Registration of Temporally Separated CT Colonography Cases

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Abstract. Robust registration between prone and supine data acquisitions for CT colonography (CTC) is a useful tool for assessing clinically significant changes but a challenging problem. This is especially the case for polyp follow-up when scans are temporally separated. We investigated the ability of automatic registration to align CTC cases, acquired several months apart. 26 initial and follow-up cases were investigated and registration measured using the locations of 35 polyps in all available scans. Robust non-rigid feature-based initialization allowed registration of prone and supine CTC scans from patient cases not only acquired on the same day but also when acquired several months apart. A mean registration error of 17.4 (std. dev. 12.1) mm (median 14.9 mm, range 1.7 to 49.7 mm) was achieved when transforming polyp locations between longitudinal scans. The level of accuracy achieved was similar to previous studies that aligned CTC images acquired at the same sitting. Automatic registration of follow-up CTC investigations could be a useful adjunct for radiologists interpreting CTC for surveillance of colonic polyps.

Keywords: Abdominal imaging, CT colonography, follow-up investigations, registration, oncology applications, computed tomography, computer-aided diagnosis.

1 Introduction

Follow-up CT colonography (CTC) scans are necessary when a polyp detected on initial CTC is relatively small and so left in-situ. This is done when the risk of resection during subsequent optical colonoscopy (OC) outweighs the risk of leaving the polyp in-situ and monitoring its growth. Polyp growth, if any, is monitored by sequential CTC, taken months or years later [6]. Clearly, it is essential that the radiologist can identify the polyp under surveillance in both the initial prone/supine and the follow-up prone/supine data sets. Manual matching

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of polyps across longitudinal CTCs can be even more challenging and time-consuming than manual matching between prone and supine scans taken on the same day.

This study investigates the ability of a recently reported registration method [8] to temporally align separated CTC cases, acquired several months apart. No other study has investigated registration accuracy for methods that establish full surface correspondence between follow-up CTC examinations.

A polyp observed over several months is shown in Fig. 1 in coronal CTC views and in Fig. 2 using virtual fly-through renderings of the endoluminal surfaces.

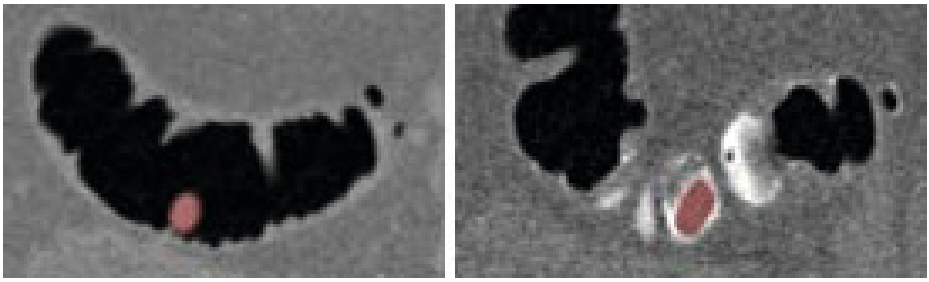

Fig. 1. Coronal views of a polyp in prone position (left) and prone position scanned 43 months later (right), highlighted using manual segmentation. The same polyp on the right is now covered by tagged fluids.

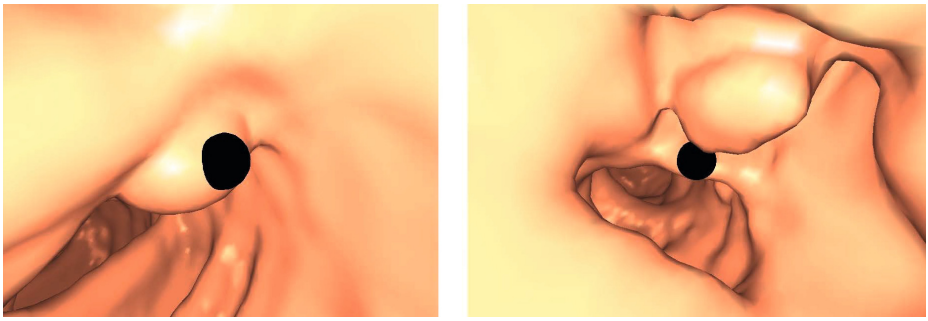

Fig. 2. Virtual fly-through renderings of a polyp in prone position (left) and prone position scanned 43 months later (right), after 'digital cleansing' of the tagged fluids. The polyps has now grown to about 11 mm in size. The black dot indicates corresponding locations using the registration result of the method described in [8].

