Conflict Management in the Fusion of Complementary Segmentations of Deformed Kidneys and Nephroblastoma

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Abstract

The fusion of multiple segmentations aims to improve their accuracy in order to make them exploitable. However, conflicts may appear. In this paper, two conflict-management models are proposed for the fusion of complementary segmentations. This conflict-management and fusion procedure, integrated into the SAIAD project, carries out the fusion of deformed kidneys and nephroblastoma using the combination of six independent methods. These methods are based on different criteria, like the adjacent segmented slices, the variation of information, the Dice, the neighbouring labels, the pixel intensity by scanner images, and the fully connected CRFs. The performances of our fusion models was evaluated on 139 scans for three patients with nephroblastoma, and the results demonstrate its effectiveness and the improvement of the resulting segmentations.

Keywords: Fusion, Conflict management, Segmentation, Cancer tumour

1. Introduction

Nephroblastoma, also called Wilms tumour, is the abdominal tumour the most frequently observed in children (generally 1- to 5-years-old boys and girls). This cancer disease represents 5% to 14% of malignant paedriatric tumours. As

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- ⁵ indicated by its name, this type of tumour is situated in the kidney. Most of the time, its initial diagnosis is based on imaging. Generally, ultrasound observations are planned first in order to confirm its existence and approximate its position. Then, a medical scanner provides its position, and the healthy tissues and organs are reached with higher accuracy. Radiologists and surgeons
- need 3-dimensional (3D) representation of the tumour and the border organs in order to establish the diagnosis, plan surgery (estimated quantity of blood, specialized equipment required, estimation of the duration of the surgery, etc.), and also guide the actions of the surgeon during the surgery.
- This 3D representation is currently done through manual segmentations, ¹⁵ which is a time-consuming task. The French-Swiss border project SAIAD (Automated Segmentation of Medical Images Using Distributed Artificial Intelligence) aims at obtaining automatic segmentations of the kidney tumours and nephroblastoma through artificial intelligence methods. There is a lot of research in publications on automatic segmentation using AI like Deep Learning
- with Convolutional Neural Networks (CNNs) (Long et al. (2015); Ronneberger et al. (2015)), Random Markov Fields (Kato et al. (2012)), and also the Fully Connected Conditional Random Fields (CRFs) Krähenbühl & Koltun (2011) coupled with CNNs to refine segmentations Chen et al. (2018); Noh et al. (2015); Kamnitsas et al. (2017), genetic algorithm (Tosta et al. (2017); Khan & Jaffar
- (2015)), and Case Based Reasoning (CBR) (Marie et al. (2018); Kausar et al. (2016); Frucci et al. (2008)). But a single method is not efficient enough to achieve a correct segmentation of all structures on an image. Each structure can be calculated using one optimal method of its own in order to obtain its best segmentation. Thus, in the SAIAD project, a method based on CBR and
- $_{30}$ region growing is used in order to segment the kidney deformed by nephroblastoma on each of the patients' 2D images (Marie et al. (2018)), and the OV² ASSION method, based on CNN, is used to segment nephroblastoma (Marie et al. (2019)).

The next step is the fusion of the nephroblastoma and kidney segmentations in order to obtain the final segmentation of a scanner image. This fusion can cause conflicts between pixels, and a conflict-management protocol must determine the true labels. Most of the conflicts are found at the intersection of the pathological kidney and the nephroblastoma. These border zones are the most difficult to label because there are no clear and/or visible boundaries

- on the scanned images. Only advanced algorithms or an experienced expert (radiologist or surgeon) could succeed in determining these boundaries. In our approach, we consider all the segmentations of deformed kidneys and nephroblastoma calculated for one patient in order to resolve the conflicts using a fusion and conflict-management model based on several combined methods.
- ⁴⁵ After the study of works related to segmentation fusion in Section 2, this paper presents, in Section 3, the fusion and conflict-management model we have designed for kidney and nephroblastoma segments. Section 4 explains the experiments for our methods and the discussions around the results.

2. Related work

- ⁵⁰ Information fusion has emerged in order to manage data from multiple sources. The fusion of information can also be applied to the fusion of images. Image fusion is applied in a wide scope of applications, including remote sensing (Ghassemian (2016)), surveillance (Jin et al. (2017)), photography (Ma et al. (2015)), and medicine (James & Dasarathy (2014); Liu et al. (2014)). Sev-
- ⁵⁵ eral fusion techniques are used, such as the wavelet transform (Li et al. (1995)), image pyramids decomposition (Mertens et al. (2007)), etc. These methods are categorized according to different fusion levels : pixel-level fusion, feature-level fusion, and decision-level fusion (Pohl & Van Genderen (1998)). However, there are also other methods specific to the merging of multiple segmentations.
- The main strategy for segmentation consists in determining the best algorithm with optimal parameters, but these algorithms can be costly and complex. Another strategy aims at combining several segmentations into a single, consensual one. The best strategy or the best criterion for fusion is then applied to the consensual segmentation. Multiple segmentations are then calculated applying

