Registration of 3D angiographic and X-ray images using Sequential Monte Carlo sampling

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Abstract. Digital subtraction angiography (DSA) reconstructions and 3D Magnetic Resonance Angiography (MRA) are the modalities of choice for diagnosis of vascular diseases. However, when it comes to treatment through an endovascular intervention, only two dimensional lower resolution information such as angiograms or fluoroscopic images are usually available. Overlaying the preoperative information from high resolution acquisition onto the images acquired during intervention greatly helps physician in performing the operation. We propose to register pre-operative DSA or MRS with intra-operative images to bring the two data sets into a single coordinate frame. The method uses the vascular structure, which is present and visible from most of DSA, MRA and x-ray angiogram and fluoroscopic images, to determine the registration parameters. A robust multiple hypothesis framework is built to minimize a fitness measure between the 3D volume and the 2D projection. The measure is based on the distance map computed from the vascular segmentation. Particle Filters are used to resample the hypothesis, and direct them toward the feature space's zones of maximum likelihood. Promising experimental results demonstrate the potentials of the method.

1 Introduction

Digital subtraction angiography (DSA), which is based on conventional X-ray, and Magnetic Resonance Angiography (MRA) are the modalities of choice for many diagnostic vascular imaging procedures, as well as for performing and monitoring endovascular interventions. The main advantage is that the DSA and/or MRA data are usually of high resolution and since they are three dimensional in nature, they provide much needed information with regard to the topology of the vessel tree. The drawback is that these acquisitions can not be performed, while the intervention is underway. Mainly because the fact that DSA takes a long time to acquire and requires certain spatial clear-ance around the patient and MRA scanner are not usually available in the interventional rooms. What is available, and is fast to acquire, is two dimensional conventional projection x-ray images. In order to take advantage of high resolution, three dimensional info from either DSA or MRA, it is desirable to have a registration method, which brings in the two data sets (i.e., x-ray and 3D DSA or MRA) into a single coordinate frame. The problem at hand is 2D-3D registration problem, which has been investigated in the literature for various applications [4][16][13][25]. Image registration [15] methods can be categorized in two distinct groups: intensity-based and features-based techniques.

Feature-based methods [1, 3] are quite popular and rely on a pre-processing often pre-segmentation step where local structures of particular interest like points are determined. Once such structures have been recovered in both images, and correspondence between them have been established registration is obtained through a parametric transformation that aligns the retained local structures. Such methods exhibit low registration complexity once features have been recovered, an important strength. On the other hand their performance heavily depends on the feature extraction that can be viewed as an important limitation.

Global and local similarity measures between the Digitally Reconstructed Radiographs (DRR) and the 2D images are the base of intensity-based methods. Simple criteria like linear correlation [5, 12] or correlation ratio [19] were considered to address such a problem. More advanced methods [14, 17, 22] require the generation of DRRs in an iterative optimization loop. In order to decrease complexity induced by the computation of DRRs in [26] partial DRR were considered, or DRRs have been pre-computated for different starting positions/orientations [20]. The similarity measure is critical for any registration algorithm performance [20]. Mutual information [23] is a prominent approach that was also considered in therapy [18]. Gradient descend methods are the most common approach to recover the registration parameters once the problem has been expressed with an energetic formulation. Nevertheless one can claim that these methods are subject to local minima and have a limited capture range.

To circumvent this limitation, in [21] a technique was proposed that starting from low-order estimates - valid in a limited region - does perform a progressive refinement where the region associated with it is expanded. This method can be qualified as hybrid between a gradient descent and simulated annealing, and showed good results for retinal images. Nevertheless, besides the limitation of having an initial model such a method presents certain limitations: (i) the initial model needs to be close enough to the minimum solution, (ii) the algorithm could not converge when the image features are dispatched into different geometrical clusters. One can address this limitation through a multiple hypothesis assumption that can overcome the case of converging to local minima. Such an approach could be implemented in an efficient fashion if a limited number of features is retained and use similarity measures that exhibit robust scoring of patient position proposals.

To this end, instead of registering the whole volume, we propose to register the vascular structures. To explore different hypothesis without prior models suggests the use of stochastic processes. Recent improvements in computer capabilities dramatically increased the popularity of Monte-Carlo methods, in particular Particle Filters for tracking problem. We propose here to use the Condensation form of sequential Monte Carlo sampling to estimate a cost function gradient, and find the global minimum.

The reminder of this paper is organized as follows: first, the 2D-3D registration problem is presented, along with a function that measures the fitness of any patient



Fig. 1. Contrast enhanced X-ray image of right hemisphere vessels

position/orientation proposal. Then, the Condensation framework is presented to direct the multiple hypothesis toward the most probable projection hypothesis. Finally, results are presented and compared with standard Nonlinear Least Squares Fitting methods [2].

