Revisiting Mid-Level Patterns for Cross-Domain Few-Shot Recognition

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\textbf{ABSTRACT}

Existing few-shot learning (FSL) methods usually assume base classes and novel classes are from the same domain (in-domain setting). However in practice, it may be infeasible to collect sufficient training samples for some special domains to construct base classes. To solve this problem, cross-domain FSL (CDFSL) is proposed very recently to transfer knowledge from general-domain base classes to special-domain novel classes. Existing CDFSL works mostly focus on transferring between near domains, while rarely consider transferring between distant domains, which is even more challenging. In this paper, we study a challenging subset of CDFSL where the novel classes are in distant domains from base classes, by revisiting the mid-level features, which are more transferable yet under-explored in mainstream FSL work. To boost the discriminability of mid-level features, we propose a residual-prediction task to encourage mid-level features to learn discriminative information of each sample. Notably, such mechanism also benefits the in-domain FSL and CDFSL in near domains. Therefore, we provide two types of features for both cross- and in-domain FSL respectively, under the same training framework. Experiments under both settings on six public datasets, including two challenging medical datasets, validate the rationale of the proposed method and demonstrate state-of-the-art performance. Code will be released\textsuperscript{1}.

\textbf{CCS CONCEPTS}

- Computing methodologies → Computer vision; Image representations; Transfer learning.

\textbf{KEYWORDS}

Cross-domain few-shot learning; Mid-level features; Few-shot learning

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\section{INTRODUCTION}

Few-shot learning (FSL) \cite{41} has been proposed recently to recognize objects in novel classes given only few training samples, with knowledge transferred from base classes (classes with sufficient training samples). Existing FSL works \cite{31,41} usually assume the in-domain setting, where base classes and novel classes are from the same domain. However, such setting may not stand in practice, because for domains where data is hard to obtain, it may be infeasible to collect sufficient training samples from them to construct the base classes either, as shown in Fig. 1. To solve this problem, very recently, cross-domain FSL (CDFSL) \cite{5,40} has been proposed to handle a more realistic setting where data from the general domain (which is easier to collect \cite{5}, e.g., ImageNet \cite{8}) are sampled as base classes, while data from other domains are defined as novel classes. Compared with the general domain, the novel-class domains may contain semantic shift (general-domain to birds \cite{5}), style-shift (natural images to pencil-paintings \cite{49}), or both \cite{14} (general-domain to medical microscopic images, as shown in Fig. 1). The novel-class domains may vary from being close to being distant against the base-class domain \cite{14}, because no assumptions could be made about what novel classes would appear and no one could enumerate all possible classes in base classes.

However, existing CDFSL works \cite{5,40} mostly focus on the transferring between domains that are close to each other, while rarely consider that for distant domains. For instance, some specialized domains such as medical domains usually lack labeled training samples and are very different from the general domain. It is beneficial while challenging to transfer knowledge from general-domain to facilitate recognition of novel classes in these specialized domains. Therefore in this paper, we aim to solve a more challenging subset of the CDFSL problem where base classes and novel classes are from distant domains, termed as distant-domain FSL for abbreviation. Moreover, to facilitate the definition of distant domains, we also use the Proxy-A-Distance (PAD) \cite{4,10} to quantitatively measure domain distances (as shown in Tab. 1 and section 4.2).

To address distant-domain FSL, the model should learn transferable patterns from general-domain base classes and transfer them to distant-domain novel classes. Much work \cite{46} on transfer learning suggests features from shallower (mid-level) layers are more transferable than those from deeper layers. Intuitively, as shown in Fig. 1 (top), high-level patterns from the general domain, such as wings and limbs, can hardly be transferred to distant-domain novel classes, while mid-level patterns, such as circle and dot, are easier to be transferred. Quantitatively, as shown in Fig. 1 (bottom), mid-level features from the third and second blocks of ResNet \cite{16}
When transferring base-class trained model to distant-domain datasets, where mid-level features (3rd and 2nd blocks) could show better performance compared with the high-level features (4th block, i.e., the last layer).

