Aggregation of MRI biomarkers in Multiple Sclerosis clinical trials using geometric PCA

S. Rebbah[1,2], I. Berry[1,3], S. Puechmorel[2], F. Nicol[2], D. Delahaye[2], P. Maréchal[4]

[1]INSERM ToNIC (Toulouse Neuroimaging Center) ; [2] ENAC (Ecole Nationale de l'Aviation Civile) ; [3] CHU Rangueil ; [4] IMT (Institut de Mathématiques de Toulouse)

Magnetic resonance imaging (MRI) of the brain plays an important role in the diagnosis and the treatment of Multiple sclerosis (MS), an inflammatory, demyelinating disease that is characterized by the presence of multiple lesions in the central nervous system and clinically by relapses and accumulation of neurological disability.
Disability progression, unlike relapses, are poorly associated to macroscopic lesion progression and we still lack a simple and robust marker to implement in clinical practice. Since progression mechanisms are complex and diffuse, the identification of effective markers requires multimodal approaches to generate combined measures reflecting the respective weight of mechanisms leading to permanent disability.
Thanks to scientific progress, we have access to many MRI procedures, and each of them offers us biomarkers e. g. Apparent Diffusion Coefficient ADC and the Fractional Anisotropy FA from the diffusion tensor, the Magnetization Transfer Ratio MTR from the magnetization transfer imaging and Cortical thickness CTH from T1-weighted images… But unfortunately, none of them individually have the power to reflect all the MS mechanisms.
The aim of this study is to propose a combined biomarker approach, with the goal to conclude more easily on the effect of a treatment in a clinical trial.

The study is based on the clinical trial MS-SPI population composed of progressive MS patients receiving high dose biotin MD1003 (n=29) and progressive MS patients receiving placebo (n=11).
In our study, the biomarkers ADC, FA, MTR and CTH are measured in the whole brain and are represented with histograms on which a parametric estimation is performed.
Principal Component Analysis (PCA) is the main linear technique for dimensionality reduction. It performs a linear mapping of the data to a lower-dimensional space in such a way that the variance of the data in the low-dimensional representation is maximized. But since we work with Gamma distributions (i.e. biomarkers distributions) a standard PCA cannot be performed. Indeed, the standard PCA is limited, it only works on data lying in a Euclidean vector space and doesn't handle more complex representations of shape. A Geometric PCA is a generalization of PCA to a non-Euclidean, non-linear setting of manifolds and can be applied to our data.
This poster will present some of the results of this approach.