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Hybrid boundary-medial shape description for biologically variable shapes

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Abstract

Knowledge about the biological variability of anatomical objects is essential for statistical shape analysis and a discrimination between healthy and pathological structures. This paper describes ongoing research on a novel approach that incorporates variability of a training set into the generation of a characteristic 3D shape model. The proposed shape representation is a hybrid of a fine-scale global boundary description and a coarse-scale local medial description. The hybrid overcomes inherent limitations of pure medial based or pure boundary based descriptions. The medial description composed of a net of medial primitives (M-rep) with fixed graph properties is derived from the shape space spanned by the major deformation eigenmodes of a boundary description based on spherical harmonic descriptors (SPHARM). The topology of the M-rep is determined by studying pruned 3D Voronoi skeletons in the given shape space. Shapes are characterized by its SPHARM descriptors and an individually deformed M-rep model. The hybrid shape description gives an implicit correspondence on the boundary and on the medial manifold, thus enabling a more powerful statistical analysis.

1. Introduction

Shape is one of the most characteristic features of objects in the real world. While humans have no apparent difficulty dealing with shapes, research in computer vision faced the usual problem when imitating human perception: Humans *can* do it, but nobody knows exactly *how*. Representation and especially analysis of shape proved to be a rather complex problem to solve. It has been shown that a generally applicable solution is not possible and that specific shape descriptions have to be established.

Davatzikos et al [8] proposed an analysis of shape morphometry via a spatially normalizing elastic transformation. Inter-subject comparisons were made by comparing the individual transformations. The method is applied in 2D to a population of corpus callosum. A similar approach in 3D has been chosen by Csernansky et al [7] to compare hippocampi. Using the elastic transformation proposed by Miller et al [5], inter-subject comparisons were made by analyzing the transformation fields. The *analysis* of transformation fields in both methods has to deal with the high dimensionality of the transformation and the sensitivity to the initial position. Although the number of subjects in the studied populations is low, both show a relatively stable extraction of shape changes. The changes provided by the deformation fields are hard to interpret and cannot be expressed intuitively.

The approach taken by Kelemen [13] evaluates a population of 3D hippocampal shapes based on a boundary description by spherical harmonics basis functions (SPHARM), which was proposed by Brechbühler [3]. The SPHARM shape description delivers an implicit correspondence between shapes on the boundary, which is used in the statistical analysis. As in the approaches discussed before, this approach has to handle the problem of high dimensional features versus a low number of subjects. Also, the detected shape changes cannot be captured intuitively, but are expressed as changes of coefficients.

Golland [12] in 2D and Pizer et al [10, 18] in 3D propose two different approaches using a medial shape description to perform statistical shape analysis. Blum [2] claims that medial descriptions are based on the idea of a biological growth model. He argues that they are a 'natural geometry for biological shape.' The medial axis in 2D captures shape intuitively and can be related to human vision (see Burbeck [4] and Kimia [20]). Changes of shape are captured locally in an intuitive fashion. Both Pizer and Golland propose a sampled medial model that is fitted to individual shapes. By holding the topology of the model fixed, an implicit corre-

spondence is given by the model. There has not yet been an effort to automatically construct the medial model, rather it has been determined manually.

In this paper we present a scheme for a new approach that combines the SPHARM boundary description of Brechbühler [3] and the medial M-rep model of Pizer [18] into a novel hybrid description. The M-rep model is derived automatically from the SPHARM description of a shape space spanned by the principal component analysis of a shape population. The topology of the M-rep is calculated by studying the topological changes of pruned 3D Voronoi skeletons in the given shape space. Voronoi skeletons as representations of shapes have been studied intensively in past. The pruning of Voronoi skeletons has been examined by Ogniewicz [16] in 2D, and Naef [15] or Attali [1] in 3D. The proposed hybrid description efficiently captures biological variability and has a given implicit correspondence on both the boundary and the medial model. Both parts of the hybrid are computed automatically.

This paper is organized as follows. In section 2, we study following properties of shape descriptions: localization, scale, boundary vs. medial representation. In the next section, we discuss how we combine the SPHARM and M-rep representation. In section 4 the method used to generate the medial M-rep model is described. It is followed by the description of the fit process for the M-rep model to an individual shape. Lastly, applications of the hybrid description are delineated.

