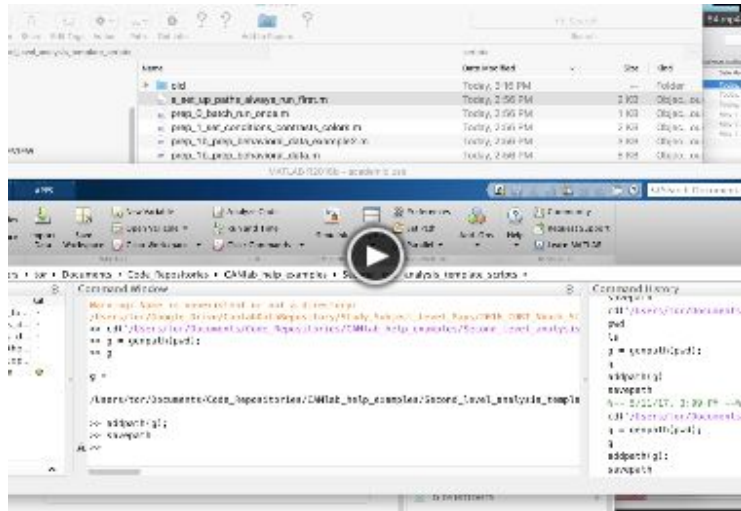
DAT.between_condition_contrastnames = {};

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_contrasts_colors.m** in MATLAB
5. Run prep_2, 3, and 4
6. It will be saved here in **data_objects.mat**

Name	Date Modified
▼ scripts	Today, 3:18 PM
m prep_1_set_conditions_contrasts_colors.m	Today, 3:22 PM
m a_set_up_paths_always_run_first.m	Today, 3:19 PM
▶ old	Today, 3:16 PM
m prep_0_batch_run_once.m	Today, 2:56 PM
m prep_1b_prep_behavioral_data_example2.m	Today, 2:56 PM
m prep_1b_prep_behavioral_data.m	Today, 2:56 PM
m z_batch_load_and_prep.m	Today, 2:56 PM
m z_batch_publish_analyses.m	Today, 2:56 PM
m z_batch_publish_image_prep_and_qc.m	Today, 2:56 PM
study_info.json	Today, 2:56 PM
▼ results	Today, 2:00 PM
▶ figures	May 1, 2017, 3:47 PM
data_objects.mat	May 21, 2016, 2:11 PM
image_names_and_setup.mat	May 21, 2016, 2:11 PM
▼ data	May 1, 2017, 3:45 PM
▶ 50_subs_contrast_images_novel_stimuli	May 1, 2017, 3:47 PM
▶ 50_subs_contrast_images_target_stimuli	May 1, 2017, 3:46 PM

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 [youtube channel](#) to learn more ways to use the wildcards.

MORE

Look through the folder:

CANlab_help_examples/Second_level_analysis_template_scripts/**core_scripts_to_run_without_modifying**

There you can run specific additional analyses, like lasso-pcr or the buckner parcellations

For example:

5. Run **z_batch_bucknerlab_network_analyses.m**

Or load up the data_objects.mat from your results folder and run some predictions like LASSO-PCR, etc

