Supplementary Material for
Residual Aligner-based Network (RAN): Motion-Aware Structure for Coarse-to-fine Deformable Image Registration

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1 Math

The denotations of symbols in this supplementary material are shown in the Tab. 1, which are the same as in the manuscript.

1.1 Proof of Regional Dependency

The pooling mapping $\mathcal{P}$ from the original full-resolution image's coordinate $\boldsymbol{x}$ to the k_{th} feature map with pool size p_k is denoted as:

$$\mathcal{P}(\boldsymbol{x}; p_k) := \lfloor \boldsymbol{x}/p_k \rfloor, \tag{1}$$

which thus satisfy:

$$\exists\, (\boldsymbol{x}, \boldsymbol{y}) \in \{(\boldsymbol{x}, \boldsymbol{y}) | \|\boldsymbol{x} - \boldsymbol{y}\|_\infty < p_k\},\ \mathcal{P}(\boldsymbol{x}; p_k) = \mathcal{P}(\boldsymbol{y}; p_k) \tag{2}$$

As stated in the manuscript, coarse-to-fine registration implies $\forall k \in [1, K) \cap \mathbb{Z},\ p_k \geq p_{k+1}, s_k \geq s_{k+1}$, and thus:

$$\forall\, (\boldsymbol{x}, \boldsymbol{y}) \in \{(\boldsymbol{x}, \boldsymbol{y}) | \|\boldsymbol{x} - \boldsymbol{y}\|_\infty \geq p_{k'}\},\ \mathcal{P}(\boldsymbol{x}; p_k) \neq \mathcal{P}(\boldsymbol{y}; p_k), k \geq k' \tag{3}$$

because the DDF predicted by k^{th} RA module has the same resolution as feature map:

$$\begin{cases} \phi_k[\boldsymbol{x}] \equiv \phi_k[\boldsymbol{y}] \text{ if } \mathcal{P}(\boldsymbol{x}; p_k) = \mathcal{P}(\boldsymbol{y}; p_k) \\ \phi_k[\boldsymbol{x}] \not\equiv \phi_k[\boldsymbol{y}] \text{ if } \mathcal{P}(\boldsymbol{x}; p_k) \neq \mathcal{P}(\boldsymbol{y}; p_k) \end{cases} \tag{4}$$

so that:

$$\begin{cases} \exists\, (\boldsymbol{x}, \boldsymbol{y}) \in \{(\boldsymbol{x}, \boldsymbol{y}) | \|\boldsymbol{x} - \boldsymbol{y}\|_\infty < p_k\}, & \phi_k[\boldsymbol{x}] \equiv \phi_k[\boldsymbol{y}] \\ \forall\, (\boldsymbol{x}, \boldsymbol{y}, k) \in \{(\boldsymbol{x}, \boldsymbol{y}, k) | \|\boldsymbol{x} - \boldsymbol{y}\|_\infty \geq p_{k'}, k \geq k'\}, & \phi_k[\boldsymbol{x}] \not\equiv \phi_k[\boldsymbol{y}] \end{cases} \tag{5}$$

Table 1. Notation of symbols in the manuscript and the supplementary material part.

Symbol	Description
$\odot$	element-wise product
$\otimes$	tensor product
$\mid$	tensor concatenate at feature channel dimension
$\mathcal{D}$	dissimilarity metric between images
$\mathcal{L}$	loss function
$\mathcal{S}$	smoothness regularization
$\mathcal{P}$	pooling mapping from the original full-resolution image's coordinate
$\mathcal{R}$	a trainable network mapping from images/feature maps to a DDF
$\mathcal{A}$	a trainable network mapping from multiple DDFs to a refined DDF
$\mathcal{W}$	warping function from one image to another via a given DDF
$\mathcal{C}$	one/multi-layer convolution subnetwork
$\boldsymbol{I}^{\mathrm{s}}, \boldsymbol{I}^{\mathrm{t}}$	source & target images
$\boldsymbol{F}^{\mathrm{s}}, \boldsymbol{F}^{\mathrm{t}}$	feature maps extracted from source & target images
ϕ	dense displacement field
$\boldsymbol{x}, \boldsymbol{y}$	coordinates at image/ddf

