THAMP Project Documentation Overview

This document contains information, procedures, and links to relevant files for all areas of the THAMP project. This includes recruiting, running participants, pre-processing, and analysis. The THAMP project is currently split up into three areas: online, EEG, and fMRI. There is also previous work looking at valence and arousal.

If you have any questions about procedures or locations of files look through this document. If anything is unclear please reach out to me over Slack or at jlaats@gmail.com

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Location of Important Files

The THAMP Runlog is used for tracking which participants have been run for EEG and MRI. This also has all the information for how to counterbalance each subject. Located in the dropbox. HERE

Song orders for online and mri/eeg and also the page used for order/ITI generation are compiled here in this spreadsheet here

Song files used in experiment here Also the files used for eeg and mri are in the eeg and mri folders. Songs used for online are uploaded in each experiment on psytoolkit.

Raw, pre-processed, and analyzed EEG data can be found on discovery HERE.

Lab wiki for general information and THAMP tab. HERE

Repositories for code used for processing and analysis can be found in the corresponding github repo.

- Online code: HERE
- EEG code: HERE
- MRI code: HERE

For MRI, raw bids and dicom files can be found in the NUBIC folder on discovery. HERE The zipped files are stored on the pegasus drive which is on Eva's desk (lab manager).

Preprocessed MRI files can be found in the current_subs folder on discovery HERE.

MRI 1st level and 2nd level analysis can be found on discovery HERE. More details on this in the processing/analysis section for MRI.

For online data analysis after the data is analyzed in matlab, the plots are in an excel sheet here

CNS poster is in the dropbox, made by psyche

All my local scripts i just put in this folder on dropbox just in case i forgot anything. here

Major THAMP Next Steps and Gaps

Gaps / Problems to be fixed

- EEG max patches weren't working on lab computer, i think you need to update max software

- A few more than 400 participants have been run but currently only 355 have been processed with the matlab script.
    - When running the script, it collects all the subjects that cause an error in a few lists and skips them
        - `id_error_list = []; %out2 empty error`
        - `id_error_list2 = []; %table1mod empty error`
        - `id_error_list3 = []; %table2mod empty error`
        - `id_error_list4 = []; %table1mod empty error line 161`
        - `id_error_list5 = []; %table1unmod empty error line 161`

        - Not sure why these subjects dont work, there is a problem with empty matrices need to bug fix
    - There is a list of participants who completed the survey and tasks with a direct link not through prolific after i gave them the refund after the psytoolkit crash day.
        - This list is at the top of script in a variable called additional ids
        - prolific crash day ids
    - These all add up to ~396, there should be a few more in there that need to be identified and added to the id list that the matlab script uses to loop through.
    - The way to work on all this is by cross checking the qualtrics data, id list, matlab script, prolific participants
        - Psytoolkit data / id list / download qualtrics data found here
        - Matlab script is here
        - Online data is found on qualtrics here
        - Online task data is found on psytoolkit group 1 group 2
        -
    - Alternatively, we could just rerun the study and open up however many slots couldnt be bugfixed.

- There is an issue with the sorting of the online results into liked and familiar songs. The data is coming out identical for modded vs unmodded which shouldn't be happening.
    - The issue is with both sart and nback data for liked and for familiar
    - I think the problem could be caused because the variables that store the lists of songs/subs are identical between modded and unmodded (modlike is the same as unmodlike, and modfam is the same as unmodfam) So the sorting isn't working as intented
    - Lines 678, 684, 690, 696 in thamb1banalysis_nomusic_batch.m are potentially where the sorting is going awry for the nback
    - Lines 440, 449, 458, 466 are the equivalent lines for the sart
    - The plots in the sony slide deck and the plots in rctv pilot plot spreadsheet are incorrect still until this is fixed.

- I was in the middle of processing subjects 15, 16, and 17 on my last week. 15 processed correctly but 16 and 17 only were outputting the final file as wausub…. Instead of swausub, so the final step wasn't working. I think the denoising step in CONN is what the final step is but I'm not sure. When rerunning the preprocessing for subs 16 and 17, I think it was getting stuck on the denoising step and would display "saving variables" but never finished.
    - 15 is finished processing so is in the conn_project/current_subs folder
    - 16 and 17 have the unfinished 'wausub' files in the current subs folder but should be re-preprocessed from bids problably

- There are four eeg files with non fixable events/triggers (marked in the runlog). All the triggers are s65 or s75 instead of what they should have been so its hard to tell where the songs start to mark the epochs. I think this might be solvable if it is possible to tell

when each task started and then knowing the length of each song already (60.8s). So maybe these files could be included in the analysis.

- Need to get all of the online participants into the CROMS spreadsheet. Only eeg and mri subjects in so far. Probably ignore all the participants who returned it.

- The naming of the ttl .txt files in the data folders for eeg tasks are not consistent, need to be altered if included in any script analysis.

Next Steps

- Continue to run participants up to 40 eegs and 40 mris
- Statistical significance analysis for online data
- Write a script that can process the task data text files that are output from the EEG and MRI versions of the task
- More analysis on the online task performance
- More analysis on MRI data
    -

- More analysis on EEG data
    - Event related potentials for the correct and incorrect trials
        - Would have to sort through the trial triggers and grade them correct/incorrect
        - erp
        - Epoch to compare mod and unmod trials
        - Trial related spectrogram

- Sort online results by positive and negative valence?
    - Take valence and arousal ratings from the first part of the project and sort the online results in thamb1banalysis_nomusic_batch.m script

- A plot of all eeg psds averaged for all songs
    - You could pick a specific bin
    - Alternative option is to use fooof
        - fooof filter could be used for each song to show the hypothesized peak

- A plot of all rolling window response times averaged for all participants

- Look at different performance indices for the SART and NBACK
    - RT for nback, %correct for sart
    - D prime, hit rate, false alarm rate

- Volume setting is subjective based on the subject, is there some way to standardize this? High or low volume could affect how distracting the music is.

- Having the brain data from eeg and mri inform how we interpret the online behavioral data and vice versa
    - For example maybe the brain data shows that certain areas only activate in the second half of a song, so then we could only look at the second half of some of the behavioral data from the online subjects.

- Average all EEG psds together by only averaging the target bins against each other instead of the whole psd.

Other THAMP Responsibilities

CROMS

- Every 15th of the month update the two forms here. One of successfully run participants and one of screening failures. For information we don't know just enter n/a or unknown.

