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Learning spatio-temporal trajectories from manifold-valued longitudinal data

Jean-Baptiste Schiratti, Stephanie Allassonnière, Olivier Colliot, Stanley Dunnleman
Inria Paris-Rocquencourt, Sorbonne Universités, UPMC Univ Paris 06 UMR S127, CNRS UMR 7225, ICM, F-75013, Paris, France
CMAP, Ecole Polytechnique, Palaiseau, France

Introduction

Objectives

• Understanding the progression of neuro-degenerative diseases, such as Alzheimer’s Disease (AD) is necessary for early diagnosis and care planning.

• We need to validate experimentally hypothetical models of disease progression, such as [Clifford Jack et al., 2010].

• Longitudinal measurements sometimes belong to Riemannian manifolds (non-Euclidean spaces).

• Longitudinal models for such longitudinal data should be defined for manifold-valued measurements.

• Linear-in-fixed-effects models [Laird and Ware, 1982] are not defined for manifold-valued measurements.

Generic spatio-temporal model for longitudinal data

Summary

We propose a generic mixed-effects model for longitudinal manifold-valued data. The model allows to estimate an average trajectory as well as individual trajectories. Random effects allow to characterize changes in direction and pace at which individual trajectories are followed. This generic model is used to analyze the temporal progression of a family of univariate biomarkers.

The model

\[ y_i(t) = \eta_i(t) + \varepsilon_i(t) \]

where \( \eta_i(t) = \sum_{k=1}^{K} \beta_k \cdot \text{Indicator}(t > T_k) \)

- \( \beta_k \) is a subject-specific acceleration factor. \( \text{Indicator}(t > T_k) \) is 1 if \( t > T_k \) and 0 otherwise.

- \( T_k \) is a subject-specific time shift.

- \( \varepsilon_i(t) \) is a subject-specific error.

- \( \mu(t) \) is a subject-specific value at time \( t \).

Three particular cases of our generic spatio-temporal model

1. Straight line model [Clifford et al., 2015]
   - \( \theta = \beta \cdot (t - \tau) + \mu \)
   - Geodesics are straight lines

2. Logistic curve model [Clifford et al., 2015]
   - \( \theta = \beta \cdot \text{Logistic} \)
   - Geodesics are logistic curves

A hierarchical model

- To model the progression of neuro-degenerative diseases
- To model the progression of ADNI subjects using multivariate fitting

Aim : we want to model the temporal progression of a family of N biomarkers

- We assume that the measurements of each biomarker belong to a one-dimensional Riemannian manifold \( \mathcal{M} \), geodesically complete and included in \( \mathbb{R}^n \). As a consequence, \( \mathcal{M} \) is a product of one-dimensional manifolds : \( \mathcal{M} = \prod_{i=1}^{n} \mathcal{M}_i \)

The average trajectory \( \tau \Rightarrow y(t) \) is obtained by reparameterizing in time the parallel shift \( \eta_i(t) \) using the affine time reparameterization \( \alpha(t) = (t - \tau_i) + \tau_i \). This allows to account for the variability in stages of disease progression across the population.

The operation of parallel shifting, on the manifold \( \mathcal{M} \), using a tangent vector, is defined as follows:

\[ \mathcal{D}_y \mathcal{M} \subset \mathcal{M} \]

where \( \mathcal{D}_y \mathcal{M} \) is the set of all tangent vectors at the point \( y \) on \( \mathcal{M} \). The curve \( \eta_i(t) \) is defined by:

\[ \eta_i(t) = \mathcal{D}_y \mathcal{M}(y_i(t)) \]

The model

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Aim : model the progression of neuro-degenerative diseases

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A hierarchical model

- To model the progression of a family of N biomarkers

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