The kth predicted DDF ϕ_k can be decomposed as:

$$\phi_k[\boldsymbol{x}] = \phi_k \circ \phi_{k-1}^{-1}[\boldsymbol{x}] + \phi_{k-1}[\boldsymbol{x} - \phi_k \circ \phi_{k-1}^{-1}[\boldsymbol{x}]] \tag{6}$$

where $\phi_k \circ \phi_{k-1}^{-1}$ is regressed by $\mathcal{R}_k$ and $\mathcal{T}_k$ in RA module as described in the manuscript. The difference between two displacements $\phi_k[x]$ and $\phi_k[y]$ can be written as:

$$
\begin{aligned}
&\Delta\phi_k(\boldsymbol{x}, \boldsymbol{y}) \\
&:= \phi_k[\boldsymbol{x}] - \phi_k[\boldsymbol{y}] \\
&= \phi_k \circ \phi_{k-1}^{-1} \circ \phi_{k-1}[\boldsymbol{x}] - \phi_k \circ \phi_{k-1}^{-1} \circ \phi_{k-1}[\boldsymbol{y}] \\
&= (\phi_k \circ \phi_{k-1}^{-1}[\boldsymbol{x}] + \phi_{k-1}[\boldsymbol{x} - (\phi_k \circ \phi_{k-1}^{-1}[\boldsymbol{x}])]) - (\phi_k \circ \phi_{k-1}^{-1}[\boldsymbol{y}] + \phi_{k-1}[\boldsymbol{y} - \phi_k \circ \phi_{k-1}^{-1}[\boldsymbol{y}]]) \\
&= \underbrace{\phi_k \circ \phi_{k-1}^{-1}[\boldsymbol{x}] - \phi_k \circ \phi_{k-1}^{-1}[\boldsymbol{y}]}_{\text{i}} + \underbrace{\phi_{k-1}[\boldsymbol{x} - \phi_k \circ \phi_{k-1}^{-1}[\boldsymbol{x}]] - \phi_{k-1}[\boldsymbol{y} - \phi_k \circ \phi_{k-1}^{-1}[\boldsymbol{y}]]}_{\text{ii}}
\end{aligned}
\tag{7}
$$

where the range of Eq. (7)(i) is limited by the kth RA module and Eq. (7)(ii) can be substituted with $\phi_{k-1}[\boldsymbol{x}'] - \phi_{k-1}[\boldsymbol{y}']$ by $\boldsymbol{x}' := \boldsymbol{x} - \phi_k \circ \phi_{k-1}^{-1}[\boldsymbol{x}], \boldsymbol{y}' := \boldsymbol{y} - \phi_k \circ \phi_{k-1}^{-1}[\boldsymbol{y}]$, where the iterative equation of Eq. (7) can be thus written as:

$$
\begin{cases}
\Delta\phi_k(\boldsymbol{x}^k, \boldsymbol{y}^k) - (\boldsymbol{x}^k - \boldsymbol{y}^k) = \Delta\phi_{k-1}(\boldsymbol{x}^{k-1}, \boldsymbol{y}^{k-1}) - (\boldsymbol{x}^{k-1} - \boldsymbol{y}^{k-1}) \\
\boldsymbol{x}^k - \phi_k \circ \phi_{k-1}^{-1}[\boldsymbol{x}^k] = \boldsymbol{x}^{k-1} \\
\boldsymbol{y}^k - \phi_k \circ \phi_{k-1}^{-1}[\boldsymbol{y}^k] = \boldsymbol{y}^{k-1}
\end{cases}
\tag{8}
$$

starting from $\Delta\phi_0(\boldsymbol{x}^0, \boldsymbol{y}^0) := 0 \ \forall \boldsymbol{x}^0, \boldsymbol{y}^0 \in \mathbb{Z}^d$. The analytic equation is derived as:

$$
\begin{cases}
\Delta\phi_k(\boldsymbol{x}^k, \boldsymbol{y}^k) = \Delta\phi_{k''-1}(\boldsymbol{x}^{k''-1}, \boldsymbol{y}^{k''-1}) + \sum_{k'=k''}^{k} \Delta\psi_{k'}(\boldsymbol{x}^{k'}, \boldsymbol{y}^{k'}) \\
\boldsymbol{x}^k - \boldsymbol{y}^k = (\boldsymbol{x}^{k''-1} - \boldsymbol{y}^{k''-1}) + \sum_{k'=k''}^{k} \Delta\psi_{k'}(\boldsymbol{x}^{k'}, \boldsymbol{y}^{k'}) \\
\Delta\psi_{k'}(\boldsymbol{x}^{k'}, \boldsymbol{y}^{k'}) := \phi_{k'} \circ \phi_{k'-1}^{-1}[\boldsymbol{x}^{k'}] - \phi_{k'} \circ \phi_{k'-1}^{-1}[\boldsymbol{y}^{k'}]
\end{cases}
\tag{9}
$$

Substitute Eq. (5) into Eq. (9), we can conclude that

$$\exists\,(\boldsymbol{x}^k,\boldsymbol{y}^k)\in\{(\boldsymbol{x},\boldsymbol{y})|\|\boldsymbol{x}-\boldsymbol{y}\|_\infty<p_{k''-1}+\sum_{k'=k''}^k\Delta\psi_{k'}(\boldsymbol{x}^{k'},\boldsymbol{y}^{k'})\},$$
$$\Delta\phi_k(\boldsymbol{x}^k,\boldsymbol{y}^k)=\sum_{k'=k''}^k\Delta\psi_{k'}(\boldsymbol{x}^{k'},\boldsymbol{y}^{k'});$$
$$\forall\,(\boldsymbol{x}^k,\boldsymbol{y}^k,k)\in\{(\boldsymbol{x},\boldsymbol{y},k)|\|\boldsymbol{x}-\boldsymbol{y}\|_\infty\geq p_{k''}+\sum_{k'=k''+1}^k\Delta\psi_{k'}(\boldsymbol{x}^{k'},\boldsymbol{y}^{k'})\},k\geq k''\},$$
$$\Delta\phi_k(\boldsymbol{x}^k,\boldsymbol{y}^k)\geq\sum_{k'=k''}^k\Delta\psi_{k'}(\boldsymbol{x}^{k'},\boldsymbol{y}^{k'});$$

(10)

with satisfying $\sup(\Delta\phi_k(\boldsymbol{x}^k,\boldsymbol{y}^k))=\sup(\|\phi_k[\boldsymbol{x}]-\phi_k[\boldsymbol{y}]\|_\infty)$, $\sup(\Delta\psi_k(\boldsymbol{x}^k,\boldsymbol{y}^k))=2a_k$, which thus prove Theorem 1.

2   Network Architecture

The network structure details of encoder, decoder and RA modules are respectively illustrated in Tab. 2, Tab. 3 and Tab. 4.

Table 2. Network of encoder.

layer(s)	kernel	dilation	channels	scale	in	out
conv,norm,act	3	1	1/8	1	$\boldsymbol{I}^{s,t}$	r1
conv,norm,act	3	1	8/8	1	r1	f1
conv,norm	3	3	8/8	1	f1	f1
act	-	-	8/8	1	f1+r1	s1
downsample	-	-	-	-	-	-
conv,norm,act	3	1	8/16	2	s1	r2
conv,norm,act	3	1	16/16	2	r2	f2
conv,norm	3	3	16/16	2	f2	f2
act	-	-	16/16	2	f2+r2	s2
downsample	-	-	-	-	-	-
conv,norm,act	3	1	16/16	4	s2	r3
conv,norm,act	3	1	16/16	4	r3	f3
conv,norm	3	3	16/16	4	f3	f3
act	-	-	16/16	4	f3+r3	s3
downsample	-	-	-	-	-	-
conv,norm,act	3	1	16/32	8	s3	r4
conv,norm,act	3	1	32/32	8	r4	f4
conv,norm	3	3	32/32	8	f4	f4
act	-	-	32/32	8	f4+r4	s4
downsample	-	-	-	-	-	-

3   Training Detail

For the experiments on inter-subject alignment of abdomen and lung CT, the models are first pre-trained for 100k iteration on synthetic DDF $\tilde{\phi}$ combining rigid spatial transformation with rotation angle $\beta\sim\mathcal{U}(-\pi/4,\pi/4)$ at an arbitrary axis and deformation

