Bijan Afsari, Center for Imaging Science, Johns Hopkins University

Averaging on Riemannian Manifolds: The curses of curvature and topology

A Riemannian manifold differs from a Euclidean space in its (non-trivial) *curvature and topology*. Current methods for defining notions of average for manifold-valued data extend existing definitions from a Euclidean space to a Riemannian manifold. In this talk, we consider some of these definitions and examine to what extent the curvature and topology of the underlying manifold cause the corresponding averages to behave differently from their Euclidean counterparts. We will start with very basic definitions and some historical remarks. The main theme of the talk is that the curses of curvature and topology, in one way or another, haunt averaging on manifolds. In that regard, we consider both the inherent properties (e.g., existence and uniqueness, noise sensitivity, continuity, etc) as well as *algorithmic/computational* properties associated with these averages. For example, we define a property called the *averaging property*, which indicates how contaminating a set of data points with noise would change their average; and we show that on a positively curved manifold, Riemannian averaging can amplify the noise. We also study the adverse consequence of this fact on the smoothness properties of *recursive-iterative* averages on such manifolds. As another example, we argue that averaging on a Riemannian manifold can become increasingly difficult as the curvature increases (in absolute values). Throughout the talk, we will consider numerous examples, introduce the latest available results, and allude to open problems.

This talk is partly based on the speaker's PhD thesis under the supervision of P.S. Krishnaprasad and K. Grove at the University of Maryland. The rest of the talk is based on the joint work with R. Tron and R Vidal at JHU. The present research has been supported, in part, by grants from NSF, NIH, and ARL.

Miroslav Bacak, Max Planck Institute for Mathematics in the Sciences, Leipzig

On some new algorithms in Hadamard spaces

Several new approximation algorithms in Hadamard spaces will be presented. Namely, the alternating projection method for finding a point in the intersection of a given pair of convex closed sets, the proximal point algorithm for finding a minimizer of a convex lsc function, and finally, I will discuss algorithms for computing the Frechet mean in Hadamard spaces. As an application, computational results in the tree space based on a real data set will be presented.

Martin Bauer, Universität Wien

Constructing reparametrization invariant metrics on spaces of curves

Metrics on shape space are used to describe deformations that take one shape to another, and to determine a distance between them. I will present a family of metrics on the space of curves, that includes several recently proposed metrics, for which the metrics are characterised by mappings into vector spaces where geodesics can be easily computed. This family consists of Sobolev-type Riemannian metrics of order one on the space $\mathrm{Imm}(S^1, \mathbb{R}^2)$ of parametrized plane curves and the quotient space $\mathrm{Imm}(S^1, \mathbb{R}^2)/\mathrm{Diff}(S^1)$ of unparametrized curves. For the space of open parametrized curves I will give an explicit formula for the geodesic distance and show that the sectional curvatures vanish on the space of parametrized and are non-negative on the space of unparametrized open curves. Furthermore I will present a numerical algorithm that computes geodesics between unparameterised, closed curves and in the final part I will discuss possible extensions of this approach to higher dimensions, i.e., space curves and hypersurfaces in n-space.

Jim Damon, Department of Mathematics, University of North Carolina

Medial/skeletal linking structures for multi-object configurations

For a configuration of objects in a 2D or 3D space, there are a number of questions involving their interaction and how their shapes and relative positions allow for improved information for various imaging questions. This includes analyzing the contributions of both the shapes of the objects and their relative positions to the properties of the configuration. Such configurations may involve collections of physiological features such as organs, bones, glands, arteries, etc, in medical images, or collections of objects in biological structures. Such configurations can generally be modeled by a collection of regions in $\mathbb{R}^n$ which may intersect on their piecewise smooth boundaries. In the talk we introduce medial/skeletal linking structures which are mathematical structures which simultaneously capture the shapes of individual regions and the positional geometry of the configuration. It is formed from *skeletal structures* for each region, consisting of *Whitney stratified sets* and multi-valued radial vector fields on them. These radial vector fields are extended to *linking vector fields* which capture the relative geometry of objects. This structure allows for the introduction of mathematical operations which capture the geometric and shape properties of individual objects. It overcomes problems with the lack of C^1-stability of classical Blum medial axes, and their lack of flexibility, by allowing both more complex models but also simplifying models for regions. This has allowed for its discretization as *s-reps* by the MIDAG group at UNC for modeling individual objects as deformable templates. In turn, this has allowed for its use for statistical analysis in medical imaging questions such as segmentation of regions and statistical comparison of individual objects in a population of patients. The linking structure further augments this providing mathematical methods for separating shape change from positional change, measure closeness and significance of portions of objects, and providing an approach for understanding their deformations. This talk will describe these structures and their features.

