FlexR: Few-shot Classification with Language Embeddings for Structured Reporting of Chest X-rays

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Abstract

The automation of chest X-ray reporting has garnered significant interest due to the time-consuming nature of the task. However, the clinical accuracy of free-text reports has proven challenging to quantify using natural language processing metrics, given the complexity of medical information, the variety of writing styles, and the potential for typos and inconsistencies. Structured reporting and standardized reports, on the other hand, can provide consistency and formalize the evaluation of clinical correctness. However, high-quality annotations for structured reporting are scarce. Therefore, we propose a method to predict clinical findings defined by sentences in structured reporting templates, which can be used to fill such templates. The approach involves training a contrastive language-image model using chest X-rays and related free-text radiological reports, then creating textual prompts for each structured finding and optimizing a classifier to predict clinical findings in the medical image. Results show that even with limited image-level annotations for training, the method can accomplish the structured reporting tasks of severity assessment of cardiomegaly and localizing pathologies in chest X-rays.

Keywords: Structured report generation, Contrastive language-image pretraining, Few-shot classification, Chest X-ray diagnosis

1. Introduction

Radiologists often spend a significant amount of time on documentation and report-writing, rather than focusing on individual patient needs. Therefore, structured reporting is highly valued in the field of radiology for not only saving valuable time but also for standardizing content and terminology (Nobel et al., 2021; Hong and Kahn, 2013). According to Nobel et al. (2020), structured reporting can be defined as an IT-based method to import and arrange the medical content into the radiological report. It facilitates the generation of standardized reports with a structured representation of clinical findings. Professional radiology societies such as RSNA and ESR endorse structured reporting and standardized reports, as it simplifies communication and makes the reports machine-readable. These features are beneficial for a variety of purposes, such as quality assurance, clinical trials, and the internationalization of data.

In contrast, most deep learning methods proposed for automated reporting focus on the generation of free-text reports. However, despite their potential benefits, generated free-text reports can suffer from the same limitations as manually written free-text reports, such as a lack of standardization and, therefore, difficulties in assessing clinical accuracy (Pino et al., 2021). A significant challenge in automating structured reporting is the lack of extensive, high-quality collections of structured annotations that are publicly available.

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Furthermore, the lack of standardization in reporting templates across hospitals and countries adds complexity to the task. Therefore, a method is needed to use the abundance of unstructured free-text radiology reports and images available and adapt to new structured reporting templates with limited annotations.

To this end, we present FlexR, a flexible few-shot learning method for predicting fine-grained clinical findings for structured reporting. We use self-supervised pretraining on pairs of chest X-rays and free-text radiology reports to extract knowledge from large amounts of unstructured data and utilize it to predict structured findings defined by sentences of reporting templates that can easily be adjusted. Our results demonstrate that even with minimal image-level annotations, FlexR can predict the severity of cardiomegaly and localize pathologies in chest X-rays.

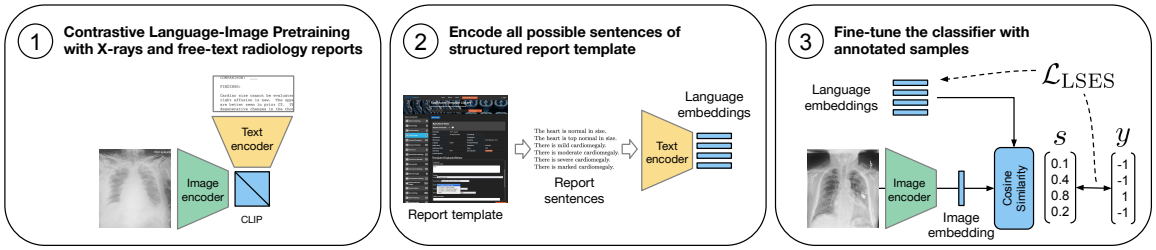

Figure 1: The Few-shot classification with Language Embeddings for chest X-ray Reporting (FlexR) method leverages self-supervised pretraining to predict fine-grained clinical findings in radiology images, using only a few high-quality annotations. The process is composed of three key steps: (1) contrastive language-image pretraining on a dataset of radiology images and unstructured reports, (2) encoding of clinical findings from structured reports, and (3) fine-tuning of the resulting language embeddings.

1.1. Related work

Recent advances in computer vision and natural language processing led to significant progress in the automated diagnosis of chest X-rays and the generation of radiology reports. In contrast to the generation of free-text radiology reports, only a few works focus on automating structured reporting. Pino et al. (2021) proposed structured report generation with a classification model of high-level pathologies used to select sentences from a template. Bhalodia et al. (2021) used an object detector to localize pneumonia and an additional classifier to predict further attributes about the lesions, which could be used in a structured reporting setting. Similar to our work, Syeda-Mahmood et al. (2020) classified the clinical findings in X-ray images on a fine-grained level as a one-hot-encoded vector and used this to retrieve similar reports to generate customized free-text reports.