2. Properties of shape descriptions

This section studies a selection of general shape description properties that can be used to broadly categorize most shape descriptions. The objects of interest are biological objects that were segmented by selecting a region of interest from volumetric medical images resulting in a binary segmentation. The effect of the presence of biological variability for each of the following properties is emphasized.

2.1. Localization: Local versus Global

Global 3D surface shape descriptions of interest in this paper, like Staib and Duncan's sinusoids [21] and Brechbühler's spherical harmonics [3], are based on a parameterization $\mathbf{X} = (x(u,v), y(u,v), z(u,v))$, where u and v vary over the shape. Global representation other than (u,v) parametrized manifolds are not taken into account in this paper. A specific shape is described by a set of coefficients weighting the given basis functions. Local shape properties like derivatives can be computed analytically from the functional parameterization. Deformations are not well localized in a global description but rather are distributed over the whole set of coefficients. Changes of the coefficients cannot be interpreted intuitively. Moreover, small deformations applied to the shape can lead to quite a different set of coefficients.

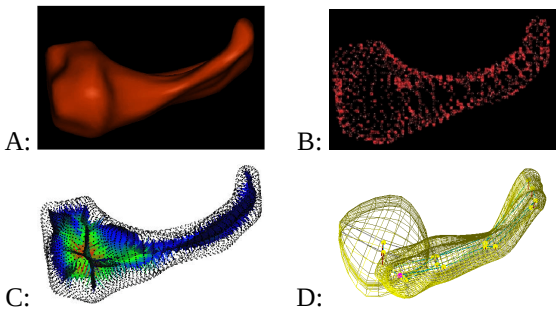


Figure 1. Different shape descriptions of a human right hippocampus: A. SPHARM: Global, Fine Scale, Boundary. B. Point Distribution Model: Local, Fine Scale, Boundary. C. Voronoi Skeleton: Local, Fine Scale, Medial. D. Manual M-rep (dots = medial atoms) + implied boundary (mesh) : Local, Coarse Scale, Medial.

Local shape descriptions are composed of a set of primitives, such as points, edges or faces, which locally describe the shape well, but deliver no global information about the shape. Deformations are captured locally and can be visualized and understood intuitively. In order to accurately define local shape properties like curvatures, primitives have to be densely sampled. A shape description is said to be efficient if shapes are described by *concise* sets of parameters or features. Thus, a finely sampled local shape description is not as efficient as a global description, since the same shape can be described by a lower number of parameters. Sparse sampling, to achieve a more efficient local description, can be used if we are not interested in accurate local shape properties or if we can determine them by additional means other than the primitives.

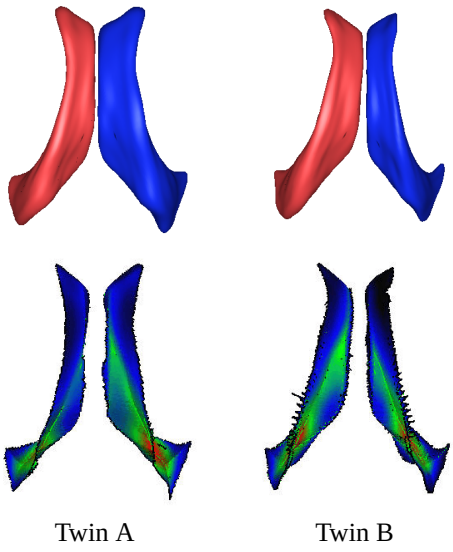
As we deal with biological shapes, we aim to pinpoint deformations intuitively as changes of anatomical landmarks. This criterion clearly favors a local description. Global parametrized descriptions are favored by the need for an accurate computation of geometric shape properties, which are used for registration and establishing correspondence.

