

Visualization and Exploration of Shape Variance for the Analysis of Cohort Study Data

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Abstract

In epidemiological studies, a group of people with common characteristics or experiences (a cohort) is studied including an analysis of socio-demographic as well as biological factors and correlations indicating per subject the absolute risk of getting a disease. Longitudinal studies are carried out over years or even decades comprising up to thousands of individuals. More recently, such studies include the acquisition of image data such as MRI to answer crucial epidemiological questions. For instance, how is the shape of an anatomical structure related to behavioral or clinical factors, e.g., liver shape related to drinking habits and obesity?

We propose a pipeline for shape variance analysis in cohort study data which comprises the definition of groups of individuals and control groups based on socio-demographic and biological factors or attributes derived from the image data as well as the visualization of intra-group shape variance and inter-group shape difference. We employ different shape variance models and investigate the applicability of the pipeline for liver and spine related epidemiological research.

Categories and Subject Descriptors (according to ACM CCS): J.3 [Computer Graphics]: Life and Medical Sciences—Medical information systems

1. Introduction

Cohort studies such as the long-term Study of Health in Pomerania (SHIP) [V*11] produce a huge amount of data which makes them consequently hard to analyze. An outstanding characteristic for SHIP is the data acquisition, which was carried out without focussing on a certain disease. This way the data sets can be analyzed with respect to many different aspects. The work in this field is currently based on *statistical* measurements of socio-demographic and medical data. Measurements on medical image data are commonly based on simple calculations such as computing distances via a ruler tool and have therefore a high intra- and inter-observer variability.

Morphometric analysis of a certain structure of interest has to be carried out in an algorithmic way to ensure objective and reproducible statements, especially with respect to intra-individual variability in follow-up studies. Automatic analysis of shape variability in epidemiology is an even larger problem given the large number of subjects and the complexity of certain structures. To support this, a pipeline for visualizing shape variances of structures in co-

hort study data is proposed. It captures the group definition phase which divides a population based on certain attributes. It also takes the different modalities of the data into account which are acquired through such a study and includes them into the selection of interesting individuals. Two different techniques for creating a data structure used for shape comparison are suggested. The first one allows for comparing objects and requires a binary segmentation. The second one takes a complete structure into account without prior knowledge of domain specific context.

2. Data

Our work comprises the collaboration with SHIP, which contains approximately 9.000 subjects with both image- and non-image data [V*11]. To provide insight into these huge data sets, information visualization methods, shape variance analysis and medical image visualization techniques need to be combined. To compare high dimensional data as well as scalar, nominal and qualitative data sophisticated visualization techniques beyond traditional approaches are required. The medical images are wb-MRI scans and were acquired

standardized on a 1.5-Tesla scanner by four trained technicians. Subjects were placed in the supine position. Five phased-array surface coils were placed to the head, neck, abdomen, pelvis, and lower extremities for whole-body imaging. The MRI software composed a whole spine sequence from the two T1- and T2-weighted sequences [HKV*09].

3. Visualization of Shape Variance

We integrated all the necessary steps for producing meaningful shape variance visualizations into a pipeline. It incorporates both medical image data and other data like socio-demographic and laboratory data. In the first step the user defines groups of individuals by selecting them using the available information produced by the study. This also includes data derived from medical images like the size of a certain structure. Along with standard tasks like finding outliers and missing data, suitable information visualization mechanics need to be applied to support the grouping step.

The shape variance analysis step comprises two different approaches on creating structures that allow for the visualization of inter-object differences. They arise from different requirements given by the underlying image data and the morphology of the structure of interest.

For liver data, we applied the growing and adaptive meshes (GAMES) algorithm [FOP*07] to create shape distribution models of a preliminary dataset consisting of five (up to twelve) binary segmented livers. This approach can easily be extended to more instances. We use the ShapeSpaceExplorer-Tool [BBP10] to visualize the resulting shape distribution model. The tool requires one of the created meshes as the basis for the mesh morphing algorithms which interpolates between the different volumes. The eponymous shape-space is a 2d projection of the principal component analysis. This space allows to navigate the different shapes, while the object space is a morphed representation of the current selected object in shape space, showing the amount of local deformation to the reference volume.

For spine data, we used statistical deformation models, that allow for visualization of inter-object differences. Due to the sparse sagittal depth resolution a segmentation based on knowledge of the structure of vertebrae is only possible with an active shape model. We decided to use statistical deformation models, which bypasses the need of a prior segmentation. We manually cut out cuboid blocks which contain the single vertebrae out of a reference data set and align them via affine registration piecewise onto a new data set. The next step is a b-Spline registration of the vertebrae which results in a deformation model. The deformation fields have the same dimensionality, because the same model is deformed for every instance of a vertebra. We applied standard visualization techniques like glyphs and streamlines as presented in Figure 1 (b) and (c). The Jacobian determinant of the deformation field which describes the local expansion

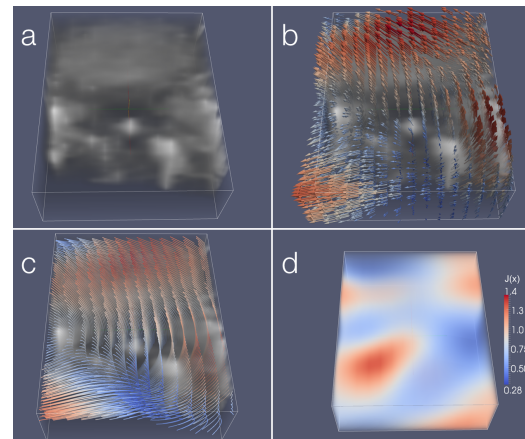


Figure 1: (a) Visualization of a b-Spline registered l4 vertebra. (b) Deformation field rendered with glyphs and (c) streamlines. (d) Visualization of the Jacobian determinant.

and compression can be seen in Figure 1 (d). Another possibility is, similar to the ShapeSpaceExplorer approach, the deformation of a reference object with morphing algorithms as the user specifies its parameters. The framework should be able to handle both statistical deformation fields and shape distribution models to create a consistent way of analyzing the data.

4. Summary

Together with a pipeline for analyzing shape variance in cohort study data, we presented two methods which derive deformation information from different data types. If an automated segmentation is possible, the use of Shape Distribution Models is recommended. Deformation Fields can be used to compare structures with no morphological background knowledge provided.

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