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THE NEUROANATOMICAL SIGNATURES OF TIME IN WORKING MEMORY

INRIA pariétal / NEUROSPIN

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Résumé

L'évaluation de la durée est l'une des capacités fondamentales du cerveau. Cependant, nous ne savons pas comment cette information est stockée en mémoire. Ici, nous utilisons un paradigme de reproduction temporelle récemment développé pour étudier la neuroanatomie du temps dans la mémoire de travail. Les participants ont écouté des séquences non rythmiques composées d'intervalles temporels, qu'ils devaient ensuite reproduire le plus fidèlement possible. Nous avons fait varier la longueur totale des séries temporelles ainsi que le nombre d'intervalles (n-item) les composant. L'expérience a été menée et enregistrée par magnétoencéphalographie ($N = 24$). Au cours de mon stage, j'ai développé des méthodes mathématiques pour analyser ces enregistrements. Nous procédons en deux étapes : 1. Nous procédons à une analyse temps-fréquence des données et nous trouvons les principaux clusters informationnels. 2. Nous utilisons les clusters temps-fréquence identifiés pour analyser les données dans l'espace source. Nos résultats suggèrent que la mémoire de travail temporelle est stockée principalement dans la bande alpha (8-14 Hz), et qu'elle est localisée dans l'aire somato-sensorielle complétée par le cortex occipital.

Mots clés : Mémoire de travail, perception temporelle, magnétoencéphalographie, analyse temps-fréquence, aires somato-sensorielles.

Abstract

Evaluating duration is one of the fundamental capacities of the brain. However, we do not know how this information is stored in memory. Here, we use a recently developed temporal reproduction paradigm to investigate the neuroanatomy of time in working memory. Participants listened to non-rhythmic sequences composed of temporal intervals, which they then had to reproduce as accurately as possible. We varied the total length of the temporal series as well as the number of intervals (n-item) composing them. The experiment was conducted and recorded by magnetoencephalography ($N = 24$). During my internship, I developed mathematical methods to analyze these recordings. We proceed in two steps: 1. We proceed to a time-frequency analysis of the data and we find the main informational clusters. 2. We use the identified time-frequency clusters to analyze the data in the source space. Our results suggest that temporal working memory is stored predominantly in the alpha band (8-14 Hz), and that it is located in the somato-sensory area complemented by the occipital cortex.

Keywords: Working memory, Temporal perception, Magnetoencephalography, Time-frequency analysis, somato-sensory areas.

Synthèse du rapport en français

À utiliser dans le cas des rapports rédigés en anglais (4 pages minimum).

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Host organizations

My internship was a bit particular in the sense that it took place between two research institutes.

I worked in parallel with :

- Inria, within the Parietal team
- and Neurospin, in the Cognition and Brain Dynamics team.

Inria

The French National Institute for Research in Computer Science and Control (Inria) is a French national research institution focused on computer science and applied mathematics. Inria employs 3800 people, including 2800 researchers and doctoral students located all over France.

Inria - Parietal

The parietal team is a laboratory of about 30 researcher dedicated to Learning brain structure, function and variability from neuroimaging data. The parietal team focuses on mathematical methods for statistical modeling of brain functions from neuroimaging data (fMRI, MEG, EEG), with a particular interest in machine learning techniques, applications to human cognitive neuroscience and scientific software development.

Within inria parietal, I have particularly worked with the team of developers now **MNE-Python**, and **MNE-BIDS-Pipeline**, especially with Richard Höchenberger and Alexandre Gramfort. But I was able to be present at the team presentations every Tuesday afternoon during the parietal talks. Every Tuesday afternoon, we had team presentations, which gave us the opportunity to follow the work of the other members of the parietal team, and to present our work.

Neurospin

Neurospin is a brain imaging center in Saclay, south of Paris. The INSERM-CEA Cognitive Neuroimaging Unit, comprises five teams:

- Languages of the Brain, which attempts to answer the question: Why are we the only species with a sophisticated communication system?
- Neuroimaging of Development, which studies human cognitive development in infants and children, both structurally and functionally, and aims to develop new imaging techniques appropriate for human infants.
- Neuromodulation which focuses on brain function in primates.
- Computational Brain, which studies the different functions of the human brain from the perspective of computation and information coding.
- **Cognition and Brain Dynamics** which is interested in the processing of multisensory information, their temporal organization and in particular the representation of temporal information in the human brain, using magnetoencephalography (MEG) as the main methods.

I did my internship in this last team: Cognition and brain dynamics with Sophie Herbst but I was also able to interact with some of the people from the other teams, especially during the Friday afternoon meetings that allows the 5 teams to get together.

Introduction

I divided this report into two parts that roughly follow the chronological order of my internship.

The first chapter gives the scientific context of my internship. This part is an account of the environment in which I am inserted and of the knowledge required to understand my work hereafter. Scientific activity is no longer a solitary activity, especially in neuroscience, where the tools used are based on years of collective work. I notably explain in this chapter the ins and outs of the pilot study paper [6] on which I rely. The goal of my internship is to complete this pilot study by analyzing magnetoencephalography (MEG) data, by finding appropriate mathematical methods to analyze the MEG data, and to implement these mathematical methods in an open source automatic analysis pipeline, the MNE-BIDS-Pipeline. This pipeline aims to allow future cognitive science researchers to analyze electroencephalogram data in a snap, while promoting replicability and open science. This part could constitute the introduction part of a future paper.

The second chapter presents the more technical aspects of my contribution to the reproduction of the pilot study. This replication using MEG imaging, I detail the method used to analyze the parts of the brain in action during the use of the working memory. We used the MNE-BIDS-Pipeline to analyze the data. But we had to adapt the MNE-BIDS-Pipeline by using new algorithms in order to meet the requirements of our experimental paradigm. An important part of my work has been allocated to implement in open-source these methods rigorously, while optimizing the computation time. This part could constitute the method part of a futur paper.

The third part presents the results obtained. The beginning of a discussion is also outlined.

An appendix provides more information on the algorithms used and on some mathematical subtleties. An important point is made on the optimization of the computation time. Indeed, even if the optimization of the computation time does not change the results, it was critical in the practical feasibility of our project.

Chapter 1

Scientific Context

1.1 The Time in Working Memory (TiWM) paradigm

Cette partie présente the *time in Working Memory* paradigm, qui a été exposé dans le papier [6]. Le but de mon stage est d'aider à la reproduction de ce papier mais cette fois ci en utilisant des donnée venant de MEG.

1.1.1 Description of the Pilot Study

Planning for the future relies on the ability to remember the duration of events, but it is unknown how durations are stored in the brain's working memory. The paper abstracting time in working memory proposes a new n-item delayed duration reproduction task to assess whether elapsed time is stored in memory as a continuous feature or as an abstract element.

The participants listened to sequences composed of empty time intervals that they had to reproduce as precisely as possible. For each sequence, one can manipulate the number of time intervals and the overall duration of the sequence to separate their effects on recall accuracy. The figure 1.1 presents the paradigm. Temporal reproduction accuracy decreased systematically with an increasing number of items. These results suggested that the number of time intervals, not their duration, determines recall precision. According to the brain clock models proposed by cognitive science, these results are interpreted as evidence of the existence of a symbolic representation of duration in working memory.

1.1.2 Goal of the internship: reproduce the pilot study using MEG data

Thus, according to this first study, we know that durations are not represented in a continuous way, but in a symbolic way. But we still do not know in which part of the brain the information

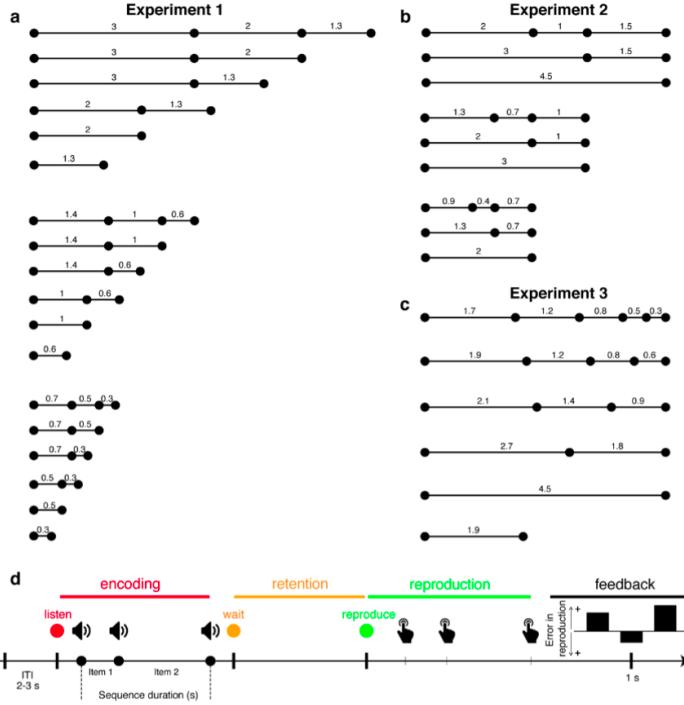


Figure 1.1: n-item delayed reproduction task, taken from [6] - Panels a–c depict the individual items and sequences used in Experiment 1, 2, and 3, respectively. Black dots represent 1kHz tones. All numbers are durations in seconds. (a) The set of sequences used in Experiment 1, in which the number of items in a sequence and the full sequence duration covaried. A sequence was composed of 1, 2 or 3 items, and its duration varied from 0.3s to 6.3 s. (b) In Experiment 2, the number of items and the sequence duration were orthogonalized. A sequence was composed of 1, 2 or 3 items with sequence duration fixed to 2 s, 3 s, or 4.5 s irrespective of the number of items composing it. (c) In Experiment 3, a sequence was composed of 1 to 5 items. Only two sequence durations were used (1.9 s and 4.5 s). (d) Example trial. In all experiments, each trial was composed of four phases: First, participants listened to a sequence of pure tones demarcating time intervals of varying duration. Following a retention interval, participants were asked to reproduce the temporal sequence as precisely as possible. In the example depicted here, the sequence was composed of two items. Following the reproduction (green), feedback was provided showing the relative temporal reproduction error for each item in the sequence.

is stored. In order to visualize in which part of the brain the working memory is encoded, we reproduced the experiment this time by recording the cerebral data with magnetoencephalograms. In this new experiment, we no longer concentrate on the analysis of the accuracy of the restitution of the duration of the time intervals, but we will concentrate more on the visualization of the frequencies and cerebral areas at stake for the working memory.

