

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.

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 [Insert Embedded Citation for the Manuscript Here – e.g. Endnote, BibTex].

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
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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.

Best Wishes!
Kai Miller,
Stanford University, 2015
kai.miller@stanford.edu, kjmiller@gmail.com