

Active contour model

An ACM method based on improved level set²⁵ was implemented in this work for ACR. This method was originated from the Chan-Vese model,²⁶ a region-based level set algorithm in which the contour evolves by minimizing an energy functional. For a given image $I(x, y)$ in the domain Ω , let C represent the segmenting curve. The object of Chan-Vese algorithm is to minimize the following energy functional:

$$F(c_1, c_2, C) = \mu \cdot \text{Length}(C) + \lambda_1 \cdot \int_{\text{inside}(C)} |I(x, y) - c_1|^2 dx dy + \lambda_2 \cdot \int_{\text{outside}(C)} |I(x, y) - c_2|^2 dx dy \quad (1)$$

where c_1 and c_2 are the average intensities inside and outside C , μ , λ_1 and λ_2 are positive constant parameters that are usually determined arbitrarily. This energy minimization problem can be redefined in the level set formulation, which provides an easier and more flexible way to find out the solution.²⁶ In the level set formulation, the unknown segmenting curve C is replaced by the level set function $\phi(x, y)$: $\phi(x, y) > 0$ if the point (x, y) is inside C , $\phi(x, y) < 0$ if (x, y) is outside C , and $\phi(x, y) = 0$ if (x, y) is on C . The energy functional (1) can be reformulated in terms of $\phi(x, y)$:

$$F(c_1, c_2, \phi) = \mu \cdot \int_{\Omega} \delta(\phi(x, y)) |\nabla \phi(x, y)| dx dy + \lambda_1 \cdot \int_{\Omega} |I(x, y) - c_1|^2 H(\phi(x, y)) dx dy + \lambda_2 \cdot \int_{\Omega} |I(x, y) - c_2|^2 (1 - H(\phi(x, y))) dx dy \quad (2)$$

where $H(z)$ and $\delta(z)$ are the Heaviside function and Dirac delta function defined as follows:

$$H(z) = \begin{cases} 1 & \text{if } z \geq 0, \\ 0 & \text{if } z < 0, \end{cases} \quad \delta(z) = \frac{d}{dz} H(z). \quad (3)$$

In (2), $H(\phi(x, y))$ and $1 - H(\phi(x, y))$ are used to specify the interior and exterior regions of C , and $\delta(\phi(x, y))$ represents the narrow band around C . The parameter μ penalizes the total length of the curve C , where a larger value can lead to more smooth boundaries. Since this study was designed to accommodate complex abdominal organs, we set $\mu = 0.01$. The

weighting parameters λ_1 and λ_2 can affect the motion of the curve evolution,²⁷ and the optimal values of these two parameters usually need to be chosen specifically for different cases. In this study, instead of manually adjusting the parameters for a large amount of inaccurate contours, we followed the approach proposed by Hatamizadeh et al.²⁵ to generalize the scalar parameters λ_1 and λ_2 to 2D parameter maps using the probability maps obtained from the above DL models. The probability map $Y_{prob}(x, y)$, as the output of the CNN segmentation models, specifies the probability of each pixel belonging to the target organ. The 2D λ_1 and λ_2 maps are calculated using the following equations:

$$\lambda_1(x, y) = \exp\left(\frac{2-Y_{prob}(x,y)}{1+Y_{prob}(x,y)}\right), \quad \lambda_2(x, y) = \exp\left(\frac{1+Y_{prob}(x,y)}{2-Y_{prob}(x,y)}\right). \quad (4)$$

The probability map $Y_{prob}(x, y)$ is also converted to a signed distance map as the beginning $\phi(x, y)$ to initialize the level set in ACM. The contour is then evolved iteratively to minimize the energy functional and better match to the desired boundary. For the ACR application in this study, the number of iterations was set to be 600, as large changes were expected for the initial inaccurate contours. For more details on the ACM method, readers are referred to the relevant publications.²⁵⁻²⁷

Table S1. The contour correction performance of MR-SIM scans.

