Dear Fellow ECoG Researcher,

These are the finger flexion data described in the PLoS Computational Biology 2012 manuscript titled *“Human Motor Cortical Activity Is Selectively Phase- Entrained on Underlying Rhythms”*. These are illustrated in figures 1-5, 8, 9, 11-12, S1-10, S16-17, S19-20.

Miller, Kai J., Dora Hermes, Christopher J. Honey, Adam O. Hebb, Nick F. Ramsey, Robert T. Knight, Jeffrey G. Ojemann, and Eberhard E. Fetz. "Human motor cortical activity is selectively phase-entrained on underlying rhythms." *PLoS computational biology* 8, no. 9 (2012): e1002655.

Please keep in mind that these anonymized data are from real patients who donated time in a difficult period of their lives to advance our understanding of the brain. Any publication involving these data **MUST** include the following in the methods section of the manuscript, without modification:

**Ethics statement:** All patients participated in a purely voluntary manner, after providing informed written consent, under experimental protocols approved by the Institutional Review Board of the University of Washington (#12193). All patient data was anonymized according to IRB protocol, in accordance with HIPAA mandate. These data originally appeared in the manuscript *“Human Motor Cortical Activity Is Selectively Phase- Entrained on Underlying Rhythms”* published in PLoS Computational Biology in 2012 [Reference].

During the finger movement task, subjects were cued with a word displayed on a bedside monitor indicating which finger to move during 2- second movement trials. The subject performed self-paced movements in response to each of these cues, and they typically moved each finger 2–5 times during each trial, but some trials included many more movements. A 2-second rest trial (blank screen) followed each movement trial. There were 30 movement cues for each finger, and trials were interleaved randomly. Finger positions were recorded using a 5 degree-of-freedom dataglove sensor (5 dt, Irvine, CA).

The basic datafiles (in MATLAB format) are named “##\_fingerflex.mat” in the folder data/##, where ## denotes the 2 letter patient code. This code is not the patient’s initials. The corresponding subject number for each patient from the manuscript is:

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
|  | Subject | Age | Sex | Handedness | Array location |
| bp | 1 | 18 | F | R | L Frontoparietal |
| cc | 2 | 21 | M | R | R Frontotemporal |
| zt | 3 | 27 | F | R | L Fronto-temporal-parietal |
| jp | 4 | 35 | F | R | L Fronto-Temporal |
| ht | 5 | 26 | M | R | L Parietal - Temporal - Occipital |
| mv | 6 | 45 | F | R | L Frontotemporal |
| wc | 7 | 32 | M | R | L Fronto-temporal-parietal |
| wm | 8 | 19 | F | R | R Fronto-parietal |
| jc | 9 | 18 | F | R | L Frontal |

Each datafile has 7 variables:

"subject": This is the 2-letter patient code

"brain": This is a structure representing the tessellated brain surface. It can easily be plotted with the CTMR package *(see “Automated electrocorticographic electrode localization on individually rendered brain surfaces” by D Hermes, et al in Journal of Neuroscience Methods, 2009)*

"locs" (number of channels x 3): Electrode locations, for plotting on the rendered brain.

"elec\_regions" (number of channels x 1): A numerical code for the anatomical location of the associated channel. The code is as follows:

1 – dorsal M1

3 – dorsal S1

4 – ventral sensorimotor (M1+ S1)

6 – frontal (non-rolandic)

7 – parietal (non-rolandic)

8 – temporal

9 – occipital

"data" (time x number of channels): These are the data.

* sampled at 1000Hz
* scale factor: 1 amplifier unit = .0298 microvolts
* built-in band pass 0.15 to 200 Hz,

- but a 1 pole band pass, so there is no sharp corner at 200Hz.

-The amplitude roll-off function is in the file “ns\_1k\_1\_300\_filt.mat”

"flex" (time x number of fingers): These are the finger flexions. Note that they are in the raw form input. They are in 40ms blocks, and have non-zero offset. The 5 columns correspond to the digits thumb-index-middle-ring-little in order.

"cue" (time x 1): Screen cue. This is the cue on the screen at each point in time (note that this might be different than the actual behavior).

0 – Inter-stimulus interval

1 – thumb

2 – index finger

3 – middle finger

4 – ring finger

5 – little finger

There is an additional file, are named “##\_stim.mat” in the folder data/##, where ## denotes the 2 letter patient code. This file contains a variable “stim”, which are labeled epochs encasing the actual movement types. The code is as follows:

0 – Inter-stimulus interval

1 – thumb

2 – index finger

3 – middle finger

4 – ring finger

5 – little finger

In order to reproduce the analyses from the manuscript, open and examine the file “call\_subs\_processing.m”. Each step of analysis is shown clearly in the functions called from this file. Intermediate processed data are saved automatically in the data/## folder (where ## denotes the 2 letter patient code).

In order to plot the data for each patient in all of the various ways illustrated in the manuscript, open and examine the file “call\_subs\_figs.m”. I have annotated the code in a manner that clearly states how and what is being plotted. As figures are generated, they are deposited into the figs/## folder (where ## denotes the 2 letter patient code).

Please note that I use a “code-section” approach to programming (each section headed by “%%”), and it is intended that you evaluate each section (control-enter or command-enter) in sequence to understand each step.

Note that the folders “ctmr” and “toolbox” from the root directory (zip files of the ECoG library) must be included in your MATLAB path for the analyses / figure generation to work properly.

Best Wishes!

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Stanford University, 2015 (revised 2018)

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