**UMAP data description:**

Location: /mnt/genzel/Rat/OS\_Ephys\_RGS14\_analysis/UMAP

*Rat folders:*

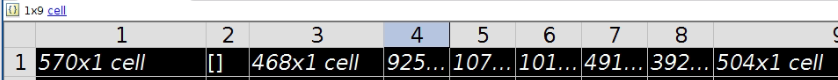
Includes data of rats used in RGS14 paper: 1,2,3,4,6,7,8,9.

*Within each folder:*

1. GC\_window\_ripples:

1x9 cell array which contains detections per trial considering PT5 split in 4.

Within each trial one finds X cells which represent X ripples. For each ripple one finds a 2x15001 matrix. The rows represent the brain regions (PFC and HPC pyramidal layer). The 15001 contains 6 seconds of recordings centered on the ripple peak using a sampling rate of 2500 Hz. The traces stored here are **not filtered**.



1. Ripple\_waveforms\_umap.

This has a similar structure to the variable above (1x9 cell). The difference is that the data within each trial has the form X x 127, with X being the number of ripples. Essentially what happened is that the cortical data was ignored.

1. Aligned\_ripple\_waveforms\_umap

Very similar to the data above but in this case each ripple was first aligned to the minimum value which is closest to the ripple peak. After this alignment, a window of ±50ms is extracted from the new aligned center of the ripple, giving a total of 127 samples per ripple.

1. Filtered\_aligned\_ripple\_waveforms\_umap

It has the same structure as “Aligned\_ripple\_waveforms\_umap”. The only difference is that the traces have been filtered in the ripple range (100-300Hz).

1. Once the data has been filtered, it is then stored in a Matlab table (analogous to a python dataframe) which we have called “T”. The description of each column of T is the following:

Column 1: Treatment

Column 2: RatID

Column 3: StudyDay

Column 4: Trial

Column 5: Ripple waveforms.

Column 6: Amplitude (Using own method)

Column 7: Mean frequency.

Column 8: Amplitude2 (Method from Pridalab)

Column 9: Frequency (Method from Pridalab)

Column 10: Entropy

Column 11: AUC

Column 12: AUC2 (not sure what’s difference between both AUC methods)

1. Ripple\_Waveforms\_Rat\_OS: These files contain the raw ripple waveforms with the actual duration of each ripple. NOTE: The amount of ripples found here may differ from that of the GC files. This is because the traces extracted for the GC file are 6-second long, so in case a ripple is too close to a sleep stage transition and there are no 6 seconds of signal available, this ripple is then discarded from the GC files. The structure is 1x9 and for each trial one would find X columns representing X ripples. For each ripples the signal length is Dx1 with D being the individual duration of each ripple. The data is not filtered.

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*Outside of Rat folders:*

1. RGS.mat: Contains a structure with preprocessed data for all rats with increased cortical plasticity using RGS.
2. RGS\_raw.mat. Same as above but using raw data, i.e., not filtered in the ripple band.
3. RGS\_ripples.mat: Contains waveforms of all RGS rats based on their individual duration. (Not UMAP format). The data is not filtered.

The three above also apply to the VEH data. Just replace RGS with VEH.

1. Ripples.mat: Cell array which length is the total number of trials. Within each cell one finds the ripples in the UMAP format.
2. T.mat: Main variable for python scripts. Contains all data.
3. T\_bk.mat: It is just a back up of T.mat.
4. T\_raw: Table which contains unfiltered ripples.
5. T\_ripples. Table which contains the ripple waveforms based on their individual duration.
6. T\_cell: Contains the same data as T but instead of being a table it is a cell array.
7. T\_cell\_ripples.mat: Discontinued. Can ignore and eventually erase.