

### Densely Semantically Aligned Person Re-Identification

#### CVPR 2019

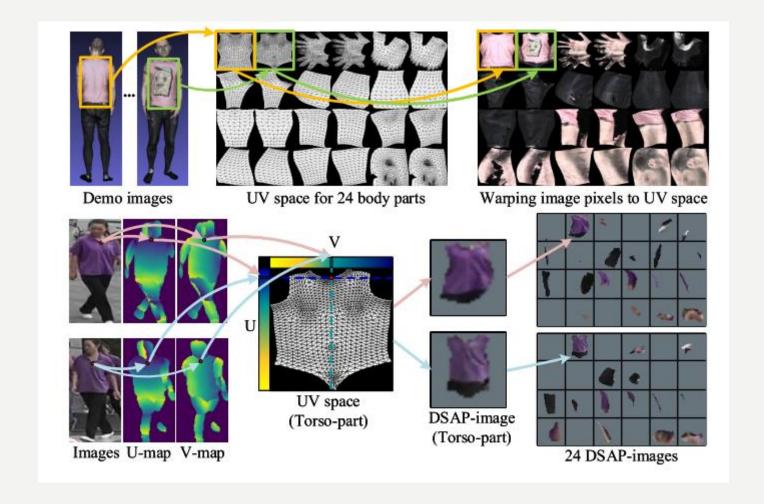
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#### Contributions:

propose making use of dense semantic alignment for person Re-ID, addressing the misalignment challenges. The first one to make use of fine grained semantics to address the misalignment problems for effective person re-ID.

DSAG removes the dependency on the performance of the dense semantics estimator during interference, making the inference model more computationally efficient and robust to dense semantics estimation errors

# Densely Semantically Aligned Person Re-Identification ---- uv space



## Densely Semantically Aligned Person Re-Identification ---- Method Overview

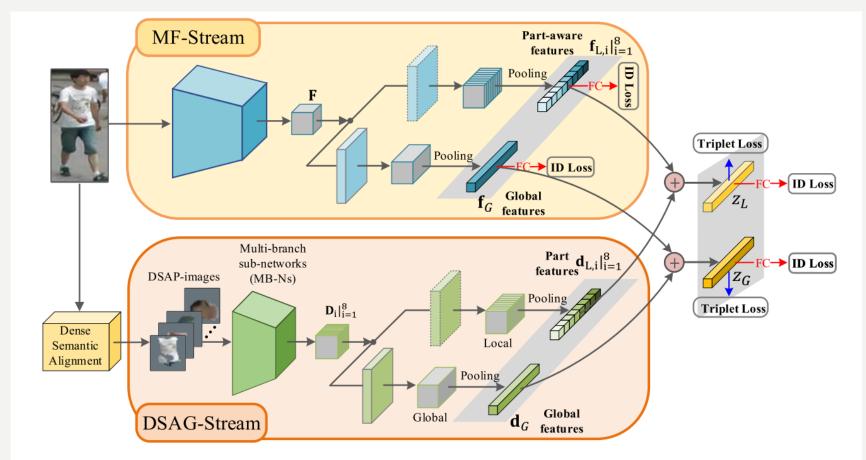
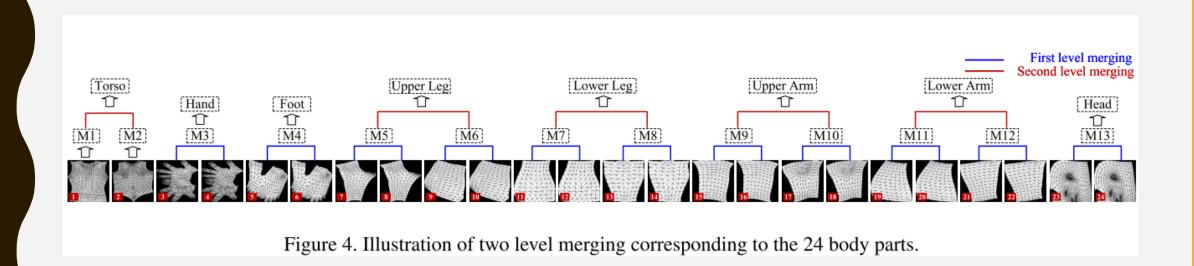


Figure 3. Flowchat of the proposed densely semantically aligned person re-ID (DSA-reID). It consists of two streams: *MF-Stream* and *DSAG-Stream*, which are jointly trained through our fusion and supervision design. The *DSAG-Stream*, with the input DSAP-images that are densely semantically aligned, plays the role of a regulator which facilitates the joint optimization of the entire network. In the inference, to be computationally efficient, the *DSAG-Stream* is discarded. The global features  $\mathbf{f}_G$  and part-aware features  $\mathbf{f}_L = \mathbf{f}_{L,i}|_{i=1}^8$  are used as the final features for re-ID. They are simultaneously exploited to make use of the global information and local detailed information.

