

Person Re-Identification by Manifold Ranking

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1 Introduction



Problem:

Re-identify a person at different locations and time.

Existing learning-to-rank methods are not scalable:

- The learning process requires exhaustive supervision on pairwise individual correspondence between camera pair.
- The value of unlabelled gallery instances is generally overlooked.

Contributions:

- Investigate the importance of using unlabelled gallery data for rank diffusion.
- Systematically formulate and validate manifold ranking models [3, 4].
- Performance significantly boosted by manifold ranking (14% performance gain at rank-1 matching rate)

2 Re-id by Manifold Ranking (MRank)

Step 1. Feature extraction

2784-dimensional feature vector:

- RGB
- YCbCr
- HSV
- Gabor
- Schmid

$$\mathbf{x} = (x_1, \dots, x_d)^T \in \mathbb{R}^d$$

Step 2. Compute pairwise affinity, A , between all n gallery images and probe

$$A \in \mathbb{R}^{(n+1) \times (n+1)}$$

$$A_{ij} = \exp(-\text{dist}^2(\mathbf{x}_i, \mathbf{x}_j)/\sigma^2)$$

Step 3. Estimate graph Laplacian

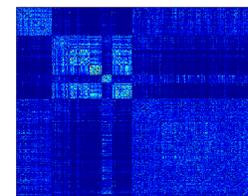
Normalised:

$$L_n = I - D^{-1/2} A D^{-1/2}$$

Unnormalised:

$$L_u = D - A$$

$$\text{where } D_{ii} = \sum_j A_{ij}$$



Step 4. Manifold ranking

$$\text{MRank-}L_n : \mathbf{c} = (\beta I + L_n)^{-1} \mathbf{y}$$

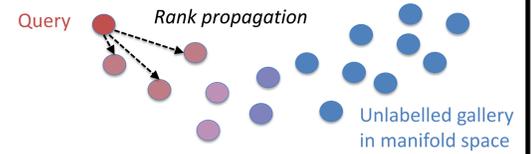
$$\text{MRank-}L_u : \mathbf{c} = [(\beta I + L_u)^{-1}]^m \mathbf{y}$$

where

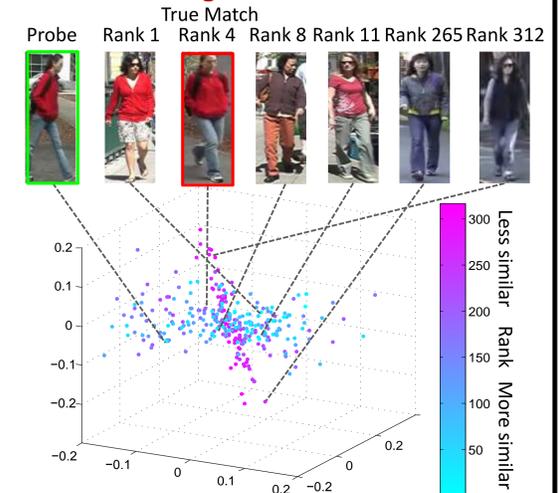
\mathbf{c} is the final ranking score vector

$$\mathbf{y} = (y_1, \dots, y_{n+1})^T \quad y_i = 1 \text{ if } \mathbf{x}_i \text{ is a query}$$

$$\beta \geq 0 \quad m \geq 0$$



Manifold ranking based on vector \mathbf{c} :



3 MRank vs. Conventional Methods without Manifold Ranking

Datasets:



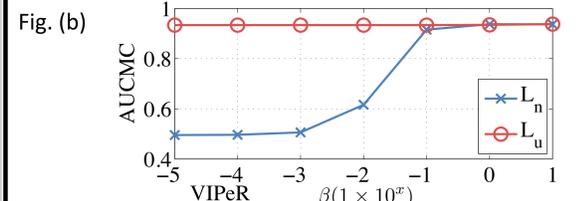
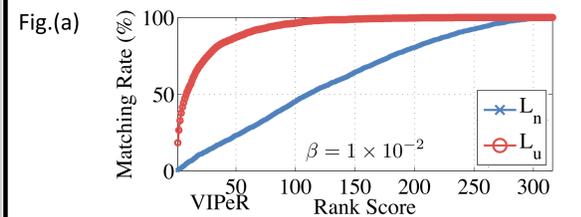
Highlights:

