\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_

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#>

[GENERAL INFORMATION](#_tskv90lun358)

[Videos (see below):](#_40u6r6sicaxx)

[Example HTML output from these scripts:](#_qt2nldgkra6f)

[What you will need to run:](#_oxgrko1ktczt)

[1. INSTALL THE CANlab\_help\_examples FOLDER FROM GITHUB](#_vs9k05w3o2lf)

[2. ADD ALL THE FOLDERS TO PATH](#_72rk6plfk0ho)

[3. SET UP YOUR DATA ANALYSIS FOLDER](#_n2y5cvjtc01n)

[STEP A - SET UP NEW FOLDERS](#_o3kirxdq3syx)

[STEP B - SET UP THE STUDY INFO DOCUMENT](#_ttia5w4im954)

[4. MODIFY THE TEMPLATE SCRIPTS](#_91u6k4b6e14a)

[4. RUN THE BATCH AND PUBLISH](#_rxvyfr84wv25)

[MORE](#_9lwz713avi7o)

\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_

# GENERAL INFORMATION

## 

## Videos (see below):

On Youtube [note: youtube video audio not working] and CANlab slack

Or on [Drive](https://drive.google.com/drive/folders/0B-FyQiYIUnS5MkRIeFU1M1VmYjg?usp=sharing)

## 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>

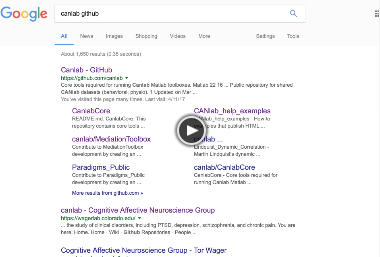
To do: add instructions on the behavioral data

\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_

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

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

This video provides further instruction.

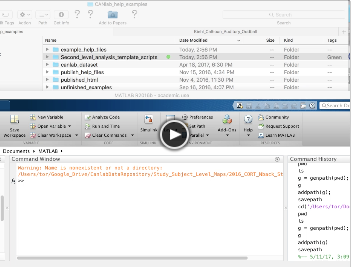


# 2. ADD ALL THE FOLDERS TO PATH

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](https://drive.google.com/open?id=0B_iGd2quo0mAR2k5bWQ5bEpJOTA) 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](https://github.com/mariannnne/Bash-Tools/blob/master/Move_Rename.sh) 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.

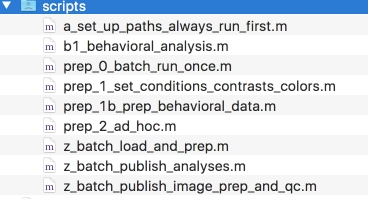
## STEP A - SET UP NEW FOLDERS

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:

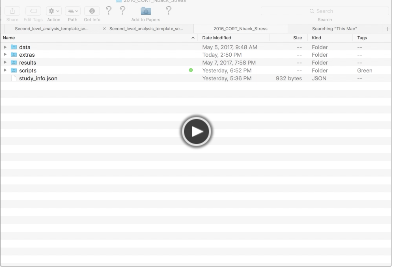
* data
* extras
* results
* scripts
  + Here copy in a series of scripts from CANLab\_help\_examples



## STEP B - SET UP THE STUDY INFO DOCUMENT

* Copy over to your **Analysis** folder ‘study\_info.json’

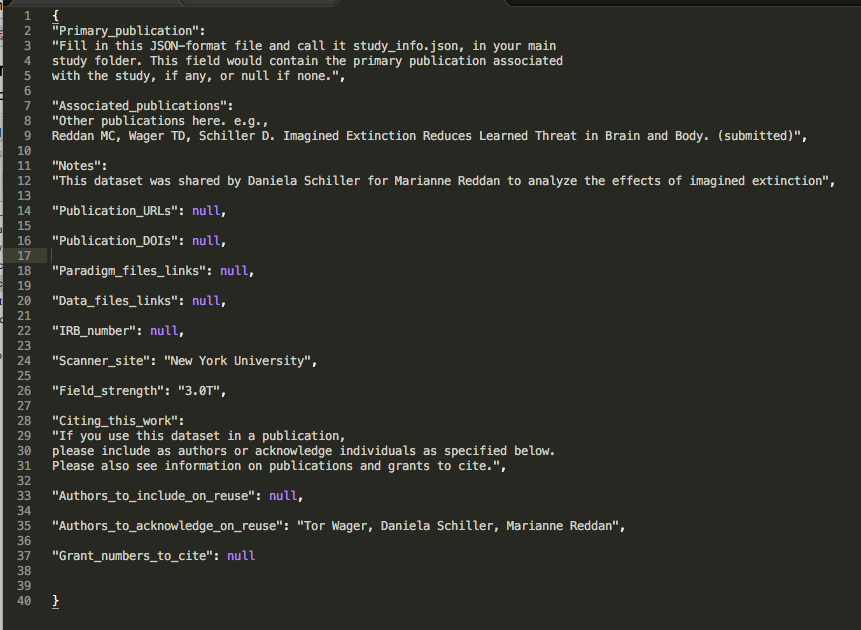
*This video provides further instruction.*