In all, our contributions can be summarized as follows:

- To solve CDFSL in distant domains, we revisit mid-level features to explore their transferability and discriminability, which is seldom studied in the main stream FSL work.
- To enhance the discriminability of mid-level features, we propose a residual-prediction task to explore the unique character of each class.
- Our method is effective for not only the distant-domain FSL but also the in-domain FSL and near-domain CDFSL.

To avoid ambiguity, we denote the feature/pattern of the last layer of the backbone network as high-level feature/pattern, and denote the feature/pattern of the layers other than the first and the last layer as the mid-level feature/pattern.

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with different types of descriptive features. Experiments under both settings on six public datasets, including two challenging medical datasets, demonstrate state-of-the-art performance. Code will be released.

2 RELATED WORK

Few-shot learning methods can be roughly grouped into embedding based method [11, 41, 44, 55–57], meta-learning based method [2, 9, 28, 54], and hallucination based method [15, 43]. The pseudo-novel-class strategy is also adopted in [12]. Very recently, some works [5, 6, 39, 40, 49] studied the problem of cross-domain FSL, which train the model on general-domain classes and evaluate it on novel classes from other domains. [40] proposed to insert affine transformations sampled from the Gaussian distribution to directly apply mid-level features to the classification. In all, the usage of mid-level features is far from being well explored in FSL.

Transferability of deep networks has been researched in the field of transfer learning [46], which shows an decreasing trend of transferability when going deeper into the deep network. Such phenomenon has also been applied in applications such as [25, 48, 50]. Some works [21, 23, 24] in FSL utilize features of multiple appended layers to handle the hierarchy of classes. The only work makes use of mid-level features, to the best of our knowledge, is [18], which directly applied mid-level features to the classification. In all, the usage of mid-level features is far from being well explored in FSL yet, which we revisit in this paper to boost both the distant-domain and the in/near-domain FSL.

3 METHODOLOGY

To learn transferable and discriminative mid-level features, we propose a residual-prediction task to explore the unique character of each class, which will benefit both the distant- and in/near-domain FSL. The framework is shown in Fig. 2.

3.1 Preliminaries

Few-shot learning (FSL) aims at recognizing novel classes given only few training samples. Following the setting of current works [34], we are provided with both base classes $C_{\text{base}}$ with sufficient training samples, and novel classes $C_{\text{novel}}$ where only few training samples are available. Note that $C_{\text{base}}$ and $C_{\text{novel}}$ are non-overlapping. The difference between in-domain FSL and cross-domain FSL lies in whether $C_{\text{base}}$ and $C_{\text{novel}}$ are from the same domain [5]. Few-shot learning is conducted on the training set (a.k.a. support set) of $C_{\text{novel}}$, and the evaluation is carried on the corresponding testing set (a.k.a. query set). For a fair comparison, current works always conduct a K-way n-shot evaluation, which means K novel classes $\{C_i\}_{i=1}^K$ will be sampled from $C_{\text{novel}}$ with n novel-class training samples $\{x_{ij}\}_{j=1}^n$ in each class. For each sampled dataset (i.e., K · n training samples + testing samples, a.k.a. episode), the nearest neighbor classification will be performed, which is represented as

$$y_q = \arg\max_{y_i} P(y_i|x_q^U) = \arg\max_i \frac{e^{s(F(x_q^U), p_i^U)}}{\sum_{k=1}^K e^{s(F(x_q^U), p_k^U)}}$$

where $F()$ is the feature extractor, $x_q^U$ is the testing sample (a.k.a. query sample), $y_i$ refers to class $C_i$, $y_q^U$ is the estimated label for $x_q^U$, $s(\cdot, \cdot)$ is the similarity function (e.g., cosine similarity), and $p_i^U$ is the estimated prototype for class $C_i$, which is typically calculated as $p_i^U = \frac{1}{n} \sum_{j=1}^n F(x_{ij}^U)$ [36]. Based on $y_q^U$, the performance will be evaluated on the sampled dataset. Repeat this sampling-evaluation procedure for hundreds of times, the performance of the evaluated model will be obtained.