Compared to the original study, we changed two main points:

- We did not repeat the 3 experiments using MEGs, but only experiment 2, which orthogonalizes the number of items and the total sequence duration.
- In the original Experiment 2, three sequences durations were tested (2 s, 3 s and 4.5 s) and the number of items was 1, 2 or 3 items for each sequence. In our replication of this

experiment, we use only sequences of either 1 or 3 items, which allows to maximize the effect size.

[add what do we expect : alpha, hippocampus. Cite the other paper from the sujet de stage]

1.1.3 Glossary

In the context of MEEG, the vocabulary used is very specific, and is essential to the understanding. The table 1.1 gives the main vocabulary of the neural oscillation theory. The table 1.2 gives the usual vocabulary used in experimental protocols.

EEG-MEG	The Electro-magnetoencephalography is a non-invasive methods for studying brain function that reflect the electrical activity of neuronal populations with millisecond temporal resolution.
Local field potential (LFP)	electric potential in the extracellular space around neurons. LFP is a widely available signal in many recording configurations, ranging from single-electrode recordings to multi-electrode arrays
Neuronal oscillations	prominent feature of spontaneous and task-related brain activity that occur at the level of single units, local field potentials (LFPs), and EEG/MEG recordings. The traditional view is that neuronal oscillations reflect inhibition-based fluctuations of neuronal activity that emerge from the synchronous activation of large neuronal ensembles.
Spectral power	reflects the amplitude of neural oscillations computed through a time-frequency transformation (TFT).

Table 1.1: Glossary of the Neural Oscillation and of the Theory of the working memory as defined in [10]

1.2 EEG, MEG

EEG and MEG measure the electrical activity of our brain using electrodes placed on the scalp. It tells us, from the surface measurements, how active the brain is. It is possible to measure both eeg and meg data, which is why the acronym meeg is used to designate these data.

For our experimental paradigm, it is much more important to have high temporal precession than high spatial precision. This is why we choose to use MEEG rather than fMRI to study this paradigm.

Indeed, the temporal sampling rate of MEG is high, with more than 1000 Hz per sencode. This high temporal resolution contrasts with that of functional magnetic resonance imaging, which essentially detects changes in the concentration of oxygen in the blood, a system with a much slower response in the human brain, with a lag of several seconds, and therefore not suitable for our temporal reproduction paradigm.

Session	A logical grouping of neuroimaging and behavioural data collected consistently across participants. A session includes the time involved in completing all experimental tasks. This begins when a participant enters the research environment until he/she leaves it.
Run	An uninterrupted period of continuous data acquisition without operator involvement.
Event	An isolated occurrence of a presented stimulus, or a subject response recorded during a task
Epoch	In the MEEG literature, the term epoch designates the outcome of a data segmentation process. Typically, epochs in event-related designs (for analysis of event related potentials or event related spectral perturbations) are time-locked to a particular event (such as a stimulus or a response)
Evoked data	Evoked objects typically store an EEG or MEG signal that has been averaged over multiple epochs, which is a common technique for estimating stimulus-evoked activity.
Sensors	Sensors are the physical objects or transducers that are used to perform the analogue recording, i.e., EEG electrodes and MEG magnetometers/ gradiometers. Sensors are connected to amplifiers, which not only amplify, but also filter the MEEG activity.
Channels	Channels refer to the digital signals that have been recorded by the amplifiers. It is thus important to distinguish them from sensors. A ‘bad channel’ refers to a channel that is producing a consistently artifactual or low-quality signal.
Sensor space	Sensor space refers to a representation of the MEEG data at the level of the original sensors, where each of the signals maps onto the spatial location of one of the sensors.
Source space	Source space refers to MEEG data reconstructed at the level of potential neural sources that presumably gave rise to the measured signals (according to an assumed biophysical model). Each signal maps onto a spatial location that is readily interpretable in relation to individual or template-based brain anatomy.

Table 1.2: Glossary of MEEG terminology commonly used to describe stimulation and task parameters and protocols as defined in [9].

1.2.1 MEG in comparison to EEG

MEG is a cutting-edge functional brain imaging technology. MEG is extremely sensitive and measures very weak magnetic fields produced by the electromagnetic activity of neurons. MEG is the safest of the various brain imaging technologies: no energy is deposited in the individual being monitored. The machine does not even touch the head. MEG is particularly important in basic and clinical research and especially in studies with young child populations.

The advantage of measuring magnetic fields, rather than electric fields as in electroencephalography (EEG), is that they pass through the skull and other tissues between the active neurons and the MEG detectors without distortion, unlike EEG, where the signal is less accurate.

1.2.2 Equipment: MEG in Neurospin

MEGs are extremely rare in France, and MEG equipment in France can be counted on the fingers of one hand. But Neurospin is one of them. Our center has a shielded chamber protecting a MEG recording device from electromagnetic noise.

The MEG at Neurospin is an Elekta Neuromag device. The MEG helmet consists of 102 sensors-triplets (1 triplet = 2 orthogonal planar gradiometers and 1 magnetometer). The MEG data I am manipulating during the internship are composed of 204 gradiometer channels and 102 magnetometer channels (Figure 1.2) This organization between gradiometer and magnetometer will be important when we try to speed up the algorithms in the section A.1.1

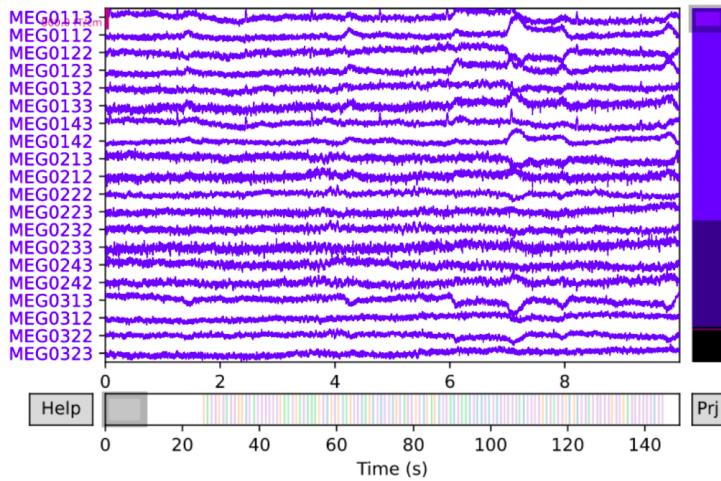


Figure 1.2: Example of an MEG recording of a passive session. Here 20 of the 306 channels are represented.

1.2.3 Frequency band

The high temporal accuracy of MEG data allows the study of signals in the frequency domain. The main frequency bands used are defined in Table 1.3.

Table 1.3: Comparison of EEG bands for a typical adult

Band Delta	Frequency (Hz) ≤ 4	Location frontally in adults, high-amplitude waves	Normally slow-wave sleep
Theta	4–8	Found in locations not related to task at hand	Drowsiness or idling. Associated with inhibition of elicited responses.
Alpha	8–14	posterior regions of head	relaxed, inhibition control
Beta	14–30	mainly frontally, low-amplitude waves	active thinking, focus
Gamma	≥ 30	Somatosensory cortex	Cross-modal sensory processing or short-term memory

1.3 The MNE ecosystem

The MNE ecosystem is composed (among other things!) of three different libraries, nested by increasing dependency.

- MNE-Python, which is an open-source Python package for exploring, visualizing, and analyzing human neurophysiological data mainly in EEG and MEG format. This library contains everything needed to manipulate EEG signals, from visualization to machine learning.
- MNE-BIDS. The Bids format is a convention for structuring MEEG datasets. MNE-BIDS is a library that facilitates the use of this convention in python.
- MNE-BIDS-Pipeline is a library allowing to automate the analysis of meeg data for datasets using the Bids format.

1.3.1 MNE-Python

MNE-Python [5] is an open-source python library allowing to analyze brain data from EEG or MEG. The figure 1.3 allows to visualize the flow of the data from the collection of the anatomical information (T1) and the raw data collected by MEEG to the estimation of the tridimensional Sources.

For the comprehension of this report, the most important steps are on the left of the figure:

- Raw data: The recording of the data is done in a continuous way during runs of 10 minutes. The recording is not stopped during this period. A run is composed of about 30 events.
- The data is pre-processed: defective sensors are removed, a low-pass filter is applied to keep only the useful brain signals, and an artifact removal technique such as ICA is used. The artifact rejection pipeline is presented in section 2.1.2.
- Epoch data : After cleaning the run, we split the run into different events. In our study, the events are either composed by intervals of 3 items or intervals of one item.
- Evoked data : We average the events in order to obtain exploitable results. In our case we mainly calculate two averages, one for each number of items.
- Source Estimate. All the previous steps are carried out in the sensor space, that is to say in the space of the 306 sensors of the MEG, which represent 306 temporal series. The calculation of the source estimate allows to convert these temporal series into a 3D or 4D representation.

