



Transductive Zero-Shot & Few-Shot Adaptation of Large Medical Vision Language Models



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Jose Dorz



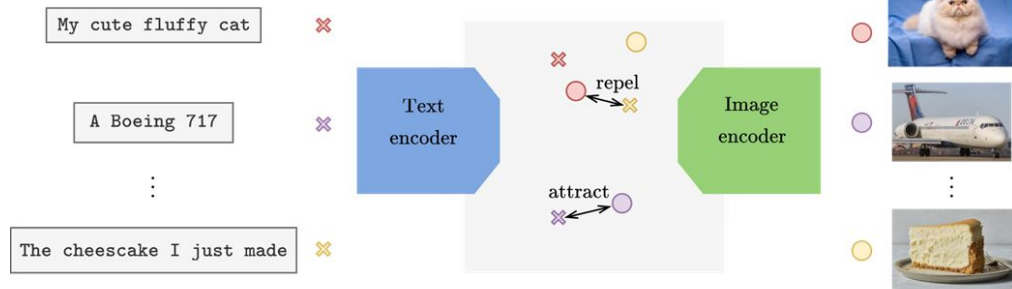
Houda Bahig

Fereshteh Shakeri
Jan 2026

Lots of different Vision-Language Models out there

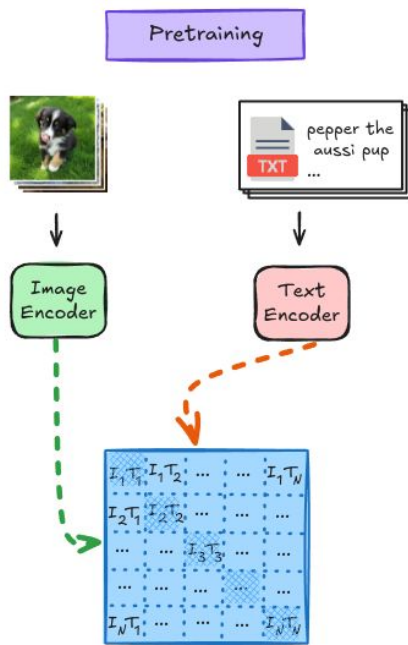
Among them...

- **CLIP: generic text-image pairs of internet**



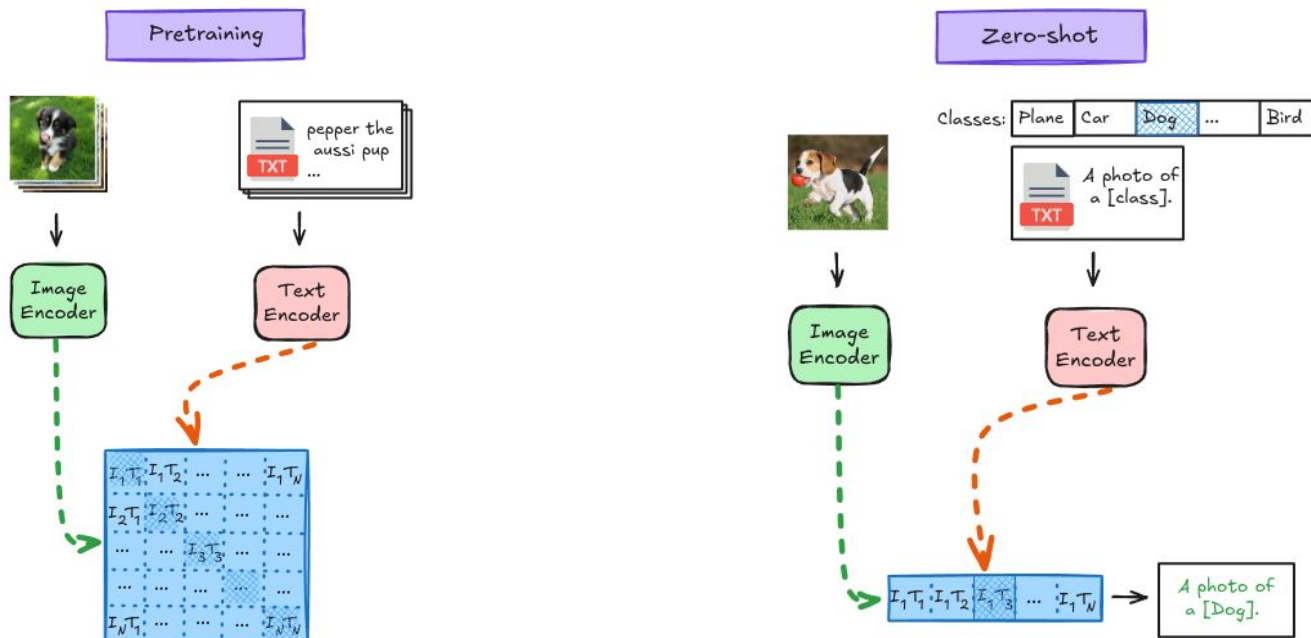
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Generalist Vision-language Models (CLIP)



Radford, Alec, et al. "Learning transferable visual models from natural language supervision." PMLR, 2021.

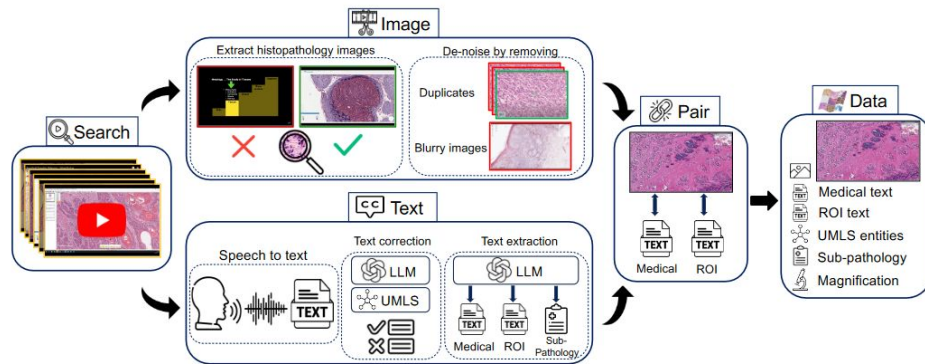
Generalist Vision-language Models (CLIP)



Lots of different Vision-Language Models out there

Among them...

- CLIP: generic text-image pairs of internet
- Quilt: from Youtube



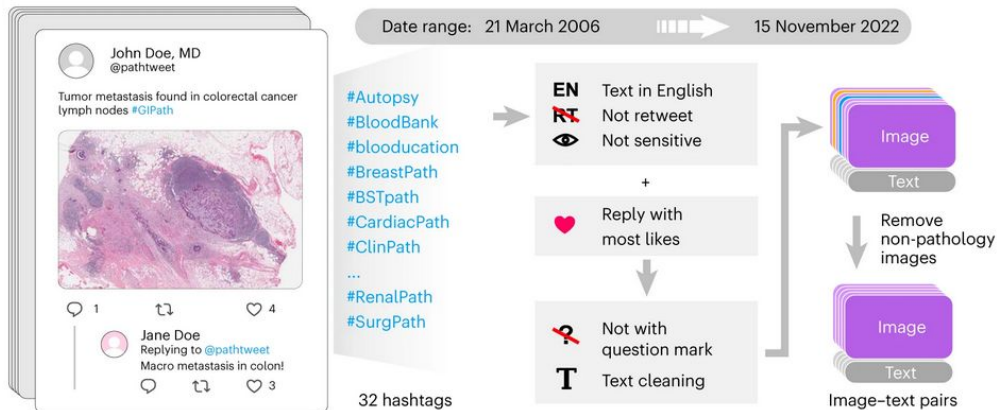
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Lots of different Vision-Language Models out there

Among them...

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- PLIP: from Twitter



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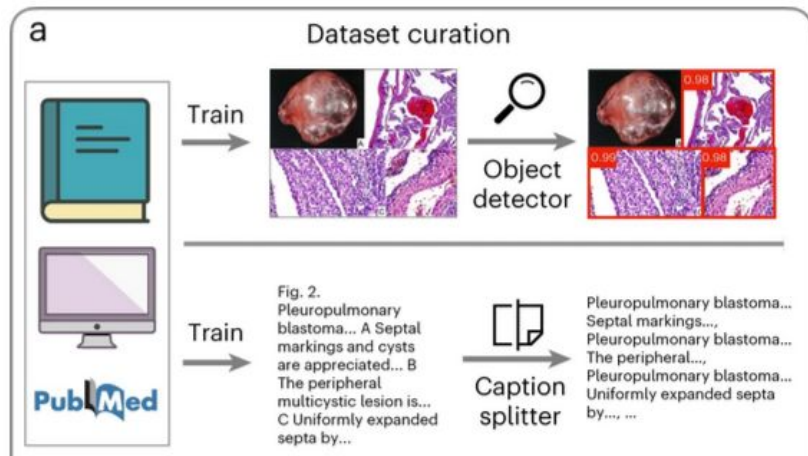
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Lots of different Vision-Language Models out there

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- CLIP: generic text-image pairs of internet
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- **CONCH** : from PubMed



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Lots of different Vision-Language Models out there

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How to leverage their representational power?

