**How to make a match: Neural representation of memories in the human brain during a memory card game**

# Experimental data

The experimental data can be found in **the .zip files**.

* **data\_iEEG**:
	+ **nf\_subject\_(n).mat** : n\_channels x n\_time, raw voltages
	+ **trigger\_info.mat** : time information
* **data\_localization**:
	+ **hdr\_subject\_(n).mat** : 1 x n\_channels struct, info about electrodes’ localization
* **data\_psychophysics**:
	+ **behavior\_subject\_(n)**.**mat** : 1 x n\_boards (# of boards played). Important fields:
		- mouse\_click\_timing: time at click
		- mouse\_click\_timing: position of click on the board
		- subject\_score: score after each click
		- piece\_status: matrix representing the board at each click. 0: tile faces down, 1: tile clicked, 2: tiles matched.
		- piece\_coordinates: coordinates (corners) of each piece on the board
		- board\_coordinates: coordinates (corners) of each piece on the board
		- list\_of\_images: index of the images included, from COCO dataset
		- object\_position: n x n, position of the images (list\_of\_images) on the board
			* e.g., list\_of\_images=[10, 400, 300, 500]. Object\_position=[4, 3, 1; 3, 1, 5; 4, 2, 2]. Images are distributed as : [500, 300, 10; 300, 10, distractor; 500, 400, 400].
		- list\_of\_objects: 1 x n2, vectorized representation of object\_positions
		- piece\_number: index of piece clicked
	+ **b\_data.mat** : Important params:
		- inter\_1img\_2img: RT between 1st and 2nd click.
		- Inter\_1img\_reset: time between 1st click and time trial is reset.

# Code

The code scripts are in **code.zip**.

## Preprocessing

Computation of behavioral parameters, time-frequency decomposition (TFD), and area under the curve (AUC). All .mat files and folders start with **P**. Results are saved in the folder with the same name as the .mat file. The scripts have to be run in order.

* **P00\_behavioral\_data.m**: for each subject, create behavioral data from *data\_psycohpysics*, including predictors used in the GLM. It computes: match (n\_trials x 1), random\_match (n\_trials x 1), n\_since\_pair (n\_tiles x 1), n\_since\_last\_click (n\_tiles x 1), n\_times\_seen (n\_tiles x 1), reaction\_time (n\_trials x 1), board\_size (n\_tiles x 1), position\_x (n\_tiles x 1), position\_y (n\_tiles x 1), distance (n\_trials x 1), image\_category (n\_trials x 1).
* **P01\_TFD\_chronux\_tile\_(1/2).m**: for each trial, computes TFD from raw voltages (*data\_iEEG*) using the chronux toolbox. It allows to select the desired frequency band: gamma (most used), beta or alpha. Data is aligned to the 1st (1) or 2nd (2) tile.
* **P02\_AUC\_tile\_(1/2)**: for each trial, computes the AUC of the selected frequency band from the TFD computed using *P01\_TFD\_chronux\_tile\_(1/2).*
* **P04\_VIF\_correlation:** for each subject and subjects’ average, it computes and plots the VIF and pair-wise correlation across predictors used in the GLM.
* **P05\_group\_regions\_tile\_(1/2) .m:** creates a new folder where data of all subjects are organized by brain regions, instead of by subject.

## Generalized Linear Model (GLM)

All .mat files and folders that start with **P**. Results are saved in the folder with the same name as the .mat file. It is necessary to have the results from **P00\_behavioral\_data** and **P03\_AUC\_tile\_(1/2)** before running the code. **G01\_compute\_GLM** has to be run first. The rest can be run in any order.

* **G01\_compute\_GLM.m**: for each subject and each channel, computes the GLM. It saves the beta coefficiengs (GLM\_b), t-statistics (GLM\_t) and p-values (GLM\_p) for each predictor and channel. It also saves the models’ R2 and p-value (GLM\_R2). Plots t-statistics for each channel.
* **G04\_table\_predictos.m**: Creates a table with the results of all channels selective for the indicated predictor and selected tile.
* **G05\_regions\_statistics.m**: Statistical testing to check whether a region has more significant channels than expected by chance for a specific predictor. Results are saved on a table

## Decoding match

All .mat files and folders that start with **D**. Results are saved in the folder with the same name as the .mat file. Code used to analyze latency of different brain regions. It is necessary to have the results from **P00\_behavioral\_data**,  **P01\_TFD\_chronux\_tile\_(1/2)** , and **P03\_AUC\_tile\_(1/2)** (only for those ended with \_glm)**.**

* **D01\_decoding.m:** to decode match versus mismatch, with data organized by brain region.
* **D02\_analyze\_decoding.m:** Script to plot decoding results. Important! It is necessary to run D01\_decoding 2 times: using both times EXACTLY the same features, but one with randomize = false, and other with % randomize = true. It computes whether the non-randomize is significant for a p-value of 0.01.

## Figures

All .mat files and folders that start with **M**. Results are saved in the folder with the same name as the .mat file. Plot figures on the paper. It is necessary to have the results from **P00\_behavioral\_data**,  **P0(1/2)\_TFD\_(chronux/fieldtrip)\_tile\_(1/2)** , **P03\_AUC\_tile\_(1/2)** and **G01\_compute\_GLM.**

* **F01\_behavior\_figures.m**:
	+ Plot: predictor bar plot for match vs. mismatch for each subject
	+ Plot: predictor bar plot for match vs. mismatch for each board size – across all subject
	+ Linear model: Test whether a predictor increases/decreases with board size, for match and mismatch, and for each tile.
* **F02\_electrodes\_tile\_(1/2).m:** plot results for single electrodes (paper).
	+ 1: GLM t-statistic of each predictor
	+ 2: Power match vs. mismatch, w/wo statistical testing
	+ 3: Raster plot match vs. mismatch trials, ordered (or not) by a specific predictor
	+ 4: Rasper plot for all trials, ordered (or not) by a specific predictor. 4a: from bigger to smaller, 3b: from smaller to bigger
	+ 5: Gamma power for different ranges of predictors' values
	+ 6: Scatter plot of the AUC vs. a predictor
	+ 7: Plot power for different image categories