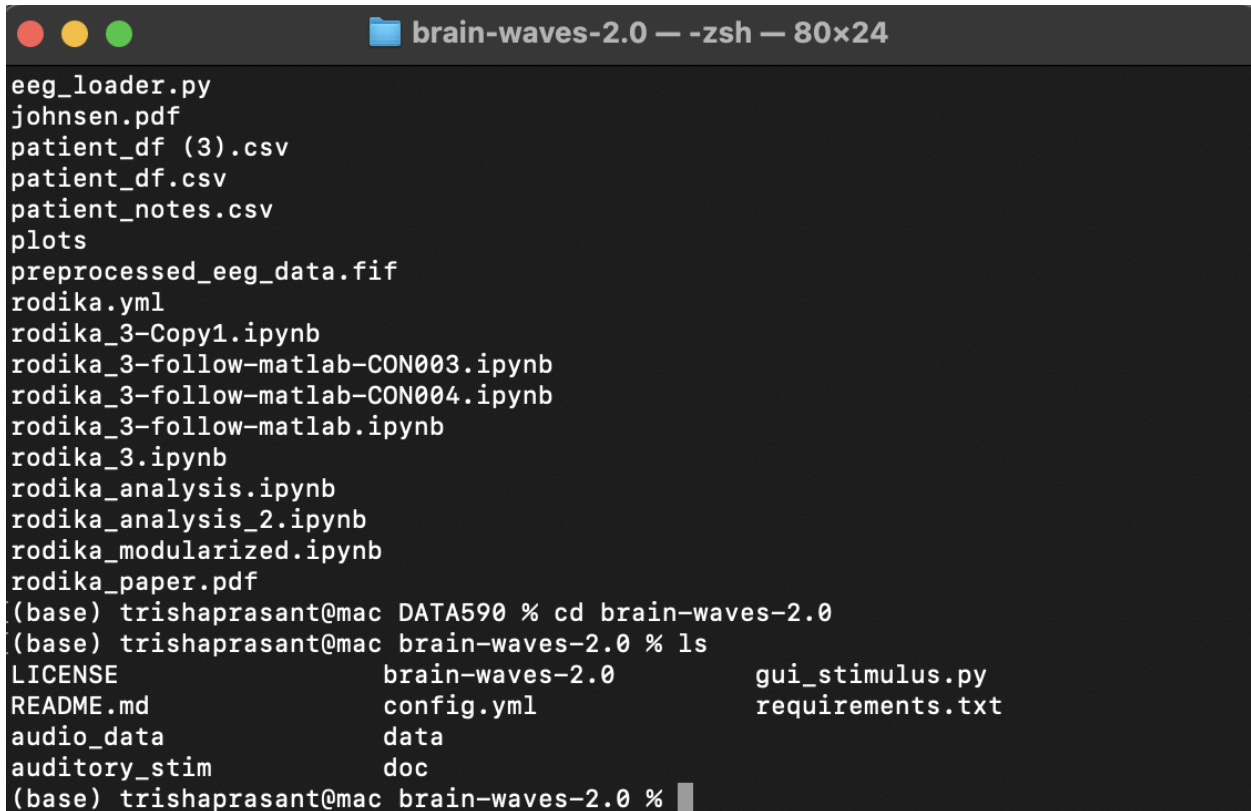# Brain Waves *Application* Step-by-Step Guide

Below is a **step-by-step** guide on how to use the Streamlit application. These instructions follow general workflow of our application,, so someone can replicate the process closely.