...

Boosting Vision-Language Models
for Histopathology Classification:
Predict all at once

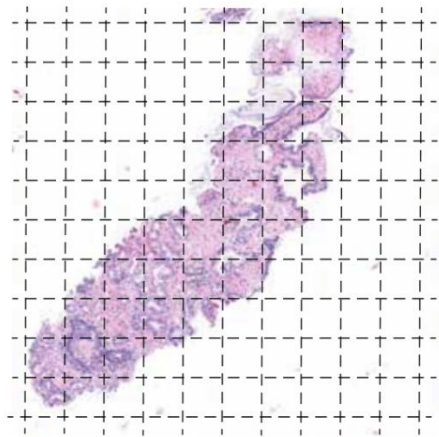
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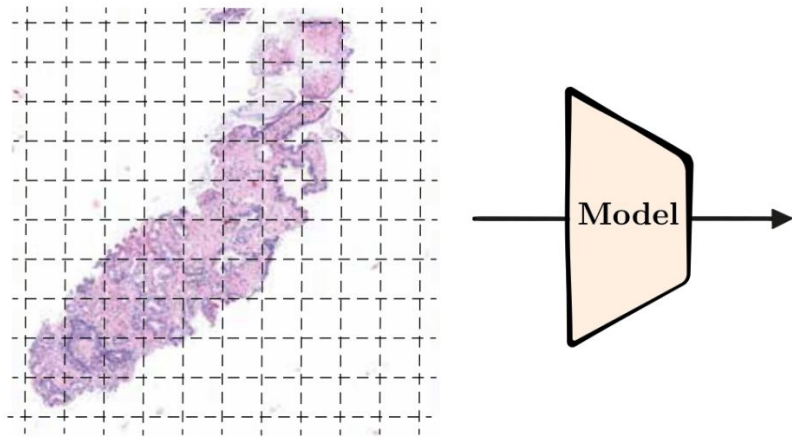
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Inductive inference



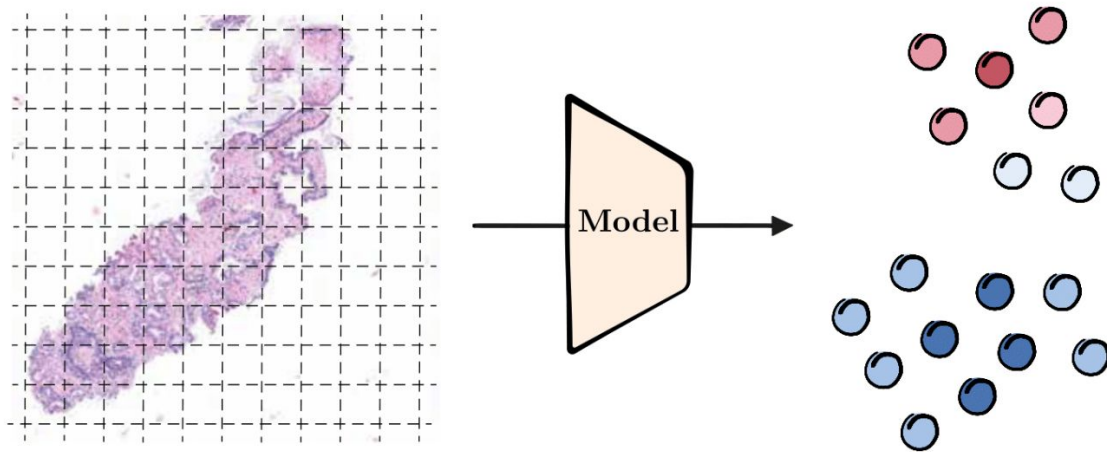
Large whole slides divided per patches, large-scale database, ...

Inductive inference



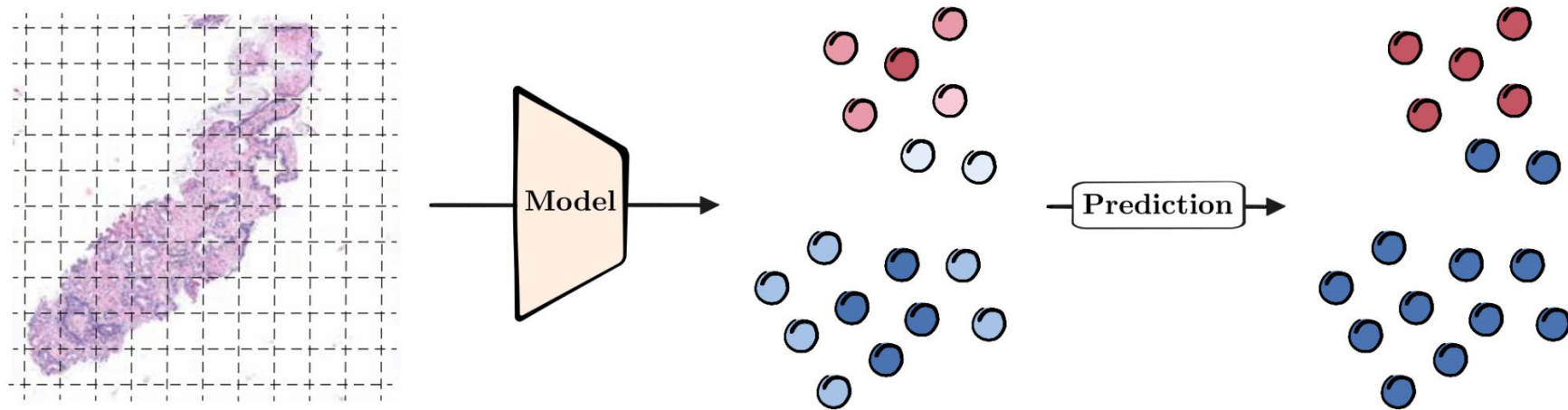
(1) If we have **enough annotated data**, we can train a Model and use it at inference time...

Inductive inference



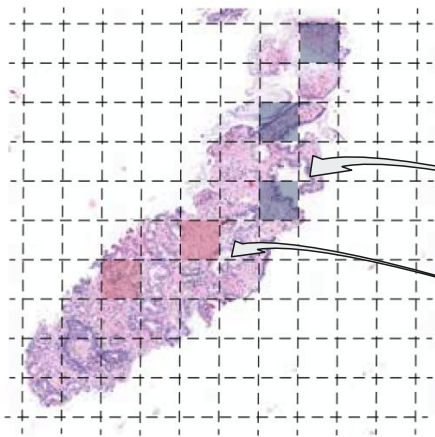
... which gives us more or less confident predictions ...

Inductive inference



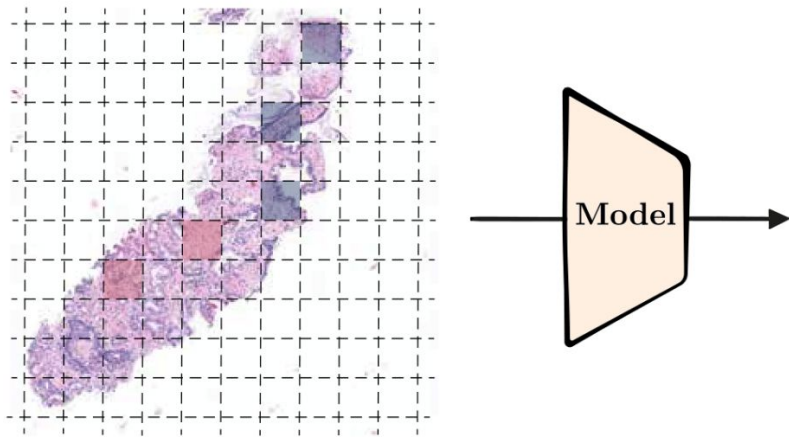
... and we take the most probable class for **each patch independently**.

Few-shot transductive inference



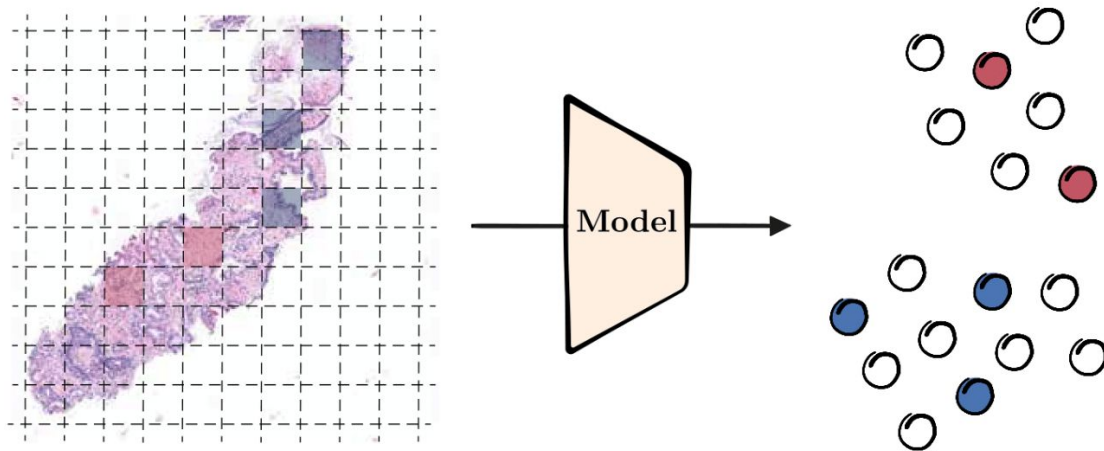
Large whole slides divided per patches, large-scale database, ... + a **few annotated patches**