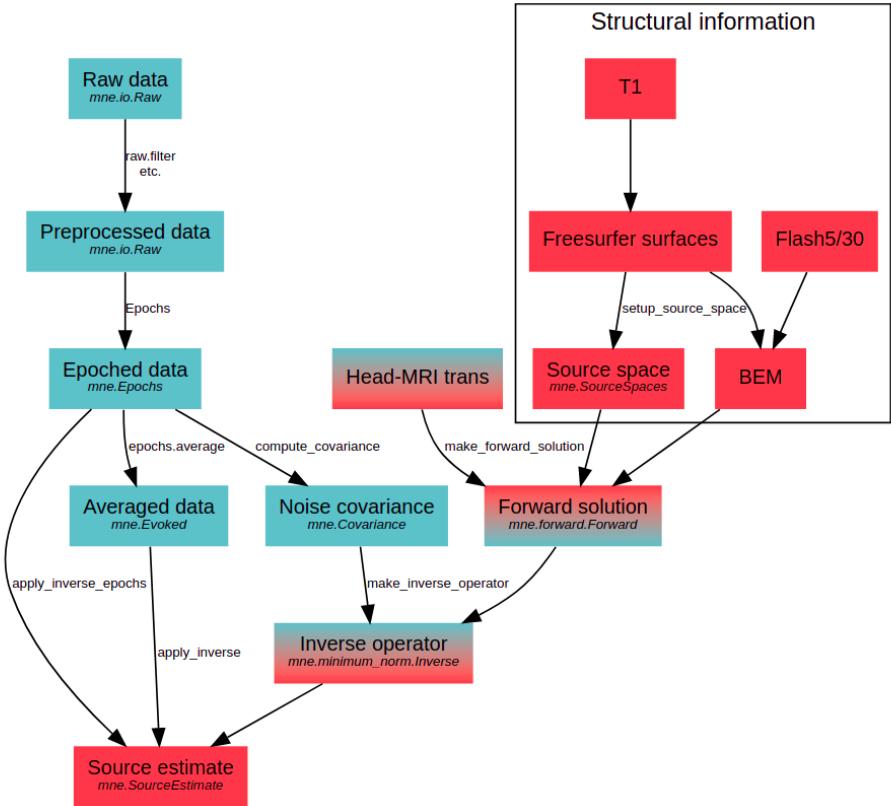


Figure 1.3: Workflow of the MNE software [5]

1.3.2 the Brain Imaging Data Structure (BIDS) format

The brain imaging data structure was created to provide a simple way to organize neuroimaging data. The goal of this structure is to be a standard format to make the data accessible to everyone and avoid confusion. Using a Python package called MNE-BIDS [1], datasets can easily be converted to BIDS format. Datasets in BIDS format are supported by many tools. BIDS is the result of a collaborative effort to standardize brain data for easy analysis and sharing.

Figure 1.4 gives an example of a file architecture in BIDS format. Figure 1.5 shows an example of the use in python of the MNE-BIDS library. In the absence of a standard format, to access a file, the full path must be written. A path is specific to a file, so if you want to access another file or even another dataset, you will have to change the full path. If the dataset is in BIDS format, it is possible to use the BIDSPath function of MNE-BIDS to call a file. In this case, if you want to call another file or another BIDS-compatible dataset, you only need to change a few arguments of this function, such as the subject name or the root of the file, without having to worry about the full path, which makes it much more modular.

Thus, by implementing the BIDS format support, it is possible to switch from one BIDS-compatible dataset to another in the blink of an eye by changing only a few elements of the scripts.

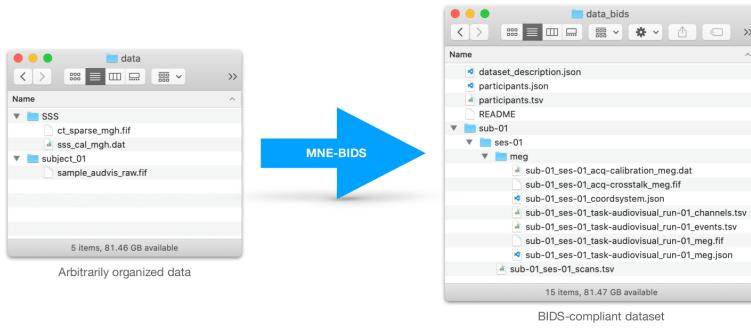


Figure 1.4: An example of the use of the BIDS format.

```
# Before BIDS
fname = '/storage/store/data/camcan/BIDSep/rest/sub-CC110033/ses-rest/meg/sub-CC110033_ses-smt_task-smt_meg.fif'

# With BIDS
root = '/storage/store/data/camcan/BIDSep/rest'
kind = 'rest'
subject = 'CC110033'
fname = BIDSPath(
    subject=subject,
    task=kind,
    session=kind,
    datatype="meg",
    extension=".fif",
    root=root,
    check=False,
)
```

Figure 1.5: Example of the use of MNE-BIDS in Python: we transform the initial long path into a modular function.

1.3.3 Automatic preprocessing with the MNE-BIDS-Pipeline

Using BIDS-compatible datasets enables us to apply the MNE-BIDS-Pipeline to the preprocessing part of the model. The MNE-BIDS-Pipeline is an automatic preprocessing and processing pipeline for MEG and EEG data stored following the BIDS format [4]. To apply the preprocessing steps wanted, the MNE-BIDS-Pipeline only requires to set the corresponding parameter in a configuration file. Once it is done for one dataset it can be used on other datasets just by changing one line in the configuration file.

It is very useful to employ this pipeline for the following reasons:

- It improves reproducibility, as only a config file contains all the information required to reproduce the results.
- The pre-processing and analysis steps of MEEG studies are common to most studies.
- Many of the meta parameters are hard to calibrate, especially for cleaning and when going through the source space. Without expertise, it is better to use the default parameters used in the pipeline.
- The pipeline allows to process the different participants in parallel, which allows to considerably accelerate the calculation times.

Chapter 2

Method

[résumer la situation et dire ce qu'il se passe dans ce chapitre. Raconter une histoire.]

Our exploration of the MEG data for the paradigm follows the classical steps of a MEG study:

- Pre-Processing of the data. Our study started with the verification and cleaning of the data.
- Analysis in the sensor space. In this step we visualized the Evoked response of the different conditions. In order to find out when and how often the information is stored at the time of retrieval, we implemented a new procedure, based on Common Spatial Patterns (CSP). After determining the most salient time and frequency, we check the statistical significance of the response using cluster permutation tests.
- Source analysis. After having determined the frequency and the moment of maximum activation of the Working memory, we visualize the 3D response.

In order to pre-process the data, and to analyze the data in the sensor and source space, I based myself on the [MNE-BIDS-Pipeline](#), which is still under development. As I wanted to use it for the time in working memory paradigm, I had to help implement the missing features I needed. The list of features to which I contributed is presented in the table [2.1](#).

This chapter aims to detail the list of algorithms I implemented or improved in the pipeline to analyze our MEG data.

2.1 Preprocessing of the data

Before this internship, I had already worked on EEG data for the "Dream, sleep apnea" challenge or for the Kaggle "Inria - BCI Challenge". But on these two occasions, the data I had manipulated

Type	Title
New feature	Add possibility to exclude runs from the analysis via the new exclude run setting.
Code health	Files docstrings in the preprocessing steps were updated.
Behavior changes	Warn if using ICA and no EOG- or ECG-related ICs were detected.
New feature	Added the possibility to have different runs for different subjects.
Behavior changes	Check that the baseline interval falls into the epoch interval.
Behavior changes	ica.reject now also applies to ECG and EOG epochs.
Bug fix	The sanity check comparing the rank of the experimental data and the rank of the empty-room after Maxwell-filtering did not use the maxfiltered data.
Bug fix	epochs_tmin and epochs_tmax were named incorrectly in some test config files.
Bug fix	We now reject bad epochs by using ica.reject before producing the "overlay" plots that show the evoked data before and after ICA cleaning in the 'proc-ica-report'.
New feature	It is now possible to analyze the contrast using the Common Spatial Patterns in the time-frequency domain using the new script: 03b-time_frequency_csp.py. We also test the significance of the contrast between the two conditions using cluster permutation statistics.

Table 2.1: List of my contributions to the MNE-BIDS-Pipeline on [GitHub](#).

had already been cleaned by the competition organizers. This internship allowed me to realize the complexity of preprocessing data in brain imaging.

2.1.1 The different steps of the preprocessing

The different phases of the data preprocessing are as follows:

[duplicates]

- Finding bad channels: some channels of MEG recordings may be noisy or flat. They need to be identified and marked as bad so they are not taking into account during the analysis;
- Applying Maxwell filter : help to remove part of the sensors noise;
- Frequency filter: to remove non desired frequency bands;
- Creating epochs: epochs are data structures to represent equal-duration chunks of MEG signals. When the recording session includes stimuli, epochs are often defined from 0.2 seconds before the stimulus to 0.5 seconds after. Otherwise, like in rest session, epochs are fixed and overlapping frames of the MEG signal.
- Computing evoked data: they are created by averaging MEG signal over several epochs. It is useful to study stimulus-evoked brain activity.

The figure 2.1 summarizes the preprocessing step in the pipeline. At the beginning of my internship,

I created this table in order to familiarize myself with the different scripts of the pipeline. Then, I added the main problems that occur in practice associated with each step as well as the main ideas of sanity checks to be performed after the execution of the pipeline.

mne-bids-pipeline preprocessing					
	01. Maxwell-filter MEG data	02. Apply freq filter	03. Construct epochs	04. Run ICA	05. Apply ICA
description	Import data, find bad channels, apply Maxwell filter	Bandpass filter, resample	Construct the epochs, decimate	Fits ICA on epoched data filtered with 1 Hz highpass	EEG/ECG artifacts detected and corresponding ICA components are removed
Main mne method	mne.preprocessing.maxwell_filter(raw)	raw.filter() ► l_freq ► h_freq ► runs ► subjects ► resample_streq	mne.Epochs(raw) ► epochs_tmin ► epochs_tmax ► decim ► conditions ► baseline	ica.fit(epochs)	ica.apply(epochs.copy())
Main parameters	*proc-sss_raw.fif *_bads.tsv NaN	*proc-filt_raw.fif NaN	*epo.fif NaN	► ica_reject ► ica_fif *_proc-ica_components.tsv	► ica_reject ► reject ► conditions ► contrasts
File output				*proc-clean_epo.fif	*proc-clean_epo.fif
Report output				*proc-ica_components_report.html	*proc-ica_report.html
How to inspect the data?	mne_bids.inspect()	mne.io.read_raw_fif()	mne.read_epochs("*_epo.fif") epochs.get_data().ptp()	Check the reports	Check the reports
Main figure in the report					
What to look for?	- Check the number of events, number of runs - Check the number of runs in your Bids dataset	- Check out bad channels, they are easily spotted in the psd plot	- Epochs should not overlap	- Check the peak to peak amplitude: the parameter ica_reject should only reject (massive) non biological artifacts - Multiple iterations: augment ica_max_iterations - No IC related component detected for EEG or ECG or too much variance in the IC plot : that's probably because of artifacts: lower ica_reject	- There shouldn't be massive artifacts anymore here - The evoked data and the timing of the roc-auc decoding should make sense with the paradigm
Potential problems	- Config file not set properly and path incorrect - Take a moment to mark bad channels with the mne-bids inspector	- The pipeline takes a long time to run. Do not hesitate to use decimate and resample to speed up the calculations. Parallelizations with N_JOBS	- Baseline not set properly - epochs_tmax too big (we see the beginning of the following event)		

Figure 2.1: Summary of the preprocessing of the pipeline.

