**This document** (editable version, may be updated) :
**https://tinyurl.com/y9r98ozw**

# CANLAB 2ND LEVEL ANALYSIS SCRIPTS: WHAT THEY ARE AND WHAT THEY DO

This is a set of scripts that is designed to facilitate second-level analysis across beta (COPE), or contrast images from a group of participants. The idea is to have a standardized set of scripts that extract and process data in the same way across studies, which (a) increases readability and understanding of the data structure, (b) decreases the need to re-write custom code to perform the same analyses over and over, and (c) facilitates analysis of defined measures across studies. The CANlab scripts are also designed to be easily customizable, so you can add study-specific analyses to your workflow by adding short, modular scripts with few lines of code.

The workflow does several things, saving data and output in standardized formats, and creating time-stamped HTML reports with plots, tables, images, and stats in one document so you have an archival record of the whole analysis. This also facilitates writing papers and sharing data and results with others. The two main stages are:

**Data preparation:**
- Load data from image files and meta-data spreadsheet(s), create and save data structures
- Image data outlier analysis and scaling (use is optional in analyses)
- Extraction of global gray, white, and CSF components (assumes MNI space)
- Image data quality control metrics; HTML report
- Extract pre-defined “signatures”, data from standard pre-defined networks and brain parcels
- Bootstrapping of support vector machine analyses for contrasts (optional)
- Save all results in standardized data structures

**Analysis workflows:**
- Load saved data structures, run sequences of short, customizable modular scripts
- “Coverage and contrasts”: Voxel-wise brain maps for all contrasts, whole-brain support vector machine classifiers
- “Signature analyses”: Expression of CANlab pre-defined signatures, e.g., NPS (requires private repository with signatures)
- Create your own: Network polar plots, meta-analysis masks, parcels, etc.

# HOW TO RUN CANLAB 2ND LEVEL ANALYSIS TEMPLATE SCRIPTS

walkthrough by Marianne Reddan, 2017

code & videos by tor, 2017



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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

### 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

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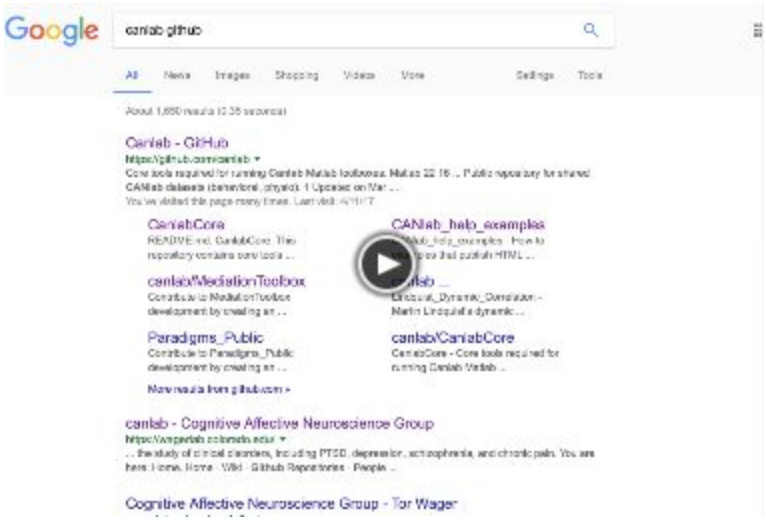
# 1. INSTALL THE CANlab_help_examples FOLDER FROM GITHUB

Found here https://github.com/canlab

This video provides further instruction.

