Generic 3D Segmentation in Medicine based on a Self-learning Topological Model

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Abstract: Three-dimensional segmentation of medical image data is crucial in modern diagnostics and still subject of intensive research efforts. Most fully automated methods, e.g. the segmentation of the hippocampus, are highly specific for certain morphological regions and very sensitive to variations in input data, thus robustness is not sufficient to achieve sufficient accuracy to serve in differential diagnosis. In this work a processing pipeline for robust segmentation is presented. The flexibility of this novel generic segmentation method is based on entirely parameter-free pre-segmentation. Therefore a hybrid modification of the watershed algorithm is developed, employing both gradient and intensity metrics for the identification of connected regions depending on similar properties. In a further optimization step the vast number of small regions is condensed to anatomically meaningful structures by feature based classification. The core of the classification process is a topographical model of the segmented body region, representing a sufficient number of features from geometry and the texture domain. The model may learn from manual segmentation by experts or from its own results. The novel method is demonstrated for the human brain, based on the reference data set from brainweb. Results show high accuracy and the method proves to be robust. The method is easily extensible to other body regions and the novel concept shows high potential to introduce generic segmentation in the three-dimensional domain into a clinical work-flow.

1 INTRODUCTION

The accurate and preferably fully-automated segmentation of medical image data is of high importance for a broad range of medical applications. The importance of computer-based support for surgery planning, disease monitoring and general diagnostics, by allowing for precise estimation of volume, size and relative position of anatomical structures, will constantly grow in clinical practice. As an example, after automated segmentation of liver parenchyma, hepatic vessels and possible lesions utilizing level sets, the tumour position can be analyzed with respect to the supporting vessels and liver lobes which is of high importance for surgery planning (Zwettler et al., 2009). The informative value image data from the functional imaging domain like SPECT or PET can be raised by combining high anatomical resolution of tomographic modalities like MRI and CT. Thereby, the metabolic activity can be quantified utilizing patient specific segmentation masks derived from the anatomical imaging (Beyer et al., 2010).

In this work we present a concept for model-based segmentation of 3D tomographic medical image data based on a generic, parameter-free pre-segmentation process and texture feature driven region merging for classification. Our novel pre-segmentation strategy combines aspects of gradient based watershed transform (Beare and Lehmann, 2006), confidence connected region growing, region merging and new variations in a hybrid algorithm (Zwettler and Backfrieder, 2012). Starting at local minima positions besides gradient height of classical watershed transform, region intensity statistics are used as merge metric. For region merging of the initially pre-processed regions, several metrics, namely watershed level tolerance, geometric properties and similarity of the intensity profile are combinded. Thus, an arbitrary input image can be

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pre-classified at a user specified number of target regions, defining the granularity of this pre-processing step. Based on the pre-segmented regions, the final segmentation is achieved by feature-based classification utilizing cost optimization. Besides texture features, also geometric properties are incorporated, all derived from a statistical a priori model calculated from manual reference segmentations. For precise reference segmentations at low user interactions, rapid prototyping image processing chains have been evaluated. The graph-based topographic modelling of the anatomical context to segment allows the segmentations at different hierarchical levels. Applicability for future multi-modal image processing will be evaluated in future.

2 DATA

For testing purposes concerning manual reference segmentations, automated pre-segmentation and feature-based classification, *n=20 T1-weighted* MRI datasets from the simulated *brainweb* database (Kwan et al., 1999) and the associated reference segmentations are used.

Further test runs and validations are performed utilizing n=12 anonymous multi-modal patient studies, comprising morphologic image acquisitions (*T1, T2, PD,...*) as well as related functional imaging (*SPECT, PET*). For the patient data sets, the required reference segmentations required for model training and leave-one-out validation are achieved in a semi-automated way by applying image processing pipelines utilizing *MeVisLab* modules (Ritter, 2007) a discussed in the later sections.