2.2. Scale: Fine versus Coarse

In medical image analysis studies, 3D objects are defined as a binary segmentation of regions of interest in volumetric images. In the present routine, such anatomical objects

are segmented based on human expert interaction. These segmentations are often processed as if free of error. Because fine scale descriptions reconstruct the object accurately, they are perceived to be anatomically correct. However, the presence of noise, partial volume effects, intensity inhomogeneities and other artifacts suggests that the view of an error-free object is not accurate. A fine scale description is therefore not efficient. Also, statistical shape analysis, to detect and discriminate shape changes, demands an efficient description in order to handle the problem of high dimensional features. On the other hand, we would like to be able to precisely pinpoint the shape changes, which demands a high anatomical correctness. Thus, the choice of scale can be interpreted as balancing the tradeoff between descriptive efficiency and anatomical correctness.

2.3. Boundary versus Medial shape description



Twin A Twin B

Figure 2. Lateral ventricles of 2 monozygotic twins. The shapes are similar, but twin A has a larger right ventricle (Volume L/R = 0.75). Twin B shows a reversed symmetry (Volume R/L = 0.79). The medial description (bottom), with color coded thickness, captures more intuitively the 3D structure of the object than the boundary representations (top).

The main advantage of medial descriptions is the separation of the local shape properties: location, orientation and thickness (see Fig. 2). The main disadvantages of medial descriptions include their inability to capture non-symmetric information and the sensitivity of its branching topology to small changes on the boundary. Because the non-symmetric part of shape can be regarded as being less stable, some researchers view this property as an advantage rather than a disadvantage. Considering the presence of biological variability, the sensitivity of the branching topology to small changes cannot be left unsolved. A statistical analysis of a set of medial manifolds based on similar biological objects would be very challenging if the branching topology is not the same for all objects. Recent research about this topic in 2D has been done by Siddiqui et al ([19], [17]), but none have been done so far for 3D objects.

The discussion above leads to the proposition that boundary descriptions are well suited for fine scale, as medial descriptions are well suited for coarse scale (see also Pizer [18]). If we can resolve the problem of the branching topology sensitivity, the medial description can be well suited for statistical shape analysis. This is especially the case if we perform the analysis for the medial properties of location, orientation and thickness separately.

3. A hybrid boundary/medial approach

We propose a hybrid shape description that combines both the boundary-based spherical harmonic description (SPHARM) [3] and a description via a net of medial primitives (M-rep) [18]. A hybrid approach of these two descriptions can combine its advantages and overcome some of the inherent disadvantages.

The SPHARM description is a hierarchical, global, unconstrained, fine scale description that can only represent shapes of sphere topology. The basis functions of the parameterized surface are spherical harmonics, which have been demonstrated by Kelemen to be non-critical to issues of shape deformations [13]. SPHARM is a smooth, accurate shape representation, given that one chooses the approximation error of the truncated harmonic series expansion to be sufficiently small. Based on a uniform icosahedron-subdivision of the spherical parameterization, we can obtain a Point Distribution Model (PDM) (see Cootes et al [6]) directly from our coefficients via a linear mapping $x = A \cdot c$. Using this relationship, local shape properties can be computed analytically for every point of the PDM. The PDM is a local shape description and it has a better localization of shape changes. Nevertheless, the PDM is not well suited as a partner with SPHARM in a hybrid description, because it is dual to SPHARM and still fine scale and boundary based.

A M-rep is a linked set of medial primitives, called medial atoms, $m = (x, r, \underline{F}, \theta)$ (see Pizer et al [18]). The atoms are composed of: 1) a position x, 2) a width r, 3) a frame $\underline{F} = (\vec{n}, \vec{b}, \vec{b^{\perp}})$ implying the tangent plane to the medial manifold and 4) an object angle θ. The medial atoms are connected in a graph with edges representing either inter- or intra-figural links. A figure is defined as an

unbranching planar medial sheet forming a planar graph of medial atoms connected by intra-figural links. Figures are connected via inter-figural links. An example of a M-rep is visualized in figure 1. In the generic case, the graph of the whole M-rep is overlapping when displayed in a 2D diagram, i.e. the medial graph is non-planar.