- different segmentation methods or using the same method but with different parameters. Many techniques use the over-segmentation method in order to obtain a large number of regions and a large amount of information about each segmentation (Huang et al. (2016); Li et al. (2012)). Other fusion methods are applied to the multi-atlas based segmentation (Aljabar et al. (2009); Nguyen et al. (2015)). The atlas, which contains a set of images and corresponding segmentations, is used to determine the images that are the most similar to
- segmentations, is used to determine the images that are the most similar to the target image and fuse the segmentations of the images chosen to obtain the segmentation of the target image.
- It is possible to group most of these fusion strategies into different ap-⁷⁵ proaches. The first and most intuitive approach is the democratic approach with fusion voting techniques like majority vote, global weighted vote, local weighted vote, and so on (Artaechevarria et al. (2009)). Another approach is the morphological approach, which uses contours and shapes of the elements in the segmentations. The Shape-Based Averaging (SBA) method (Rohlfing &
- Maurer (2007)) uses the signed Euclidean distance maps in order to determine the segmentation contours of each possible label. F-Measure Martin et al. (2004) is a criterion used in Mignotte & Hélou (2014) which evaluates the quality of the resulting contours and uses the notions of precision and recall.
- Many other methods are based on probabilistic approaches, like the STAPLE method (Warfield et al. (2004)), which estimates the optimal combination of segmentations to fuse, weighting each segmentation according to the estimated performance level using the Expectation-Maximization algorithm (Dempster et al. (1977)). Mignotte (2010) used a method based on the Probabilistic Rand Index (PRI) criterion (based on pairwise relationships), as well as the method based
- on the Variation of Information (VoI) criterion (Mignotte (2014)). This method uses mutual information metrics and entropies in order to measure the amount of information lost or gained when turning one label into another. Another VoI-based fusion procedure is used in Nguyen et al. (2018) in order to merge multiple atlases of X-ray images. This method is successfully applied to complex
- ⁹⁵ bone regions like the patella, talus, and pelvis.

The Global Consistency Error (GCE) criterion is used in Khelifi & Mignotte (2017c) for the fusion of multiple segmentations. This method measures the extent to which one segmentation can be viewed as a refinement of another segmentation, based on segmentation regions. The K-Mean method (Mignotte (2008); Harrabi & Braiek (2012)) aggregates pixels with similar characteris-

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(2008); Harrabi & Braiek (2012)) aggregates pixels with similar characteristics. A method using weakly supervised trace-norm multi-task learning (Liang & Huang (2018)) consists of considering the segmentation fusion problem as a weakly supervised learning problem, in order to use the information from superpixels. In this method, the multiples segmentations are treated as multiple closely related tasks and utilise multi-task learning methods to evaluate the reliability of the segmentations. The segmentation maps obtained are then aggregated according to a fusion strategy. Finally, another approach uses the spatial and intensity information of an image (i.e. using the 2D information) for the fusion of the MR-T2 brain images segmentation map (Feng et al. (2017)).

Furthermore, a recent multi-objective methods combines several criteria like the combination of the VoI criterion with the F-Measure criterion and the GCE criterion with the F-Measure criterion (Khelifi & Mignotte (2017a,b)), and then a new classification is proposed: mono-objective methods and multi-objective methods.

- However, most of these approaches have not been implemented on medical images, and they fuse concurrent segmentations of the same initial image. Only Nguyen et al. (2018) and Feng et al. (2017) use medical images and merges the corresponding segmentations. Our approach aims at carrying out fusion of complementary segmentations, i.e. the fusion of kidney segmentations and tumour segmentations together, and resolving the pixels in conflict (labelled as belonging to the kidney and the tumour in the fused segmentation) by retrieving the patient's 3D information (i.e. all other segmented slices of the patient). Two conflict-management models are defined and presented in the next section of this paper and are based on the set of combined methods using the informations.
- ¹²⁵ from the Adjacent Segmented Slices (ADS2) method, a method based on VoI (Mignotte (2014)), on Dice, on the spatial and intensity information of one

image (renamed here NandI for Neighbours and Intensity) (Feng et al. (2017)), on a 3D-NandI method which is an improvement of the NandI method and on the Fully Connected CRF (Krähenbühl & Koltun (2011)).

¹³⁰ 3. Proposed method

The general architecture of the system designed in the SAIAD project is described in Figure 1. It is composed of three layers. The first one is the data layer, which contains a database for each segmentations system. Each database has access to all the scanned images and corresponding manual segmentations and expert knowledge like the information from scanner images in Dicom files but they have their own case base. The definition of a case can be different from one segmentation system to another. The second layer is the segmentation layer, where images are segmented by artificial intelligence systems. For example, the deformed kidney can be segmented by a CBR system coupled with region

¹⁴⁰ growing (Marie et al. (2018)), and the tumour can be segmented by a Deep Learning system (Marie et al. (2019)). At the end of the segmentation process, the system gives two complementary segmentations for each image. Finally, the fusion layer combines the complementary segmentations and resolves the conflicts.

