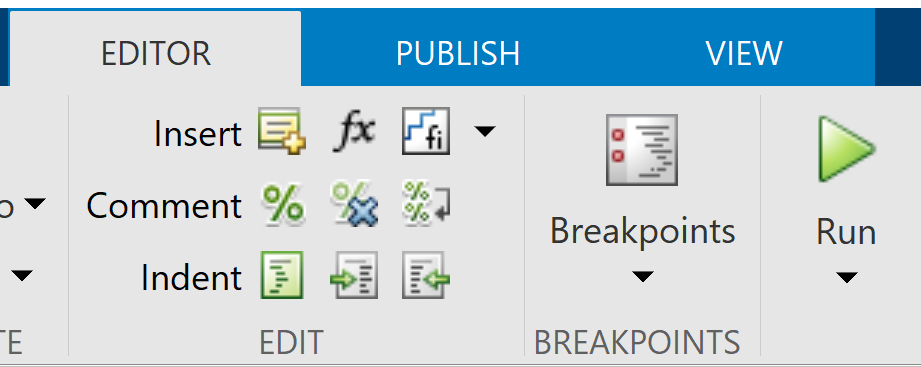
**HAPPE Task-Related User Guide**

**Run HAPPE:**

1. Navigate to the main HAPPE folder in your file browser.
2. Open HAPPE\_v2.m in MATLAB.
3. In the Editor tab, hit “Run.”
4. Follow the prompts in the command window of MATLAB
   * For detailed instructions regarding the prompts, see below.

**Following Command Line Prompts:**

Prompts as they appear in the command window are written in Courier New, like this, followed by a brief description of what to enter, with an example, also in Courier New. Sometimes a certain choice will result in a different set of prompts - in which case they will be indented under a heading that describes the choice needed for them to appear.

Enter the path to the folder containing the dataset(s):

The first step asks you to input the folder where the raw data is located. If running HAPPE for the first time, the folder with the data should ONLY include the raw files you wish to run through the pipeline; no other folders or files should live inside that folder. If reprocessing data, all outputs (folders and documents) should be in the folder in the same file structure as they were created during the original HAPPE run in addition to the raw data.

**Example (Mac):** /Users/laurelg-d/Desktop/Data Folder

**Example (PC):** C:\Users\laurelg-d\Documents\Data Folder

Select an option:

raw = Run on raw data from the start

reprocess = Run on HAPPE-processed data starting post-waveleting/ICA

If this is your first time processing the raw data file(s), input raw. If you wish to re-run raw data that has previously been processed, starting with post-waveleting (ICA is not used for low density), input reprocess. Depending on your choice, you may be asked to follow additional prompts (see below).

If you selected to reprocess existing data:

Name of previously created dataQC .csv file:

If no file exists, enter "none" (without quotations).

If you have the dataQC .csv file from the previous run, input the name of the file here. Confirm that it is located in the “quality\_assessment\_outputs” folder before running HAPPE. Otherwise, input noneand HAPPE will still be able to reprocess your data, but some quality control outputs may be missing.

Files, such as processed data and quality metrics, may already exist for this dataset.

overwrite = Overwrite existing files

new = Save new files

If you do not want to keep your previous files for this dataset, input overwrite. To keep both the previous files and the current files, input new**.**

Ifyou selected to save new files:

Use default or custom suffix for processed set?

default = Default name (\_rerun\_dd-mm-yyyy.mat).

custom = Create your own file name.

To create your own suffix for the processed data, input custom**.** You will then be prompted to enter your custom suffix. We recommend starting your custom suffix with an underscore. Otherwise, input default, which will save your files with a suffix in the format shown above.

Load pre-existing set of input parameters? [Y/N]

If parameters have previously been set through HAPPE for this dataset or another dataset with parameters that support the current dataset, you can load these parameters, if desired. Depending on your choice, you will be asked to follow a different set of prompts (see below).

If you chose to load pre-existing parameters:

Path to the folder containing the input parameters:

The default folder name will be **input\_parameters**. NOTE: the input parameters folder does not have to be in the same path as the datasets you are currently running.

**Example (Mac):** /Users/laurelg-d/Desktop/Data Folder/input\_parameters

**Example (PC):** C:\Users\laurelg-d\Documents\Data Folder\input\_parameters

Name of file containing pre-existing parameters:

The default file name is **inputParameters\_DD-MM-YYYY.mat**. If you chose a custom file name for the pre-existing parameters, input this name instead.

You will then be presented with a list of your current inputs.

Change an existing parameter? [Y/N]

To change any of the inputs saved in this file, input Y (case insensitive).