http://openaccess.thecvf.com/content\_CVPR\_2019/papers/Zhang\_Densely\_Semantically\_Aligned\_Person\_Relation\_CVPR\_2019\_paper.pdf

## Densely Semantically Aligned Person Re-Identification ---- Method Overview



# Densely Semantically Aligned Person Re-Identification ---- Experiment

Table 2. Performance (%) comparisons with the state of the art methods. Bold numbers denote the best performance, while numbers with underlines denote the second best. Superscript \* indicates that model is pre-trained on CUHK03 and fine-tuned on CUHK01.

					CUE	IK03		G11111101			
	Method		01 (SQ)	Labe	led	Detected		CUHK01		DukeMTMC-reID	
		Rank-1	mAP	Rank-1	mAP	Rank-1	mAP	Rank-1	Rank-5	Rank-1	mAP
Basic-CNN	IDE(ECCV18) [35]	85.3	68.5	43.8	38.9	-	-	-	-	73.2	52.8
(ResNet-50)	Gp-reid(Arxiv18) [2]	92.2	81.2	-	-	-	-	-	-	85.2	72.8
	Spindle(CVPR17) [49]	76.9	-	-	-	-	-	79.9	94.4	-	-
	PIE(Arxiv17) [53]	78.7	53.9	-	-	-	-	-	-	-	-
	MSCAN(CVPR17) [15]	80.8	57.5	-	-	-	-	-	-	-	-
	PDC(ICCV17) [33]	84.1	63.4	-	-	-	-	-	-	-	-
	Pose Transfer(CVPR18) [22]	87.7	68.9	33.8	30.5	30.1	28.2	-	-	68.6	48.1
	PN-GAN(ECCV18) [26]	89.4	72.6	-	-	-	-	-	-	73.6	53.2
	PSE(CVPR18) [28]	87.7	69.0	-	-	30.2	27.3	67.7	86.6	79.8	62.0
-related	MGCAM(CVPR18) [32]	83.8	74.3	50.1	33.8     30.5     30.1     28.2     -     -     68.6       -     -     -     -     -     73.6       -     -     30.2     27.3     67.7     86.6     79.8       50.1     50.2     46.7     46.9     -     -     -       -     -     -     84.3     -     78.9       -     -     -     80.7*     94.4*     84.4       -     -     -     88.1     96.7     76.8	-					
	MaskReID(Arxiv18) [25]	90.0	75.3	-	-	-	-	84.3	-	78.9	61.9
	Part-Aligned(ECCV18) [34]	91.7	79.6	-	-	-	-	80.7*	94.4*	84.4	69.3
	AACN(CVPR18) [45]	85.9	66.9	-	-	-	-	88.1	96.7	76.8	59.3
	SPReID(CVPR18) [14]	92.5	81.3	-	-	-	-	-	-	Rank-1  73.2 85.2  68.6 73.6 79.8 - 78.9 84.4	71.0
	AlignedReID(Arxiv17) [48]	91.8	79.3	-	-	-	-	-	-	-	-
Stripe	Deep-Person(Arxiv17) [3]	92.3	79.6	-	-	-	-	-	-	80.9	64.8
-	Method   Rank-1   mAP   Rank-1   mAP   Rank-1   mAP   Rank-1   mAP   Rank-1   Rank-5   Rank	83.3	69.2								
34354	MGN(MM18) [39]	95.7	86.9	<u>68.0</u>	<u>67.4</u>	<u>66.8</u>	<u>66.0</u>	-	-	Rank-1 73.2 85.2 68.6 73.6 79.8 - 78.9 84.4 76.8 84.4 - 80.9 83.3 88.7 - 80.5 81.8 84.9	78.4
	DLPAP(ICCV17) [50]	81.0	63.4	-	-	-	-	76.5*	94.2*	-	-
Attention	HA-CNN(CVPR18) [19]	91.2	75.7	44.4	41.0	41.7	38.6	-	-	80.5	63.8
	DuATM(CVPR18) [31]	Rank-1   mAP   mAR   m	81.8	64.6							
	Method   Rank-1   mAP   mAP   Rank-1   mAP   Rank	65.5	60.5	-	-	84.9	71.8				
Dense Semantics -based (Ours)	DSA-reID	95.7	87.6	78.9	75.2	78.2	73.1	90.4*	97.8*	86.2	74.3

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## Densely Semantically Aligned Person Re-Identification ---- Experiment

Table 3. Performance (%) comparisons of baselines and our schemes on the Market-1501 dataset.