Table 3. Network structure of decoder for Residual Aligner Network (RAn_0,RAn_3,RAn_4,RAn_4^+) with varying channels (c_0=32,32,36,48; c_1=64,48,44,48; c_2=48,48,44,48; c_3=32,32,28,32, c_4=24,32,28,32), pooling scales and layer inputs.

layer(s)	ker	dila	chns	RAn_0 scale	in	RAn_3 scale	in	RAn_4 scale	in	RAn_4^+ scale	in	out
upsample				×		✓		✓		✓		
conv,norm,act	3	1	c_0/32	16	s4	2	s4,s3	1	s4,s3,s2	1	s4,s3,s2	r5
conv,norm,act	3	1	32/32	16	r5	2	r5	1	r5	1	r5	f5
conv,norm	3	3	32/32	16	f5	2	f5	1	f5	1	f5	f5
act	-	-	32/32	16	f5+r5	2	f5+r5	1	f5+r5	1	f5+r5	$F_0^{s/t}$
upsample				✓		×		×		×		
conv,norm,act	3	1	c_1/32	8	$F_0^{s/t}$|s4	2	$F_0^{s/t}$|s4	1	$F_0^{s/t}$|s4	1	$F_0^{s/t}$|s4	r6
conv,norm,act	3	1	32/32	8	r6	2	r6	1	r6	1	r6	f6
conv,norm	3	3	32/32	8	f6	2	f6	1	f6	1	f6	f6
act	-	-	32/32	8	f6+r6	2	f6+r6	1	f6+r6	1	f6+r6	$F_1^{s/t}$
upsample				✓		×		×		×		
conv,norm,act	3	1	c_2/16	4	$F_1^{s/t}$|s3	2	$F_1^{s/t}$|s3	1	$F_1^{s/t}$|s3	1	$F_1^{s/t}$|s3	r7
conv,norm,act	3	1	16/16	4	r7	2	r7	1	r7	1	r7	f7
conv,norm	3	3	16/16	4	f7	2	f7	1	f7	1	f7	f7
act	-	-	16/16	4	f7+r7	2	f7+r7	1	f7+r7	1	f7+r7	$F_2^{s/t}$
upsample				✓		×		×		×		
conv,norm,act	3	1	c_3/16	2	$F_2^{s/t}$|s2	2	$F_2^{s/t}$|s2	1	$F_2^{s/t}$|s2	1	$F_2^{s/t}$|s2	r8
conv,norm,act	3	1	16/16	2	r8	2	r8	1	r8	1	r8	f8
conv,norm	3	3	16/16	2	f8	2	f8	1	f8	1	f8	f8
act	-	-	16/16	2	f8+r8	2	f8+r8	1	f8+r8	1	f8+r8	$F_3^{s/t}$
upsample				✓		✓		×		×		
conv,norm,act	3	1	c_4/8	1	$F_3^{s/t}$|s1	1	$F_3^{s/t}$|s1	1	$F_3^{s/t}$|s1	1	$F_3^{s/t}$|s1	r9
conv,norm,act	3	1	8/8	1	r9	1	r9	1	r9	1	r9	f9
conv,norm	3	3	8/8	1	f9	1	f9	1	f9	1	f9	f9
act	-	-	8/8	1	f9+r9	1	f9+r9	1	f9+r9	1	f9+r9	s9
conv	1	1	8/d	1	s9	1	s9	1	s9	1	s9	$F_4^{s/t}$

synthesized by thin plate spline as well as gaussian deformation by 20 random seeds located uniformly randomized within the image domain. , with the loss function set as:

$$\mathcal{L}_{\text{syn}} = \sum \|\phi - \tilde{\phi}\|_2^2 + \lambda \sum \|\nabla \phi\|_2^2 \tag{11}$$

where λ denotes the weight of regularization.

