

Towards Interpretable Deep Metric Learning with Structural Matching

Supplementary Material

A. Implementation of DIML

A.1. The Sinkhorn Algorithm

The Sinkhorn algorithm [1] modifies the original optimal transport problem (Eq.4) into the following one:

$$\begin{aligned} T^* = \arg \min_{T \geq 0} & \text{tr}(CT^\top) + \lambda \text{tr}(T(\log(T) - \mathbf{1}\mathbf{1}^\top)^\top), \\ \text{subject to } & T\mathbf{1} = \mu^s, \quad T^\top \mathbf{1} = \mu^t, \end{aligned} \quad (\text{A.1})$$

where λ is a non-negative regularization parameter. By adding the entropic regularizer, the Equation (A.1) becomes a convex problem, which can be solved with Sinkhorn-Knopp algorithm [12]. Starting from an initial matrix $K = \exp(-C/\lambda)$, the problem can be solved by iteratively projecting onto the marginal constraints until convergence:

$$\mathbf{a} \leftarrow \mu^s / K\mathbf{b}, \quad \mathbf{b} \leftarrow \mu^t / K^\top \mathbf{a}. \quad (\text{A.2})$$

After converged, we can obtain the optimal transport plan:

$$T^* = \text{diag}(\mathbf{a})K\text{diag}(\mathbf{b}). \quad (\text{A.3})$$

A.2. Testing

In all of our experiments, we use ResNet50 [6] as our backbone. Therefore, the size of the feature map before the pooling layer is 7×7 . To reduce computational costs, we first use ROI Align [5] to pool the feature map to $G \times G$ and $G = 4$ in most of our experiments unless otherwise noted. According to the multi-scale matching algorithm, for each image as a query, we first sort the images in the gallery using the standard cosine similarity to obtain the indices of top- K candidates \mathcal{I}_K (we use $K = 100$ in most of the experiments). We then calculate the proposed structural similarity of all the images in \mathcal{I}_K . To combine both global and structural information, we use the sum of the cosine similarity and the structural similarity for the top- K images to compute their ranks. The regularization parameter λ in Equation (6) is set to 0.05.

A.3. Training

Incorporating DIML into the training objectives is quite straightforward. Generally, the loss functions in metric learning can be roughly categorized into distance-based methods

(*e.g.*, Contrastive [4], Triplet [3], Margin [16]) and similarity-based methods (*e.g.*, Multi-Similarity [15], Arcface [2], N-Pair [13]). For distance-based methods, we replace the original distance function d with the average of d and our structural distance d_{struct} ; For similarity-based methods, we replace the original similarity function s with the average of s and our structural similarity s_{struct} . In this section, we will use several loss functions as examples to demonstrate how to apply DIML during training.

Margin [16] The Margin loss [16] is defined as

$$\mathcal{L}_{\text{margin}}(k, l) = \left(\sigma + (-1)^{I(y^k \neq y^l)} (D_{k,l} - \beta) \right)_+, \quad (\text{A.4})$$

where σ and β are learnable parameters, and D_{kl} is used to measure the distance between image k and l :

$$D_{k,l} = \frac{1}{2} (d_{\text{struct}}(z^k, z^l) + d(\bar{z}^k, \bar{z}^l)), \quad (\text{A.5})$$

where d is Euclid distance and d_{struct} is derived from d using Equation (10).

Multi-Similarity [15] The original Multi-Similarity is defined as:

$$s^*(k, l) = \begin{cases} s(k, l), & s(k, l) > \min_{p \in \mathcal{P}_k} s(k, p) - \epsilon \\ s(k, l), & s(k, l) < \max_{n \in \mathcal{N}_k} s(k, n) + \epsilon \\ 0, & \text{otherwise} \end{cases} \quad (\text{A.6})$$

$$\begin{aligned} \mathcal{L}_{\text{MS}} = & \frac{1}{B} \sum_{k \in \mathcal{B}} \left[\frac{1}{\alpha} \log \left[1 + \sum_{p \in \mathcal{P}_k} \exp(-\alpha(s^*(k, p) - \lambda)) \right] \right. \\ & \left. + \frac{1}{\beta} \log \left[1 + \sum_{n \in \mathcal{N}_k} \exp(\beta(s^*(k, n) - \lambda)) \right] \right], \end{aligned} \quad (\text{A.7})$$

where $s(k, l) = s(\psi^k, \psi^l)$ is the cosine similarity of the embeddings ψ^k, ψ^l of the two images. To utilize DIML, we

can replace s with

$$s(k, l) \leftarrow \frac{1}{2} (s(\bar{z}^k, \bar{z}^l) + s_{\text{struct}}(z^k, z^l)). \quad (\text{A.8})$$

Note that in our notation both ψ^k and \bar{z}^k represent the same embedding in \mathbb{R}^D .

ProxyNCA [8] It is also worth mentioning there are slight difference when applying DIML to proxy-based methods during training. Taking ProxyNCA [8] as example, the original objective is

$$\mathcal{L}_{\text{proxy}} = -\frac{1}{B} \sum_{k \in \mathcal{B}} \log \left(\frac{\exp(-d(\psi^k, \eta^{y^k}))}{\sum_{c \in \mathcal{C} \setminus \{y^k\}} \exp(-d(\psi^k, \eta^c))} \right), \quad (\text{A.9})$$

where d is Euclid distance and $\eta^c \in \mathbb{R}^D$ is the proxy for the c -th class. To use DIML, we need to use proxies with the size $\mathbb{R}^{H \times W \times D}$, denoted as $\{\rho^c, c \in \mathcal{C}\}$. Then, we can replace the $d(\psi^k, \eta^c)$ with

$$d(\psi^k, \eta^c) \leftarrow \frac{1}{2} (d(\psi^k, \rho^c) + d_{\text{struct}}(z^k, \rho^c)), \quad (\text{A.10})$$

where we also note that $\text{GAP}(\rho^c) = \eta^c$.

