Inverse consistency error in the registration of prone and supine images in CT colonography

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Abstract. Robust registration between prone and supine data acquisitions for CT colonography is pivotal for medical interpretation but a challenging problem. One measure when evaluating non-rigid registration algorithms over the whole of the deformation field is the inverse consistency error, which suggests improved registration quality when the inverse deformation is consistent with the forward deformation. We show that using computed landmark displacements to initialise an intensity based registration reduces the inverse consistency error when using a state-of-the-art non-rigid b-spline registration method. This method aligns prone and supine 2D images derived from CT colonography acquisitions in a cylindrical domain. Furthermore, we demonstrate that using the same initialisation also improves registration accuracy for a set of manually identified reference points in cases exhibiting local luminal collapse.

Keywords: CT colonography, image registration, computer aided diagnosis and interventions

1 Introduction

Recently, Roth et al. [1] presented a method for establishing spatial correspondence between prone and supine colonic surfaces derived from computed tomographic (CT) colonography (CTC) data. This method involves the conformal mapping of both endoluminal surfaces derived from colon segmentations to cylindrical 2D domains, in order to simplify this challenging 3D registration problem. This is followed by a non-rigid cylindrical registration based on the well-accepted b-spline registration method [2, 3]. The similarity metric used to drive the cylindrical registration is the sum-of-squared differences (SSD) of the shape index (SI). Shape index [4] has also been used for detection of colonic polyps by computer-aided detection (CAD) methods also applied to CT colonography data [5]. The SI values are computed on the original surface meshes which describe the endoluminal colon surface with the patient in the prone and supine positions. Regions of possible local colonic collapse can be ignored during computation of the similarity measure when performing this cylindrical registration. This is important since luminal collapse is commonly encountered during clinical interpretation.

The registration method promises good accuracy in regions where the colon is well-distended in both orientations and when no segmentation errors are present. The reported mean (± std. dev.) registration error of 13 polyps was 5.7 (±3.4) mm when tested in 13 validation cases. However, the method might be less accurate if marked differences in distension or segmentation between prone and supine acquisitions are encountered, since this can precipitate marked dissimilarities in derived surface features: similar feature patterns for driving the registration are required to align both surfaces accurately.

*** et al. [6] show that landmark features (e.g. haustral folds) matched robustly between prone and supine acquisitions can further improve algorithm accuracy by providing an initialisation for the cylindrical registration along the length of the colon. Registration accuracy improved significantly from 9.7 (± 8.7) mm to 7.7 (± 7.1) mm in cases exhibiting local luminal collapse. The registration error was unchanged at 6.6 mm for 8 cases where the colon was already adequately distended.

The present paper aims to further investigate the effect of this initialisation on the registration, via evaluation of the inverse consistency error (ICE). The ICE was proposed by Christensen et al. [7] as an important criterion for evaluation of non-rigid registration methods.

2 Inverse consistency error

The cylindrical registration can be computed in two directions: prone to supine and supine to prone. We arbitrarily denote the prone to supine direction as the forward transformation T_{ps}, e.g. prone as source and supine as target image. Supine as source and prone as target is denoted as the inverse (supine to prone) transformation T_{sp}. The standard b-spline registration method is not inverse consistent, with the result that registration can result in different solutions depending on the transformation direction; i.e. prone to supine or supine to prone. The inverse consistency error ICE measures this inconsistency as follows [8]: any point p on the prone surface S_p can be transformed to the supine surface S_s using the forward transformation T_{ps}. The inverse transformation T_{sp} is then applied to map the transformed point back to p' on S_p. The Euclidean distance $\|\cdot\|$ between point p and p' in 3D space gives the value of ICE for any point p. This principle is illustrated in Fig. 1 for a point p in the transverse colon and can be formulated as

$$ICE = \|p' - p\| = \|T_{sp}\left(T_{ps}\left(p\right)\right) - p\| \,. \tag{1}$$

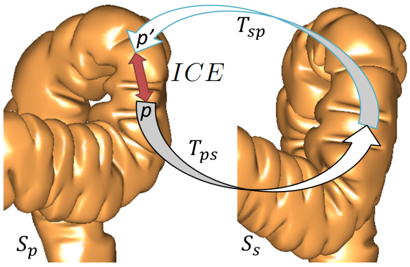

Fig. 1. Computing the inverse consistency error (ICE).

3 Evaluation of inverse consistency

3.1 Data

For the following experiments, we used anonymised CTC data acquired during normal clinical practice and following generally-accepted recommendations for CTC data acquisition [9]. These data consist of a total of 13 validation cases of which 5 exhibited local luminal collapse in at least one patient orientation. A radiologist (experienced in over 400 validated colonography studies) manually identified haustral folds of confident correspondence. This was achieved using cylindrical image representations and virtual 3D fly-through renderings for navigation through the prone and supine acquisitions. This procedure resulted in a total of 1175 pairs of corresponding landmarks with an average of 90 pairs of haustral folds per case.

