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

## GENERAL INFORMATION

Videos (see below):

Example HTML output from these scripts:

What you will need to run:

1. INSTALL THE CANlab\_help\_examples FOLDER FROM GITHUB

2. ADD ALL THE FOLDERS TO PATH

3. SET UP YOUR DATA ANALYSIS FOLDER

STEP A - SET UP NEW FOLDERS

STEP B - SET UP THE STUDY INFO DOCUMENT

4. MODIFY THE TEMPLATE SCRIPTS

4. RUN THE BATCH AND PUBLISH

MORE

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## 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/rt8xzf6yq4h0h6e/Example\\_CANlab\\_second\\_level\\_html\\_output.zip?dl=0](https://www.dropbox.com/s/rt8xzf6yq4h0h6e/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](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>

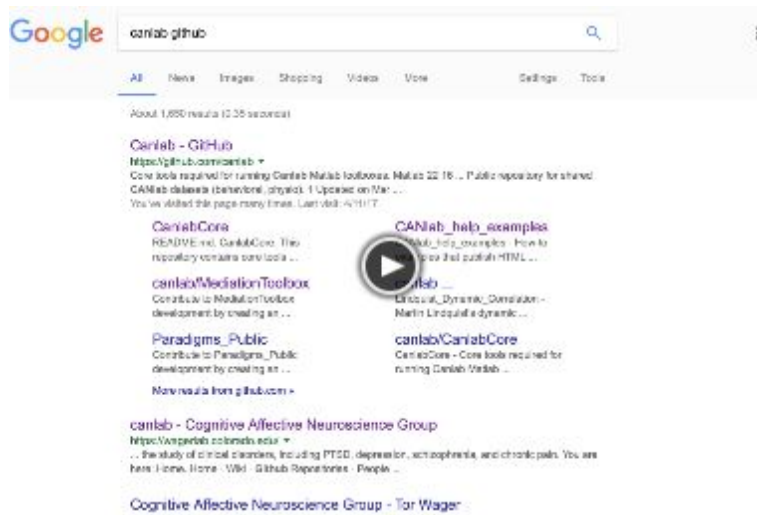
<https://slack-files.com/T09S4HMUL-F1J0TF0H5-2885e964cc>

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.

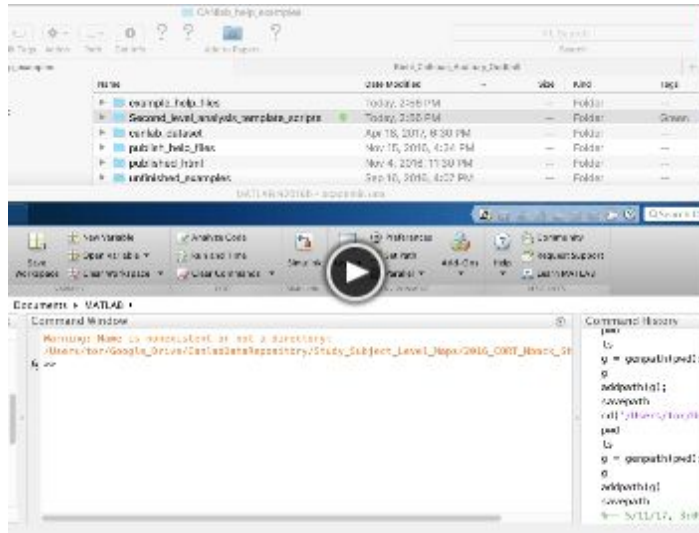


## 2. ADD ALL THE FOLDERS TO PATH

In MATLAB

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

*This video provides further instruction.*



Check and make sure you have all the paths and dependencies before you get started by running this script (found in CANLab\_help\_examples):

- `run('/CANlab_help_examples/Second_level_analysis_template_scripts/a2_second_level_toolbox_check_dependencies.m')`

You may need files from our [lab's google drive](#) which is \*not\* public. However, these are not necessary for all analyses.

### 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.

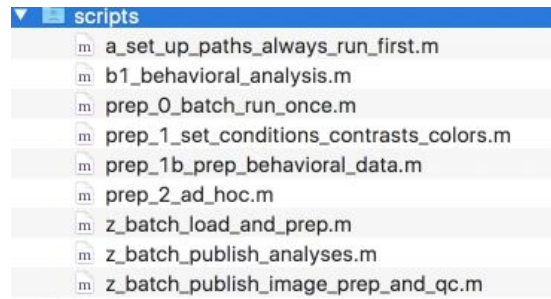
#### **STEP A - SET UP NEW FOLDERS**

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:

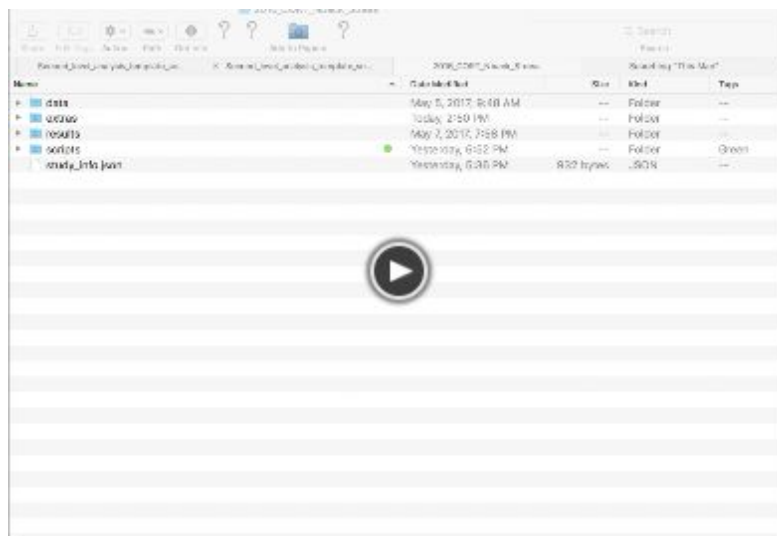
- data
- extras
- results
- scripts
  - Here copy in a series of scripts from CANLab\_help\_examples



## **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**

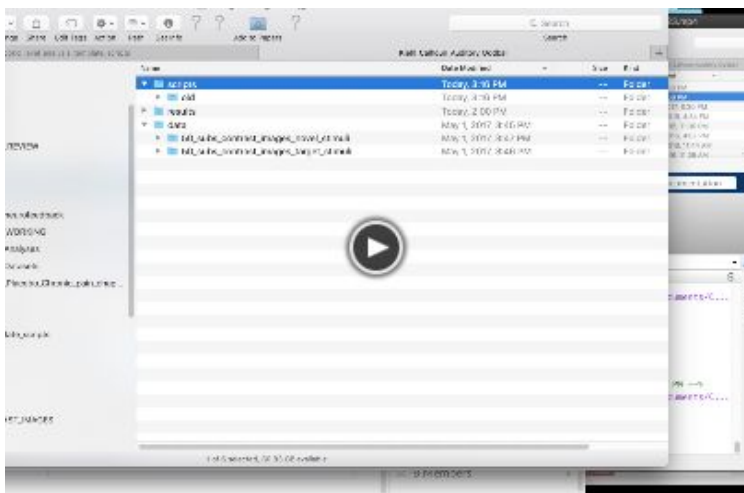
1. In a text editor, edit the **study\_info.json** file to fit your data  
For example:

```

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 = [];

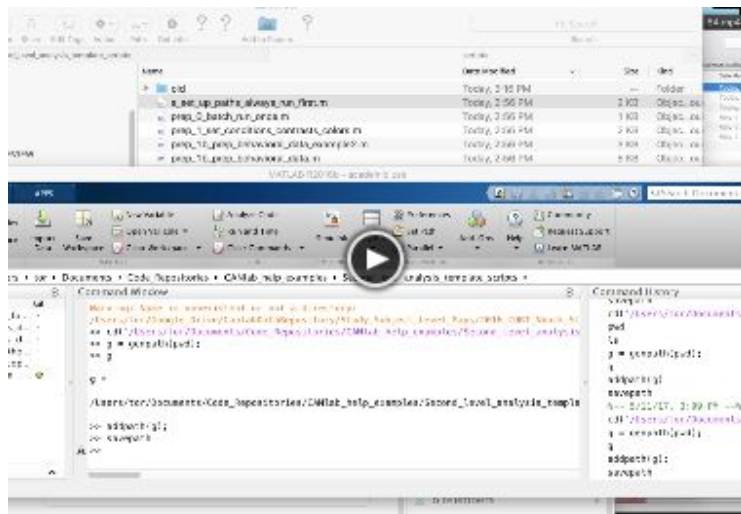
DAT.between_condition_contrastnames = {};

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.

## USER OPTIONS FOR CLASSIFICATION

**c2\_SVM\_contrasts** has user-controlled functionality. Prep script

**prep\_3b\_run\_SVMs\_on\_contrasts\_and\_save** runs SVMs and saves results.

**c2\_SVM\_contrasts** reloads them from the saved mat files and displays results.

You can copy this script **a2\_set\_default\_options** to your analysis/scripts folder and change the following options:

- Bootstrapping -- Default OFF
- Save the stats maps -- Default ON

Those options will be called by the classification analysis scripts.

## 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