B. Experimental Details

B.1. Evaluation Metrics

We implement the same evaluation metrics as [9], including Precision at 1 (P@1), R-Precision (RP), and Mean Average Precision at R (MAP@R).

P@1 is also known as Recall@1 in metric learning. Given a sample x^q and feature encoder $\phi(\cdot)$, the set of k nearest neighbors of x^q is calculated as the precision of k nearest neighbors:

$$\mathcal{N}_q^k = \arg \min_{\mathcal{N} \subset \mathcal{X}_{\text{test}}, |\mathcal{N}|=k} \sum_{x^f \in \mathcal{N}} d_e(\phi(x^q), \phi(x^f)) \quad (\text{B.1})$$

where $d_e(\cdot, \cdot)$ is the euclidean distance. Then P@ k can be measured as

$$\text{P@}k = \frac{1}{|\mathcal{X}_{\text{test}}|} \sum_{x^q \in \mathcal{X}_{\text{test}}} \frac{1}{k} \sum_{x^i \in \mathcal{N}_q^k} \begin{cases} 1, & y^i = y^q, \\ 0, & \text{otherwise} \end{cases}, \quad (\text{B.2})$$

where y^i is the class label of sample x^i . We only report P@1 in our experiments, i.e. $k = 1$.

R-precision is defined in [9]. Specifically, for each sample x^q , let R be the number of images that are the same class with x^q and R-precision is simply defined as P@ R (see Equation B.2). However, R-precision does not consider the ranking of correct retrievals, so it is not informative enough.

To tackle this problem, [9] introduced Mean Average Precision at R.

MAP@R is similar to mean average precision, but limit the number of nearest neighbors to R. So it replaces *precision* in MAP calculation with *R-precision*:

$$\text{MAP@}R = \frac{1}{R} \sum_{i=1}^R P(i), \quad (\text{B.3})$$

where

$$P(i) = \begin{cases} \text{P@}i, & \text{if the } i\text{-th retrieval is correct;} \\ 0, & \text{otherwise.} \end{cases} \quad (\text{B.4})$$

MAP@R is more informative than P@1 and it can be computed directly from the embedding space without clustering as post-processing.

B.2. Experimental Setups

For most of the baseline methods, we follow the implementation and the hyper-parameters in [14]. For Proxy Anchor [7], we use their original implementation but set the hyper-parameters as [14] (batch size 112, embedding size 128, etc.). Besides various loss functions, we also experiment with different sampling methods. In Table 1 of the original paper, we use suffixes to represent the sampling methods (-R: Random; -D: Distance [16]; -S Semihard [11]; -H: Softhard [10]).

C. Detailed Results

In the original paper, we have demonstrated the effects of truncation number K and feature map size G using charts. In this section, we provide the original numerical results that were used to plot those charts in Table 1 and Table 2.

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Table 1: **Comparisons of different truncation numbers.** We test for different truncation number K ranging from 0 to 500. Experimental results show that a small K can already bring considerable performance improvement.

Baseline	K	CUB-200			Cars196			SOP		
		P@1	RP	M@R	P@1	RP	M@R	P@1	RP	M@R
Margin[16]	0	62.47	34.12	23.14	72.18	32.00	20.82	78.39	45.64	42.34
	10	65.16	34.56	23.87	76.65	32.52	21.72	79.26	46.44	43.20
	50	65.16	35.43	24.54	76.65	33.64	22.83	79.26	46.44	43.19
	100	65.16	35.48	24.54	76.65	33.93	22.95	79.26	46.44	43.19
	500	65.16	35.48	24.54	76.65	33.93	22.95	79.26	46.44	43.19
Multi-Similarity[15]	0	62.56	32.74	21.99	74.81	32.72	21.60	77.90	44.97	41.54
	10	64.89	33.21	22.73	78.50	33.26	22.50	78.53	45.60	42.24
	50	64.89	34.04	23.37	78.50	34.46	23.72	78.53	45.60	42.23
	100	64.89	34.12	23.38	78.50	34.70	23.81	78.53	45.60	42.23
	500	64.89	34.12	23.38	78.50	34.70	23.81	78.53	45.60	42.23

Table 2: **Effects of the size of feature map.** Generally, the performance of our DIML is better with higher G . DIML with $G = 4$ yields good results within relatively low computational costs.

Baseline	G	CUB-200			Cars196			SOP		
		P@1	RP	M@R	P@1	RP	M@R	P@1	RP	M@R
Margin[16]	1	62.47	34.12	23.14	72.18	32.00	20.82	78.39	45.64	42.34
	2	64.15	34.79	23.83	75.04	32.59	21.85	79.06	46.29	43.03
	4	65.16	35.48	24.54	76.65	33.93	22.95	79.26	46.44	43.19
	7	65.58	35.58	24.79	76.96	32.93	22.66	79.59	46.83	43.62
Multi-Similarity [15]	1	62.56	32.74	21.99	74.81	32.72	21.60	77.90	44.97	41.54
	2	63.77	33.33	22.60	77.45	33.25	22.60	78.39	45.56	42.15
	4	64.89	34.12	23.38	78.50	34.70	23.81	78.53	45.60	42.23
	7	65.45	34.15	23.55	78.93	33.64	23.50	78.76	45.90	42.57

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