Recruiting, Scheduling, and Running Subjects

EEG

Qualtrics EEG behavioral surveys (https://neu.co1.qualtrics.com/jfe/form/SV_3I2IzcMXI44PmXc)

Consent form (https://www.dropbox.com/preview/MINDLabWes/EthicsProtocols/NU%20IRB/Adult_IRB/ConsentForm_Adults.docx?context=standalone_preview&role=personal)

Recruiting and Scheduling

Post a time slot on Psylink. The time slot should be 90 minutes and can be posted whenever the basement lab space is available as well as an additional RA to help with gelling/clean up.

The EEG is scheduled through the "TR2 (jam room with EEG system)" calendar through the mindlab gmail. If no one else is scheduled to use the large testing room, you can create an event at the time you want to run the EEG to reserve the space.

Update the Run Log

Update this sheet with the participant ID, research assistants present, and experimental notes. Song order and task order is also counterbalanced here.

Testing Triggers on the EEG

You will also need to use the laptop with the mindlab sticker to test triggers for the EEG. Basically, you want to make sure that the signals being sent from the laptop during the EEG are being recorded properly. To do this either just run the task max patch for a few seconds before starting the recording or follow these steps:

1. Plug in the EEG battery into the EEG system in the booth
2. Open PyCorder on the desktop computer on the right side of the basement lab (app can be found on the desktop
3. In PyCorder, go to the box in the right corner of your screen and click on "Default Mode"
4. Go into the booth, and plug the lab laptop (the one with the sticker) into the black cord (the one connected with the arduino). Make sure you plug the cord into the second port, not the first.
5. On the laptop, navigate to `/Desktop/Synchrony_Gamma/Experiment` and open `TriggerTestCode`
6. Next, open the PsychoPy app. Go to "View" at the top and click "Open Coder View". When the window comes up, press Return to start the Python session.
7. Copy and paste the three lines of code in the `TriggerTestCode` into PyCorder
8. Paste line three again and change the 1 to 23
9. Paste line three again and change the 1 to 156
10. Leave the booth to see if 1, 23, and 156 showed up at the bottom of the EEG screen. If they did, then you are good to go!
11. If there are many overlapping triggers being sent. Double check the connection of the pins in the arduino and try again.

EEG Set up

- Open the run sheet on the desktop computer on the right side of the basement lab and update it with the participant ID
- Make note of the "Task Order" in the run log and the "Song Order"
- Take out gel, syringes, gloves, and paper towels and put them in the EEG booth
- Put EEG electrodes on the counter (box 1 to the left, box 2 to the right, ground in the middle). Put the styrofoam head in the middle of the two boxes. Take out the two laminated EEG guides.

- Bring the measuring tape and caps upstairs with you so you can measure the participant's head right after the consent process
- EEG Experiment: Participants's EEG activity is recorded while completing the SART task and the 2BACK task while listening to music with and without the amplitude modulation effect. On the day of, welcome the participant and tell them about the EEG and the two tasks they will be completing today. After showing a demo of the two tasks, have them complete the young adult consent form, and then start the Qualtrics behavioral surveys. After they sign the consent form, measure their head. While they are completing the surveys, prepare the appropriate cap with the both electrode boxes.

Running the EEG Max patch:

- Open nback_Thamp_pl.maxpat or sart_thamp_final.maxpat
- Here is where the files for running the experiment and data folders here
- Follow the steps in the max patch for starting the experiment
    - Plug in headphones
    - Change audio status output device
    - Hit the loadbang button if nback
    - Turn on sound with X
    - Set the participant name
    - Load the song order
    - Fullscreen
    - Presentation mode
    - Hit 5 to start
    - After finished hit write for the .txt (example: write 230929SCOE_sart_thamp_0.txt)
    - And hit the 'write' button above (write 230929SCOE_sart_thamp_0_ttl.txt) and save to the data folder.

Once finished gelling you can start the recording in pycorder. Open the first task as indicated in the run sheet. Plug the headphones into the computer. In Max, ensure the audio device is correct, the participant ID is entered, the sound is turned on, and the patch is in presentation mode and fullscreen. Hit 5 to start the patch and 1 for the response key. Continue the recording and run the second task. If the participant has finished the surveys they are then free to leave. Grant the credits and clean up.

Saving to Discovery

Log into FileZilla on the desktop in the basement (the one you collected the EEG data from):

1. Open FileZilla.
2. In the Host field, type sftp://xfer.discovery.neu.edu
3. In the Username field, type your Northeastern username.
4. In the Password field, type your Northeastern password.
5. In the Port field, type 22

The documents and folders on the left are the documents on the desktop computer. The documents and folders on the right are the ones in discovery in `/work/mindlab`.

Navigate to the folder where you saved the data on the desktop (left side). Navigate to `/work/mindlab/Projects/GammaMBI/EEG Data/raw/ pre` or `post` on discovery (right side). Drag the file from the left side of the screen to the right. Once the sync process is done, you can close FileZilla.

fMRI

Posting on Psylink

Post a time slot on Psylink when you believe Fred is available and an additional RA to help you is free. Do this at least a week and a few days out. Post the start of the Psylink slot to be 30 minutes before the official scan time with Fred.

Prescreening

Have participants fill out the MRI Screening Form (pdf or Google Form) and send it to Fred; wait for his approval before scheduling MRI. The form is linked on the psylink sign-up and participants are instructed to complete and sign the form and email to j.laats@northeastern.edu.

If the participant marks yes for anything on the form follow up with them either by phone or email to confirm the details. For example, if they have piercings make sure they are all removable.

Once you feel confident that the participant could be scanned, use outlook to schedule the time with Fred (next section). Make sure that you book with Fred at least a week before the hypothetical slot. If it's less than a week, sometimes he shifts around his schedule. You can also book outside of the usual two slots if Fred is free.

Send an email to Fred with the prescreening form at the same time of shortly after booking his calendar time. This email can be titled: FLLL - THAMP - MIND Lab. Attach

the screening form and in the top right of outlook select the sensitivity tag (looks like a little paintbrush kind of) and select level four, critical risk. In the body of the email include any notes and follow up answers you had about the participant.

Scheduling with Fred

MRI's are booked through Fred Bidmead's Outlook calendar. To access his calendar, go to the calendar tab of your outlook calendar and click "Add Calendar" on the left panel. Next, click "Add From Directory" and type in "Fred Bidmead". MIND Lab has two reserved times lots every week at the MRI. (Correct times as of Spring 24)

- Monday 11:15 to 12:45 pm
- Thursday 11:45 to 1:15 pm

To book one of these slots, create an event in your own calendar called "MIND Lab - Participant ID". Invite Fred as well as your 3rd MRI person to this event. When Fred accepts the invitation, you have officially booked a slot at the MRI. If there are any other open time's in Fred's schedule, you can book an MRI outside of the two times listed above. You would use the same procedure described above to do this.

