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| **Multilayer approach to diagnose and classify Multiple Sclerosis phenotypes using graph theory measures** | |
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| Shape, rectangle  Description automatically generated | **Joan Ginard Illescas**  Master in Science in Data Science  Machine Learning in Medicine  **Project supervisor**  Eloy Martínez de las Heras  **Coordinating professor**  Ferran Prados Carrasco  **Date of submission**  XX-XX-2023 |



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**SUMMARY OF THE FINAL PROJECT**

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| Title of the project: | Multilayer approach to diagnose and classify Multiple Sclerosis phenotypes using graph theory measures |
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| Abstract | |
| Multiple sclerosis (MS) is a chronic disease that affects the central nervous system and is a leading cause of disability in young adults. Magnetic resonance imaging (MRI) is a key tool for disease diagnosis, but lesions seen on an MRI do not always correlate with disease progression, known as the "clinical-radiological paradox."  Network science has proved to be a powerful tool for characterizing brain connectivity patterns, and in this work, we propose using network connectivity measures to classify MS patients. We will construct a three-layer network per subject based on MRI data and obtain a set of measures to enable the application of machine learning algorithms to differentiate between healthy subjects and MS patients and distinguish patients with worse clinical outcomes.  During this process we will find most suitable connectivity measures and determine the usefulness of considering the network layers separately or integrating them into a single-layer network. | |

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# Introduction

Multiple sclerosis is a chronic disease of the central nervous system and is the first non-traumatic cause of disability in young adults (D. T. Chard et al. 2021) It is characterized by inflammation, demyelination and progressive neurodegeneration (Haider et al. 2016).

Patients can evolve from a clinically isolated syndrome (CIS) into a primary progressive course (PPMS) or a relapsing-remitting course (RRMS), which will evolve into a secondary progressive course (SPMS) within in a period that may vary between 10 and 20 years (Kocevar et al. 2016).

It is of paramount importance to determine which patients will follow each disease course as early treatment can delay disease progression (Comi et al. 2009) and improve living standards of these patients.

## Context and motivation

Magnetic resonance imaging (MRI) is established as a key tool for the disease diagnosis, although lesions shown by this test seem to have no direct correlation with the evolution of the disease (Chard and Trip 2017). Those who have more lesions on an MRI do not necessarily present more symptoms, which is known as the "clinical-radiological paradox." (Barkhof 2002).

Currently, we do not have any other tools that can measure the progression of the disease. Therefore, it is of great interest to find a system that can classify patients based on the available diagnostic tests, primarily MRI, according to the progression of the disease.

On the other hand, increasing size and complexity of neurobiological data is met with theoretical and computational advances in data analysis (Bassett and Sporns 2017). Network science has proved to be a powerful tool to cope with this challenge and to characterize brain connectivity patterns (Fornito, et al. 2016)

In this work, we propose using network connectivity measures to classify MS patients. For this purpose, we will use data obtained from MRI resulting in the construction of a 3 layer network per subject, with 76 nodes each layer. Based on the connectivity properties of the network, we will obtain a set of measures that will enable us to apply different machine learning algorithms, which we hope will help us distinguish patients with worse clinical outcomes, or at least to differentiate between healthy subjects and MS patients.

Previous studies have explored the feasibility of several machine learning models (Kocevar et al. 2016) or (Zhao et al. 2020), but few, to the best of our knowledge, have focused on using connectivity measures (Solana et al. 2019)

## Personal motivation

One of the subjects that I have enjoyed the most during this Master Degree has been graph theory. That is why I decided I wanted to do my Master Thesis on something related to it. However, I did not want to explore typical examples in graph theory like as social networks or transportation.

While reviewing available thesis topics, my wife, a pediatrician, pointed out this one as the most original one.

I delved into the specific topic of the project and I found very attractive to be able to relate the functioning of the brain or model some aspect of it with a mathematical model such as a graph. As I learned more about this area, my interest grew, and I believe we are at an important moment in advancing our knowledge of how the brain works.

## Goals

In this work we aim to investigate the potential of using network analysis and machine learning algorithms applied to MRI data to classify MS patients.

Our main goal is to find algorithms or an ensemble of algorithms that can classify individuals into healthy subjects and MS patients and discriminate patients in different stages of the disease.

