

VLEER: Vision and Language Embeddings for Explainable Whole Slide Image Representation

Sep. 27th, 2025

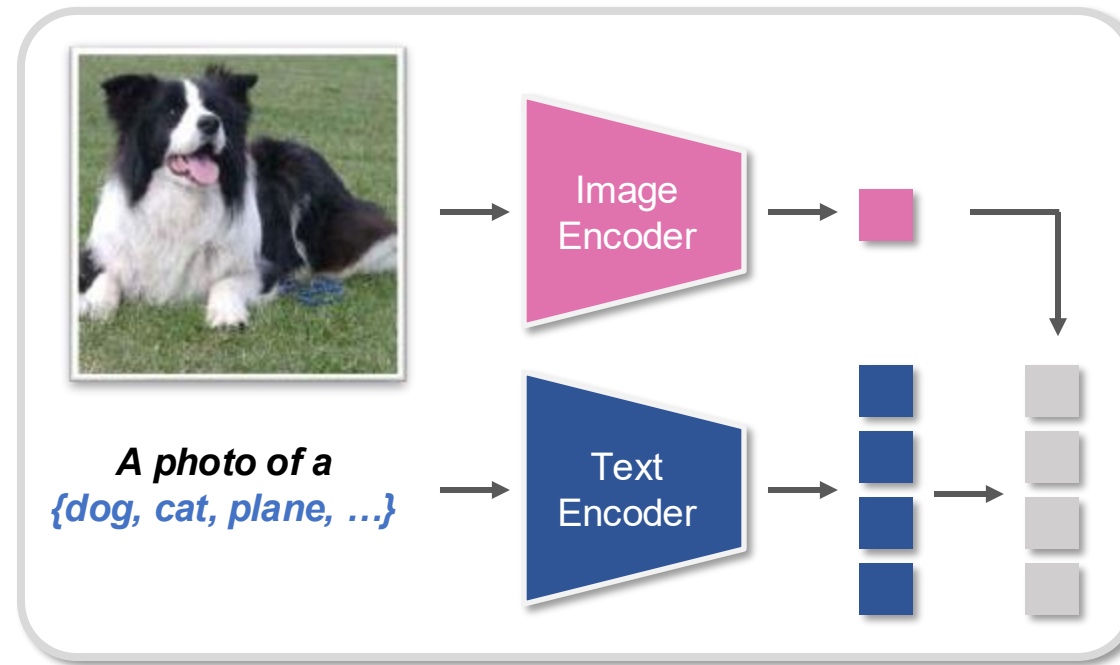
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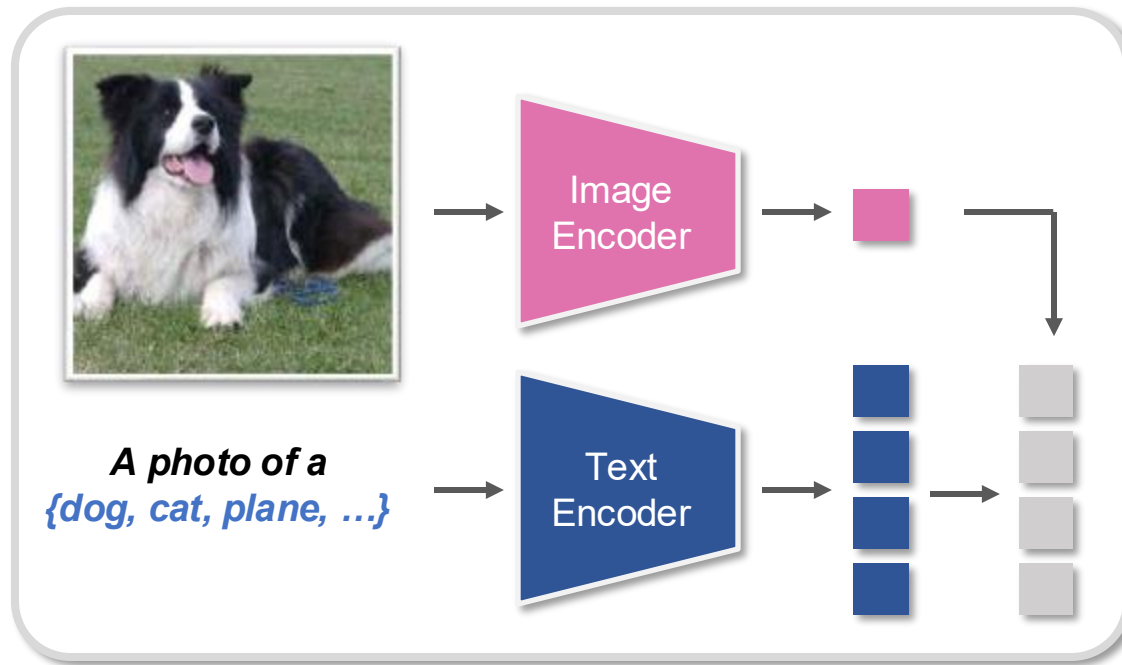
□ Vision-Language Model

- There has been growing interest in vision-language models (VLMs), which **integrate vision and language** modalities by jointly learning from image-text datasets.



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CLIP

Radford et al. (2021)

CoCa

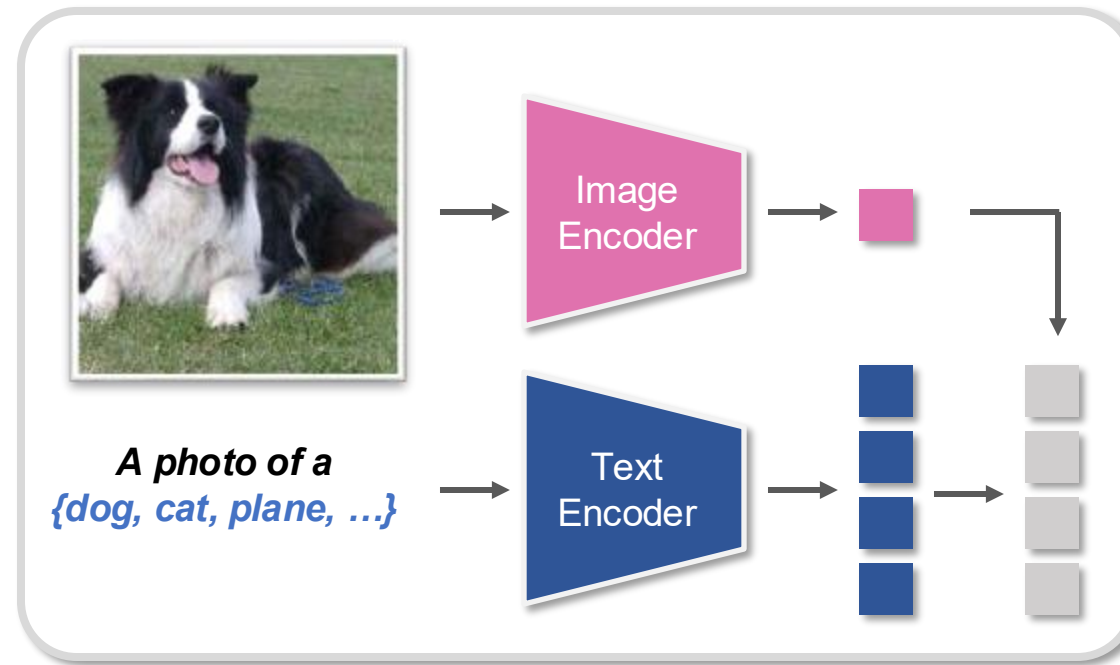
Yu et al. (2022)

FLAVA

Singh et al. (2022)

