WATERSHED SEGMENTATION OF MEDICAL VOLUMES WITH PAINT DROP MARKING

A. Signoroni, G. Zanetti, R. Grazioli and R. Leonardi

Signals & Communication Lab., University of Brescia, Brescia, Italy

ABSTRACT

We present an improvement of the classical marker-controlled watershed approach in the direction of a better exploitation of user-defined markers. The combined action of a partial flooding and paint drops falling downwards on the gray value relief from marker locations, leads to a robust and meaningful identification of the candidate basins, which is a prerequisite for an accurate segmentation. This is useful for user-controlled segmentation of biomedical volumes in that it facilitates robust identification of complex 3D structures with inhomogeneous borders. To this end, a visual interactive segmentation system has been implemented where different user-data interaction tools can be selected by physicians to generate machine-understandable knowledge in a quick and compact way. Experimental results on selected use-cases demonstrate the strengths of the proposed solutions.

Index Terms— Image segmentation, Interactive systems, Watershed, 3D Biomedical Datasets

1. INTRODUCTION

Segmentation is a fundamental step in many medical image analysis pipelines. Its performance critically depends on how clinical information is conveyed to the segmentation algorithms. In general, the higher the target variability (related to anatomo-physiological or pathological factors) the lesser the amount of information that can be established a priori. Therefore, fully automatic methods are specialized with respect to a precise application domain in terms of image modality and diagnostic question and may have limitations in successfully handling target variabilities or discrepancies with respect to basic hypothesis. Conversely, interactive (also user-guided) systems can be designed starting from a more general level of knowledge to act in situations where automatic solutions do not guarantee sufficient degree of accuracy or robustness. They should therefore be characterized and evaluated in terms of the joint level of segmentation accuracy vs variability robustness they can reach. The role of user-guided techniques is not always recognized, and new ideas in this area are subject to the risk to be judged only for the user burden they entail in comparison with eventually existing fully automatic alternatives. However a more articulated vision should be adopted in that there are many situations, of relevant clinical interest, that can not be addressed by automated tools because either they have not been sufficiently investigated or they are too vunerable to target variability. In some cases such variability may lead outside the parameters of the models to which automatic methods refers to, while in other cases it may hamper the very definition of any model. Hence, the need of methods that may be deemed valid under more general hypothesis, and for a fairly wide range of problems, arises, even at the cost of an interaction with the user. Desirable charachteristics of the interactive segmentation systems, for 2D biomedical images, have been recognized in [1]: the user burden must be kept low and the application should converge to the desired result in an intuitive, robust, efficient and repeatable way. For the reasons stated above we try to define and use another desirable feature, that could be called *generality*, in the design of our novel algorithmic and methodological solutions. Generality can be thought as the aptitude of a segmentation system for the successful completion of a given segmentation task, with respect to different types of problems and imaging modalities, according to some suitable mechanism of knowledge from markers (i.e. an expressive transfer of information from the user about the specific task to be accomplished)[2]. Particularly interesting are methods which foresee meaningful and compact primitives to be used in a quick and intuitive user-data interaction, while another key point for an effective and robust user-guided segmentation system is a sound concordance between interaction tools and the algorithmic solutions. Morphology-based techniques and, in particular, marker-based watershed ones [3] are good candidates for this matching in that, many cues coming from user world can be effectively translated in algorithmic parameter or conditions to be used for guaranteeing accuracy and fast convergence to the desired result. If, from one side, the use of markers (deriving from interaction primitives) solves the typical over-segmentation problem of a WS analysis, for reasons that will be clear, not all markers set by the user could be equally exploited by the algorithms, and this can to the contrary generate under-segmentation problems.

In the following sections, after a concise background introduction on WS related aspects (Sec.2), we present a solution to the above problem by proposing a variant to the classical marker-based WS segmentation that we called Paint-Drop Marking, which increases the possibility of user-defined markers to be significantly exploited (Sec.3). Our algorithmic solution has been included within a fully-featured interactive segmentation system (Sec.4). Finally, we present some experimental results on representative use-cases (Sec.5).