Day of testing session

The participant should arrive 30 minutes before the scan time. When they arrive for the first 15 minutes they should complete the consent form, as much of the survey on qualtrics as they can, and show them the two tasks. 15 minutes before scan time, head over to the MRI room. Sit them down in the waiting room on the far side of the room, and have them complete the screening form again.

Consent

https://www.dropbox.com/preview/MINDLabWes/EthicsProtocols/NU%20IRB/Adult_IRB/ConsentForm_Adults.docx?context=standalone_preview&role=personal

Surveys (Qualtrics)

Complete these surveys before the MRI time slot if there is time. Finish afterwards.
https://neu.co1.qualtrics.com/jfe/form/SV_a9o5Kv4OXQWGD0q

MRI Notes

Print this page and bring it with you to the scan. Replace the first and second tasks with SART/nBACK depending on order.

MRI Task Practice (do this and above in the lab)

Show participants a demo of the SART & 2back tasks before going into the MRI room

- The SART max patch can be found in the dropbox at /MINDLabWes/projects/THAMP/thampsartfmri_1/sart_thamp_final.maxpat
- "When the task starts you will hear music playing and will see numbers appearing on the screen. Press button 1 after each number that you see except for the number 3. Be sure to give equal importance to the speed and accuracy of your answers."

- The 2BACK max patch can be found in the dropbox at /MINDLabWes/projects/THAMP/thamp2backfmri_1/nback_Thamp_pl.maxpat
- "When the task starts you will hear music playing and will see letters appearing on the screen. Press button 1 only if the letter currently shown matches the letter shown two letters ago. Otherwise do not press button 1. Be sure to give equal importance to the speed and accuracy of your answers."

Setup MRI

- Take the script, the MRI notes form, the blue earplugs, and MIND Lab laptop with you
- Make sure both participant and RAs arrive at the MRI room 15 minutes before your scheduled time
- MRI technician will guide the participant to fill out MRI screening form and change
- Fred will ensure participants do not have any metal on them using the portable metal detector after they change.
- While the MRI technician is talking to the participant, one RA should set up the sheets and cushions and connect MRI button boxes, while the other RA should set up the computer and the silver box to the top right of the computers. Make sure you are not wearing any metal and have nothing in your pockets before you go into the MRI.
- Based on the runlog, the button box will be placed in the participants left or right hand. Only button 1 is required for the SART and 2BACK tasks. Button 1 and 2 are required for the volumeset task.

To set up the computer:

- Connect the MIND Lab laptop to the HDMI cord
- Open Max8 on the MIND Lab laptop
- Check the flat black box on the desk under the MRI computers to see if the triggers get sent to the laptop or desktop. The white light should be beside the "laptop" label (whichever computer you are running the maxpatch on). If not, hit the round button to switch it to the correct side.
- Press the "laptop" button on the black box to the left side of the computers to make sure the laptop screen is projecting on the MRI screen and the ViewSonic computer screen
- Open the "Relax Hold Still" document. Click control + L to make the pdf fill the screen. (Control + Q can be used for to quit the document)

To test the button box:

- There is a silver box right above the computer you are sitting at. Ensure the box is set to the following:

`USB

HHSC- 2x2

HID KEY 12345`

- If it isn't, press "autoconfiguration" and then select "HHSC- 2x2" (NEED TO CHECK WITH FRED)
- Open the "Button_box_test.txt" file in the THAMP folder
- Have the RA in the MRI room press the buttons and see if the corresponding lights on the silver box shines and if responses are recorded in the .txt file.
- Delete the numbers in the .txt file before you close it.

To prepare participants for the MRI scan:

- The MRI technician will bring the participant into the space and you can help set up the participant on the table. Before they lay back, show them the button boxes and make sure they understand which button is for which rating.
- The MRI technician will show you how to set the participant up the first couple of times you run a session, but it will be your responsibility moving forward. Make sure the participant can read the "Relax Hold Still" slide while they are in the scanner.

Runlog and Counterbalancing

- The Thamp MRI and EEG runlog can be found in the dropbox (https://www.dropbox.com/scl/fi/wnxbvpqxwqy5bmoeiyn60/THAMP_runlog.xlsx?rlkey=ukpwd1unq7pbocmu0d2eotek7&dl=0)
- The counterbalancing is indicated on the runlog as follows: the participants alter doing the SART task first or the 2back first, and every two participants will start with modded or unmodded songs first.
- To choose which task is run first simply open the appropriate max patches during each task block.
- The appropriate song orders will be listed in the runlog which also determine whether the songs are modded first or unmodded first.

MRI Scans

- Fieldmap 2min
- Resting state 8min
- Volume set 2min
- Task-based fMRI:
    - SART 6min
    - 2back 6min
- Structural scan (T1) 7min
- DTI 12min
- Right before starting the first scan, go to the right-hand-side DELL computer, type FIRMM in the terminal, hit enter to run, which will open FIRMM. Click on "Start", select the participant you are running, and then click on "Run". This will measure participant's movement while in the scanner. If FIRMM shows they are moving too much (i.e. in the red/grey zone a lot), ask them to stay still.
- While you are scanning, make notes in the "MRI Notes" form.
- During the scan use this script for instructing the participant while in the scanner. https://www.dropbox.com/scl/fi/0sij2bczdt1oo7mhbjtlr/THAMP_MRI_Protocol.docx?rlkey=yirdb5tnfodakkwi51zdkuzej&dl=0
    - This form is printed and in the filing cabinet with the rest of the THAMP EEG and MRI forms.

Clean up

- Towards the end of the scan, go into the small office (MRI technician will direct you) to make a copy of the MRI screening form. Make sure the technician has signed it before you make a copy. Keep the copy and give the technician the original.

- The MRI technician will guide you through the clean up process. Use Clorox wipes to wipe down all the surfaces and button boxes and throw the used sheets in the red laundry bag outside of the room. Bring the blue earplugs back to the lab to wash them. As with set up, once you do it a few times, you can do this on your own with the help of your third MRI person.

Copy and upload MRI Data

After your MRI session, plug the USB into the right-hand-side computer.