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This part of the paper presents our conflict-management models and our different methods used within our models.

3.1. Fusion of complementary segmentations

Since nephroblastoma and kidneys are segmented individually, it is necessary to fuse them in order to obtain segmentation with both of these structures. In order to manage the possible conflicting pixels, we need to obtain fused segmentation for all methods used except the method based on the Fully Connected CRF.

As shown in Figure 2, during this first step of fusion, each structure is merged and a new temporary label is assigned to the pixels in conflict (i.e. the pixels labelled as belonging to different structures the complementary segmentations).



Figure 1: General schema of the SAIAD project.

3.2. Adjacent segmented slices information

The segmentations of adjacent slices may give information about a pixel in conflict. Indeed, we assumed that the segmentations of adjacent slices are relatively similar, since the structures presented have more or less the same shapes and positions. For that reason, we have designed the Adjacent Segmented Slices (ADS2) method for the resolution of conflicts. This method examines the labels of each conflicting pixel in the adjacent slices.

Deformed kidney segmentation



Consensus segmentation with conflicts Merging

Figure 2: Merging of deformed kidney and nephroblastoma segmentations.

Algorithm 1: ADS2-based conflict resolution method.					
for each segmented slice s do					
for each conflicted pixel p with label l_s^p do					
if l_{s-1}^p and l_{s+1}^p do not conflict then					
$ \qquad \qquad \mathbf{if} \ l^p_{s-1} == l^p_{s+1} \ \mathbf{then} \\$					
$l_{s}^{p} = l_{s-1}^{p} = l_{s+1}^{p};$					
end					

The pseudo-code of the ADS2 method is shown in Algorithm 1. Considering a conflicting pixel p labelled with l_s^p in slice s, if the labels l_{s-1}^p and l_{s+1}^p of p in the adjacent slices of s are equal to l (i.e $l_{s-1}^p = l_{s+1}^p = l$), then we assume that l_s^p is equal to l. Unfortunately, this method cannot resolve all the conflicts. Indeed, ADS2 can only be applied in specific situations where adjacent pixels are not in conflict. For this reason, we have also designed and implemented other methods.

3.3. Method based on the variation of information criterion

The Variation of Information (VoI) criterion (Meilă (2003)) is based on an information theory that compares two samples in a set of data. It is also used in order to compute the similarity between two segmentations and thus to quantify the quality of a segmentation regarding its ground truth given by an expert

(Sathya & Manavalan (2011); Mobahi et al. (2011)). Its formula is based on a probabilistic approach using the entropy and the mutual information of the segmentations to be compared. The VoI score is between 0 and 1, and the lowest scores indicate similar segmentations. The highest scores indicate mostly
different segmentations.

In the case of the comparison of two segmentations S and S', the VoI is defined as:

$$VoI(S, S') = H(S) + H(S') - 2 * I(S, S')$$
(1)

where H(S) and H(S') represent the entropy of S and S', and I(S, S') represents the mutual information between the two segmentations.

185 The entropy is defined as:

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$$H(S) = -\sum_{i=1}^{R} P(i) \log P(i) = -\sum_{i=1}^{R} \frac{n_i}{n} \log \frac{n_i}{n}$$
(2)

where R is the number of regions of S, and P(i) is the probability that a pixel belongs to the class i based on the total number n of pixels in the segmentation. In imagery, the entropy can be calculated by the normalized histogram of the considered image. ¹⁹⁰ The mutual information is also defined as:

$$I(S,S') = \sum_{i=1}^{R} \sum_{j=1}^{R'} P(i,j) \log(\frac{P(i,j)}{P(i)P(j)}) = \sum_{i=1}^{R} \sum_{j=1}^{R'} \frac{n_{ij}}{n} \log(\frac{\frac{n_{ij}}{n}}{\frac{n_{ij}}{n}})$$
(3)

where P(i, j) is the probability that a pixel belongs to the class i of S and to the class j of S'.

In this method, considering a set of L segmented slices $\{S_k\}_{k \leq L}$, the comparison of S to $\{S_k\}_{k \leq L}$ is based on the computation of the mean VoI:

$$\overline{VoI}(S, \{S_k\}_{k \le L}) = \frac{1}{L} \sum_{k=1}^{L} VoI(S, S_k)$$
(4)

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The theoretical consensus segmentation is simply the segmentation having the weakest \overline{VoI} among all the possible labels of each pixel:

$$\hat{S}_{\overline{VoI}} = \underset{S \in S_n}{\operatorname{argmin}} \overline{VoI}(S, \{S_k\}_{k \le L})$$
(5)