2. BACKGROUND

Morphological image processing approaches like the WS analysis are based on modeling n-dimensional scalar datasets I as $(n+1)$-dimensional surfaces G representing topographic reliefs to be flooded by rainfall [3]. Rainfall gradually fill the so called 'catchment basins' $CB(M)$, related to local minima $m_i \in M$. These can be used as atoms for the final segmentation, usually consisting in some form of CB selection/aggregation. CB identification is obtained by a WS induced partition on G. On a continuous domain D, the watershed of I is the set of points that doesn't belong to any CB, $WS(I) = D \cap \left(\bigcup_j CB(m_j)\right)^c$, while the watershed transform $WST(I) : D \to M \cup W$ is a labeling of I in its $CB(m_j), j = 1 \ldots \aleph(M)$ plus a special label W for the set WS. Alternative to the rainfall model is the so called immersion model [4], where the WS corresponds to the set of dams raised to separate different CB's, while the water level gets higher and higher, entering from holes located on G's local minima. A more direct association between crest lines of G and object boundaries in I can be reached considering G as derived from I', the (morphological) gradient of I. The watershed (WS) transform [3] has computationally effective implementations [4, 5], while WS-based approaches extends efficiently for discrete domains and multiple dimensions, being suitable for 3D and 4D biomedical imaging segmentation tasks involving spatially complex structures. In classical marker-based WS approaches, a set of markers (marking function, MF) can be acquired by pattern recognition tools or directly by the user. An homotopy modification of the surface G in a new G_h is carried out, where MF are forced to behave as local minima during the flooding [3].

A WS analysis finds the most pronounced boundaries between adjacent basins, even in presence of low contrasted signals. This is important because the boundaries of interesting structures do not always correspond to the most contrasted contours, or the same structure may have variously contrasted borders (e.g. white-matter/gray-matter is less contrasted than gray-matter/CSF boundary in MR imaging). Some of these facets have been also recognized by Grau et.al [6] and characterize several medical image segmentation problems. Regrettably, the classic usage of a MF to guide the segmentation could nullify the above advantage of using a WS approach. In fact, as markers are freely placed by the users, some of them can be positioned near most contrasted borders, and this generates a relevant problem in the segmentation of the target structures. This is depicted in Fig.1 (a-c) where a sectioned portion (1-D view) of the surface G, derived from I', is shown with a couple of markers selected by the user (a). When filled by water, the MF-modified homotopy of G (b) leads to an incorrect result (c). To help envision a concrete case we can imagine the depicted profile as a path crossing a GM sulci, as suggested in Fig.1(a). In the next section, we propose a simple and effective technical solution to the described problem.

3. PAINT DROP MARKERS FOR BASIN SELECTION

The proposed solution (which is valid for any data dimensionality) improves candidate CB identification by exploiting user-defined marker functions in a mixture of 'flooding by immersion' and 'rainfall (here paint drops)' approaches. This is based on a two-step CB selection and does not require homotopy modifications of G: 1) 'partial flooding' and 2) identification of candidate basins by CBs' water color change using 'paint drops' falling from marker locations.

Partial flooding. At first, we take the gradient function I' and start flooding the corresponding surface G, from its zero level minima, until a partial flooding height h_{pf} is reached. Proper h_{pf} values can be estimated and controlled by interactive tools (see next section). The partial flooding is implemented by assigning a special label (say A) to all pixels (or voxels) p of the ordered queue, having $I'(p) \leq h_{pf}$. This produces some beneficial effects, even on the computational cost, in that partial flooding is an intrinsic denoising tool and allows to skip the detection and merging of a vast population of minor basins, rarely representative of real structures. The morphological gradient $I' = grad(I) = \max_{\eta_{ijk}}\{abs(I(i,j,k) - I(\eta_{ijk}))\}$ is used here, with η_{ijk} being a 18-voxel connected neighborhood. The so obtained partially-flooded basins (see Fig.1(d) and Fig.2(b)) can be thought as thick skeleton (or portions of it) of structures that we would find by reaching their watershed lines, and this is functional to the subsequent CB identification step.

