
Medical Imaging Summer School 2014

28 July - 1 Aug 2014 Favignana, Sicily

Medical Imaging meets Computer Vision

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Lecture 1: Demonology, or a short retrospective of Demons in medical image registration

In this talk, we will present the evolution of the demons' algorithm over a decade from a historical point of view. Originally proposed by Thirion as an efficient procedure for non-linear registration, the algorithm was revisited several times to be recast in a sound minimization framework, in particular through Cachier's pair and smooth (PASHA) method. Additional modifications were performed by Stefanescu to make it fully parallelizable and to include a non-stationary adaptive regularization that could take into account pathologies (areas that do not correspond).

More recently, Vercauteren adapted the efficient optimization procedure to work on a space of diffeomorphic transformations. Experiments show that the diffeomorphic demons results are similar in terms of image similarity metric, but more regular and closer to the true transformation in controlled experiments, particularly in terms of Jacobian. This efficient algorithm was further enhanced by parameterizing the deformation using one parameter subgroups, following the proposition of Arsigny. This new parameterization allows to obtain inverse consistency very easily, and opens the way to a sound statistical setting for deformation-based morphometry.

To wrap up, we will present recent works demonstrating that the efficient and sound principles of demons provide a diffeomorphic registration framework which is also quite versatile and can be easily adapted to tackle new problems such as incompressibility for cardiac motion tracking.

Lecture 2: Geometric Structures for Statistics on Shapes and Deformations in Computational Anatomy

Syllabus: Riemannian and affine Geometry, statistics on manifolds and Lie groups, computational anatomy, Alzheimer's disease, longitudinal deformations

Computational anatomy is an emerging discipline at the interface of geometry, statistics, image analysis and medicine that aims at analysing and modelling the biological variability of the organs shapes at the population level. The goal is to model the mean anatomy and its normal variation among a population and to discover morphological differences between normal and pathological populations.

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For instance, the analysis of population-wise structural brain changes with aging in Alzheimer's disease requires first the analysis of longitudinal morphological changes for a specific subject. This can be evaluated through the non-rigid registration. Second, To perform a longitudinal group-wise analysis, the subject-specific longitudinal trajectories need to be transported in a common reference (using some parallel transport).

To reach this goal, one needs to design a consistent statistical framework on manifolds and Lie groups. The geometric structure considered so far was that of metric and more specially Riemannian geometry. Roughly speaking, the main steps are to redefine the mean as the minimizer of an intrinsic quantity: the Riemannian squared distance to the data points. When the Frechet mean is determined, one can pull back the distribution on the tangent space at the mean to define higher order moments like the covariance matrix.

In the context of medical shape analysis, the powerful framework of Riemannian (right) invariant metric on groups of diffeomorphisms (aka LDDMM) has often been investigated for such analyses in computational anatomy. In parallel, efficient image registration methods and discrete parallel transport methods based on diffeomorphisms parameterized by stationary velocity fields (SVF) (DARTEL, log-demons, Schild's ladder etc) have been developed with a great success from the practical point of view but with less theoretical support.

In this talk, I will detail the Riemannian framework for geometric statistics and partially extend it to affine connection spaces and more particularly to Lie groups provided with the canonical Cartan-Schouten connection (a non-metric connection). In finite dimension, this provides strong theoretical bases for the use of one-parameter subgroups. The generalization to infinite dimensions would ground the SVF-framework. From the practical point of view, we show that it leads to quite simple and very efficient models of atrophy of the brain in Alzheimer's disease.