



Bad moods may affect brain connectivity



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INTRODUCTION

- Aim of this study: provide new insights into the dynamics of brain activity and their relationship with psychological functions.
- This relationship is explored by connecting different types of data, measured on the same subject over one year:
 - brain data**, collected through resting-state and task-based *fMRI*
 - behavioral data**, i.e. scores assigned by the subject himself to psychological indices characterizing his emotions

BRAIN DATA ANALYSIS

Goal: measure the connectivity between two brain points along different sessions.
Data: *fMRI* acquisitions of a single subject's brain activity during T different sessions. For each session, we have τ time values for each of the 17281 brain points in the template mesh. To reduce the dimensionality of the problem and to increase the robustness and interpretability of the results, the brain points are clustered in 83 regions.

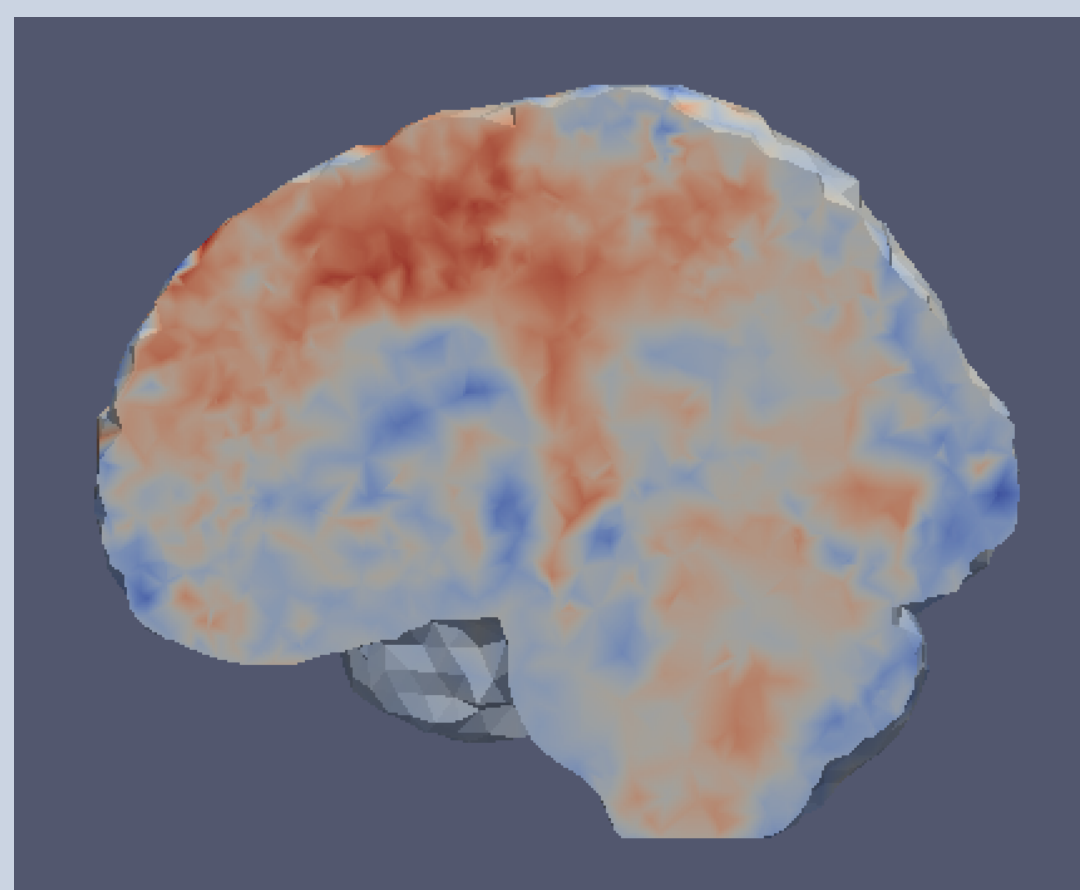


Figure 1 – Connectivity between brain points

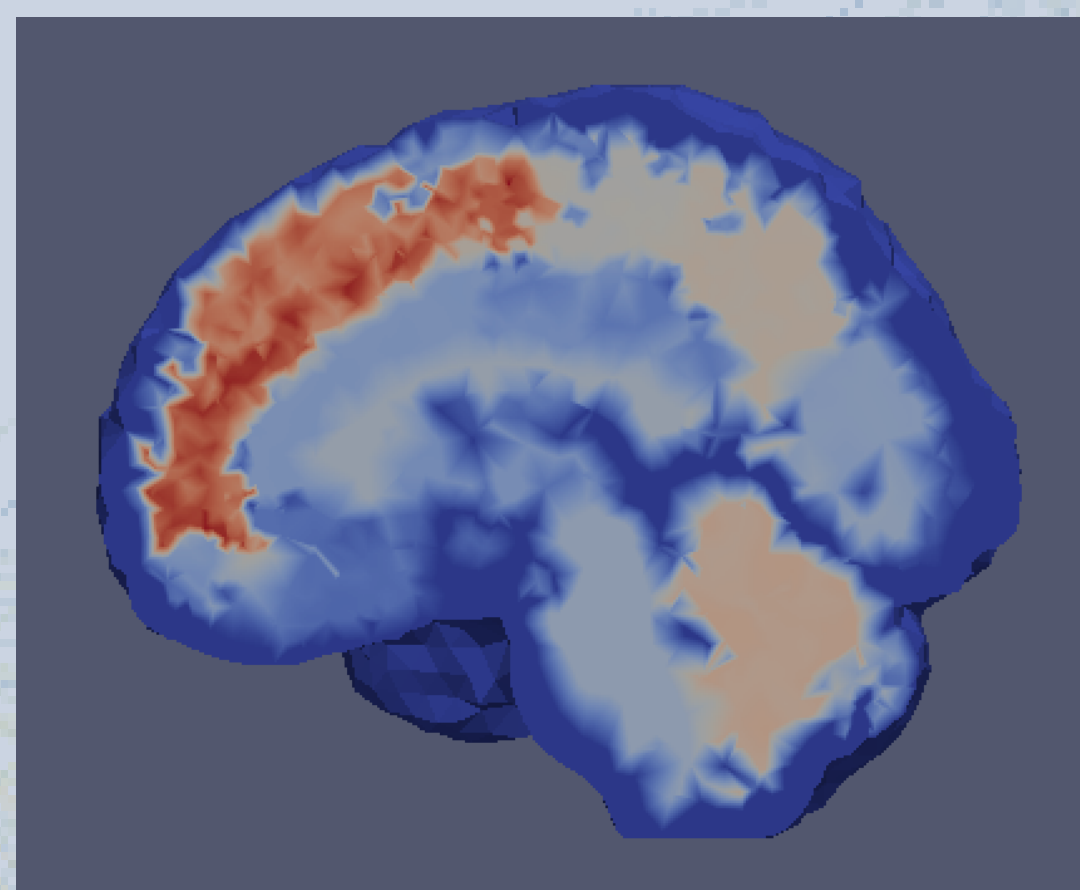


Figure 2 – Connectivity between brain regions

From *fMRI* to graphs: the connectivity between two brain regions is measured through the correlation between their activity level during each session \Rightarrow we obtain T correlation matrices that we interpret as the adjacency matrices of T graphs. For each graph, the nodes represent the regions and the weight of each edge (i,j) represents the correlation among region i and region j in the given session.

Goal of network analysis: measure the importance and the connections among the regions in each graph (**centrality** property), obtaining a $T \times 83$ dataset.

Results:

- resting-state** case: three regions (*hippocampus*, *nucleus accumbens* and *temporal horn*) have a significantly higher centrality than the mean of the other regions
- task-based** case: connectivity graphs are in general very different from the resting state ones, but those three regions are often among the most central

MODULARITY DETECTION

Goal: evaluate how network nodes are connected and grouped together in **communities**, i.e. subsets of nodes highly connected among each other, but sparsely connected to the rest of the network (**modularity** property).

Data: the time signals on the brain mesh are averaged over the 83 regions. The resulting average time signals are split into *time windows* of 30 seconds. For each time window, an 83×83 correlation matrix is computed and converted to an adjacency matrix. The series of adjacency matrices defines a *multigraph*.

Results: across the resting-state sessions, the networks show an approximately random pattern, thus it is not easy to identify recurrent communities.