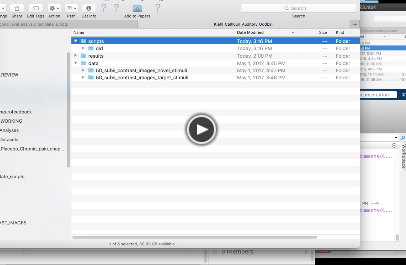


# 4. MODIFY THE TEMPLATE SCRIPTS

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

For example:

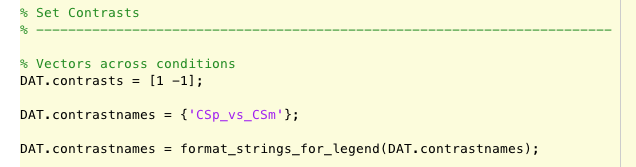


*This video provides further instruction.*

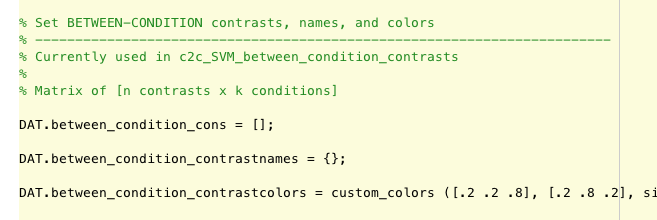
1. Next, in MATLAB open **a\_set\_up\_paths\_always\_run\_first.m** and change:
   1. basedir *to the filepath of your analysis folder*
2. Next, open up **prep\_1\_set\_conditions\_constrasts\_colors.m** and change the paths and wildcards referring to the contrast images in your data folder:
   1. Update the *conditions* to reflect how \*your\* data are set up
      1. DAT.subfolders
      2. DAT.conditions
      3. DAT.structural\_wildcard



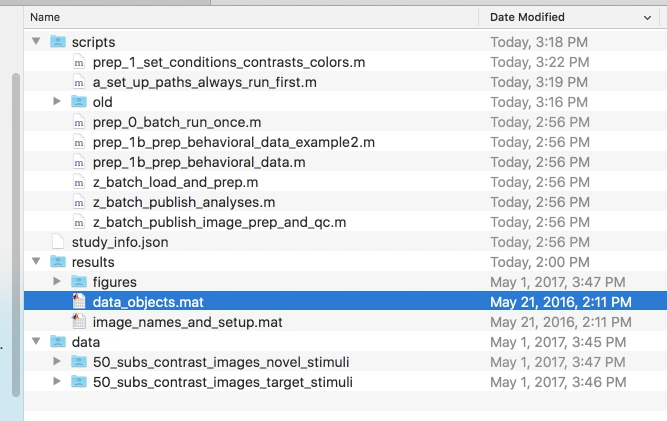
* 1. Update the *contrasts* to reflect what contrasts you are interested in
     1. DAT.contrasts
     2. DAT.contrastnames



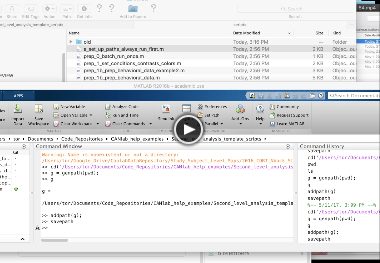
* 1. Update the *colors* or leave to default
  2. Update *between-condition* *contrasts* if you have more than one subject group. If you only one group - leave it empty.



1. Save & run your **a\_set\_up\_paths\_always\_run\_first.m** and **prep\_1\_set\_conditions\_constrasts\_colors.m** in MATLAB
2. Run prep\_2, 3, and 4
3. 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 channe](https://www.youtube.com/channel/UCKlRfGa03PZqu349IiexlNg)l 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