Organs	Subregions groups based on initial DSC and MDA	Percentage of subregions with improved DSC and improved MDA after ACR	Percentage of subregions with DSC ≥ 0.8 and MDA ≤ 3 mm after ACR	Mean DSC change after ACR	Mean MDA change (mm) after ACR	Mean sDSC change after ACR	Mean APL change (mm) after ACR
Small bowel	Major errors	679/844 (80%)	82/844 (10%)	0.32 → 0.56 *	7.72 → 6.11 *	0.28 → 0.43 *	89.04 → 72.16 *
	Minor errors	877/1612 (54%)	459/1612 (28%)	0.71 → 0.76 *	3.71 → 3.65 ($p=0.114$)	0.54 → 0.58 *	96.28 → 87.19 *
Large bowel	Major errors	450/574 (78%)	53/574 (9%)	0.33 → 0.56 *	8.71 → 7.06 *	0.29 → 0.44 *	79.25 → 63.09 *
	Minor errors	729/1162 (63%)	381/1162(33%)	0.72 → 0.78 *	3.81 → 3.66 ($p=0.001$)	0.56 → 0.62 *	71.25 → 58.88 *
Combined bowels	Major errors	551/622 (89%)	83/622 (13%)	0.33 → 0.60 *	6.57 → 4.62 *	0.31 → 0.50 *	89.90 → 68.46 *
	Minor errors	1269/1963 (65%)	911/1963 (46%)	0.72 → 0.80 *	3.09 → 2.81 *	0.59 → 0.66 *	95.45 → 86.22 *
Pancreas	Major errors	92/132 (70%)	6/132 (5%)	0.32 → 0.51 *	6.18 → 5.15 *	0.25 → 0.40 *	66.09 → 48.93 *
	Minor errors	267/573 (67%)	140/573 (24%)	0.70 → 0.72 *	3.28 → 3.58 *	0.49 → 0.52 *	59.56 → 46.92 *
Duodenum	Major errors	149/236 (63%)	7/236 (3%)	0.33 → 0.50 *	6.46 → 5.78 *	0.28 → 0.39 *	67.50 → 51.70 *
	Minor errors	245/613 (40%)	115/613 (19%)	0.69 → 0.70 ($p=0.008$)	3.31 → 3.79 *	0.52 → 0.52 ($p=0.901$)	52.64 → 43.59 *
Stomach	Major errors	37/80 (46%)	5/80 (6%)	0.46 → 0.57 *	10.10 → 10.11 ($p=0.969$)	0.29 → 0.34 ($p=0.014$)	81.58 → 70.89 ($p=0.001$)
	Minor errors	198/428 (46%)	86/428 (20%)	0.77 → 0.78 ($p=0.083$)	4.17 → 4.57 *	0.47 → 0.48 ($p=0.431$)	96.99 → 85.59 *

* indicates paired t-test p value <0.001 .

Table S2. The contour correction performance of MRL scans.

Organs	Subregions groups based on initial DSC and MDA	Percentage of subregions with improved DSC and improved MDA after ACR	Percentage of subregions with DSC ≥ 0.8 and MDA ≤ 3 mm after ACR	Mean DSC change after ACR	Mean MDA change (mm) after ACR	Mean sDSC change after ACR	Mean APL change (mm) after ACR
Small bowel	Major errors	277/374 (74%)	22/374 (6%)	0.35 \rightarrow 0.54 *	8.96 \rightarrow 7.12 *	0.28 \rightarrow 0.41 *	130.54 \rightarrow 110.46 *
	Minor errors	239/538 (44%)	75/538 (14%)	0.69 \rightarrow 0.71 *	4.53 \rightarrow 4.98 *	0.54 \rightarrow 0.54 ($p=0.422$)	103.55 \rightarrow 101.32 ($p=0.090$)
Large bowel	Major errors	204/324 (63%)	23/324 (7%)	0.36 \rightarrow 0.53 *	9.86 \rightarrow 9.23 ($p=0.002$)	0.30 \rightarrow 0.41 *	86.01 \rightarrow 69.10 *
	Minor errors	226/527 (43%)	119/527 (23%)	0.71 \rightarrow 0.73 ($p=0.030$)	4.23 \rightarrow 4.83 *	0.56 \rightarrow 0.56 ($p=0.827$)	68.04 \rightarrow 62.62 *
Combined bowels	Major errors	202/278 (73%)	22/278 (8%)	0.39 \rightarrow 0.57 *	8.03 \rightarrow 6.60 *	0.33 \rightarrow 0.46 *	111.66 \rightarrow 95.60 *
	Minor errors	437/962 (45%)	233/962 (24%)	0.72 \rightarrow 0.76 *	3.88 \rightarrow 4.29 *	0.57 \rightarrow 0.59 ($p=0.001$)	111.48 \rightarrow 112.39 ($p=0.513$)
Pancreas	Major errors	68/72 (94%)	17/72 (24%)	0.32 \rightarrow 0.64 *	8.15 \rightarrow 3.87 *	0.20 \rightarrow 0.51 *	96.02 \rightarrow 55.65 *
	Minor errors	149/194 (77%)	76/194 (39%)	0.68 \rightarrow 0.78 *	4.38 \rightarrow 3.34 *	0.42 \rightarrow 0.51 *	82.66 \rightarrow 62.35 *
Duodenum	Major errors	35/66 (53%)	2/66 (3%)	0.31 \rightarrow 0.47 *	7.64 \rightarrow 7.15 ($p=0.215$)	0.24 \rightarrow 0.30 ($p=0.012$)	63.23 \rightarrow 54.82 *
	Minor errors	50/195 (26%)	28/195 (14%)	0.70 \rightarrow 0.66 *	3.81 \rightarrow 5.18 *	0.55 \rightarrow 0.46 *	47.14 \rightarrow 48.47 ($p=0.363$)
Stomach	Major errors	17/31 (55%)	1/31 (3%)	0.40 \rightarrow 0.55 *	9.62 \rightarrow 8.92 ($p=0.280$)	0.21 \rightarrow 0.28 ($p=0.030$)	93.73 \rightarrow 78.05 *
	Minor errors	36/173 (21%)	13/173 (8%)	0.78 \rightarrow 0.76 *	4.31 \rightarrow 5.72 *	0.45 \rightarrow 0.38 *	96.02 \rightarrow 102.30 ($p=0.006$)