2.1.2 Highlight on the management of artifacts

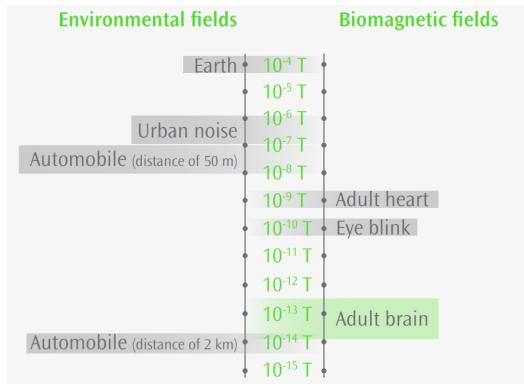


Figure 2.2: Scale of magnitude of different magnetic fields

An important point is the order in which the data is rejected. Indeed, a major difficulty with raw data coming from cortical signals is the fact that these signals are extremely small. Although the data is recorded in a shielded chamber, the slightest noise can totally overwhelm the signal. Figure 2.2 shows the scale of orders of magnitude, which makes it clear that the external noise is of an order of magnitude immeasurably larger than the neurological signals of interest.

Even after removing all the noise from the external environment, some of the so-called biological artifacts, such as heartbeats and blinks, must be removed by either discarding the contaminated time interval or separating the sources by using independent component analysis (ICA), which separates the heartbeat and blink sources from the rest of the signal.

The figure 2.3 allows to visualize the pipeline rejection of the MNE-BIDS-Pipeline.

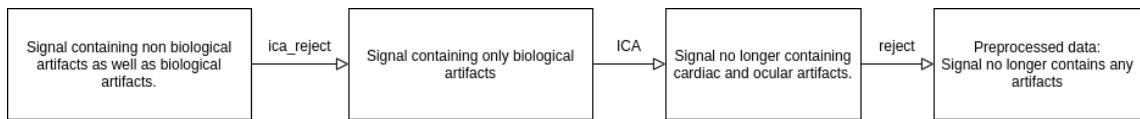


Figure 2.3: Flow of the BIDS-Pipeline rejection process.

Here are the details of the procedure:

- At the beginning the signal contains both biological artifacts (eye blink, heartbeat), and non biological artifacts. The latter are of an order of magnitude larger than the biological artifacts.
- We can start by filtering the different epochs using rejecting the epochs whose peak-to-peak amplitude exceeds the amplitude specified by the "ica.reject" parameter. This parameter allows to filter signals that are 50 times larger than the nominal amplitude and therefore allows to make a first screening.
- The resulting signal does not contain any more redhibitory non-biological artifact, which allows to improve the convergence of the ICA, allowing to separate the sources for the ocular and cardiac artifacts.
- The ICA source separation does not work perfectly, so an additional step is required to reject the last artifacts using the "reject" parameter, which allows to filter the signals with a peak-to-peak amplitude 10 times higher than the nominal amplitude. The result is the preprocessed signal.

Even if the global pipeline rejection method was already established before my arrival, the experimental data revealed problems in the order of the filtering operations, and we thus improved a lot the automatic data preprocessing especially for difficult data that contains simultaneously biological and non-biological artifacts such as phase inversion fields. Figure 2.4 shows an example of ICA enhancement before and after our Pull request that changes the order of operations, in particular by filtering out non-biological signals before the ICA.

[put an example of a heart or EOG ? Example of preprocessing reports.]

2.2 Sensor Space: Finding the main time-frequency cluster

[rappeller le source space]

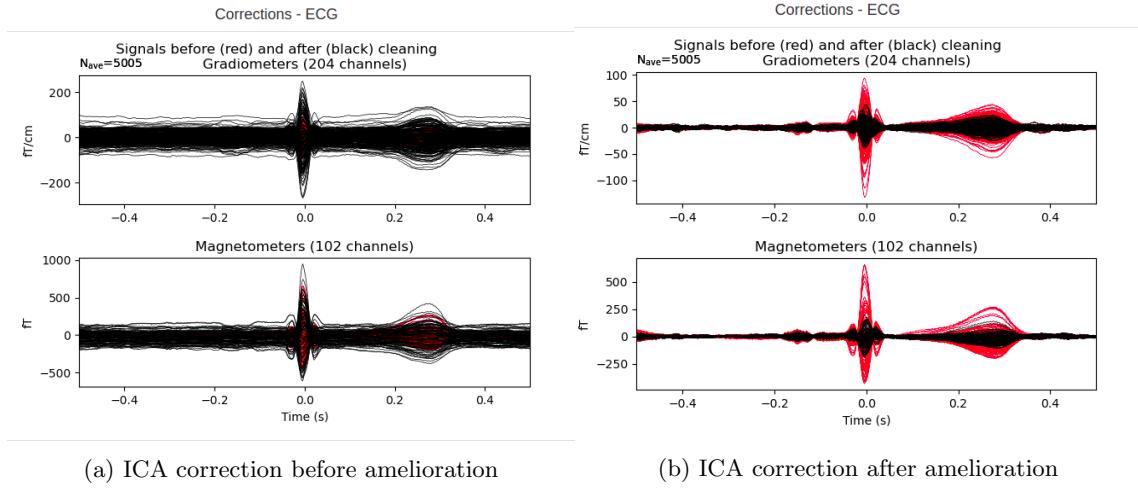


Figure 2.4: We can see that after amelioration, we no longer obtain a discontinuity, and the ICA is capable of reducing almost by 4 the peak to peak amplitude of the ECG artifact.

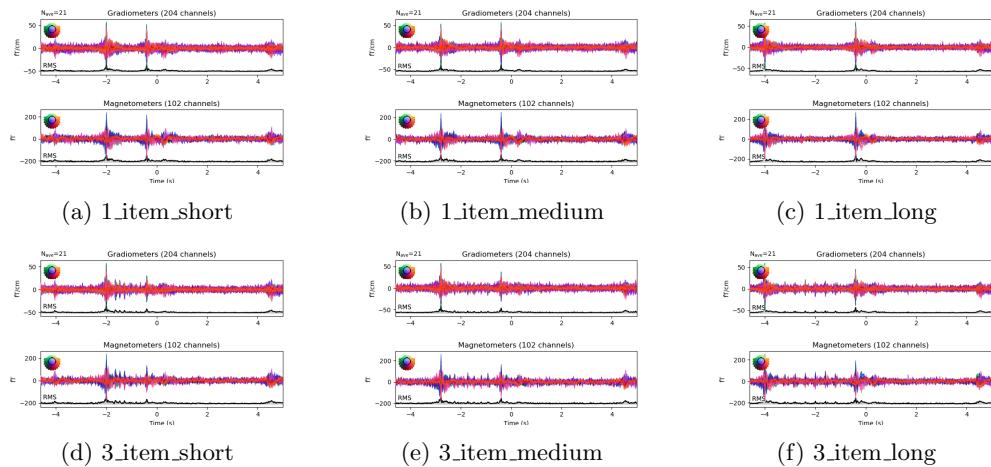
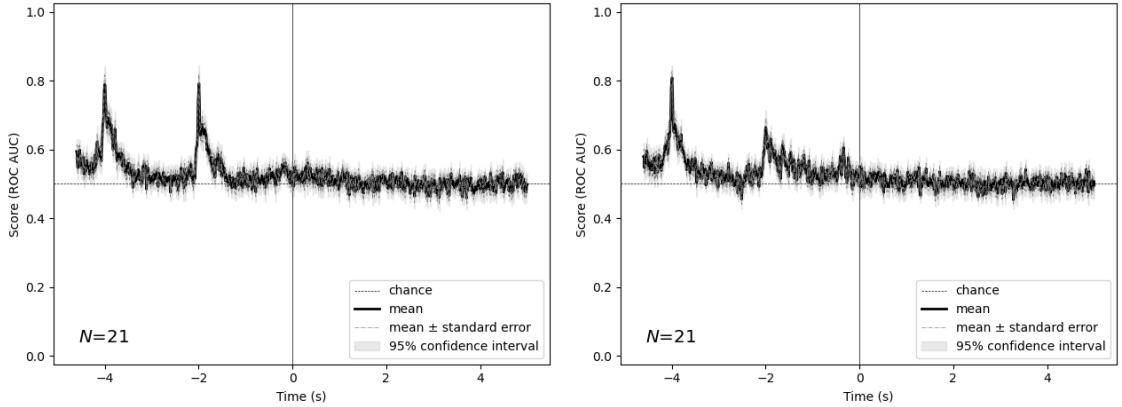


Figure 2.5: Evoked data for our 6 different items.

2.2.1 Insufficiency of the pipeline to analyze in a relevant way the MEG

At the beginning of my internship, the MNE-BIDS-Pipeline allowed us to quickly obtain figures such as 2.5 and such as 2.6. These figures show that the preprocessing went well since the results are clean. But these two figures also present some limits in the framework of our paradigm.

- The figure 2.5 presents the evoked data for each of our 6 different items. The three top figures are temporal sequences containing only one interval (1 item), while the three bottom figures contain sequences of 3 intervals (3 items). When there is only one item, we observe two very clear peaks before $t \leq 0$. These two peaks correspond to the pure tone which give the beginning and the end of the interval. After $t \geq 0$ begins the restitution phase, i.e. the phase during which the participant must recall the sequence in his head as precisely as possible. We see that during this restitution phase, the evoked data does not present any particular phenomenon, there is no peak to exploit.
- In the same way for the figure 2.6, even if we can see that the decoder used in the pipeline



(a) Decoding between 1_item_short and 1_item_long. (b) Decoding between 3_item_short and 3_item_long.