Model	mAP	Rank-1	Rank-5	Rank-10
Baseline	76.4	91.2	96.5	97.9
Baseline (RE)	78.6	92.3	97.6	98.3
Baseline (RE+LS)	81.2	93.4	97.8	98.5
Baseline (Two branches)	83.4	94.0	98.0	98.7
DSA-Global(Single)	84.7	94.8	98.2	98.9
DSA-Local(Single)	83.2	94.0	97.9	98.6
DSA-Global(Joint)	87.4	95.6	98.6	99.1
DSA-Local(Joint)	86.5	95.2	98.4	99.0
DSA(Two streams fused)	87.5	95.8	98.4	99.1
DSA-reID(Only MF-Stream)	87.6	95.7	98.4	99.1

DSA-Global/Local(Single): denotes the design with only the global/local branch in our two stream framework for both training and inferencing.

DSA-Global/Local(Joint): train with two branch and test with Global/Local features

Table 4. Performance (%) comparisons between dense and coarse semantic alignment in our framework on the Market-1501 dataset.

Model	mAP	Rank-1	Rank-5	Rank-10
Baseline (RE+LS)	81.2	93.4	97.8	98.5
CSA(Only MF-Stream)	84.1	94.1	98.1	98.8
DSA(Only MF-Stream)	87.6	95.7	98.4	99.1

## CSA: coarsely semantically aligned, cropping images into 24 parts

Table 5. Performance (%) comparisons on the designs of the two-stream fusion, on the Market-1501 dataset.

Fusion method	mAP	Rank-1	Rank-5	Rank-10
Concatenation+fc	81.6	93.0	97.6	98.6
Elem-add	87.6	95.7	98.4	99.1

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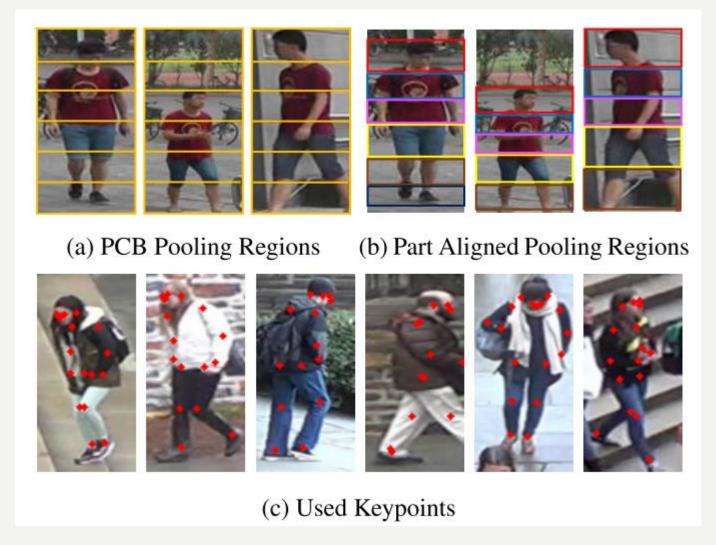
arXiv 2018.12.29

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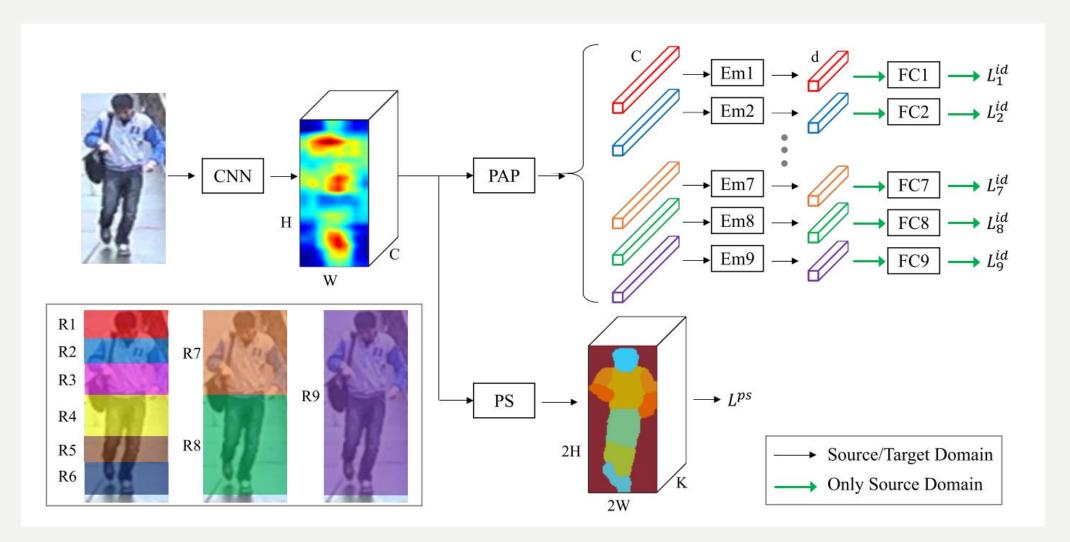
#### Contributions:

address cross-domain ReID and make contributions for both model generalization and adaptation; propose Part Aligned Pooling (PAP) that brings significant improvement for cross-domain testing. design a Part Segmentation (PS) constraint over ReID feature to enhance alignment and improve model generalization.

# EANet: Enhancing Alignment for Cross-Domain Person Re-identification ------Motivations



### -----Method OverView



### ---- Effectiveness of PAP

	$M{ ightarrow}M$	C→C	$D \rightarrow D$	M→C	$M \rightarrow D$	C→M	C→D	$D{ ightarrow}M$	$D{\rightarrow}C$
GlobalPool	88.2 (71.3)	42.4 (39.6)	79.2 (61.9)	10.7 (9.3)	38.7 (21.5)	45.7 (21.8)	32.5 (15.7)	47.9 (21.6)	9.1 (7.7)
PCB	93.2 (81.1)	65.2 (60.0)	86.3 (72.7)	8.9 (7.8)	42.9 (23.8)	52.1 (26.5)	29.2 (15.2)	56.5 (27.7)	8.4 (6.9)
PAP-6P	94.4 (84.2)	68.1 (62.4)	85.6 (72.4)	11.6 (9.9)	47.6 (28.3)	54.6 (29.3)	33.9 (18.1)	59.7 (31.4)	9.2 (8.2)
PAP	94.4 (84.5)	72.0 (66.2)	86.1 (73.3)	11.4 (9.9)	46.4 (27.9)	55.5 (30.0)	34.0 (17.9)	59.5 (30.6)	9.7 (8.0)

Table 1: Effectiveness of PAP. Label M, C and D denote Market 1501, CUHK03 and DukeMTMC-reID respectively.  $M \rightarrow C$  means training on M and testing on C, and so on. Score in each cell is Rank-1 (mAP) %. Following tables share this annotation.

### ---- Effectiveness of PS

	$M{ ightarrow}M$	C→C	$D{ ightarrow}D$	M→C	$M{ ightarrow}D$	$C{ ightarrow}M$	C→D	$D{ ightarrow}M$	D→C
PAP	94.4 (84.5)	72.0 (66.2)	86.1 (73.3)	11.4 (9.9)	46.4 (27.9)	55.5 (30.0)	34.0 (17.9)	59.5 (30.6)	9.7 (8.0)
PAP-S-PS-SA	94.5 (85.7)	71.4 (66.2)	86.9 (74.2)	13.6 (11.7)	50.2 (30.9)	58.4 (32.9)	38.4 (20.6)	60.6 (31.9)	11.1 (9.5)
PAP-S-PS	94.6 (85.6)	72.5 (66.8)	87.5 (74.6)	14.2 (12.8)	51.4 (31.7)	59.4 (33.3)	39.3 (22.0)	61.7 (32.9)	11.4 (9.6)
PAP-ST-PS	-	-	-	21.4 (19.0)	56.1 (36.0)	66.4 (40.6)	45.0 (26.4)	66.1 (35.8)	15.6 (13.8)

Table 2: Effectiveness of PS Constraint.

PAP: Traing on Source Domain with PAP component and directly test on Target Domain

PAP-S-PS: Traing on Source Domain with PAP and PS component and directly test on Target Domain

PAP-ST-PS: Train on Source Domain with PAP, PS loss and Target Domain with PS loss, then directly test on

Target Domain

PAP-S-PS-SA: averaging over all pixel losses when calculating PS loss while PAP-S-PS calculating PS loss by averaging over each part pixel losses to avoid the loss dominating by large part