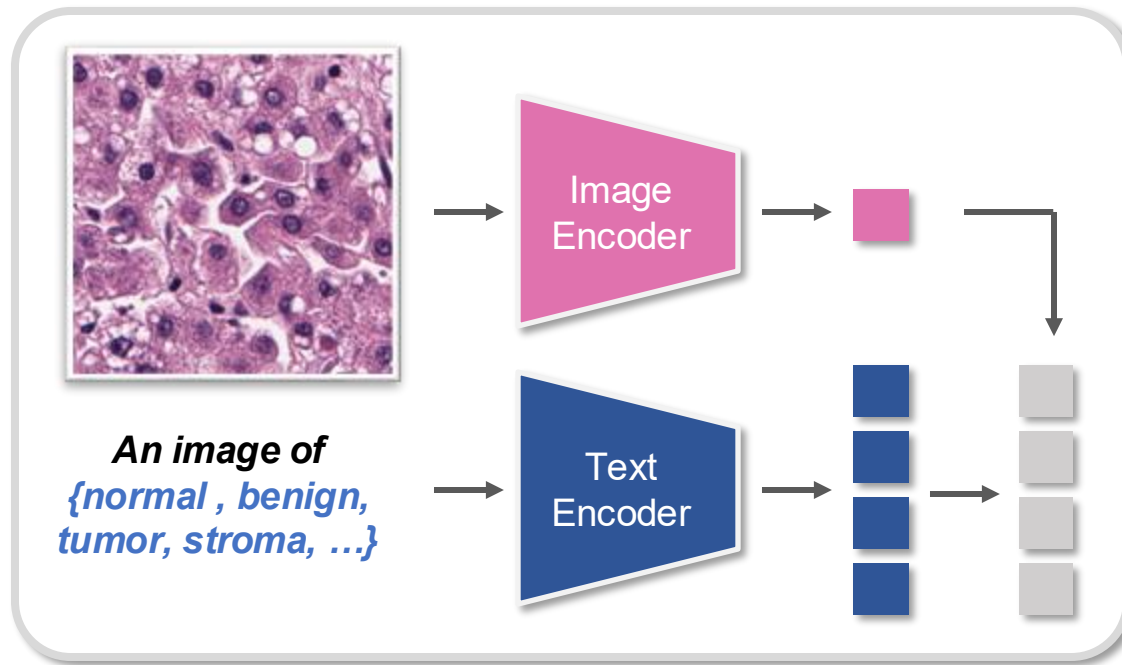
□ Vision-Language Models in Pathology

- In computational pathology, this approach has been adapted to domain-specific datasets, resulting in **pathology VLMs**



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PLIP

Huang et al. (2023)

QUILT-NET

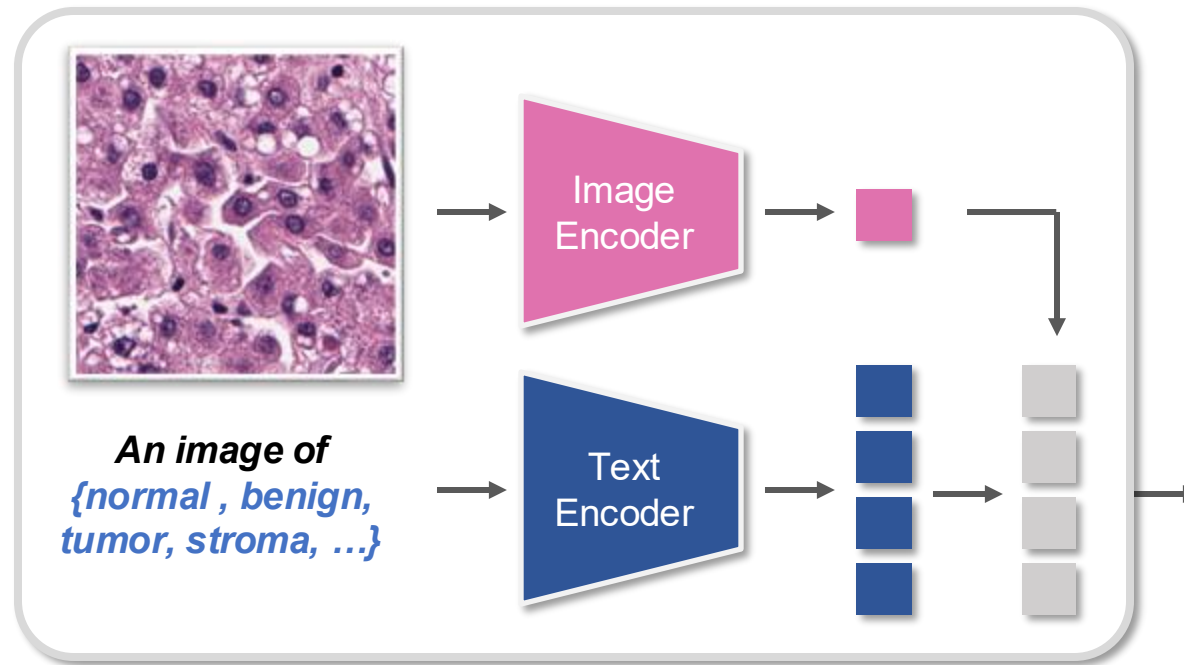
Ikezogwo et al. (2023)

CONCH

Lu et al. (2024)

□ Vision-Language Models in Pathology

- They have achieved remarkable results in various classification tasks, often **without** requiring further training or fine-tuning.



PLIP

Huang et al. (2023)

QUILT-NET

Various Classification Tasks

Tissue phenotyping

Gleason grading

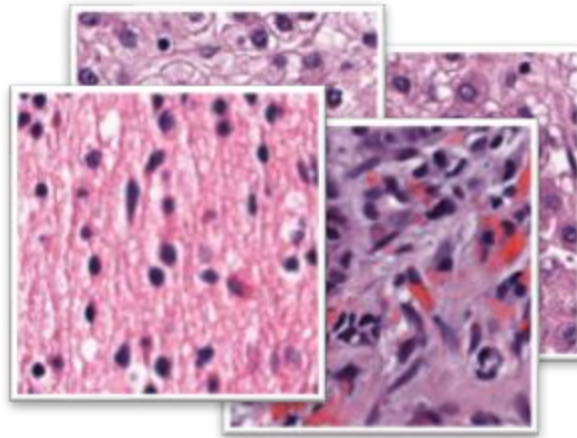
Lymph node metastasis detection

CONCH

Lu et al. (2024)

□ Motivation

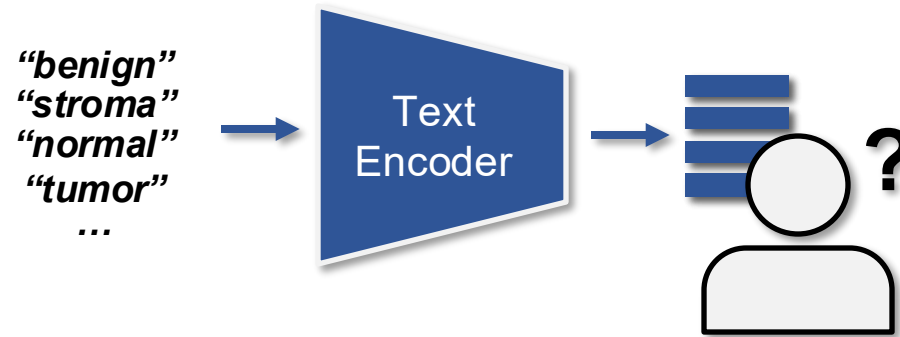
- Most studies have primarily focused on pre-training VLMs and their direct application to downstream tasks, overlooking **two key limitations**.



Most prior works mainly focus on **patch-level tasks**, while **WSI-level** applications remain largely unexplored.