We could use the mean VoI metric (see Eq. 4) for conflict management but the computation time would be excessive. Consequently, we use its local expression derived $\Delta \overline{VoI}$ in Eq. 6 used in Mignotte (2014) and Nguyen et al. (2018) where $s: m \to x$ is the pixel at position s with label m replaced by the label x in S, \mathcal{L}_s^l is the pixel label at position s in the segmentation $S_l \in \{S_k\}_{k \leq L}$, and $n_{m\mathcal{L}_s^l}$ is the number of pixels which have the same label m in S and the label \mathcal{L}_s^l at position s in S_l . In contrast to the mean VoI metric, the maximum value for the derived mean VoI is searched for.

$$\begin{split} \Delta \overline{VoI}(S, \{S_k\}_{k \leq L})_{s:m \to x} = L \cdot \left\{ -\frac{n_m}{n} \log\left(\frac{n_m}{n}\right) - \frac{n_x}{n} \log\left(\frac{n_x}{n}\right) \\ +\frac{n_m - 1}{n} \log\left(\frac{n_m - 1}{n}\right) + \frac{n_x + 1}{n} \log\left(\frac{n_x + 1}{n}\right) \right\} \\ - 2 \cdot \sum_{l=1}^{L} \left\{ \frac{n_m \mathcal{L}_s^l}{n} \log\left(\frac{n_m \mathcal{L}_s^l}{n} \cdot \frac{n}{n_m} \cdot \frac{n}{n_{\mathcal{L}_s^l}}\right) \\ + \frac{n_x \mathcal{L}_s^l}{n} \log\left(\frac{n_x \mathcal{L}_s^l}{n} \cdot \frac{n}{n_x} \cdot \frac{n}{n_{\mathcal{L}_s^l}}\right) \\ - \frac{(n_m \mathcal{L}_s^l - 1)}{n} \log\left(\frac{(n_m \mathcal{L}_s^l - 1)}{n} \cdot \frac{n}{n_m - 1} \cdot \frac{n}{n_{\mathcal{L}_s^l}}\right) \\ - \frac{(n_x \mathcal{L}_s^l + 1)}{n} \log\left(\frac{(n_x \mathcal{L}_s^l + 1)}{n} \cdot \frac{n}{n_x + 1} \cdot \frac{n}{n_{\mathcal{L}_s^l}}\right) \right\} \end{split}$$

$$(6)$$

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The maximization of the Eq. 6 can be realized by an ICM algorithm Besag (1986) (Iterative Conditional Modes) an iterative steepest local energy descent. Like the pseudo-code of the VoI-based method shown in Algorithm 2, for each conflicting pixel, the derived mean VoI is calculated for each possible label. The final label will be the one with the highest value. As the adjacent slices are similar, this method only takes into account the segmentations of the n_n adjacent slices of S. For example, for $n_n = 2$ and S = 4, segmentations $\{2, 3, 4, 5, 6\}$) are taken into account. This step is repeated until $p < T_{max}$ and for each segmented slice.

Data:

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 $\{S_k\}_{k < L}$: The set of L segmented slices

 n_n : The number of adjacent slices taken into account

 ε : The set of possible labels for a pixel

 T_{max} : The maximal number of iterations

for each segmented slice S in $\{S_k\}_{k \leq L}$ do $\{S_k\}_{k \in \{k-n_n,...,k+n_n\}}$: Set of neighbor fused segmentations to Ssegmentation of one patient with conflicting pixels while $i < T_{max}$ do for each conflicted pixel p with label l_s^p of segmentation S do Compute $VoIMax = \arg \max_{x \in \varepsilon} \Delta \overline{VoI}(S, \{S_k\}_{k \in \{k-n_n,...,k+n_n\}}) l_s^p \rightarrow x$ Replace label l_s^p by label x of VoIMax at the segmentation Send i = i + 1end end

3.4. Method based on the dice criterion

The Dice-based method is inspired by the VoI-based one: the VoI criterion is replaced by the Dice. This metric is commonly used in the medical field. The F-Measure (Martin et al. (2004)) is also based on the Dice for the segmentation fusion (Mignotte & Hélou (2014)) at the region level. In the present approach, the Dice criterion is used for the segmentation fusion at the pixel level. The Dice is defined as:

$$Dice(S, S') = \frac{2 * TP_{S,S'}}{2 * TP_{S,S'} + FP_{S,S'} + FN_{S,S'}}$$
(7)

where $TP_{S,S'}$ is the number of true positive pixels between S and S'(pixels labelled true in both of the segmentations). FP is the number of false positive pixels (pixels labelled true in S and false in S') and FN the number of false negative pixels (pixels labelled false in S and true in S').

Like the VoI-based method, the mean Dice of S_i is computed considering a set of L segmented slices $\{S_k\}_{k \leq L}$. In addition, a weight is associated to each slice in order to give a bigger Dice to the nearest slices. The equation then becomes:

$$\overline{Dice}(S_i, \{S_k\}_{k \le L}) = \frac{1}{L} \sum_{k=1}^{L} Dice(S_i, S_k) * r_{i,k}$$
(8)

with weight $r_{i,k}$:

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$$r_{i,k} = 1 - \frac{|i-k|}{n_n * 2 + 1} \tag{9}$$

where n_n is the number of adjacent slices taken into account at each side of S_i .