If you are not loading a pre-existing set of input parameters:

Low-density data? [Y/N]

For HAPPE, low-density data contains 30 channels or less.

For HAPPE, always enter N (case insensitive).

Enter data type:

rest = Resting-State EEG

task = Task-Related EEG

Input task for HAPPE with task-related EEG.

Performing event-related potential (ERP) analysis? [Y/N]

Input N (case insensitive) for HAPPE task-related, non-ERP EEG.

File Format:

0 = .mat (MATLAB array)

1 = .raw (Netstation simple binary)

2 = .set (EEGLAB format)

3 = .cdt (Neuroscan)

4 = .mff (EGI)

This is the file format of your raw data. Depending on your choice, you may need to follow a different set of prompts. Note that .raw format is not available for resting-state EEG.

**Example:** 2

Acquisition layout net type:

1 = EGI Geodesic Sensor Net

2 = EGI HydroCel Geodesic Sensor Net

3 = BioSemi

4 = Brain Products Standard BrainCap (BC)

5 = Brain Products Wet-Sponge R-Net for actiCHamp Plus (RNP-AC)

6 = Neuroscan Quik-Cap

7 = Other

Select the type of cap for your acquisition layout. Different choices will result in different prompts.

**Example:** 1

If you select .mat for your file format, you will get the following prompts:

If you selected an EGI GSN net, an EGI HydroCel GSN net, or a BioSemi net, HAPPE will list the number of electrodes that are compatible with HAPPE for that net.

If you selected a BC net, a RNP-AC net, or a Quik-Cap, you see the following:

Do you have a channel locations file for your data? [Y/N]

NOTE: A list of supported files can be found in the HAPPE user guide.

Accepted EEGLAB channel location file formats (from EEGLAB documentation) include:

1. .loc, .locs, .eloc - EEG polar coordinates
2. .ced - EEGLab with polar, cartesian, and spherical
3. .sph - MATLAB spherical coordinates
4. .elc - Cartesian 3-D from EETrack
5. .elp - Polhemus Cartesian coordinates
6. .elp - BESA spherical coordinates
7. .xyz - MATLAB/EEGLab Cartesian coordinates
8. .asc, .dat - Neuroscan Cartesian polar coordinates
9. .mat - Brainstrom channel locations
10. .sfp - BESA/EGI xyz Cartesian coordinates

If you do not have channel locations, you will not be able to proceed with HAPPE for high-density data.

Enter the name of the file containing the chanlocs, including the full path and file extension:

Enter the name of the file with the chanlocs in a file format that is listed above as supported by HAPPE.

**Example (Mac):** /Users/laurelg-d/Desktop/chanlocs.sfp

**Example (PC):** C:\Users\laurelg-d\Documents\chanlocs.sfp

Number of channels:

The number of channels in the net used to collect the data. Make sure to use that number, even if your data does not use or include all possible channels in the net.

Enter the potential EEG variable names, one at a time.

Press enter/return between each entry.

NOTE: variable names containing "segment" may cause issues.

For .mat files, you need the name of the variable that stores the EEG data. Between each entry, press your newline key (enter - Windows, return - Mac). When you are done entering potential variable names, enter done.

**Example:** Category\_1

Path to .txt files containing task event info:

Enter the path to the .txt files that have your task event info here.

If you select .raw for your file format, you will get the following prompts:

If you selected an EGI GSN net or an EGI HydroCel GSN net, HAPPE will list the number of electrodes that are compatible with HAPPE for that net.

Number of channels:

The number of channels in the net used to collect the data. Make sure to use that number, even if your data does not use or include all possible channels in the net.

If you select .set for your file format, you will get the following prompts:

Does your file have the 10-20 channels labeled? [Y/N]

HAPPE currently requires the 10-20 channels to be labeled in the dataset to run.

Number of channels:

The number of channels in the net used to collect the data. Make sure to use that number, even if your data does not use or include all possible channels in the net.

If you select .cdt for your file format, you will get the following prompts:

Number of channels:

HAPPE supports 32, 64, and 128 channels.

The number of channels in the net used to collect the data. Make sure to use that number, even if your data does not use or include all possible channels in the net.

Examine all channels (all) or only channels of interest (coi)?

To process all possible channels within each EEG file, input all**.** If you wish to only process a subset of channels in each data file, input coi.

If you selected to only examine channels of interest, you will get the following prompts:

Choose an option for entering channels:

include - Include ONLY the entered channel names.

exclude - Include every channel EXCEPT the entered channel names.