□ Motivation

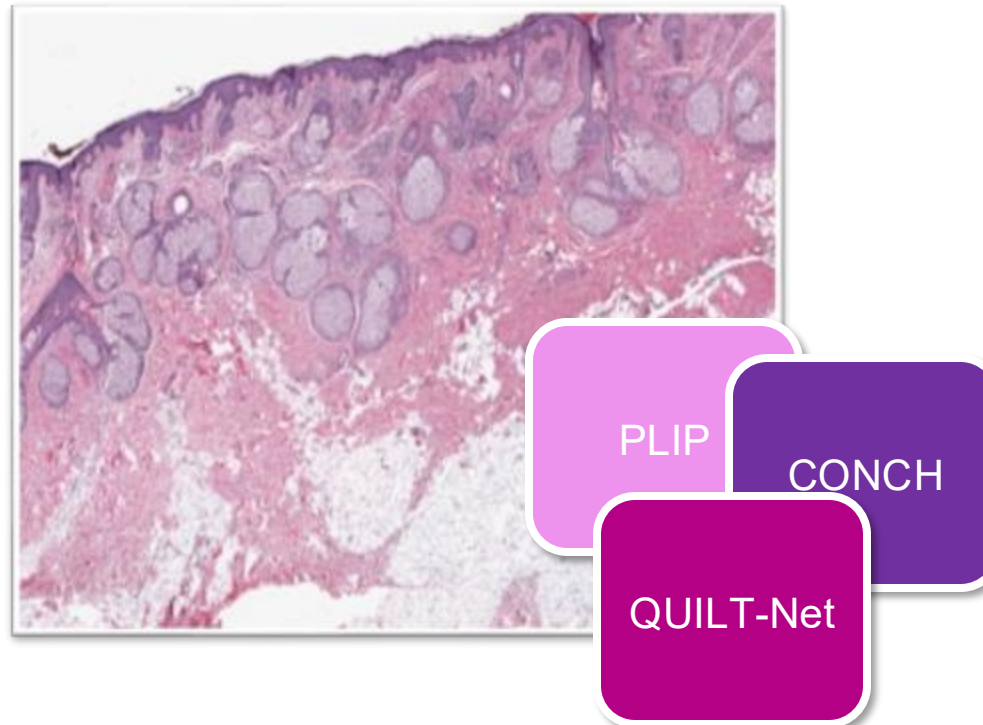
- Most studies have primarily focused on pre-training VLMs and their direct application to downstream tasks, overlooking **two key limitations**.



The **interpretability of textual embeddings** in VLM has not been thoroughly explored.

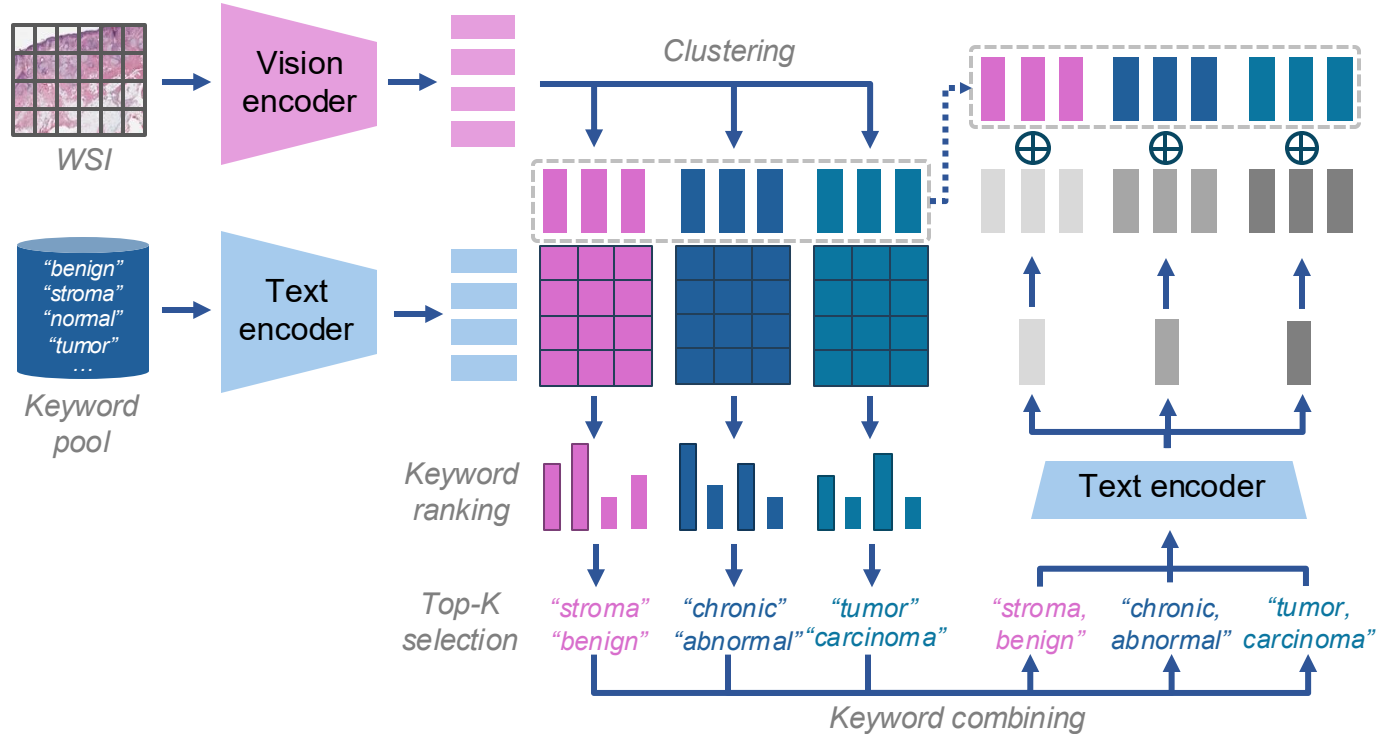
□ Our Approach

- We hypothesize that **pre-trained VLMs can inherently represent WSIs** in a quantitative and interpretable manner.



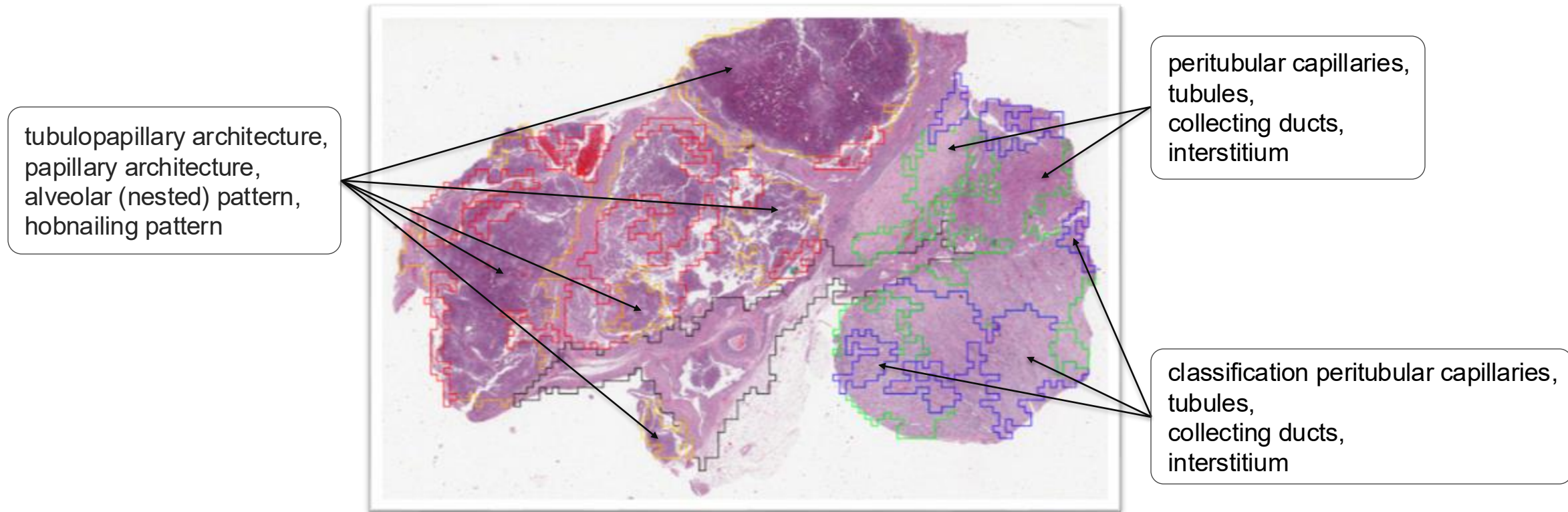
Our Approach

- We introduce **Vision and Language Embeddings for Explainable WSI Representation (VLEER)**.