Before the non-parametric training and testing on novel classes, the model also needs to be (pre-)trained on the base classes [34] to learn prior knowledges. In this work, we utilize the cosine classifier [5, 21] to be our baseline model, which is regarded as a simple but effective baseline. Given N base classes $\{C_i\}_{i=1}^N$, it trains the model by the cross-entropy loss given the input x and its label y as

$$L_{\text{cls}} = -\log(P(y|x)) = -\log\left(\frac{e^{w^Tf(x)}}{\sum_{k=1}^K e^{w_i^Tf(x)}}\right)$$

where $f(x) \in \mathbb{R}^{d \times 1}$ is the extracted feature using the backbone $f()$, $W \in \mathbb{R}^{N \times d}$ is the parameter for the fully connected (FC) layer, the
We follow [31] to abandon the biases term of the FC layer. As the forward pass of the FC layer is equivalent to the calculation of the cosine similarity of $W^c$ and $f^c(x)$, this baseline is named the cosine classifier. After the training on $C_{\text{base}}$, the backbone will be applied directly as the feature extractor for novel classes (i.e., set $F = f$ in Eq. 1), and the nearest neighbor classification will be performed.

3.2 Residual-prediction task

Although mid-level patterns could be more transferable than high-level ones [46], they may not be discriminative enough. Therefore, to boost the discriminability of mid-level features, we propose a residual-prediction task for the base-class training which encourages mid-level features to learn the discriminative information in each sample. Intuitively, for example, to describe zebra with knowledge from dogs, it is easy to transfer high-level patterns such as feet, tail to zebra. But for zebra’s unique character, zebra stripes, it is hard to transfer high-level patterns (e.g., semantic parts [37]) from dogs, but it is much easier to transfer mid-level patterns such as stripe itself to describe it. Also, as an example, such stripe-like pattern could help the medical analysis [32], i.e., distant-domain recognition. Inspired by this, we assume every class has its unique character that could not be easily described by high-level patterns from other classes, for which mid-level patterns can be more effective, providing discriminative information suitable for mid-level features to learn. To improve mid-level features with such information, the residual prediction task can be divided into the following steps as shown in Fig. 2 (top): we first extract the feature for each base-class sample (e.g., zebra) with the backbone network being trained by the classification loss in Eq.2. Then, for each sample, we design to use high-level patterns from other classes (e.g., dogs, birds, human) to reconstruct the extracted feature (high-level reconstruction), and we remove the reconstructed feature (e.g., zebra without stripe, maybe a white horse) from the extracted feature, outputting a discriminative residual feature (e.g., stripes), which contains the discriminative information for this sample that is suitable for mid-level features to learn. Finally, we constrain mid-level features to predict such discriminative residual feature, which pushes mid-level features to be discriminative. Our method is jointly trained with $L_{cls}$ and the residual-prediction task. Details are in the following.

3.2.1 High-level Reconstruction. Firstly, given a training sample $x$, we use high-level patterns from other base classes to represent (reconstruct) its extracted feature $f(x)$. Current works [12, 31] suggest that the parameters of the base-class FC parameters $W$ could be viewed as the prototypes of base classes, and each row of $W$ (a prototype) contains the overall information of the corresponding class, which refers to the high-level patterns because it exists in the same feature space as that of the backbone’s final layer. Therefore, prototypes are used to reconstruct $f(x)$. The prototypes of the other $N - 1$ base classes for $x$ is denoted as the prototype set $\{W_i\}_{i \neq y}$ where $y$ is the label of $x$ and $W_i \in \mathbb{R}^d$ is the same as the corresponding row in the FC parameters $W$.

The reconstruction is based on the feature and prototypes averagely split along the channel axis. For easy understanding, we begin with the situation where no splitting is applied. Specifically, we use the extracted feature $f(x)$ to apply the nearest neighbor search over $\{W_i\}_{i \neq y}$, and query top $m$ prototypes with the highest cosine similarities to form the neighboring prototype set $\{W^k_i\}_{k=1}^m$. Then, the reconstructed feature is calculated as the mean of all queried prototypes as $R(x, W) = \frac{1}{m} \sum_{i=1}^m W_i$.