---

## 1. Launching the Application

1. **Open a terminal** (or command prompt).
2. **Navigate to your project folder** containing `gui_stimulus.py`.



```
eeg_loader.py
johnsen.pdf
patient_df (3).csv
patient_df.csv
patient_notes.csv
plots
preprocessed_eeg_data.fif
rodika.yml
rodika_3-Copy1.ipynb
rodika_3-follow-matlab-CON003.ipynb
rodika_3-follow-matlab-CON004.ipynb
rodika_3-follow-matlab.ipynb
rodika_3.ipynb
rodika_analysis.ipynb
rodika_analysis_2.ipynb
rodika_modularized.ipynb
rodika_paper.pdf
(base) trishaprasant@mac DATA590 % cd brain-waves-2.0
(base) trishaprasant@mac brain-waves-2.0 % ls
LICENSE                 brain-waves-2.0         gui_stimulus.py
README.md               config.yml              requirements.txt
audio_data              data
auditory_stim           doc
(base) trishaprasant@mac brain-waves-2.0 %
```

*Navigating to the location of brain-waves-2.0 on local computer*

3. **Activate your Python/Conda environment** (e.g., `conda activate eeg`).

**Run the Streamlit app** by typing:

`streamlit run gui_stimulus.py`

```
rodika.yml
rodika_3-Copy1.ipynb
rodika_3-follow-matlab-CON003.ipynb
rodika_3-follow-matlab-CON004.ipynb
rodika_3-follow-matlab.ipynb
rodika_3.ipynb
rodika_analysis.ipynb
rodika_analysis_2.ipynb
rodika_modularized.ipynb
rodika_paper.pdf
(base) trishaprasant@mac DATA590 % cd brain-waves-2.0
(base) trishaprasant@mac brain-waves-2.0 % ls
LICENSE                 brain-waves-2.0         gui_stimulus.py
README.md               config.yml              requirements.txt
audio_data              data
auditory_stim           doc
(base) trishaprasant@mac brain-waves-2.0 % streamlit run gui_stimulus.py

  You can now view your Streamlit app in your browser.

  Local URL: http://localhost:8501
  Network URL: http://192.168.86.37:8501
```

*Running streamlit app using* `streamlit run gui_stimulus.py`

4. **Open your web browser** to the URL displayed in your terminal (often [http://localhost:8501](http://localhost:8501)).

---

# 2. Administer Stimuli (Tab 1)

## A. Patient ID & Trial Types

1. **Look for the field** labeled **"Enter Patient/EEG ID"**.
   - **For example:** typing in the patient ID "CON004", ensures that any stimuli you administer will be recorded under this ID.
2. **Click** the **"Prepare Stimulus"** button.
   - This often randomizes or fetches the trial types from your back-end code. You'll see a message or have trials assigned in memory if successful.

*First tab of application with patient ID entered, and stimulus prepared*

## B. Playing the Stimulus

1. **Check** that your patient ID is still set.
2. **Click "Play Stimulus"**.
   - The system shows a progress bar, updating as each trial is administered.
   - In the background, the software logs the start and end times of each stimulus in a CSV (the `patient_df.csv` or a similar file).
3. **Watch** for any console output.
   - The terminal shows messages/ status updates in the Streamlit interface confirming how many stimuli were played.
   - This will take time!

*Terminal output when audio is being played*

## C. Adding Notes

1. **Scroll down** to **"Add Notes to your Selected Patient and Date."**
2. **Type** any relevant note in the text box (e.g., "Patient responded slowly after the second beep.").
3. **Click "Add Note".**



*Example note added on Tab 1 of application*

## D. Reviewing Existing Notes

1. **Look under "Find Patient Notes".**
2. **Select** a patient ID and date from the drop-down menus (if available).
3. **Read** any existing notes that are displayed.

---

# 3. Upload EEG Files (Tab 2)

## A. Patient ID, Date, & EDF Upload

1. **Type** the patient ID (e.g., "CON004") in the "Patient ID" field.