Figure 2.6: Decoding ititialelement dans la pipeline.

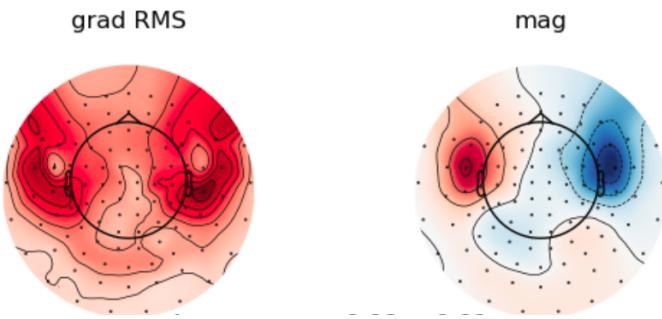


Figure 2.7: Topographic map of the first peak from 1_item_short evoked data 2.5a. We can see that during these peaks which appear on the figures 2.5, it is above all the auditory cortex which is involved.

manages to decode the signals before $t = 0$ in a very satisfactory way, especially at the location of the auditory stimuli, the performance of the decoders is null during the restitution phase.

In this study, we are not interested in the auditory cortex, but in the working memory. We therefore do not concentrate on the listening phase before $t \leq 0$, but rather on the restitution phase after $t \geq 0$. This means that the algorithms currently in place in the pipeline were not sufficient at the beginning of my internship, and that we must find an adequate method to study the working memory.

2.2.2 Strategy: analysing the contrast in time-frequency space

Classically the sensor space is decomposed in the following steps:

- creation of the evoked data sets are created by averaging different conditions.
- Using a sliding estimator with a logistic regression model for every time point.
- Time frequency decomposition: the epoched data is transformed to time-frequency domain.
- Computation of the group average results.

This order of operations is fine for most studies. But in the case of our study it is crucial to obtain results in the time-frequency space. We therefore need to combine the features of the "sliding estimator" script to study a contrast between two conditions and the "time frequency decomposition" script to study the signal in time and frequency space. It is to fill this gap that I implemented a new script in the pipeline allowing to visualize which are the time-frequency bin which present in the most salient way the working memory by studying the contrast between the sequences of an item and the sequences of 3 items.

Indeed, 3_items load the working memory much more than a single item. The reason for contrasting 3_items with 1_item and not 3_item with 0_item (rest) is that the contrast should not be based on a difference in the nature of the tasks, but rather a difference in load.

My [pull request](#) adds a new script to the pipeline, designed to analyze in the time-frequency domain a contrast between two conditions. There are two main steps in this script:

1. Decoding: for each time-frequency bin: For each time-frequency bin, we use a csp classifier in order to distinguish between the two conditions. We compute the roc-auc score for each time-frequency bin.
2. Permutation statistics at the group level: we try to answer the following question: is the difference between the two conditions statistically significant? We use the classic permutations cluster tests on the time-frequency roc-auc map.

2.2.3 Why using CSP?

CSP is based on a geometrical analysis of the brain response, which is called pattern-based. CSP is used to identify the most salient time-frequencies. CSP classifies between 1-item events and 3-item events. To be able to classify between these two items is to be able to recognize a working memory with two different loads.

We use CSP to identify the most salient times and frequencies for our task: we just have to look at which frequency interval and which time interval our classifier performs best. A good discrimination between the two conditions (1 item vs. 3 items) is characterized by a roc-auc close to 1 while a roc-auc close to 0.5 means that the neural code that encodes the working memory is not detectable by high level geometric features.

2.2.4 Decoding with Common Spatial Patterns (CSP)

The time-frequency decomposition is estimated by iterating over raw data that has been band-passed at different frequencies. This is used to compute a covariance matrix over each epoch or a

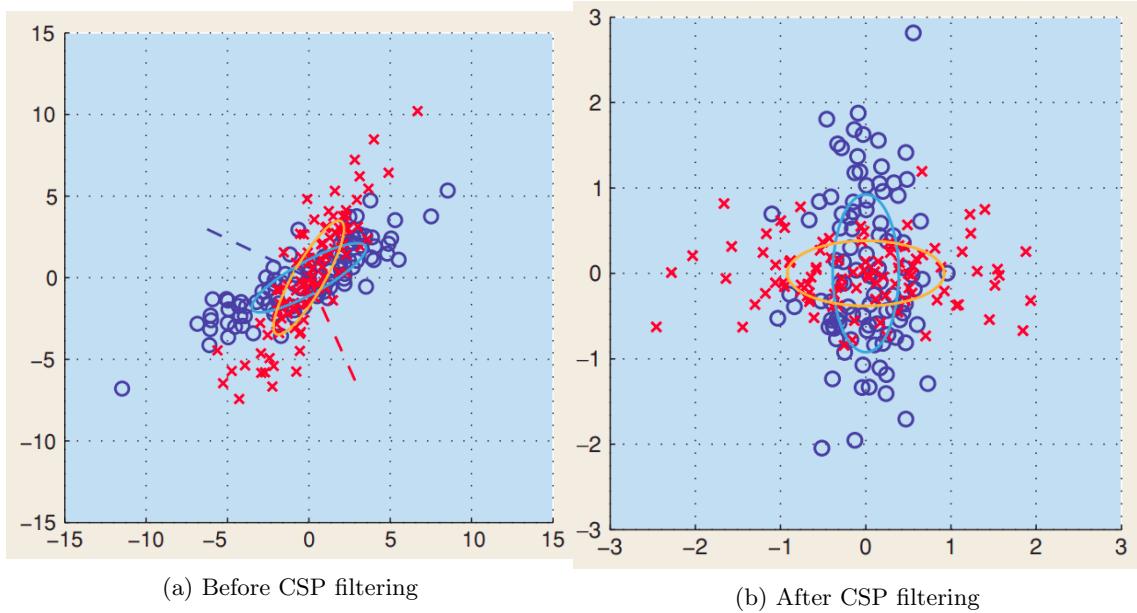


Figure 2.8: Toy example showing the functioning of the CSP transformation.

rolling time-window and extract the CSP filtered signals. A linear discriminant classifier is then applied to these signals.

CSP is a technique to analyze multichannel data based on recordings from two classes qui a été introduite dans le contexte des EEG par [7].

Intuitive explanation

I took the figure from [2] which also contains a comprehensive tutorial on CSP.

[je peux faire un shema mieux]

If we have two Gaussian signals, both centered in zeros, but with different principal directions, we can try to transform the two scatterplots in such a way that the principal directions of the two scatterplots in the CSP space are orthogonal so as to maximize the ratio of the variances following the principal directions.

For example on the figure 2.8, we start from two point clouds, red and blue, very correlated, which we transform into decoupled red' and blue' point clouds.

The main vector of the red' cloud is aligned on the absice axis, while the main vector of the blue' cloud is aligned on the ordinate axis.

By this process, we maximize the variance ratio along the abscissa axis between the red' and the blue' clouds.

In our usage, a point cloud corresponds to an event, and each color corresponds to a different

condition. Here, we do not try to classify points individually as in machine learning, but we classify a whole point cloud. If we try to guess the color/condition of a point cloud, we just have to transform the point cloud with the same transformation as before (i.e. apply the unmixing matrix as we will see later), and take the projection on the x axis of the new point cloud. We can then calculate the variance along the x axis and then train a linear classifier to discriminate among the different variances. By combining the csp algorithm, and for example a logistic regression, we can classify between the two conditions.

Technical Description (to be skipped in a first reading)

The above explanation only explains intuitively the algorithm for the first component of the CSP. But it does not explain how to obtain the other orientations. An efficient formulation to obtain all components of the CSP while being computationally reasonable is to formalize the problem as a generalized eigenvector problem. [mettre les deux autres formulations]

General Eigenvalue Problem Formulation Let $X \in \mathbb{R}^{C*T}$ be a matrix containing C channels and T time points. The data at a single time point is denoted by $x(t) \in \mathbb{R}^C$. Common spatial pattern (CSP) finds a decomposition that projects the signal in the original sensor space to CSP space using the following transformation:

$$x_{\text{CSP}}(t) = W^T x(t) \quad (2.1)$$

where each column of $W \in \mathbb{R}^{C*C}$ is a spatial filter and each row of $x_{\text{CSP}}(t)$ is a CSP component. Let $\Sigma^+ \in \mathbb{R}^{C*C}$ and $\Sigma^- \in \mathbb{R}^{C*C}$ be the respective covariance matrices of the two different conditions. CSP analysis is given by the simultaneous diagonalization of the two covariance matrices.

$$W^T \Sigma^+ W = \lambda^+ \quad (2.2)$$

$$W^T \Sigma^- W = \lambda^- \quad (2.3)$$

Where the two λ are diagonal matrices whose entries are the eigenvalues of the following generalized eigenvalue problem in $(w, \lambda) \in (\mathbb{R}^C, \mathbb{R})$:

$$\Sigma^+ w = \lambda \Sigma^- w \quad (2.4)$$

Large entries in the diagonal matrix corresponds to a spatial filter which gives high variance in one class but low variance in the other. Thus, the filter facilitates discrimination between the two

classes.

The unmixing matrix Another way to read the two equations 2.2 and 2.3 is to remember that $w^T \Sigma w$ computes the variance of the covariance Σ along the w direction. Thus, $W^T \Sigma^+ W$ and $W^T \Sigma^- W$ just compute diagonal matrices, whose diagonal elements are the variances of the covariances along the different columns of W , namely the variances along the different spatial filters.

By finding all the w which satisfy the equation 2.4, we construct the matrix W also called *unmixing matrix*.

After having found all the couples (w_i, λ_i) which satisfy the generalized eigenvalue equation 2.4, we can order the solutions by decreasing eigenvalues. The first filter corresponds to the direction maximizing the ratio of the variances between the two scatter plots. Indeed, if we replace in the equation 2.2, 2.3, we obtain:

$$w_i^T \Sigma^+ w_i = \lambda_i^+ \quad (2.5)$$

$$w_i^T \Sigma^- w_i = \lambda_i^- \quad (2.6)$$

And it is then enough to replace in 2.4 then to multiply on the left by w^T to obtain

$$\lambda_1 = \lambda_1^+ / \lambda_1^- \quad (2.7)$$

2.2.5 Significance of time-frequency bins with Permutation statistics

We try to answer the following question: is the difference between the two conditions statistically significant? We use the a permutations cluster tests on the time-frequency roc-auc map in order to check the significance of the activation.