To provide a better reconstruction of the extracted feature, we split the extracted feature $f(x)$ averagely into $S$ splits along the channel axis, denoted as $\{f^k(x)\}_{k=1}^S$ where $f^k(x) \in \mathbb{R}^{d/S \times 1}$, i.e., concatenate all split features in $\{f^k(x)\}_{k=1}^S$ could obtain the original feature $f(x)$. We also split each prototype into $S$ splits along the channel axis, where each split of prototypes is denoted as $\{W^k_i\}_{i \neq y}$, where $W^k_i \in \mathbb{R}^{d/S \times 1}$. Then, the above nearest neighbor searching are conducted split-wisely between each $f^k(x)$ and $\{W^k_i\}_{i \neq y}$, outputting a split of reconstructed feature $R^k(x, W) \in \mathbb{R}^{d/S \times 1}$, and finally the reconstructed feature $R(x, W) \in \mathbb{R}^{d \times 1}$ is the concatenation of all splits of reconstructed features, as shown in Fig. 3. As the queried neighboring prototypes can be different across each split group $k$, the splitting operation can provide a closer reconstruction of $f(x)$ compared with directly applying the whole feature (Tab. 10).

Then, we constrain the reconstructed feature to be close to $f(x)$ in the cosine similarity space with the loss

$$L_{\text{recon}} = ||f^c(x) - R^c(x, W)||_2^2$$

where $R^c(x, W)$ is the $L_2$ normalized $R(x, W)$. Note that by applying this loss, we are also trying to decompose $f(x)$ into the split prototypes, which can implicitly integrate the composition information of base classes into the feature, thus helping the in-domain FSL.

3.2.2 Residual Calculation. In experiments (Tab. 10), we find that for the best case that $f(x)$ could be improved for in-domain FSL, $L_{\text{recon}}$ remains about 0.11 to 0.25. Keeping enlarging the weight of $L_{\text{recon}}$ will largely decrease the performance, indicating the best case that the high-level reconstruction can reach, which verifies our assumption that every class has its character that could not be easily represented by high-level patterns from other classes. By removing the high-level patterns from $f(x)$, we will get a discriminative residual feature which contains the discriminative information suitable for mid-level features to learn.

As both $f^c(x)$ and $R^c(x, W)$ are $L_2$ normalized, these vectors can be viewed to be distributed on a unit circle (left figure). Intuitively, the residual term and the high-level reconstructed term should not be representative of each other, which implies they should be orthogonal. Therefore, we prolong the $L_2$ normalized feature $f^c(x)$ to $f^p(x)$ by $f^p(x) = \frac{f^c(x)}{||f^c(x)||_2}$.
\[ f^c(x)/\cos(f^c(x), R^c(x, W)) \], where the cosine value could be obtained as \( 1 - L_{\text{recon}}/2 \). Moreover, this prolonging could also stabilize the training. Thus, the residual is calculated as \( r(x, W) = f^c(x) - R^c(x, W) \in \mathbb{R}^{d \times 1} \).

### 3.2.3 Residual Prediction

Then, to boost the discriminability of the mid-level features, we utilize the mid-level feature to predict the residual term. The predicted residual term is the weighted combination of multiple transformed mid-level features from a fixed mid-layer set \( \{m_l(x)\}_{l=1}^L \) where \( L \) is the number of total candidate mid-layers and \( m_l(x) \in \mathbb{R}^{d \times 1} \) is the mid-level feature for layer \( l \).

For better understanding, we begin with the scenario where only one mid-layer \( m_l(x) \) is used for the residual prediction, and the weighted combination of multiple layers will be included afterwards.

As a vector can be decomposed into its direction (\( L_2 \) normalized vector) and length (\( L_2 \) norm), we can re-write the residual term as

\[ r(x, W) = \frac{r(x, W)}{||r(x, W)||_2} - r^c(x, W) \cdot ||r(x, W)||_2 \]

In practice, we find it beneficial to predict the direction \( r^c(x, W) \) and the length \( ||r(x, W)||_2 \) of the residual term separately. For better understanding, we first introduce the prediction of the residual term’s direction, which is similar to the prediction of its length.

Therefore, firstly our aim is to transform a mid-level feature \( m_l(x) \) to predict \( r_l(x, W) \). As it is the mid-level feature instead of another high-level feature that is what we want, we should avoid learning another high-level feature by utilizing any deep and complex transformation network during the prediction. Therefore, we simply transform the mid-level feature by multiplying a matrix and adding a bias on it, which is calculated as

\[ r^c_l(x, W) = \frac{W^c_l m_l(x) + b^c_l}{||W^c_l m_l(x) + b^c_l||_2} \]

where \( W^c_l \in \mathbb{R}^{d \times d_l} \) and \( b^c_l \in \mathbb{R}^{d \times 1} \) are the weights and the biases for the transformation, and \( d_l \) is the dimension of layer \( l \). The prediction is also \( L_2 \) normalized to represent a direction, which simplifies the prediction.