With this method, The fused segmentation is the one which obtains the biggest \overline{Dice} :

$$\hat{S}_{i\overline{Dice}} = \underset{S \in S_n}{\operatorname{argmax}} \overline{Dice}(S_i, \{S_k\}_{k \le L})$$
(10)

Finally, the pseudo-code of the Dice-based method is the same as Algorithm 2 where $\Delta \overline{VoI}$ is replaced by \overline{Dice} .

3.5. 2D and 3D method based on neighbouring information

3.5.1. NandI method

The method based on neighbouring information, like the pixel's grey level and the neighbour's labels, is used in Feng et al. (2017) for the fusion of brainimages segmentation. This method, known as NandI (Neighbours and Intensity), calculates a similarity index between two pixels p and q of the same slice, defined as:

$$Sim(p,q) = exp\left(-\frac{d^2(p,q)}{2\alpha^2} - \frac{dif^2(p,q)}{2\beta^2}\right)$$
 (11)

where d(p,q) = ||p - q|| is the Euclidean distance between p and q, and dif(p,q) = |I(p) - I(q)| is the difference of intensity between them. α and β are two weights.

A set of coherent neighbours must then be determined for each conflicting pixel p in order to determine their final label. Let E_p^r be the set of an effective neighbourhood of p. A pixel q must satisfy the next three conditions in order to become an effective neighbour of p:

²⁵⁰ 1. d(p,q) < r: The Euclidean distance between p and q must be smaller than radius r,

2. $l^q \in S = l^q \in S'$: q is not a conflicting pixel,

3. $l^q \in \varepsilon$: The label of q belongs to the set of possible labels, i.e the tumour label or the kidney label.

The new label of p is also obtained by:

$$l^{p} = \begin{cases} tumour \text{ if } \sum_{q \in E_{p}^{r}, l^{q} = tumour} Sim(p,q) > \sum_{q \in E_{p}^{r}, l^{q} = kidney} Sim(p,q), \\ kidney \text{ else} \end{cases}$$
(12)

Finally, the pseudo-code of the NandI method for the conflict resolution of the set of segmented slices for one patient is shown in Algorithm 3.

Algorithm 3: The NandI-method algorithm.
Data:
$\{S_k\}_{k \leq L}$: The set of L segmented slices
r: The radius
for each segmented slice S in $\{S_k\}_{k \leq L}$ do
for each conflicted pixel p of segmentation S do Compute E_p^r
Compute l_s^p
end
end

3.5.2. 3D-NandI method

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In order to manage the conflicts of a slice, the NandI method only uses the information from this slice. However, as we are working on a set of segmented slices corresponding to a patient's abdomen, 3D information can also be taken into account. The 3D-NandI method is an evolution of the NandI method, in which a 3D effective neighbourhood and a 3D Euclidean distance are calculated.

²⁶⁵ 3.6. Fully connected CRF based method

The fully connected CRF (Krähenbühl & Koltun (2011)) is mainly used as CNN post-processing, from the generated probability maps, in order to refine the calculated segmentations (Chen et al. (2018); Noh et al. (2015); Kamnitsas et al. (2017)). Indeed, they refine the edges of the structures while taking into account the possible dependencies through fast and accurate inferences. Unlike the widespread use of Fully Connected CRF to refine segmentation results, we use them here to resolve the conflicts generated by the fusion of complementary segmentations.

Figure 3 shows the process of this method. At first, the probability maps of
the CNN segmentations of each structure of the image are used and modified.
These values, between 0 and 1 and corresponding to the percentage of membership in each class, are adjusted to 0 or 1 for non-conflicting pixels. On the contrary, the values of the conflicting pixels stay in this interval. These modified probability maps are given as input to the Fully Connected CRF (in addition to
the corresponding scanner images), which will determine the labels of the pixels

in conflict by outputting consensus segmentation without conflicts.

3.7. Conflict-management model

Figures 4 and 5 show our two versions of the conflict-management process based on the combination of all the methods described above. The set of calculated complementary segmentations and the corresponding scans are the inputs for the entire process. In the first version in Figure 4, the conflicts are first positioned and treated with all the methods presented above in parallel.

The results of all the methods can then be aggregated in two different ways. The first is based on a majority vote for the association of the final labels of each pixel in conflict. However, with the majority vote, there may be a tie for pixels that can be resolved by the ADS2 method because there is then an even



Figure 3: Fusion and conflict management of segmentations with the Fully Connected CRF-based method.

number of results to be processed. In this case, several choices are possible, such as choosing the final label determined by a certain method, or deciding that the pixels in the tie be labelled as belonging to the tumour or the kidney.

