Improving Pathology Foundation Models for Brain Tissue using Parameter Efficient Fine-tuning

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Project Page

Introduction

- **Significance:** Adaptation of pathology foundation models to brain tissue is essential for extending AI-assisted diagnostics to rare and complex neurological conditions.
- **Foundation Models:** Large-scale vision transformers pretrained on histopathology data have shown strong generalization across multiple cancer types.
- **But here's the challenge:** These models often face domain shift when applied to brain tissue as brain histology is fundamentally different from other tissues.
- **Why not retrain?** Full fine-tuning of large models like Virchow2 is computationally expensive and risks losing valuable pretrained knowledge.
- **Interpretability:** Leverage EAGLE pipeline (specifically CHIEF) to identify most diagnostically relevant tiles.
- **Combined solution:** Facilitate domain adaptation through parameter-efficient fine-tuning (PEFT), preserving interpretability and reducing computational overhead.
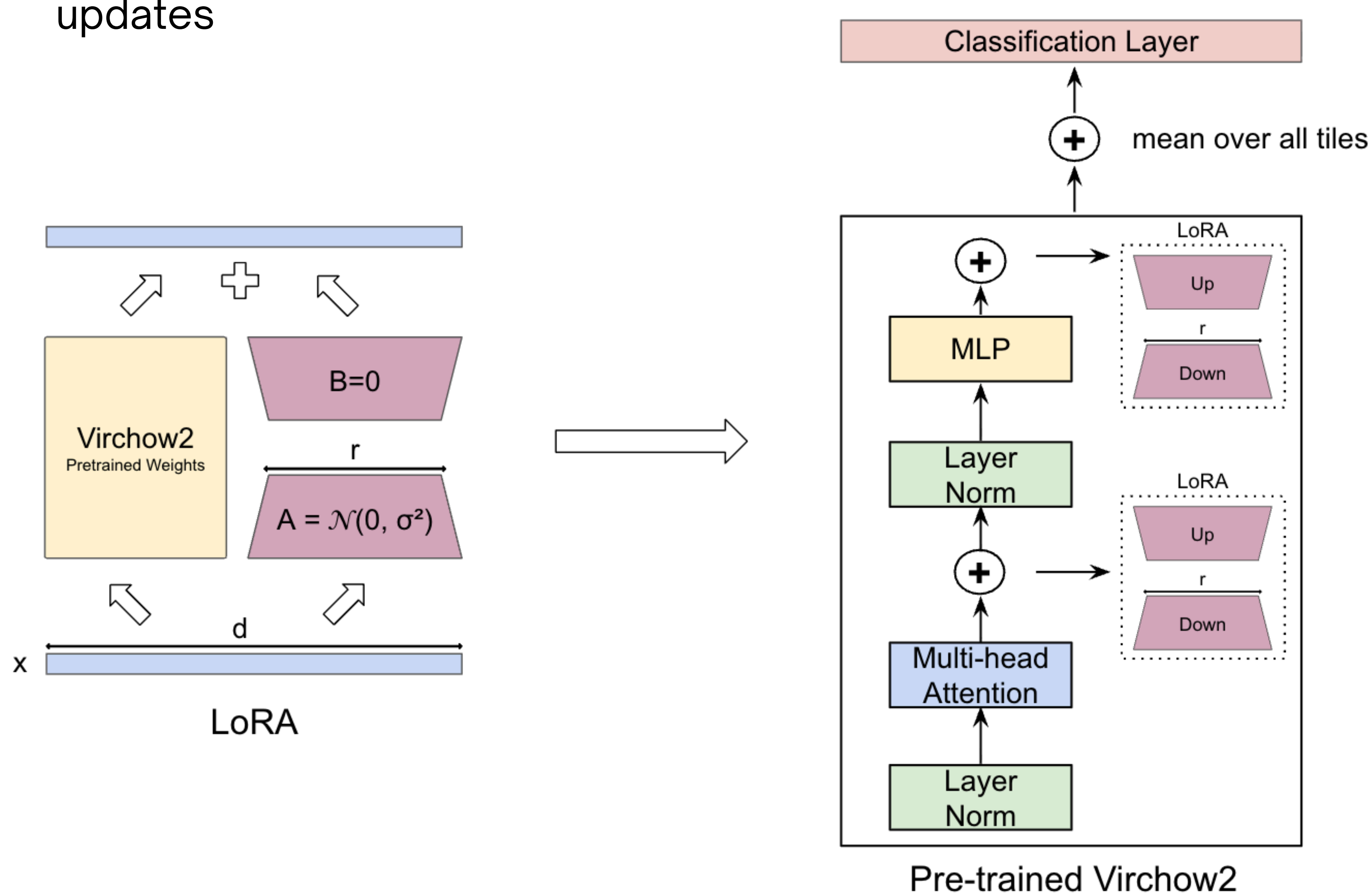
Methodology