Paint drop marking. From the set of markers MF (made of single voxels or connected components) we let paint drops fall down on the partially flooded G and change the water color. By doing so, some drops will directly splash in the partially flooded basins,

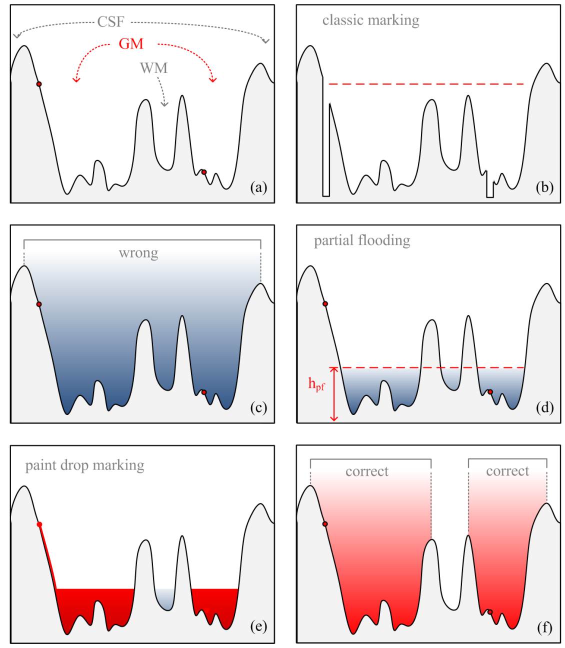


Fig. 1. Representation of the segmentation process with classical marker-controlled approach (a-c), and the proposed paint-drop marking (a),(d-f).

while others will come down, slipping on G. In this case, we consider all spreading descending paths ($\pi_k = (p_0, ..., p_l)$ such that $I'(p_{i+1}) < I'(p_i)$) of a paint drop staining the G function (with a special label, say B) until partially flooded basins, or other no more descending levels (minima), are reached. So there are two possibilities: (1) At least one π_k meets a voxel in a partially flooded basin, causing water color change; here a new label C propagates and substitutes label A within the joined basins (see Fig.1(e)); (2) No π_k joins partially flooded basins, this means that a higher basin has been reached and that the marker cannot be reliably used. However, with a proper choice of h_{pf}, the probability of failed marker exploitation becomes negligible. When all markers have been considered, immersion (voxel labeling) continues only with colored basins (labeled C) towards their watershed crest lines (Fig.1(f)). Voxels resulting to share the label C correspond to the segmented object. A real segmentation case with and without using paint drop marking method is shown in Fig.2. In our 3D extension of the 'flooding by immersion' approach we use pre-ordered voxel queues, where voxels are processed only once during the immersion. The gradient plateau management and the problem of finding a correct implementation of the immersion recursion, within a fast watershed implementation, comply with what suggested in [5]. The proposed solution can be 'immersed' (included and interfaced) in a full-featured interactive segmentation system, as shown in the next section.

4. USER-DRIVEN 3D SEGMENTATION SYSTEM

A graphical interactive segmentation environment for the visualization, interaction and processing of biomedical volumes (e.g. MR and CT datasets), has been implemented in C++ language (Borland C++, with Visual Component Libraries). Its design principles and some modules derives from previous works on 3D connected component processing and denoising [7],[8] and interactive 3D region growing

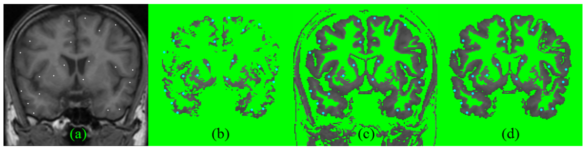
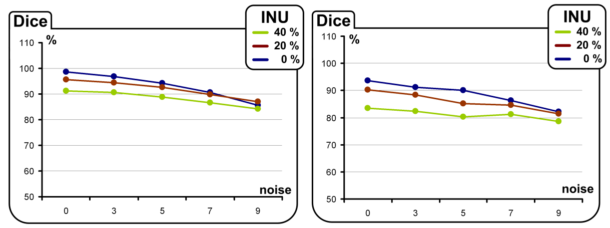


Fig. 2. Segmentation of GM: (a) slice with seeds, (b) partial flooding, (c)/(d) wrong/correct result without/with paint drop masking.



(a) WM Dice Coefficient (b) GM Dice Coefficient

Fig. 3. WM and GM segmentation results: K (Dice) parameter at different noise and INU (without denoising).