The second method resulting in segmentation fusion uses the CRF. During the CRF algorithm, probability maps are generated. For each conflicting pixel, the value of this pixel in the probability maps is the number of times that this label is chosen divided by the total number of results. For example, if there are two possible labels (kidney and tumour), four results in favour of the kidney label and two in favour of the tumour label, then the value of this pixel in the 300 probability map of the kidney label will be 4/6 and 2/6 in the probability map of the tumour label.

The second version of the conflict-management process is described in Figure 5. The ADS2 method performs a pre-treatment in order to obtain an odd result. Then, the other methods are applied, and a majority vote or a decision based on the CRF probability map is launched in order to obtain the final segmentations.

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Figure 4: First version of the conflict-management model, for the fusion of tumorous kidney segmentations.



Figure 5: Second version of the conflict-management model, with a pretreatment, for the fusion of tumorous kidney segmentations.

4. Experiments

4.1. Generation of segmentation set

We have tested the performance of our models over a set of 139 segmented scans of three patients. Patients 1, 2, and 3 have 47, 62, and 30 scans, respectively. All of the scans and calculated segmentations have the same size: 512 x 512. The pathological kidney and the nephroblastoma of each patient were segmented by Deep Learning (the convolutional neural network FCN-8s first trained with the PASCAL VOC 2012 database in Everingham et al. (2015)) enhanced with the OV²ASSION (Marie et al. (2019)) with 10000 iterations for training. The learning protocol OV²ASSION is adapted to small learning sets.

We also have the ground truth segmentations of our three patients, carried out by experts (surgeons and radiologists) at the *Centre hospitalier Régional Universitaire de Besançon*. These ground truths are used in order to verify the reliability of our processes and the resulting fused segmentations.

4.2. Results

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4.2.1. Optimal parameters

We first determined the optimal parameters for each fusion method. In particular, we determined the optimal number of adjacent slices for the VoIbased and the Dice-based methods. Figure 6 shows the results obtained for the VoI and Dice-based methods regarding the number of adjacent slices taken into account. For all the patients, the best average performance of the VoI-based method and Dice-based method is obtained with two adjacent slices at each side of the considered segmentations for $T_{max} = 3$. Three loops were sufficient to become stable because the initial image is very close to the expected image, and there are only a few pixels in conflict (compared to the total number of image pixels).

The performance of the NandI and the 3D-NandI methods have been evaluated according to the size of the chosen radius. The results of both methods are 335 shown in Figure 7. The average performance of the 3D-NandI method stagnates



Figure 6: Evolution of the performance of the VoI-based method and the Dicebased method regarding the number of adjacent slices at each side of the considered segmentations.

after a radius of 5. Consequently, a radius of 3 has been retained for the NandI method and a radius of 5 for the 3D-NandI one.



Figure 7: Evolution of the performance of the NandI method and the 3D-NandI method regarding the size of the chosen radius.

4.2.2. Results of both of the versions

Table 1 shows the performance of the ADS2 method for three patients. This table presents the number of conflicting pixels that have been correctly classified and, in between brackets, the number of conflicting pixels that were correctly classified by the total number of conflicting pixels that could be resolved by this method. We obtained 88.87% of good resolution for Patient 1 (1.749 correctly classified pixels for 1.968 pixels that could be resolved), 92.11% for Patient 2,

and 86.82% for Patient 3. An average of 89.56% of good resolution was obtained, which makes ADS2 a good method for a little less than a quarter of the pixels in conflict. However, this method cannot be applied to all conflicting pixels. Indeed, we must be in the favourable case where the pixels of adjacent slices have the same non-conflicting label for the conflicting pixel. Table 2 shows the

percentage of conflicting pixels that can be resolved by the ADS2 method, which represents on average of 23.30%.

	Patient 1	Patient 2	Patient 3	Total Mean
ADS2	0.8887	0.9211	0.8682	0 8956
	(1749/1968)	(1004/1090)	(448/516)	0.0350

Table 1: Average performance on different patients and for the ADS2 method.

	Patient 1	Patient 2	Patient 3	Mean
ADS2	31.2%	26.3%	12.5%	23.3%

Table 2: Percentage of conflicting pixels that can be resolved by the ADS2 method for three patients.

Table 3 shows the average performance in the first version for each of the methods, in parallel to the ADS2 method. We have 67.32% of correct resolution for the VoI-based method, 74.39% for the Dice-based method, 73.31% and 78.49% for the NandI and 3D-NandI methods, and 75.03% for the CRF-based method. The final results are shown in regards to the type of fusion applied in Table 4.