Use the following instructions to save the MRI data to the USB:

1. Go to the second computer from the left if the MRI is to your left.
2. Right click on the participant in the list
3. Click "Export to DICOM Files(s)
4. Navigate to /Documents/Loui/MCIMBI/ in the pop-up window and click "Choose"
5. The folder will export. You can track the activity in the "Activity" area on the bottom left of the screen.
6. Once the folder is done exporting, open a finder window, and navigate to /Documents/Loui/THAMP/. Right click the folder and click "Compress "Folder Name""
7. A pop-up will come up to show the progress. Once this is done, go to the computer you plugged the USB into and click on "Documents (Mac Pro) in the top right corner of the screen.
8. Navigate to /Loui/THAMP/
9. In a new tab, open the USB and drag the zipped folder from the "Documents (Mac Pro)" folder to the one on the USB. It might ask you if you trust the file, and you can say yes.
10. Once this process is done, eject the USB and bring it with you.

Once the data is on the USB, go to the analysis computer at Eva's desk. Use these instructions to copy the data from USB to the Promise_Pegasus hard drive. Follow these instructions except use the THAMP-Study folder instead of GammaMBI.

After making sure data is saved at the right place, delete the previous participant's data from the USB.

Then, upload the raw data to discovery by syncing the Promise_Pegasus folders to the corresponding folders on Discovery. This could be done on any computer. You should only need to use the section titled "Uploading the zip folder to the lab computer".

The zipped data files and unzipped dicom files will then be present in /work/mindlab/NUBIC/THAMP-Study

If you are capable, continue with the following sections to convert dicom to bids on Discovery and preprocess the data. This could also be done on any computer.

Text files cataloguing the participants from sub001 to sub042 are stored in the /work/mindlab/NUBIC/THAMP-Study/raw_bids/ folder in the same format as the Gamma MBI study folders. Update these text files after syncing the zipped folder, the dicom folder, and converting the dicom files to bids.

Online

Prolific was used to recruit online participants for this study.

- If new subjects are needed, use this prolific study and add more slots. Here.
- Subjects are linked from prolific to this qualtrics survey. Here.
    - The survey is already published but if edits are required it can be republished and the link stays the same
- Subjects complete the survey on qualtrics and then are linked from qualtrics to psytoolkit for the tasks (Online task surveys on psytoolkit group 1 group 2)
    - The way that psytoolkit is structured is that there is a survey for group1 and group2 which are mod or unmod first. Then each survey links to a subset of 5 experiment tasks which change the song order. The data is downloaded in the survey pages not the exp pages.

Pre-processing and Analysis

EEG

Pre-processing

This is a guide for preprocessing using the script: Jakob_THAMP_Preprocessing.m. It is also very simple to do without the script, just click through the eeglab gui for each step.

- Move the eeg files from the recording machine to discovery. The files should be stored in /work/mindlab/Projects/THAMP/EEG Data/raw
- Download the desired participant folder to your local machine that you will be doing the preprocessing on. (Or on discovery)

- If using a local machine ensure that eeglab and all the necessary plugins are installed and added to path. Either download plugins from the internet or copy from this folder /work/mindlab/Programs/eeglab2021.1/plugins. On discovery simply add eeglab to path from /work/mindlab/Programs/eeglab2021.1
- Download all of the .m files found HERE or in /work/mindlab/Projects/THAMP/EEG Data. (Or start a virtual matlab session on discovery and open the .m files)
- In the Jakob_THAMP_preprocessing change the path, ID, and ID_I variables (lines 19, 23, 24) to the correct folder and participant id that you would like to process.
    - Also change lines 53, and 62 to point the appropriate local location file, and output directory
    - Also line 99
- Run Jakob_THAMP_Preprocessing. While running there are several manual stops that require input for it to keep running.
    - The full list of preprocessing steps are as follows
        - Load channel locations
        - Change song trigger labels, remove extra triggers.
        - Filter from .5 Hz to 50 Hz
        - Re-reference to TP9 and TP10
        - Resample from 5000 to 500
        - Automatic Rejection
        - Manual Rejection
        - Independent Component Analysis
        - Reject Components
        - Analysis Script
            - Epoching
            - PSD
            - Topos Plots
    - How to update Events
        - Look at already processed subject txt files for examples.
        - Export triggers in eeglab as txt. (the code automatically exports this file)
        - Copy and paste into excel or sheets.
        - Create a new column on the write.
        - Use this formula
        - =if(AND((H2=H1),NOT(H2=H3)), TRUE, if(AND(H2=H4,not(H2=H5)),TRUE,FALSE))
        - The 'H' column should be referring to the trigger value column.
        - The new column header name should be called 'remove' and the values should all be TRUE/FALSE
        - In the sheet change the onset and offset triggers (invert for unmoved first)
        - SART onset (modded first) (unmodded first)
        - s111 -> s211 s_11 -> s101
        - s112 -> s212 s_12 -> s102

        - s113 -> s213 s_13 -> s103
        - s_14 -> s104 s114 -> s214
        - s_15 -> s105 s115 -> s215
        - s_16 -> s106 s116 -> s216
        - NBACK onset (modded first) (unmodded first)
        - s111 s_21 -> s201
        - s112 s_22 -> s202
        - s113 s_23 -> s203
        - s_24 -> S204 s114
        - s_25 -> S205 s115
        - s_26 -> S206 s116
      - Make sure any extra triggers in the 100's and 200's are changed. (Change them to s240 or s255)
      - Save the sheet with the replaced triggers and put it in the folder. Save as FLLL_triggers_repl.tsv
      - Copy the values column into a new txt file and save it as FLLL_type.txt
      - Copy the remove column into a new txt file and save it as FLLL_remove.txt
      - Optional: remove the rows containing TRUE if response duplicate triggers need to be deleted
        - go to edit/select_epochs_or_events
        - in the keep field enter in the Selection box false
        - check keep only selected events and remove all others
      - From this point on the code will be automated again and you can continue
    - Rejection
      - After automated rejection, the script will open the scroll plot. Visually inspect all 64 channels and look at the runlog to see if any channels were marked as noisy. Remove any channels that the automated rejection may have missed that seem obviously noisy.
    - Component Rejection
      - After ica runs, the script will plot components 1-30 with labels using ICLabel. Manually inspect the components by clicking on them to view more information. Enter the components by number to be rejected in the command window.
- Manual Epoching
    - After pruning ICA components and before running the psd script
    - tools /extract epochs
    - Each epoch is 60800 ms long.
      - So the start value is 0 and end is 60.8 for the epoch limits
    - Select the correct 12 triggers based on being either modded first or unmodded first. Triggers can be found above in the events section.
    - Save the new dataset and add '_epochs' to the end