Few-shot transductive inference



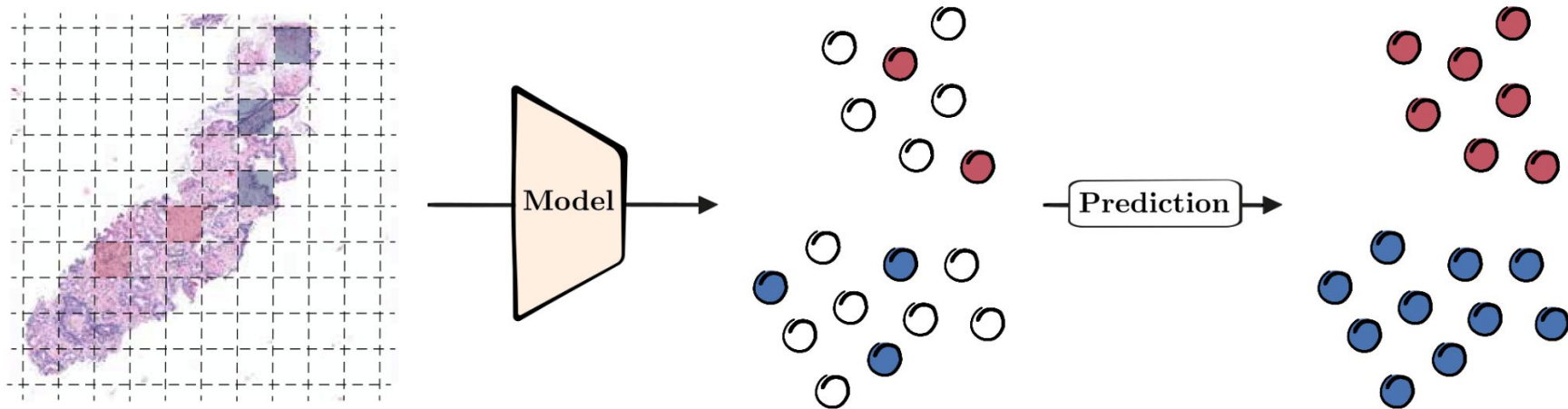
(2) We can use a good embedder (even self-supervised!) ...

Few-shot transductive inference



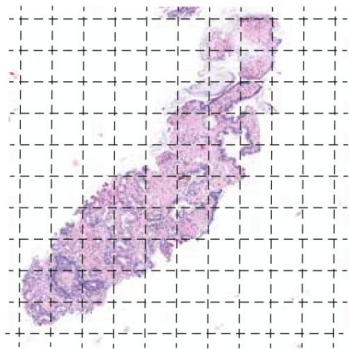
... which gives a good representation ...

Few-shot transduction inference



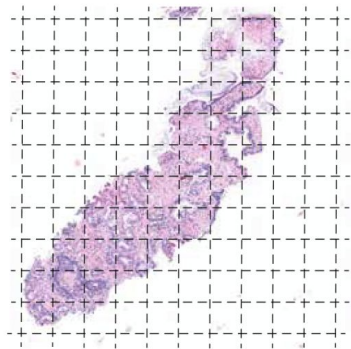
... we can leverage **data structure** and the few-labeled patches !

Unsupervised transductive inference



Large whole slides divided per patches, large-scale database, ... ~~+ a few annotated patches~~

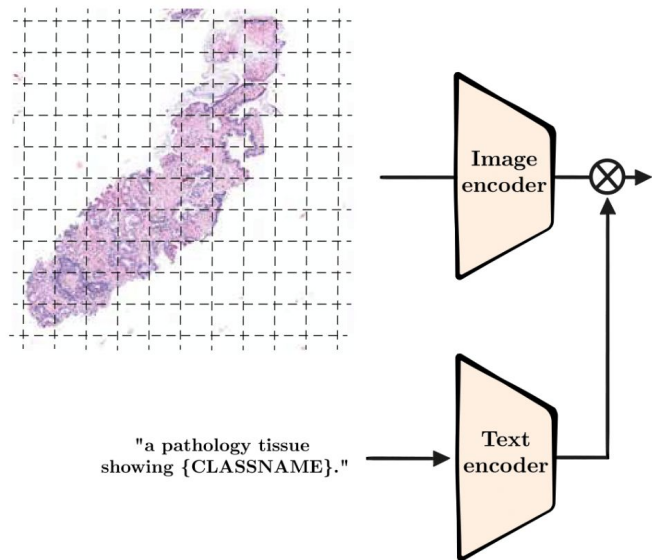
Unsupervised transductive inference



"a pathology tissue
showing {CLASSNAME}."

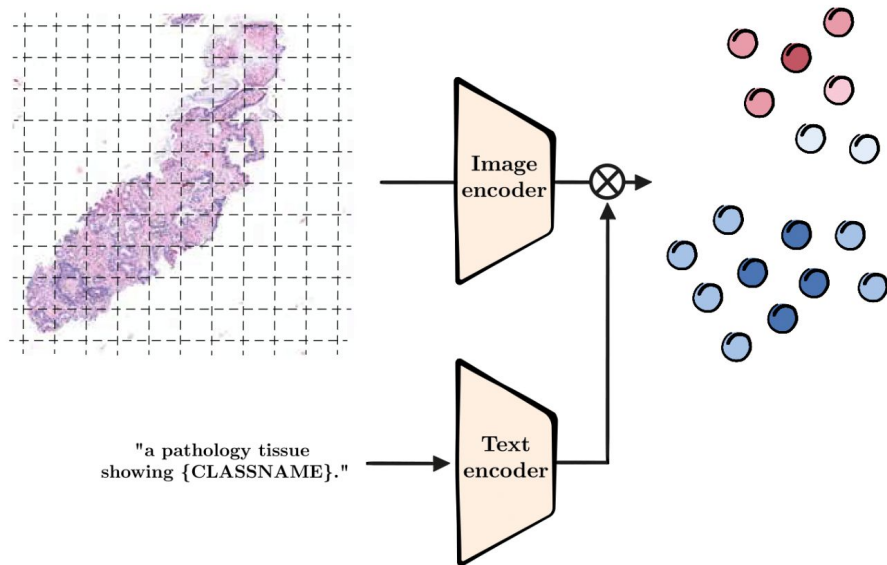
Large whole slides divided per patches, large-scale database, ... + **text description for each class**

Unsupervised transductive inference



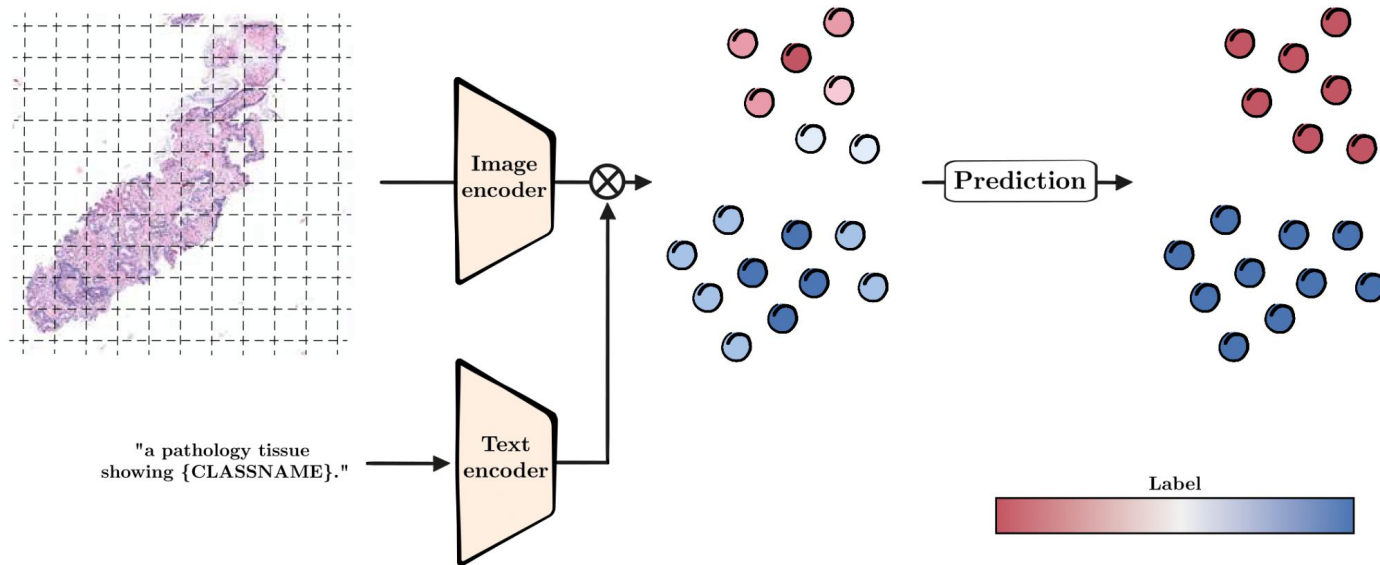
(3) we leverage **Vision-Language Models (VLMs)** trained on large-scale unsupervised text-image data...