We have additional secondary objectives that are either desirable or serve as preliminary milestones. Here the most prominent ones:

• Find out most suitable network connectivity measures for the task. This is not only relevant in improving the algorithm's subsequent performance but could also assist in the research of the disease itself. It should be noted that previous studies have already explored this selection process (Solana et al. 2018) or (Casas-Roma et al. 2022)

• Determine if it is more useful to consider the layers separately, a multi-layer network, or to try to integrate them into a single-layer network.

• Obtain results with algorithms that allow for interpretation and avoid “black box” algorithms

## Sustainability, diversity and ethical/social challenges

The Ethical and Global Engagement Competence (EGEC) is defined at the Master’s level as follows: *“Act in an honest, ethical, sustainable, socially responsible and respectful manner with respect to human rights and diversity, both in academic practice and in the professional, and design solutions to improve these practices.”* It addresses three main dimensions: Sustainability, Ethical behavior and social responsibility and Diversity and Human Rights.

Our goal could potentially lead to improved living standards for those affected by MS so we can state this work main impact is on Ethical behavior and Social responsibility.

We also address diversity in the sense we do not differentiate o discriminate patients by skin color, religion, sexual orientation or any possible source of discrimination.

We certainly have to be aware of patient sex and age in our data as it is well documented that are gender and age differences in WM (Hsu et al. 2008). This does not mean we pursue results which apply to only one sex and age, in fact quite the opposite.

## Approach and Methodology

A project like this has a previous step which is reviewing available literature. A thorough literature review is a valuable tool for ensuring the accuracy of our theoretical framework, refining project goals, and applying relevant findings to our own research.

Data science projects typically follow a set of common stages, such as exploratory data analysis and data processing, feature selection, model creation and model assessment. In addition, there may be additional stages that are specific to the particular topic or domain of the project. It's important to note that the data science process is not strictly linear, but rather an iterative one. Additionally, the boundaries between the different stages can be blurry at times, as there is often overlap and feedback loops between them.

Accordingly I have divided work with data in four major steps: Data processing, Network connectivity measures, feature selection, model creation and comparison.

**Data processing**

We have a data set provided by the tutor. It is composed of a cohort of 147 patients and 18 healthy volunteers. As it has been noted before we have a multi-layer network for each subject, encoded as 3 data matrix per subject. Those 3 matrices represent: structural white matter (WM) network, structural gray matter (GM) network and a resting-state functional network. For each subject we have some clinical information including age, sex, disease duration, EDSS score and binary classification informing whether the subject is a patient or a healthy subject.

Although data has already been processed in order to obtain the matrices, there are still some decisions to make. For instance, different factors contribute to the fact that we will have some connections in GM and WM matrices that are not really present or in functional matrix we will have to deal with negative correlations that pose as negative weights in our network.

**Network connectivity measures**

In this step, we will obtain different connectivity measures for each network and patient. We will focus mainly in those measurements that literature points out as more promising.

Also in this step we will check whether it is convenient to work with a 3 layer network, combine it into one single and/or discard one or more layers if they are not meaningful.

**Feature Selection**

In order to optimize the performance of our models, we need to select the most relevant features. This can involve conducting statistical test on our data to determine the most informative variables, or using dimensionality reduction techniques to reduce the complexity of the dataset.

**Model creation and assessment**

This stage involves training and testing different models with the same set of train and test data. To assess model performance we will use metrics like accuracy, recall and F-scores among others.

To carry out the project, R and Python, via Jupyter notebook, will be used. In R we will use specific libraries to analyze and perform network measurements, like *igraph* and *muxViz* (De Domenico, Porter, and Arenas 2015), which is a library specially focused on multi-layer networks. Besides those libraries we will also use *tidyverse* libraries.

Regarding to Python, data science most relevant libraries will be used: *Pandas, Numpy, Sckit-Learn, Matplotlib* and *Seaborn* and *Scipy*. In addition two specific libraries will also be used: *NetworkX (network measurments)* and *ComBat* to correct biases in our array due to the use of different scanners.(Behdenna et al. 2021)

## Schedule

The work plan is organized around a series of milestones, which will be completed in each Continuous Assessment Test. Each milestone is then further divided into smaller steps. As shown in the table below and in the Gantt Diagram (Fig. 1), the main phase of the project (phase 3) is based on the stages outlined in the previous section.