3 METHODOLOGY

In the preparation phase of our segmentation concept, model definition is performed with respect to the imaging modality to support and the hierarchical anatomical topography of interest. Furthermore, the classification features are chosen with respect to their correlation. Based on the anatomical topography and the chosen features, a sufficient set of reference segmentations has to be processed applying a semi-automated image processing chain to evaluate the model parameters with respect to each particular feature and each particular anatomical structure to consider.

After preparing and training the model, pre-segmentation of the tomographic patient dataset to process is performed, utilizing a hybrid approach incorporating aspects of watershed transform, confidence connected region growing and region merging. The chosen features are evaluated for all regions resulting from the pre-segmentation process step. The final segmentation is interpreted as optimization problem, as the anatomical structure labels are assigned to the particular regions in a way to achieve a classification result that minimizes the overall error with respect to the statistical feature values, see Fig 1.

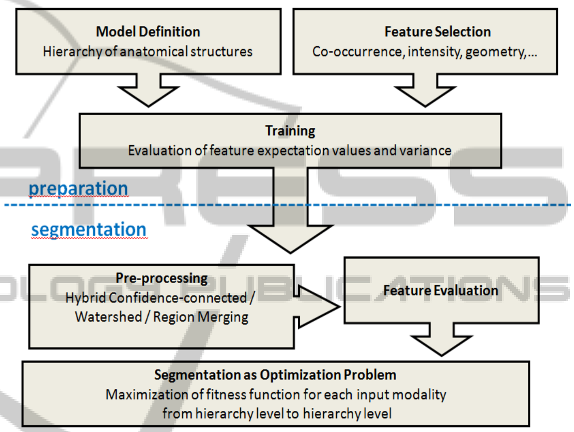

Figure 1: Illustration of our model-based segmentation strategy. After definition of anatomical topography and model training as *preparation*, pre-segmentation of the 3D tomographic data is performed and resulting regions are classified according to statistical features for final *segmentation*.

3.1 Definition of Hierarchical Anatomical Topography

For each anatomical structure to segment in the particular medical context and for the specified imaging modality, the position within the cascading hierarchy of granularity has to be defined, see Fig. 2. At level 0 the first separation into foreground as the region of interest and the background as remaining voxels is performed. Later the structures are subdivided into composing structures according to anatomical topography.

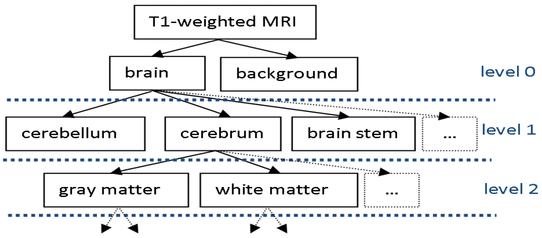

Figure 2: Illustration of topographic modelling. Granularity is increased at higher levels.

3.2 Hybrid Pre-Segmentation

A generic segmentation of arbitrary image data can be achieved utilizing an image processing chain, including anisotropic diffusion filtering for smoothing image data, gradient magnitude extraction and a hybrid watershed implementation, incorporating intensity homogeneity besides gradient borders and neighbour region boundary conditions as explained in (Zwettler and Backfrieder, 2012) and illustrated in Fig. 3.

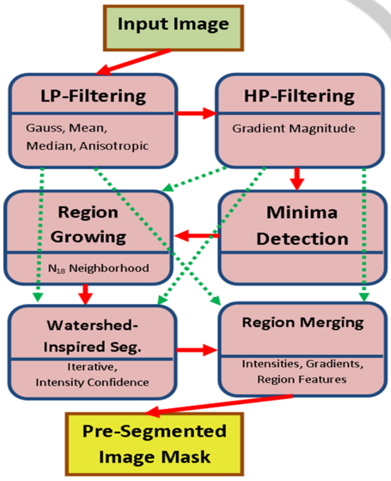

Figure 3: The sequential process chain (solid red arrows) comprises low-pass filtering, high-pass filtering, minima detection region growing, the watershed-type segmentation procedure and finally region merging until the convergence criterion is reached. Filtered input image and the gradient magnitude representation are required as input for several particular process steps (dashed green arrows).