Unsupervised transductive inference



... text-image similarities give us (noisy) **zero-shot predictions** for each patch ...

Unsupervised transductive inference



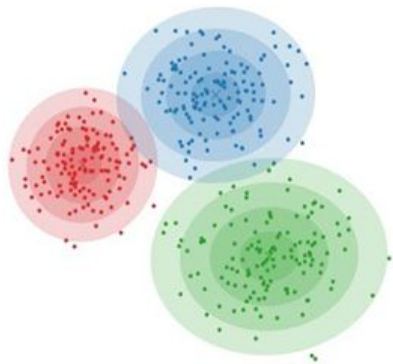
... these **zero-shot predictions** can be used in combination with the **data structure**!

Our algorithm (in short)

$$\mathcal{L}_{\text{Zero-Shot}}(\mathbf{z}, \boldsymbol{\mu}, \boldsymbol{\Sigma}) = \underbrace{-\frac{1}{|\mathcal{Q}|} \sum_{i \in \mathcal{Q}} \mathbf{z}_i^\top \log(\mathbf{p}_i)}_{\text{GMM clustering}} - \underbrace{\sum_{i \in \mathcal{D}} \sum_{j \in \mathcal{D}} w_{ij} \mathbf{z}_i \mathbf{z}_j}_{\text{Laplacian reg.}} + \underbrace{\sum_{i \in \mathcal{Q}} \text{KL}_\lambda(\mathbf{z}_i || \mathbf{j})}_{\text{Text knowledge}}$$

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We model features as a balanced Gaussian Mixture Model (**GMM**).

Our algorithm (in short)

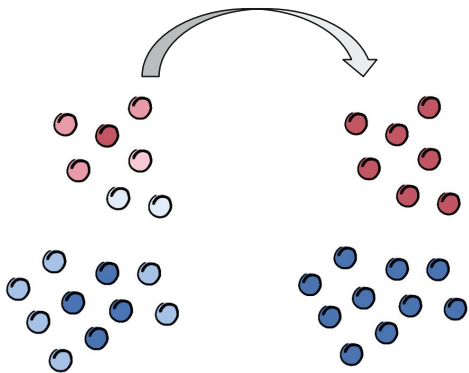
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Similar patches should have similar predictions!

Our algorithm (in short)

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New predictions should remain **as close as possible to the initial (zero-shot) ones** (while minimizing the 2 other terms!)

Our algorithm (in short)

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Solving procedure of 3 update equations
→ just a few lines of code!

```

1 function Histo-TransCLIP(f, t,  $\tau$ )
    // Text-based pseudo-labels  $\hat{y}$ 
2    $\hat{y}_i = \text{softmax}(\tau \mathbf{f}_i^T \mathbf{t}) \quad \forall i$ 
    // Initialize  $\mathbf{z}$ ,  $\mu$ ,  $\Sigma$ 
3    $\mathbf{z}_i = \hat{y}_i \quad \forall i$ 
4    $\mu_k = \text{top\_confident\_average}(\mathbf{f}, \hat{y}) \quad \forall k$ 
5    $\text{diag}(\Sigma) = \frac{1}{n\_features}$ 
    // Iterative procedure
6   while not_converged do
7     for l = 1 : ... do
8        $\mathbf{z}_i^{(l+1)} = \frac{\hat{y}_i \odot \exp(\log(\mathbf{p}_i) + \sum_{j \in \mathcal{Q}} w_{ij} \mathbf{z}_j^{(l)})}{(\hat{y}_i \odot \exp(\log(\mathbf{p}_i) + \sum_{j \in \mathcal{Q}} w_{ij} \mathbf{z}_j^{(l)}))^T \mathbb{1}_K} \quad \forall i$ 
9        $\mu_k = \frac{\sum_{i \in \mathcal{Q}} z_{i,k} \mathbf{f}_i}{\sum_{i \in \mathcal{Q}} z_{i,k}} \quad \forall k$ 
10       $\text{diag}(\Sigma) = \frac{1}{|\mathcal{Q}|} \sum_{i \in \mathcal{Q}} \sum_k z_{i,k} (\mathbf{f}_i - \mu_k)^2$ 
11   return  $\mathbf{z}$ 

```

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→ just a **few lines of code!**

Really fast to solve
→ just a **few seconds for 100,000 patches**

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#Patches	Features	Histo-TransCLIP
10^2	~ 1 sec.	~ 0.1 sec.
10^3	~ 4 sec.	~ 0.2 sec.
10^4	~ 28 sec.	~ 0.4 sec.
10^5	~ 5 min.	~ 6 sec.

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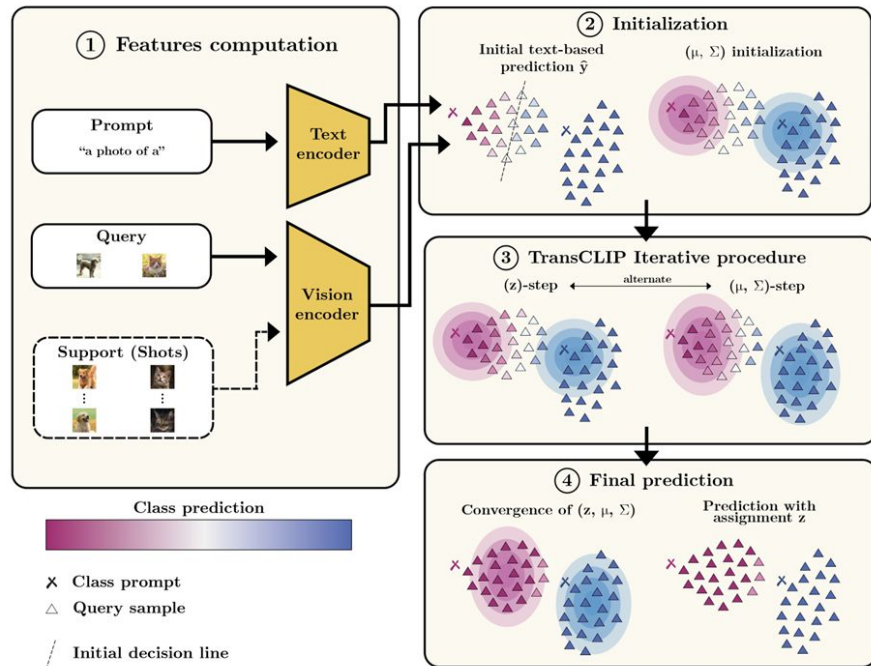
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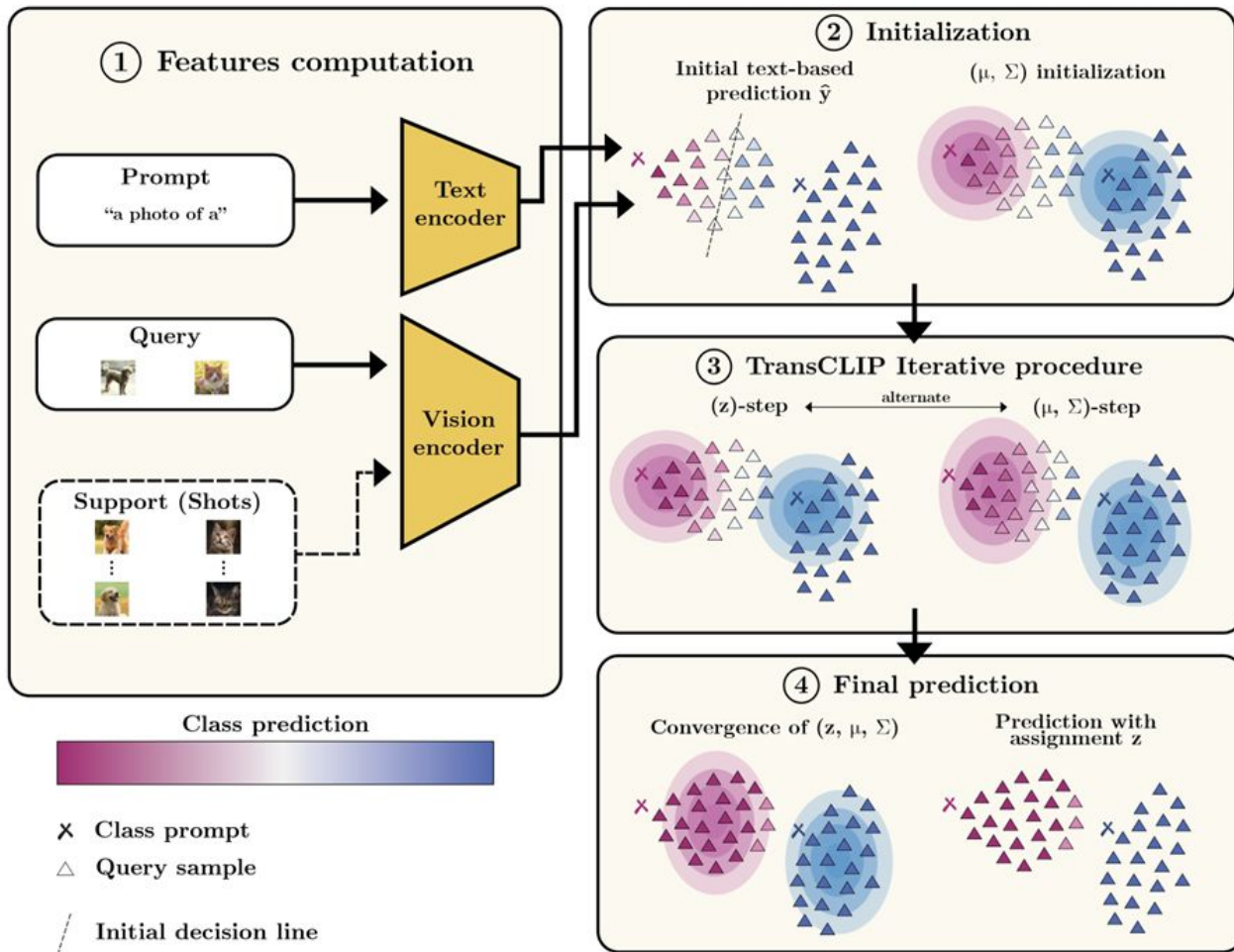


