

Statistical computing on manifolds for computational anatomy

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In standard medical image analysis, many of the features extracted from images or from their processing are geometric by nature and noisy (e.g. transformations in registration, surfaces in segmentations). Likewise, the usual method for computational anatomy, an emerging discipline that aims at analyzing and modeling the biological variability of the human anatomy, is to identify anatomically representative geometric features (points, tensors, curves, surfaces, volume transformations), and to describe and compare their statistical distribution in different populations. Unfortunately, geometric features most often belong to manifolds that are not vector spaces, which prevents the use of standard statistical tools.

Based on a Riemannian manifold structure, we will detail how one can develop a consistent framework for statistical computing on manifolds, starting with the notions of mean value and covariance matrix of a random element, normal law, Mahalanobis distance and test. Then, we will extend the Riemannian computing framework to PDEs for smoothing and interpolation of fields of geometric elements with the example of positive definite symmetric matrices (tensors). We show that the choice of a convenient Riemannian metric allows to consistently generalize many important geometric data processing algorithms — such as interpolation, filtering, diffusion and restoration of missing data — to tensor fields.

The framework will be exemplified with the statistical estimation of Diffusion Tensor Imaging images from Diffusion Weighted Imaging under a Rician noise assumption, and with the modeling of the brain variability from a dataset of lines on the cerebral cortex.