segmentation [9]. The visual environment allows the user (physician) to interact with images with a set of different tools he can be freely select and use on any number of 2D slices in different orientations. The tools can be chosen among: a) set of seeds, b) couple of crossing lines, c) ellipses/rectangles with seeds, d) free-hand closed lines with seeds. Each tool has its own application vocation [9] and, depending on the spatial characteristics of the structures, one or more tools can be considered as appropriate. Associated to each tool there are specific methods to extract the MF and to determine initial values of the algorithm parameters: a suitable preflooding height h_{pf} and the gray-level range $[\lambda_{min}, \lambda_{max}]$ of the target structures in I. The gray-level range can be used to restrict the domain of computation D of the marker-controlled WS with additional savings in terms of computational load. In our software, the user can use as much as visual tools he wants, giving them an unique name or ID which identify the collected descriptors (MF and parameters). Then he can freely select a subset of descriptors and use them to segment the desired structures. He can also manually trim pre-estimated parameters and have immediate visual feedbacks for an effective conditioning of the subsequent segmentation. In fact, he can see (e.g. by semiopaque mask layers on slices and a quick navigation in various orientations) both the domain restriction and the partially flooded thick skeleton and, when necessary, he can properly adjust the λ_{min}, λ_{max} and h_{pf} parameters, helped by real-time and intuitive visual feedbacks. Then, after the above freely choosen sequence of quick actions, he can trustfully launch the paint-drop marker-controlled segmentation (which takes few seconds on a common PC architecture) and visualize the results. The software also offers other possible operations with previously segmented structures or components (SC): a) a certain SC can work as inclusion/exclusion domain to refine the result or to avoid compenetration with other SC's, b) additional SC's can be generated by the union/intersection of other freely chosen already available SC's.

5. EXPERIMENTAL RESULTS

To assess the *generality* performance of the proposed system is not a simple task. An exhaustive 'accuracy vs variability' performance evaluation would require a wide variety of datasets and segmentation target applications. This is quite impractical and what it has been done instead is to choose representative use-cases to assess accuracy performance and infer on variability related aspects. To this purpose, we first considered brain structure (gray matter, GM and white matter, WM) quantification on neurological MR datasets. This also gave us meaningful information about the adequacy of our paint drop marking solution to handle complex structures with inhomogeneous borders. Other evidences on variability attributes will be derived from qualitative evaluations on tumor brain segmentation in MR volumes. Our main use-case is a widely known and challenging problem, and we are well aware that today best solutions for these problems comes from the world of statistical data analysis (e.g. Expectation Maximization approaches incorporating a-priori information deriving from brain atlases and statistical models). As stated in the introduction, it should be clear to the reader that our intent here is not to compete with highly specialized methods with respect to the classification performance, but to derive some sound evidences on the capabilities of the proposed system to handle difficult problems starting from general hypothesis and counting solely on the potentialities offered by the implemented (algorithmical and interaction based) knowledge from markers solutions. Therfore no kind of task specialization is considered here while our term of comparison are both general and task specialized techniques which can be meaningfully compared to ours in terms of technological approach to the same segmentation problem.

GM and WM segmentation. We considered 3D-datasets from the BIC simulated brain repository [10]: 15 MR volumes (T1 mode, 181x217x181 voxels, 1mm slice thickness) in all combinations of noise (in % wrt brightest tissue: 1,3,5,7,9%) and intensity non uniformity (INU) due to RF bias (0, 20,40%). Each volume has been segmented 'semi-independently' i.e. loading the same marker functions (selected once) and letting the user (a volounteer neuroradiologist - from the Neuroradiology Unit of the Civil Hospital of Brescia, Italy - which undergone a proper software usage training) free to trim h_{pf}, λ_{min} and λ_{max} parameters with real time visual feedbacks. This was motivated by the need to maintain some degree of structural consistency of the results, without alteration of the user experience and freedom in using the segmentation environment. MF selection can take from about one minute to few minutes depending on the task and user experience, while the rest of the procedure (interaction and computational time) takes 30-40 sec. on a common PC architecture. Among the available tools, seeds collected on various and freely selected slices have been preferred for GM, while couples of crossing lines was used for a compact sketching of the WM. In this case the first line must be traced inside the WM and the second one should cross nearby structures (typically CSF and GM) allowing proper h_{pf} estimation. Only, in few cases (high noise or RF values) the user desired to repeat the segmentation, by refining the MF (the system allows it in a comfortable way). WM is segmented first and used as domain exclusion to prevent WM-GM compenetration. The following segmentation evaluation parameters have been measured for each segmented structure: the set of voxels belonging to the segmented structure N_S, the ground truth set N_G (provided in the BIC database), the True Positives $TP = \frac{N_G \cap N_S}{N_G}$, False Negatives $FN = \frac{N_G - N_G \cap N_S}{N_G}$ and False Positives $FP = \frac{N_S - N_G \cap N_S}{N_G}$ fractions, the Overlap Metric coefficient $OM = \frac{TP}{1+FP}$ and the Dice coefficient $K = \frac{2(N_G \cap N_S)}{N_G + N_S}$. In Fig.3, K performance results are shown for all the 15 tested datasets, while in Tab.1 all performance parameters are compared with available ones from [11] and [6] (3%,