A M-rep description is a local and medial shape description per se. In our approach, the sampling of medial atoms is low and thus leads to a coarse scale description. We derive the M-rep from the SPHARM description, constrained by a medial model with a fixed medial graph. This implies that the branching topology and the sampling of the medial atoms is fixed. Every shape is expressed by the same medial graph varying only the parameters of the individual medial atoms. This, of course, only makes sense for shapes of similar nature. Thus, our approach is to define a M-rep model for each anatomical object, that incorporate the biological variability of this object. The M-rep shape description of an individual object is thus constrained by 2 aspects: 1) The medial topology and sampling is constrained by the fixed medial graph of the model. 2) The geometric properties of the medial atoms are constrained by their statistical distribution regarding a given shape space incorporating the biological variability. The generation of such a statistical, fixed-graph M-rep model is described in the next section.

The proposed shape description is a hybrid description consisting of a fine-scale SPHARM and a coarse-scale M-rep derived from the SPHARM with the shape space spanned by the principal component analysis (PCA) capturing the biological variability.

4. M-rep model generation incorporating shape variability

Sampled medial models such as the M-rep are currently created manually by human interaction, as human experts decide on the properties of such a model. The model is derived from one representative sample shape of a population of biological objects. Thus, it is assumed that the sample's topology and geometry represent a set of similar shapes with respect to the population and that a human expert can reliably extract this topology and geometry. Our new approach takes a step further towards a stable statistical description by taking into account a whole population and automatically deriving the model from statistical observations of the shape.

We start from a smooth SPHARM shape representation for every individual shape of our population. We can calculate the population average and its major deformation modes (eigenmodes) of the population by applying principal component analysis (PCA). The calculation of PCA from SPHARM coefficients is described by Kelemen [13]. We assume that the average model and the first few eigenmodes describe the biological variability of the shape appropriately and span the space of all similar biological shapes with respect to the studied population. From this SPHARM shape space, we generate the sparsely sampled medial model in 2 steps. First, we compute the branching topology of the M-rep using Voronoi skeletons. Secondly, we calculate the sampling of the M-rep taking into account a predefined maximal approximation error.

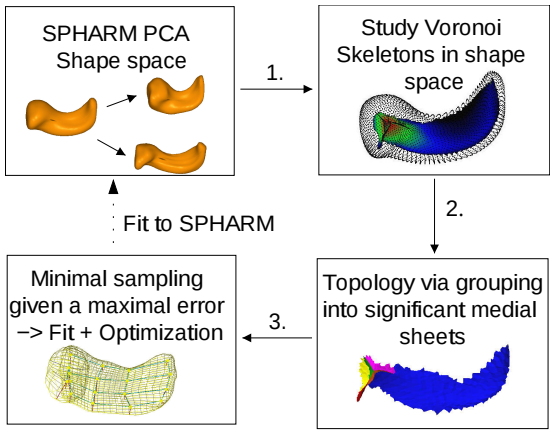


Figure 3. Schematic overview of the medial model generation, that incorporates shape variability. The average model and the first few eigenmodes span a shape space. In this shape space, we study the topology of the Voronoi skeleton and extract a common medial topology. As a last step the sampling of the medial sheets is determined.

The computation of the branching topology can be interpreted as grouping parts of the medial manifold into figures of medial sheets connected by a net of inter-figural links. Each of the medial sheets is sampled by medial atoms connected by a net of intra-figural links. The intra-figural net is constrained to be composed of quadrilateral connections.

4.1. Branching Topology - division into figures

The branching topology of the M-rep model is derived via the Voronoi skeleton medial representation (see Attali [1]). In order to calculate the 3D Voronoi skeleton from the SPHARM description, we first calculate a finely sampled PDM from the SPHARM, which can be done directly from the coefficients via a linear mapping $x = A \cdot c$ (see Kelemen [13]). From the PDM, the full inside 3D Voronoi diagram and Delaunay triangulation is calculated. The Voronoi diagram is well behaved due to the fact that SPHARM is a smooth description and the PDM is a fine