*Tab 2 of Application with patient ID and Recording Date inputted*

2. **Select** a date from the calendar widget under "Recording Date."
3. **Upload** the EDF file by clicking on "Browse files" (or dragging the file) into the "Upload EDF File" widget.
   ○ Ensure your file is named in a way that the system can use it or that you keep track of the name for future reference.
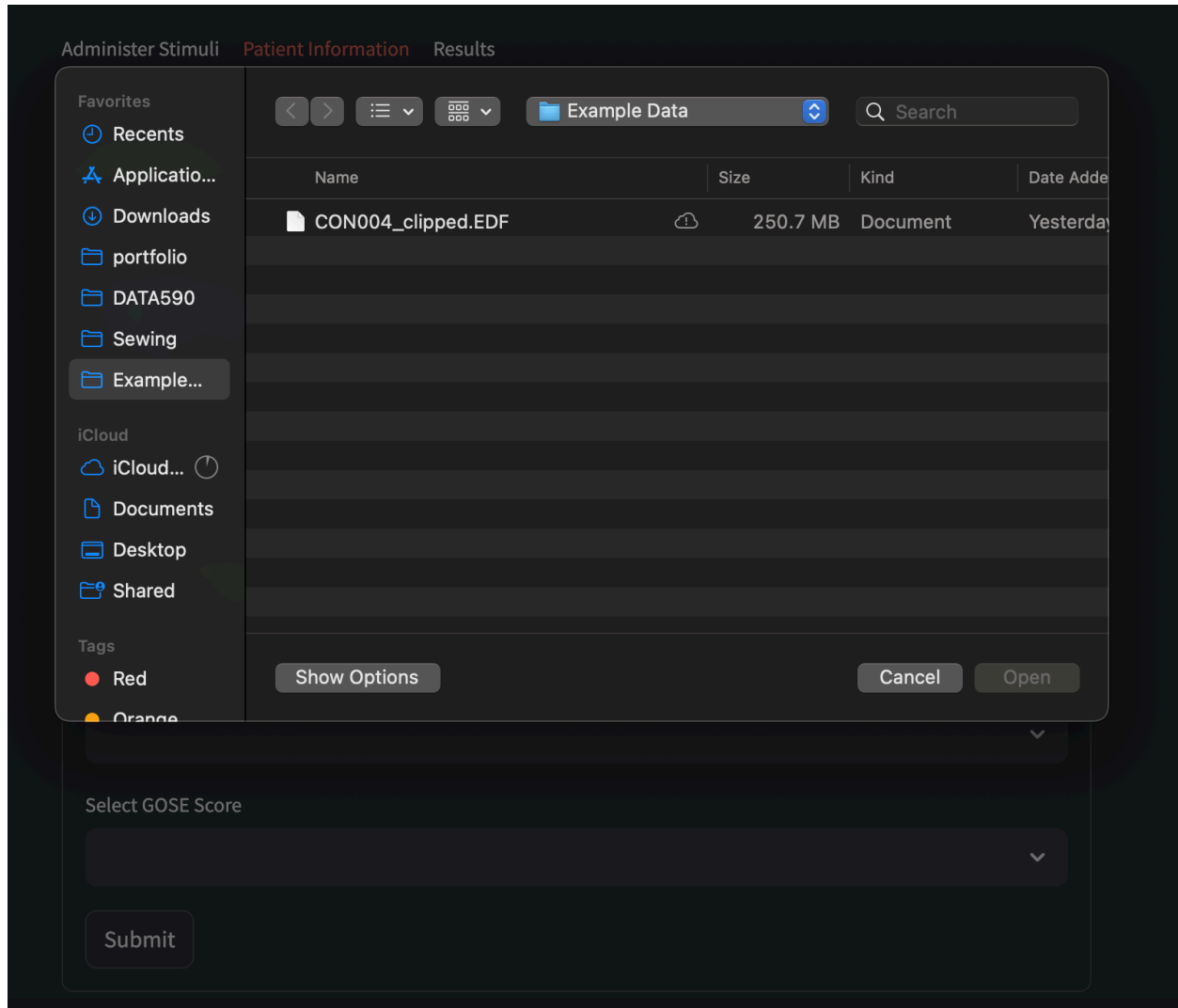


*Selected a new EEG reading (in the form of .edf file) to upload on to application*

## B. CPC / GOSE Scales

1. **Pick** the relevant CPC (Cerebral Performance Category) from the drop-down.
2. **Pick** a GOSE (Glasgow Outcome Scale Extended) level from the second drop-down.