* indicates paired t-test p value <0.001 .

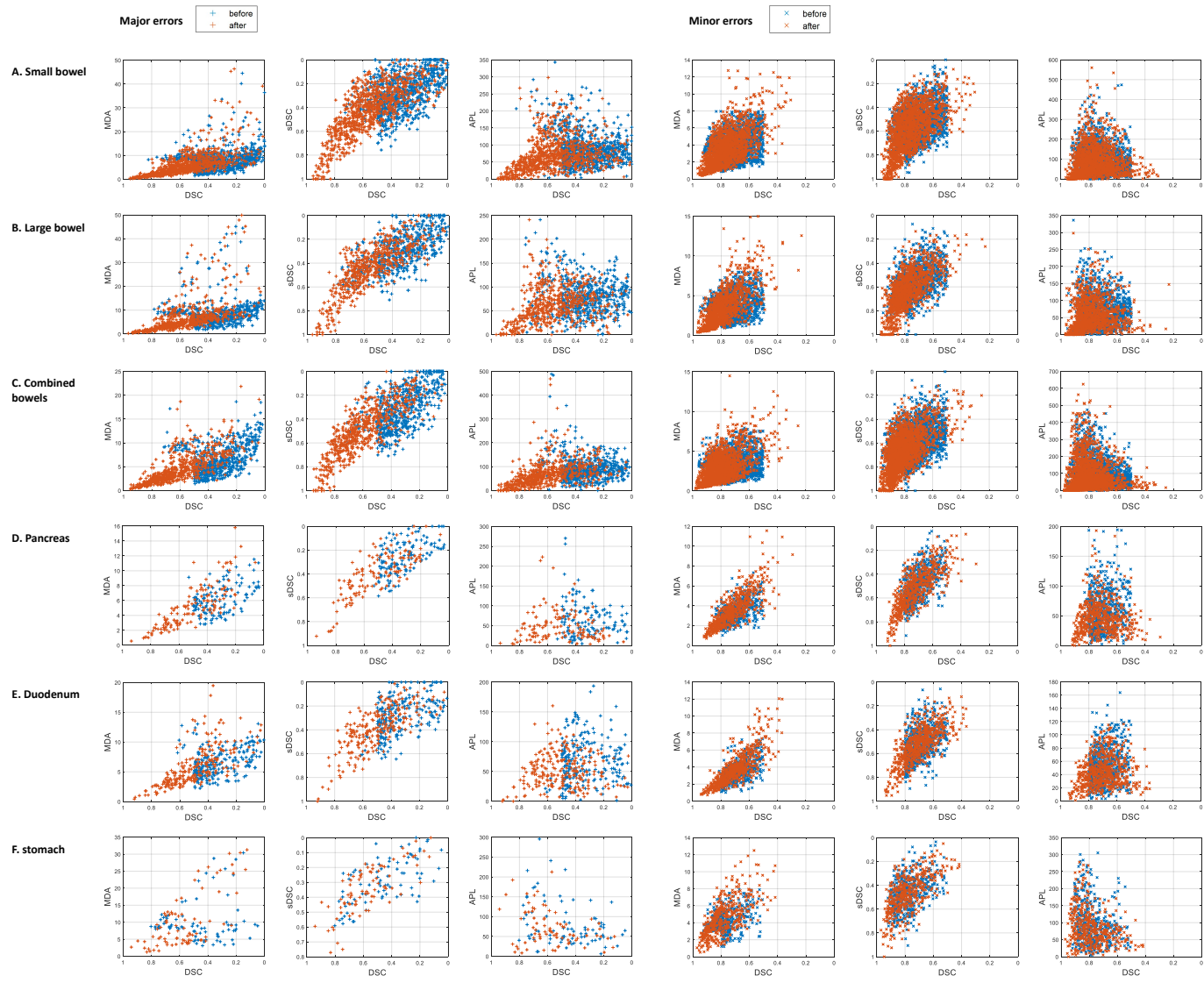


Figure S1. Changes of the contour accuracy metrics for MR-SIM data before and after the ACR process.