Similarly, the prediction of the residual term’s length \( ||r(x, W)||_2 \) is also performed by a simple transformation as

\[ r^s_l(x, W) = W^s_l m_l(x) + b^s_l \]

where \( W^s_l \in \mathbb{R}^{d \times 1} \) and \( b^s_l \in \mathbb{R} \) are the corresponding parameters.

Given the predicted direction and length from \( m_l(x) \), the predicted residual term can be represented as \( r_l(x, W) = r^c_l(x, W) \cdot r^s_l(x, W) \in \mathbb{R}^{d \times 1} \), and we design a loss as \( ||r_l(x, W) - r^c_l(x, W)||^2_2 + \alpha (r_l(x, W) - ||r_l(x, W)||_2)^2 \) to separately push the direction and length to be close to the residual term.

For the prediction from multiple mid-layers, we learn two weights for each layer’s predicted direction and predicted length respectively, which are denoted as \( a_l(x) \) and \( a^2_l(x) \) and calculated as

\[ a_l(x) = \frac{t_l(m_l(x))}{\sum_{k=1}^L t_k(m_l(x))}; \quad a^2_l(x) = \frac{t^2_l(m_l(x))}{\sum_{k=1}^L t^2_k(m_l(x))} \]

where \( t_l \) and \( t^2_l \) are implemented as two independent single-layer perceptrons appended to the corresponding mid-level feature \( m_l(x) \) and each will output a scalar value. With these layer-wise weights, we can simply use a fixed candidate mid-layer set to include all layers other than the first and the last layer.

Then, the weighted combination of the predicted direction and length from multiple mid-layers can be represented as

\[ r^c(x, W) = \frac{\sum_{l=1}^L a_l(x) \cdot r_l^c(x, W)}{||\sum_{l=1}^L a_l(x) \cdot r_l^c(x, W)||_2} \]

Finally, the prediction loss which separately pushes the direction and length to be close is calculated as

\[ L_{\text{mid}} = ||r^c(x, W) - r^c_l(x, W)||^2_2 + \alpha (r^c(x, W) - ||r^c(x, W)||_2)^2 \]

where \( r^c(x, W) \) and \( ||r(x, W)||_2 \) is the direction and length of the residual term respectively, and \( \alpha \) is a pre-defined hyper-parameter. The first part of \( L_{\text{mid}} \) is the direction prediction loss, and the second part is the length prediction loss. This process is shown in Fig. 4.

The final loss for base-class training is

\[ L = L_{\text{cls}} + \lambda_1 L_{\text{recon}} + \lambda_2 L_{\text{mid}} \]

where \( \lambda_1 \) and \( \lambda_2 \) are predefined hyper-parameters.

### 3.3 Novel-class Recognition

Although we aim to boost mid-level features for distant-domain classes, this framework is also effective for in-domain FSL and CDFSL in near domains. We provide two novel-class features under the same training framework, for both the distant- and in/near-domain settings respectively as shown in Fig. 2 (bottom), according to the quantitative domain distance measure by PAD \([10]\).

#### 3.3.1 Distant-domain

As all mid-level features within the candidate mid-feature set are improved but they are of different feature dimensions, we use the weighted concatenation of all mid-level features as the final feature as
Table 1: Datasets and quantitative domain distances.

| Dataset          | Classes | Samples | Train/val/test class number | PAD |
|------------------|---------|---------|----------------------------|-----|
| minilimageNet    | 100     | 60,000  | 64 / 16 / 20               | 0.53|
| CUB-200-2011     | 200     | 11,788  | 100 / 50 / 50              | 0.60|
| Kinetics         | 100     | 6,400   | 64 / 12 / 24               | -   |
| Pencil-paintings*| 36      | 21,600  | - / 16 / 20                | -   |
| TBN cell*        | 3       | 363     | - / - / 3                  | 1.80|
| Malaria cell*    | 2       | 27,558  | - / - / 2                  | 2.00|

\[
F(x) = \text{concatenate} \left( \{a_j(x) \cdot m^*_j(x)\}_{j=1}^L \right)
\]

where \(F(x)\) is the final feature in Eq. 1, and \(\{m^*_j(x)\}_{j=1}^L\) is the L₂ normalized candidate mid-feature set with the weight \(a_j(x)\) in Eq. 7 for each layer. For clarity we denote this distant-domain feature as \(F_k(x)\). The ablation study of each mid-feature is validated in Tab. 8.