2 Methods

2.1 Evaluation Data

Ethical approval and patient consent were obtained. All cases were selected from patients with two or more CTC investigations undertaken for the identification

and subsequent follow-up of colonic polyps. No attempt was made to select 'perfect cases' or exclude cases with poor distension from the study. These data had not been used previously for the development of the registration method. The evaluation sample consisted of 26 patients. From this group the radiologist (Emma Helbren) was able to identify 35 polyps present in both acquisitions in both the initial and subsequent CTC studies.

2.2 CT Colonography Registration

We build upon methods described previously [8,3] that establish full spatial correspondence between prone and supine endoluminal surfaces. The entire colon surfaces extracted from the initial and follow-up prone/supine CTC scans are mapped to cylinders utilizing a conformal mapping method based on Ricci flow [4]. The original surfaces' curvature information is preserved during this step. Initialization is provided by robust haustral fold matching between all four cylindrical views [3,2]. Full surface correspondence is then achieved using a non-rigid, cylindrical version of a B-spline registration method [5]. Registration is driven by local shape measurements, i.e. shape index (SI) computed on the colon surface. The sum-of-squared differences (SSD) of these SI measures are used to drive the cylindrical registration [8]. After convergence of the algorithm, any point on the 3D surface can be mapped between both CTC acquisitions. Figure 3 illustrates the principle of this registration method. Fig. 3 further illustrates how correspondence between all data sets of a follow-up study can be achieved. The follow-up prone (P) and supine (S) data sets acquired on the first or second occasion are superscripted with $_1$ or $_2$ respectively. The registration allows the transformation of any surface location between all temporally separated (longitudinal) and same-day acquisitions. One could transform points between all data sets by only computing three registrations: $P_1 \rightarrow P_2$, $S_1 \rightarrow P_1$ and $P_2 \rightarrow S_2$. Therefore,

$$S_1 \rightarrow S_2 = S_1 \rightarrow P_1 \circ P_1 \rightarrow P_2 \circ P_2 \rightarrow S_2. \quad (1)$$

However, $S_1 \rightarrow S_2$ is also computed in order to reduce any accumulated error that would occur when composing three transformations as in equation 1. Furthermore, the computation of $S_1 \rightarrow S_2$ allows the generation of a "consistency error" over the whole colonic surface. This would measure how similar the registration results are (e.g. resulting in the same anatomical correspondence) when transforming one point around the full transformation 'loop' ($S_1 \rightarrow S_2 \rightarrow P_2 \rightarrow P_1 \rightarrow S_1$). This might be a good indicator for judging the successfulness of the registration without referring to a reference standard at the polyps positions ('consistency registration error').

3 Results

Registration was performed on all 26 patients, and polyp locations in all subsequent acquisitions were estimated using the registration result. Table 1 lists the

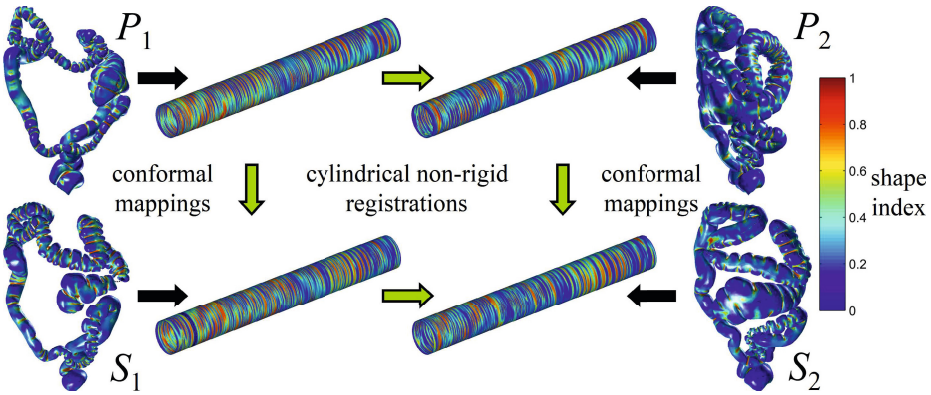

Fig. 3. Establishing correspondence between the follow-up prone (P) and supine (S) data sets acquired on the first or second occasion is superscripted with $_1$ or $_2$ respectively. Non-rigid registration of all colon surfaces is performed in cylindrical space after conformal mapping. The color coding indicates the local shape index (SI) measurements (see color scale) [8]. The different appearances of the 3D endoluminal surfaces between each scan illustrate the challenge of this registration task. A short section of endoluminal collapse (dotted line) is visible in the ascending colon of S_1. This translates to a 'ring' of missing data in the cylindrical representation of S_1 (left hand side of cylinder).