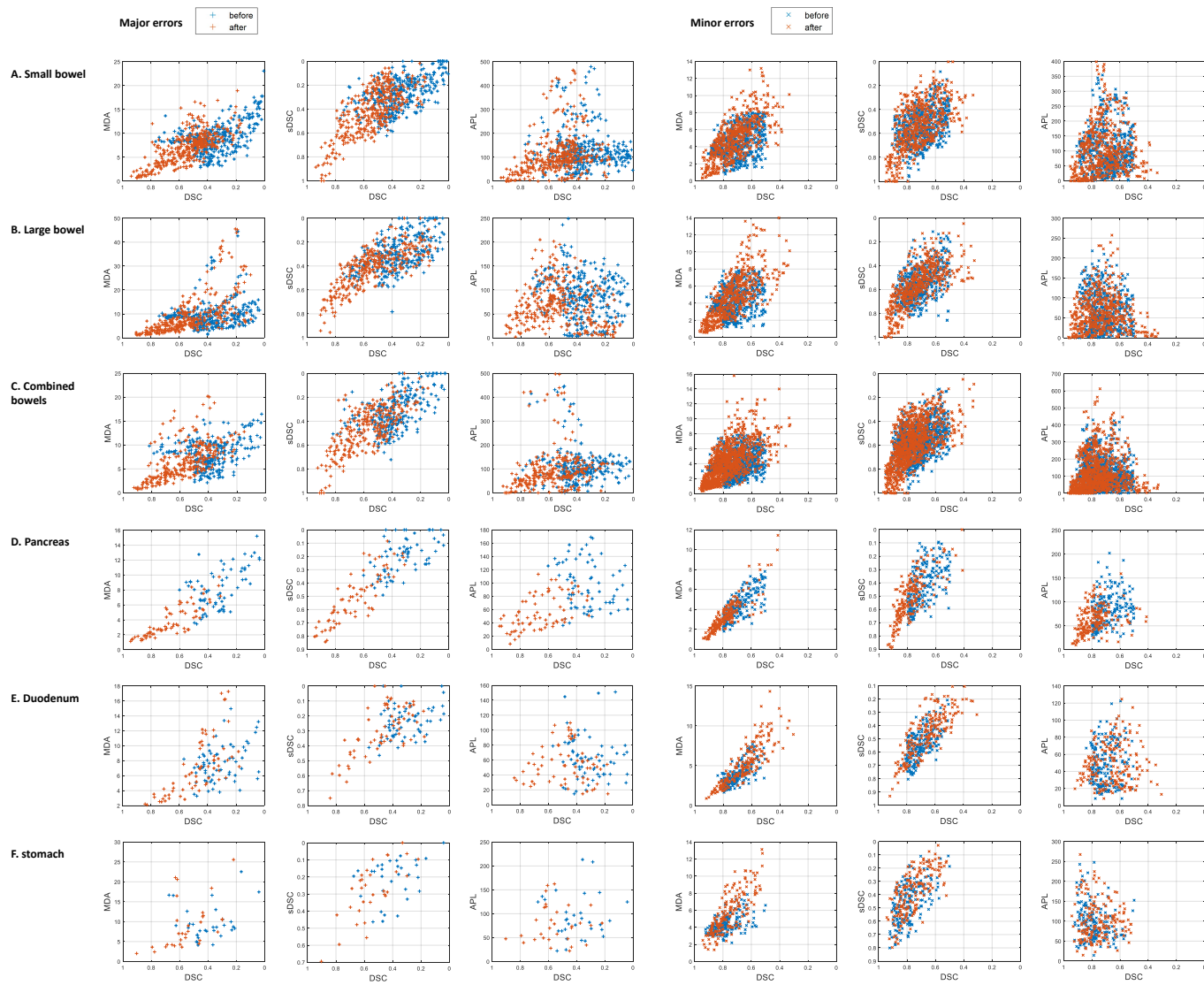


Figure S2. Changes of the contour accuracy metrics for MRL data before and after the ACR process.