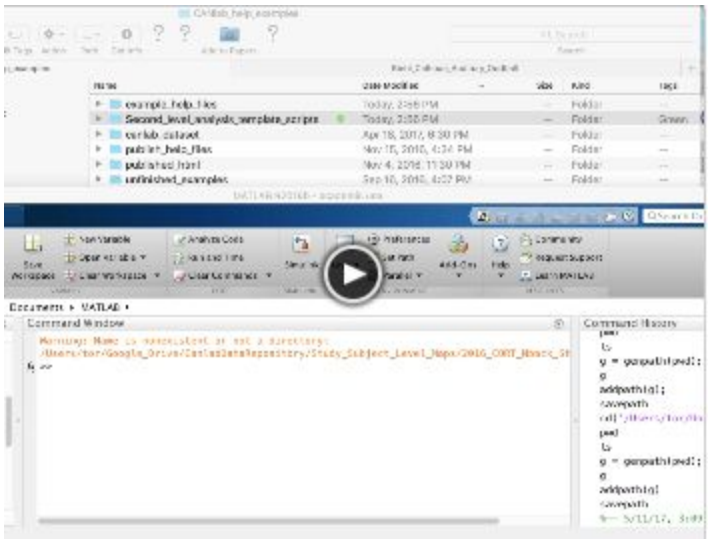



# 2. ADD ALL THE FOLDERS TO PATH

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.

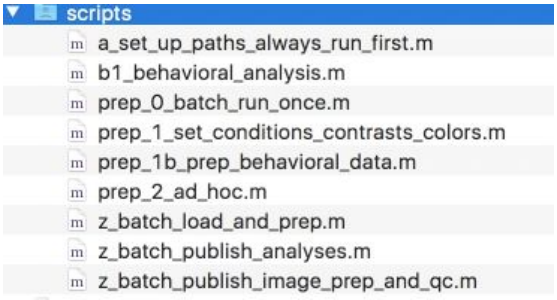
### STEP A - SET UP NEW FOLDERS

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:

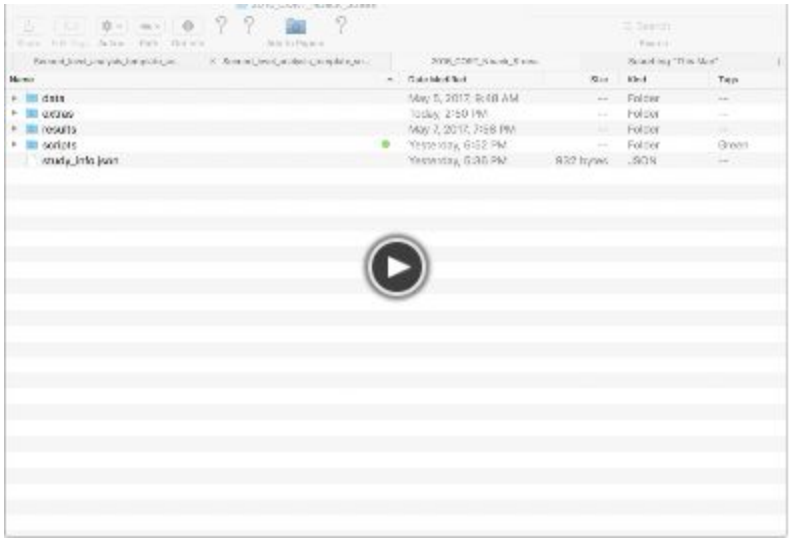
- data
- extras
- results
- scripts
    - Here copy in a series of scripts from CANLab_help_examples