Our algorithm

Solving problem
→ just a few

Really fast to
→ just a few

#I



Results

Dataset	Method	Model				
		CLIP	Quilt-B16	Quilt-B32	PLIP	CONCH
<i>SICAP-MIL</i>	Zero-shot	29.85	40.44	35.04	46.84	27.71
	Histo-TransCLIP	24.72	58.49	28.18	53.23	32.58
<i>LC(Lung)</i>	Zero-shot	31.46	43.00	76.24	84.96	84.81
	Histo-TransCLIP	25.62	50.53	93.93	93.80	96.29
<i>SKINCANCER</i>	Zero-shot	4.20	15.38	39.71	22.90	58.53
	Histo-TransCLIP	11.46	33.33	48.80	36.72	66.22
<i>NCT-CRC</i>	Zero-shot	25.39	29.61	53.73	63.17	66.27
	Histo-TransCLIP	39.61	48.40	58.13	77.53	70.36
<i>Average</i>	Zero-shot	22.73	32.1	51.18	54.47	59.33
	Histo-TransCLIP	25.35	47.69	57.26	65.32	66.36
	$\Delta_{\text{transductive}}$	+2.62	+15.59	+6.08	+10.85	+7.03

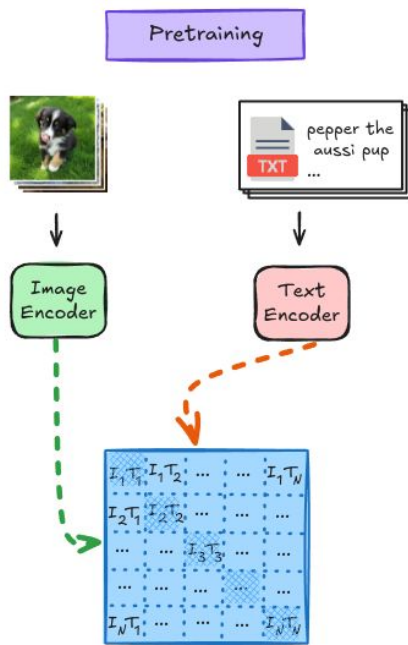
Results: generic pre-training

Dataset	Method	Model				
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Results: histopathology pre-training

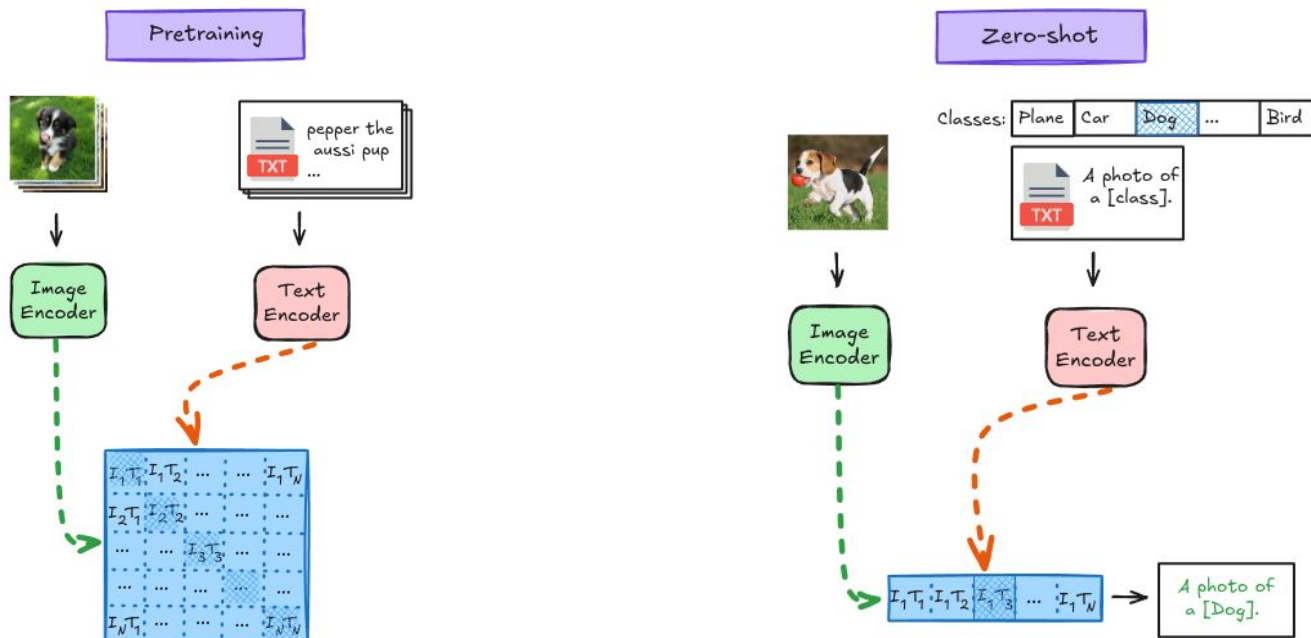
Dataset	Method	Model				
		CLIP	Quilt-B16	Quilt-B32	PLIP	CONCH
<i>SICAP-MIL</i>	Zero-shot	29.83	40.44	35.04	46.84	27.71
	Histo-TransCLIP	24.75	58.49	28.18	53.23	32.58
<i>LC(Lung)</i>	Zero-shot	31.40	43.00	76.24	84.96	84.81
	Histo-TransCLIP	25.67	50.53	93.93	93.80	96.29
<i>SKINCANCER</i>	Zero-shot	4.20	15.38	39.71	22.90	58.53
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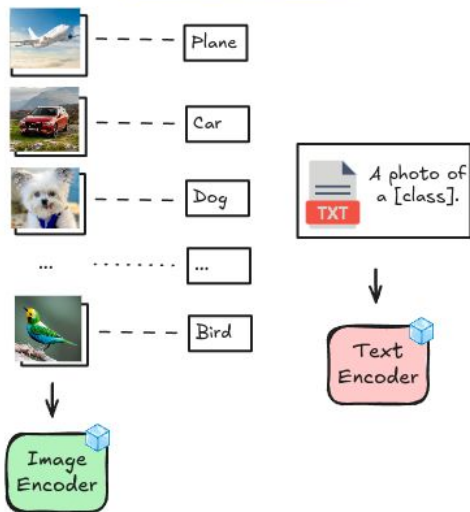