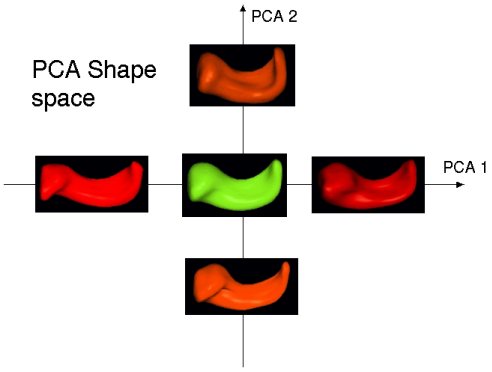


Figure 4. The proposed shape space is spanned by the first few eigenmodes of deformation. In this figure, the first 2 dimensions of the shape space are visualized. The computed M-rep model will be representative for this whole shape space

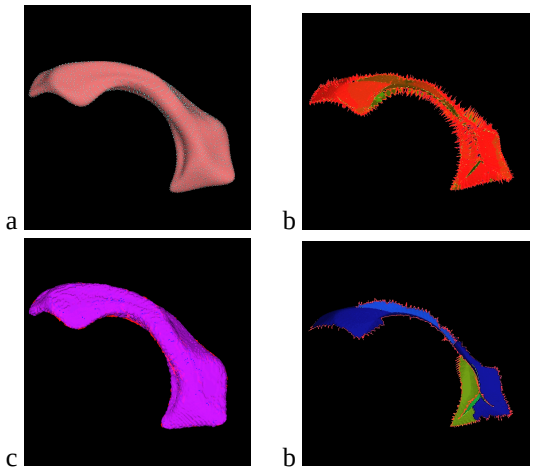


Figure 5. Proposed Voronoi skeleton grouping/deletion scheme applied to a lateral ventricles (side views). a. Original ventricle. b: Original Voronoi skeleton ($\sim$ 1600 sheets). c: Object reconstructed from pruned skeleton. d: Pruned skeleton (3 sheets).

sampling of this smooth description. The medial manifold of a Voronoi skeleton is described by Voronoi vertices connected by Voronoi edges forming planar Voronoi faces. A conservative adaption of the grouping algorithm proposed by Naef [14] groups the Voronoi faces into medial sheets. These medial sheets are then weighted by their volumetric contribution to the overall object volume. This is followed by a topology preserving deletion of the medial sheets with low volumetric contribution. We are aware that this grouping/deletion scheme can lead to problems when dealing with very complex objects like the whole brain cortex.

The previously described Voronoi skeleton extraction is first applied to the average shape of the SPHARM description, yielding the initial approach to the branching topology of the M-rep model. We then study stepwise the changes of the branching topology in the shape space spanned by the average shape and the deformations *along* the first few eigenmodes $\pm 2 \cdot \sqrt{\lambda_i}$ from a PCA on the SPHARM description. Corresponding sheets can be identified using the given correspondence on the boundary. For all studied deformations, significant additional medial sheets are incorporated into the M-rep model. Sheet significance is measured by the volumetric contribution to the shape. Thus, the topology of the M-rep model is refined step by step by incorporating medial sheets necessary to describe the given shape space. The determined final branching topology for the M-rep model captures efficiently the biologically variable topology of the medial surface with respect to the proposed PCA shape space.

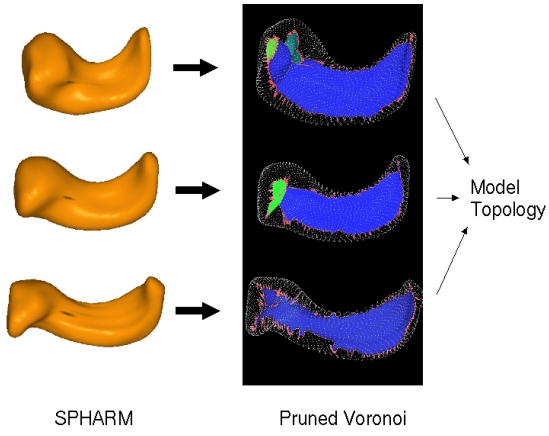


Figure 6. Extraction of a common topology. After determining the branching topology of pruned Voronoi skeletons in the shape space, we combine significant sheets to build a common model topology. In this case, this would result in a M-rep topology of 3 medial sheets.