Choose whether the channels you enter will be the channels of interest or the channels of disinterest. If you select include, the channel names you enter in the following prompt will be the only channels included in processing. If you select exclude, the channels you enter will be the only ones not included in processing.

Enter channels, including the preceding letter, one at a time.

Press enter/return between each entry.

Examples: E17

M1

When you have entered all channels, input 'done' (without quotations).

NOTE: 10-20 channels are already included.

Enter the channels you wish to include/exclude one at a time. You should include the preceding letter, if applicable. You do not need to include the names of the 10-20 channels, as they are automatically included. If you have any questions about your channel names, refer to your acquisition layout. Ensure that quotations are not used when inputting electrodes as well. Between each entry, press your newline key (enter - Windows, return - Mac). When you are done entering channels, enter done.

Perform bad channel detection? [Y/N]

If you wish to have channels that have high impedances, damage to the electrodes, insufficient scalp contact, and excessive movement or electromyographic (EMG) artifact throughout the recording removed, input Y (case insensitive).

If you select to perform bad channel detection:

Bad channel detection method:

default = Default method optimized in HAPPE v2.

legacy = Method from HAPPE v1 (NOT RECOMMENDED).

You can choose to run either the default or the legacy version of bad channel detection. The legacy version was used in the original HAPPE software, and is outdated and thus not recommended. The default uses the new method of bad channel detection with the Clean Rawdata function with preset criterion that has been optimized.

Frequency of electrical (line) noise in Hz:

USA data probably = 60; Otherwise, probably = 50

This input is necessary to help accurately detect line noise in the data, so ensure that you have chosen the correct frequency based on where the data was collected.

Line noise reduction method:

default = Default method optimized in HAPPE v2.

legacy = Method from HAPPE v1 (NOT RECOMMENDED).

Legacy line noise reduction method uses the CleanLine plugin for EEGLAB from a far less effective version release. For this reason, we recommend inputting default to process your data with the new line noise reduction method in HAPPE that uses an improved version of CleanLine to reduce line noise.

Run HAPPE with visualizations? [Y/N]

By choosing Y(case insensitive) you will run HAPPE in the semi-automated setting, with several visualizations for every file.

If you have selected to run with visualizations, the following prompts will appear:

Minimum value for power spectrum figure:

The minimum value for the plot of the power spectrum.

Maximum value for power spectrum figure:

The maximum value for the plot of the power spectrum.

Enter the frequencies, one at a time, to generate spatial topoplots for:

When you have entered all frequencies, input 'done' (without quotations).

This input asks you to select any particular frequencies you would like to see topoplots for (spatial distribution of power in that frequency across the scalp) in the same image as the power spectrum for that file. Between each entry, press your newline key (enter - Windows, return - Mac). When you are done entering channels, enter done.

Resample data? [Y/N]

NOTE: Resampling is recommended for files <= 60 seconds long.

If you wish to resample your data, input Y, otherwise input N. Either option is case-insensitive.

If you chose to resample your data, the following prompt will appear:

HAPPE supports resampling to 250, 500, and 1000.

Resample frequency:

Choose one of the three possible frequencies above to resample your data to.

Method of wavelet thresholding:

default = Default method optimized in HAPPE v2.

legacy = Method from HAPPE v1 (NOT RECOMMENDED).

The new wavelet method uses a soft Empirical Baysian level-dependent threshold for the wavelets. Wavelet family is coiflet (level 4). This method has been optimized on EEG data. The legacy method of waveletting uses a soft, global threshold for the wavelets. The wavelet family is coiflet (level 5). Threshold multiplier is used to remove more high frequency noise. This method has not been optimized, so it is not recommended.

Segment data? [Y/N]

To segment your data, input Y. Otherwise, input N. If you choose to segment your data for your analysis, you will be asked to answer additional prompts.

If you have selected to segment your data, the following prompts will appear:

Segment start, in MILLISECONDS, relative to stimulus onset:

Example: -500

The starting latency for your segments, relative to the stimulus onset. Including a baseline will result in a negative latency, whereas starting at the stimulus onset would be 0.

Segment end, in MILLISECONDS, relative to stimulus onset:

The ending latency for your segments, relative to the stimulus onset. Stimulus onset is 0, so this number should be greater than 0.

Interpolate the specific channels' data determined to be artifact/bad within each segment? [Y/N]

This option allows you to evaluate within each epoch whether any channels have bad data for that segment by using only the channels that have been marked “good” channels overall from the channel rejection step. Channels flagged with bad data for that segment will then have their data interpolated only for that segment.