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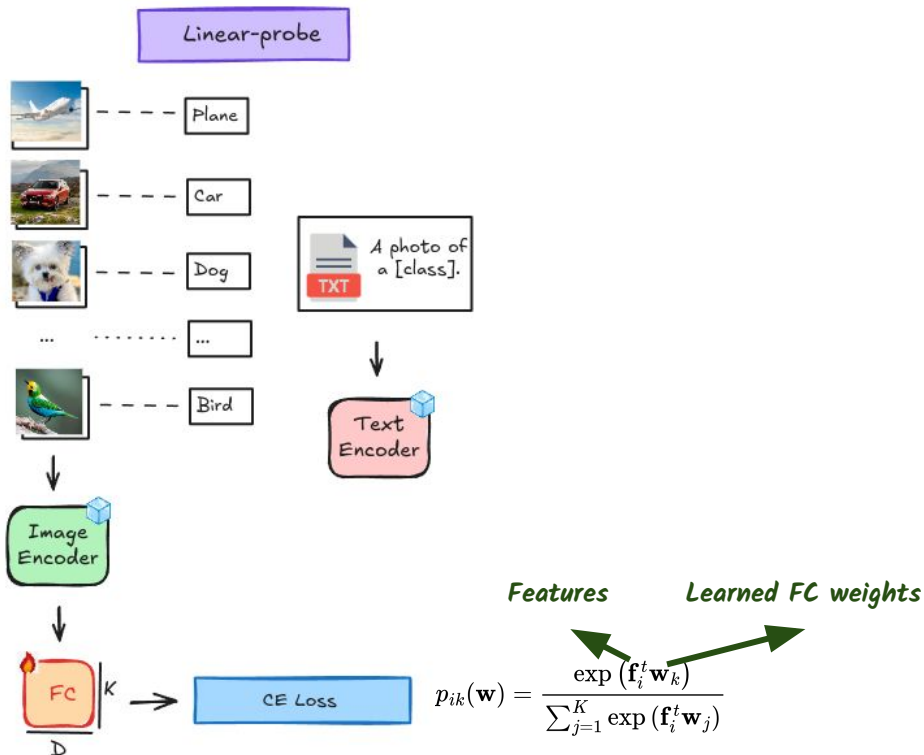
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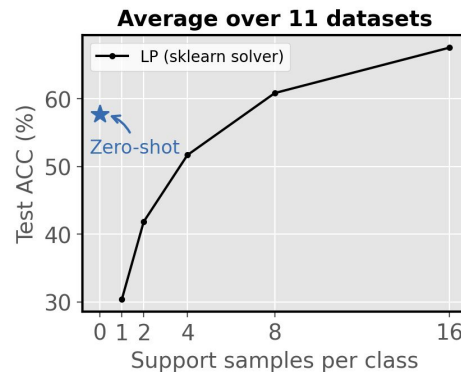
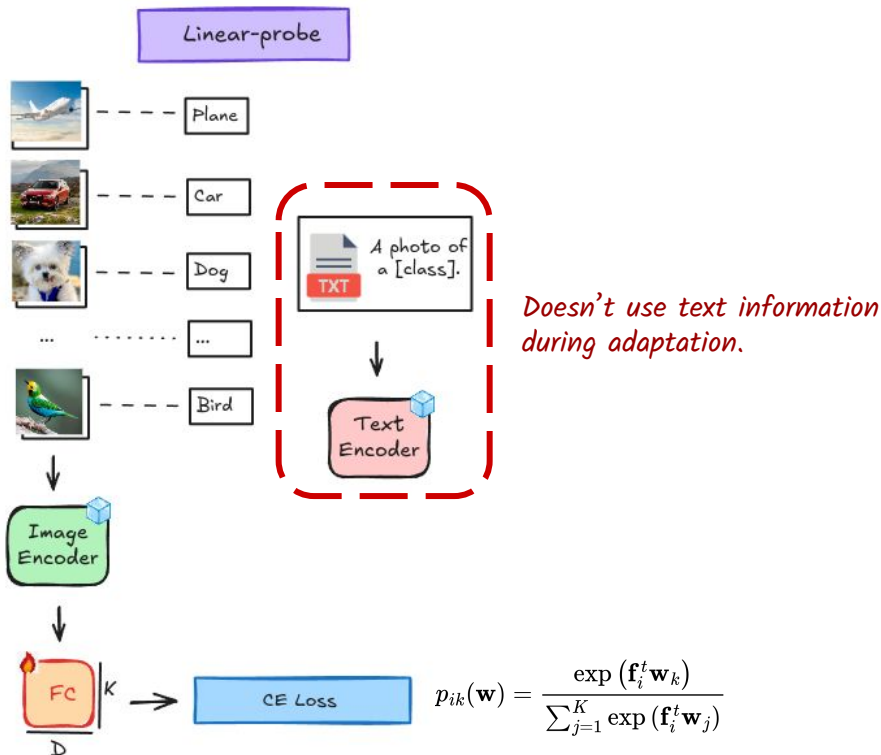
Few-Shot Adaptation (linear probe)



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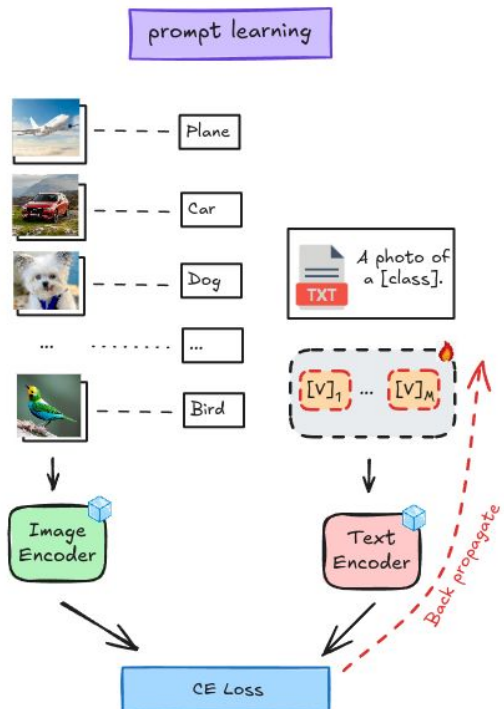


Few-Shot Adaptation (linear probe)



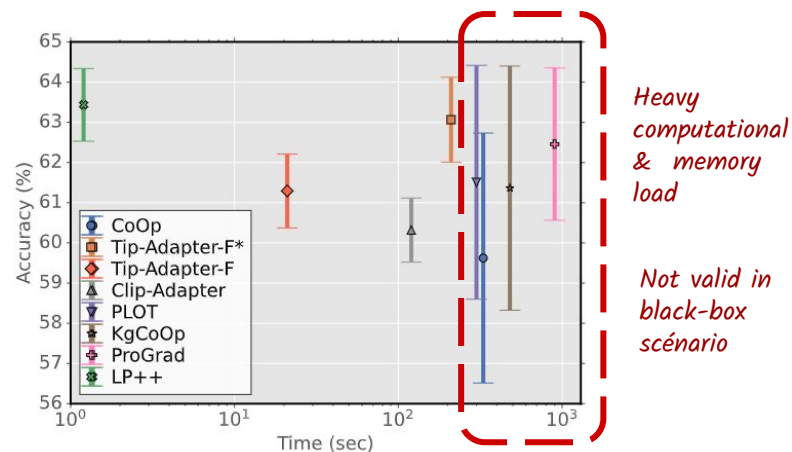
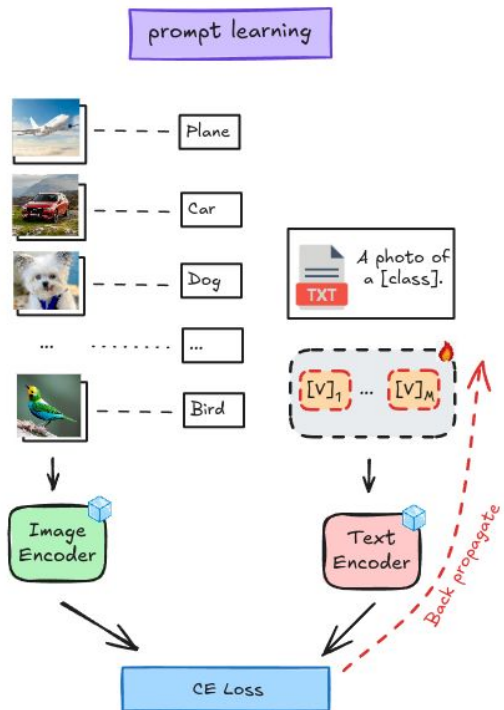
Linear Probe below Zero shot!!

Few-Shot Adaptation (prompt learning)



Prompt learning: Zhou, Kaiyang, et al. "Learning to prompt for vision-language models." *IJCV* (2022).

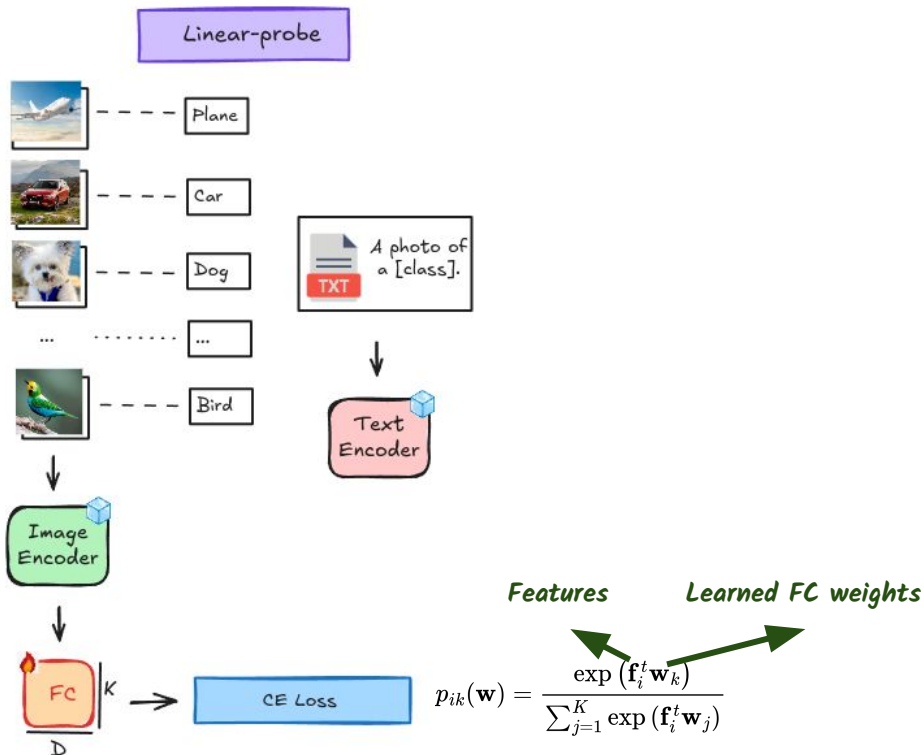
Few-Shot Adaptation (prompt learning)



Prompt learning: Zhou, Kaiyang, et al. "Learning to prompt for vision-language models." *IJCV* (2022).