|  |  |  |
| --- | --- | --- |
| STAGE | START DATE | END DATE |
| 1. Work planning | 01/03/2023 | 12/03/2023 |
| 1. State of the art – Bibliographic review | 08/03/2023 | 21/03/2023 |
| * 1. Literature review | 08/03/2023 | 17/03/2023 |
| * 1. Draft | 18/03/2023 | 25/03/2023 |
| 1. Work implementation | 26/03/2023 | 27/05/2023 |
| * 1. Data preprocessing | 26/03/2023 | 12/04/2023 |
| * 1. Network connectivity | 13/04/2023 | 27/04/2023 |
| * 1. Feature selection | 28/04/2023 | 12/05/2023 |
| * 1. Creation of Models | 19/05/2023 | 27/05/2023 |
| 1. Writing Report | 29/05/2023 | 25/06/2023 |
| * 1. Draft | 29/05/2023 | 11/06/2025 |
| * 1. Final version | 12/06/2025 | 25/06/2025 |
| 1. Project Defense | 26/06/2023 | 02/07/2023 |
| * 1. Slides and Video | 26/06/2023 | 02/07/2023 |
| * 1. Public Defense | Date to be determined | |

Table 1. Project Schedule

Gráfico

Descripción generada automáticamente

Fig. 1. Project Gantt Diagram

Fig 1. Project Gantt diagram

There are several reasons why planned schedules may be disrupted, including over-optimistic planning, illness, technological setbacks, and excessive workload at the workplace. That is precisely why we have allocated more time in Phase 3, as it allows for the review of the process thus far and adjustments to be made if necessary.

## Summary of the outputs of the project

## Brief description of the remaining chapters of the report

# State of the art

As previously mentioned, Multiple Sclerosis (MS) is a neurodegenerative disease that poses a challenge when it comes to relating MRI-detected lesions to physical disability and cognitive impairment in patients. (Fleischer et al. 2016) and (Schoonheim, Meijer, and Geurts 2015) have suggested that during the early stages of the disease, a compensatory mechanism may exist that allows for the reorganization of brain functional networks to cope with disease progression. However, this mechanism is only possible when structural damage is not yet severe (Schoonheim, Broeders, and Geurts 2022). While the proposal of such a mechanism remains controversial (Schoonheim, Broeders, and Geurts 2022), it nevertheless suggests that there is something happening with brain networks in MS, which has led to the classification of MS as a network disease (Schoonheim, Broeders, and Geurts 2022; D. T. Chard et al. 2021). Hence, utilizing network analysis and graph-based measures to study MS, as we propose in this work, is a valid and appropriate approach.

## Brain networks

Although the focus of this work is on the characteristics of brain networks in individuals with MS, it is worth noting that a healthy brain is characterized by a combination of segregated and integrated processing. In a comprehensive review of the literature on brain structure and function, (Schoonheim, Broeders, and Geurts 2022) describe how a healthy brain is represented by high local clustering and short average path lengths between distant regions. The measures of network integration in this kind of network are characteristic path length and global efficiency, while segregation is quantified by modularity and clustering of local efficiency. This organization of networks is referred to as rich club organization (Heuvel and Sporns 2011; Fornito et al. 2016). In rich club networks, high-degree nodes (or network hubs) are more densely connected to each other than to lower-degree nodes.

As (Fornito, et al. 2016) point out, there are 2 main networks studied in brain connectivity: Structural and Functional networks. Structural networks are based on the anatomical connections between different regions of the brain, while functional networks are based on the patterns of synchronized activity between those regions. This means that while the structural network provides information about the anatomical pathways that connect different brain regions, the functional network provides information about the strength and efficiency of the communication between those regions.

## Single layer networks applied to MS

In their review, (Fleischer et al. 2019) enumerated all network measures found in the literature up to that point (Table 2) to distinguish between healthy subjects and MS patients or between patients in different clinical stages of the disease. Some studies have focused on studying structural network disruption, such as (Kocevar et al. 2016; Shu et al. 2016; Llufriu et al. 2016), while others have focused more on functional networks, such as (Welton et al. 2020)

|  |  |  |
| --- | --- | --- |
|  | **Measures** | **Interpretation** |
| Measures of centrality | Degree Centrality | The higher the value the higher the influence of the region |
| Eigenvector Centrality | Higher values correspond to regions which are connected to regions that are central in the network |
| Nodal Efficiency | A higher value indicates a higher ability of the region to propagate information with the other nodes |
| Measures of segregation | Clusteriing coefficient | Fraction of a node’s neighbor that also neighbors. So, it will indicate an organization principle which is cost-efficient |
| Transitivity | Variant of clustering coefficient |
| Local efficiency | It shows the capacity of the network to transfer information between neighboring regions |
| Modularity | Modules are densely connected nodes that are sparsely connected to the rest of the network. Increased values represents an optimized network in response to changing environments |
| Measures of integration | Global efficiency | Information transfer across the whole brain is more efficient |
| Path length | An increase will show a lower ability to transfer information in parallel |
| Measures of network resilience | Assortativity | Increase describes brain ability to continue functioning as response to continuous damage. |

