

Programme on**“Infinite-dimensional Riemannian geometry with applications to
image matching and shape analysis”****January 7 – February 27, 2015****organized by****Martin Bauer (U Vienna), Martins Bruveris (Brunel), Peter W. Michor (U Vienna)****Week 2****“Mathematical methods for computational anatomy”****February 9 – 13, 2015****• Lecture course****Tuesday – Friday, 10:00 – 11:00****Geometric structures for statistics on shapes and deformations in computational anatomy***Xavier Pennec*

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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. For instance, the analysis of population-wise structural brain changes with ageing 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.

Lecture 1 will focus on the most powerful geometric structure considered so far for statistics on manifolds: Riemannian geometry. The main idea is to redefine the mean as the minimizer of an intrinsic quantity: the Riemannian squared distance to the data points. When the Fréchet 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. Conversely, we can define a normal law (and more generally an exponential family) on a manifold by choosing the distribution that minimizes the entropy knowing the first moments. Statistical distances such as the Mahalanobis distance are also well defined and can be used to define some simple statistical tests on manifolds. The framework will be exemplified on medical imaging application such as shape of the spine in scoliosis and the evaluation of the accuracy of rigid-body registration.

Lecture 2 will extend the Riemannian computing framework to manifold valued images with the example of positive definite symmetric matrices (tensors). The choice of a convenient Riemannian metric allows to generalize consistently to tensor fields many important image processing algorithms such as interpolation, filtering, diffusion and restoration of missing data. This framework will be exemplified on diffusion tensor image processing and on the modeling of the brain variability from a dataset of lines on the cerebral cortex.

Lecture 3 will extend the Riemannian framework for geometric statistics to affine connection spaces and more particularly to Lie groups provided with the canonical Cartan-Schouten connection (a non-metric connection). 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 morphometric analyses in computational anatomy. In parallel, efficient image registration methods and discrete parallel transport methods based on diffeomorphisms parametrized by stationary velocity fields (SVF) (DARTEL, log-demons etc) have been developed with a great success from the practical point of view but with less theoretical support. Our affine connection structure provides strong theoretical bases for the use of one-parameter subgroups in finite dimension, and the generalization to infinite dimensions would ground the SVF-framework.

Lecture 4 will focus on the analysis of longitudinal deformations. The main theoretical problem is that the longitudinal evolution of each subject is described in its own geometry. Thus we have to transport small longitudinal deformations along large inter-subject deformations to compare the trajectories of different subjects in a common reference frame. We designed for that discrete parallel transport algorithms called Schild's and Pole ladders. We show that it leads to quite simple and very efficient models of atrophy of the brain in Alzheimer's disease.

All talks take place at the ESI, Boltzmann Lecture Hall.