number of days separating each CTC study together with *longitudinal* and *consistency registration errors*. Using direct *longitudinal* transformations over time ($P_1 \rightarrow P_2$ and $S_1 \rightarrow S_2$), a mean longitudinal registration error of 17.4 (std. dev. 12.1) mm (median 14.9 mm, range 1.7 to 49.7 mm) was achieved. All errors measured using the Euclidean distance between transformed polyp location and the location of the targeted polyp.

Measuring the 'consistency error' around the loop (predicting polyp location through all acquisitions from the specified location on the initial supine scan alone) a mean Euclidean registration error of 26.9 (std. dev. 20.8) mm (median 28.0, range 0.9 to 84.5 mm) was achieved. For comparison, the mean registration errors between prone and supine CTCs acquired on the same day was 16.9 (std. dev. 17.6) mm (median 13.8 mm, range 1.5 to 83.9 mm). There is no significant difference between *longitudinal* and *same-day registration errors* ($p = 0.451$[1]).

Both, the *longitudinal errors* and *consistency errors* are not correlated to the number of days between the two CTC studies with $p = 0.105$ and $p = 0.055$ respectively[2].

[1] Related-Samples Wilcoxon Signed Rank Test, 1% significance level.
[2] Two-tailed Pearson Correlation, 1% significance level.

Table 1. Registrations of follow-up studies on external CTC data. The number of days separating each colonography study are listed together with *longitudinal*, *consistency* and *same-day registration errors* (averaged over the number of polyps per case).

Patient #	Days #	Polyps*	Longitudinal Error [mm]	Consistency Error [mm]	Same-day Error [mm]
1	1500	3	23.6	42.7	21.6
2	734	1	12.9	56.4	83.9
3	741	1	34.5	44.1	21.5
4	779	1	1.7	2.9	1.5
5	730	1	5.2	7.7	1.9
6	1524	2	30.1	30.0	15.3
7	779	1	49.7	84.5	50.3
8	1905	1	17.5	28.8	8.9
9	742	1	18.1	8.7	20.1
10	755	1	5.4	10.1	1.8
11	1886	1	9.3	11.5	9.3
12	865	1	8.5	9.5	13.8
13	757	1	15.3	29.0	13.8
14	369	2	13.3	28.2	22.3
15	1842	2	4.3	3.3	8.4
16	1498	1	8.0	31.0	24.5
17	747	2	21.4	15.3	3.3
18	371	3	33.7	33.7	26.6
19	755	2	8.9	18.6	14.7
20	375	1	6.3	0.9	4.1
21	405	1	17.1	27.8	21.5
22	753	1	29.0	53.3	4.7
23	749	1	38.2	49.0	4.2
24	266	1	14.5	18.9	6.0
25	777	1	16.7	51.0	27.4
26	735	1	9.1	2.6	8.3
Mean	**898**	**1.3**	**17.4**	**26.9**	**16.9**
Std. dev.	**480**	**0.6**	**12.1**	**20.8**	**17.6**
Minimum	**266**	**1.0**	**1.7**	**0.9**	**1.5**
Maximum	**1905**	**3.0**	**49.7**	**84.5**	**83.9**

*The total number of polyps is 35.

4 Discussion

The challenge of automatically registering the endoluminal colonic surface acquired by CTC separated by several months or years is potentially more challenging than registration between scans taken during the same CTC sitting. It was previously demonstrated that the proposed registration algorithm can accurately match prone and supine datasets acquired on the same day [8]. In the present study we explored a wider application – the follow-up of polyps on subsequent CTC taken months and years later.

Temporal separation increases the chance of dissimilarity between bowel preparation, distension, and overall quality of CTC when comparing data sets, which might make automatic registration between these data sets more difficult. Despite this challenge, the level of accuracy achieved by the registration algorithm was similar to studies registering between prone and supine on the same day; and these results agree with previous studies aligning CTC images obtained at same-day investigations using data that reflects clinical practice, i.e. including collapsed regions [9,7,1]. For example, Boone et al. reported a polyp registration error (mean $\pm$ standard deviation) of 19.9 mm $\pm$ 20.4 mm in 51 CTC patients [1] and Suh and Wyatt reported an average registration error of 30.1 mm for four polyps in four CTC cases [9]. Registration errors of less than 100 mm could already be clinically useful when relating between CTC scans. For example, Summers et al. found an accuracy of 100 mm useful in linking CTC findings to optical colonoscopy (100 mm corresponds to one mark on a standard colonoscope) [10].