4   More Results

To clearly show the performance detail of the previous relevant models compared with our RANs as well as the ablation studies on the nine organs: spleen (Fig. 1), right kidney (Fig. 2), left kidney (Fig. 3), esophagus (Fig. 4), liver (Fig. 5), aorta (Fig. 6), inferior vena cava (Fig. 7), portal splenic vein (Fig. 8), and pancreas (Fig. 9).
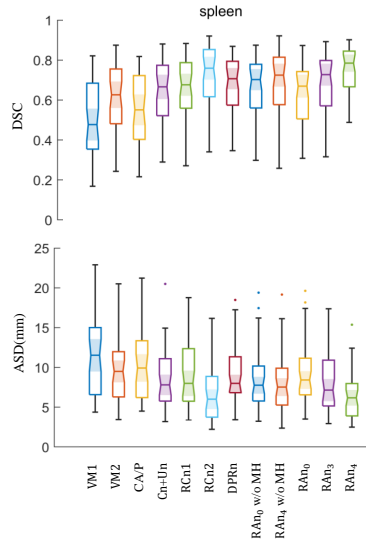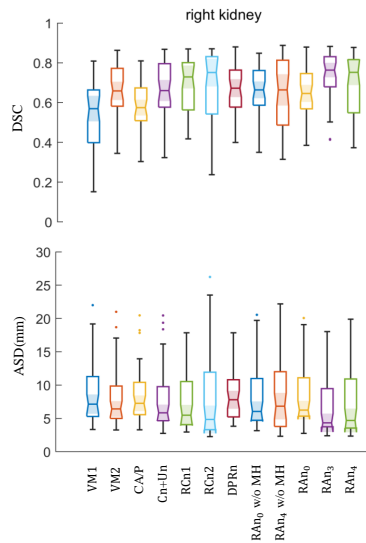
Fig. 1. Results on spleen.

Fig. 2. Results on right kidney.

Table 4. Network structure of Residual Aligner (RA) module for Residual Aligner Network ($RAn_0, RAn_3, RAn_4, RAn_4^+$) with varying scales and dilation rates.