□ Our Approach

- *VLEER* facilitates direct interpretation of results through **human-readable** and **understandable** textual representations.



□ Overall,

- *VLEER* utilizes two components to learn explainable WSI embeddings:
*a task-related **text pool** of pathology keywords*
*a pre-trained **pathology VLM***

□ Task-related pathology text pool

- We collect **task-specific keywords** illustrating the histology of tissues for each task.



Keyword pool

□ Task-related pathology text pool

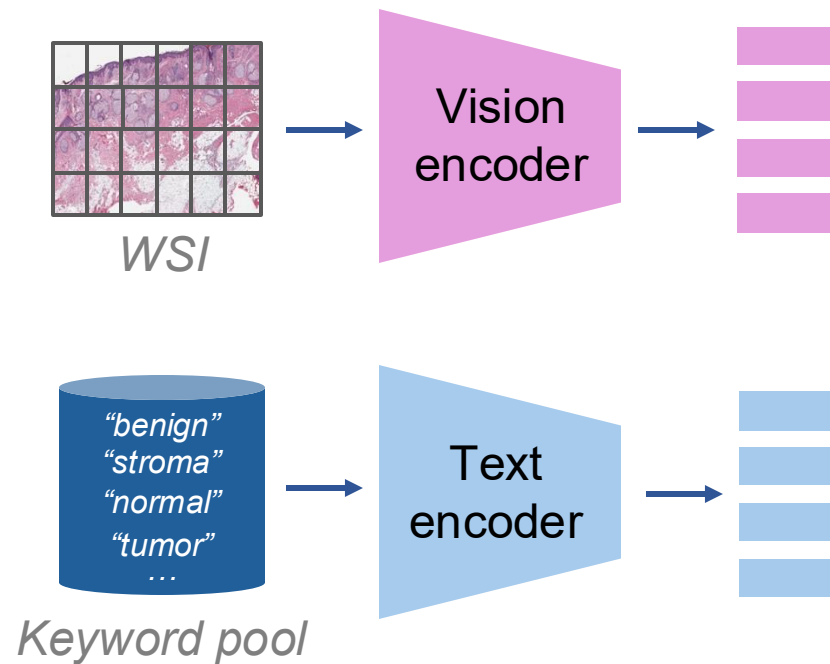
- These keywords include pathological terms that are relevant to **both normal and abnormal** conditions.
- All collected keywords are then **reviewed and validated** by a board-certified, experienced pathologist.



Keyword pool

□ Textual and visual embedding extraction

- WSI is tiled into a bag of patches, the **vision encoder** transforms these patches into **vision embeddings**.
- We adopt the **text encoder** to embed all keywords in the pool into **textual embeddings**.



□ Textual and visual embedding extraction

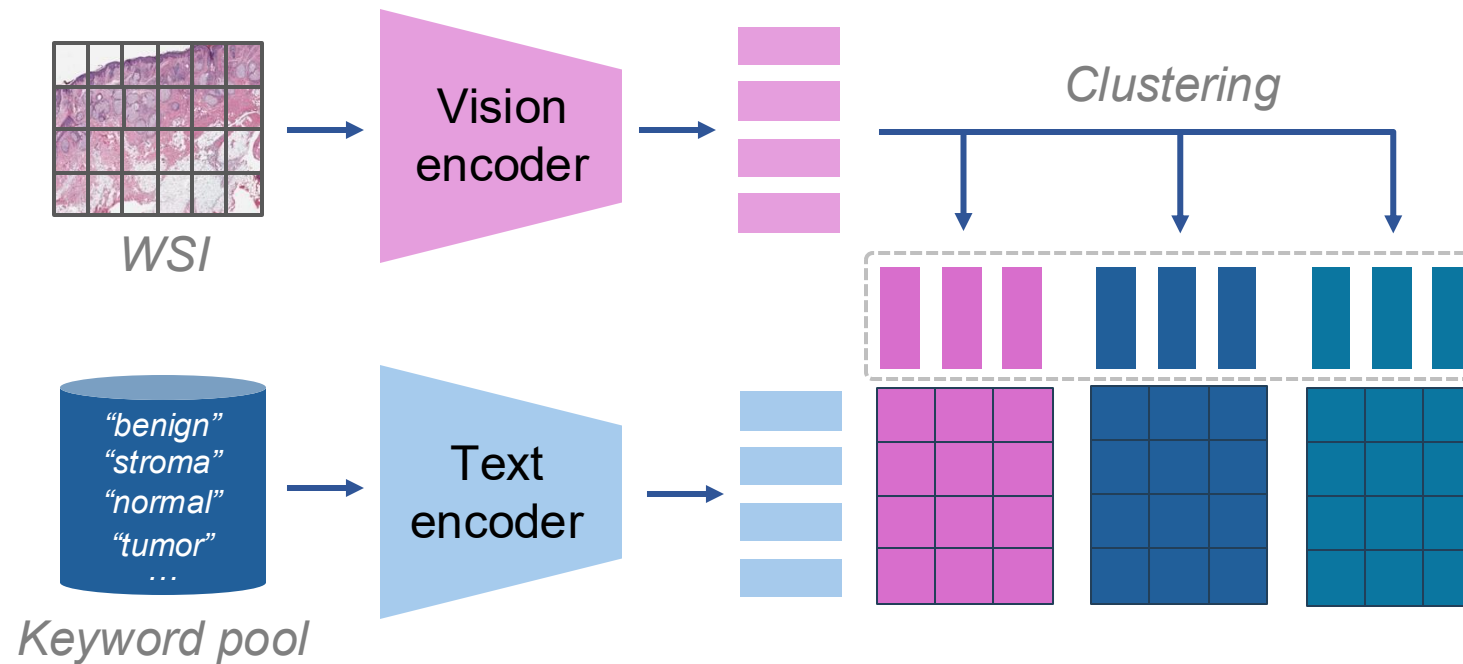
- We employ **various templates** to generate diverse text prompts for each keyword.

an image of CLASSNAME.
an image showing CLASSNAME.
an example of CLASSNAME.
a histopathological image showing CLASSNAME.
a histopathological image of CLASSNAME.
CLASSNAME is shown.
this is CLASSNAME.
there is CLASSNAME.
a histopathological photograph of CLASSNAME.
a histopathological photograph showing CLASSNAME.
...

Lu, Ming Y., et al. "A visual-language foundation model for computational pathology." Nature medicine 30.3 (2024): 863-874.

