# Seminar (Contrastive learning)

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# (MICCAI2021) Positional Contrastive Learning for Volumetric Medical Image Segmentation

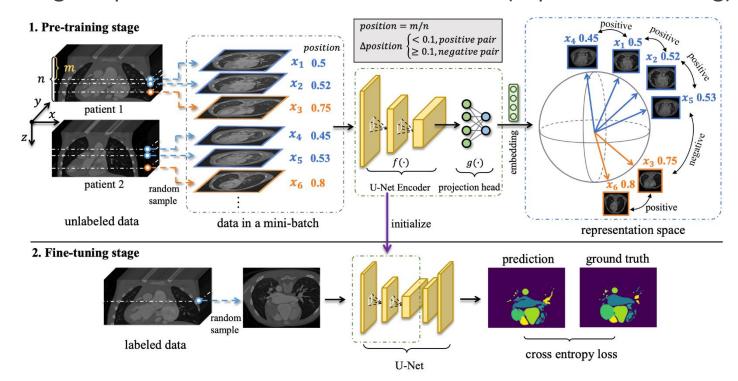
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#### Motivation and Contribution

- 1. The scarcity of annotated medical images
- 2. False negative pairs due to the similarity of different images
- 3. The doubtful attempt to divide volumes into partitions and consider the slides of corresponding partitions in different volumes as positive pairs and those of different partitions as negative pairs
- 4. Propose a novel positional contrastive learning (PCL) framework: generating pairs based on the position of a slice in volumetric medical images

#### Method

- 1. Pre-train a 2D U-Net (contrastive learning)
- 2. Fine-tune using the pre-trained encoder as initialization (supervised learning)



#### Dataset

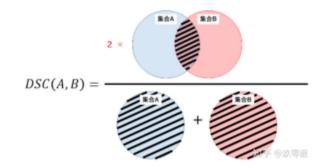
- 1. Congenital Heart Disease (CHD) dataset, CT
- 2. MMWHS dataset, CT (same annotation types as CHD)
- 3. ACDC dataset, MRI
- 4. HVSMR dataset, MRI (a bit different annotation types from ACDC)

#### Evaluation

#### Dice

对于分割过程中的评价标准主要采用Dice相似系数(Dice Similariy Coefficient,DSC),Dice系数是一种集合相似度度量指标,通常用于计算两个样本的相似度,值的范围 0-1 ,分割结果最好时值为 1 ,最差时值为 0

$$Dice(P,T) = rac{|P_1 \wedge T_1|}{(|P_1| + |T_2|)/2} \Leftrightarrow Dice = rac{2TP}{FP + 2TP + FN}$$



# Experiment(Semi-supervised Learning)

Table 1: Comparison of the proposed PCL method with baseline methods on CHD and ACDC. M is the number of patients used in the fine-tuning process. Results are reported in the form of mean(standard deviation) on 5-fold cross-validation. PCL provides better results than the baselines for all values of M.

CHD (68 patients in total)							
Method	M=2	M=6	M=10	M = 15	M = 20	M = 30	M = 51
Random	0.184(.06)	0.508(.06)	0.584(.05)	0.627(.05)	0.658(.04)	0.693(.04)	0.754(.02)
Rotation [6]	0.171(.06)	0.488(.07)	0.575(.04)	0.625(.04)	0.651(.04)	0.691(.04)	0.749(.03)
PIRL [14]	0.196(.07)	0.504(.08)	0.617(.05)	0.658(.03)	0.674(.04)	0.714(.04)	0.761(.03)
SimCLR [3]	0.192(.06)	0.515(.06)	0.599(.06)	0.631(.05)	0.666(.05)	0.699(.05)	0.756(.03)
GCL [2]	0.255(.10)	0.564(.04)	0.646(.03)	0.669(.04)	0.697(.04)	0.725(.04)	0.766(.03)
PCL	0.356(.08)	0.600(.06)	0.661(.05)	0.686(.05)	0.716(.04)	0.735(.05)	0.774(.03)
ACDC (100 patients in total)							
		AC	CDC (100 pa	tients in tot	al)		
Method	M=2	M=6	CDC (100 pa M=10	tients in tot $M=15$	al) $M=20$	M = 30	M = 80
Method Random	M=2 0.588(.07)		-			M=30 0.909(.01)	M=80 $0.928(.00)$
	841,0801 B181	M=6	M=10	M = 15	M=20	325000 2000000	Section Sections
Random	0.588(.07)	M=6 $0.782(.03)$	M=10 $0.840(.03)$	M=15 $0.876(.01)$	M=20 $0.894(.01)$	0.909(.01)	0.928(.00)
Random Rotation [6]	0.588(.07) 0.572(.08)	M=6 $0.782(.03)$ $0.809(.03)$	M=10 $0.840(.03)$ $0.868(.02)$	M=15 $0.876(.01)$ $0.886(.01)$	M=20 $0.894(.01)$ $0.898(.01)$	0.909(.01) 0.910(.01)	0.928(.00) 0.925(.00)
Random Rotation [6] PIRL [14]	0.588(.07) 0.572(.08) 0.492(.03)	M=6 $0.782(.03)$ $0.809(.03)$ $0.823(.04)$	M=10 $0.840(.03)$ $0.868(.02)$ $0.865(.01)$	M=15 $0.876(.01)$ $0.886(.01)$ $0.880(.02)$	M=20 $0.894(.01)$ $0.898(.01)$ $0.896(.02)$	0.909(.01) 0.910(.01) 0.912(.01)	0.928(.00) 0.925(.00) 0.927(.00)