*Selecting CPC Scores for Patient CON004*
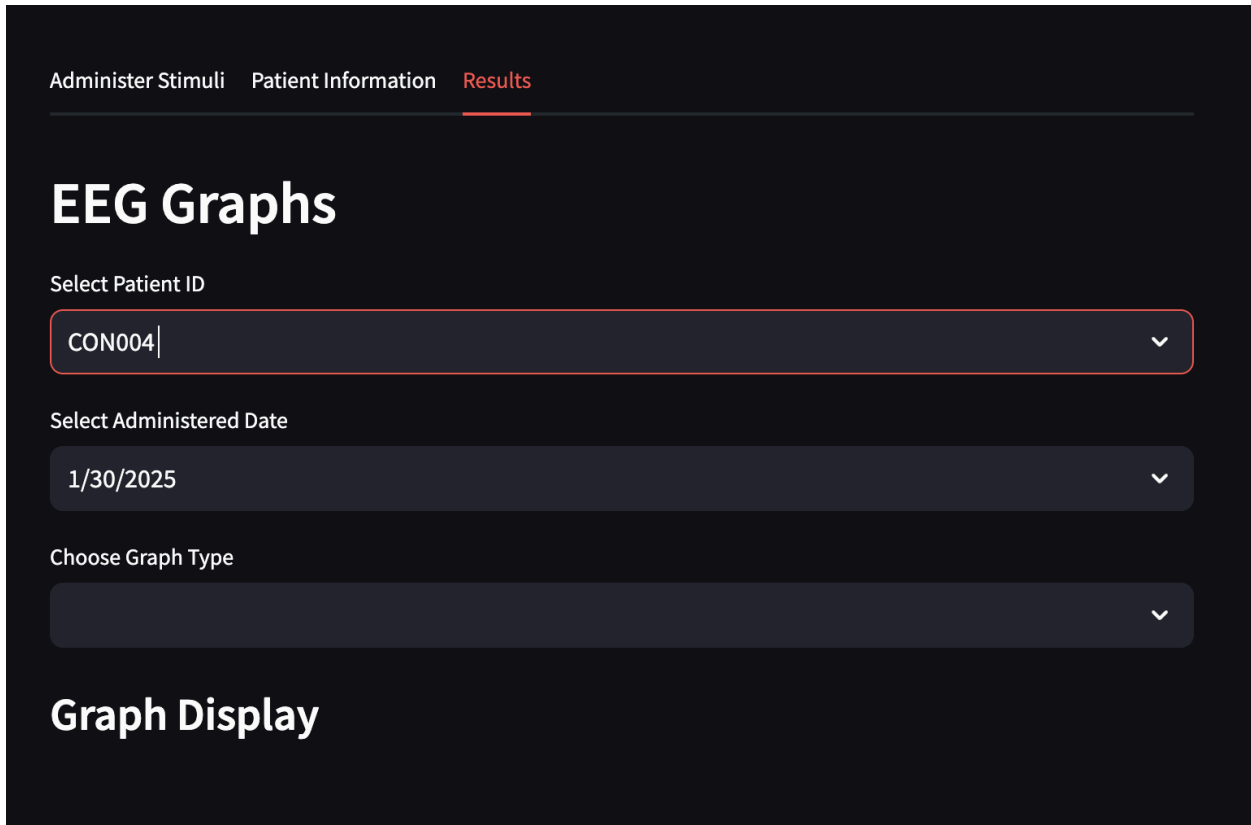
## C. Submitting

1. **Click "Submit".**
   - The app saves your uploaded EDF file to the designated folder (`edf_dir`) and logs the CPC/GOSE labels in a CSV (like `patient_label_path`).

---

# 4. Viewing Results / Graphs (Tab 3)

## A. Selecting Patient & Date

1. **Select** a patient from the drop-down labeled **"Choose Patient"**.
2. **Pick** a relevant date from **"Recording Date"** (or another date selector).
   - The app constructs a filename (e.g., `PatientID_Date.edf`) based on your selection.