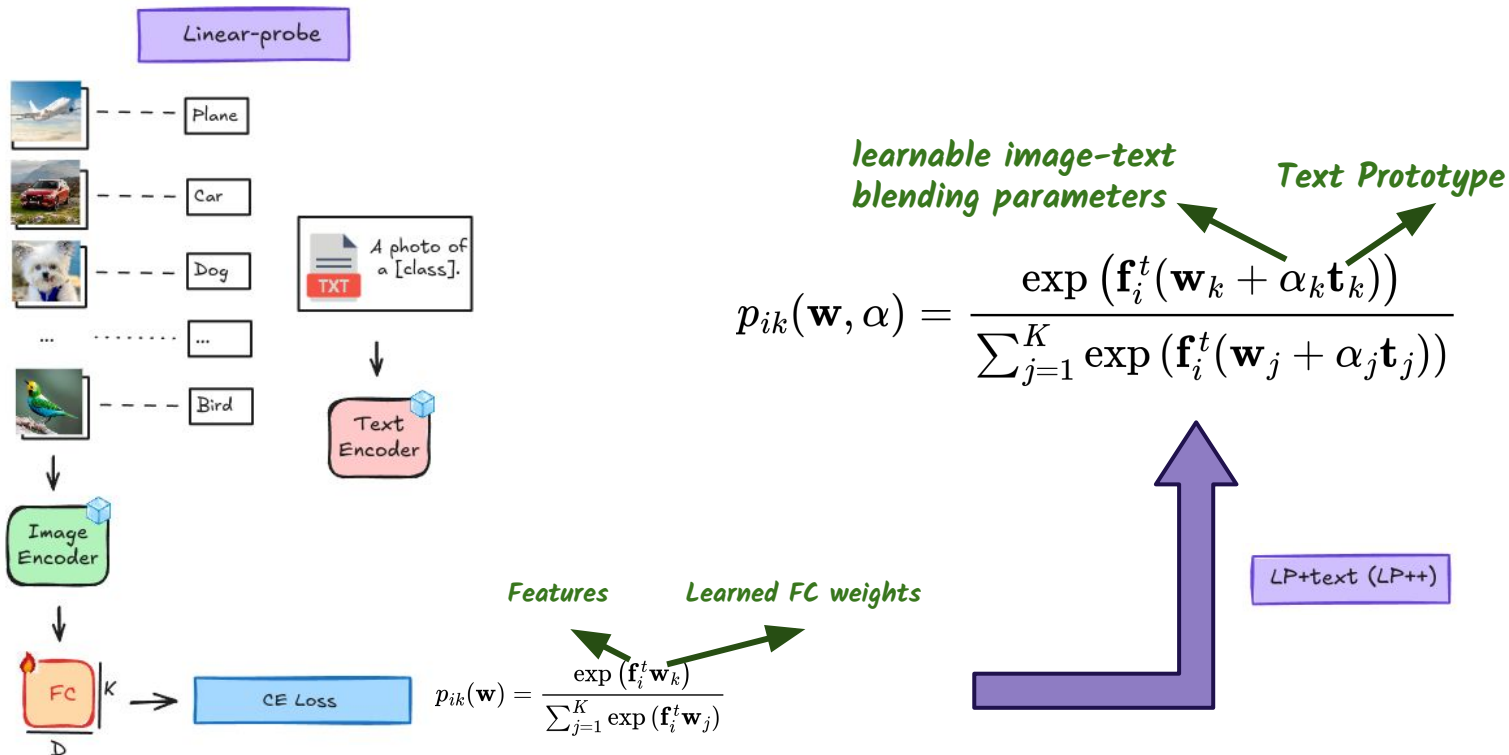
Figure from: Huang, Y, et al. . "LP++: A Surprisingly Strong Linear Probe for Few-Shot CLIP" . *CVPR* (2024).

Few-Shot Adaptation (linear probe)

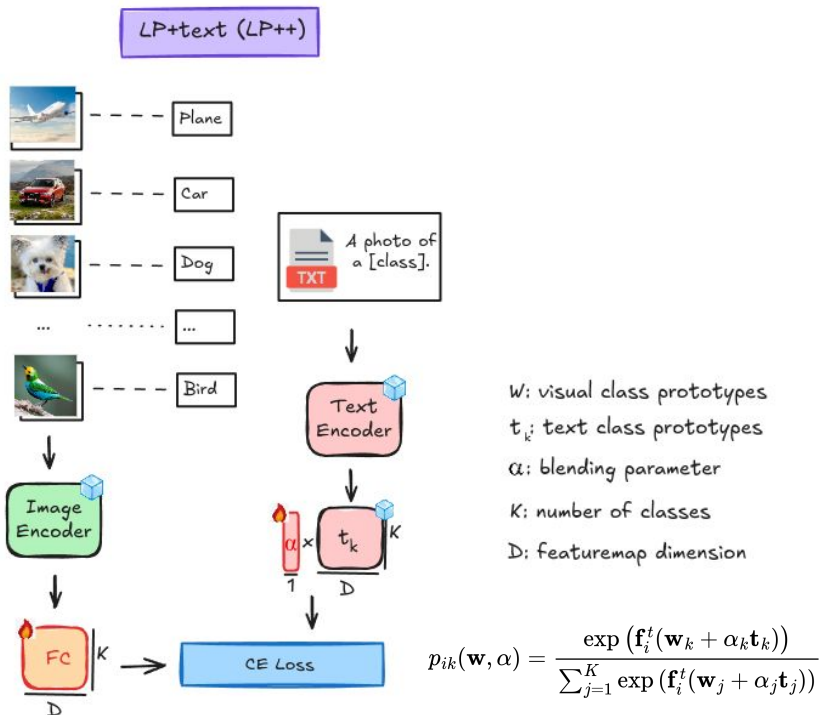


Radford, Alec, et al. "Learning transferable visual models from natural language supervision." PMLR, 2021.

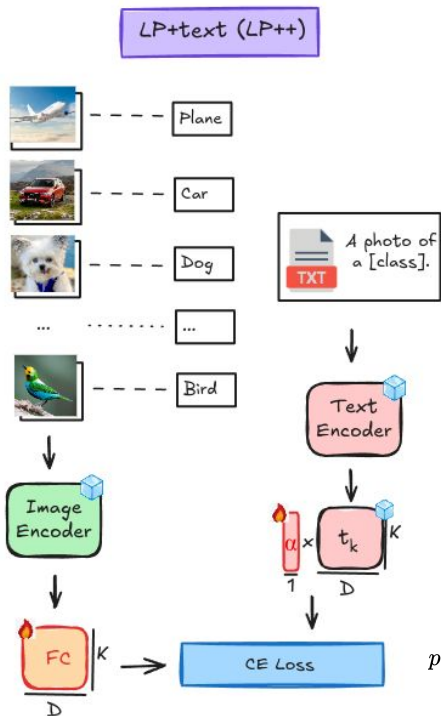
Few-Shot Adaptation (linear probe)



Few-Shot Adaptation (LP++)



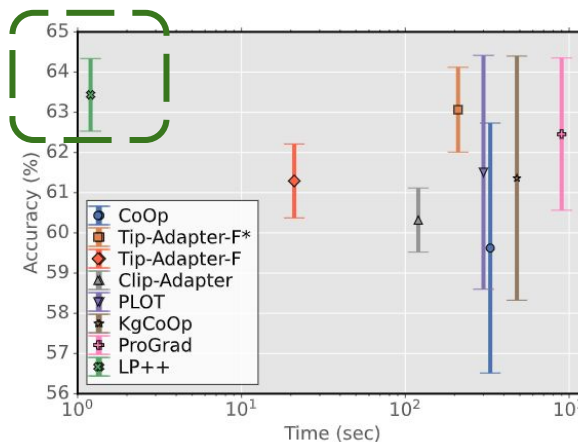
Few-Shot Adaptation (LP++)



