**UMAP data description:**

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

*Rat folders:*

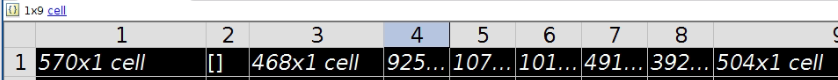
Includes data of rats used in RGS14 paper: 1,2,3,4,6,7,8,9.

*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.

1. Ripple\_Waveforms\_Rat\_OS: These files contain the 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.