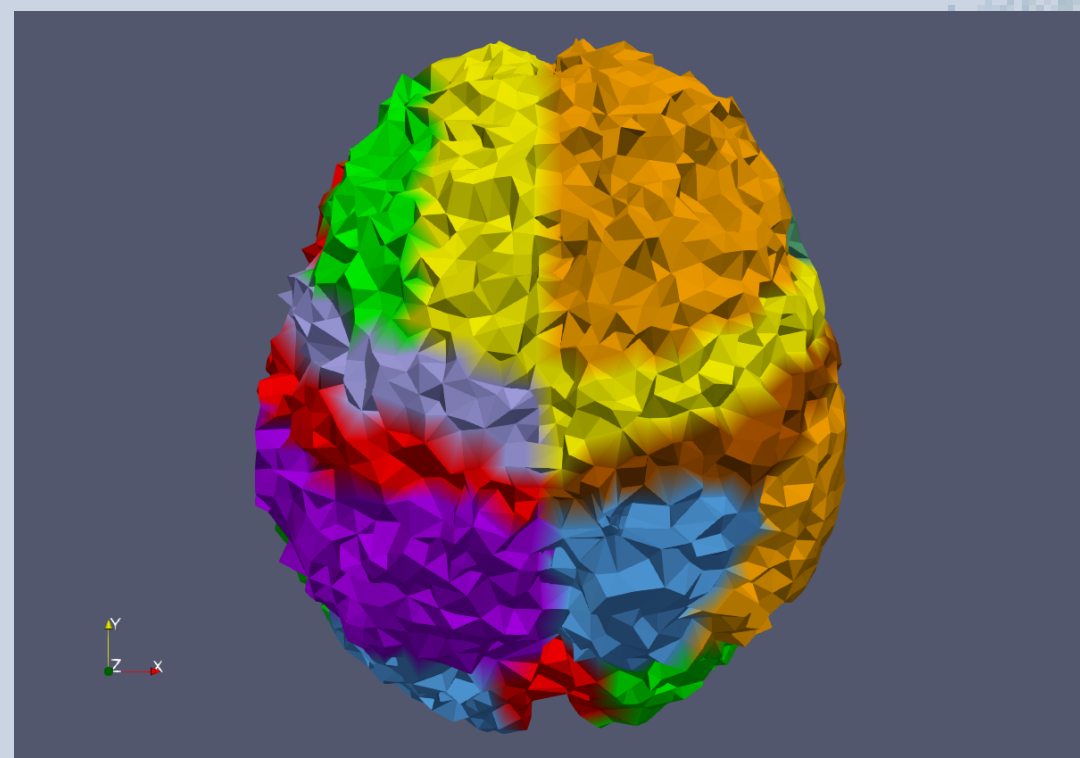


Figure 3 – Communities - session 11

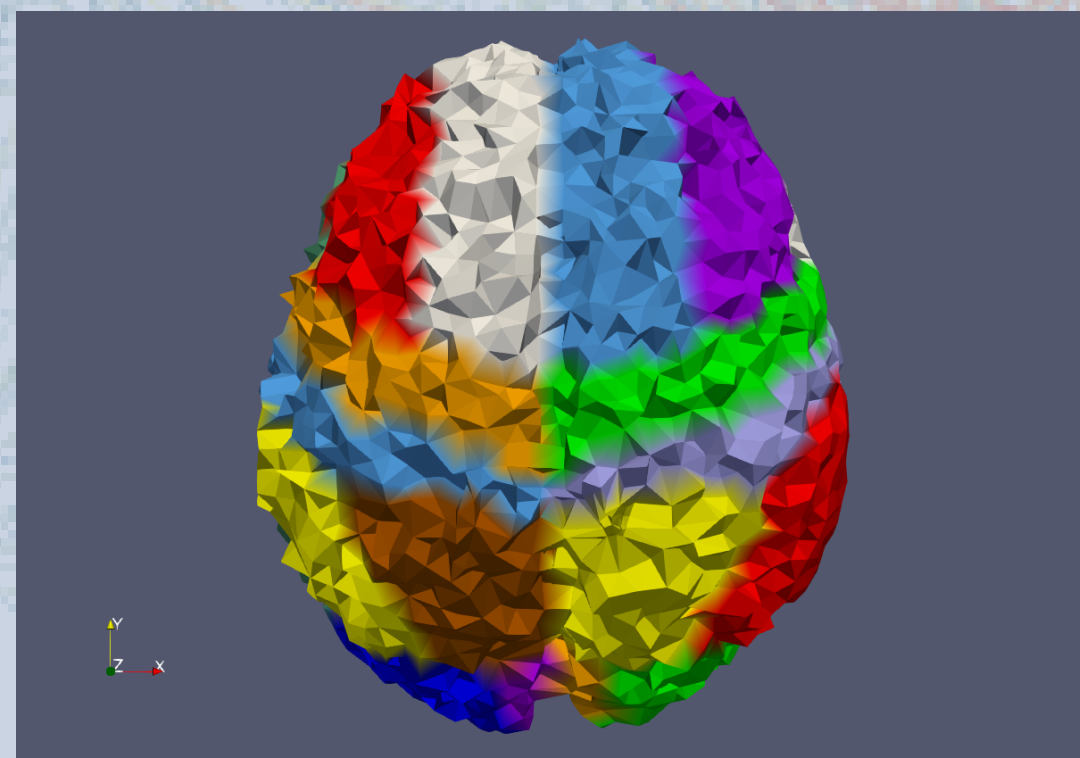


Figure 4 – Communities - session 38

A **linear regression** on the dataset joining the modularity measures with the three PCs of behavioral data does not provide interesting correlation results \Rightarrow the resting-state functional brain connectivity is to some extent non behavior dependent.

CONCLUSIONS

- Behavioral** data: are interpreted from the result of Principal Component Analysis.
- fMRI** data: the graph approach is useful to underline central regions of the brain, partially dependent on the task performed during the session.
- Modularity detection:** shows that brain regions, in the resting-state case, cannot be grouped in larger communities according to their functionality.
- JIVE** algorithm: proves that behavioral data and *fMRI* data are completely uncorrelated for resting-state sessions, while they are correlated in the task-based case: in-task working memory performance are affected by emotions.

BEHAVIORAL DATA ANALYSIS

Goal: extract relevant information about the psychological attitude of the subject during the analysis, in order to connect it with his brain activity.

Data: mood of the subject, described through 57 variables that quantify his principal emotions (e.g. sadness, excitement, etc.)

Results: the first three components of a PCA (see Figure 5) explain the 60% of the total variance, while the remaining ones do not have a clear interpretation.