- Fetch most **diagnostically** relevant tiles which can be interpreted by pathologist
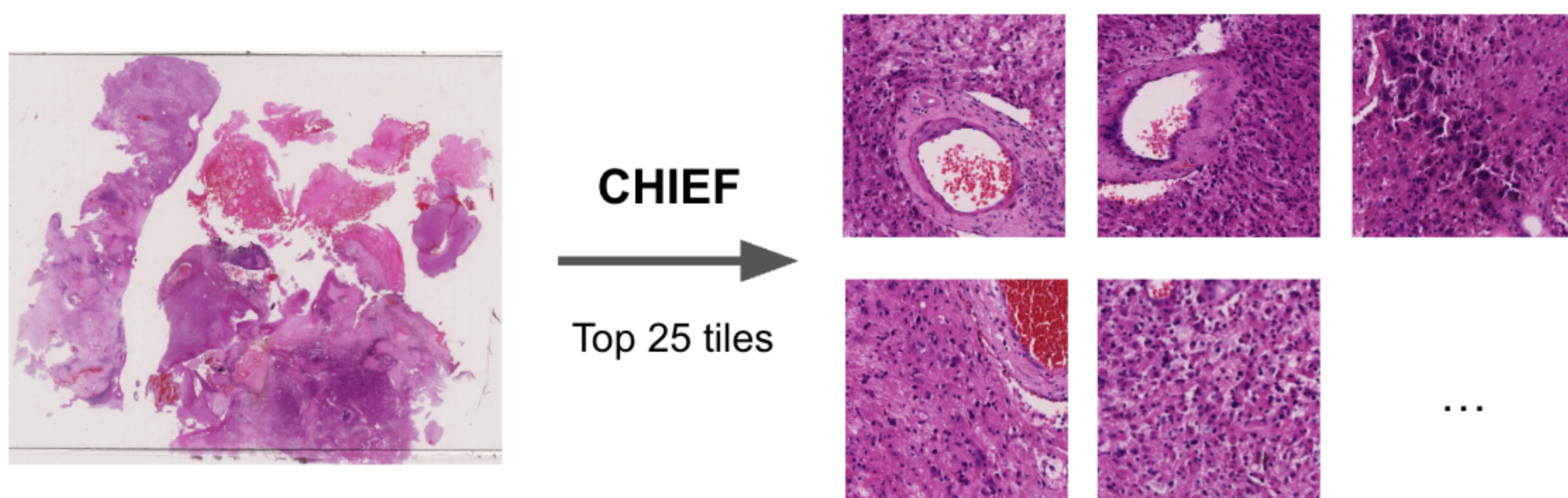
1) Top 25 tiles filtered from CHIEF

- LoRA adapter applied on **MLP and attention layers** for low-rank updates

2) Fine-tuning Virchow2 with LoRA

Research objectives

Our study focuses on advancing the adaptation of foundation models in brain histopathology. The key objectives of our research are:

- **Address domain shift** between general pathology models and brain-specific morphology.
- **Apply LoRA-based fine-tuning** to adapt Virchow2 for brain tissue without full retraining.
- **Demonstrate performance gains** in underrepresented tumor classes while maintaining computational efficiency.
- **Deliver an interpretable, lightweight, and clinically relevant** adaptation pipeline for computational pathology foundation models.
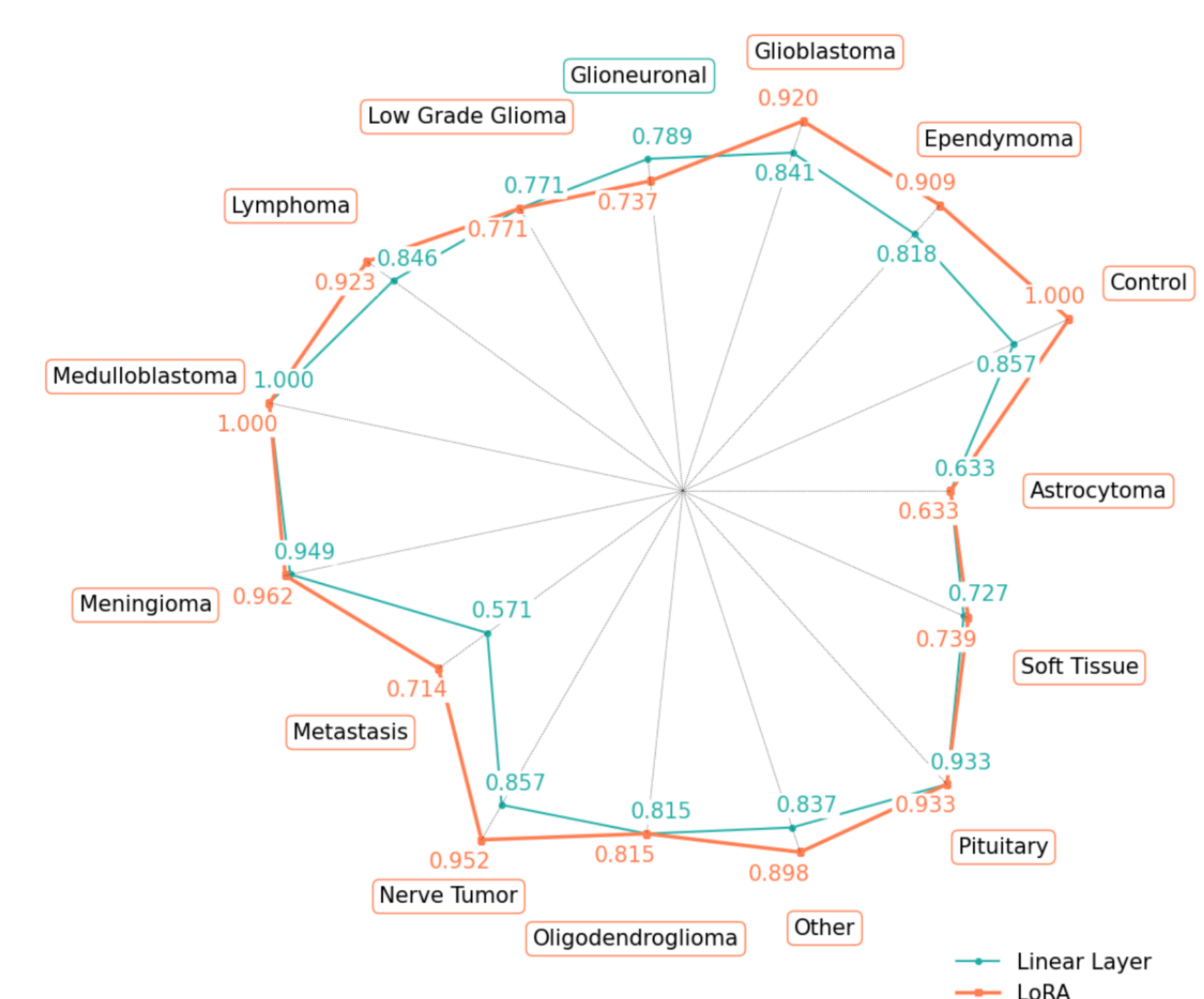
Experimental results

PEFT adaptation of EAGLE on The Digital Brain Tumor Atlas (TDBTA) results in significant perforamance improvements.