Overview of the cluster permutation statistics method

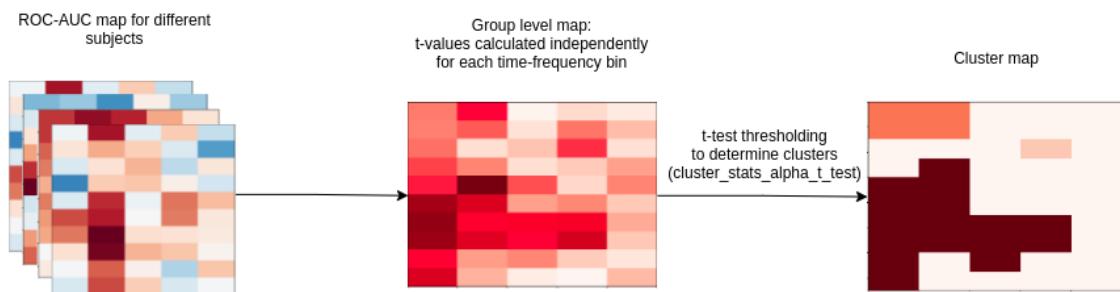


Figure 2.9: Overview of the permutation statistics pipeline.

[harmoniser les images]

The figure 2.9 gives an overview of the cluster creation pipeline.

We start by collecting all the time-frequency roc-auc maps of all the subjects. For each time-frequency bin, we compute a t-value, independently for each bin (the details of the computations can be found in the Appendix). We then obtain the t-value map. Then, in order to find the location of the clusters, we use a threshold, for example corresponding to a chance level of 0.05 or 0.01. This threshold is not very important mathematically, but in practice, it allows to control the size of the clusters. Once the threshold is applied, we potentially get one or more clusters. In order to assign a p-value to each cluster, we have to use the permutation mechanism.

The permutation mechanism consists in computing a metric on our clusters: which can be either the size of the cluster, or the maximum of t-values within the cluster, or the sum of t-values within the cluster. [us?] Then we compare this metric to the distribution of this metric simulated for the permutation: We reverse the sign of the difference for each bin in each subject. We obtain the distribution of the metric in the null hypothesis where the distribution of spatial cluster sizes is independent of the sign of the data.

[detailler]

2.3 Source Space Analysis

After going into the sensor space. The natural direction is to go to the source space. [detailler ou retravailler]

2.3.1 Generalités source space.

[Mettre les différents scripts.]

2.3.2 New script: Contrast in source space

Motivation: Insufficient classical pipeline, and inability to average from individual CSPs component.

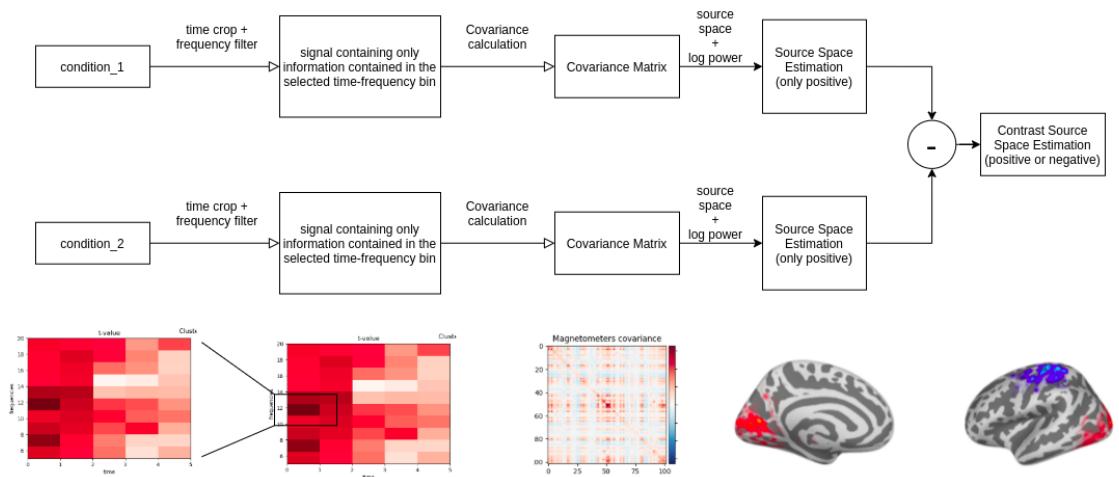


Figure 2.10: Shema of the procedure to visualize the contrast in source space.

Chapter 3

Results

Dans ce chapitre, nous présentons les résultats de la méthode exposée précédemment.

3.1. Sensor Space : Nous commençons par étudier la donnée dans le time-frequency space afin de trouver les temps et les fréquences les plus importantes: - La classification par CSP nous a permis d'obtenir une time-frequency map qui permet d'associer à chaque temps et fréquences une roc auc. Cette roc auc indique à quel point l'information stockée dans la mémoire de travail est décodable par des informations géométrique. - Les statisitques par permutation permettent de vérifier la significativité du time-frequency cluster obtenu.

3.2. Source space. Après avoir vérifié la significativité statistique de notre cluster, nous utilisons ce cluster pour projeter l'information dans un espace tridimensionnel, (aka l'espace des sources), afin d'y visualiser le contraste entre la mémoire de travail chargée avec 3-items contre 1-item. C'est principalement cette étape qui permet d'extraire les informations neuroanatomiques.

3.1 Sensor space results

3.1.1 CSP results

In the figure 3.1, we observe the roc-auc score of the classifier composed of (CSP, logistic regression) for different frequencies distributed linearly between 5 Hz and 20 Hz as well as for times between $t = 0$ and $t = 5$ seconds (the figures 2.5, 2.6 presented the times $t \leq 0$ only for pedagogical purposes). We can see that the CSP algorithm succeeded in highlighting the alpha frequency band between 8 and 12 Hz, and the results are consistent between the frequency map 3.1a and the time-frequency map 3.1b.

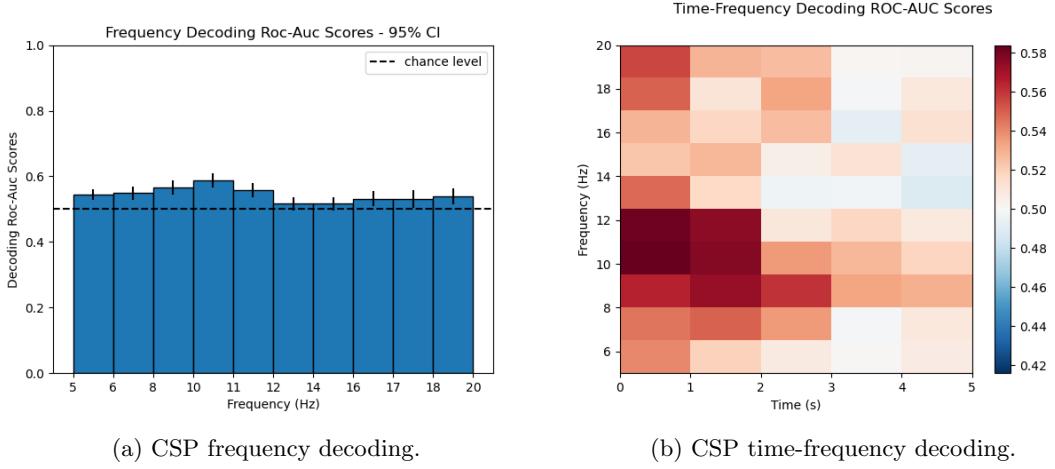


Figure 3.1: CSP results for the average subject.

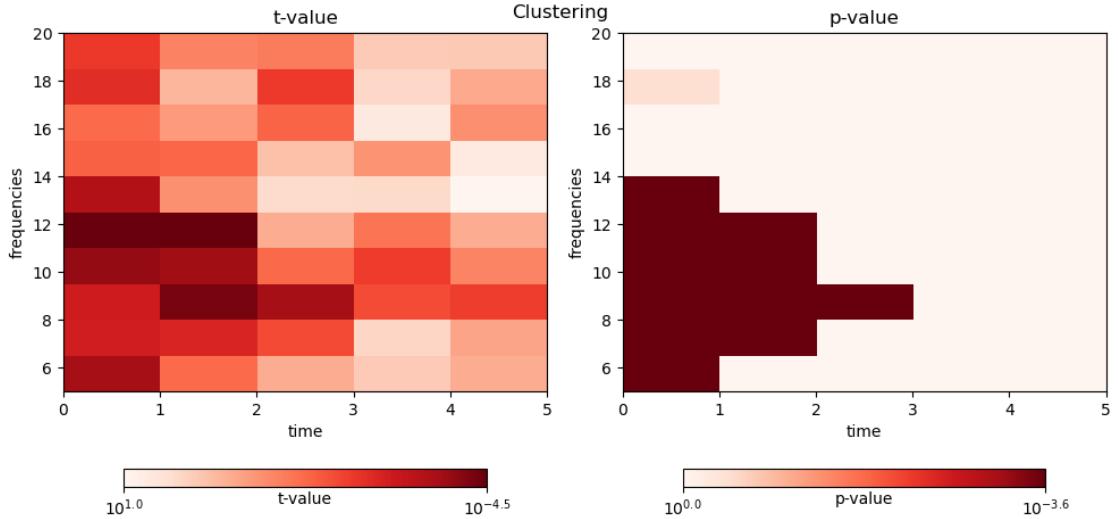


Figure 3.2: Permutation statistics results.

3.1.2 Cluster Permutation Test results

3.2 Sensor results discussion

Quantitative analysis An AUC of 0.6 is not high in absolute terms but not bad in neuroscience on intervals of only 0.5 seconds. If we combine all the bins we would get a much better AUC. Furthermore, statistics by permutation of clusters show that the results are very significant at the group level.