Administer Stimuli    Patient Information    Results

# EEG Graphs

Select Patient ID

CON004

Select Administered Date

1/30/2025

Choose Graph Type

## Graph Display

*Tab 3 of Application with Patient ID Selected*

## B. Graph Type

1. **Choose** the **Graph Type** from the drop-down. Typically, you'll see options like **"CMD," "Language Tracking,"** or **"EEG Reactivity."**
2. **If you pick "CMD,"** the code will load classification plots for motor command analysis.
3. If you pick "Language Tracking," you will see ITPC plots generated for all electrodes or a selected channel.

## C. Running the Analysis (If Provided)

1. If there is a button (e.g., **"Run Analysis"** or **"Run Language Tracking Analysis"**), **click** it.
   - The system may call functions from your `eeg_auditory_stimulus` package (like `claassen_analysis.run_analysis(...)` or `rodika_modularized.main(...)`).

# EEG Graphs

Select Patient ID

CON003

Select Administered Date

1/14/2025

Choose Graph Type

CMD

## Graph Display

Run Analysis

```
nanops.py", line 52, in <module>
    bn = import_optional_dependency("bottleneck", errors="warn")
  File "/Users/trishaprasant/anaconda3/lib/python3.11/site-packages/pandas/compa
t/_optional.py", line 135, in import_optional_dependency
    module = importlib.import_module(name)
  File "/Users/trishaprasant/anaconda3/lib/python3.11/importlib/__init__.py", li
ne 126, in import_module
    return _bootstrap._gcd_import(name[level:], package, level)
  File "/Users/trishaprasant/anaconda3/lib/python3.11/site-packages/bottleneck/_
_init__.py", line 7, in <module>
    from .move import (move_argmax, move_argmin, move_max, move_mean, move_media
n,
35, in import_optional_dependency
    module = importlib.import_module(name)
  File "/Users/trishaprasant/anaconda3/lib/python3.11/importlib/__init__.py", li
ne 126, in import_module
    return _bootstrap._gcd_import(name[level:], package, level)
  File "/Users/trishaprasant/anaconda3/lib/python3.11/site-packages/bottleneck/_
_init__.py", line 7, in <module>
    from .move import (move_argmax, move_argmin, move_max, move_mean, move_media
n,
AttributeError: _ARRAY_API not found
AttributeError: _ARRAY_API not found
14%|          | 70/500 [00:11<01:02,  6.91it/s]
```