3.3.2 In/near-domain. The base-class training stated above is actually a pseudo-novel training strategy, which views the current sample \(x\) as a pseudo-novel-class sample and views other classes as pseudo-base classes for it, providing simulated in-domain novel-class data. As adequate information is provided for \(większ\), the extracted pseudo-novel feature \(f(x)\) can be viewed as the ground truth for such pseudo-novel training. By encouraging the high-level reconstruction from pseudo-base classes, we are trying to predict the pseudo-novel feature \(f(x)\) merely based on pseudo-base prototypes \(\{W_l\}_{l \neq y}\). By predicting the discriminative pseudo-novel residual feature, we are also encouraging the model to be able to predict the real discriminative residual feature for the (real) novel-class feature. After such training, on base classes the model will be able to predict the discriminative pseudo-novel feature \(f(x)\), merely based on the pseudo-base-class prototypes \(\{W_l\}_{l \neq y}\) and mid-level features, which makes it able to predict the discriminative in/near-domain (real) novel-class feature, thus helping the in/near-domain FSL.

Therefore, we use all base-class prototypes to conduct the high-level reconstruction, and then the reconstructed feature together with the predicted residual term will be combined to be the final feature, which is calculated as

\[
F(x) = R^c(x, W) + r^c(x, W) \cdot r^c(x, W)
\]

For clarity we denote this in/near-domain feature as \(F_k(x)\).

Finally, the nearest neighbor classification based on Eq. 1 will be conducted and obtain the final performance.

4 EXPERIMENTS

Extensive experiments are conducted under both distant-domain and in-domain FSL settings. Due to space limitation, more details are included in the supplementary material.

4.1 Datasets and Settings

Datasets used for evaluation are summarized in Tab. 1, where val denotes validation, and * denotes distant-domain datasets, including Pencil-paintings dataset [49] and two medical datasets3 (TBN Cell [30] and Malaria Cell [33]). minilimageNet [41] is a subset of ImageNet [8] and the pencil-paintings dataset contains novel classes of minilimageNet converted to the pencil-painting images.

The CUB [42] dataset is a fine-grained dataset of birds, and the Kinetics dataset [53] contains video actions. Some examples can be found in Fig. 2 (bottom). For the distant-domain setting, the listed datasets are used as novel classes, and the base classes of minilimageNet are used as base classes [5]. Following existing methods [41], the mean accuracy (%) and the 95% confidence intervals of randomly generated K-way n-shot episodes from test sets (novel classes) will be reported.

4.2 Quantitative Measure of Domain Distances

We first utilize Proxy-A-Distance (PAD) [4, 10] for quantitative domain distance measuring. As minilimageNet is used as the base classes for all the distant-domain evaluation, we calculate the PAD between all candidate domains’ novel classes with base classes from minilimageNet. Details are in supplementary materials, results are listed in the last column of Tab. 1.

As minilimageNet’s base and novel classes are from the same domain [41], the distance between these two set could be viewed as the lower bound for the PAD. From Tab. 1 we can see that the PAD of CUB is quite close to this lower bound, indicating this dataset should be used as the CDFSL dataset that is in the near domain of minilimageNet. The pencil-paintings is the third distant domain. Unsurprisingly that it is closer than two medical datasets as it shares semantically similar classes with base classes of minilimageNet, but is much more distant than CUB. Therefore, we use this dataset as a distant domain. The two medical datasets are the furtherest datasets, with the Malaria cell dataset reaches the upper bound of PAD (2.0), so these two datasets are also selected as distant domains.