EEG Analysis

- Now open the THAMPcalcPSD_1stlevel.m script.
    - Edit the id variable, songorder variable, task order variable and mod order variable. Look at the thamp runlog for this information. Also change the file path to where you have the processed
    - Run the script to view the PSD and topos plots for each song.
    - Plot additional plots as needed.
- Next open THAMPcalcPSD_2ndlvl_bytask.m
    - Edit the id variable, songorder variable, task order variable and mod order variable for whichever participants are to be included
    - The code should be commented about what does what
    - The output are the psd plot with Modded vs unmodded plotted together and the two topos plots
    - There should be 1 plot for each task for each song so 60 plots total.
    - The script organizes and takes data from each participant that heard each specific song and averages each psd by song
        - Each subject has the 12 psd files for each song after the lvl 1 script

fMRI

If you are doing this for the first time, please see this page to install and activate miniconda before getting started with the instructions below. You only have to install it the first time you do the bids conversion.

Uploading the zip folder to the lab computer

1. Put the Thing2 usb onto the lab computer and copy the latest participant's zipped folder to /Volumes/Promise_Pegasus/THAMP_Study/Raw_data_zipped.
2. Unzip the folder by double clicking it, and move the unzipped participant folder to /Volumes/Promise_Pegasus/THAMP_Study/dicom folder.
3. You will notice that the participant's folder has the file structure below:

THAMP_Study/dicom/**Thamp_230622Cpar**/Loui_Goutama_1031_Thamp - 1 The space between the "Mcimbi" and the "-" and the "1" are problematic for the dicom to bids conversion on discovery, so please delete those two spaces so the folder structure looks like this:

THAMP_Study/dicom/**Thamp_230622Cpar**/Loui_Goutama_1031_Thamp - 1

4. Use the rsync command below to rsync the dicom folder to your scratch workspace on Discovery.

rsync -rltDvu /Volume/Promise_Pegasus/THAMP_Study/dicom <yourusername>@xfer.discovery.neu.edu:/scratch/<yourusername>/THAMP_Study/

(More rsync commands can be found in /Volumes/Promise_Pegasus/rsync_backup_codes.txt.)

Dicom to Bids on Discovery

1. Open a terminal on discovery and go to the compute node by using the command below:

srun --partition=short --nodes=1 --cpus-per-task=1 --pty /bin/bash

2. rsync the MCI_Study folder from /work/mindlab/NUBIC/dicom/ to scratch (/scratch/<yourusername>/THAMP_Study/dicom/). This will take some time as the files that are copying are quite large, so please plan for that, especially if you are doing this for the first time. This step can take about 2.5 hours. You can use the command below for this:

rsync -rltDvu --exclude 'ignore' /work/mindlab/NUBIC/THAMP_Study/dicom/ /scratch/<yourusername>/THAMP_Study/dicom/

You will have to do this every time you do this conversion in order to ensure that you are working with the most up to date data. If you do not sync the whole folder at least make sure the new participants you wish to process are in the scratch dicom folder.

3. In the file explorer, find the makebids_withfacename_discovery.py script in the THAMP_Study folder on your scratch. Click on the 3 dots to the right and then choose "Edit". Scroll to line 48. This line defines the base path, so make sure you change that path to /scratch/<yourusername>/. You might have to do this every time you run the script.
4. In the discovery File Explorer, change the name of the dicom folder you would like to convert to include a "z" at the beginning, so 210719BFOR1 would become z210719BFOR1. Make sure that only one folder that has not been put through the dicom to bids script is in the dicom folder at a time. If you are trying to process two participants at a time, remove the second one from the dicom folder temporarily
5. Delete all files containing ant or anat at the beginning EXCEPT the following:

anatT1w_acqmprageNav4e_RMS_XX

anatT1w_acqmprageNav4e_RMS_XX

6. Now we are ready to run the script!
7. First make sure the folder /scratch/<your username>/THAMP_Study/raw_bids exists and is empty.

a. Raw bids files in scratch exist in the raw_bids_main folder.
b. Raw bids in the middle of being preprocessed exist in the raw_bids_preprocessing folder
c. Rename raw_bids_in to raw_bids
    i. First rename raw_bids to raw_bids_main

Running the Script

0.
Follow these instructions first if not already installed.
https://github.com/mind-lab-bos/MBI_Project_MRI_Analysis/wiki/1.-Installing-SPM-and-Conn-on-Discovery
Installing miniconda:
https://github.com/mind-lab-bos/MBI_Project_MRI_Analysis/wiki/Creating-a-Miniconda-Environment-(for-dcm-to-bids-conversion)

1. Load anaconda and activate your miniconda environment

module load anaconda3/2022.01

source activate my_dcm2bids_env

2. Load python

module load python/3.8.1

3. cd into your scratch folder

cd /scratch/<yourusername>/

run before dcm to bids conversion

source /home/j.laats/miniconda/bin/activate

conda activate my-py38env

conda activate my_dcm2bids_env

4. Before running the script, move all the files from the dicom folder into a temp folder. Leave only the subject or subjects you want to process. (This is necessary because the script doesnt run only the subject with the z in front it seems to try to do all of them. This is a bug and the workaround that I have used (jakob))
    a. Run the script.

/scratch/<yourusername>/THAMP_Study/makebids_withfacename_discovery.py --project "THAMP_Study" --all

The script should process only the one with the z in front, but it may process them all.

5. Check the data. By running the script, each participant will have a folder made in the raw_bids folder that has been assigned a numeric ID. Make sure that within the participants folder (raw_bids/sub-040), you see the following folders: fmap, func, anat, dwi.
    a. Each participant will be called sub-001 so manually change the sub-001 to the appropriate number, and copy into raw_bids_main folder from the raw_bids folder.
6. Add the participant ID to the README.txt file in /scratch/<yourusername>/MCI_Study/raw_bids/. Ensure to include the numeric ID the participant was given in the bids conversion.
7. Using the File Explorer, remove the "z" at the beginning of the participant's data in the dicom folder.

Repeat the above "Dicom to Bids on Discovery" and "Running the Script" steps until you finished converting all new participants' data (one by one). After that, continue to the following steps.