*Side–by–side output of terminal when clicking "Run Analysis" for CMD Analysis*

Select Patient ID

CON004

Select Administered Date

1/30/2025

Choose Graph Type

Language Tracking

## Graph Display 🔗

## Language Tracking Options

Select Bad Channels

T7 ×    Fp1 ×    Fp2 ×

Select EOG Channels

Fp1 ×    Fp2 ×    T7 ×
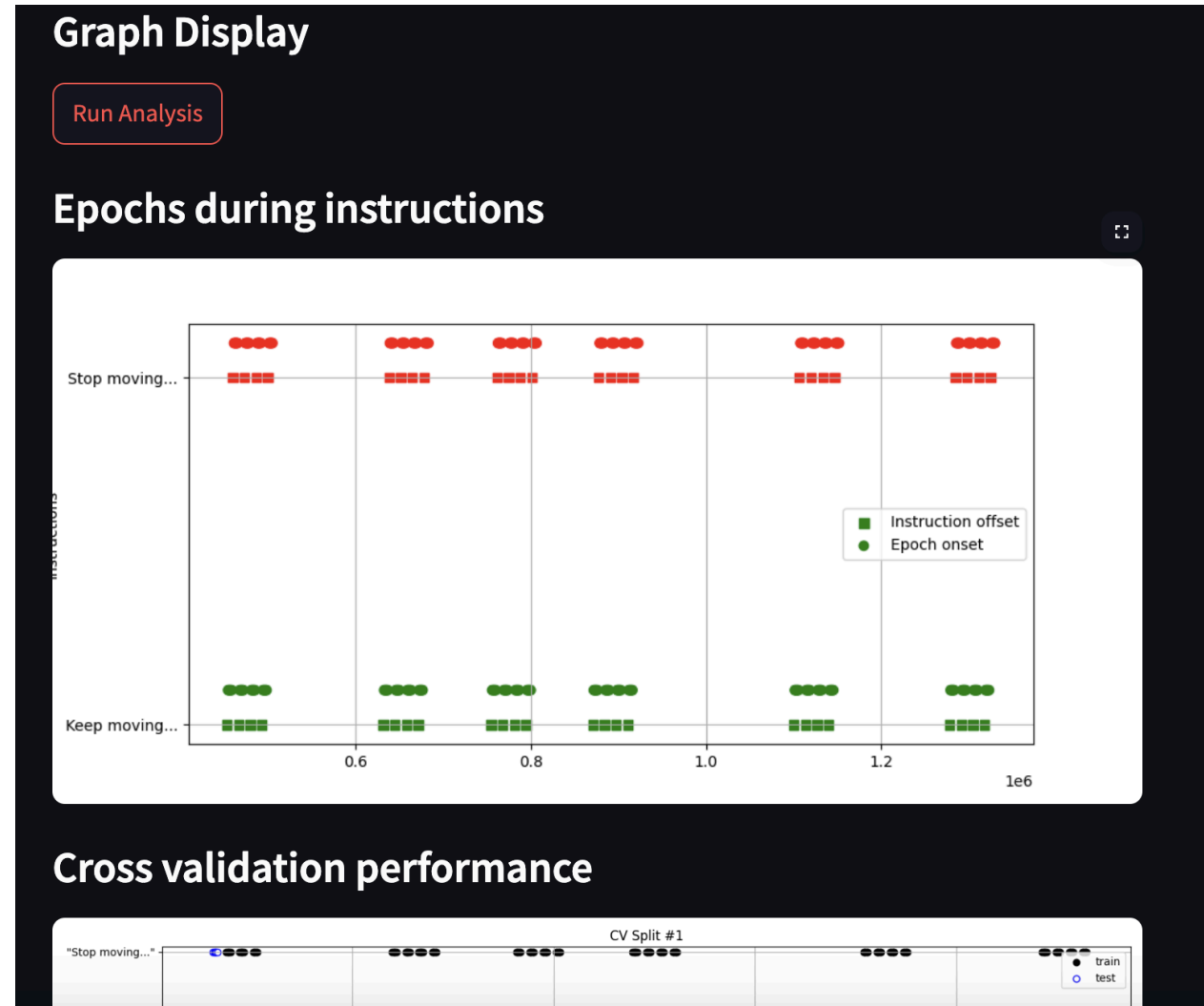
Select Graph to Display

Average ITPC

Run Language Tracking Analysis

*Preparation for ITPC graph results, before clicking "Run Language Tracking Analysis"*

2.  **Wait** for the app to generate results or show a success message

## D. Displaying Graphs

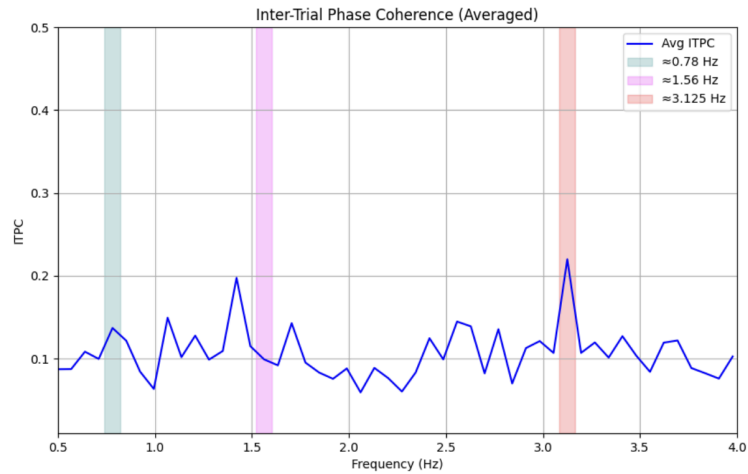1.  **Scroll down** to see any auto-loaded plots (SVM classification scores, or speech-entrainment ITPC at 3 Hz).