4.3 Implementation Details

Due to the space limitation, detailed parameter settings are in the supplementary material. For the CUB benchmark, we follow current works [31, 38, 45] to use the provided bounding boxes to crop the images. For the Kinetics dataset, to handle the temporal information, we uniformly sample 8 frames from the video, and a temporal convolution layer with the kernel of \(8 \times 1 \times 1\) is appended to the backbone network. Following [53], we use the pre-trained weights from the ImageNet. For all the above models, the mid-level feature maps of size \(h_l \times w_l \times d_l\) (\(t_l \times h_l \times w_l \times d_l\)) is global averaged in all dimensions except the last one to obtain the mid-level feature. As all elements in extracted features are positive due to the ReLU [13] activation, to constrain prototypes in the same feature space as the extracted features, we also apply an \(\text{abs}()\) function to use the absolute values. For medical datasets, to preserve resolutions, we use raw images from ImageNet as base classes.
Table 2: Distant-domain performance on pencil-paintings.

| Method            | 5-way 1-shot | 5-way 5-shot |
|-------------------|--------------|--------------|
| MatchingNet [41]  | 23.35 ± 0.64 | 32.42 ± 0.55 |
| RelationNet [44]  | 23.87 ± 0.82 | 33.29 ± 0.96 |
| PPA [31]          | 23.86 ± 0.42 | 33.74 ± 0.41 |
| SGM [43]          | 23.49 ± 0.29 | 32.67 ± 0.32 |
| ProtoNet [36]     | 23.23 ± 0.32 | 32.92 ± 0.41 |
| MetaOptNet [20]   | 24.53 ± 0.28 | 33.23 ± 0.63 |
| Baseline++ [5]    | 24.06 ± 0.46 | 32.74 ± 0.81 |
| LFT-GNN [40]      | 27.02 ± 0.43 | 34.28 ± 0.43 |
| DAPN [49]         | 27.25 ± 0.25 | 37.45 ± 0.25 |
| Cosine Classifier | 29.18 ± 0.24 | 37.21 ± 0.37 |
| Ours_5           | 29.45 ± 0.22 | 40.38 ± 0.35 |

Table 3: Distant-domain performance on medical datasets.

| Method            | TBN cell (3-way) | Malaria cell (2-way) |
|-------------------|------------------|----------------------|
|                  | 1-shot | 5-shot | 1-shot | 5-shot |
| Pixel             | 44.03 ± 0.27 | 51.95 ± 0.38 | 53.01 ± 0.40 | 53.79 ± 0.53 |
| Random Init       | 48.38 ± 0.33 | 55.87 ± 0.44 | 52.75 ± 0.36 | 55.78 ± 0.58 |
| MatchingNet [41]  | 44.40 ± 0.31 | 60.52 ± 0.43 | 53.92 ± 0.38 | 57.65 ± 0.54 |
| DAPN [49]         | 54.18 ± 0.38 | 64.56 ± 0.29 | 55.22 ± 0.40 | 63.88 ± 0.37 |
| ProtoNet [36]     | 59.56 ± 0.28 | 68.68 ± 0.39 | 58.12 ± 0.37 | 67.68 ± 0.35 |
| Baseline++ [5]    | 56.89 ± 0.32 | 66.25 ± 0.40 | 60.47 ± 0.37 | 71.35 ± 0.48 |
| MatchingNet++ [6] | 51.54 ± 0.31 | 62.57 ± 0.39 | 59.97 ± 0.39 | 64.47 ± 0.52 |
| ProtoNet++ [6]    | 60.07 ± 0.28 | 68.95 ± 0.38 | 59.85 ± 0.38 | 70.06 ± 0.52 |
| LFT-GNN [40]      | 54.20 ± 0.39 | 67.13 ± 0.31 | 62.54 ± 0.52 | 74.51 ± 0.38 |
| Multi-net [18]    | 61.71 ± 0.28 | 68.95 ± 0.40 | 60.86 ± 0.39 | 72.60 ± 0.54 |
| Cosine Classifier | 60.65 ± 0.28 | 68.96 ± 0.36 | 59.16 ± 0.35 | 70.41 ± 0.39 |
| Ours_5            | 64.12 ± 0.26 | 72.88 ± 0.36 | 63.82 ± 0.41 | 76.94 ± 0.32 |

4.5 Ablation Study

For better understanding, we report the ablation studies first for the
in-domain FSL and then for the distant-domain FSL.

