# Joint Disentangling and Adaptation for Cross-Domain Person Re-Identification



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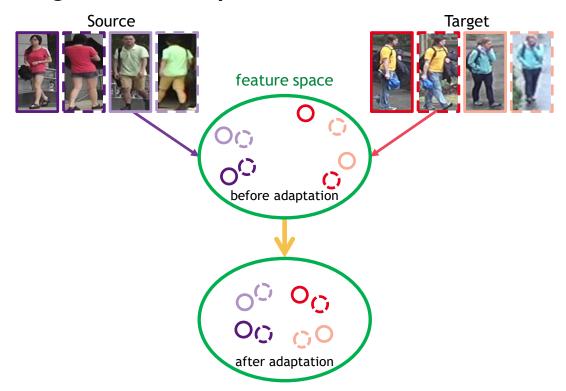
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#### Background: Unsupervised Cross-Domain RelD

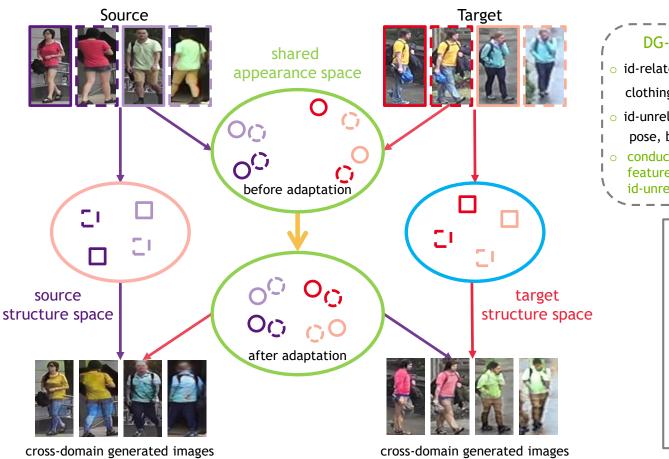


#### DG-Net [1] (for a single domain)

- o id-related features (appearance codes): clothing color, textures, styles, etc.
- o id-unrelated features (structure codes): pose, background, illumination, etc.

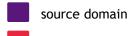
- source domain
- target domain
- identity in source
- identity in target
- different images of
- the same identity

#### Motivation: Joint Disentangling and Adaptation



#### DG-Net++ (for cross-domain)

- id-related features (appearance codes):
   clothing color, textures, styles, etc.
- id-unrelated features (structure codes):
   pose, background, illumination, etc.
- conduct adaptation in the id-related feature space exclusively to prevent id-unrelated interference



target domain

identity in source

identity in target

different images of the same identity

appearance code

structure code

adaptation loss term

#### Approach: DG-Net++

 $E_{app}$ 

 $E_{app}$ 

 $E_{str}^{s}$ 

Source

**Target** 

dom adv

 $L_{
m adv}^{
m dom}$ 

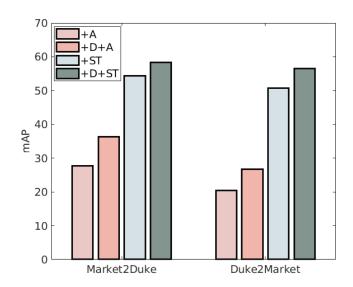
disentangling loss:  $L_{\rm adv}^{\rm img}$  +  $L_{\rm id}^{\rm s_1}$  +  $L_{\rm id}^{\rm s_2}$  +  $L_{\rm cyc}$  $L_{\mathrm{adv}}^{\mathrm{dom}}$  +  $L_{\mathrm{id}}^{\mathrm{t_1}}$  +  $L_{\mathrm{id}}^{\mathrm{t_2}}$ adaptation loss: self-training  $E_{app}$ shared appearance encoder source structure encoder target structure encoder source decoder target decoder image discriminator  $|\overline{L}_{
m cyc}|$ domain discriminator  $E_{app}$ disentangling loss term  $L_{\mathrm{id}}^{\mathrm{t_2}}$ 

# Quantitative Results: Comparison with SOTA

	M 1 (	1501 . D	1 MTM	, II)	D 1 M/I	MC ID	. M. 1	1501
Methods			ukeMTMC				→ Market	
			Rank@10				Rank@10	
SPGAN [6]	41.1	56.6	63.0	22.3	51.5	70.1	76.8	22.8
AIDL [55]	44.3	59.6	65.0	23.0	58.2	74.8	81.1	26.5
MMFA [30]	45.3	59.8	66.3	24.7	56.7	75.0	81.8	27.4
HHL [68]	46.9	61.0	66.7	27.2	62.2	78.8	84.0	31.4
CAL [36]	55.4	-	-	36.7	64.3	-	-	34.5
ARN [29]	60.2	73.9	79.5	33.4	70.3	80.4	86.3	39.4
ECN [69]	63.3	75.8	80.4	40.4	75.1	87.6	91.6	43.0
PDA [28]	63.2	77.0	82.5	45.1	75.2	86.3	90.2	47.6
CR-GAN [3]	68.9	80.2	84.7	48.6	77.7	89.7	92.7	54.0
IPL [43]	68.4	80.1	83.5	49.0	75.8	89.5	93.2	53.7
SSG [10]	73.0	80.6	83.2	53.4	80.0	90.0	92.4	58.3
DG-Net++	78.9	87.8	90.4	63.8	82.1	90.2	92.7	61.7
Methods	$Market-1501 \rightarrow MSMT17$				$DukeMTMC-reID \rightarrow MSMT17$			
	Rank@1	Rank@5	Rank@10	mAP	Rank@1	Rank@5	Rank@10	mAP
PTGAN [56]	10.2	-	24.4	2.9	11.8	-	27.4	3.3
ENC [69]	25.3	36.3	42.1	8.5	30.2	41.5	46.8	10.2
SSG [10]	31.6	-	49.6	13.2	32.2	-	51.2	13.3
DG-Net++	48.4	60.9	66.1	22.1	48.8	60.9	65.9	22.1
Methods	$MSMT17 \rightarrow Market-1501$				$MSMT17 \rightarrow DukeMTMC-reID$			
	Rank@1	Rank@5	Rank@10	mAP	Rank@1	Rank@5	Rank@10	mAP
PAUL [59]	68.5	-	-	40.1	72.0	-	-	53.2
DG-Net++	83.1	91.5	94.3	64.6	75.2	73.6	86.9	58.2

## **Quantitative Results: Ablation Study**

Methods	$Market-1501 \rightarrow DukeMTMC-reID$				$DukeMTMC-reID \rightarrow Market-1501$			
	Rank@1	Rank@5	Rank@10	mAP	Rank@1	Rank@5	Rank@10	mAP
Baseline	37.4	52.4	58.4	19.3	39.7	57.9	64.3	15.0
+A+ST	71.4	81.8	85.7	57.5	75.7	86.4	90.1	57.1
+D	44.5	60.6	66.7	24.2	50.1	68.0	73.9	26.8
+D+A	53.2	68.7	73.8	36.3	52.2	70.7	77.0	28.6
+D+ST	74.2	82.8	86.5	58.4	78.0	87.1	90.3	56.5
+D+A+ST	78.9	87.8	90.4	63.8	82.1	90.2	92.7	61.7



- o D: disentangling
- A: adversarial alignment
- ST: self-training

### **Qualitative Results: Image Synthesis**



# **Qualitative Results: Comparison with SOTA**



### **Qualitative Results: Ablation Study**