4.2. Sampling of sheets - division into medial atoms

Holding the branching topology fixed, we aim to determine the sampling of the medial sheets given a tradeoff between sampling rate and approximation error. The computation of the sampling is done in parallel for all sheets simultaneously. A low number of sampled medial atoms is desirable to improve localization, statistical stability and descriptive efficiency of the model. A low approximation error is desirable from the viewpoint of maintaining both high accuracy and a correct description of the original shape. Because the role of the M-rep in the hybrid description is to represent the coarse-scale shape, the aim is to keep the number of medial atoms as low as possible while keeping the approximation error in certain bounds for all shapes in the proposed shape space. In order to determine the bounds of the approximation error, a M-rep model with a proposed sampling is fitted to the center and the extrema of the shape space. The algorithm to fit a M-rep model to a single shape given by its boundary description is discussed in section 5.

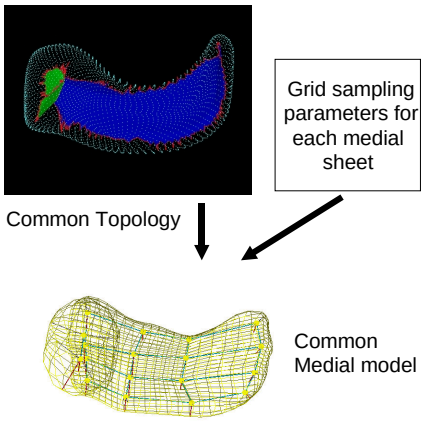


Figure 7. The common topology and a set of grid parameters ($n_i \times m_i$ grid points for sheet i) determine the final M-rep model. Grid sampling parameters are optimized for minimal number given a predefined maximal approximation error for all shapes in the given shape space.

We constrain the medial atoms on a medial sheet to be organized in a planar net of quadrilateral connections, holding its dimensions fixed. Thus, the topological structure of the medial graph is a grid and can be represented by the numbers of medial atoms sampled along the two grid directions. The sampling of the M-rep is defined by the grid densities of the individual medial sheets.

An exhaustive search of the minimal sampling for a M-rep-model given a branching topology and a shape space is only achievable for simple shapes due to the computational cost of fitting a M-rep-model to the whole shape space. Thus, we propose an evolutionary algorithm to solve this optimization problem.

5. Fit of a M-rep model to the boundary

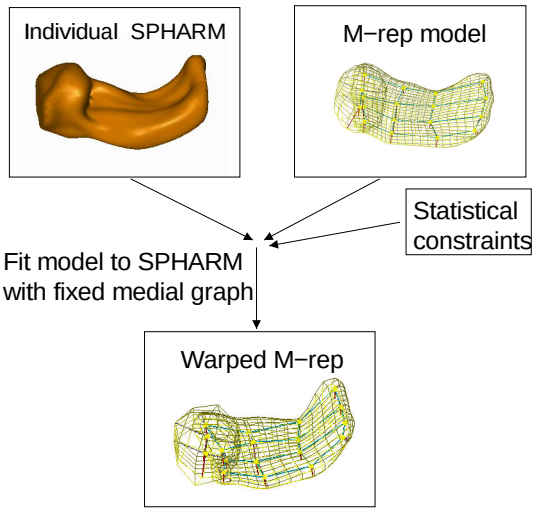
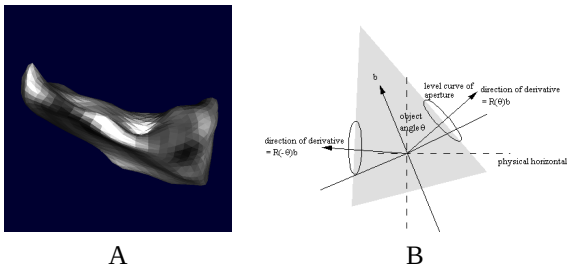


Figure 8. Determination of the medial part of the proposed hybrid from the SPHARM part by fitting a M-rep model (dots = medial atoms, mesh = implied boundary), with fixed medial graph and statistical constraints.