3.3 Feature-based Classification

Our segmentation strategy is defined as hierarchical multi-feature optimization problem for classification of pre-defined anatomical structures with respect to their statistical feature values. For each anatomical object at each hierarchy level, a statistical feature vector must be preserved as a-priori information. The chosen features comprise classic metrics derived from co-occurrence matrix, like entropy and energy (Felipe, 2003), the deviation of the intensity profile, results of structural analysis with Hessian eigenvalues (Sato et al., 1998) and others. Beside these textural parameters, shape information, like deviation of the size and extent is incorporated.

The segmentation itself is now defined as an optimization problem of assigning the pre-classified 3D elements to the defined objects at lowest hierarchy level to minimize the cumulated total feature error. Due to recursive dependencies, only one hierarchy level is optimized at each time and the results are used as input for the next level in an iterative top-down and bottom-up cycle. As first initialization, the best matching regions for the particular anatomical structures are iteratively assigned with respect to expected size of the particular structure. Results after this first classification run are currently our final results.

In future, refinement of the segmentation results is expected to be achieved utilizing heuristic optimization based on evolution strategy (Rechenberg, 1973) and classic genetic algorithms (Goldberg, 1989).

4 RESULTS

Utilizing hybrid pre-segmentation, precision of common watershed segmentation can be increased from *0.88* to *0.91* and *0.92* respectively for our static and adaptive intensity interval region merging on average. The target number of regions to be pre-segmented is reliably reached and misclassifications only occur in border areas between neighbouring anatomical structures, see Fig. 4.

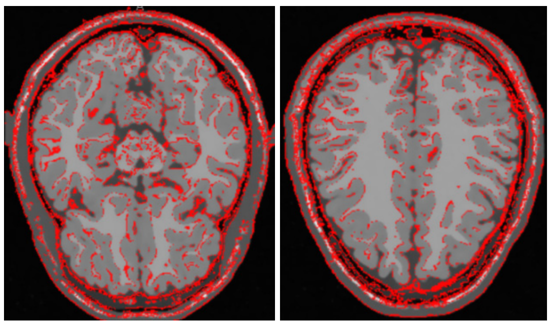

Figure 4: Misclassified voxel (red) of AII4_WS segmentation strategy in slices #70 and #150 compared to brainweb reference segmentations displayed with respect to original image data of dataset subject 04.

Concerning classification, for each feature the prediction reliability is calculated based on distributions with mean μ and variance δ calculated as statistical average of all reference segmentations and each particular anatomical structure to distinguish. The reliability thereby indirectly correlates with the error due to overlapping areas. The overall prediction reliability is calculated via stepwise integration over the entire feature value range. The distributions of the anatomical structures are normalized with respect to their overall probability, i.e. statistical differences in anatomical structure size.

Currently we evaluate 34 different feature types for their prediction reliability when training an anatomical topography model. Some of the most notable are presented in Table 1 for analysis on brainweb datasets. For construction of the feature vector, a number of 10 of the best discriminating features, should be selected. Despite choosing the features with highest prediction reliability, it has to be assured, that correlation within the feature vector is low.

Table 1: Different types of features and their reliability for classifying the different anatomical structure feature value distributions.

feature ID	*description*	*prec.*
1	maximum intensity value	67.93
3	median intensity value	87.07
4	mean intensity value	88.43
5	quantile 25 intensity	90.37
7	anatomical structure size	82.34
21	surface-to-volume-ratio	82.29
22	entropy of intensities	75.40
23	energy of intensities	74.12
25	mean probability of intensities	78.46

5 CONCLUSIONS

A generic segmentation concept for fast model-based adjustment to particular image segmentation tasks and imaging modalities has been presented. Hybrid pre-segmentation is perfectly applicable for context-free pre-processing of arbitrary image data for first region labelling. Correlation of the analyzed texture and geometric features shows promising results for future heuristics-based classification according to pre-defined anatomical topography.

The discussed and continuously refined rapid prototyping image processing chain is perfectly applicable for fast and robust preparation of reference segmentations for training the a priori model.

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