We achieved accuracies showing registration to be robust for lesion matching over time. Therefore, automatic registration could be a useful adjunct for those interpreting CTC for the follow-up surveillance of colonic polyps. Registration is likely to be especially helpful for follow-up of small polyps that are likely harder to locate and to identify without assistance. The fact that there is no dependency of *longitudinal errors* and *consistency errors* on the length of time between the initial and follow-up CTC studies highlights that registration errors are more likely caused by differences in distension and bowel-preparation than by any anatomical changes that might occur over the months and years between studies.

Further applications of follow-up registration could include automatic detection of structural abnormalities on the endoluminal surface. One could use the similarity measure of the registration cost-function not only to achieve alignment between colonic surfaces but also to automatically identify areas of dissimilarity that might be caused by abnormalities arising between follow-up scans. Furthermore, the deformation fields resulting from the registration could be used to estimate the growth or change of anatomical structures such as polyps.

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References

1. Boone, D.J., Halligan, S., Roth, H.R., Hampshire, T.E., Helbren, E., Slabaugh, G.G., McQuillan, J., McClelland, J.R., Hu, M., Punwani, S., Taylor, S.A., Hawkes, D.J.: CT colonography: External clinical validation of an algorithm for computer-assisted prone and supine registration (2013)
2. Hampshire, T.E., Roth, H.R., Boone, D.J., Slabaugh, G., Halligan, S., Hawkes, D.J.: Prone to supine CT colonography registration using a landmark and intensity composite method. In: Yoshida, H., Hawkes, D., Vannier, M.W. (eds.) Abdominal Imaging 2012. LNCS, vol. 7601, pp. 1–9. Springer, Heidelberg (2012)

3. Hampshire, T., Roth, H.R., Helbren, E., Plumb, A., Boone, D., Slabaugh, G., Halligan, S., Hawkes, D.J.: Endoluminal surface registration for CT colonography using haustral fold matching. Medical Image Analysis (2013)
4. Jin, M., Kim, J., Luo, F., Gu, X.: Discrete surface Ricci flow. IEEE Trans. Vis. Comput. Graphics 14(5), 1030–1043 (2008)
5. Modat, M., Ridgway, G., Taylor, Z., Lehmann, M., Barnes, J., Hawkes, D., Fox, N., Ourselin, S.: Fast free-form deformation using graphics processing units. Comput. Meth. Prog. Bio. 98(3), 278–284 (2010)
6. Pickhardt, P., Hassan, C., Laghi, A., Zullo, A., Kim, D., Iafrate, F., Morini, S.: Small and diminutive polyps detected at screening CT colonography: a decision analysis for referral to colonoscopy. American Journal of Roentgenology 190(1), 136–144 (2008)
7. Roth, H.R., Boone, D.J., Halligan, S., Hampshire, T.E., McClelland, J.R., Hu, M., Punwani, S., Taylor, S., Hawkes, D.J.: External clinical validation of prone and supine CT colonography registration. In: Yoshida, H., Hawkes, D., Vannier, M.W. (eds.) Abdominal Imaging 2012. LNCS, vol. 7601, pp. 10–19. Springer, Heidelberg (2012)
8. Roth, H.R., McClelland, J.R., Boone, D.J., Modat, M., Cardoso, M.J., Hampshire, T.E., Hu, M., Punwani, S., Ourselin, S., Slabaugh, G.G., Halligan, S., Hawkes, D.J.: Registration of the endoluminal surfaces of the colon derived from prone and supine CT colonography. Medical Physics 38(6), 3077–3089 (2011), http://link.aip.org/link/?MPH/38/3077/1
9. Suh, J.W., Wyatt, C.L.: Registration of prone and supine colons in the presence of topological changes. In: SPIE Med. Imaging: Physiology, Function, and Structure from Medical Images, vol. 6916(1), p. 69160C (2008)
10. Summers, R., Swift, J., Dwyer, A., Choi, J., Pickhardt, P.: Normalized distance along the colon centerline: a method for correlating polyp location on CT colonography and optical colonoscopy. Am. J. Roentgenol. 193(5), 1296–1304 (2009)