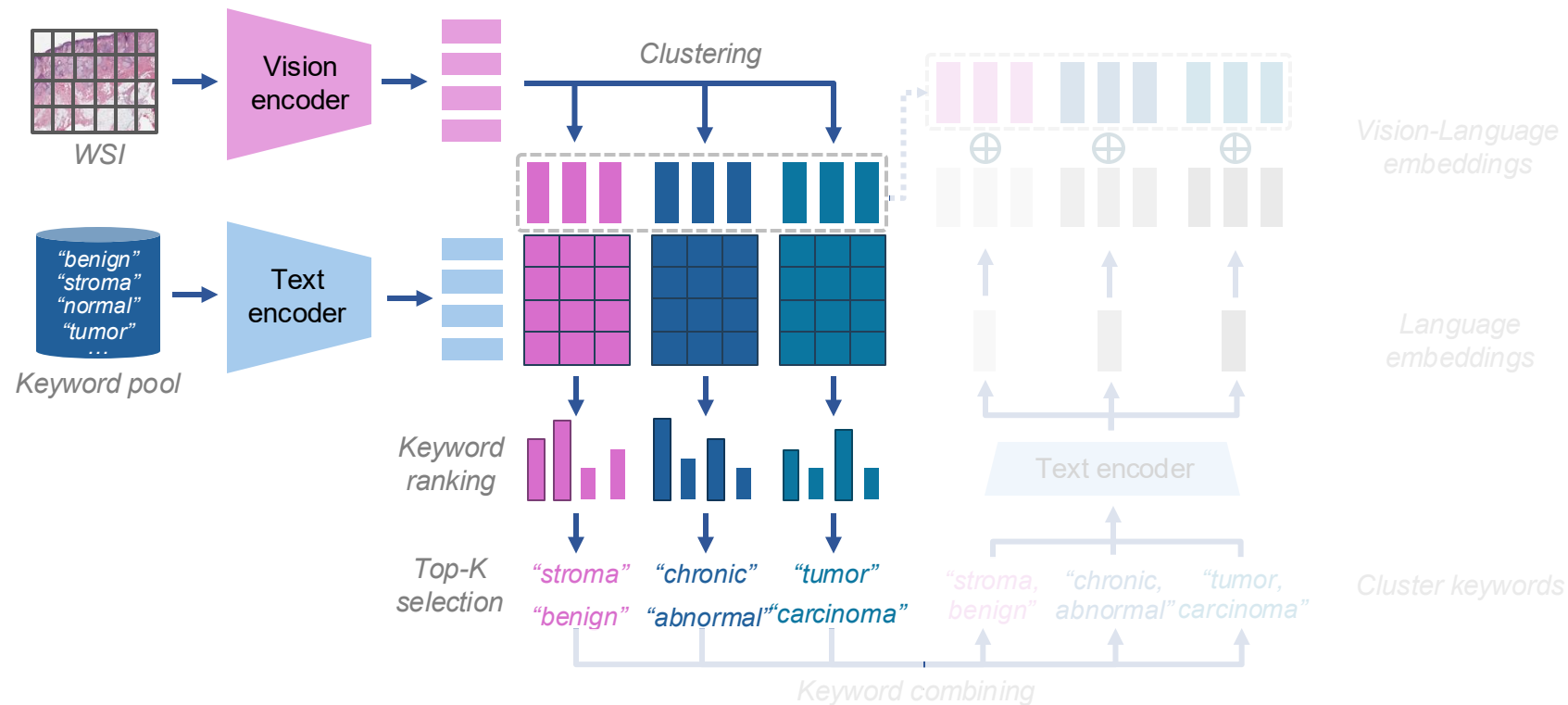
□ Vision-Text alignment

- We **cluster patches** into distinct groups to improve the semantic meaning.
- For each cluster, **similarity scores** are calculated between all visual and textual embeddings.



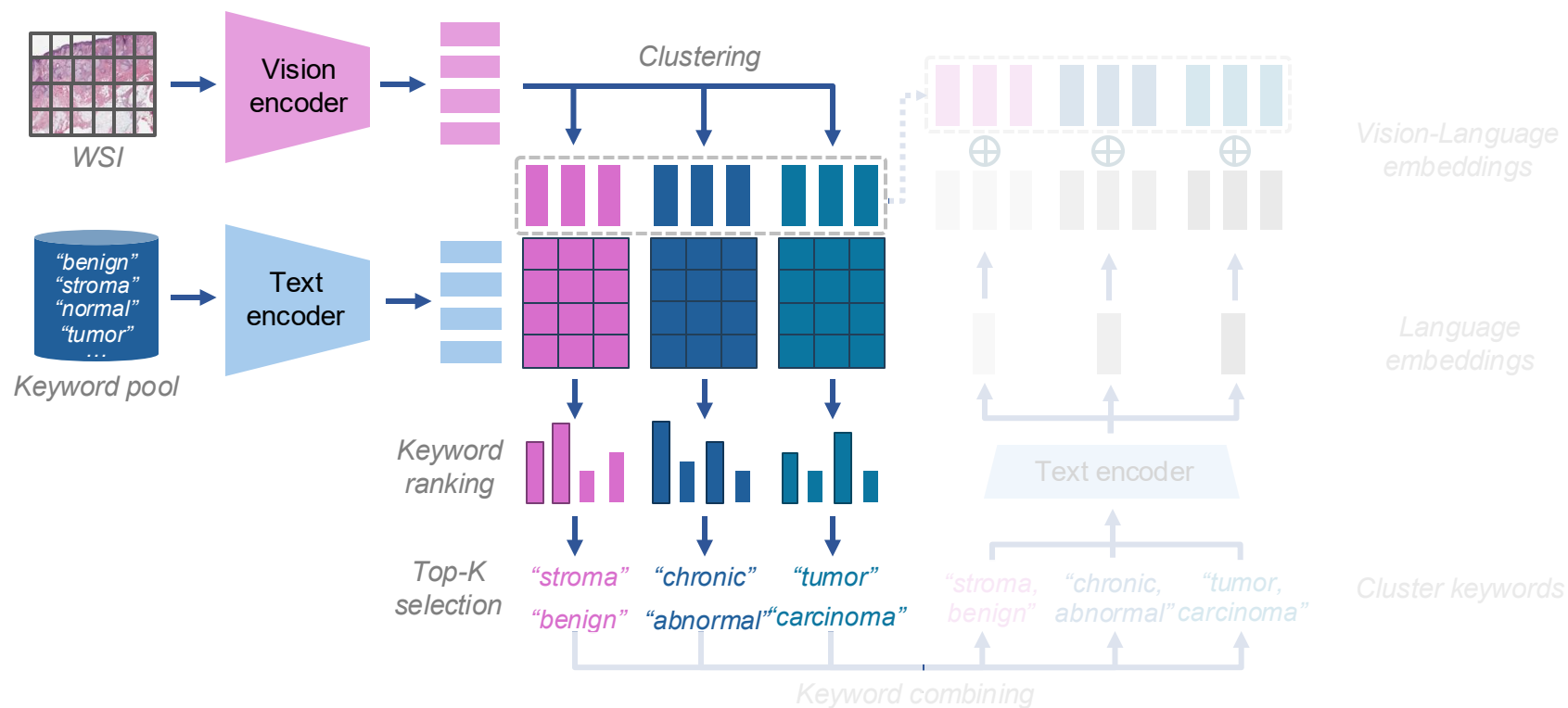
Cluster representative keywords retrieval

- We **rank all keywords** based on their similarity scores with each patch image, **aggregate** these rankings and retrieve the **most representative keywords** for each cluster.



