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Automated segmentation and shape characterization of volumetric data

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ABSTRACT

Characterization of complex shapes embedded within volumetric data is an important step in a wide range of applications. Standard approaches to this problem employ surface-based methods that require inefficient, time consuming, and error prone steps of surface segmentation and inflation to satisfy the uniqueness or stability of subsequent surface fitting algorithms. Here we present a novel method based on a spherical wave decomposition (SWD) of the data that overcomes several of these limitations by directly analyzing the entire data volume, obviating the segmentation, inflation, and surface fitting steps, significantly reducing the computational time and eliminating topological errors while providing a more detailed quantitative description based upon a more complete theoretical framework of volumetric data. The method is demonstrated and compared to the current state-of-the-art neuroimaging methods for segmentation and characterization of volumetric magnetic resonance imaging data of the human brain.

Introduction

Characterization of complex shapes embedded within volumetric data is an important step in a wide range of applications. In neuroimaging applications, for example, quantitative descriptions of brain morphology play a critical role in the characterization of neurodegenerative disease progression. Standard approaches to this problem employ surface-based methods that require an initial segmentation of a surface and often a subsequent inflation of this surface to satisfy the uniqueness or stability of subsequent surface fitting algorithms. These methods are inefficient and time consuming because of the need for segmentation prior to fitting and the computationally intensive inflation process, the latter of which being also a significant source of errors due to creation of topological defects. Here we present a novel method that overcomes several of these limitations by directly analyzing the entire data volume, obviating the segmentation, inflation, and surface fitting steps, significantly reducing the computational time and eliminating topological errors while providing a more detailed quantitative description based upon a more complete theoretical framework of volumetric data. The method is based on a spherical wave decomposition (SWD) of the data and we present an application of this technique to volumetric magnetic resonance imaging (MRI) data of the human brain.

This novel 3D signature-based method produces rotationally invariant compact shape descriptors that can be efficiently computed over 3D data sets without the need for explicit preliminary surface segmentation. The approach is appropriate for compact representation, fast decomposition, and automated segmentation and morphometry analyses of volumetric magnetic resonance imaging data. The SWD representation uses a direct expansion of volumetric data in a linear combination of basis functions that include both angular (spherical harmonics) and radial (spherical Bessel functions) parts. The 3D descriptors are easily archived and facilitate statistical comparison at multiple spatial scales: low frequency information describes gross shape, while high frequency information captures more details as well as internal structures.

Direct computation of the SWD over a full volume of data is computationally expensive, and thus we developed several fast transforms applicable both to spherical harmonics and to spherical Bessel functions that allowed a fast and robust numerical implementation of the SWD that is applicable to a wide range of geometries, independent of affine transformations, for large, noisy volumetric data sets. We demonstrate this method on a high resolution MRI data set of a normal human brain by comparing it to the current state-of-the-art methods employed in neuroimaging for segmentation of gray and white matter and shape characterization of the cortical surface.

Background

Continuing progress in the development of advanced non-invasive imaging methods such as MRI and CT have facilitated the acquisition of very high resolution, high contrast volumetric data that offer the possibility of non-invasive highly informative assessment of brain morphology. However, these more informative and complex data put a greater burden on the computational methods needed to analyze them. This is particularly true of MRI data which has a wide range of contrast mechanisms by which it can produce very high contrast between complex soft tissues of different types.

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In concert with these advancements in imaging technologies, advances in computational methods, particularly in volume graphics and computer vision have resulted in tremendous increase in computational methods for morphology characterization and segmentation for comparative morphometry for both basic neuroscience studies on brain anatomy and clinical studies of disease characterization and progression in humans, and for a broad range of studies in comparative biology.

In comparative biology, geometric morphometrics has emerged as an important tool for analysis, becoming commonly used to quantify morphology, wherein landmark points are identified in photographic (2D) images and then are fit to a warped mesh that provides a common coordinate system in which different specimens can be compared (Zelditch et al., 2004). These methods allow users to define key points of known morphological interest and statistically compare morphologies based on these points. However, the current predominant methods are based on 2D digital images or on 3D surfaces and are not readily applied to volumetric 3D data, such as those acquired by MRI or CT.

Recent advances in segmentation techniques were mostly originated from fuzzy logic and supervised and non-supervised clustering (Barra and Boire, 2000; Lin et al., 2012) both in 2D (Barra and Boire, 2001; Cocuzzo et al., 2011; Pedoia and Binaghi, 2012; Razlighi et al., 2012; Suri, 2001; Zavaljevski et al., 2000) and 3D (He et al., 2011; Kiebel et al., 2000; Klauschen et al., 2009; Popuri et al., 2012; Wels et al., 2011). Unfortunately, in spite of all advances none of these methods are able to provide truly robust and automated segmentation.

The most straightforward approach to segmentation is thresholding, which involves finding an intensity value, the threshold, that distinguishes features of interest. This method is most frequently used to create a binary segmentation of an image, but it is also possible to distinguish three or more intensity classes using multithresholding (Zavaljevski et al., 2000). Thresholding works particularly well with imaging modalities such as CT data where images are often essentially binary between bone (bright) and soft tissue (very dark) and segmentation can be practically automated. Automated methods for MRI data, however, are exceedingly difficult because of adjoining regions with similar values (i.e. low contrast), partial voluming (multiple tissue types within a single voxel), image noise, and intensity inhomogeneities, all of which are common to MR images (Atkins and Mackiewich, 2000; Pham et al., 2000).