Qualitative analysis Our main cluster is centered on the alpha band. We will discuss the alpha band in more detail in section 3.3. But at first sight, the literature shows frequently significant results in the alpha band for working memory loadings [8] which is encouraging.

A surprising phenomenon is that the algorithm can decode much more easily at the beginning

of the restitution phase than at the end of the restitution phase. Given that the csp encodes a geometric information, this means that:

- either the information in the working memory is transformed in the course of restitution into information disseminated in the brain in a non-geometrical way.
- Or, given the very large number of repetitions of the experiment, the subject gets tired after a while and forgets the sequence "instantly" after having repreated it in order to save mental energy.

3.3 Results of the contrast in source space²

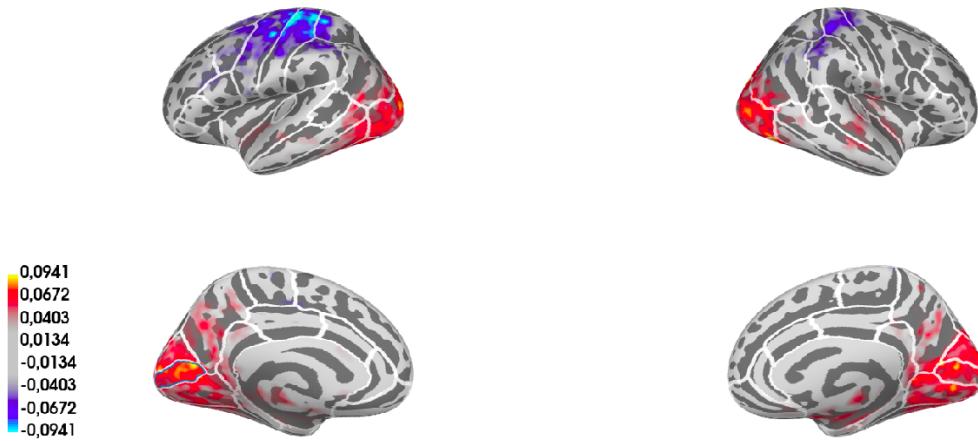


Figure 3.3: Contrast results in source space for 0s-1s, and 8Hz-14Hz (alpha).

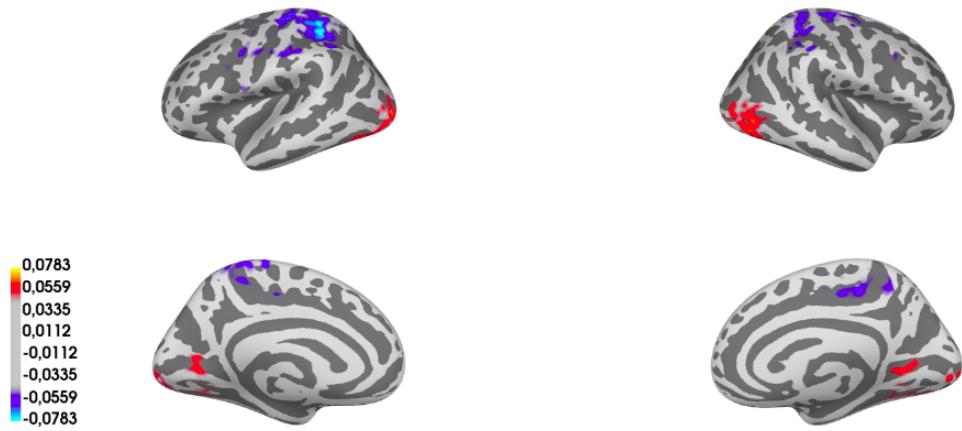


Figure 3.4: Contrast results in source space for 0s-1s, and 15Hz-20Hz (beta).

The figure 3.3 presents the results of the contrast in source space for the most significant time-frequency bin at the group level, i.e. 0s-1s, and 8Hz-14Hz. In this figure the red regions are the regions activated for 3 items, while the blue regions are more activated for 1 item. We recall that

3 items are supposed to load the working memory more than 1 item.

Occipital cortex (visual) The red region activated here is the visual area. The fact that we see the visual area here is not surprising. Indeed, we have to remember that we are visualizing here the alpha band which is a classically inhibitory band in the literature. Thus, the classical interpretation of an activation in the alpha band corresponds to an inhibition of the function of the associated region. This is confirmed by the fact that when we look at the activation in the beta 3.4 of our contrast, the activation of the visual cortex (the red region) disappears almost completely.

The literature presents other results similar to this one. For example [8] shows that "Enhanced alpha oscillations (8-13 Hz) during retention of items in working memory are often interpreted to reflect increased demands on storage and inhibition".

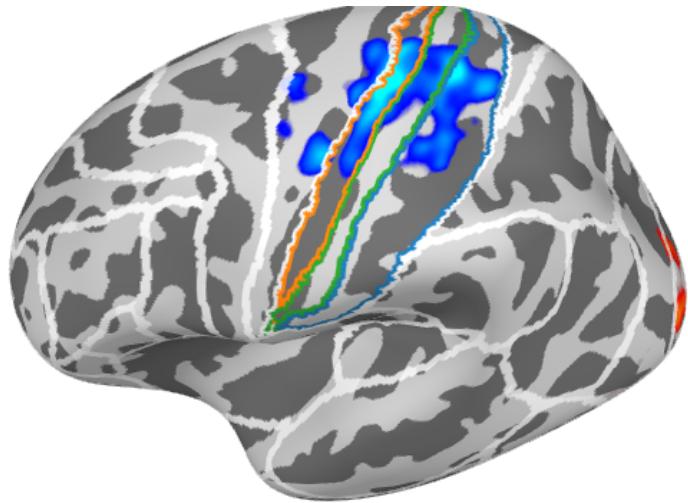


Figure 3.5: Focus on the Brodmann areas 1 (green), 2 (blue) and 3 (orange), from the alpha band in the left hemisphere.

Sensori-Motor Areas The blue region activated at the top of the brain is the sensori-motor area, centred on the postcentral gyrus (Brodmann areas 1, 2 and 3). Before the MEG experiment, subjects were trained to reproduce the task by pressing a button, which explains the activation here. And the region of the somatosensory cortex activated here corresponds to the location of the hand receptors 3.5. This is also supported by the fact that the activation is stronger in the left hemisphere which is consistent with the fact that the subjects are right-handed.

A possible interpretation is that time is represented by the imagination of the movement of one of the body parts, here the hand. We can also reason by analogy by noting that musical children learn to master rhythms by beating the beat or walking to the rhythm of the pulse. The rhythmic information is embodied. Therefore, even if here the analogy has limits since the temporal signal is not organized in a rhythmic and regular way, this interpretation seems to us to be the most

natural one.

Auditory area The regions close to the ears are deactivated while the cue is an auditory one. There are several interpretations: - To see an activation in the auditory zones one must place oneself at $t \leq 0$, as on the figures 2.7: After $t \geq 0$, the auditory cortex is no longer involved - The signal is abstracted from the auditory region to transform it into a purely rhythmic information, thus no longer restricted to the auditory areas. - The auditory region is activated, but we do not see it in this group figure. As a matter of fact, the auditory regions are visible in the csp components of the subjects as in the figure A.2b. But there is a lot of inter-subject variability: After looking at the csp components for the different subjects, it appears that only subjects with a marked beta peak show activation in auditory cortex, and this peak is not restricted to $0 \leq t \leq 1$ but are spread across all subjects between 0s – 5s. In order to see an auditory signal at the group level, one would have to align and average the first extracted components for each peak from each subject. But averaging the components presents mathematical difficulties [ref. Appendix], and could be a research topic in itself.

[Image beta et pour csp aussi.]

Conclusion et Bilan personnel

Insérer ici le texte de votre conclusion La conclusion doit porter sur les travaux que vous avez réalisés. Quelles sont les questions que vous vous êtes posées et les réponses que vous y avez apportées ? Pensez à porter un œil critique et à élargir votre réflexion. Il est important de souligner vos acquis personnels et professionnels et de dresser un bilan de cette expérience en le mettant en perspective de votre formation et de votre projet professionnel. N'oubliez pas d'effacer ce texte quand vous n'en aurez plus besoin.

References

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Appendix A

Sensor

A.1 CSP algorithm

A.1.1 CSP running time optimization

The optimization of the computation time does not change the neuroanatomical results presented, and therefore is not integrated in the "method" part, but still required a considerable amount of work.

My first implementation of the CSP algorithm took a whole day to compute for a single subject, which corresponds to a 15 days computation for our cohort. It was therefore crucial to find ways to greatly accelerate the calculations, which will then be reiterated at each commit of the pipeline as part of the continuous integration with Circle CI.

A great deal of research and engineering effort was then put into reducing the calculation time.

Classic software engineering techniques Classic software engineering techniques have been key to massively reduce computation times: factoring of all steps, use of tools such as the line-profiler - which allows to visualize the execution time of each line - use of multi-processing. On the other hand, even if mathematically some operations are commutative, in practice, the choice of the order of the operations allows to save computation time: for example even if the operations (time crop, frequency filter) are commutative, it is better to start by cropping the data and then filtering, because the filtering operation is very expensive.

Dimensionality reduction Once all the software improvements have been made, we can also make improvements coming from machine learning techniques by using dimensionality reduction techniques: We can either select the type of channels, or use a PCA.