2 2D-3D registration

2.1 Problem

2D-3D registration consists in finding the limited number of parameters that define the perspective projection from a given 3D volume to a 2D image (see [FIG. (1)]). A perspective projection from a 3D homogeneous point P to a 2D homogeneous point p is defined with matrix as

$$p = \mathbf{PCT}P,\tag{1}$$

where **T** is a 4×4 matrix of the pose relating the pre-operative coordinate frame to the iso-centric coordinate frame of intra-operative imaging device. **C** is a 4×4 matrix defining the transformation between the iso-centric coordinate frame and the coordinate frame centered at the x-ray imaging source, which also depends on gantry angles. **P** is a 3×4 projection matrix defining the projection cone related to the source-detector geometry. We assume **P** and **C** are known from a calibration step. **T** is the unknown pose that encodes the three translation and three rotation parameters. The problem thus consists of formulating different hypothesis for **T**, measuring the fitness of each pose hypothesis, and optimizing the best ones.

2.2 Pose fitness measure

Intensity based registration approaches require DRR generation, which is then compared with the x-ray or fluoro images at each step of the process. The main bottleneck for intensity based approaches is the speed. In [26], the authors mentioned several minutes for registering the whole intensity volume, most of the time spent on generating the DRR. For this application, we use the vascular structures as features for registration. Vascular structures are easy to segment in most of cases, sparse enough for the



Fig. 2. The projected vascular structure and the distance map associated with it

registration to be faster than intensity-based methods, but yet generally well distributed throughout the organs to capture potential misalignments. One obstacle here is to define a fast and robust measure that characterizes the fitness of the pose. The proposed method uses a prior segmentation of the vessels in the 3D volume of interest and the 2D image. From the 2D segmentation result, a distance map[8] is computed (see [FIG. (2)]). For a given pose matrix **T**, the measure of fitness is the sum of distances (i.e. D) to the 2D structure for each projected 3D point from the segmented vessel tree:

$$F(\mathbf{T}) = \int_{P \in vessel} D(\mathbf{PCT}P).$$
 (2)

3 Bayesian process and Condensation

3.1 Bayesian process

The Bayesian problem can be simply formulated as the computation of the present state x_t pdf of a system, based on observations from time 1 to time t $z_{1:t}$: $p(x_t|z_{1:t})$. Assuming that one has access to the prior pdf $p(x_{t-1}|z_{1:t-1})$, the posterior pdf $p(x_t|z_{1:t})$ is computed according to the Bayes rule:

$$p(x_t|z_{1:t}) = \frac{p(z_t|x_t)p(x_t|z_{1:t-1})}{p(z_t|z_{1:t-1})}$$

where the prior pdf is computed via the Chapman-Kolmogorov equation

$$p(x_t|z_{1:t-1}) = \int p(x_t|x_{t-1})p(x_{t-1}|z_{1:t-1})dx_{t-1},$$

and

$$p(z_t|z_{1:t-1}) = \int p(z_t|x_t) p(x_t|z_{1:t-1}) dx_t$$

The recursive computation of the prior and the posterior pdf leads to the exact computation of the posterior density. Nevertheless, in practical cases, it is impossible to compute exactly the posterior pdf $p(x_t|z_{1:t})$, which must be approximated. This approximation is performed using Condensation [SEC. (3.2)].



Fig. 3. *The resampling process: a random selection chooses the samples with the highest weights where a local perturbation is applied.*

3.2 Sequential Monte Carlo and Condensation

Condensation [6, 11] (Conditional Density Propagation) is a sequential Monte-Carlo technique that is used to estimate the Bayesian posterior probability density function (pdf) with a set of samples [9, 24]. A prior set of particles (hypothesis) is used to estimate the probability of different situations (posterior pdf), given the current observation. In terms of a mathematical formulation, such a method approximates the posterior pdf by M random measures $\{x_t^m, m = 1..M\}$ associated to M weights $\{w_t^m, m = 1..M\}$, such that

$$p(x_t|z_{1:t}) \approx \sum_{m=1}^M w_t^m \delta(x_t - x_t^m).$$

where each weight w_t^m reflects the importance of the sample x_t^m in the pdf, as shown in [FIG. (3)].

The samples x_t^m are drawn using the principle of *Importance Density* [10], of pdf $q(x_t|x_{1:t}^m, z_t)$, and it is shown that their weights w_t^m are updated according to

$$w_t^m \propto w_{t-1}^m \frac{p(z_t | x_t^m) p(x_t^m | x_{t-1}^m)}{q(x_t^m | x_{t-1}^m, z_t)}.$$
(3)

Once a set of samples has been drawn, $p(x_t^m | z_t)$ can be computed out of the observation z_t for each sample, and the estimation of the posteriori pdf can be sequentially updated.

Such a process will remove most of the particles and only the ones that express the data will present significant weights. Consequently the model will lose its ability to track significant changes on the pdf; therefore a resampling procedure has to be executed on a regular basis. Such a process will preserve as many samples as possible with respectful weights. One can find in the literature several resampling techniques. We chose the most prominent one, Sampling Importance Resampling [9], for its simplicity to implement, and because it allows more hypothesis with low probability to survive, compared to more selective techniques such as Stratified Resampling [7].