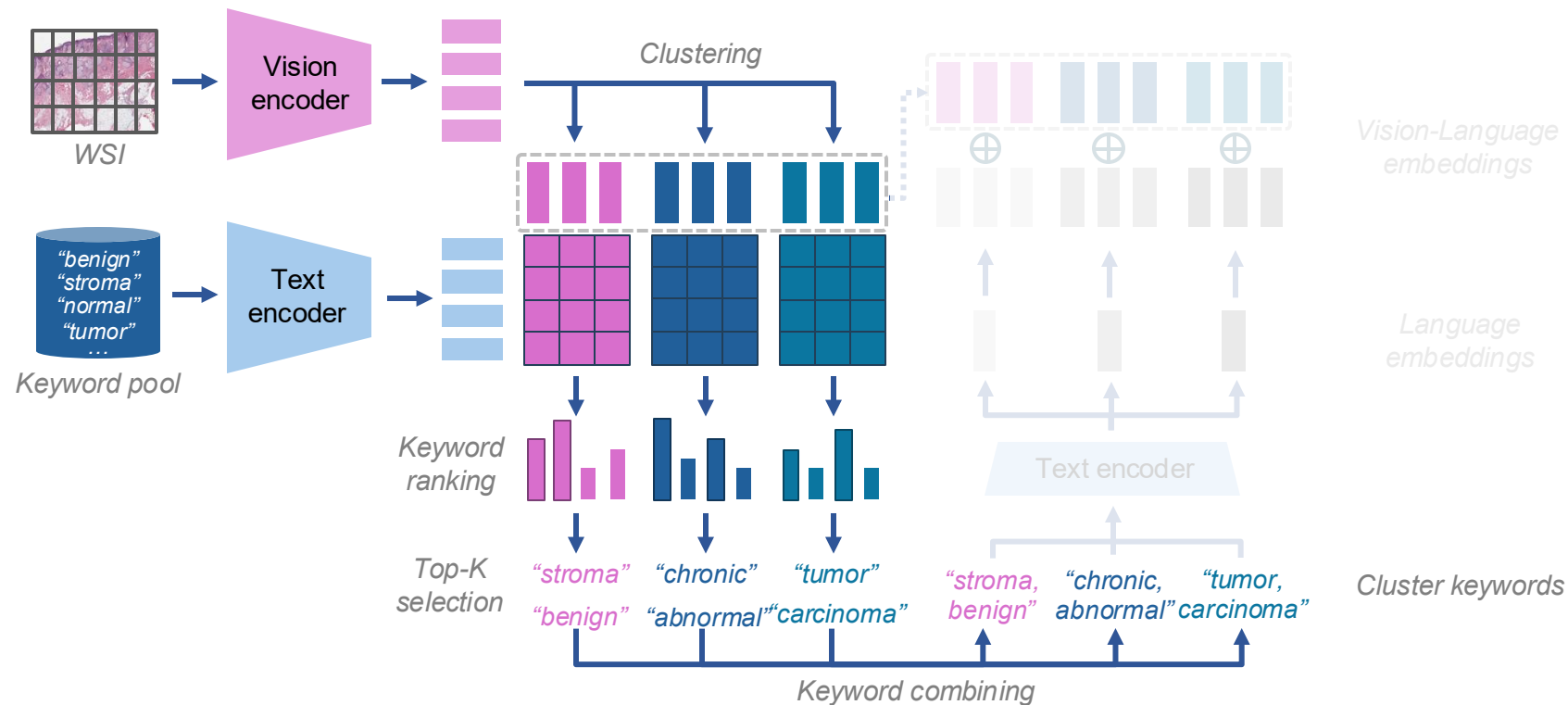
□ Language embedding generation

- The representative **keywords** are concatenated by commas



□ Language embedding generation

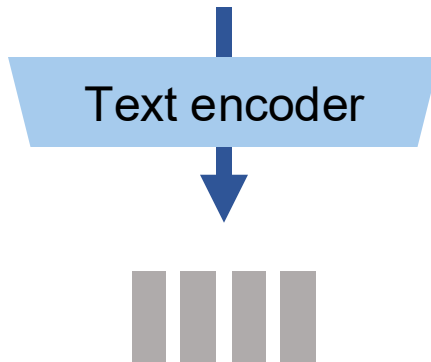
- and forwarded through the text encoder to obtain the **cluster-level language embeddings**.



□ Language embedding generation

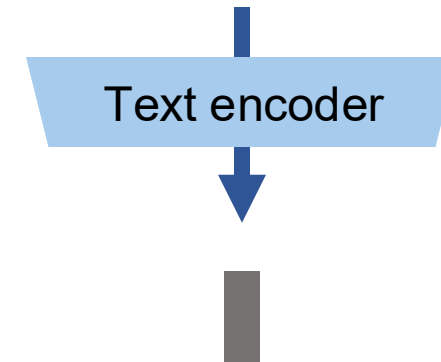
- With combined keywords, the model can understand their **contextual relationships**.

“papillary architecture”
“alveolar (nested) pattern”
“hobnailing pattern”
“abundant cytoplasm with reticular pattern”



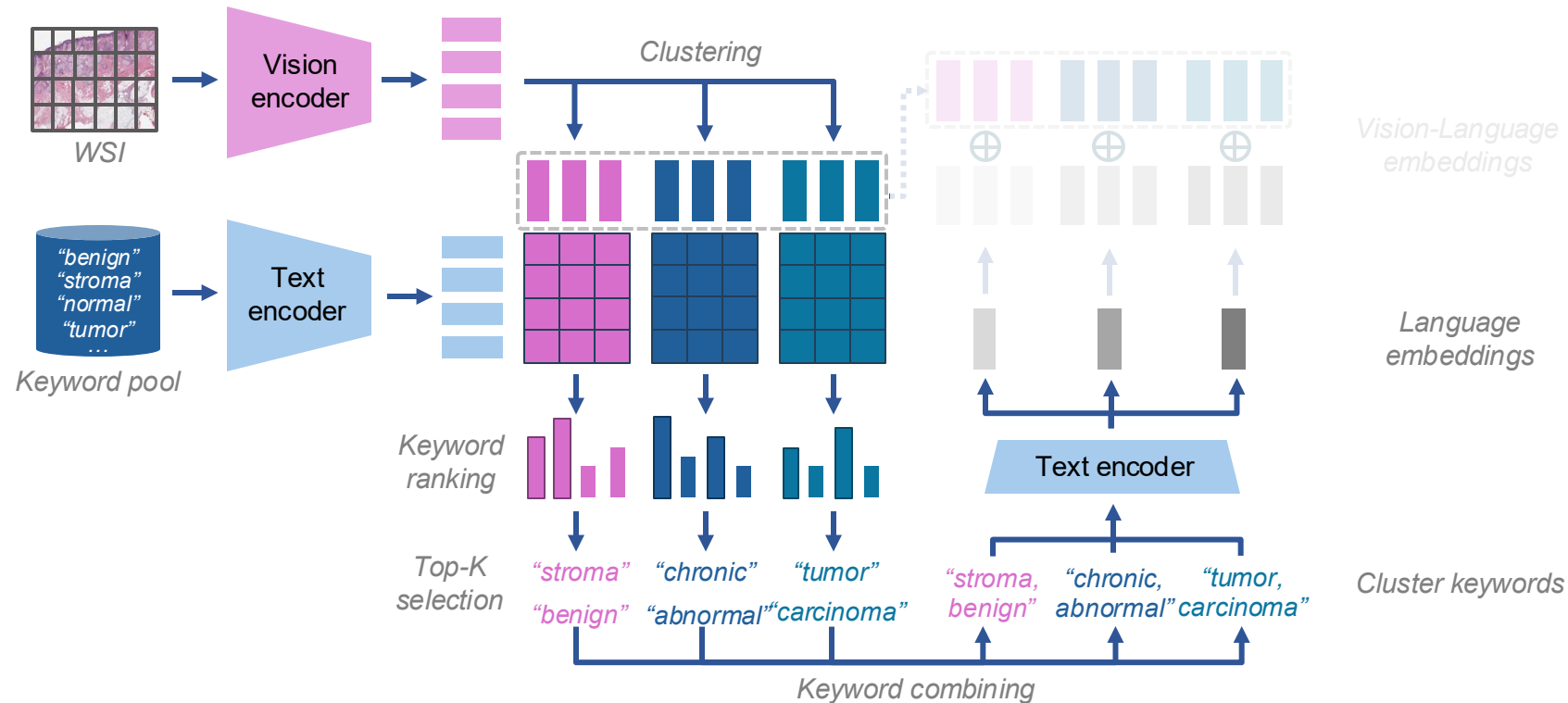
→
*Keyword
combining*

*“papillary architecture, alveolar (nested)
pattern, abundant cytoplasm with reticular
pattern, hobnailing pattern”*



□ Vision-language embedding generation

- **Language** embeddings are then **concatenated** with the corresponding **vision** embeddings.
- These embeddings are then aggregated into a WSI-level embedding using a trainable MIL aggregator.



