

TDAPM: Target Distribution Alignment via Progressive Matching for Multi-Source-Free Domain Adaptation

– *Supplementary Materials*

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In what follows, we provide a more detailed theoretical derivation for the progressive prediction alignment strategy employed in TDAPM.

1. Theoretical Derivations for Progressive Prediction Alignment

We provide a more detailed theoretical derivation for the progressive prediction alignment strategy employed in TDAPM, specifically focusing on bounding the generalization error of the target model. Our analysis draws inspiration from established frameworks in domain adaptation theory, adapting them to the source-free, iterative prediction alignment context.

Let P_S and P_T denote the true data distributions of the source and target domains, respectively. In the MSFDA setting, we have access to m source models $\{\theta_S^j\}_{j=1}^m$ pre-trained on $S_j \sim P_S$, and unlabeled target data $T \sim P_T$. Our goal is to learn a target model θ_T that performs well on P_T .

1.1. Generalization Bound for Iterative Adaptation

We define a sequence of target models $\{\theta_k\}_{k=0}^K$, where θ_0 is the initial target model constructed from a weighted ensemble of source models, and θ_k is the model at iteration k after adapting to the target data. Let $L(\theta, P)$ denote the loss of model θ on distribution P . We are interested in bounding $L(\theta_K, P_T)$.

Following a chain rule for generalization error, the error of the final model θ_K on the true target distribution P_T can be related to the error of the initial model and the accumulated shifts during the iterative process. We can express the target risk of θ_K as:

$$L(\theta_K, P_T) = L(\theta_0, P_T) + \sum_{k=1}^K [L(\theta_k, P_T) - L(\theta_{k-1}, P_T)] \quad (1)$$

This decomposition is generally difficult to bound directly. Instead, we leverage the concept of distribution discrepancy between successive model predictions.

Let P_{θ_k} denote the prediction distribution (output probabilities) of model θ_k on target domain samples. The core idea of progressive prediction alignment is to minimize the discrepancy between P_{θ_k} and $P_{\theta_{k-1}}$. Specifically, TDAPM optimizes θ_k such that the pairwise alignment loss $\mathcal{L}_{\text{align}} = -I(P_{\theta_{k-1}}(x'), P_{\theta_k}(x))$ is minimized. This can be viewed as an attempt to make P_{θ_k} “close” to $P_{\theta_{k-1}}$.

Let $D(P_1, P_2)$ be a suitable discrepancy measure between two prediction distributions P_1 and P_2 (e.g., KL divergence). We make the following assumptions:

1. **Bounded Prediction Shift:** The progressive alignment strategy ensures that the discrepancy between consecutive prediction distributions is bounded. That is, for each iteration k , there exists a $\pi_k \in [0, \Pi_{\max}]$ such that $D(P_{\theta_k}, P_{\theta_{k-1}}) \leq \pi_k$. This π_k quantifies the “progress” or “shift” in the prediction distribution from one iteration to the next. In TDAPM, the mutual information maximization loss $\mathcal{L}_{\text{align}}$ directly aims to keep this shift small.
2. **Regularization Contribution:** Each iteration might include regularization terms, denoted by $\mathcal{R}(\theta_k)$, which add to the total loss. We assume these regularization terms contribute $\lambda_k \mathcal{R}(\theta_k)$ to the error at iteration k .

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3. Relationship between Model Change and Risk: A crucial step is to relate the prediction distribution shift to the change in target risk. While a direct equality $L(\theta_k, P_{\mathcal{T}}) - L(\theta_{k-1}, P_{\mathcal{T}}) \leq D(P_{\theta_k}, P_{\theta_{k-1}})$ is generally strong, under conditions of sufficient model capacity and smooth loss landscapes, it is reasonable to assume that controlling the prediction distribution shift helps control the risk change. Specifically, we can write:

$$L(\theta_k, P_{\mathcal{T}}) \leq L(\theta_{k-1}, P_{\mathcal{T}}) + \gamma_k D(P_{\theta_k}, P_{\theta_{k-1}}) + \lambda_k \mathcal{R}(\theta_k) \quad (2)$$

where γ_k is a scaling factor that depends on the properties of the loss function and model. For simplicity in the initial theoretical insight, we can consider $\gamma_k \approx 1$ for a direct relationship.

Applying this iteratively from $k = 1$ to K :

$$L(\theta_K, P_{\mathcal{T}}) \leq L(\theta_0, P_{\mathcal{T}}) + \sum_{k=1}^K [\gamma_k D(P_{\theta_k}, P_{\theta_{k-1}}) + \lambda_k \mathcal{R}(\theta_k)] \quad (3)$$

Substituting the bounded prediction shift assumption:

$$L(\theta_K, P_{\mathcal{T}}) \leq L(\theta_0, P_{\mathcal{T}}) + \sum_{k=1}^K [\gamma_k \pi_k + \lambda_k \mathcal{R}(\theta_k)] \quad (4)$$

This is the general form of Eq. (1) in the revised manuscript:

$$L(\theta_K, P_{\mathcal{T}}) \leq L(\theta_0, P_{\mathcal{T}}) + \sum_{k=1}^K (D(P_{\theta_k}, P_{\theta_{k-1}}) + \lambda_k \mathcal{R}(\theta_k)). \quad (5)$$

1.2. Simplification and Interpretation

To simplify further and provide a clearer interpretation, let's assume:

- The prediction shift is uniformly bounded: $D(P_{\theta_k}, P_{\theta_{k-1}}) \leq \pi$ for all k . This is a reasonable assumption if the iterative steps are small and controlled.
- The regularization strength is constant per iteration: $\lambda_k \mathcal{R}(\theta_k) = R$ for all k . This R encapsulates the contribution of all regularization terms (e.g., diversity loss, domain indicator loss) to the overall generalization error in each step.

Under these simplifying assumptions, the sum becomes:

$$\sum_{k=1}^K (D(P_{\theta_k}, P_{\theta_{k-1}}) + \lambda_k \mathcal{R}(\theta_k)) \leq \sum_{k=1}^K (\pi + R) = K(\pi + R) \quad (6)$$

Substituting this back into the bound:

$$L(\theta_K, P_{\mathcal{T}}) \leq L(\theta_0, P_{\mathcal{T}}) + K(\pi + R). \quad (7)$$

Let $\alpha_0 = L(\theta_0, P_{\mathcal{T}})$ represent the initial loss on the target distribution before any iterative adaptation. Then, we arrive at my revised manuscript Eq. (2):

$$L(\theta_K, P_{\mathcal{T}}) \leq \alpha_0 + K(\pi + R). \quad (8)$$