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Learning spatio-temporal trajectories from manifold-valued longitudinal data

Jean-Baptiste Schiratti, Stéphanie Allassonnière, Olivier Colliot, Stanley Dunnleman

Inria Paris-ROUSS|sou, Sorbonne Université, UPMC Univ Paris 06 UMR S127, CNRS UMR 7225, ICM, F-75013, Paris, France
C|MAIP, Ecole Polytechnique, Palaiseau, France

AM: model the progression of neuro-degenerate diseases

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

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

Working with longitudinal data in the context of neuro-degenerate diseases raises two difficulties:

- Two individuals of the same age might be at very different stages of disease progression
- Statistical models based on the regression of measurements with age are inadequate to model disease progression and age should not be treated as a covariate but as a random variable.

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

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

Linear mixed-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 model is used to analyze the temporal progression of a family of univariate biomarkers.

- \( (B, \gamma^B) \) smooth Riemannian manifold included in \( \mathbb{R}^d \)
- \((M, g_M)\) sub-Riemannian manifold of \( M \), assumed to be geodesically complete
- \( p \in M, \nu \in T_p M \), \( Ey_p(\nu) \) : Riemannian exponential in \( M \) at \( p \) of the tangent vector \( \nu \)
- \( \gamma : B \to M \) : geodesic of \( M \)
- \( \gamma_{t_0} \in \gamma \) : parallel transport in \( B \) along \( \gamma \) from \( p = \gamma(0) \) to \( \gamma(t) \)
- \( \gamma(\gamma, p) : \text{geodesic of } M \text{ which goes through } p \text{ at time } t \) with velocity \( \nu \).

A hierarchical model:

- At each individual:
  - \( \gamma_{t_0} : \mathbb{R} \to M \)
  - \( \gamma_{t_0} = \gamma_{t_0}(p) : \mathbb{R} \to M \)
  - \( \gamma_{t_0} = \gamma_{t_0}(p) : \mathbb{R} \to M \)

A progression model for a family of univariate biomarkers:

- We assume that the measurements of each biomarker belong to a one-dimensional Riemannian manifold \( I \), geodesically complete and included in \( M \).

The average trajectory \( \gamma_{t_0} \) is chosen among a parametric family of geodesics of \( M \):

- \( \gamma_{t_0} \) is a geodesic of the one-dimensional Riemannian manifold \( I \) (straight line, logitudinal curve, ..)

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