3.2 Inverse consistency without feature initialisation

Accuracy of registration can only be evaluated where corresponding features have been manually identified. This is only feasible when there are easily identifiable corresponding features (e.g. polyps) in both acquisitions (i.e. where the registration is more likely to give a good result). In contrast, the ICE can be calculated anywhere on the cylindrical representations and does not require manually identified landmarks, thus simultaneously eliminating any error due to landmark mismatching.

The ICE values can vary for different regions of the images. Large ICE values often occur where the surface features in the two acquisitions appear very different, since the registration algorithm is unable to align the different features successfully. Figure 2 illustrates the ICE computed for each pixel of the cylindrical images and mapped back to the endoluminal colon surface in Fig. 3. The total mean ICE for all 13 validation patients is 3.7 mm. The mean ICE is slightly higher in the 5 collapsed cases; 4.9 mm as opposed to the mean ICE of 3.0 mm for the 8 well insufflated cases.

We propose that areas of high ICE precipitate more uncertainty in both images regarding which features need to be aligned with which. Therefore, registration does not necessarily converge towards the same solution in forward and inverse directions. However, a registration result with low ICE does not necessarily suggest good correspondence between two images [7]; further evaluation of registration accuracy is necessary. The manual selected fold correspondences can be used to establish a fold registration error (FRE) which measures misalignment of reference points in 3D after cylindrical non-rigid registration as an index of accuracy, resulting in a mean ($\pm$ std. dev.) FRE of 7.7 ($\pm$7.4) mm for all 13 cases. The 5 cases exhibiting local colonic collapse have a higher FRE : 9.7 ($\pm$8.7) mm compared to 6.6 ($\pm$6.3) mm for the 8 well insufflated cases.

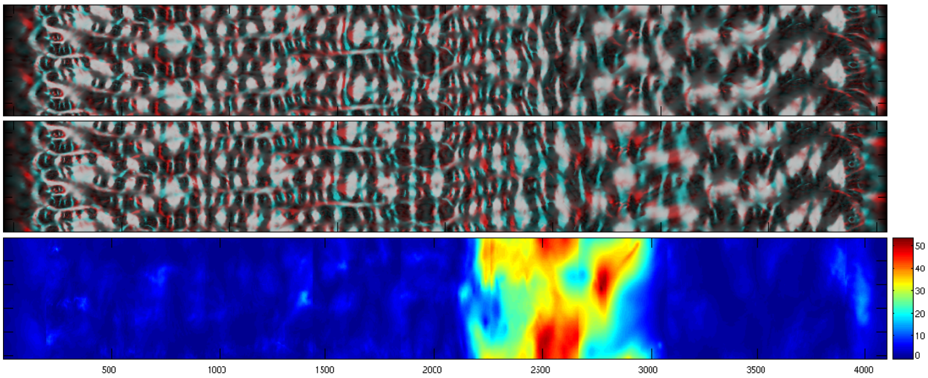

Fig. 2. Difference between forward (top) and inverse (middle) registrations for patient 4. The registration results are shown using a false colour scheme which displays source features as blue and target features as red. After non-rigid alignment, overlapping features are displayed in grey. The forward (top) and inverse (middle) registrations show areas of inconsistency, especially around 2500 pixels in x-direction (along the colon). This is reflected in the ICE values in these areas (bottom).

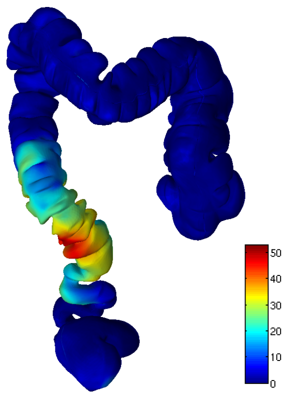

Fig. 3. ICE values for patient 4 mapped onto the colon surface.

3.3 Inverse consistency after feature initialisation

*** et al. [6] show that an initialisation of the registration method using robustly matched features (e.g. haustral folds) can improve the registration accuracy. Using a good initialisation can roughly align the correct folds of the cylindrical images leading to convergence to the correct solution in the subsequent b-spline registration. A significant improvement from 9.7 (± 8.7) mm to 7.7 (± 7.1) mm was reported in the cases where the dissimilarity of features is higher (e.g. the 5 cases exhibiting local colonic collapses) while it stays unchanged at 6.6 mm in 8 well-distended cases.