- Move the sub-xxx folder in raw bids into raw bids main (including the sub-xxx folder in tmp_dcm2bids)
    - Then rename raw_bids to raw_bids_in and raw_bids_main to raw_bids

8. In terminal, rsync the raw bids folder in your scratch with the one in the /work/mindlab/ location.

rsync -rltDvu /scratch/<yourusername>/THAMP_Study/raw_bids /work/mindlab/NUBIC/THAMP_Study/

9. Run the following command to change the permissions on the most recent participant's folder to ensure everyone in /work/mindlab/ can access the folder:

chmod -R 770 /work/mindlab/NUBIC/THAMP_Study/raw_bids/<latestparticipant>

10. In the long run, Raw_data_zipped and dicom should be stored on Promise_Pegasus, and raw_bids onward should be stored on Discovery.

PREPROCESSING
Preprocessing (Automated)

Generate a directory in your scratch workspace named 'raw_bids_preprocessing'. Copy new participant data from NUBIC/THAMP_Study/raw_bids_preprocessing folder into this directory. Only add raw bids for *new subjects* that are being added to the project.

It has been shown that we cannot run more than 5 subjects at a time. While unlikely, if you have more than 5 new subjects, please add the first 5 to the raw_bids_preprocessing folder first. After the following steps has been done, repeat for the next 5 subjects.

Copy the *contents* of /work/mindlab/Projects/THAMP/CONN_Project into your scratch workspace, including the Current_Subs folder including the THAMP_Generate_Batch.m, THAMP_Batch_submit.sh, and THAMP_CONN_Submit.m files, and THAMP_Conn_Project.mat in work/mindlab/Projects/THAMP/. You could either click the copy and paste buttons or use the following code in terminal.

rsync -rltDvu /work/mindlab/Projects/THAMP/CONN_Project/
/scratch/<yourusername>/THAMP_Study/

rsync -rltDvu /work/mindlab/Projects/THAMP/CONN_Project/THAMP_Conn_Project.mat
/scratch/<yourusername>/THAMP_Study/

Important: Edit file path in first line of THAMP_CONN_Submit.m to match the path to your scratch workspace (/scratch/<yourusername>).

Please check each participant's fMRI data in the ~/func folder. Each subject should have 1 runs for sart, 1 run for nback, and 1 run for rest. If they have more than that, check the MRI note sheet in lab manager's drawer to see what happened during the MRI session and delete all the unwanted scans. Most likely, the last run should be the one to keep, but it is always good practice to check before deleting.

Run Preprocessing Batch

SSH into your scratch workspace. (Go to your scratch workspace on OOD, and click on "Open in Terminal", type in your password as prompted).

Paste the following code into command line: sbatch MBI_Gamma_Batch_submit.sh

Use scontrol show jobid -d "job number" or click on Jobs -> Active Jobs on OOD to check on job status, or check matching output file (slurm-<jobnumber>.out) in your scratch workspace. This job will take several hours (23h max). It is OK to log out of OOD or let your computer go to sleep while the job is running. After the job is completed, the .out file should end like this:

Update Project folder in /work/mindlab

Once the job completes, check the /raw_bids_preprocessing/sub-*/func/ folder. It should have more than what you started with (should have 78 in total). Start an interactive Matlab session, checking boxes to use GPU and Gurobi, and allocating 10 GB of memory.

Change the working directory to /scratch/yourusername on the top. Then, set path and open conn toolbox, using the following code:

addpath('/work/mindlab/Programs/conn')

addpath('/work/mindlab/Programs/spm12')

conn

In conn, open the project file (THAMP_Conn_Project.mat) from your scratch workspace. If you are prompted to select a location for a specific file in a pop-up window. Locate this within the Current_Subs folder of *your scratch*, select the appropriate file of that exact name, and click "Open". Do not end this interactive session.

Ensure that existing participants are present and new ones have been added. You could do that by clicking on each tab on the left and hovering your cursor above each scan on the right. The file names for the scan in each of the tabs should be as follows:

- Structural (T1): wc0c*
- Functional: swau* (e.g. swausub-094_task-musbid_bold.nii; session 1 = rest, session 2 = mus-bid, session 3 = face name study (run 1), session 4 = face name test (run 2))
- ROIs: wc1c* (Grey Matter), wc2c* (White Matter), wc3c (CSF)
- Covariates 1st level: rp_*
- Covariates 2nd level: no regular names, but make sure each sub has a distinct pattern

Once the project is confirmed to be accurate, copy the project .mat file and MBI_Gamma_Conn folder into /work/mindlab/Projects/GammaMBI/CONN_Project. Also copy the data from the RAW_BIDS folder in your scratch space into the Current_Subs folder in both your scratch and /work/mindlab directories. You can either do this manually on OOD or use rsync in terminal.

rsync -rltDvu /scratch/<yourusername>/MBI_Gamma_Conn.mat /work/mindlab/Projects/GammaMBI/CONN_Project/

rsync -rltDvu --ignore-existing /scratch/<yourusername>/MBI_Gamma_Conn/ /work/mindlab/Projects/GammaMBI/CONN_Project/MBI_Gamma_Conn/

Move raw_bids_preprocessing data to the Current_Subs folder in your scratch manually, and then - rsync -rltDvu --ignore-existing /scratch/<yourusername>/Current_Subs/ /work/mindlab/Projects/GammaMBI/CONN_Project/Current_Subs/

Returning to your interactive Matlab session, open the updated conn project .mat file located in /work/mindlab/Projects/GammaMBI/CONN_Project. You will likely be prompted to select a location for a specific file in a pop-up window. Locate this within /work/mindlab/Projects/GammaMBI/CONN_Project/Current_Subs, and select the appropriate file of that exact name. Additional filepaths should then be updated automatically. If you can't find the file in the pop-up window, that mostly likely means preprocessing wasn't done correctly. If that's the case, you should look at the slurm-*.out file to troubleshoot. Ask Alex if you need help.

Save and exit the project, terminate the interactive session, and the project should now be fully updated.

If you have more than 5 subjects, repeat the above steps for new subjects.

Preprocessing Manually

1. Start a matlab session on discovery and open conn
2. Copy over THAMP_Conn_Project folder and THAMP_Conn_Project.mat from work to scratch, and CONN_Project
    a. Also copy over spm_thamp_batch_modfirst.mat and spm_thamp_batch_unmodfirst.mat
3. Open THAMP_Conn_Project.mat in conn.
    a. Update file paths if asked. Locate the right anat and func files it asks for in scratch. Find these paths in ~/CONN_Project/Current_subs/
        i. For example: wc1csub-001_run-01_T1w.nii exists in ~/CONN_Project/Current_subs/sub-001/anat/
    b. Update the file paths
4. Ensure the subjects being added are in raw_bids_preprocessing in scratch
    a. Copy over from raw_bids_main. (If not already, sync over raw_bids_main from /work/mindlab/ or copy over the desired subjects from /work/mindlab/NUBIC/THAMP_Study/dicom/ to raw_bids_preprocessing)
5. Open the THAMP_Conn_Project.mat file in conn
6. In the basic tab increase the number of subjects based on how many are being added.
7. In the Structural tab for each subject locate anat file wc0c-sub###_run-01_t1w.nii
8. In the Functional tab for each subject locate the 3 func files.
    a. SART is session 1, NBACK is session 2, and rest is session 3.

