

Neuronexus EEG Probe Mapping

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Overview

This protocol describes how to map the location of the Mouse EEG v2 H32 Probe with the OM Amplifier Adapter. For better or worse, like all custom probes mapping must be confirmed manually.

Per Neuronexus the recordings are stored in the following format:

Radiens saves primary time-series data sets (e.g., neural recordings) in a simple, open format. Each dataset (i.e. recording) is saved in a file set named ‘XDAT’ that consists of three files: (i) flat binary file containing the matrix of all sample values (typical in uV) across the multiple channels, (ii) flat binary file containing all timestamps, (iii) json text file containing enriched metadata. [link](#)

We can import metadata from the json file which contains information about the probe layout and recording:

```
% MATLAB code to extract metadata from XDAT dataset

str = fileread([xdat_filename '.xdat.json']);
jsonData = jsondecode(str);

% extract metadata for probe mapping
H32Metadata = jsonData.sapiens_base.biointerface_map;

% remove non-array fields
H32Metadata = rmfield(H32Metadata, 'samp_freq');
H32Metadata = rmfield(H32Metadata, 'sig_units');
```

```
% save metadata as CSV
writetable(struct2table(H32Metadata), 'NeuroNexusMouseEEGv2H32_Map.csv');
```

For convenience, I have hosted the resulting CSV file on [github](#) for further analysis.

Examining the Probe Metadata

We will evaluate the metadata in R to more easily plot and wrangle the data. First, we will load the CSV file from github and view the first 5 rows of the metadata.

```
# Load CSV file from github

H32Metadata <- read_csv("https://raw.githubusercontent.com/cincibrainlab/vhtp/main/chanfil

# View the first 10 rows of the metadata
tb1 <- H32Metadata %>% head(5) %>% kable()
```

Table 1: Table of XDAT dataset metadata for the Mouse EEG v2 H32 Probe.

```
\begin{tabular}{l|l|r|l|r|r|r|r|l|r|r|r|l|r|r|r|r|r|r|l|l|r} \hline chan\_name & chan\_type & nt\end{pre}
```