Herbert Edelsbrunner, Duke University and Institute of Science and Technology Austria

Persistent homology: theory and practice.

Persistence is a recent extension of the classic concept of homology in algebraic topology. Motivated by the instability of homology to slight changes in the space, we start with a filtration and use the induced maps connecting the homology groups to trace the classes. The information is collected in a planar diagram, which is an invariant of the filtration.

Overcoming the instability of the classic theory is one reason why persistence has found many applications in the sciences and engineering, the existence of fast algorithms is another. They take only seconds to compute diagrams of complexes that reach hundreds of thousands or millions of elements, sizes that are not unusual in applications, which we find in geometry processing, data visualization, medical imaging, biological shape analysis, high-dimensional data analysis, and other areas.

Aasa Feragen, Department of Computer Science, University of Copenhagen

On the uniqueness of geodesics between geometric trees

In this talk we shall consider the uniqueness of geodesics in the space of geometric ordered or unordered trees of any finite size. We prove that there exists a set W_0 of trees such that i) W_0 has meagre intersection with any space of trees of bounded size, ii) the set W_1 of trees T_1 that have more than one geodesic to T_0 intersects any space of trees of bounded size in a meagre set.

Jacob Hinkle, Scientific Computing and Imaging Institute, University of Utah

Polynomial regression on Riemannian manifolds

In this talk I will describe the theory of parametric polynomial regression on Riemannian manifolds. Riemannian polynomials enable parametric analysis in a wide range of applications, including rigid and non-rigid kinematics as well as shape change of biological structures due to growth and aging. We describe the application of Riemannian polynomial regression to shape analysis in Kendall shape space and on diffeomorphically deforming landmarks. Results are presented demonstrating polynomial regression on the classic rat skull growth data of Bookstein and the analysis of the shape changes associated with aging of the corpus callosum from the OASIS Alzheimer's study.

Stephan Huckemann, Georgia Augusta University Goettingen

On means and their asymptotics under positive curvature: From circles to shape spaces

The classical central limit theorem (CLT) states that suitably translated and root n rescaled independent sample means tend to a multivariate Gaussian. Essentially under three conditions this translates to stratified spaces: Uniqueness, manifold stability (i.e. that the mean is assumed on the highest dimensional stratum) and omitting of the cut locus (i.e. no mass near the cut locus of the mean).

Since shape spaces are a quotient with respect to a Lie group action, curvatures increase thus providing for manifold stability of intrinsic means. The underlying argument cannot be applied to the well known Procrustes means, however, they can hit singular strata.

Furthermore, the omitting property is studied on circles. Here, certain scenarios give arbitrary slow rates for the CLT. For practical applications, however, only the Gaussian's covariance is affected.

We conclude by noting that higher dimensional descriptors such as geodesic PCs can also be viewed as means, and by applying this thought to biological growth analysis.

Daniel Hug, Karlsruhe Institute of Technology Germany

What is the shape of large cells in Poisson driven random tessellations?

A random tessellation (mosaic) is a random partitioning of space into countably many cells. The most prominent examples of tessellations are the Voronoi and the hyperplane tessellations. Under appropriate distributional assumptions on a random tessellation, mean values of geometric characteristics of the cells and relations between these are well known. On the other hand, results involving information on the shape of the cells are much harder to obtain and of more recent vintage. In this context, a conjecture by D.G. Kendall suggests that in the case of a stationary isotropic Poisson line tessellation in the Euclidean plane the asymptotic shape of cells, under the condition that they have large size (e.g. large area), should be approximately spherical. This question has been thoroughly investigated and generalized in recent years, for instance in a non-isotropic setting and to arbitrary dimensions. The talk provides an introduction to the study of large cells in Poisson driven random tessellations. Some tools from geometry which turn out to be useful will be explained as well.

The talk is based on joint work with Rolf Schneider and (partly with) Matthias Reitzner.