9. Click on Preprocessing in the bottom left.
    a. Uncheck preprocess all subjects, and select the subjects you want to process in the scroll menu.
    b. Accept the default 11 preprocessing steps.
    c. Accept all the default settings except change the kernel size from 8mm to 5mm and select slice order from BIDS.
    d. After preprocessing all new subjects, click done in the bottom left.
10. The denoising tab on the top of the screen should now be available. Using default settings click through the denoising steps.
11. Copy the processed files from raw_bids_preprocessing into CONN_Project/Current_subs
    a. Sync /scratch/<your username>/THAMP_Study/CONN_Project/Current_subs/ to /work/mindlab/Projects/THAMP_Study/CONN_Project/Current_subs/
12. Also copy over THAMP_Conn_project.mat back over to /work/mindlab
    a. When you do reopen THAMP_Conn_project.mat from work and not scratch you will have to point it to the new filepaths again. It should only ask for one and then figure out the pattern for the rest of the paths.

1st Level Analysis

1. Sync the thamp_spm_sart_nback_rest folder from /work/mindlab/Projects/THAMP/thamp_spm_sart_nback_rest/ to scratch/<your username>/THAMP_Study/thamp_spm_sart_nback_rest/
2. Create a new folder for each new subject in thamp_spm_sart_nback_rest in scratch.
    a. sub-XXX-FLLL
    b. In each folder create folders named output_sart and output_nback
3. For each participant copy the preprocessed file for each task into the new folder you just created.
    a. swausub-XXX-taskthampsart_bold.nii
    b. swausub-XXX-taskthamp2back_bold.nii
    c. swausub-XXX-task-rest-bold.nii
    d. These files are found in ~/CONN_Project/Current_subs/sub-XXX/func/
4. Copy over or rsync the batch files for 1st level analysis. These are found in /work/mindlab/Projects/THAMP/spm_thamp_batch_modfirst.mat and /work/mindlab/Projects/THAMP/spm_thamp_batch_unmodfirst.mat and copy them into /scratch/j.laats/THAMP_Study/

Converting from 4D to 3D using SPM

1. Open up a MatLab GUI on discovery and type the following in the command line:

    addpath('/work/mindlab/Programs/spm12')

spm fmri

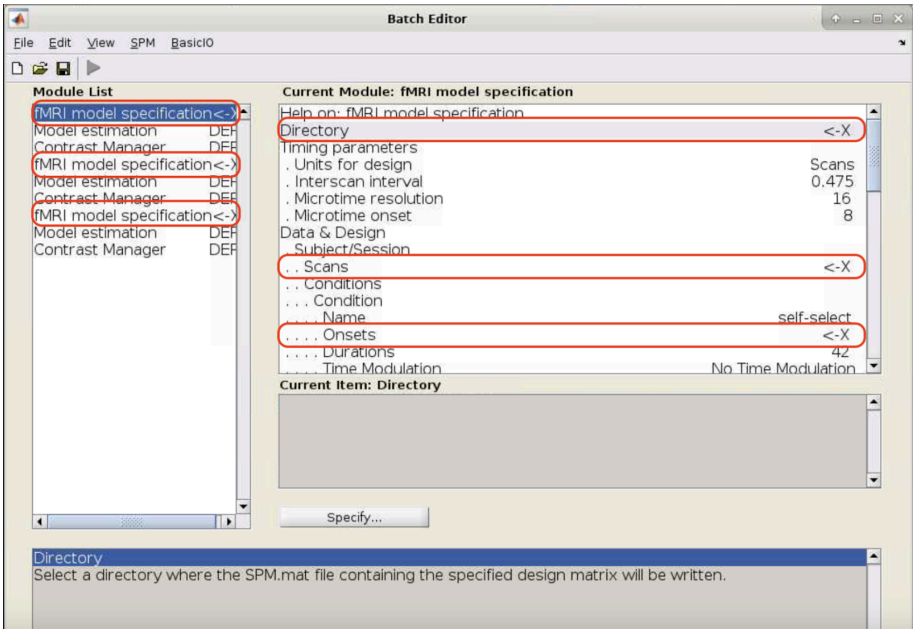
2. In the SPM GUI, select the button that says Batch, which will open up the batch editor.
3. In the batch, navigate to SPM > Util > 4D to 3D File Conversion. This will add "4D to 3D File Conversion" to your Module List (left panel).
4. Double click each of the fields listed below and select the following information to fill them.
    - 4D Volume --> Select the swausub-XXX_taskthampsart_bold.nii and swausub-XXX_taskthampnback_bold.nii volume you copied into your home directory, /home/<yourusername>/mus_bid_data/<subjectfolder>/swausub-XXX_task-musbid_bold.nii from the popup window. (Ensure this file is listed in the bottom part of the popup window then click Done.)
    - Output Directory --> select the folder you want the files outputted to. In this case, it will be the into the same folder as the .nii files.
5. Click the green triangle button on the left corner of the batch window to Run the batch. This could take a few minutes, so make sure you do not type anything in the MatLab command window while this is processing. Once the batch has run, close out the batch window.
5.

1. Now you are ready for the 1st level analysis! Open spm in matlab on discovery and in spm click batch and go to file load existing batch. Open the appropriate .mat file either modfirst or unmodfirst for each specific participant.
2. To open this pipeline, follow the steps below:

a. Click Specify 1st-level b. In Batch Editor, Click File> Load Batch c. Load musbid_pipline_newbp.mat (from your home directory)

3. Input Directory, Scans, and Trigger onsets for 2 models: Sart and NBACK. Note that you should only have to be making changes to the three fMRI model specification modules unless the participant has missing data for a particular condition.
    a. Check the runlog. If it was recorded that there was a different order of unmodded/modded songs played, then the contrast will need to be adjusted

accordingly.



b. When selecting directories in the gui be sure to unselect whatever is selected before selecting something new.
c. The output directory for sart should be in ~/thamp_spm_sart_nback_rest/sub-xxx-FLL/output_sart/ and ~/thamp_spm_sart_nback_rest/sub-xxx-FLL/output_nback/ for back
d. The scans are in /scratch/<your_username>/THAMP_Study/thamp_spm_sart_nback_rest/sub-xxx-FLLL/ and there should be 768 of them for each task.
e. IMPORTANT: If the participant was marked as doing the NBACK task first in the runlog, then load the nback scans for the sart task, and the sart scans for the back tasks.
f. If there are 768 for each then the onsets should not need to be adjusted. They should be equally split the 768 scans into 6 equal lengths for the 6 songs in each task.
g. In the model estimation tab, select the spm.mat file in output_sart and output_nback for each task. If there is no spm.mat file yet then select dependency instead of specify and reference from the fMRI model specification directly before the model estimation in the batch.
    i. Do the same for the SPM.mat file in the contrast manager tab.