3.3 Sampling Importance Resampling

The Sampling Importance Resampling (SIR) algorithm [9] consists of choosing the prior density $p(x_t|x_{t-1})$ as importance density $q(x_t|x_{1:t}^m, z_t)$. This leads to the following condition, from [Eq. (3)]

$$w_t^m \propto w_{t-1}^m p(z_t | x_t^m). \tag{4}$$

The samples are updated by selecting $x_t^m \propto p(x_t | x_{t-1}^m)$, and perturbed according to a random noise vector.

The SIR algorithm is the most widely used resampling method because of its simplicity from the implementation point of view. Nevertheless, the SIR uses mostly the prior knowledge $p(x_t|x_{t-1})$, and does not take into account the most recent observations z_t . Such a strategy could lead to an overestimation of outliers. On the other hand, because SIR resampling is performed at each step, fewer samples are required, and thus the computational cost may be reduced with respect to other resampling algorithms.

Since the resampling is based on the prior $p(x_t|x_{t-1})$, and not $p(x_t|x_{t-1}, z_t)$, it does not take into account the most recent observation; the resampling is suboptimal. Nevertheless, one can notice the process is stationary (the statistics of x_t do not vary with time). Therefore, $p(x_t|x_{t-1})$ can be considered optimal. Further research will investigate the use of Nonlinear Gradient Descent during the resampling step to drive the particles toward the region of interest.

It is important to note that the statistics of x_t (the projection parameters) do not change in time ; the process is stationary. Therefore, if the posterior pdf estimation is put aside, such a Particle Filter is nearly equivalent to some kind of Genetic Algorithm³. Nevertheless, if the observation z_t changes in time (e.g. registration of a 3D pre-operative volume with a sequence of fluoro images) and if the registration at one time-step constitutes a prior for the next time step (in other words, if registration for one portal image helps registering the next image), Condensation is exploited to its full extent. This will be explored in further studies.

4 Results and Discussion

4.1 Condensation performs better than random search

First, experiments were conducted to compare the method presented in this paper with a purely random search, and the results proved that Condensation used with x particles during z time steps reach a better registration than $x \times z$ random trials (in the experiments, x=64 and z=100).

4.2 Condensation performs better than Levenberg-Marquardt gradient descent

Second, experiments were conducted to compare Condensation performance (with respect to the measure presented in [SEC. (2.2)]) with classic nonlinear least square

³ although Genetic Algorithm cannot be used in this case, since the parameters are dependent



Fig. 4. Comparison of Condensation (blue) and Levenberg-Marquardt (red) performances when gaussian noise is introduced in the portal image

methods to find the minimum of a nonlinear function: Levenberg-Marquardt[2] and Gauss-Newton algorithms. Both Levenberg-Marquardt and Gauss-Newton are highly dependent on initialization, and never led to better results than Condensation (over 100 experiments were made with synthetic portal images from real pre-operative volumes, and random patient poses).

The perspective projection may not be perfect, and for optimal parameters, the subtraction of the two registered images may not be exactly null in real cases. For that matter, white noise has been added to the portal image to test the sensibility of the two algorithms, Condensation and Gradient Descent. The results are presented in [FIG. (4)] and [FIG. (7].

Tests have been performed about the method sensitivity to segmentation error, and the conclusions are presented in [FIG. (5)]. Whereas the Gradient Descent performances decrease as the segmentation error increases (in Hounsfield units), the Condensation results do not vary. As the error level increases, the global minimum's basin of attraction (for Gradient Descent) diminishes; consequently, the probability for the Gradient Descent to be correctly initialized diminishes. Since the particles are uniformly initialized in any case, the results are independent of the segmentation error.

For a similar reason, Condensation is independent of the capture range, while any Gauss-Newton / Gradient Descent method inherently depends on the global minimum's basin of attraction width. Furthermore, when features are missing, local minima are created, which are likely to attract the Gradient Descent method. Particle Filters still converge toward the global minimum (see [FIG. (6)]).

4.3 Further investigation

Condensation can be combined with Gradient Descent, for a more efficient resampling. During the resampling stage, the particles with the most significant weights are selected, and moved along the steepest direction.

Further investigations will also focus on observations that change in time, issues that are naturally handled by Bayesian processes. For a sequence of X-ray images, the



Fig. 5. Comparison of Condensation (blue) and Levenberg-Marquardt (red) performances when segmentation error is introduced

Condensation can estimate the parameters pdf at a given time, and use this estimation to actualize the pdf at at the next time step. This application is particularly relevant for features that may or may not be present at time t. Several local minimas can be detected using Particle Filter at time t, and observation at time t+1 may solve the ambiguity.

Last but not least, biplanar acquisition can be exploited to resolve ambiguities and local minimas.

In conclusion, the solution presented in this paper is both computationally light compared to intensity-based methods, and more robust than gradient descent algorithm applied on the same feature-based framework. With a limited number of particles (64 in our experiments), the computational cost (of the order of one minute, using non optimized Matlab code) gives reasonable hopes for real-time applications in the future.





Fig. 6. Condensation converges toward global minimum with missing features



Fig. 7. (*L*) Comparison between Condensation and Levenberg-Marquardt method performance. (*R*) Registered vascular structure with 2D projection simulated from original CT data

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