# Experiment(Transfer Learning)

Table 2: Transfer learning comparison of the proposed PCL method with the baselines. Except for Random, all the methods are pre-trained on CHD and ACDC without labels and fine-tuned on MMWHS and HVSMR respectively.

CHD transferring to MMWHS (20 patients in total)							
Method	$M{=}2$	$M{=}4$	M=6	M=8	M = 10	M = 16	
Random	0.232(.14)	0.661(.10)	0.732(.07)	0.769(.06)	0.808(.05)	0.834(.05)	
Rotation [6]	0.247(.16)	0.659(.13)	0.751(.07)	0.768(.07)	0.803(.06)	0.850(.04)	
PIRL [14]	0.251(.10)	0.670(.11)	0.755(.07)	0.774(.06)	0.821(.05)	0.851(.04)	
SimCLR [3]	0.269(.17)	0.683(.10)	0.751(.07)	0.783(.06)	0.818(.05)	0.850(.04)	
GCL [2]	0.262(.11)				0.820(.04)		
PCL	0.339(.15)	0.748(.08)	0.792(.05)	0.820(.05)	0.840(.04)	0.869(.03)	

ACDC transferring to HVSMR (10 patients in total)							
Method	M=2	$M{=}4$	M=6	M=8			
Random	0.742(.06)	0.813(.05)	0.842(.03)	0.842(.04)			
Rotation [6]	0.737(.07)	0.816(.06)	0.845(.03)	0.844(.03)			
PIRL [14]	0.740(.05)	0.826(.04)	0.849(.03)	0.846(.03)			
SimCLR [3]	0.700(.07)	0.779(.05)	0.808(.04)	0.815(.04)			
GCL[2]	0.770(.05)	0.818(.05)	0.842(.03)	0.843(.03)			
PCL	0.781(.05)	0.832(.05)	0.857(.03)	0.857(.03)			

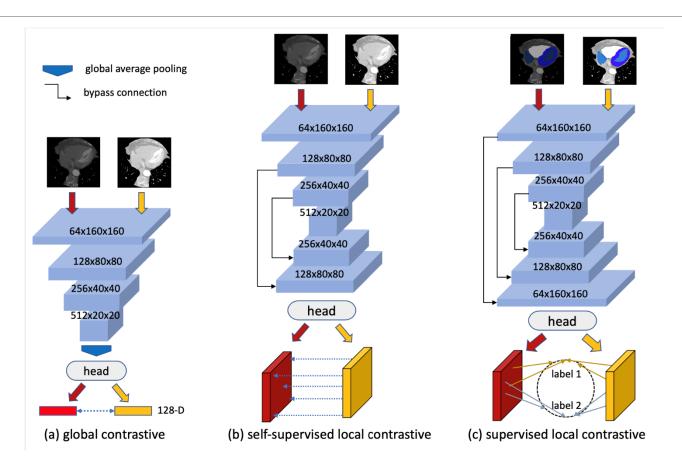
#### (MICCAI2021) Semi-supervised Contrastive Learning for Label-efficient Medical Image Segmentation