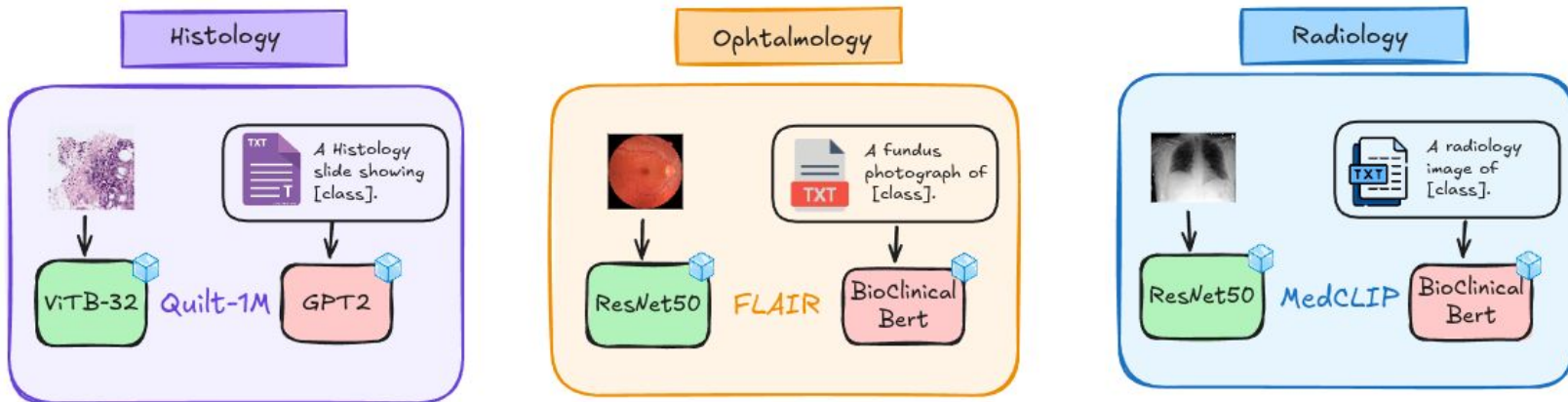
$$p_{ik}(\mathbf{w}, \alpha) = \frac{\exp(\mathbf{f}_i^t(\mathbf{w}_k + \alpha_k \mathbf{t}_k))}{\sum_{j=1}^K \exp(\mathbf{f}_i^t(\mathbf{w}_j + \alpha_j \mathbf{t}_j))}$$

Orders-of-magnitude faster

Preserve black-box



Medical VLMs

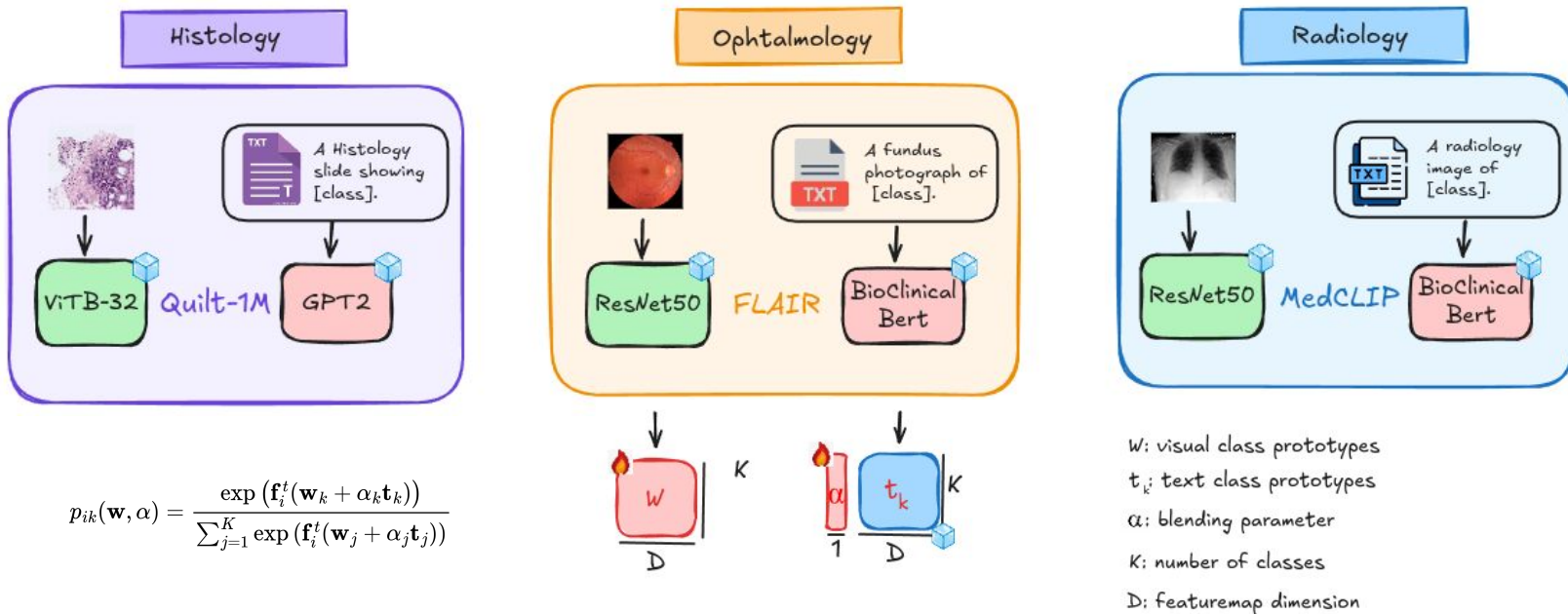


FLAIR: Silva-Rodríguez et al., A Foundation Language-Image Model of the Retina, MedIA 2024

Quilt-1M: Ikezogwo et al., One Million Image-Text Pairs for Histopathology, NeurIPS 2023

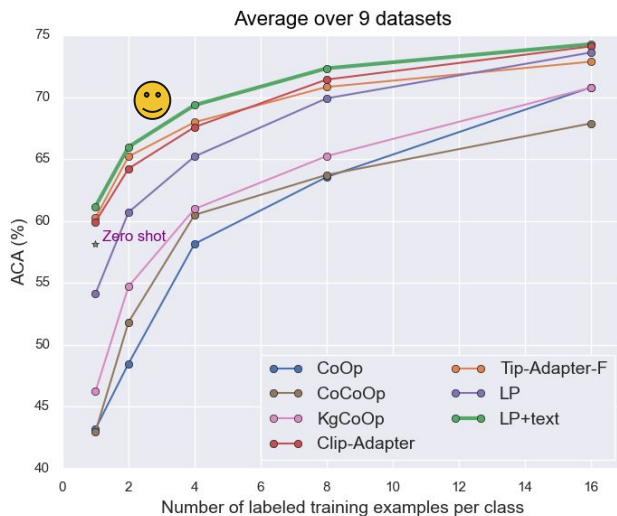
MedCLIP: Wang et al., Contrastive Learning from Unpaired medical images and text, EMNLP 2022

Few-Shot Adaptation in Medical VLMs



Few-Shot Adaptation in Medical VLMs

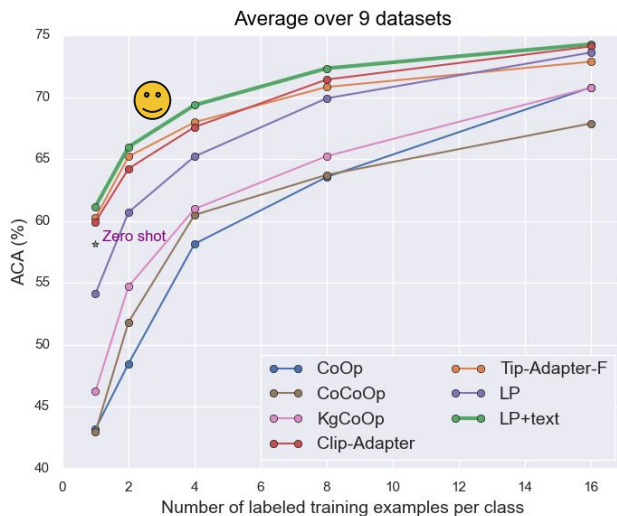
3 modalities / 9 datasets



LP+text is competitive!

Few-Shot Adaptation in Medical VLMs

3 modalities / 9 datasets



LP+text is competitive!

LP+text is extremely efficient!

- Adaptation in a matter of seconds
- Trainable on commodity GPUs
- Black-box adaptation

Methods	Category	Training Time	Black-box	#Parameters
Zero-shot [21]		n/a	✓	n/a
CoOp [35]	Prompt-Learning	3min	✗	$K \times n_{ctx1} \times D$
CoCoOp [34]		12min	✗	$n_{ctx2} \times D + C$
KgCoOp [31]		3min	✗	$K \times n_{ctx1} \times D$
Clip-Adapter [5]	CLIP-based Adapters	2min	✓	$2(D_1 \times D_2)$
Tip-adapter-F [32]		2min	✓	$K \times S \times D$
LP	Linear probe	43s	✓	$K \times D$
LP+text [7]		4s	✓	$K(D + 1)$

References

- **Few-shot Adaptation of Medical Vision Language Models [Spotlight]**

F Shakeri, Y Huang, JR Silva, H Bahig, A Tang, J Dolz, IB Ayed
IMedical Image Computing and Computer Assisted Intervention (MICCAI), 2024

- **LP++: A Surprisingly Strong Linear Probe for Few-Shot CLIP**

Y Huang, F Shakeri, J Dolz, M Boudiaf, H Bahig, IB Ayed
IEEE/CVF Conference on Computer Vision and Pattern Recognition (CVPR), 2024



- **Boosting Vision-Language Models for Histopathology Classification: Predict all at once [Best Paper Award]**

M Zanella, F Shakeri, Y Huang, H Bahig, IB Ayed
MICCAI Workshop on Foundation Models for General Medical AI (MedAGI), 2024



Questions? :)



Thank you for your attention!

