

Detailed description of the **source code file** (Matteucci_et_al_source_code.7z) and **source data file** (Matteucci_et_al_source_data.7z) for the article “A template-matching algorithm for laminar identification of cortical recording sites from evoked response potentials” by Giulio Matteucci, Margherita Riggi and Davide Zoccolan.

Source code file

The source code file is an archive file in 7z format (.7z) containing 5 Matlab functions and 1 Matlab script file (.m). Recommended Matlab version to run this code is R2018 or higher. The code files are the following:

- **MTM_layer_prediction_example.m**: script the user should run to execute a small example of prediction of the cortical depths and laminar position of channels of a test session using the reference template described in the paper (this script is meant to demonstrate the usage of the provided functions).
- **get_VEP_template_for_MTM.m**: function needed to build a new VEP template starting from a histologically annotated VEP dataset.
- **get_MTM_predicted_depth.m**: function implementing the core of the algorithm described in the paper to predict cortical depths of recording channels of a test session (using the template that can be build using the previous function).
- **get_MTM_predicted_layers.m**: function using histologically inferred layer border depths to map predicted depths (outputted by the previous function) into predicted layer labels.
- **inspect_MTM_template.m**: visualization function that can be used to inspect the VEP template being used by the algorithm.
- **inspect_MTM_prediction_results.m**: visualization function that can be used to inspect the results of the depth and layer prediction performed by the algorithm on the session provided as input.

Functionality of the code is extensively commented in the code files themselves.

Source data file

The source data file is an archive file in 7z format (.7z) containing 4 data files in Matlab format (.mat). The data files are the following:

- **VEP_dataset.mat**: .mat file containing 1 matrix (X) with dimensions = (channels,timesamples) containing downsampled VEPs (in μV) for each channel of each recording sessions discussed in the paper; 2 vectors (Y and Y_layer) containing ground-truth histological annotations for each channel (for depth, in μm , and laminar location respectively) and 2 scalars storing the number of sessions (N_sess) and the sampling frequency (S_freq in Hz) of data in X.

- **VEP_template.mat:** .mat file containing 2 matrices (VEP_template_mu and VEP_template_std) containing the reference VEP templates obtained from the paper dataset (average, and standard deviation respectively) and 1 scalar storing the sampling frequency (S_freq in Hz) of the template traces.
- **layers_borders_from_histology.mat:** .mat file containing 1 vector (V1_layer_bins) storing, in order, upper and lower boundaries (in μm) between cortical layers as obtained from histological annotation of our dataset and 1 cell array with layer labels (V1_layer_bins_names).
- **example_session_data.mat:** containing 1 matrix (X_test) and 2 vectors (Y_test and Y_layer_test) organized in a similar way as X, Y and Y_layer from the VEP_dataset.mat file but containing data (observed VEPs for each channel and their ground-truth depths and laminar location respectively) meant to be used to demonstrate depth and layer prediction by the MTM_layer_prediction_example.m script.

Usage note: To run the demonstrative depth and layer prediction example provided here unzip the content of both .7z files in a folder on your Matlab path and then simply run the script MTM_layer_prediction_example.m.