*Output of CMD Analysis Charts (should be 6 charts in total)*

*Output of ITPC graph display: averaged ITPC scores over all electrodes*
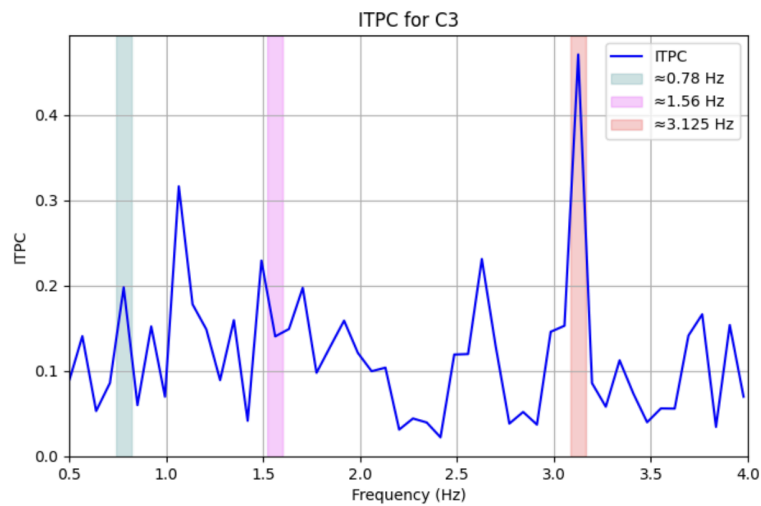


*Output of ITPC graph display: ITPC score for one select electrode*

## 5. Troubleshooting Tips

- **File Path Issues**: Make sure your EDF file or stimulus CSV path is correct in the config or user interface.
- **No Patient or Date Shown**: If a drop-down is empty, it may mean no data for that ID/date combination is in your CSV or the patient never had a stimulus trial in Tab 1.
- **Progress Bars & Logging**: Tab 1's "Play Stimulus" might show a progress bar. This typically means it's writing each stimulus trial into `patient_df.csv` for future reference.

## 6. Workflow Summary

1. **Tab 1**: Enter a patient ID → prepare trials → click "Play Stimulus" → optionally add or review notes.
2. **Tab 2**: Upload your EEG data (EDF files) for that patient and date → specify outcome scales.
3. **Tab 3**: Select the same patient and date → pick an analysis or graph → (optionally) run advanced analysis → review displayed plots or classification metrics.

## 7. Closing or Stopping the App

1. **Return to your terminal** where you started `streamlit run gui_stimulus.py`.
2. **Press** `Ctrl + C` (or `Cmd + C` on macOS) to stop the Streamlit server.

```
from .move import (move_argmax, move_argmin, move_max, move_mean, move_media
n,
35, in import_optional_dependency
    module = importlib.import_module(name)
  File "/Users/trishaprasant/anaconda3/lib/python3.11/importlib/__init__.py", li
ne 126, in import_module
    return _bootstrap._gcd_import(name[level:], package, level)
  File "/Users/trishaprasant/anaconda3/lib/python3.11/site-packages/bottleneck/_
_init__.py", line 7, in <module>
    from .move import (move_argmax, move_argmin, move_max, move_mean, move_media
n,
AttributeError: _ARRAY_API not found
AttributeError: _ARRAY_API not found
100%|████████████████████████████████████| 500/500 [01:20<00:00,  6.21it/s]
Permutation p-value = 0.9320
Empirical AUC = 0.42 +/- 0.19
Shuffle AUC = 0.50
p-value = 0.9321
Test run: False
Test run: False
Test run: False
Test run: False
^C  Stopping...
(base) trishaprasant@mac brain-waves-2.0 %
```

*Stopping streamlit app, by using Ctrl + C*

3. **Deactivate** your Conda environment if you wish (`conda deactivate`).