Eva B. Vedel Jensen, Centre for Stochastic Geometry and Advanced Bioimaging, Aarhus University

Spatial point processes on linear networks

In the last decades, models for spatial point patterns, typically planar point patterns, describing inhomogeneity as well as interaction, have been a very active research area in spatial statistics. Different types of model classes have been introduced, including intensity reweighted second-order stationary models, transformation models and local scaling models.

As emphasized by Okabe and coauthors, there are many kinds of phenomena that are represented by points on a network. For the analysis of such point patterns, it is needed to transfer methods of analyzing point patterns in the plane to point patterns on networks. This has been done in a series of papers by Okabe and coauthors, mainly in geographical journals. In particular, the question of transforming an inhomogeneous point pattern such that the transformed point pattern has unit intensity has been studied.

Very recently, a theoretical framework has been put down for modelling of point patterns on linear networks. In particular, a correction to the network K-function has been proposed that intrinsically compensates for the network geometry. Also, inhomogeneity due to intensity reweighting was introduced.

In this talk, I will study inhomogeneous point processes on linear networks obtained by transformation and local scaling of point processes, respectively, and the interrelationships between these two model classes.

Sarang Joshi, Department of Bioengineering, University of Utah

Simple statistics on interesting spaces for developing imaging biomarkers analysis

A primary goal of Computational Anatomy is the statistical analysis of anatomical variability. Large Deformation Diffeomorphic transformations have been shown to accommodate the geometric variability but performing statistics of Diffeomorphic transformations remains a challenge. I will start with the simple concept of defining the 'Average Anatomy' and then extend this to the study of regression and co-variation of anatomical shape with independent variables. The motivation is to model the inherent relation between anatomical shape and clinical measures and evaluate its statistical significance. We use Partial Least Squares for the multivariate statistical analysis of the deformation momenta under the Large Deformation Diffeomorphic framework. The statistical methodology extracts pertinent directions in the momenta space and the clinical response space in terms of latent variables. We report the results of this analysis on 313 subjects from the Mild Cognitive Impairment group in the Alzheimer's Disease Neuroimaging Initiative (ADNI).

Kwang-Rae Kim, Georgia Augusta University Goettingen

Geometry and statistics in biomechanical knee motion analysis

In this research we approach the problem of analyzing space-time curves. In terms of classical geometry, the characterization of space-curves can be summarized in terms of a differential equation involving functional parameters curvature and torsion whose origins are from the Frenet-Serret framework. In particular, curvature measures the rate of change of the angle which nearby tangents make with the tangent at some point. In the situation of a straight line, curvature is zero. Torsion measures the twisting of a curve, and the vanishing of torsion describes a curve whose three dimensional range is restricted to a two-dimensional plane. By using splines, we provide consistent estimators of curves and in turn, this provides consistent estimators of curvature and torsion. We illustrate the usefulness of this approach on a biomechanics application.

Marco Lorenzi, INRIA, France

Divergence-induced topology of deformation processes: analysing the anatomical changes as networks of regional flow

Non rigid registration describes the morphological changes between medical images as deformation fields. The deformation fields implicitly encode the spatial location of relevant anatomical processes, such as the atrophy induced by pathologies, and novel analysis techniques are required to consistently extract and analyse these features. According to the Helmholtz decomposition, the vector field which parametrizes the deformation can be decomposed into irrotational and divergence-free components. If we assume that the atrophy can be completely described by a change of volume, then it is completely encoded by the irrotational part, while the divergence-free one accounts for the tissue reorganization. Thus, the critical points of maximal/minimal irrotational potential define the centers of expanding and contracting regions, and may represent a promising measure for morphometric studies. Theoretically, one could partition the whole space into critical areas of positive and negative divergence, each of them containing a critical point of local maximal/minimal pressure. From the divergence theorem, the flux across the boundaries of these areas is either flowing inward or outward. The saddle points for the pressure are on the boundaries of those regions, and identify a change in the flow. The analysis of the critical points of a pressure map can be addressed by the Morse-Smale theory as a topological problem, leading to a complex of regions, boundaries, edges and vertices. Although intriguing, the application of such concepts to the medical imaging is still difficult, due to the missing statistical version of the Morse theory, i.e. the ability to incorporate the uncertainties characterizing medical data. The presentation aims to introduce the preliminary concepts and the theoretical background of the topology induced by deformation fields, and to highlight new potential directions of investigation. A preliminar application to the study of neurodegenerative diseases is finally proposed.

