Longitudinal models for Parkinson’s Disease

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Introduction

• Gain understanding the progression of Parkinson’s disease
• Infer a template of the average disease progression
• Infer each patient disease stage and future evolution
• Two individuals at the same age might be at different stages of disease progression

Methods

Generic spatio-temporal model for longitudinal data

• A hierarchical model

\[ \begin{align*}
\text{Average trajectory:} & & \mu_i(t) = \mu(t) + \epsilon_{t,i} \\
\text{Trajectory of the } i\text{th individual:} & & \mathbf{y}_i(t) = \mathbf{y}(t) + \mathbf{e}_{t,i}
\end{align*} \]

Observations: \( \mathbf{y}_i(t) = \mathbf{y}(t) + \mathbf{e}_{t,i} \)

1. The average trajectory \( \mu(t) \) is chosen to be the geodesic \( \Gamma_\alpha(t) \) of the tangent vector \( \mathbf{v}_0 \) in \( \mathcal{M} \), which we choose orthogonal to \( \mathbf{v}_0 \).
2. The trajectory of the \( i \)-th individual is obtained in two steps. We start by constructing the parallel shift of the average trajectory \( \Gamma_\alpha(t) \) using a tangent vector \( \mathbf{v}_i(t) \), which we choose orthogonal to \( \mathbf{v}_0 \).

\[ \mathbf{y}_i(t) = \mathbf{y}(t) + \mathbf{e}_{t,i} \]

The trajectory \( \mathbf{y}(t) \) is then obtained by reparameterizing in time the parallel shift \( \mathbf{y}(t) \) using the affine reparameterization \( \mathbf{y}(t) \mapsto \mathbf{y}(\tau(t)) \). The above is for the case of stages progression across the population.

\[ \left( \begin{array}{c} \mu(t) \\
\mathbf{v}_0 \\
\mathbf{v}_i(t) \\
\mathbf{e}_{t,i} \end{array} \right) \] (smooth Riemannian manifold \( \mathcal{M} \) \( \xrightarrow{\text{par}} \) (\( \mathbb{R}^d \) sub-Riemannian manifold of \( \mathcal{M} \) \( \xrightarrow{\text{par}} \) (\( \mathbb{R}^d \) sub-Riemannian manifold of \( \mathcal{M} \) \( \xrightarrow{\text{par}} \) (\( \mathbb{R}^d \) sub-Riemannian manifold of \( \mathcal{M} \) \( \xrightarrow{\text{par}} \) (\( \mathbb{R}^d \) sub-Riemannian manifold of \( \mathcal{M} \))

Results

The model in practice for single longitudinal data

Univariate Linear Model

\[ \mathbf{X}_i(t) = \mathbf{X}(t) + \mathbf{e}_{t,i} \]

Multivariate Linear Model

\[ \mathbf{X}_i(t) = \mathbf{X}(t) + \mathbf{e}_{t,i} \]

Multivariate Logistic Model

\[ \mathbf{X}_i(t) = \mathbf{X}(t) + \mathbf{e}_{t,i} \]

Multivariate Logistic model for 3 different motor scores (cerebellar, motor, and cognitive) as output of the non-sparse \( \mathcal{M} \) model.

Multivariate Logistic model for 3 different motor scores (cerebellar, motor, and cognitive) as output of the non-sparse \( \mathcal{M} \) model.

Conclusion

We use a mixed-effect model which is able to evaluate a group-representative spatiotemporal propagation of biomarkers. Moreover, individual parameters characterizing personalized patterns of propagation as variations of the mean scenarios are estimated. The evaluation of this model is made with the MCMC-SAEM algorithm.

Tools and Data

Univariate Logistic Model

\[ \mathbf{X}_i(t) = \mathbf{X}(t) + \mathbf{e}_{t,i} \]

Multivariate Logistic Model

\[ \mathbf{X}_i(t) = \mathbf{X}(t) + \mathbf{e}_{t,i} \]

References