- Performance is measured using matching rate at rank- r = the expectation of finding the correct match in the top r matches
- MRank can be initialised with supervised distance metrics, denoted as MRank- L_u ($dist$) and MRank- L_n ($dist$) for unnormalised and normalised Laplacians
- A relative improvement of 14% at rank-1 recognition rate over the state-of-the-art learning to rank methods (RankSVM [1] and PRDC [2]).

Method	i-LIDS ($p = 50$)					VIPeR ($p = 316$)					GRID ($p = 900$)				
	$r=1$	$r=5$	$r=10$	$r=15$	$r=20$	$r=1$	$r=5$	$r=10$	$r=15$	$r=20$	$r=1$	$r=5$	$r=10$	$r=15$	$r=20$
ℓ_1 -norm	29.60	54.80	67.60	74.60	81.00	9.43	20.03	27.06	30.95	34.68	4.40	11.68	16.24	19.12	24.80
MRank- L_n (ℓ_1 -norm)	31.40	54.40	68.40	75.60	83.60	8.48	18.70	24.40	28.83	32.66	7.12	12.32	17.68	20.64	25.36
MRank- L_u (ℓ_1 -norm)	30.60	53.40	68.20	76.00	82.80	8.35	17.06	22.47	26.33	30.76	6.00	13.28	17.92	21.12	24.00
ℓ_2 -norm	28.20	54.00	66.20	72.40	79.40	10.95	23.92	31.39	38.86	44.11	4.88	14.24	20.32	22.40	26.24
MRank- L_n (ℓ_2 -norm)	31.40	55.60	67.60	77.40	82.20	11.42	24.27	33.73	38.92	44.11	5.76	14.96	21.76	25.12	30.96
MRank- L_u (ℓ_2 -norm)	31.00	56.00	67.40	77.00	81.20	10.57	24.24	33.42	38.83	43.42	5.76	15.44	21.28	24.96	28.40
RankSVM [1]	42.60	67.60	78.80	86.00	92.00	14.87	37.12	50.19	58.48	65.66	10.24	24.56	33.28	39.44	43.68
MRank- L_n (RankSVM)	42.80	70.40	81.80	86.40	92.40	19.27	42.41	55.00	63.86	70.06	12.24	27.84	36.32	42.24	46.56
MRank- L_u (RankSVM)	41.80	69.60	81.40	87.00	91.40	19.34	42.47	55.51	64.11	70.44	11.44	27.60	36.40	42.24	46.24
PRDC [2]	44.80	68.00	77.60	84.20	88.20	16.01	37.09	51.27	59.43	65.95	9.68	22.00	32.96	38.96	44.32
MRank- L_n (PRDC)	47.80	71.60	80.60	85.00	90.60	19.37	42.78	54.78	63.77	69.62	10.88	24.96	35.84	41.44	46.40
MRank- L_u (PRDC)	49.00	70.60	80.60	85.60	90.60	18.45	41.74	53.67	62.72	69.27	11.12	26.08	35.76	41.76	46.56

L_u = Unnormalised Laplacian; L_n = normalised Laplacian; r = rank; p = number of person in a test set

4 L_u vs. L_n



β is an important parameter that controls the convergence of manifold ranking.

Fig. (a) Matching rate curves with $\beta = 10^{-2}$

Fig. (b) Area under the curve with β varied from 10^{-5} to 10.

* Unnormalised Laplacian, L_u , is less sensitive to β in comparison to normalised Laplacian, L_n .

5 Examples

The leftmost image is the probe. The true match within the ordered gallery candidates is highlighted with red border. MRank gains better retrieval results as compared to PRDC [2] without manifold ranking. (And higher visual consistency at top ranks).