This improvement in registration accuracy suggests the method is more robust when initialisation is good. Increased accuracy is also reflected in the ICE metric. Figure 4 shows the reduction of an area of high ICE after initialisation for patient 4. The mean ICE for this patient is reduced from 7.6 mm to 2.2 mm. Another example is shown in Fig. 5 and confirms this assumption for patient 12 in which a short section of colon is collapsed. The mean ICE for this patient is reduced from 8.2 mm to 3.9 mm. The total mean ICE for all 13 validation patients is reduced from 3.7 mm to 2.6 mm. Table 1 lists the mean FRE and mean ICE before and after using a feature-based initialisation for each patient. In all but two cases (patient 6 and 13) a reduction of mean ICE can be observed after feature-based initialisation. Here, the ICE was low before initialisation and the increase of the ICE is negligible (0.2 mm and 0.1 mm respectively).

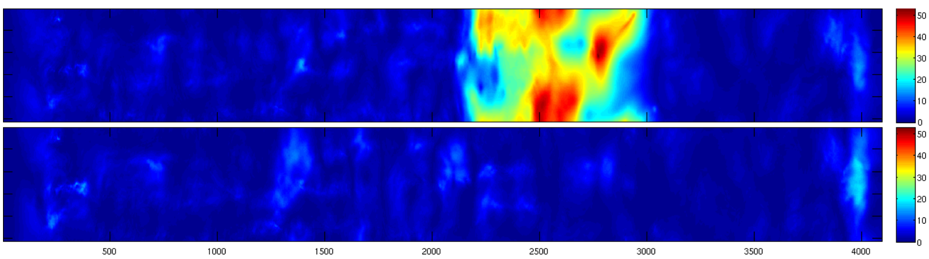

Fig. 4. The inverse difference metric (ICE) before (top) and after (bottom) initialisation using feature correspondences for patient 4.

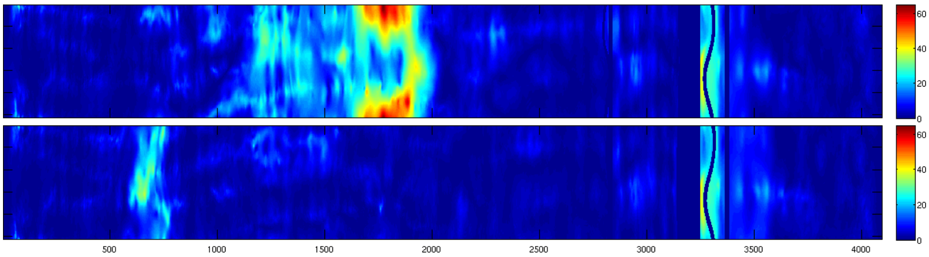

Fig. 5. The inverse difference metric (ICE) before (top) and after (bottom) initialisation using feature correspondences for a collapsed case (patient 12).

Table 1. The mean fold registration error $\overline{FRE}$ and mean inverse consistency error ($\overline{ICE}$) in mm for 13 patients used for validation before ($_1$) and after ($_2$) using a feature-based initialisation. The locations of where the colon is collapsed are given (DC: descending colon, SC: sigmod colon).

Patient	**Collapse in prone**	**Collapse in supine**	$\overline{FRE_1}$ [mm]	$\overline{FRE_2}$ [mm]	$\overline{ICE_1}$ [mm]	$\overline{ICE_2}$ [mm]
1	none	none	11.5	11.5	2.9	2.6
2	none	none	8.6	7.2	3.4	2.6
3	none	none	5.3	5.5	2.0	1.9
4	none	none	5.7	5.7	7.6	2.2
5	none	none	5.5	5.8	2.1	2.0
6	none	none	5.2	5.5	1.7	1.9
7	none	none	5.8	6.1	2.1	2.0
8	none	none	6.7	6.9	2.3	2.3
9	none	1 x DC	9.6	9.1	4.1	2.3
10	none	1 x SC	7.8	7.8	5.6	3.4
11	1 x DC	1 x DC	6.5	5.8	3.3	3.2
12	3 x (DC, SC)	none	13.5	8.7	8.2	3.9
13	1 x DC	1 x DC	12.2	7.9	2.9	3.0
Total [mm]			7.7	7.0	3.7	2.6

4 Conclusion

We show that a robust initialisation can improve the inverse consistency of the cylindrical b-spline registration method. While improved inverse consistency alone does not guarantee good correspondence, concomitant improvement in registration accuracy suggests that registration is more robust when using a feature-based initialisation.

Further improvement might be achieved by implementing an inverse-consistent non-rigid registration method. This might help optimise registration in cases where false local minima in the similarity function that is being optimised are present. Information from both forward and inverse direction may enforce convergence towards the correct solution.

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