We interpret the problem of fitting a deformable M-rep model to a SPHARM description as an optimization process that can be solved using a non-linear optimization technique. The goal function of the optimization is composed of 2 terms $f(\text{M-rep}) = E_{approx} - log(M_{medial})$ with E_{approx} as approximation error and $M_{medial} = \Sigma m_{medial,i}$ as the sum of measures of medialness strength at the medial atoms. The approximation error is calculated as the Mean Squared Distance between the model-implied boundary and the given SPHARM boundary. The strength of medialness at a medial atom is defined by the application of a set of medial strength kernels at different scales (see Pizer et al [9],[18], [11] and figure 9). The optimization is further constrained to smooth changes of the medial atom properties within a medial sheet. The actual implementation is purely based on the medial strength measurement and does not yet include the approximation error.

As a first step, we fit the model to the average case. All following fit computations can take advantage of the known correspondence on the boundary by the SPHARM descrip-



A B

Figure 9. Visualization of Energy terms for fitting a medial model to a boundary surface. A - Mean Squared Distance of boundaries: Distance between corresponding PDMs of 2 individual shapes mapped onto one of them (low intensity = low distance). B - Medialness: Example of a medial strength kernel.

tion between the average shape and the actual shape. Using the PDM, dual to SPHARM, we define a transformation field using a thin-plate spline algorithm. Warping the average M-rep-model according to this transformation yields an appropriate initialization for the optimization.

As a byproduct of calculating the optimal sampling (see previous section 4.2), we gain a statistical distribution of the properties of the medial atoms in regard to the proposed shape space. The statistical distributions of the location, orientation and thickness information of medial atoms are incorporated into the final M-rep fitting procedure. These statistics are used to constrain the fit of the Mrep-model to the individual cases.

6. Application

The main application of the hybrid shape description is statistical shape analysis discriminating normal from pathological shape. The hybrid model gives an implicit correspondence on the boundary and on the medial manifold. Thus, statistical analysis can be applied directly. The proposed statistical shape analysis is based on Principal Component Analysis (PCA) and discrimination analysis. Preliminary results of such an analysis have already been reported on pure SPHARM descriptions (see Kelemen [13]) and on pure 2D M-rep descriptions (see Yushkevich [22]). The detected changes via SPHARM were not intuitively interpretable and only captured global changes. The shape analysis by Yushkevich was performed in 2D and was based on a manually derived model from a single case. The results in both cases are encouraging.

First applications include a first-episode schizophrenia study of hippocampi and a monozygotic twins schizophrenia study of lateral ventricles. Both exhibit promising preliminary results.

7. Conclusion and Discussion

We present a new approach to the description of shape for objects in the presence of biological variability. The proposed description is a hybrid of the boundary based SPHARM and the medial M-rep. The hybrid captures both fine scale using SPHARM and coarse scale properties using the M-rep. The hybrid model gives an implicit correspondence on the boundary and on the medial manifold. Thus, statistical analysis can be applied directly.

We have to be aware that the M-rep is constrained to the assumption that the biological variability can be captured based on the shape space spanned by the principal component analysis of SPHARM. A consequence of this assumption is that we cannot describe pathological shapes that are not represented in the PCA shape space. However, we are able to detect such pathological shapes by inspecting the approximation error.

The choice of a *fixed* topology for the M-rep has several advantages, e.g. enabling an implicit correspondence for statistical analysis. On the other hand, a fixed topology M-rep model cannot accurately capture the topology of an individual object. The determined M-rep is therefore always an approximation, which emphasizes our decision of a coarse scale M-rep description.

The SPHARM description and thus also our hybrid approach is constrained to objects of sphere topology. The proposed algorithm to compute the branching topology is designed for objects whose major deformation eigenmodes of the fine-scale boundary incorporate the coarse scale deformations. We expect that objects like the cortex of a human brain are hard to handle without further adaption of our algorithms.

The generation of the medial part of the hybrid takes into account the biological variability of a set of training shapes, which is a novel concept. The biological variability is captured efficiently, and therefore the hybrid description is a step towards a natural shape representation

This paper describes a scheme for a hybrid shape description which is work in progress and ongoing research at our laboratories. Parts of the scheme have already been implemented, applied and tested. Applications to clinical studies in Schizophrenia and other neurological diseases are in progress.

8. Acknowledgments

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