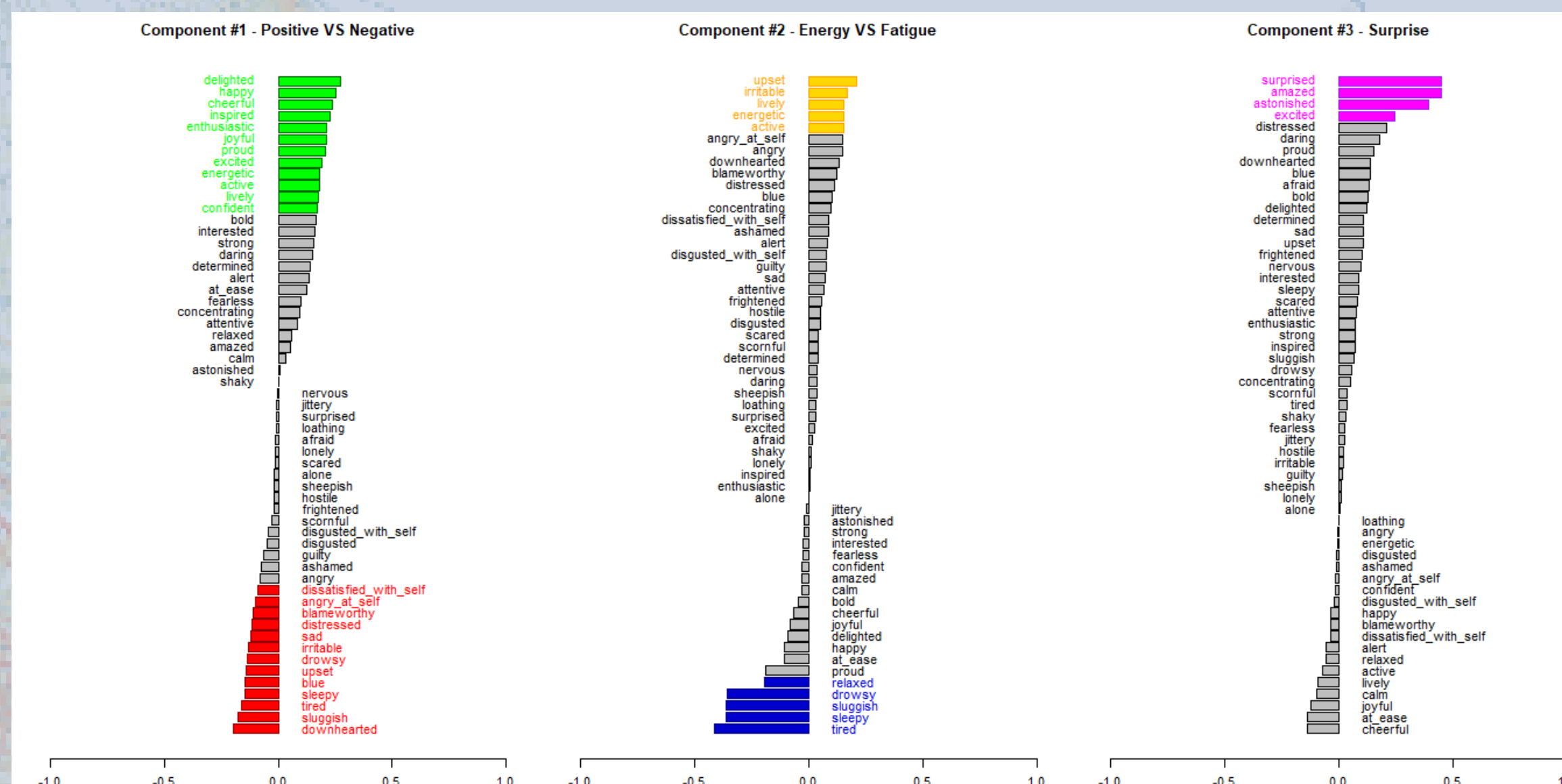


Figure 5 – PCA of the behavioral data

Using euclidean distance and complete linkage on the three scaled PCs, we obtain four clusters (see Figure 6): common days (**green**), tiring days (**red**), nervous and negative days (**blue**), and positive days of surprise (**violet**).

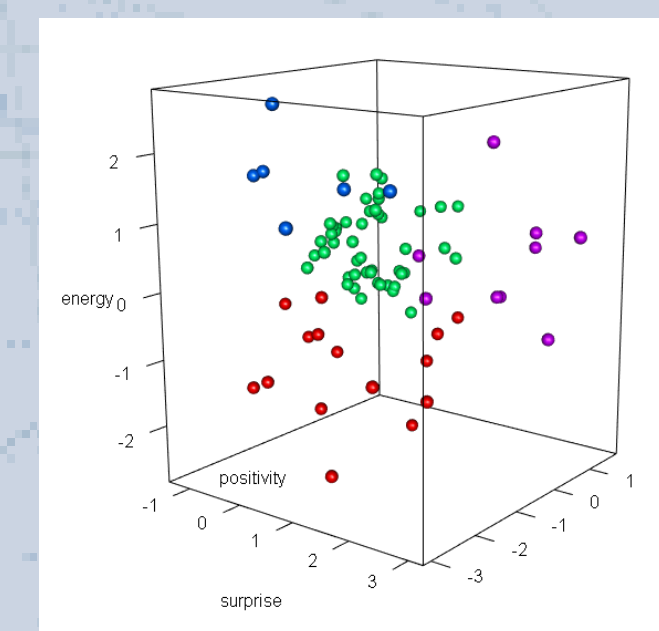


Figure 6 – Clustering on the PCs

JIVE COMBINED ANALYSIS

JIVE: variance decomposition technique that combines information from different datasets measured on a common set of experiments. It compares the *joint variation* between datasets with the *individual variation* of each dataset.

Goal: understand how **human behavior** affects the **working memory** capacity.

Data: three pairs of datasets are compared:

- resting-state correlation of each brain region w.r.t. *amygdala* VS behavioral data.
- N-back* task-based correlation of each brain region w.r.t. *amygdala* VS behavioral data.
- working memory network indicators (*centrality* and *modularity*) VS behavioral data.