- Results on **tumor classification**

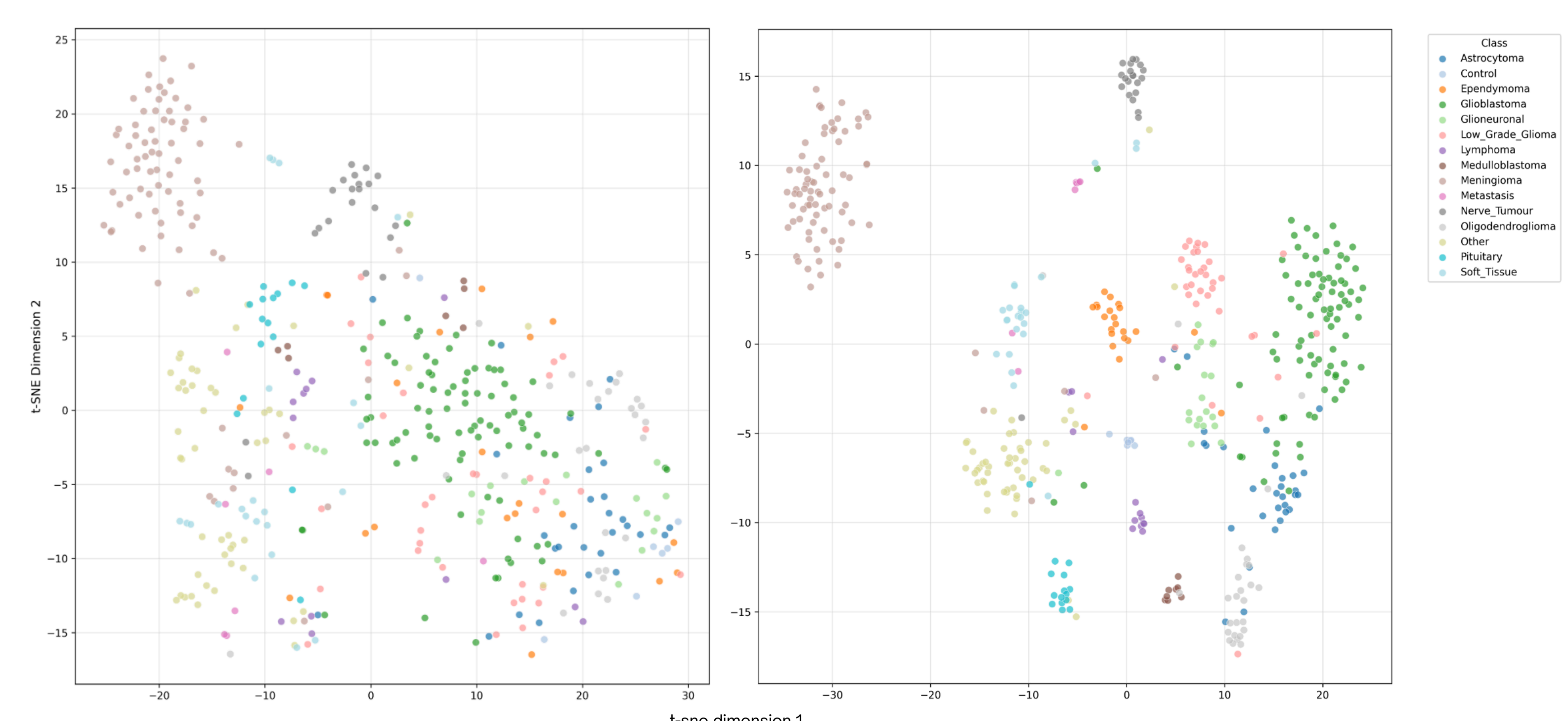Table: Performance on EBRAINS (TDBTA) test set

	Accuracy	Balanced Accuracy
Linear Probing (Baseline)	83.21	81.64
LoRA (Fine-tuning)	**87.07**	**86.04**

- Improved performance in **under-represented classes**

3) Tumor Classification

- PEFT closely **aligns embeddings** of similar classes

4) t-SNE plot before and after fine-tuning