# General Information

* multi-FRAME requires access to the MATLAB packages SPM12 and CoSMoMVPA (both are linked in the Github to download)
* For the longer scripts (estimateModel.m, runMVPAclassification.m, and runRSA.m), it is faster to run through a PBS script
* multi-FRAME does not assume the data are preprocessed. It is currently equipped to preprocess the data through SPM12 or handle data that has been processed through fMRIprep. After preprocessing, the scripts will look for the following files:

*fMRIprep Preprocessed Data:*

Anat file: \*desc-preproc\_T1W.nii.gz

Func files: MNI\*\_bold.nii.gz

* All files are referenced in BIDS naming format:

beh (behavioral)

func (functional)

anat (anatomical

**File Structuree:**

You need a folder structure as seen below for the scripts to work properly. “masks” refers to where you will put your masks prior to analysis. “models” will be where all of your output goes.

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Multivariate

* masks
* models

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*Important Notes:*

* *Specify, preprocess and estimate must be performed in the order outlined below.*
  + *If you tag all trials from the start - you only need to run these once per study*
* *Most scripts require SPM12 to be open, so it is generally good to open that via matlab before doing any of these scripts*
* *Be sure to check over the entire scripts - some portions require you to change txt to csv, or to match your beh excel columns*

# Script Order

## createParams.m - can Run in Matlab 2022a

* 1. This step creates a params file that will be read into every step following this for each model/analysis you would like to run
  2. This step requires you to specify all aspects of the current task (i.e. conditions, paths to BIDS/preprocessed data)
  3. **May need to change:** line 279 for tagging correct subjects
     1. i.e., specify if you want sub-o or sub-y or all subs ‘sub-’
  4. Enter path to parent directory:
     1. Don’t need a / at the end of this path
  5. Enter path to raw functional data starting from the parent directory input in the preivous step to path to wherever the preprocessed data is stored within that project folder
     1. Don’t need a “/” at the end or beginning of this path
  6. Enter Path to behavioral file starting from the parent directory input previously to path to wherever the BIDS formatted data is stored within that project folder
     1. Don’t need a / at the end or beginning of this path
     2. Oftentimes you just need to type *BIDS*
     3. Enter Trial Tag File Extension: enter the suffix for whatever format (tsv, csv, xlsx, etc.) your BIDSified data is in
        1. Do not put a . at the beginning, only enter the file extension
     4. Select Preprocessing Pipeline: Usually fmriprep
     5. Enter Task Name: enter the tag for whatever part of the task you’re looking at
        1. Examples: enc, ret, time1, time2, etc.
           1. **Be careful with capitalization and spelling – RSA analyses require lowercase**
     6. Enter Conditions of Interest: enter the trial tag for the types of trials you’re looking at. Make sure it is exactly how they are tagged behaviorally
        1. Examples: single\_target, far\_target
        2. **When running an RSA, there needs to be no capitalized letters**
     7. Is accuracy possible?: Usually no
     8. How many volumes?: enter the number of volumes in that part of the task
        1. Ex: 126
        2. If you dont know, type in a new terminal:
           1. module load fsl
           2. fsl &
           3. Then your directory to a subject's func folder and find an enc or ret “desc\_preproc\_bold.nii” file.
           4. fslnvols “file.nii”
           5. Should output volumes
     9. How many runs?: Enter the # of runs for whatever part of the task you’re looking at
        1. Example: 4
     10. How many trials per run?: Enter the # of trials per run of whatever section of the task you’re looking at
         1. Ex: 36
     11. Enter TR *in seconds*
         1. usually 2 or 2.5
     12. Select Multivariate: choose whatever analysis you want to run
         1. RSA, MVPA etc.
     13. Select Analysis Level for Multivariate Test: Usually ROI
         1. If you are running an RSA searchlight - you will need to specify whether you want this to be run with radius or count; and the size of the searchlight numerically
     14. NO to Regress out RT, Perform Bootstrap
         1. You can perform bootstrapping after the fact in a separate coding program. HOWEVER, the MVPA classification does require bootstrapping to be selected.
     15. Are there subconditions: generally no
         1. If you are unsure, select no
  7. Will output in whatever directory you are in (in matlab) so navigate to your folder you want an output in ahead of time

## preprocessData.m - can Run in Matlab 2022a

* 1. Only needs to be run once for each participant in each study (once for each task – i.e., once for encoding & retrieval).
     1. Meaning run it with one enc params file and then one ret params file, but no need to do this with every single params file
  2. If you’ve already preprocessed in fmriprep (i.e., you preprocessed the imaging data much earlier and clicked fmriprep when the “Select Preprocessing Pipeline” prompt came up during step 1), then this script will edit that output to work with SPM conventions and move the motionRegressor files to the Singletrialmodelenc or ret folders in multivariate/model path. Should take ~ 2 mins to run
     1. This script only needs to be done once per participant per study
     2. Usually Click - Automated - all subjects
  3. If the params file you made in step 1 specifies to run preprocessing in SPM (i.e., you clicked SPM12 when the “Select Preprocessing Pipeline” prompt came up), then this step will run through preprocessing for each participant and thus take much longer than 2 mins

## specifyModel.m ~1 min

* 1. This script tags trial types and spits out corresponding onsets - if you specify/tag every trial type possible for run - you should only have to run this once for each block type (e.g., once for encoding and retrieval) as you will have tagged everything necessary for subsequent models and analyses.
  2. Make sure to double check with behavioral data of at least a few subjects that trials and onsets are being tagged correctly
  3. This script will output “multiple\_conditions.mat” files for every run (e.g., enc or ret - whichever you specified in params file) with onsets and trial tags
  4. **May need to change**: change line 52 for correct type of run (enc/ret); change lines 113-116 to match names of what you want to be tagged from behavioral files
  5. The script is set up to accept tsv files – however, can be updated to accept other beh datafile types.

## estimateModel.m ~1 hour

* 1. This step outputs betas for every volume, job.mat and SPM.mat files into the multivariate/models/SingleTrialModel folders
  2. Essentially ties behavioral and neural data together
  3. If specifyModel has tagged all trials types possible this should also only have to be run once per participant per study

## Mask Registration

1. Each analysis requires a mask folder that contains masks for each subject that have been co-registered (atlas-based mask) or segmented (freesurfer mask).
2. The corresponding mask folder for each analysis should be named exactly the same as the params file output from createParams.m
3. This step must be done before running the subsequent analyses

## runMVPAclassification.m - needs to be run in matlab2017b

* 1. Requires unzipped betas
  2. Asks for params files

## runRSA - can Run in Matlab 2022a

* 1. Requires zipped betas
  2. Asks for params files

## runERS - can Run in Matlab 2022a

## This requires both specify and estimate to be run for encoding and retrieval

* 1. Asks for params files

1. **RunRSASearchlight.m** - can Run in Matlab 2022a
   1. The RSA searchlight is set up to run a dissimilarity correlation matrix - i.e. the between-category similarity in each voxel of whatever mask you choose
      1. Requires a params file input
      2. Output of RSA\_Searchlight: The script will output a .nii for each subject in a corresponding model/params file. The nii is an intensity map of all of the voxels that exhibit similarity between your two conditions. We will use this for analysis.