□ MIL aggregators

- We compare vision-only and vision-language embeddings using **four MIL aggregators**,
 - *ABMIL, CLAM-SB, CLAM-MB, and TransMIL.*

□ Datasets

- **Three public TCGA datasets** are used for evaluation.
 - *TCGA-NSCLC: Lung cancer subtyping*
 - *TCGA-RCC: Renal cell carcinoma subtyping*
 - *TCGA-BRCA: Breast invasive carcinoma subtyping*

□ For qualitative analysis,

- We generate **heatmaps** using the normalized attention scores from the MIL aggregator.
- Following clustering, adjacent patches within the same cluster are merged into a region of interest (RoI).
- Each RoI is annotated with the **representative keywords**,
which is **region-specific** and is generated using **Vision-Language embeddings (ReVL annotation)**.

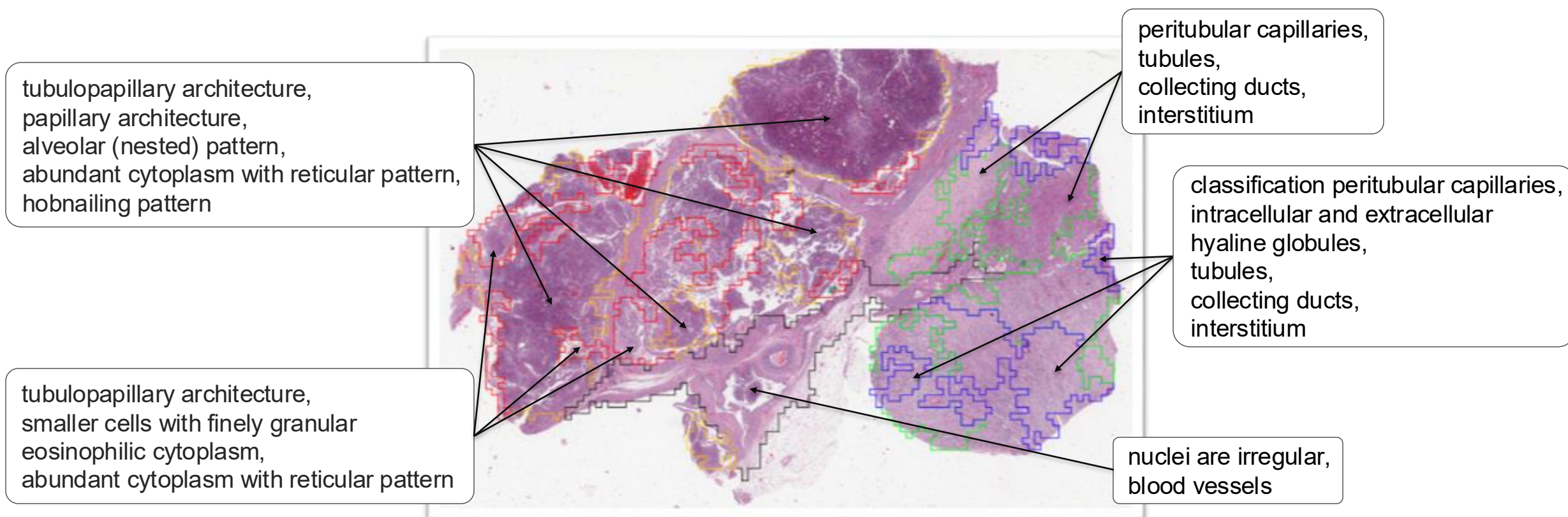
Quantitative evaluation

Aggregator	Emb.	TCGA-NSCLC			TCGA-RCC			TCGA-BRCA			Average		
		<i>Acc</i>	<i>F1</i>	<i>AUC</i>	<i>Acc</i>	<i>F1</i>	<i>AUC</i>	<i>Acc</i>	<i>F1</i>	<i>AUC</i>	<i>Acc</i>	<i>F1</i>	<i>AUC</i>
ABMIL	V	0.9035	0.9033	0.9739	0.9425	0.9338	0.9949	0.9313	0.9005	0.9707	0.9257	0.9126	0.9798
	V-L	0.8989	0.8988	0.9679	0.9310	0.9205	0.9961	0.9479	0.9225	0.9762	0.9259	0.9139	0.9800
CLAM-SB	V	0.9012	0.9011	0.9715	0.9402	0.9282	0.9951	0.9271	0.8915	0.9649	0.9228	0.9069	0.9771
	V-L	0.9058	0.9056	0.9696	0.9333	0.9181	0.9954	0.9479	0.9196	0.9770	0.9290	0.9144	0.9806
CLAM-MB	V	0.8989	0.8988	0.9691	0.9333	0.9191	0.9949	0.9292	0.8949	0.9650	0.9205	0.9043	0.9764
	V-L	0.9103	0.9103	0.9699	0.9287	0.9131	0.9964	0.9479	0.9196	0.9780	0.9290	0.9143	0.9814
TransMIL	V	0.8736	0.8729	0.9603	0.9333	0.9247	0.9882	0.9146	0.8517	0.9741	0.9072	0.8831	0.9759
	V-L	0.8920	0.8918	0.9688	0.9379	0.9236	0.9903	0.9125	0.8479	0.9728	0.9141	0.8878	0.9773

- On average, vision-language embeddings consistently achieved **higher performance** than vision-only embeddings across all evaluation metrics, aggregators, and datasets.

□ Qualitative evaluation of *VLEER*

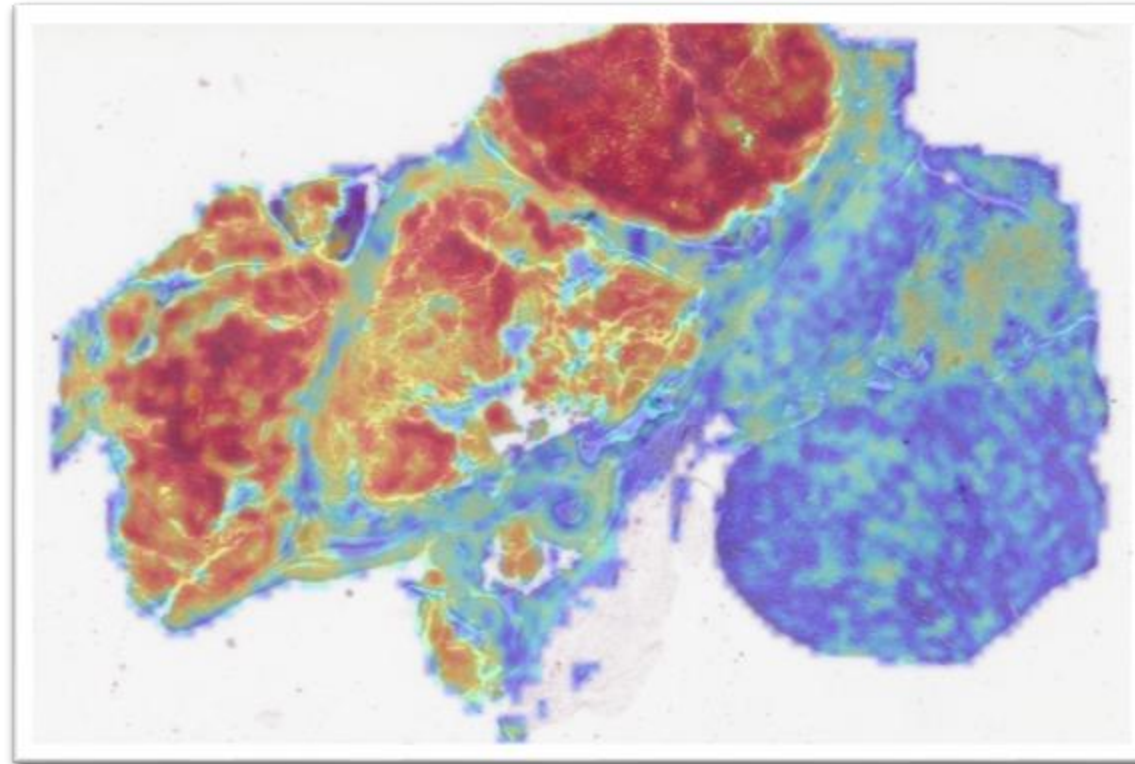
- The ReVL annotations of a papillary renal cell carcinoma in TCGA-RCC