4.5.1 In-domain Setting. The performance of models implemented
with different modules is in Tab. 9. Each row in the second
column represents the model with modules of all the above rows plus
the module in the current row. For the cosine classifier, +abs, and
+L_recon, we use the backbone extracted feature as the final feature
(i.e., $F = f$ in Eq. 1). For +L_mid, we use $F_{50}$ as the final feature.

From this table we can see that each module contributes to the
performance respectively. abs contributes because all the proto-
types are constrained to be positive, which is the same as the
extracted features, simplifying the training. L_recon also improves
the performance because by encouraging the pseudo-novel feature
close to the reconstructed feature, the network is pushed to learn
the composition of base-class prototypes. Moreover, we can see that
L_recon contributes the most to CUB by around 4%, exceeding
that to all other datasets. On the other hand, for $l_{mid}$ on CUB this
term contribute less than that on minImageNet. This is because
CUB is a fine-grained dataset for birds. As nearly all birds contain similar high-level patterns (e.g., wings, beak), the high-level feature reconstruction on CUB will be much easier than on miniImageNet. In miniImageNet, various classes exist, such as dogs, cars, ships, which means these classes may not contain as many overlapped high-level patterns as that on CUB, making the high-level feature reconstruction harder. Therefore, $L_{\text{recon}}$ promotes more on CUB. Moreover, it can also explain why $L_{\text{mid}}$ promotes more on miniImageNet than CUB: As there are larger residual terms on miniImageNet that could not be well reconstructed by prototypes, the mid-level prediction helps more.

4.5.2 Distinct-domain Setting. The ablation study is in Tab. 8, with the feature of the forth (i.e., final), the third, the second block and the concatenation of the third and second block (i.e., $F_3()$). We can see that almost all forth blocks’ features are outperformed by that of the third blocks, which is consistent with the study [46] that mid-level features can be more transferable than final-layer’s feature, and verifies the choice of distant domain datasets. For this challenging setting, methods that helps the in-domain FSL cannot show significant improvements now, because by fitting the base classes (especially $L_{\text{recon}}$), the model is likely to learn more about the domain-specific information which may harm the transferability. Meanwhile, by applying $L_{\text{mid}}$, we can see a clear improvement of mid-level features over baselines and the forth layer features, which verifies the our motivation: boosting the discriminability of mid-level features by the residual-prediction task.

4.5.3 Comparison of high-level reconstruction. We trained our model with $L_{\text{recon}}$ on miniImageNet with different splits in Tab. 10, with the optimal performance and the $L_{\text{recon}}$ value. We can see by splitting the extracted feature and prototypes, the reconstructed feature gets closer to the extracted feature ($L_{\text{recon}}$ decreases as splits increase), leading to the best feature implicitly encoded with base-class prototypes (setting splits to 4, obtaining the accuracy at 59.15). Also, we can see that for the best improved feature, $L_{\text{recon}}$ remains larger than 0.1, which coarsely corresponds to an angle of 20° in the degree measure, verifying the existence of residual terms.

4.6 Visualization

To verify the contribution of mid-level patterns, we visualize the activated regions on novel classes of miniImageNet in Fig. 5. As the high-level and mid-level representations are already implicitly encoded in the extracted feature, we visualize the final-layer feature maps of models trained with (w/) and without (w/o) $L_{\text{mid}}$, together with the transformed mid-layer feature maps (t. mid), by means of summing up and resizing all the feature maps [51]. We can see the model trained without $L_{\text{mid}}$ covers less activated regions than that trained with $L_{\text{mid}}$, indicating regions that are unable to be described by the baseline method are now better described by our model. The difference in the covered activated regions coarsely corresponds to the activated regions of the transformed mid-layer feature maps, which verifies the contribution of mid-level patterns.

5 CONCLUSION

To learn transferable and discriminative mid-level features for the distant-domain FSL, we proposed a residual-prediction task consisting of the high-level feature reconstruction and the mid-level residual prediction, which consistently achieves state-of-the-art performance and better. Extensive experiments on both the distant- and in-domain settings including image recognition and video recognition show the rationale and the insights of the proposed method.
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