

Analysis of changes in time series of medical images

Abstract

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May 5, 2004

This thesis focuses on the development of a tool chain to analyze time series of medical images automatically. Time series of medical images are acquired when monitoring disease progression or medical treatment by using, e.g., *magnetic resonance tomography* (MRT) or *computer tomography* (CT). If the disease or treatment induces structural change of tissue and/or bone, this change may result in differences between the images that can be quantified and further analyzed.

However, additional differences between the images may be present due to the imaging process only. They have to be eliminated prior to the quantification of relevant changes. Besides noise and artifacts, which are only discussed in brief, rigid registration is used to eliminate altered positions of the patient during image acquisition. A review on the established methods is given, and two voxel based approaches are finally selected to be included in the tool chain. Also, MR image series often represent identical materials at different intensities even when acquired by using the same protocols, e.g. due to the imperfection in the scanner hardware. Therefore, a variety of approaches was investigated to automatically adjust the intensity of pairs of MR images of the head. It is shown that the optimization of statistical measures is useful to improve the material-intensity consistence.

With these preprocessing steps, the images of a time series are adjusted for

position, orientation, and intensity distribution. Hence, the residual differences between the images are assumed to be induced by the disease/treatment process only. Non-rigid registration based on fluid dynamics is employed to quantify these differences. Since fluid dynamics based registration is known to be computational intensive, approaches are tested to speed up registration. As a result of this work, it is shown that a variant of the Gauss-Southwell-relaxation is best suited to solve the registration problem with a sufficient accuracy on a workstation class computer.

With non-rigid registration, the differences between the images of a time series are given as large scale vector fields that are difficult to interpret. Therefore, I propose contraction mapping to detect critical points in order find deformation spots in the time series images. The accuracy of this method is demonstrated by its application to synthetically generated vector fields.

As the last analysis step, a visualization of the anatomical image data, overlaid with the deformation fields, and in conjunction with possible critical points is used, to illustrate the monitored anatomical change.

This tool chain was applied to pathological MRT data, such as data acquired during the progression of Alzheimer's disease or during the post-acute phase following an intra-cerebral hemorrhage. It is illustrated how a better understanding of the disease process may be achieved. Another example, CT examinations during midfacial distraction osteogenesis demonstrate the usefulness of a proper 3D analysis of a treatment process. These examples demonstrate that this tool chain even captures minute changes in time series data that are easily overlooked. In addition, it allows the quantification and qualification of structural changes on a high level description.