| layer(s)	ker	chns	RAn$_0$ scale	dila	RAn$_3$ scale	dila	RAn$_4$ scale	dila	RAn$_4^+$ scale	dila	in	out
conv,act,conv,act	3	64/18/18	16	1	2	8	1	16	1	16	$F_0^s\vert F_0^t$	m0
conv,act,conv	3	18/27/md	16	1	2	1	1	1	1	1	m0	φ_0
conv,act,conv	3	18/18/m	16	1	2	1	1	1	1	1	m0	ϑ_0
conv,norm,act	3	18/1	16	1	2	1	1	1	1	1	ϑ_0	ϑ_0'
conv	1	m/m	16	0	2	0	1	0	1	0	ϑ_0	θ_0
reshape,conv	3	md/m/9	16	1	2	1	1	1	1	1	$\sigma(\theta_0)\odot\varphi_0$	df0
conv,reshape	3	9/1/d	16	1	2	1	1	1	1	1	$\vartheta_0'\odot$df0	ϕ_0
upsample			✓		×		×		×		ϕ_0,θ_0	ϕ_0,θ_0
conv,act,conv,act	3	64/18/18	8	1	2	4	1	8	1	8	$\phi_0(F_1^s)\vert F_1^t$	m1
conv,act,conv	3	18/27/md	8	1	2	1	1	1	1	1	m1	φ_1
conv,act,conv	3	18/18/m	8	1	2	1	1	1	1	1	m1	ϑ_1
conv,norm,act	3	18/1	8	1	2	1	1	1	1	1	ϑ_1,θ_0	ϑ_1',θ_0'
conv	1	$2m/m$	8	0	2	0	1	0	1	0	$\vartheta_1\vert\theta_0$	θ_1
reshape,conv	3	md/m/9	8	1	2	1	1	1	1	1	$\sigma(\theta_1)\odot\varphi_1$	df1
reshape,conv	3	md/m/9	8	1	2	1	1	1	1	1	$\sigma(\theta_1)\otimes\phi_0$	dp1
conv,reshape	3	18/1/d	8	1	2	1	1	1	1	1	$\vartheta_1'\odot$df1$\vert\theta_0'\odot$dp1	ϕ_1
upsample			✓		×		×		×		ϕ_1,θ_1	ϕ_1,θ_1
conv,act,conv,act	3	32/18/18	4	1	2	2	1	4	1	4	$\phi_1(F_2^s)\vert F_2^t$	m2
conv,act,conv	3	18/27/md	4	1	2	1	1	1	1	1	m2	φ_2
conv,act,conv	3	18/18/m	4	1	2	1	1	1	1	1	m2	ϑ_2
conv,norm,act	3	18/1	4	1	2	1	1	1	1	1	ϑ_2,θ_1	ϑ_2',θ_1'
conv	1	$2m/m$	4	0	2	0	1	0	1	0	$\vartheta_2\vert\theta_1$	θ_2
reshape,conv	3	md/m/9	4	1	2	1	1	1	1	1	$\sigma(\theta_2)\odot\varphi_2$	df2
reshape,conv	3	md/m/9	4	1	2	1	1	1	1	1	$\sigma(\theta_2)\otimes\phi_1$	dp2
conv,reshape	3	18/1/d	4	1	2	1	1	1	1	1	$\vartheta_2'\odot$df2$\vert\theta_1'\odot$dp2	ϕ_2
upsample			✓		×		×		×		ϕ_2,θ_2	ϕ_2,θ_2
conv,act,conv,act	3	32/18/18	2	1	2	1	1	2	1	2	$\phi_2(F_3^s)\vert F_3^t$	m3
conv,act,conv	3	18/27/md	2	1	2	1	1	1	1	1	m3	φ_3
conv,act,conv	3	18/18/m	2	1	2	1	1	1	1	1	m3	ϑ_3
conv,norm,act	3	18/1	2	1	2	1	1	1	1	1	ϑ_3,θ_2	ϑ_3',θ_2'
conv	1	$2m/m$	2	0	2	0	1	0	1	0	$\vartheta_3\vert\theta_2$	θ_3
reshape,conv	3	md/m/9	2	1	2	1	1	1	1	1	$\sigma(\theta_3)\odot\varphi_3$	df3
reshape,conv	3	md/m/9	2	1	2	1	1	1	1	1	$\sigma(\theta_3)\otimes\phi_2$	dp3
conv,reshape	3	18/1/d	2	1	2	1	1	1	1	1	$\vartheta_3'\odot$df3$\vert\theta_2'\odot$dp3	ϕ_3
upsample			✓		✓		×		×		ϕ_3,θ_3	ϕ_3,θ_3
conv,act,conv,act	3	16/18/18	1	1	1	1	1	1	1	1	$\phi_3(F_4^s)\vert F_4^t$	m4
conv,act,conv	3	18/27/md	1	1	1	1	1	1	1	1	m4	φ_4
conv,act,conv	3	18/18/m	1	1	1	1	1	1	1	1	m4	ϑ_4
conv,norm,act	3	18/1	1	1	1	1	1	1	1	1	ϑ_4,θ_3	ϑ_4',θ_3'
conv	1	$2m/m$	1	0	1	0	1	0	1	0	$\vartheta_4\vert\theta_3$	θ_4
reshape,conv	3	md/m/9	1	1	1	1	1	1	1	1	$\sigma(\theta_4)\odot\varphi_4$	df4
reshape,conv	3	md/m/9	1	1	1	1	1	1	1	1	$\sigma(\theta_4)\otimes\phi_3$	dp4
conv,reshape	3	18/1/d	1	1	1	1	1	1	1	1	$\vartheta_4'\odot$df4$\vert\theta_3'\odot$dp4	ϕ
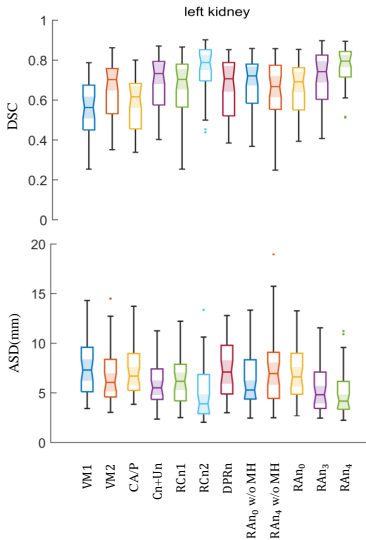
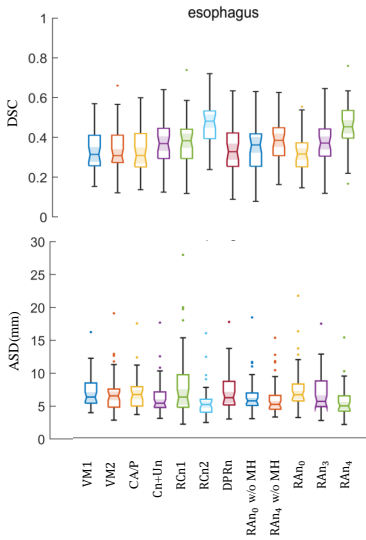**Fig. 3.** Results on left kidney.