# EANet: Enhancing Alignment for Cross-Domain Person Re-identification ---- Single Domain Comparison with SOTA

Mathad	Publication	Market	1501	CUHI	K03	DukeMT	MC-reID
Method	Publication	Rank-1	mAP	Rank-1	mAP	Rank-1	mAP
BoW+KISSME [49]	ICCV15	44.4	20.8	6.4	6.4	25.1	12.2
WARCA [14]	ECCV16	45.2	-	-	-	-	-
SVDNet [34]	ICCV17	82.3	62.1	41.5	37.3	76.7	56.8
Triplet Loss [12]	arXiv17	84.9	69.1	-	-	-	-
DaRe [39]	CVPR18	86.4	69.3	55.1	51.3	75.2	57.4
AOS [13]	CVPR18	86.5	70.4	47.1	43.3	79.2	62.1
DML [47]	CVPR18	87.7	68.8	-	-	-	-
Cam-GAN [54]	CVPR18	88.1	68.7	-	-	75.3	53.5
MLFN [2]	CVPR18	90.0	74.3	52.8	47.8	81.0	62.8
* PDC [32]	ICCV17	84.4	63.4	-	-	-	-
* PSE [29]	CVPR18	87.7	69.0	-	-	79.8	62.0
* PN-GAN [26]	ECCV18	89.4	72.6	-	-	73.6	53.2
* GLAD [41]	MM17	89.9	73.9	-	-	-	-
* PABR [33]	ECCV18	91.7	79.6	-	-	84.4	69.3
* SPReID [15]	CVPR18	92.5	81.3	-	-	84.4	71.0
MSCAN [16]	CVPR17	80.3	57.5	-	-	-	-
PAR [48]	ICCV17	81.0	63.4	-	-	-	-
JLML [19]	IJCAI17	85.1	65.5	-	-	-	-
HA-CNN [20]	CVPR18	91.2	75.7	41.7	38.6	80.5	63.8
AlignedReID [46]	arXiv17	92.6	82.3	-	-	-	-
Mancs [37]	ECCV18	93.1	82.3	65.5	60.5	84.9	71.8
PCB [35]	ECCV18	92.3	77.4	61.3	54.2	81.8	66.1
PCB+RPP [35]	ECCV18	93.8	81.6	63.7	57.5	83.3	69.2
PCB (Our Implementation)	-	93.2	81.1	65.2	60.0	86.3	72.7
* PAP (Ours) †	-	94.4	84.5	72.0	66.2	86.1	73.3
* PAP-S-PS (Ours)	-	94.6	85.6	72.5	66.8	87.5	74.6

# EANet: Enhancing Alignment for Cross-Domain Person Re-identification Cross-Domain Comparison with SOTA

Method	Publication	$M \rightarrow$	D	$D \rightarrow$	M	$C \rightarrow$	M	C→ Rank-1  23.0 17.6 42.7 32.5 29.2 39.3 45.0	D
Wethod	Fuoncation	Rank-1	mAP	Rank-1	mAP	Rank-1	mAP	Rank-1	mAP
LOMO [21]	CVPR15	12.3	4.8	27.2	8.0	-	-	-	-
BoW [49]	ICCV15	17.1	8.3	35.8	14.8	-	-	-	-
UMDL [25]	CVPR16	18.5	7.3	34.5	12.4	-	-	-	-
CAMEL [44]	ICCV17	-	-	54.5	26.3				
PUL [6]	TOMM18	30.0	16.4	45.5	20.5	41.9	18.0	23.0	12.0
PTGAN [40]	CVPR18	27.4	-	38.6	-	31.5	-	17.6	-
SPGAN [4]	CVPR18	41.1	22.3	51.5	22.8	42.3	19.0	-	-
SPGAN+LMP [4]	CVPR18	46.4	26.2	57.7	26.7	-	-	-	-
TJ-AIDL [38]	CVPR18	44.3	23.0	58.2	26.5	-	-	-	-
HHL [53]	ECCV18	46.9	27.2	62.2	31.4	56.8	29.8	42.7	23.4
GlobalPool (DT) †	-	38.7	21.5	47.9	21.6	45.7	21.8	32.5	15.7
PCB [35] (Our Imp., DT) †	ECCV18	42.9	23.8	56.5	27.7	52.1	26.5	29.2	15.2
PAP-S-PS (Ours, DT) †	-	51.4	31.7	61.7	32.9	59.4	33.3	39.3	22.0
PAP-ST-PS (Ours)	-	56.1	36.0	66.1	35.8	66.4	40.6	45.0	26.4
PAP-ST-PS-SPGAN (Ours) †	-	61.5	39.4	69.6	39.3	-	-	-	-
PAP-ST-PS-SPGAN-CFT (Ours) †	-	67.7	48.0	78.0	51.6	-	-	-	-

Table 6: Comparison with state-of-the-art methods under cross-domain setting. In each column, the 1st and 2nd highest scores (excluding methods with trailing †) are marked by red and blue, respectively. **DT** means Direct Transfer.

# THANKS