J.S. Marron, Dept. of Statistics and Operations Research, University of North Carolina

OODA of tree-structured data objects

The field of Object Oriented Data Analysis has made a lot of progress on the statistical analysis of the variation in populations of complex objects. A particularly challenging example of this type is populations of tree-structured objects. Deep challenges arise, which involve a marriage of ideas from statistics, geometry, and numerical analysis, because the space of trees is strongly non-Euclidean in nature. These challenges, together with three completely different approaches to addressing them, are illustrated using a real data example, where each data point is the tree of blood arteries in one person's brain.

This is a pretty general purpose abstract. More useful for your purposes will be some of the topics I plan to cover:

- Phylogenetic tree space
- Brain artery data set (several folks will discuss other aspects of that data), but probably I should introduce that first.
- Geodesics in the brain artery case
- Interactions between triangles, curvature, and data, using multi-dimensional scaling.

Stephen Marsland, School of Engineering and Advanced Technology, Massey University, New Zealand

A twist in the tale: Shape correspondence and the role of the connection

Shape correspondence is inextricably linked to the use of a Riemannian metric, both in terms of the tangent space, and in terms of the associated connection. Generally, when required to choose a metric connection we choose the Levi-Civita connection, which is torsion-free. However, it is not the only connection available, and when trying to do statistics on manifolds, curvature is a problem. In this talk I will introduce the Weitzenböck (or Vitali) connection, which has torsion but no curvature. I will show that using this it is possible to find some interesting variations in a set of shapes, and highlight the interesting questions in what is very much work-in-progress. This is joint work with Carole Twining at Manchester University.

Facunco Mémoli, School of Computer Science, University of Adelaide

The shape space defined by the Gromov-Wasserstein distance

The Gromov-Wasserstein distance is a metric on the collection of all metric measure spaces. We review its construction, main properties, lower bounds, and computation.

Peter Michor, Fakultät für Mathematik, Universität Wien, Austria

Overview on geometries of shape spaces and diffeomorphism groups

For a compact manifold M and a manifold N, we consider the the spaces of embeddings and of immersions of M into N, the regular Lie groups of diffeomorphisms of M and of those diffeomorphisms on N which fall rapidly to the identity, and the spaces of Riemannian metrics on M and on N. There are several actions of the groups; The space of immersions modulo the group of reparamerizations is an orbifold (with finite isotropy groups). There are several natural weak Riemannian metric of the spaces of metrics. Fixing a Riemannian metric g of bounded geometry on N induces several weak Riemannian metrics on the spaces of embeddings and of immersions and on the diffeomorphism group of N. I will review their interplays, their geodesic equations, what is known about well-posedness for them, and what is known about curvatures.

Ezra Miller, Duke University and SAMSI

Geometry for samples of metric branched structures

Processing samples of metric branched structures in structural and evolutionary biology raises fundamental pure mathematical questions in geometric probability and metric geometry of stratified spaces. This talk outlines current research, arising from analyses of phylogenetic trees, blood vessels, and fruit fly wing veins, that concerns (i) asymptotics of probability distributions in stratified settings, particularly in the presence of negative curvature; (ii) statistical methods for metric trees that take 3-dimensional embedded structure into account; and (iii) analyzing datasets that exibit topological as well as continuous geometric variation in planar shapes.

Washington Mio, Florida State University

Taming shapes and learning metrics for morphological analysis

It is often the case that morphological and functional data extracted from biological images show many irregularities. For example, shapes may contain many topological defects due to noise and imaging artifacts and they may appear nearly amorphous due to large variability across samples or the rapid changes they undergo. The problem can be particularly acute for shapes such as those found in early development or gene expression domains. In the first part of the talk, we will discuss interpolation methods and consistency of probability density estimators on compact Riemannian manifolds, as tools to tame bioimaging data and make them amenable to analysis. In the second part, we will discuss methods for learning shape metrics well suited to the detection of patterns of allometry associated with dynamical processes such as development and growth. For simplicity, we will formulate the problem for the usual landmark model of shape. We will consider a family of shape metrics and present a method to learn metrics that are able to detect regions that experience more pronounced allometric variation under the assumption that allometry is concentrated in fairly small areas.