Table 2. Graph Based Measures in literature. Adapted from Fleischer et al. 2019

Among the first group, (Llufriu et al. 2016) observed an increase in Path Length and a decrease in Global Efficiency, which could indicate a disruption in network integration. (Shu et al. 2016) found a decrease in local and global efficiency. On the other hand, (Fleischer et al. 2016) found that, at least in the early stages of the disease, there is an increase in network clustering and modularity, which could be indicative of the compensatory mechanism mentioned previously.

According to (Schoonheim, Broeders, and Geurts 2022) we could conclude that patients tend to show more segregated and less integrated structural networks overall, particularly in patients with cognitive impairment. In the same review, they pointed out that existing studies on functional networks are more complex and that hypothetical connections between network efficiency and cognition are less clear.

Some authors, such as (Pontillo et al. 2022), have concluded that to this date, there is no "hallmark of multiple sclerosis" in the sense that conflicting results still arise when studying the brain and multiple sclerosis as a single layer network.

## Brain and multilayer networks

Multilayer networks are a relatively new approach in network analysis (Bianconi 2022), and their application to the human brain is even more recent. (Schoonheim, Broeders, and Geurts 2022) note that considering the brain as a multilayer network leads to emergent properties that cannot be fully captured by analyzing individual layers separately. (Sporns 2018) predicts that the use of a multilayer framework is likely to become more widespread.

Regarding the brain, some studies explore the application or extension of single-layer measures to a multilayer setting, such as (Vaiana and Muldoon 2020; Mandke et al. 2018). Others have proposed models, such as the core-periphery organization from a multiplex point of view (Battiston et al. 2018). With respect to disease, it is worth noting that the disruption of the core-periphery structure has been studied in Alzheimer’s disease (Guillon et al. 2019).

## Multilayer networks applied to MS

Given what we have discussed about single layer networks, it's not surprising that (Pontillo et al. 2022; Schoonheim, Broeders, and Geurts 2022) suggest that multilayer networks may provide better insights into the organization of the brain and multiple sclerosis. This approach is so new that I have only found four papers applying multilayer networks to multiple sclerosis.(Kennedy et al. 2023) used five biological layers, which are quite different from the data we have, and (Martí-Juan et al. 2023). studied the relationship between functional and structural networks using a tool called The Virtual Brain. Therefore, I will focus on the other two papers.

(Casas-Roma et al. 2022). examined a three-layer network with the same layers as in our work, including a GM morphological network, a structural brain network, and a functional network. In their approach, all nodes are the same across the layers, but each layer represents a different type of relationship between nodes. One of the main innovations in their study is the use of the WM structural network to represent interlayer connections between the other two layers. They employed global and local measures to describe the properties of the multilayer network, including Strength, Degree, Betweenness centrality, Closeness centrality, and local efficiency. The authors found that all MS patients had lower local efficiency, and most of them had lower closeness centrality and node degree.

In (Pontillo et al. 2022), the researchers also used a three-layer network similar to the one in the (Casas-Roma et al. 2022). study. However, they used a different approach by constructing a multiplex network, which is a type of multilayer network where nodes have a one-to-one correspondence between layers. This allows for the integration of different layers into a single layer. They measured coreness using the definition proposed by (Battiston et al. 2018) and also introduced a Coreness disruption index, which represents a global measure of core-periphery reorganization. They found that the weakening of the multiplex core-periphery structure depends on the disease phase and is associated with physical disability and cognition. They also noted that the modeling of different layers together is still a topic of debate, and new solutions may emerge in the future.

## Machine Learning and MS

It is interesting to note that various machine learning models have been employed to predict or classify MS patients using different types of MRI data. This can be seen in the reviews of (Nabizadeh et al. 2022; Seccia et al. 2021). However, it is surprising that there are no ML algorithms applied to graph metrics, and as far as we know, only (Kocevar et al. 2016; Solana et al. 2019) have applied SVM to connectivity measures. To our knowledge, no one has applied ML algorithms to a multilayer network in the context of MS.