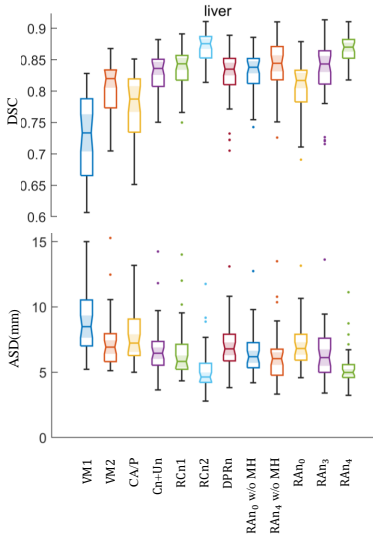
Fig. 4. Results on left kidney.
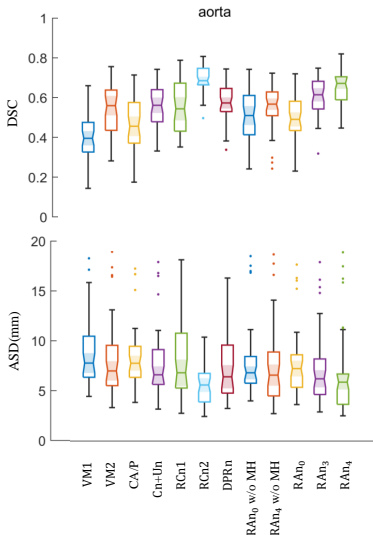
Fig. 5. Results on liver.
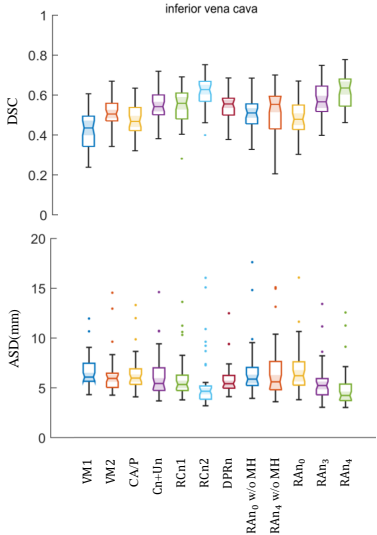

Fig. 6. Results on aorta.
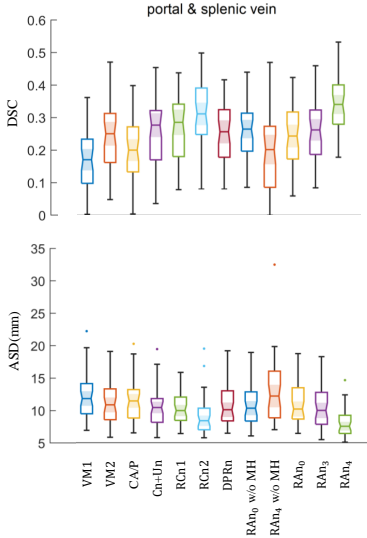
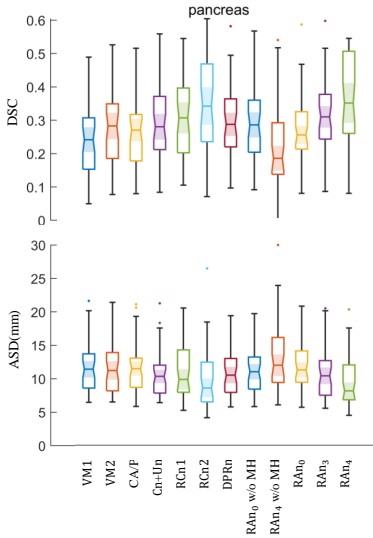**Fig. 7.** Results on inferior vena cava.

Fig. 8. Results on portal splenic vein.

Fig. 9. Results on pancreas.