Tom Nye, Newcastle University

Bayesian inference of principal components in the space of evolutionary trees

Analogs of principal components analysis (PCA) are often sought for data lying in non-Euclidean spaces. These are usually expressed without reference to probability models, for example by constructing principal components by minimizing the sum of squared distances of the data points from the principal component. In this work we use a probabilistic description of PCA on standard Euclidean space to construct an analogous model in a space of evolutionary trees. Inference under this model fits naturally into a Bayesian framework, and we describe an MCMC scheme for sampling principal lines from the posterior distribution given a sample of trees. The model and inference procedures we describe can readily be extended to other geodesic metric spaces. The method is illustrated by infering principal lines for empirical collections of evolutionary trees.

Megan Owen, David R. Cheriton School of Computer Science, University of Waterloo

Statistics and applications of tree space

Data generated in such areas as medical imaging and evolutionary biology are frequently tree-shaped, and thus non-Euclidean in nature. As a result, standard techniques for analyzing data in Euclidean spaces become inappropriate, and new methods must be developed. I will present an approach based on the representation of metric trees as points in a geometric space. This space is non-positively curved (hyperbolic), so there is a unique geodesic path (shortest path) between any two trees and a well-defined notion of mean and variance for a given set of trees. Additionally, I will discuss how we are applying this work to a diverse range of biological problems, including labelling and registration of lung airway scans and phylogenetic tree reconstruction.

Florian Pausinger, Institute of Science and Technology Austria

Stable length estimates for tube-like shapes

Motivated by applications in biology, we present two algorithms to estimate the length of tube-like shapes in three dimensional Euclidean space. We combine the tube formula of Weyl with integral geometric methods to obtain an integral representation of the length of a tube. In a next step we estimate the value of the integral with a variation of the classical Theorem of Koksma-Hlawka. Finally, tools from computational topology are used to analyze and improve the stability of the initial algorithm.

This is joint work with Herbert Edelsbrunner.

This research is partially supported by the National Science Foundation (NSF) under grant DBI-0820624, the European Science Foundation (ESF) under the Research Network Programme, and the Russian Government under the Mega Project 11.G34.31.0053.

Xavier Pennec, INRIA, Sophia Antipolis, France

Bi-invariant means on Lie groups

When a set possess a particular geometric structure, it is desirable to respect this structure. For instance in a Lie group, it would be judicious to have a notion of a mean which is stable by the group operations (composition and inversion). Such a property is ensured for Riemannian center of mass in Lie groups endowed with a bi-invariant Riemannian metric, like compact Lie groups (e.g. rotations). However, bi-invariant Riemannian metrics do not exist for most non compact and non-commutative Lie groups. This is the case in particular for rigid-body transformations in any dimension greater than one, which form the most simple Lie group involved in biomedical image registration.

In this talk, we propose to replace the Riemannian metric by an affine connection structure on the group. We show that the canonical Cartan connections of a connected Lie group provides group geodesics which are completely consistent with the composition and inversion. With such a non-metric structure, the mean cannot be defined by minimizing the variance as in Riemannian Manifolds. However, the characterization of the mean as an exponential barycenter gives us an implicit definition of the mean using a general barycentric equation. Thanks to the properties of the canonical Cartan connection, this mean is naturally bi-invariant. We show the local existence and uniqueness of the invariant mean when the dispersion of the data is small enough. We also propose an iterative fixed point algorithm and demonstrate that the convergence to the invariant mean is at least linear.

Dan Raviv, Technion, Israel

Geometric invariants in non-rigid models

Traditional models of bendable surfaces are based on the exact or approximate invariance to deformations that do not tear or stretch the shape, leaving intact an intrinsic geometry associated with it. Intrinsic geometries are typically defined by shortest paths also known as geodesic distances, or diffusion processes on the surface like diffusion distances. Both methods are implicitly derived from the metric induced by the ambientEuclidean space.