Perform. coeff. (%)	Act.Cont.1 [11]		Act.Cont.2 [11]		Paint-drop.WS		Impr.WS [6]	
	GM	WM	GM	WM	GM	WM	GM	WM
TP	78.0	84.3	93.3	95.1	89.9	91.5	–	–
FN	22.0	15.7	6.7	4.9	10.0	8.4	–	–
FP	13.0	5.7	5.6	5.8	13.7	2.5	–	–
OM	68.9	79.7	88.3	89.8	79.1	89.2	–	–
K	–	–	–	–	88.3	94.3	89.0	94.6

Table 1. Comparison of GM and WM segmentation methods.

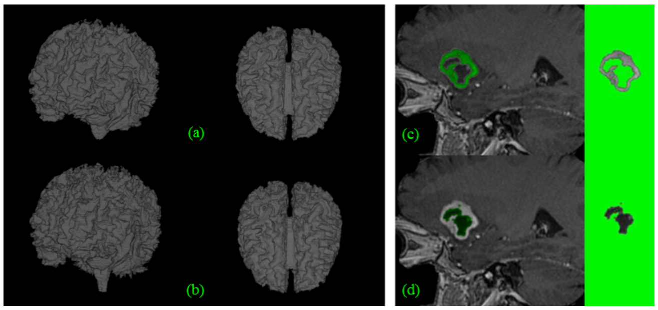


Fig. 4. Visual results. Volume rendering of (a) manual and (b) obtained WM segmentation. (c)/(d) External/internal tumor fractions.

20% INU dataset). In [11], some techniques for active contour segmentation of 3D brain are presented, a first technique (ActCont1) can be defined 'general' in that region growing is used to initialize the contour, a second technique (ActCont2) is specialized on the segmentation of brain structures, it makes use of skull stripping, histogram analysis and user interaction. In [6] a technique for automatic segmentation of GM and WM is presented which exploits a-priori knowledge, acquired through statistical analysis and atlas matching, to guide a watershed-based segmentation. Trends in the obtained results are consistent, they shows gradual degradations when noise and INU increase without breaking down. With respect to the same base technology (WS), performance of our generic (not specialized) interactive system looks aligned with state-of-art specialized and automated ones. With respect to other base technologies (active contours) our approach performs better when compared to a generic approach. As expected, application specialized techniques can perform better, as shown e.g. by the ActCont2 results, and performance improvements with higher automatism could be also obtained specializing our system, e.g. by introducing a skull stripping step before GM segmentation (most brain dedicated techniques use it) or by specific knowledge from marker strategies. Therefore, our system can be thought as scalable with respect to specialization and automation levels with good baseline performance for generic applications.

Other datasets/applications. We did similar tests on real datasets from the IBSR database[12]. We obtained, on 17 volumes for which manual segmentation results are provided, results well aligned to the above ones. In Fig.4(a)-(b) manual vs obtained segmentation results are shown for MR volume nr.8 in the database.

Another meaningful use-case regards tumor segmentation and quantification problems in brain MR datasets. Here we show a segmentation result which is composed by 2 distinct components external/internal, due to the different nature of involved tissues. Domain exclusion (internal vs external) and subsequent SC logical union have been used to produce a final result. This use-case offer additional cues on the capabilities of the the proposed system and constitutes the subject of an ongoing research activity.

6. CONCLUSION

A novel algorithmic approach for marker-controlled watershed segmentation and his setting in a 3D interactive segmentation system have been presented. The proposed solution has been described in terms of marking paint drops which fall on a partially flooded topographic relief (related to a volumetric dataset) and which identify the catchment basins of interest by means of water color changes. The combination of the two phases (partial flooding followed by CB staining) represents an elegant and simple solution for marker-driven segmentation in a watershed framework, and allows robust segmentation even when complex or extended anatomical structures present inhomogeneous borders. Marker selection, parameter tuning and rapid convergence toward the desired result are provided, guaranteeing a strong link between computationally effective algorithms and a fully featured interactive segmentation environment. The presented system shows satisfactory results on challenging tasks even without application domain specialization. This is also due to the sound matching between algorithmic solutions and interactive tools.

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