### STEP B - SET UP THE STUDY INFO DOCUMENT

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

*This video provides further instruction.*

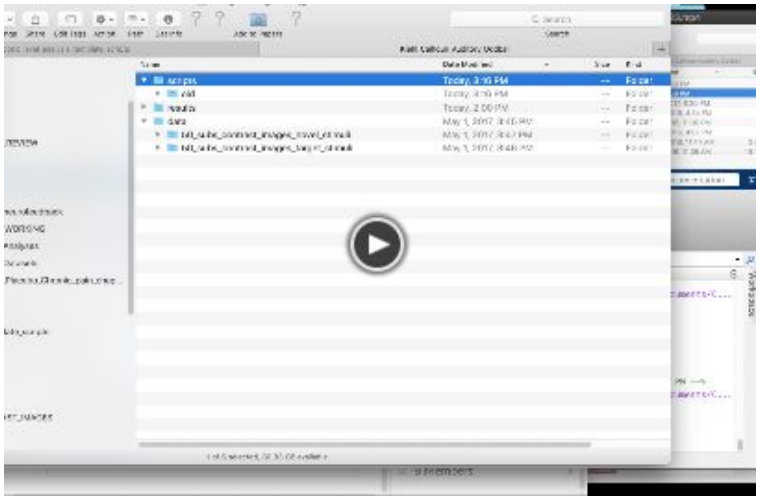


# 4. MODIFY THE TEMPLATE SCRIPTS

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

```
{
"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.",

"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.*



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_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'};
```

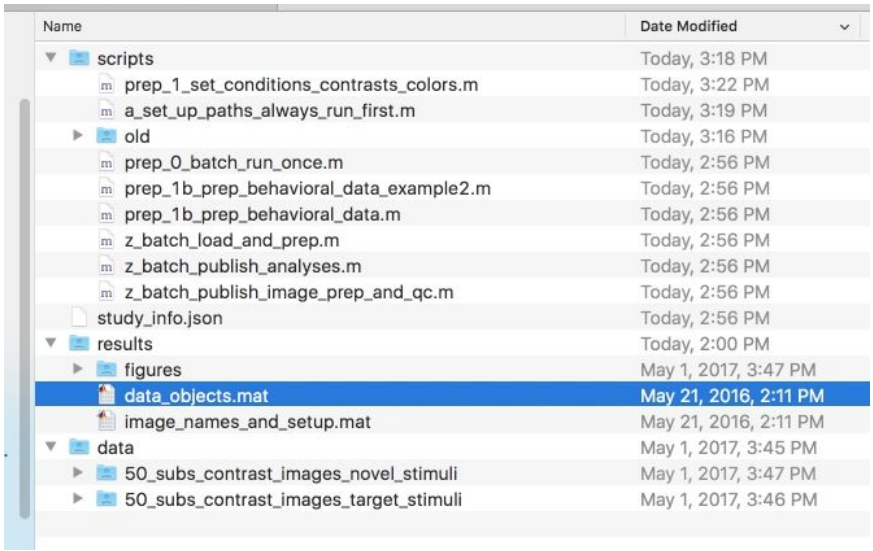
    b. Update the *contrasts* to reflect what contrasts you are interested in
        i. DAT.contrasts
        ii. DAT.contrastnames

```
% Set Contrasts
% ------------------------------------------------------------------------

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

DAT.contrastnames = {'CSp_vs_CSm'};

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

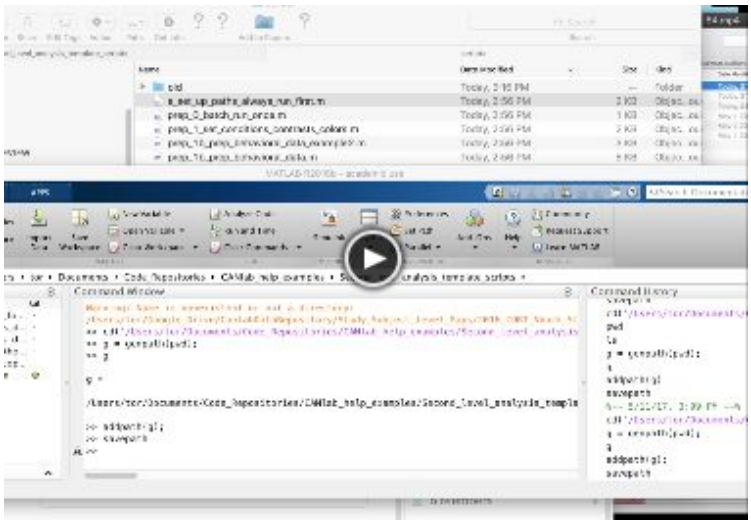
c. Update the *colors* or leave to default
d. Update *between-condition contrasts* if you have more than one subject group. If you only one group - leave it empty.

```
% 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_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 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