Here, we depart from this restrictive assumption by observing that a different choice of the metric results in a richer set of geometric invariants. We extend the classic equi-affine arclength, defined on convex surfaces, to arbitrary shapes with non-vanishing Gaussian curvature. As a result, a family of affine-invariant intrinsic geometries is obtained. We propose a computational framework that is invariant to the affine group of transformations (similarity and equi-affine) and thus, by construction, can handle non-rigid shapes. Diffusion geometry encapsulates the resulting measure to robustly provide signatures and computational tools for affine invariant analysis.

Dan Raviv, Ron Kimmel and Alfred Bruckstein, Computer Science Department, Technion, Haifa, Israel

Graph isomorphisms and automorphisms via spectral signatures

Preliminary abstract: An isomorphism between two graphs is a connectivity preserving bijective mapping between their sets of vertices. Finding isomorphisms between graphs, or between a graph and itself (automorphisms) is of great importance in applied sciences. The inherent computational complexity of this problem is yet unknown. Here, we introduce an efficient method to compute such mappings using heat kernels associated to the graph Laplacian. While the problem is combinatorial in nature, in practice we experience polynomial runtime in the number of vertices. As we demonstrate, the proposed method surpasses in performance state of the art packages on various important examples.

Sean Skwerer, UNC Chapel Hill

Optimization problems and algorithms for tree statistics

Medical imaging technology has made it possible to extract anatomical structures from images. Datasets of arteries and lungs are collected to study these anatomical structures. These structures have forms much like a graph theoretic tree. This talk focuses on the optimization problems associated with some of the basic elements required to build a statistical toolkit for analyzing samples of trees. The distance between two trees is an essential building block. Distance is useful for defining averages and variability. The first part of the talk focuses on a summary statistic called the Fréchet mean. The Fréchet mean of a sample of trees can be defined as a point that minimizes the squared distances to every tree in the sample summed together. The problem of calculating the Fréchet mean for phylogenetic trees is discussed. An algorithm and results from a simulation study are presented. The second part of the talk focuses on the distance between unlabeled trees. This problem is NP-complete. This distance is expressed naturally as the solution to a complicated nonlinear optimization problem. An integer programming reformulation is presented. This formulation makes it possible to use branch and bound or cutting plans to solve the problem.

Stefan Sommer, Department of Computer Science, University of Copenhagen

Sufficiently large subsets of diffeomorphism manifolds

Diffeomorphism manifolds allow modeling of shape and deformation by the action of their elements on the underlying domain. For both statistical, modeling, and computational purposes, it is beneficial to study the effects of restricting to finite dimensional subsets of the full manifold. We describe the subsets generated by two particular choices of parametrization: The kernel bundle framework makes it possible to represent deformation at multiple scales by using tangent bundles to hold derivative information. This increases the capacity of the deformation model and it enables sparsity in the deformation description. Secondly, we show how higher-order momentum distributions allow locally affine deformation to be described in a finite dimensional settings. Again, the increase in order extends the description capacity of traditional zeroth-order models while providing compact representation of medically relevant deformation.

Anne Marie Svane, Department of Mathematics, Aarhus University

Local digital estimators for the integrated mean curvature

Given a binary image of an r-regular set, we consider weighted 2 by 2 configuration counts as estimators for the integrated mean curvature. A natural requirement for these estimators is that they are unbiased when the observation grid is randomly translated with respect to the underlying set, at least when the grid distance goes to zero. Unfortunately, such an estimator does not exist in dimensions greater than or equal to 3. The key ingredient in the proof is a second order formula for the asymptotic volume of the hit-or-miss transform of an r-regular set with finite structuring elements, generalizing a formula of Kiderlen and Rataj.

Steven W. Zucker, Yale University

A new approach to inferring shape from shading information

Shape from shading is a classical inverse problem in computer vision. We introduce a novel mathematical formulation for calculating local surface shape based on covariant derivatives, rather than the customary integral minimization or P.D.E approaches. Motivated by neurobiology, we introduce the shading flow field (the tangent map to the image isophotes) between the image and the surface levels. Parallel transport of the shading flow field yields restrictions on surface curvatures. Under simplifying assumptions we solve exactly for the light source/surface pairs needed for a local image patch to have a given shading flow. In the frontal parallel case, the magnitude of the brightness gradient restricts this family to a single light source and surface estimate pair, up to the concave/ convex ambiguity and an additional elliptical/saddle ambiguity. The result is a fibre bundle, sections of which are possible surface/light source pairs. (Research with B. Kunsberg.)