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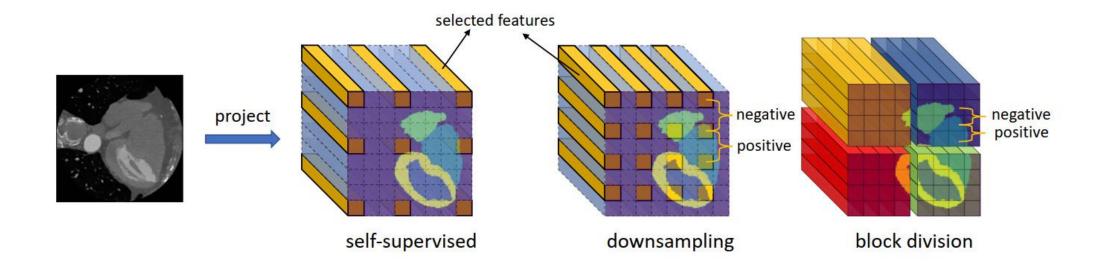
#### Motivation and Contribution

- 1. Most existing contrastive learning methods target image classification tasks
- 2. Semantic segmentation, on the other hand, requires pixel-wise classification
- Propose a semi-supervised framework consisting of self-supervised global contrast and supervised local contrast to take advantage of the available labels

#### Method



### Method



#### Dataset

- 1. Hippocampus dataset, MRI
- 2. MMWHS dataset, CT

# Experiment

Table 1: Comparison between state-of-the-art methods and the proposed methods w.r.t. subsequent segmentation dice scores on two datasets. Ablation studies of our methods (w/o global contrast) are also included.

	Hippocampus			MMWHS			
Methods	% of da	ta labele	$d in X_{tr}$	$\%$ of data labeled in $X_{tr}$			
	5	10	20	10	20	40	
random	0.788	0.833	0.852	0.328	0.440	0.715	
global [7]	0.817	0.834	0.861	0.359	0.487	0.724	
global+local(self) 4	0.808	0.843	0.858	0.367	0.490	0.730	
Mixup 18	0.818	0.847	0.861	0.365	0.541	0.755	
TCSM [14]	0.796	0.838	0.855	0.347	0.489	0.733	
local(stride)	0.818	0.845	0.860	0.354	0.485	0.743	
local(block)	0.817	0.843	0.862	0.366	0.475	0.736	
global+local(stride)	0.822	0.851	0.863	0.384	0.525	0.758	
global + local(block)	0.824	0.849	0.866	0.382	0.553	0.764	

### Experiment

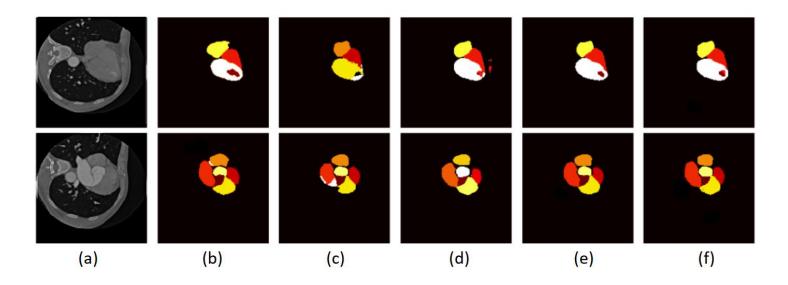


Fig. 3: Visualization of segmentation results on MMWHS with 40% labeled data. (a) and (b) represent input image and ground truth. (c)  $\sim$  (f) are the predictions of random, global+local(self), global+local(stride), and global+local(block). Different color represents different structure categories. (Better to view in colors)

### Experiment

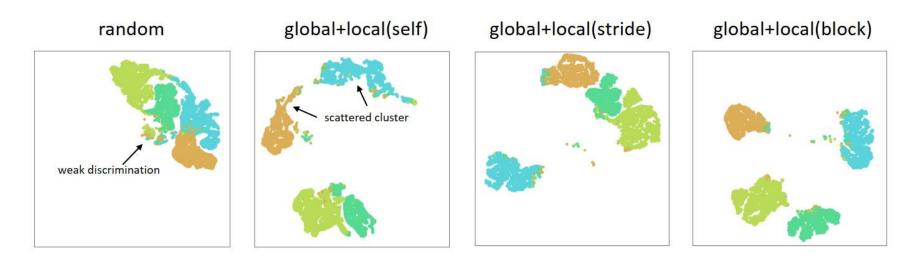


Fig. 4: Visualization of embedding features after applying t-SNE on MMWHS with 40% labeled data. Different color represents different classes. The features are all from the feature map before the last point-wise convolution. (Better to view in colors.

# Thanks