## Conclusions from the state-of-art

After reviewing the literature, it is evident that analyzing MS as a network disorder and employing graph-based measures is a valid approach. Although, it appears that there is an increasing agreement that a multilayer network approach is necessary to fully capture the complexity of MS. However, there is still no consensus on the best way to model the different layers of the network.

This presents a challenge for our work, as our main goal was to explore the use of network analysis and graph-based metrics to study MS. Given the current state of the field, it may be necessary to focus on developing and comparing different approaches to modeling the multilayer network.

# Methods and resources

## Participants

We have data from 165 subjects, with ages spanning from 22 to 72 years. Among these participants, 18 where healthy subjects (HS), who volunteered for the study, and the remaining 147 were patients with Multiple Sclerosis (PwMS). This group can be further subdivided based on the type of MS: 6 with PPMS, 16 with SPMS and the remaining 125 with RRMS. Physical disability is assessed using the EDSS.

Below is a table summarizing data from all participants:

|  |  |  |
| --- | --- | --- |
|  | PwMS ( n = 147) | HS (n = 18) |
| Female, n | 104 | 15 |
| Age years, mean | 47.3 ± 10.1 | 36.6 ± 9.6 |
| MS type |  | ---- |
| RRMS | 125 (90 female) | ---- |
| SPMS | 16 (10 female) | ---- |
| PPMS | 6 (4 female) | ---- |
| EDSS, median (range) | 2 (0 – 7.5) | ---- |
| Disease duration, year mean | 14.1 ± 10.1 | ---- |

Table 3. Participans clinical, demographic and cognitive characteristics

Gráfico, Gráfico en cascada

Descripción generada automáticamenteWe can also see our data distribution in Fig 2.

Fig 2. Participants data distribution.

Based on graphs a) and b), we can observe that our HS group tends to be younger, while patients with more advanced types of MS lean towards the higher age spectrum (b). Graphs c) and d) clearly show a significantly higher representation of females. In graph e), the disease duration appears to cluster around the 10 to 20-year mark. Finally, graph f) illustrates how disability tends to exacerbate during the more advanced stages of the illness.

## Brain networks and processing steps

As we have stated previously we have 3 matrices per subject. Although it is beyond the scope of this work, scanner data acquisition and preprocessing steps needed to obtain these matrices, it is important to note that these matrices still require some additional processing and verification..

During data acquisition, the brain was segmented into 76 regions of interest (ROIs), or nodes, leading to 76 x 76 matrices. However, preprocessing was conducted to ensure all matrices are symmetrical. Consequently, when we interpret these matrices as graphs, they will be recognized as undirected graphs, given that the connection from node i to node j is identical to that from j to i. The main diagonal in matrices represents self-connections and will be removed if present.

### Structural brain network (FA network)

As described in section 2.1., this network maps the anatomical pathways connecting different regions of the brain. To generate matrices that embodies this network, the diffusion of water molecules is studied (hence the name diffusion MR)I. Diffusion of water molecules in the brain is anisotropic, indicating that diffusion does not occur freely (and isotropically) but rather following pathways, running in parallel to the barriers imposed by brain structure. Fractional anisotropy (FA) quantifies how water diffusion is constraint in a given direction within a voxel.

Despite the preprocessing steps effectively minimizing or eliminating factors that could introduce noise in our data, we can implement a threshold to further ensure the elimination of all non-connections. We apply a threshold (Fornito, et al. 2016) to our matrices to remove these spurious connections. However, since this could inadvertently remove true, albeit weak, connections, we use an additional criterion. If a connection is present in at least 60% of the healthy subjects (HS) - that is, 11 out of 18 - we retain the connection as is.

We can summarize these conditions in the following way:

1. Eliminate all connections that fall below a threshold, which is set at **0.1**.
2. However, if these connections are present in at least **11 out of 18** healthy subjects (HS), they should be retained.

The preprocessing steps (prior to this one) proved to be precises, as no changes were observed.

In Fig 3, we observe a distribution of weights across all matrices, with a significant number of outliers at zero. This situation is partially rectified with the age and sex correction (see [section 3.3.](#_Age_and_sex)). I decided not to impute any value to remove these outliers. I considered that this values are likely to represent weak structural connections, thus any imputation will not greatly affect the overall data. Furthermore, as we applying graph measures to our matrices/graphs, these values will not pose any numerical problems.

### Structural gray matter brain network (GM network)

For each participant, we have another structural network. This network is derived from the similarities in gray matter (GM) morphological patterns according to a defined parcellation scheme. As mentioned before acquisition of this data, as well as parcellation scheme fall beyond the scope of this work.