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Applying the first method shown in Figure 4, when the fusion of results is realized by a majority vote (MV in the table) and, if in case of a tie, the kidney label is chosen, the conflicting pixels are correctly resolved at 78.61%. On the contrary, if the tumour label is chosen in case of a tie, our system gets 78.59%

	Patient 1	Patient 2	Patient 3	Total Mean	
Vol	0.7159	0.6910	0.5906	0 6722	
VOI	(4946/6909)	(3203/4635)	(2703/4577)	0.0732	
Dico	0.7497	0.7292	0.7501	0 7439	
Dice	(5180/6909)	(3380/4635)	(3433/4577)	0.7455	
NandI	0.7140	0.7070	0.7885	0 7331	
	(4933/6909)	(3277/4635)	(3609/4577)	0.1551	
3D-NandI	0.7493	0.7931	0.8305	0 7849	
	(5177/6909)	(3676/4635)	(3801/4577)	0.1043	
CRF	0.7234	0.7458	0.7955	0 7503	
	(4998/6909)	(3457/4635)	(3641/4577)	0.1000	

Table 3: Average performance on different patients and for each method with the first version of the conflict-management model.

	Patient 1	Patient 2	Patient 3	Total
	1 attent 1	I atlent 2	1 attent 5	Mean
MV with kidney	0.7746	0.7737	0.8160	0 7861
in case of a tie	(5352/6909)	(3586/4635)	(3735/4577)	0.7801
MV with tumour	0.7752	0.7730	0.8149	0 7850
in case of a tie	(5356/6909)	(3583/4635)	(3730/4577)	0.7859
CRF-based	0.7658	0.7663	0.8193	0 7819
method	(5291/6909)	(3552/4635)	(3750/4577)	0.7812

Table 4: Average performance measurements on different patients for the first model with different methods of fusion.

of correct resolution. The system also gets 78.12% of correct resolution with the CRF-based method.

For the second version of our method described in Figure 5, the performance of the ADS2 method is the same as the first model shown in Table 1. For the other methods, the performances are shown in Table 5, where the results are

	Patient 1	Patient 2	Patient 3	Total Mean	
Vol	0.6446	0.6285	0.5696	0 6157	
VOI	(3185/4941)	(2228/3545)	(2313/4061)	0.0157	
Dico	0.6871	0.6697	0.7355	0 6070	
Dice	(3395/4941)	(2374/3545)	(2987/4061)	0.0919	
NandI	0.6912	0.6894	0.7870	0 7217	
	(3415/4941)	(2444/3545)	(3196/4061)	0.1211	
3D-NandI	0.6936	0.7540	0.8239	0 7528	
	(3427/4941)	(2673/3545)	(3346/4061)	0.1528	
CRF	0.7051	0.7255	0.7936	0 7395	
	(3484/4941)	(2572/3545)	(3223/4061)	0.1335	

Table 5: Average performance on different patients and for each method with the second version of the conflict-management model.

		Patient 1	Patient 2	Patient 3	Total
		i atlent i	1 atlent 2	1 atlent 5	Mean
		0.7681	0.7786	0.8184	0 7854
	(5307/6909)	(3609/4635)	(3746/4577)	0.7854	
	CRF-based	0.7678	0.7769	0.8217	0 7857
	method	(5305/6909)	(3601/4635)	(3761/4577)	0.1001

 Table 6: Average performance measurements on different patients for the second model with different methods of fusion.

lower than the first version (Mean between 61.57% and 75.28%) because the easiest conflicts have already been solved by the ADS2 method. Table 6 shows the final results of this second method. The final results of the two models are similar but remain superior to the result of each method individually (except for the fusion using the CRF-based method in the first model, which is less efficient than the 3D-NandI method alone).

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Table 7 shows the average Dice of segmentations for each patient before and

	Type of Fusion	Mean Dice	Mean Dice	Mean Dice	
	Type of Fusion	Patient 1	Patient 2	Patient 3	
Before		0.8535	0.8491	0.8477	
	CRF-based	0.9569	0.8503	0.8501	
	method	0.8308			
	MV with kidney	0.8569	0.8504	0.8500	
After V1 model	in case of a tie	0.0000	0.0004	0.0000	
	MV with tumour	0.8569	0 8504	0 8499	
	in case of a tie	0.0000	0.0001	0.0100	
	CRF-based	0.8568	0.8505	0.8502	
After V2 model	method	0.0000	0.6909	0.0302	
Alter v2 model	MV	0.8567	0.8505	0.8501	

Table 7: Presentation of the average Dice before and after the conflict management.

after the different conflict-management processes. The values in bold correspond
to the maximum values obtained for each patient. We can see that the average Dice increased for each patient, with an average increase of 0.24%, taking into account the maximum Dice after conflict management. We can justify the slight improvement by the fact that the number of conflicting pixels is minimal compared to the total number of pixels of each image. Indeed, the conflicting pixels
represent 0.06%, 0.03%, and 0.06% of pixels for Patients 1, 2, and 3 respectively. Nevertheless, the conflict-management protocol improves the segmentations in the most important areas (the edges of the different touching structures).