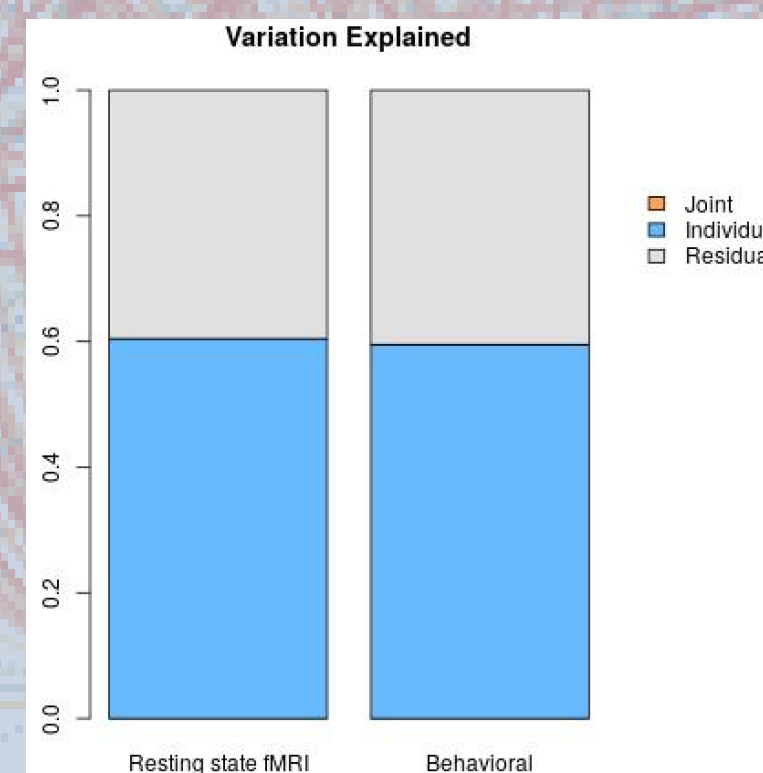


Figure 7 – Resting State *fMRI*

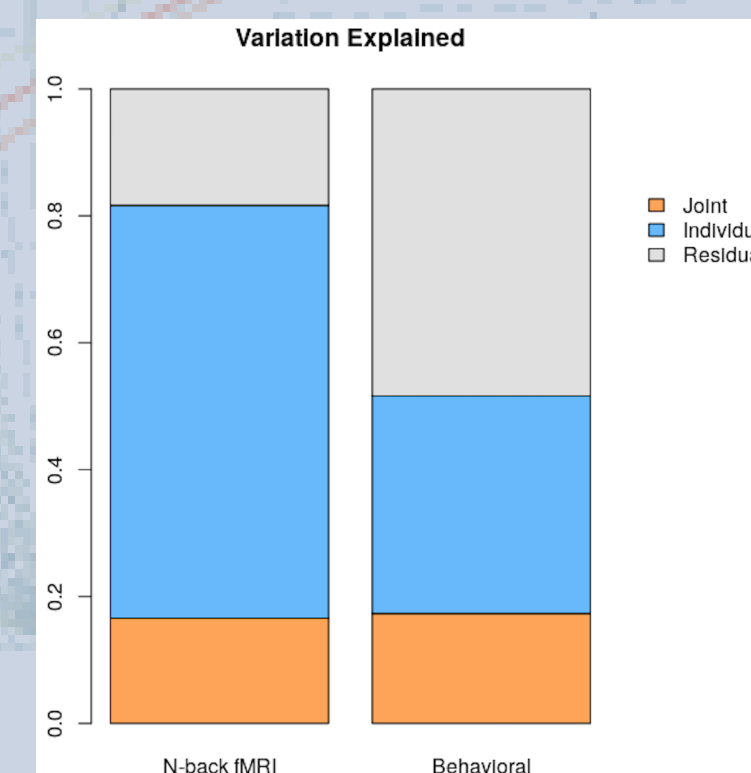


Figure 8 – N-back *fMRI*

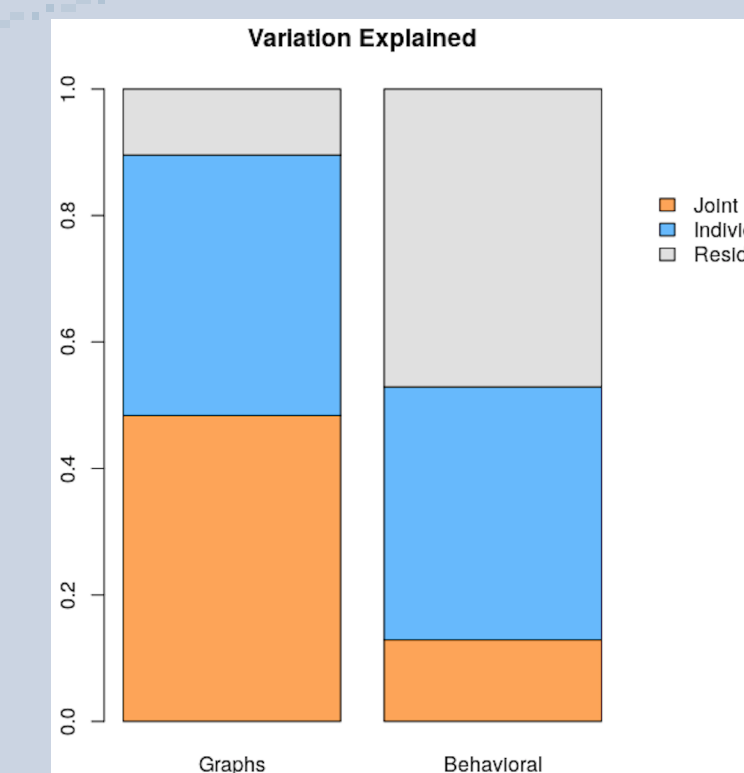
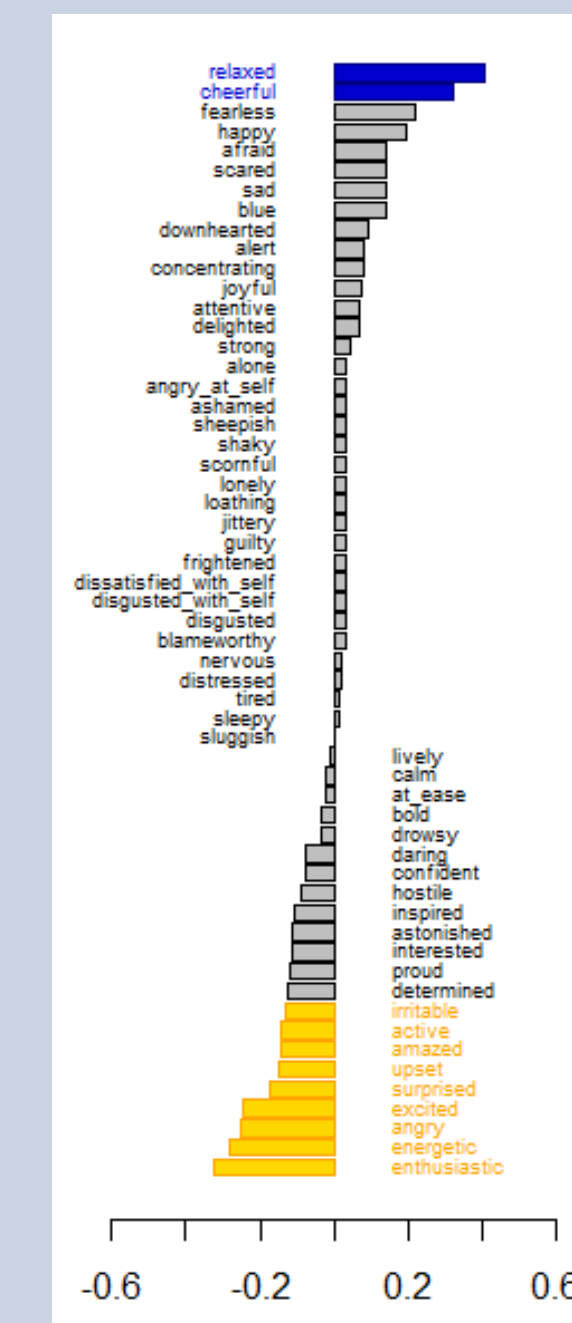


Figure 9 – Graphs indicators

Results: The percentage of joint variability progressively increases:

- resting-state** case: as expected, imaging and behavioral data are **not related**
- task-based** case: the signal associated with **working memory** is related to the **behavioral variables**
- when the task-based signal is described through **network indicators**: the principal components of an **SVD** decomposition of the JIVE joint signals **explain** the **joint variability** from the network and behavioral perspectives. The **first principal component** coming from the behavioral data **coincides** with the **second component** obtained analyzing the same data without interactions with the brain \Rightarrow this component is fundamental not only to explain the variability of the behavioral dataset on its own, but also its variability with respect to the network analysis of the *fMRI*.



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