Region growing methods extract connected regions in images based on criteria that can include both intensity and edges. These methods are susceptible to noise, which can create artificial divisions between connected regions, and partial volume effects, which can merge disconnected regions. These effects can be reduced by limiting growth to topology-preserving deformations (Mangin et al., 1995), but user input is still required to select seed regions. Clustering algorithms alternate between segmenting the image and characterizing the properties of each segmented class, iterating until a stopping criterion is reached (Barra and Boire, 2000, 2002; Liang et al., 1994; Pachai et al., 2001; Popuri et al., 2012). Clustering is generally susceptible to both noise and image inhomogeneities, though robustness to intensity inhomogeneities has been demonstrated (Pham and Prince, 1999). Given a Bayesian prior model, Markov random field models can be incorporated in clustering methods to minimize susceptibility to noise (Li, 1994).

Atlas-guided approaches provide an option that may be feasible (Klein et al., 2009). In such methods, a linear or non-linear transformation is found mapping the pre-segmented atlas image to the target image. Thus the tissue classification problem is changed to a registration or deformation problem. However, to effectively use atlas-guided methods very large and detailed databases or atlases of reference objects are needed. This puts the onus of the quantitation on an accurate and reproducible method for atlas creation.

One important and rather successful direction in brain quantifying and characterization has emerged from analyses of parameterization of surfaces for 3D shape description using spherical harmonic (SPHARM) representation (Brechbühler et al., 1995; Kazhdan et al., 2003). Shape signatures can be created using the SPHARM decomposition at several concentric spheres or just at a single surface that represents a highly convoluted geometry of the cerebral cortex. In the SPHARM method any function f is assumed to be defined on a sphere, $f(\theta, \phi)$, and decomposed as the sum of its spherical harmonics:

$$f(\theta,\phi) = \sum_{l=0}^{\infty} \sum_{m=-l}^{l} f_{lm} Y_l^m(\theta,\phi) \tag{1}$$

with low values of l corresponding to lower frequency information. Since L_2-norms of spherical functions are not affected by rotations, a rotationally-invariant shape signature may be given as $SH(f) = \{\|f_0(\theta,\phi)\|, \|f_1(\theta,\phi)\|, \ldots\}$, where the $f_l(\theta,\phi) = \sum_{m=-l}^{l} f_{lm} Y_l^m(\theta,\phi)$ are the frequency components of f. We note that an alternate signature can be calculated more quickly and directly from the coefficients, defining $SH(f) = \{A_0, A_1, \ldots\}$, where the A_1 are L_2-norms of all the coefficients f_{lm} at each l : $A_l = \sum_{m=-l}^{l} |f_{lm}|^2$. The spherical harmonic Y_l^m are continuous functions, but for computational applications, f is only sampled at N_Ω discrete angles. To create a shape signature for a 3D object, the shape is sampled at N_Ω angles and N_r radii, SH is calculated at each radius up to $l = L_{max}$, and the result is represented as a 2D grid of size $L_{max} \times N_r$. This SPHARM application described by Kazhdan et al. (2003) was more general shape classification using "clean" data (e.g. a set of 1890 "household" objects), but in noisy MRI data the SPHARM deals with noise automatically, since the noise does not appear in the lower frequencies that dominate shape descriptions. Many internal structures remain visible in data reconstructed from the signatures, while the signatures themselves require significantly less storage space than the original data. This general method was improved further by appropriate filtering (i.e. using exponentially weighted Fourier or spherical harmonic series, Chung et al., 2007; Chung, Dalton et al., 2008; Chung, Hartley et al., 2008). The weighting reduces a substantial amount of the so called ringing (or Gibbs) phenomenon and aliasing (or Moiré) patterns (Gelb, 1997), both appearing because of relatively slow convergence of Fourier series when used for representing discontinuous or rapidly changing measurements.

Overall these modifications of the SPHARM method with filtering or exponential weighting (Chung et al., 2007; Chung, Dalton et al., 2008; Chung, Hartley et al., 2008) allowed successful parameterization of the cortical surface including characterization of the local difference in gray matter concentration. Nevertheless, techniques based on the SPHARM morphometry method — tensor-based morphometry — uses the cortical surface already segmented out of noisy MRI data and quantifies the amount of gray matter only in a narrow layer along this surface via the concept of a local area element. Hence, the analysis cannot be directly used for volumetric MRI data.

An extension of spherical harmonic decomposition that naturally allows incorporating of complete 3D volume data has been known in various areas of physics for quite a long time, i.e. in quantum physics for description of waveform solutions of the Shrödinger equation (Gersten, 1971), in atomic and nuclear physics for approximation of Coulomb scattering function (Barnett, 1981, 1996), and in astrophysics for analyses of anisotropies of microwave background, as well as for quantum gravity (Abbott and Schaefer, 1986; Binney and Quinn, 1991; Leistedt et al., 2012).

In this paper we present the spherical wave decomposition (SWD) method, that combines angular-only basis functions of the SPHARM with spherical Bessel functions as the radial basis functions, forming the complete 3D basis. This basis is appropriate for expanding any function $f(r, \theta, \phi)$ defined inside a sphere of radius a. The expansion coefficients have the advantage of allowing characterization of the internal structure simultaneously with the overall shape. Because they are not surface-based, there is no need to fix topological discrepancies or to provide surface-based segmentation first. Thus this approach offers a more complete description of noisy volumetric data and is also more efficient to compute. We present timings for our implementation of the SWD