

COMPUTATIONAL SOFTWARE

DTHB3D_Reg: Dynamic Truncated Hierarchical B-Spline Based 3D Nonrigid Image Registration

Aishwarya Pawar¹, Yongjie Jessica Zhang^{1,*}, Cosmin Anitescu²,
Yue Jia³ and Timon Rabczuk²

¹ *Department of Mechanical Engineering, Carnegie Mellon University, PA 15213, United States.*

² *Institute of Structural Mechanics, Bauhaus-Universität Weimar, Germany.*

³ *School of Mechanics, Civil Engineering and Architecture, Northwestern Polytechnical University, China.*

Received 29 June 2017; Accepted (in revised version) 12 August 2017

Abstract. We present a robust approach to perform 3D nonrigid image registration suitable for large deformation and topology change, and develop a software package named DTHB3D_Reg (Dynamic Truncated Hierarchical B-spline based 3D Image Registration). The optimum spatial transformation, defined using truncated hierarchical B-splines, is obtained through the minimization of an energy functional. The optimization process minimizes sum of squared difference in the intensity values of the grayscale images. Control points are dynamically updated without constructing large matrices as in finite element method. To improve the computational efficiency, an adaptive strategy carries out refinement only in the regions with large deformation. The proposed method is demonstrated on 3D synthetic and medical images to show robustness on topology change as compared to other image registration methods.

AMS subject classifications: 65K10, 65K05

Key words: 3D nonrigid image registration, dynamic scheme, truncated hierarchical B-spline, adaptive refinement, topology change.

Program summary

Program title: DTHB3D_Reg

Nature of problem: This package performs 3D non-rigid image registration for medical and synthetic images using truncated hierarchical B-splines (THB-Splines).

*Corresponding author. *Email addresses:* jessicaz@andrew.cmu.edu (Y. Zhang), arpawar@andrew.cmu.edu (A. Pawar), cosmin.anitescu@uni-weimar.de (C. Anitescu), yuejia@nwpu.edu.cn (Y. Jia), timon.rabczuk@uni-weimar.de (T. Rabczuk)

Software licence: BSD 3-Clause License

CiCP scientific software URL: https://github.com/arpawar/DTHB3D_Reg

Programming language(s): Matlab and C++.

Computer platform: x86-64.

Operating system: Linux, Windows and Mac OS X.

Compilers: Supported and compatible compilers for MATLAB 2017a and previous releases:

- <http://www.mathworks.com/support/compilers>
- http://www.mathworks.com/support/sysreq/previous_releases.html

RAM: 16 GB and higher recommended.

External routines/libraries: None

Running time: Running time will depend upon the size of the images and the computational resources allocated to run the software.

Restrictions:

Supplementary material and references:

Additional comments:

1 Introduction

Image registration is the process of computing optimum correspondence between two images through a spatial transformation mapping. One of its most prominent applications is the alignment of medical images, where spatial correspondence is obtained between salient features of different images. These images can be obtained at different time frames, subjects or imaging modalities. Image registration plays a crucial role in obtaining a more comprehensive knowledge from separate images, thus having potential applications in aiding medical diagnosis [16, 19, 24, 31].

Image registration methods can be classified based on whether the images are obtained from the same or different imaging modalities [22, 40]. In monomodal image registration, analysis can be carried out between images obtained for the same subject (intra-subject) or different subjects (inter-subject). In intra-subject registration, changes in certain features over time are measured. These feature changes can be computed through the alignment of preoperative and postoperative images from the same patient. Moreover, motion quantification of certain features can be achieved. This plays a significant role in studying disease progression such as tumor movement and growth [39]. In inter-subject registration, images are taken from several subjects to study the variation of features between normal subjects and patients. This registration process is more challenging in terms of increased complexity of shape and topology of the features [21, 37]. The complexity of the registration problem also increases while registering image sequences