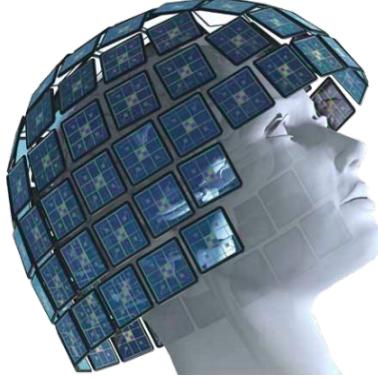
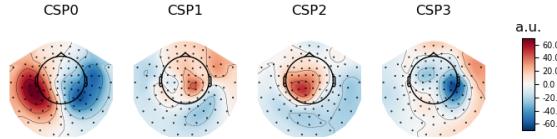


Figure A.1: MEG Sensors [[ELEkta documentation](#)]

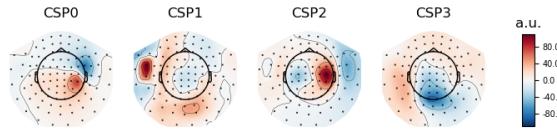
- Reduction of dimensionality by selection of the channel type: The MEG data comes from 102 sensors, which are distributed as shown in the figure A.1. Each sensor consists of 2 gradiometers measuring the gradiometric field (Tesla/meter) in the direction tangent to the sensor plane, and a magnetometer measuring the electric field in the direction normal to the sensor plane. Magnetometers are robust to external noise, while magnetometers are more exposed. But magnetometers have two crucial advantages: 1. they record localized spatial information, which is perfectly suited to the CSP algorithm, which subsequently favors the interpretability of patterns from the CSP. 2. The magnetometers are half as numerous as the gradiometers. Thus, by selecting only the magnetometers, the number of channels is divided by three. The CSP algorithm being limited by an SVD whose complexity in $\mathcal{O}(Tn^2)$ evolves as a function of the square of the number n of channels [3], we thus accelerate the algorithm by a factor 9. (T is the number of time point, in our case bigger than the number of channels. The complexity of the SVD internal to the CSP is in square of the minimum between T and n).
- The following point applies only to data from a MEG, but not to EEGs. Indeed, EEGs have only one channel type. We can therefore reduce the dimensionality using a simple PCA.

Sampling The last way to accelerate the computation time is to use sampling, i. e. to reduce the sampling frequency. This is also called decimation. For example $decim = 5$ consists in taking only one point on 5. But sampling can introduce numerical instabilities. Indeed, the CSP algorithm must start by estimating the covariance matrix of the signal. However, the estimation of a covariance matrix of dimension n requires at least approximately n points. With a sampling frequency of 100 Hz, over a time window of 0.5 seconds, we have 50 points. It is therefore necessary to reduce the dimensions to at most 50 or to use covariance regularization methods, presented in section A.1.2.

[Nyquist]



(a) Example of CSP components (alpha band)



(b) Example of CSP components (beta band)

Figure A.2: Example of csp components from the alpha and beta band.

CSP running time optimization results The choice of the order of commutativity, the reduction of the dimensionality and the resampling allow us today to obtain results in less than three hours with 8Cross validation for all subjects. These three techniques allow us to respectively accelerate by $2 * 10 * 5$ on our dataset while keeping similar performances in all points. It even seems that the PCA increases the numerical stability of the results.

A.1.2 CSP Regularization

topographic map, right hand rule

The visualization of csp patterns makes it one of the most interpretable algorithms. But in the context of MEGs, one must keep in mind that the activations are done by magnetic dipole. Thus in the CP0 of the figure, by using the right hand rule, we deduce that the magnetic field enters inside the right ear.

A.1.3 Mathematical subtleties

Why not aiming for the best classifier?

Mathematically, we are not looking here to create the best classifier, and to optimize the rocauc score, we are only looking to obtain unbiased scores that can be used later in the permutation test. This is why it is not a problem to optimize the execution time.

Moreover, in neuroscience, interpretability is much preferred to performance. And the CSP algorithm is ultra interpretable thanks to the visualization of patterns. Since our results are already significant with CSP, there is no need to struggle any further. The CSP algorithm is already one of the best compromise between intepretability and performance.

choosing the t-value threshold

Choosing a t-value threshold of 0.01 we obtain the figure 3.2, with a cluster having a p-value of $10^{-3.6}$. I chose this restrictive threshold of 0.01 for my final image in order to limit the area of my cluster and to limit it to the most significant areas. But it is possible by choosing a threshold of 0.05 to obtain a figure with a cluster going through the whole alpha band from 0 to 5 seconds.

However the obtained cluster has no physical reality and could be extended to the whole image if we had more subjects. We must therefore take a cluster of reasonable size in order to maximize the signal to noise ratio when moving to the analysis of sources.

A.2 Cluster permutations statistics algorithm

A.2.1 t-values calculation

Les t-valeur est un test paramétrique qui suppose la gaussianité des valuer souris jacentes calculé. Cette hypothèse de gaussianité n'est pas toujours vérifiée pour des données venant d'imagerie cérébrale en raison des nombreux filtres préliminaires. Mais dans notre cas, on calcule les t-valeur à partir de la différence entre le roc-auc score et le niveau de chance moyen ce qui permet de rétablir l'hypothèse de gaussianité.

Le calcul des p-valeurs se fait pour chaque time-frequency bin de manière indépendante.

On considère la liste des différences $(X_i)_{i \in [\text{Nb Subjects}]}$ pour tous les sujets entre le roc-auc et le chance level $c = 0.5$ pour une time frequency bin.

On soustrait alors toutes ces cartes au chance level d'une roc-auc à savoir 0.5. On obtient alors la différence entre le roc-auc et le chance level.

Il suffit alors de calculate the T-test for the mean of ONE group of scores.

This is a test for the null hypothesis that the expected value (mean) of a sample of independent observations a is equal to the given population mean, popmean .

Ce test permet de rejeter l'hypothèse nulle sous laquelle la moyenne d'une population d'observation indépendantes est égal à 0.

Formellement, On veut comparer la moyenne μ d'une population de loi normale et d'écart type σ non connu à 0. Pour ce faire, on calcule la moyenne empirique $\bar{x} = \frac{1}{n} \sum_{i=1}^n x_i$ et l'estimateur sans biais S_n^{*2} de sa variance σ^2 : $S_n^{*2} = \frac{1}{n-1} \sum_{i=1}^n (X_i - \bar{X}_n)^2$.

Selon l'hypothèse nulle, la distribution d'échantillonnage de cette moyenne se distribue elle aussi normalement avec un écart type $\frac{\sigma}{\sqrt{n}}$.

La statistique de test:

$Z = \sqrt{n} \frac{\bar{X} - \mu_0}{S_n^*}$ suit alors une [[loi de Student]] à $n - 1$ degrés de liberté sous l'hypothèse nulle (c'est le théorème de Cochran).

On choisit un risque α , généralement 0.05 ou 0.01 et l'on calcule la réalisation de la statistique de test :

$$z = \sqrt{n} \frac{\bar{x}_n - \mu_0}{s_n^*}, \text{ où } s_n^* = \sqrt{\frac{1}{n-1} \sum_{i=1}^n (x_i - \bar{x}_n)^2}$$

A.2.2 Limites algorithmiques

[annex]

- Choix du nombre de Bin est quelque peu aritraire. Il fut juste respecter quelques conditions telle que Nyquist, plus le fait d'avoir assez de point pour estimer la matrice de covariance. Mais ici, ce n'est pas gracve d'être arbitraire sur le nombre de point étant donné que le résultat du snesor space n'est utilisé que pour cibler le travail en allant dans le source step. - Le fait de pouvoir choisir la taille des cluster simplement en ajustant le threshold de la t-value est perturant à première vue. Mais en réalité c'est plutot un bon signe. Nous n'avons testé que deux t-velur différentes (0.01 er 0.05) et le fait d'obtenir deux cluster de taille différentes signifie simplement que notre cluster associé à 0.05 présente une différence significative tout comme notre cluster à 0.01 qui est assui significative. L'un n'exclue par l'autre.

Appendix B

Source

- Annexes : Subtilité : Neuroscience : quest ce qui constitue du bruit ? Quel choix de la matrice de covariance Subtilités mathématiques : commutativité Log + moyenne BEM model freeview

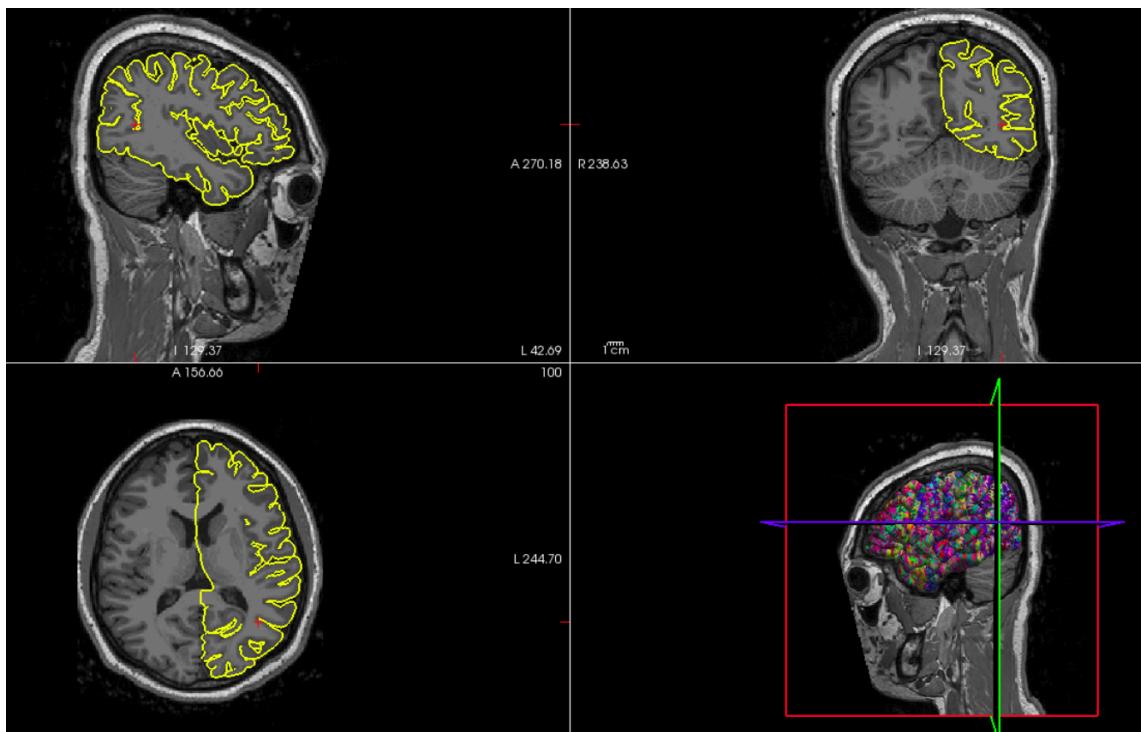


Figure B.1: BEM model used. Only one because MEG transparent.