Supplementary Material

Anonymized Authors

Anonymized Affiliations
email@anonymized.com

1 Algorithm

Algorithm 1 PID module in end-to-end PID-LRSC

Input: Feature clusters $\mathbf{Z} = \{\mathbf{Z}_1, \mathbf{Z}_2, \mathbf{Z}_3\}$, Prototype features $\mathbf{Z}^{\mathrm{PI}}$
Output: Final bag feature $\mathbf{Z}_{\mathrm{WSI}}$ and label map `label`

for $k = 1$ to 3 **do**
  $d_k \leftarrow D\big(\mathbf{Z}_k, \mathbf{Z}^{\mathrm{PIs}}\big)$ ▷ Distribution-aware CFD metric
end for
$\{w_k\}_{k=1}^{3} \leftarrow 1 - \mathtt{Normalize}(\{d_k\})$
$\mathtt{order} \leftarrow \mathtt{argsort}(\{w_k\}, \mathtt{descend})$
$\mathtt{label}[\mathtt{TIs}] \leftarrow \mathbf{Z}_{\mathtt{order}[1]}, \ \ldots, \ \mathtt{label}[\mathtt{BGIs}] \leftarrow \mathbf{Z}_{\mathtt{order}[3]}$
$\mathbf{Z}_{\mathrm{final}} \leftarrow \mathcal{A}\Big(\mathtt{concat}(\sum_{k=1}^{3} w_k\, \mathbf{Z}_k, \mathbf{Z}^{\mathrm{PI}})\Big)$
return $\mathbf{Z}_{\mathrm{WSI}}$, `label`

2 Datasets and Configurations

Datasets: We conduct experiments on two private datasets collected from some institution for squamous cell carcinoma pathological grading. **AMU-LSCC** is for laryngeal squamous cell carcinoma pathological grading and **AMU-CSCC** is for cervical squamous cell carcinoma. **AMU-LSCC** dataset includes 342 whole slide images that was divided by a 6:4 training-validation ratio for each category. Specially Grade I contains a total of 89 WSIs, Grade II contains 152 WSIs and Grade III includes 101 WSIs. **AMU-CSCC** dataset includes 262 whole slide images, where Grade I contains a total of 27 WSIs, Grade II contains 127 WSIs and Grade III includes 108 WSIs. 961 patches were grid cropped from each WSI on two datasets. Besides, we validate generalization of proposed PLoRC on two public datasets, where **DHMC-LUNG** [9] is for lung adenocarcinoma classification and **DHMC-KIDNEY** [13] is for renal cell carcinoma sub-types classification.
Compared MIL Models: Eleven SOTA models are implemented for comparison. They are ABMIL [4], CLAMs [6], TransMIL [7], DTFD-MIL [11], IBMIL [5], ILRA-MIL [10], S4MIL [3], FRMIL [1], DGRMIL [14], ACMIL [12], RRT-MIL [8]

and MFC-MIL [2]. We report metrics Accuracy and Area Under Curve (AUC) for evaluation.

Implementation: For end-to-end training, we employ Rmsprop optimizer and the learning rate schedule sets: 1×10^{-5} for epochs 1–50, 5×10^{-6} for epochs 51–75, and 1×10^{-6} for epochs 76–100. Models on two private datasets were trained with a batch size of 2 and 100 epochs. For two public datasets, batch size is set 1. The random seed was fixed 0 across all stages to ensure reproducibility. The input resolution of PLoRC was $96 \times 96 \times 3$. The hyper-parameter in loss function setting is $\gamma_1 = \gamma_2 = 0.1$, $\gamma_3 = 1 \times 10^{-4}$. The low rank hyper-parameter $r = 384$ when parameterizing $\mathbf{A}$. Patches were grid cropped from each WSI in 10x magnification and we filtered out instances with blank areas. All models are employed under the same experimental configurations with four *NVIDIA A10 Tensor Core 24GB* GPUs. The peak GPU memory usage is reported 10GB.

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