We apply same threshold and conditions to these matrices as we did for the FA networks, and we also observe no changes in this processing.

### Resting-state functional network (fMRI network)

Functional MRI is used to measure participants' brain activity during resting-state. After preprocessing, signal correlations between Regions of Interest (ROIs) form our matrices. As described in section 2.1. this networks provides information about the communication between nodes.

As matrices are formed by correlation coefficients, its values range from approximately -1 to 1, with diagonal values representing self-correlations. When interpreting these matrices as our graph adjacency matrices, their values will serve as network edge weights. This requires us to remove negative values, as they would imply negative weights. However, discarding negative correlations could lead to a loss of significant information (Fleischer et al. 2019).

Given that negative values also suggest a relation between ROIs, we have decided to take the absolute value to retain this information while setting the diagonal values to zero.

## Age and sex correction

The brain, similar to many other biological systems or structures, undergoes changes with aging and exhibits gender-related differences (Hsu et al. 2008).

To control for age and gender, and allow comparison across participants, we adjust the matrix values using a linear regression with age and gender as regressors. For each specific i,j position in all matrices, we collect 165 values, one per participant, and apply linear regression. Since the matrices are symmetric and the diagonal is zero, we only consider one linear regression for each matrix position in the upper triangle.

|  |  |  |
| --- | --- | --- |
|  |  | ( 1) |

Where are predicted values, α and β are the regression coefficients. The difference between actual value (y) and predicted value, is known as residuals.

|  |  |  |
| --- | --- | --- |
|  |  | ( 2) |

These residuals account for information not explained by our regressors, i.e., sex and age. Theoretically any changes cause by the disease will be captured in these residuals. The final value of i,j position in our matrix is our residuals plus and “standard” value for this position. This standard value should represent a normal brain, corrected for age and sex. However as this value is not uniform across all brains, we consider the mean of our healthy volunteers. Therefore, for patient m, the final value in position i,j is given by:

|  |  |  |
| --- | --- | --- |
|  |  | ( 3) |

Please note that the linear correction may result in values marginally below zero or slightly above one. Since we can't use negative values to represent graph weights, we adjust these to zero. However, we retain the values above one, as they are infrequent and only marginally exceed one.

In the following figure, the differences in values distribution before and after accounting for age and sex are clearly shown:

Gráfico, Histograma

Descripción generada automáticamente

Fig 3. Weights distribution, before and after sex and age correction.

Differences are specially noticeable in FA connections, where some values of zero appear to be corrected. Visible changes are also present fMRI connections, while no substantial differences are appreciated in GM connections.

## Data harmonization using ComBat

Participants data have been collected using two different scanners. According to existing literature (Fortin et al. 2017), diversity in data acquisition methods may lead to an increase in the variance of matrix values.

To verify if there is an increase in variance, we conduct a principal component analysis, PCA, (see Fig 4). The analysis indicate effect of data acquisition is only evident in FA data

Gráfico, Gráfico de dispersión

Descripción generada automáticamente

Fig 4. PCA before harmonization

In graph we could appreciate how only FA shows a significant effect of data acquisition.

To overcome this problem neuroCombat library (Fortin et al. 2018) is applied to FA data. And in the following figure we can appreciate data changes in PCA for FA data.

Gráfico, Gráfico de dispersión

Descripción generada automáticamente

Fig 5. PCA with FA data after ComBat

## Graphs

# Results

# Conclusions and future work

# Glossary

* *Expanded Disability Status Scale* (EDSS) is a test used to assess physical disability in MS patients. It ranges from 0, no disability, to 10, deceased.

Voxel?

## List of Abbreviations

Terms in alphabetical order

|  |  |
| --- | --- |
| TERM | ABBREVIATION |
| Clinically Isolated Syndrome | CIS |
| Expanded Disability Status Scale | EDSS |
| Fractional Anisotropy | FA |
| Functional MRI | fMRI |
| Gray Matter | GM |
| Healthy Subject | HS |
| Multiple Sclerosis | MS |
| Magnetic Resonance Imaging | MRI |
| Patient with MS | PwMS |
| Primary progressive course | PPMS |
| Principal Component Analysis | PCA |
| Region(s) of interest | ROI(s) |
| Relapsing-Remitting Course | RRMS |
| Secondary progressive course | SPMS |
| Support Vector Machine | SVM |
|  |  |

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# Appendices