ReVL annotation
(a papillary renal cell carcinoma in TCGA-RCC)

□ Qualitative evaluation of *VLEER*

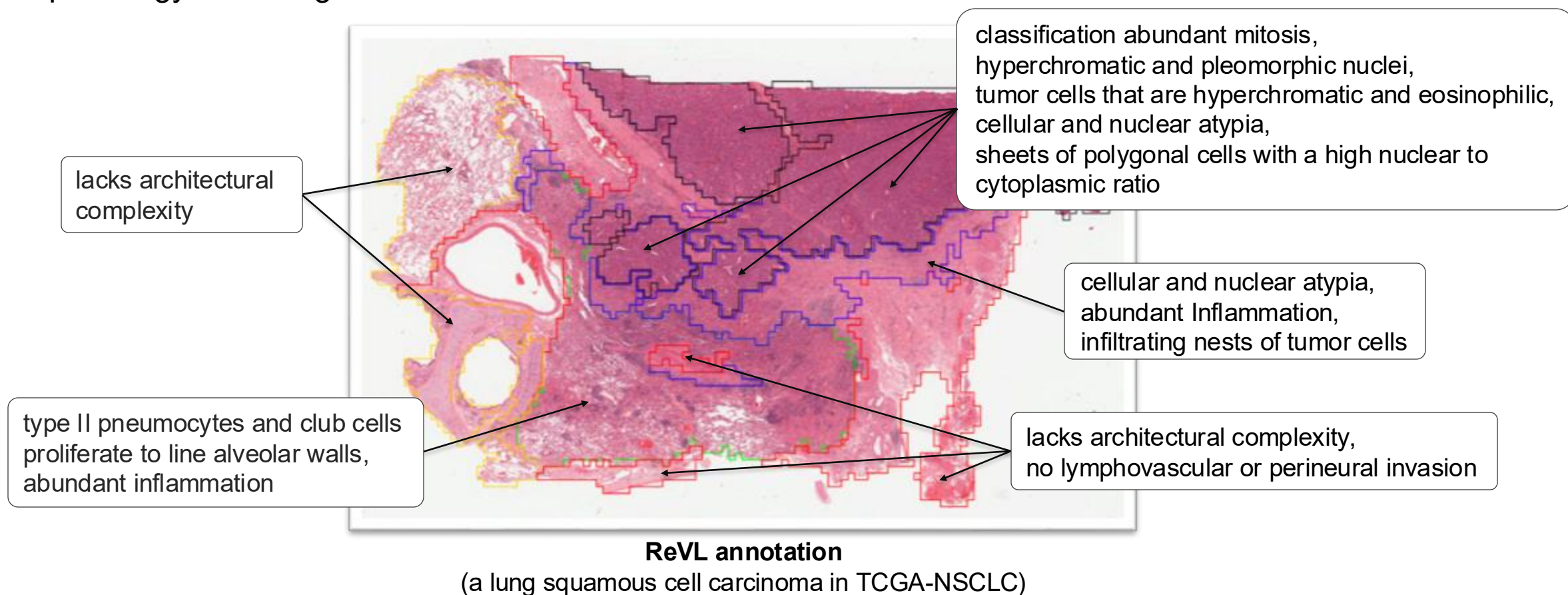
- The highly attended regions (**red**) in the heatmap are closely related to the patterns of **papillary cancer**, whereas the low attended regions (**green** and **blue**) are **normal histology of renal tissues**.



Attention heatmap
(a papillary renal cell carcinoma in TCGA-RCC)

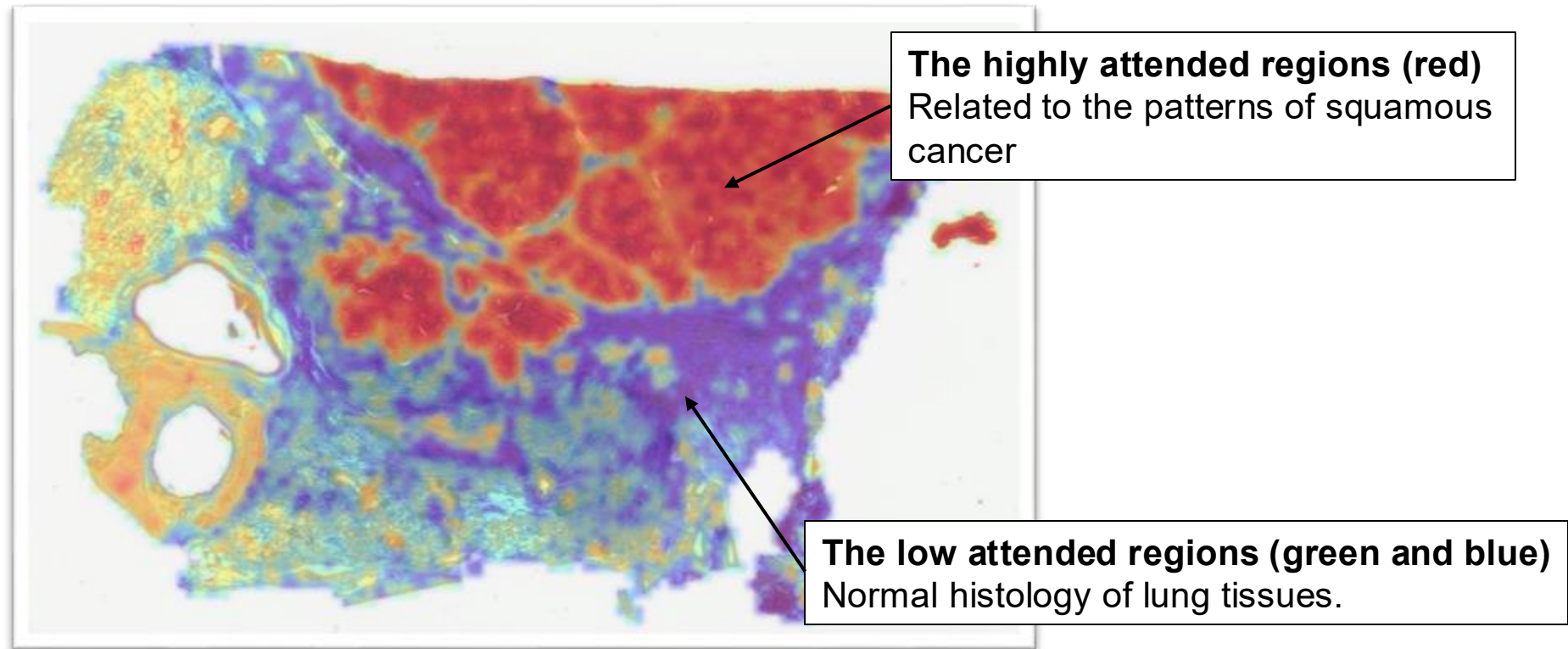
□ Qualitative evaluation of *VLEER*

- *VLEER* enhances transparency by providing text-based justifications that align with established pathology knowledge.



□ Qualitative evaluation of *VLEER*

- The combination of ReVL annotations and heatmaps enables the accurate detection of abnormal regions within a WSI along with their pathological patterns.



Attention heatmap
(a lung squamous cell carcinoma in TCGA-NSCLC)

□ *VLEER*

- We propose *VLEER* for generating vision-language embeddings in WSI representation.
- The method not only increases the performance on downstream tasks but also provides **explainability** of the prediction.
- The combination of **ReVL annotations** and **attention heatmaps** forms a powerful and interpretable framework for WSI analysis.

Thank you