4. Once you have double checked that all Directories, Scans, and Onsets are correct, click the Run (green triangle) on the top left of the batch window.
5. After the analysis has finished, check all of the subfolders in the subject's output_sart and output_nback folders. They should have the following files. Note that the number of conn and beta files will differ for each folder based on the number of contrasts associated with each.
    a. Spm.mat, beta files, cont files, spmT files

6. Save this version of the template batch to the participant's thamp_spm_sart_nback_rest folder . To save the batch, click on the File > Save Batch. You can name the batch using the participant's ID.
7. After completing the analysis, use rsync to sync the subjects‘ folders from your scratch to /work/mindlab/

rsync -rltDvu /home/<yourusername>/THAMP_Study/thamp_spm_sart_nback_rest

/work/mindlab/Projects/THAMP/thamp_spm_sart_nback_rest

8. Change the permissions on the folder you just rsync'd into /work/mindlab/ so anyone in the lab can access your data.

chmod -R 770 /work/mindlab/Projects/THAMP/thamp_spm_sart_nback_rest

Then click on the results tab in the main menu of spm.

Create four contrasts in the contrast manager menu.

- Mod vs Unmod
- Mod
- Unmod
- Unmod vs Mod

For example if the subject was modded first.

- [1 1 1 -1 -1 -1]
- [1 1 1 0 0 0]
- [0 0 0 1 1 1]
- [-1 -1 -1 1 1 1]

When viewing the results, select no mask, .05 pwe corrected.

If you want to overlay the significant results over a default image of the brain use single_subj_T1.nii which is usually in spm12/canonical/.

If you want to overlay the significant results over the subjects own brain then select the subjects structural file. (I’m not sure exactly which file to select)

2nd Level Analysis

In SPM click on specify 2nd level.

Open the batch file in /scratch/j.laats/THAMP_Study/thamp_spm_sart_nback_rest/2nd_lvl_analysis for either the sart of nback. The two existing spm.mat files are only showing contrast 1 currently

across the subjects. This could be replicated for the other 3 contrasts. (Contrast 1 is mod-unmod)

For directory select the spm.mat file in /scratch/j.laats/THAMP_Study/thamp_spm_sart_nback_rest/2nd_lvl_analysis/sart/ or /scratch/j.laats/THAMP_Study/thamp_spm_sart_nback_rest/2nd_lvl_analysis/nback/ for nback

For scans add any new con-001.nii files for each new subject. Then you can run the batch file.

Hit results and load the new spm.mat file to view the 2nd level analysis results. The contrast for 2nd level should be [1].

Rsync all folders back to /work/mindlab/ when finished.

rsync -rltDvu /scratch/<yourusername>/THAMP_Study/thamp_spm_sart_nback_rest /work/mindlab/NUBIC/THAMP_Study/

Online

There are a few scripts used for analysis of the online tasks.

- thamb1banalysis_nomusic_batch.m
    - This is the most up to date script which processes all 400 final participants at once, includes the no music condition, rolling window reaction time plots, sorting by liking/familiarity/ASRS score.
- thamp1b_liking _familiary.m
    - This script just sorts all performance results across all participants and plots the results into mod liked, unmod liked, mod familiar, unmod familiar for both tasks.
    - Only updated for the first 18 participants
- Thamb1banalysis_nomusic.m
    - Similar to the first script but not used for all 400 participants, just one at a time.
- Thamp1banlysis.m
    - First script for looking at RT and %correct for one pilot participant at a time. No music condition not included.

Guide and notes to running the thamb1banalysis_nomusic_batch.m script

This script processes all 400 of the online participants data from qualtrics and psytoolkit. The script should be fairly well commented but it is very long and does a few different things so it is

probably difficult to parse through. I will lay out what the inputs and outputs and sections are here.

- First download the data directly from psytoolkit and qualtrics, or use the already downloaded data that is in the dropbox
    - Psytoolkit data / id list / download qualtrics data found here
    - Matlab script is here
    - Online data is found on qualtrics here
    - Online task data is found on psytoolkit group 1 group 2
- Make sure all the data is downloaded and the file paths in the script are updated accordingly for your local machine
- First section opens the psytoolkit data
    - The way it works is that matches the experiment file with the survey file from qualtrics
- Then it sorts into like/fam
- Then it splits into group1 and group2 to grade the sart
- Then it splits into gruop1 and gorup2 again to do the same grading but for fam and like split
- Then it does the same two things for nback
- And then the same for no music section
- Then asrs ranking
- Then music listening habits
- At the end it compiles all the results into one large matrix
    - `final_results_all_fam`
    - `Final_results_all_like`
    - `Final_results_all`
    - `Final_results_all_asrs`
    - `Final_results_all_asrs0`
    - `Final_results_all_mus`
    - `Final_results_all_mus0`
- These final results matrices can be copy and pasted into the rctv pilot plot spreadsheet in dropbox here and edited to correctly display the response time cv and %correct plots.

Previous Work

Thamp 1a, Valence and Arousal Ratings

Prolific Page
https://app.prolific.com/researcher/workspaces/studies/63bf030b57dd0f7aea2e0e47/submissions

Qualtrics
Version 2 Section 1
https://neu.co1.qualtrics.com/survey-builder/SV_cSV1eHJsMxqNfcq/edit
Version 2 Section 2
https://neu.co1.qualtrics.com/survey-builder/SV_805lLqFiTKE2aUe/edit

Analysis File (**Thamp.R**) (**BMRQ_analysis.Rmd**)
https://github.com/mind-lab-bos/THAMP-Online

Downloaded Data
https://www.dropbox.com/personal/MINDLabWes/projects/THAMP/Study1a

Icmpc poster is in the dropbox