Perform segment rejection? [Y/N]

Instead of interpolating data within segments, users can instead select to reject segments that are determined to still be artifact-contaminated. Criteria for rejection include a choice of joint-probability criteria, amplitude-based criteria, or a combined joint-probability criteria with amplitude-based criteria.

If you select to perform segment rejection, the following prompts appear:

Choose a method of segment rejection:

amplitude = Amplitude criteria only

similarity = Segment similarity only

both = Both amplitude criteria and segment similarity

The first option is using amplitude criteria only. Amplitude-based criteria sets a minimum and maximum signal amplitude as the artifact threshold, with segments being removed when their amplitude falls on either side of this threshold. After inputting amplitude,users must set the amplitude to be used for determining artifact-segments. The second option is using segment similarity only. Segment similarity criteria considers how likely a segment’s activity is to be artifact-laden given the activity of other segments for that channel, and also other channels’ activity for the same segment. Outlier segments will be removed. The assumption is that artifact segments should be the rare segments relative to the rest of the data at this point in the processing stream. The third option includes both methods. A combined approach with segment similarity criteria and amplitude-based criteria removes outlier segments based on both standard deviations and a minimum and maximum signal amplitude set by the user. If you input both,you will be prompted to input the minimum and maximum signal amplitude to use as the artifact threshold.

If you select amplitude or both for segment rejection criteria, the following prompts appear:

Minimum signal amplitude to use as the artifact threshold:

This is the minimum signal amplitude used for segment rejection.

**Example:** -200

Maximum signal amplitude to use as the artifact threshold:

This is the maximum signal amplitude used for segment rejection.

**Example:** 200

Use all channels or a region of interest for segment rejection?

all = all channels

roi = region of interest

If you plan to analyze all of the user-specified channels in your dataset, input all.If you have a region of interest that you will be analyzing, input roiand you will be prompted to enter the channels in the region of interest.

If you selected to use a region of interest for segment rejection, the following prompts appear:

Enter the channels in the ROI, one at a time.

When you have finished entering all channels, enter 'done' (without quotations).

Enter the channels you wish to include in your region of interest one at a time. You should include the preceding letter, if applicable. If you have any questions about your channel names, refer to your acquisition layout. Ensure that quotations are not used when inputting electrodes as well. Between each entry, press your newline key (enter - Windows, return - Mac). When you are done entering channels, enter done.

Re-reference data? [Y/N]

If you wish to re-reference your data, input Y. Otherwise, input N.

If you selected to re-reference your data, the following prompts appear:

Re-Referencing Type:

subset = Re-referencing to another channel/subset of channels

average = Average re-referencing

To re-reference the data to a single (non-reference) channel or a subset of channels, input subset. To re-reference across all the user-input channels, input average.

If you selected to re-reference to a subset, the following prompts appear:

Enter channel/subset of channels to re-reference to, one at a time.

When you have entered all channels, input 'done' (without quotations).

Enter the channels you wish to include in your subset one at a time. You should include the preceding letter, if applicable. If you have any questions about your channel names, refer to your acquisition layout. Ensure that quotations are not used when inputting electrodes as well. Between each entry, press your newline key (enter - Windows, return - Mac). When you are done entering channels, enter done.

Format to save processed data:

1 = .txt file (electrodes as columns, time as rows) - Choose this for ERP timeseries

2 = .mat file (matlab format)

3 = .set file (EEGLab format)

Select your preferred format to save your processed data.

Are the above parameters correct? [Y/N]

Use this tool to check that your inputted parameters are correct. If you would like to change one or more parameters, input N.

If you selected to change a parameter, the following will appear:

Parameter to change: data file format, acquisition layout, channels of interest, bad channel detection, line noise frequency, line noise reduction, visualizations, resampling, wavelet thresholding, segmentation, interpolation, segment rejection, re-referencing, save format.

If you do not see an option, quit (Ctrl+C or Cmd+.) and re-run HAPPE.

Enter "done" (without quotations) when finished changing parameters.

Choose from the above list to change a parameter. You will be prompted with the original command to change the parameter. NOTE: this list may change depending on whether you are reprocessing your data. You may change as many parameters as needed, but must change them one at a time. Some selections may require that you answer multiple prompts.

If you created a new parameter set or changed a pre-existing set, you will be prompted to save your parameters:

Parameter file save name:

default = Default name (inputParameters\_dd-mm-yyyy.mat).

custom = Create your own file name.

The default save name for the parameter set is inputParameters\_DD-MM-YYYY.mat, with the current date.For custom save name, input custom and you will be prompted to choose a file name.