The result of one segmentation is presented in Figure 8. The initial segmentation on the left has conflicts (light colour) at the intersection between the kidney and the tumour, and inside the tumour. The latter conflict is quite easy

kidney and the tumour, and inside the tumour. The latter conflict is quite easy to solve, because they are mostly due to artefacts during the segmentation process. These artefacts are unique to the current slice. In addition, it is possible to simply determine the correct labels of these pixels by their grey intensity in

the scanner image. The two models of conflict management then give the same
result, as is the case on the right image. However, the former type of conflict is more difficult to resolve, and this is where the propositions of the different models diverge. Our different methods, which use various information like grayscale of the corresponding scanner image and of the neighbouring scanner images, as well as the labels of current segmentation and of the neighbouring segmentations are not enough in all cases to resolve the conflicts correctly.



Initial segmentation



Final segmentation

Figure 8: Example of a segmentation fusion result with the initial segmentation with conflicts (shown in light colour) on the left and the resulting segmentation on the right.

Figure 9 shows the conflict resolution between the two structures. Four pixels (shown by the arrows) were labelled "tumour" by the fusion through majority vote in both of the models and also labelled "kidney" by the fusion through the CRF-based method in both of the models.

400 *4.2.3*. Discussion

The results show that the combination of several fusion methods produces better results than each method individually. Indeed, the best way is to obtain complementary methods. The performance of the conflict management methods are different since they exploit different types of information (localization,

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statistics, probabilities, similarities between slices) and a different number of images (the slices in conflicts only, adjacent slices in addition).







Final segmentations

Figure 9: Focus on conflict resolution at the kidney-tumour intersection in Figure 8 with the initial segmentation with conflicts (shown in light colour) on the left and the resulting segmentations superimposed on the right.

The Dice-based method performs better than the VoI-based method because, even if exploit all the neighbouring segmentations, the Dice-based method associates weighting to the segmentations. The NandI, 3D-NandI, and the CRFbased methods also use the scanner images themselves as inputs for their conflict management (and thus exploit more information). In addition, the 3D-NandI method is an improvement to the NandI method since it integrates all the neighbouring-slice (segmentations and scanners) information. As with the NandI method, the CRF-based method uses the information on the current slice. For that reason, the CRF-based method is outperformed by the 3D-NandI method. In any manner, the CRF-based method is the only fusion method that uses the probability map of the segmentation, which is another source of information for the segmentation fusion.

The ADS2 method is a particular method since its strength is also its weak-⁴²⁰ ness. Indeed, it uses the information in adjacent segmentations only if they are equal and consistent. Thus, statistically and logically, it is the most efficient method because of its precautionary principle. However, this method cannot be used on all conflicting pixels: the conflict can be resolved when, and only when, pixel labels in adjacent slices match. The performance of the two proposed conflict management models are more or less equivalent; there is no model that stands out. Two fusion methods are proposed in the models but are questionable because they give close results. However, using the CRF-based method makes it possible not to be blocked a tie in the case of an even number of results (as is the case using the majority vote).

Prioritizing the ADS2 method in the second model does not seem to have a significant impact on the results. We can also imagine weighting each of the methods used as functions of the data. For example, if the scanned images are too noisy, it would be better to give more importance to the methods that exploit only the segmentations. Conversely, with segmentations very far from the ground truths, it would be better to give more important weighting to the methods exploiting the scanner images.

In addition, conflicting pixels within a structure are often easy to solve, but those within a boundary between two structures are more ambiguous. Even radiologists and surgeons use their experience to delimit these areas manually. Sometimes, the information on the scanned images and on the segmentations does not make it possible to find a clear delimitation. More powerful methods must be found to provide other types of information and improve the efficiency of our models for these particular cases. Some artificial intelligence methods using experience, such as the radiologists' and surgeons' experiences, may achieve

Finally, these models are easily flexible, and our results could be enriched by adding other methods which exploit other information, such as patient data. The models must now be tested over a larger set of patients. Indeed, at this point, we managed to have a dataset composed of 139 slices and three patients.

5. Conclusion and further work

better results on these borders.

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In this paper, we have presented new conflict-management strategies for complementary segmentations of pathological kidneys with cancerous tumours. Our methods allow the resolution of conflicts and thus improve the accuracy

of segmentations. Actually, these protocols are based on the intelligent association of single strategies for conflict management. These strategies use very different tools: the 3D information provided by the adjacent slices, neighbouring labels, the pixel intensity in scanner images, use of probability maps provided by CNN training, and criteria dedicated to the measurement of the accuracy of segmentations.

These fusion strategies are also adaptable and flexible to each case, since the different parameters can be modified according to the type of segmentation and conflicting pixels encountered.

Finally, in our case of the fully automatic segmentation of tumorous kidneys, these processes for fusion improve the Dice accuracy of the calculated segmentations by 0.24% on average and thus increase the robustness of the general system of the SAIAD project.

Further work will focus on the measurement of the robustness of the processes. In addition, we wish to add artificial intelligence methods in our systems to improve the resolution of conflicting pixels. We also wish to extend the method to other anatomical structures appearing on the scans, such as arteries, veins, and excretory cavities.

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