The concept of contrastive language-image pretraining (CLIP) (Radford et al., 2021) is to generate a joint representation of text and image pairs. This joint embedding proved to be also very useful for downstream tasks like classification and captioning. Trained originally

on general data scraped from the internet, CLIP has recently been adopted to the radiology domain to improve retrieval-based radiology report generation (Endo et al., 2021). Boecking et al. (2022) further improved this pretraining by using semantic concepts and discourse characteristics. Wang et al. (2022) added pertaining on unpaired datasets to CLIP and added a semantic matching loss. The generation of language-image representations, without CLIP, has also been investigated for the report generation task using weakly-supervised contrastive pretraining (Yan et al., 2021), joint embeddings for pulmonary edema assessment (Chauhan et al., 2020), mutual information maximization for chest X-ray classification (Liao et al., 2021), and attention-based contrastive learning (Huang et al., 2021)

Few-shot learning in medical imaging aims to overcome the challenge of obtaining large amounts of accurate labels by only requiring few annotated images. For the diagnosis of chest X-rays, Paul et al. (2021) employed a discriminative autoencoder ensemble in a few-shot setting and (Jia et al., 2020) explored the few-shot generation of reports for rare diseases. Recently, methods that use CLIP have also been evaluated for zero-shot prediction using only text embeddings of pathologies with promising results. Both Seibold et al. (2022) and Tiu et al. (2022) perform a zero-shot classification using language prompts of disease labels and their negation. Huang et al. (2021) and Boecking et al. (2022) showed the effectiveness of their improved pretraining in a zero-shot and few-shot setting in predicting chest pathologies. In contrast to our work, these works focus on classifying the multi-label presence of pathologies and do not predict more fine-grained labels like disease localization or grading.

2. Method

Our Few-shot classification with Language Embeddings for chest X-ray Reporting (FlexR) method uses self-supervised pretraining to predict clinical findings defined by text prompts for a given radiology image. Our method's primary goal is to use large amounts of unstructured radiology data to predict structured, fine-grained clinical findings with only a few high-quality annotations. Specifically, we extract all possible sentences of a structured radiology report template and define these as possible clinical findings. Next, we project them onto a joint language-image embedding space and use these language embeddings of clinical findings to predict the ones most similar to the input image embedding. As shown in Figure 1, our method consists of three steps:

1. Contrastive language-image pertaining (CLIP) with unlabeled pairs of radiology reports and images: Due to the domain gap, the CLIP model must be retrained on a dataset with radiological images and reports to be applied in our approach. Alternatively, domain-specific vision-language models like BioViL (Boecking et al., 2022) with a joint embedding space of text and images can be used.

2. Language embeddings of clinical findings: In the second step, we extract all possible options for the structured reporting template as individual sentences and encode them with the CLIP text encoder, resulting in a text embedding T_i for each clinical finding. In the example of detecting and grading cardiomegaly in chest radiographs, they could be expressed by the prompts in Table 1 like *There is mild cardiomegaly.*

3. Fine-tuning the classifier: The result of our approach, the classifier consists of a CLIP image encoder to obtain the embedding I_i of the input image, as well as the embeddings $W = \{T_1, T_2, \ldots, T_C\}$ initialized by the text embeddings of clinical findings, where C is the number of clinical findings defined by the structured reporting template. To classify the input image, we calculate the cosine similarity $s = \{s_1, s_2, \ldots, s_C\}$ between I_i and each clinical finding in W.

We use the fact that many textual prompts share common information with other sentences from similar parts of the template, providing a useful clustering of medically similar findings and label dependencies. For example, *lung opacity in the left lung* and *lung opacity in the upper left lung* have almost identical language embeddings. We even noticed that, in rare cases, two different prompts have the same embedding using the initialization W. Therefore, we propose to optimize the clinical finding embeddings in W and the image encoder using the Log-Sum-Exp Sign loss to ensure that different prompts result in different language embeddings.

We propose using the Log-Sum-Exp Sign (LSES) loss function (Jin et al., 2021) to optimize the clinical finding embeddings initialized by the text encoder. The labels of each clinical finding are defined as $y = \{y_1, y_2, \ldots, y_C\}$ with $y_i \in \{1, -1\}$, representing the presence and absence of a clinical finding in the report, respectively. Given the cosine similarity s between image and finding embedding, we define the $\mathcal{L}_{\text{LSES}}$ loss as $\mathcal{L}_{\text{LSES}} = \log\left(1 + \sum_{i=1}^{C} e^{-y_i \gamma s_i}\right)$. which inherently assigns a higher weight to misclassified classes while leaving the embeddings of correctly initialized classes largely unchanged. This effect can be adjusted with the hyperparameter γ, which further increases the loss for misclassified embeddings and decreases it for good embeddings. This mechanism is effective in classification tasks with a long-tailed distribution like human-object interaction recognition (Jin et al., 2021) and is therefore suited for the long-tailed distribution in structured reporting. In $\mathcal{L}_{\text{LSES}}$, 1 is added to the summands to give the loss a lower bound of 0.

3. Experimental setup

In this section, we detail the experimental setup and the dataset employed in our study. We evaluate the performance of our method on two structured reporting tasks: the assessment of cardiomegaly severity and the localization of pathologies in chest X-rays. For comprehensive information on the implementation, including data processing, model architecture, and training protocols, please refer to the appendix.

3.1. Dataset

We use the MIMIC-CXR-JPG v2.0.0 (Johnson et al., 2019a) dataset, which is derived from the MIMIC-CXR dataset consisting of 377,110 chest radiographs associated with 227,827 imaging studies and free-text reports (Johnson et al., 2019b; Goldberger et al., 2000). The labels for structured reports are extracted from the medical scene graph dataset Chest ImaGenome (Wu et al., 2021) consisting of 242072 anatomy-centered scene graphs for the MIMIC-CXR image data. It provides 1256 combinations of relation annotations between 29 anatomical locations and their attributes.

Table 1: The prompts were used for initializing the classifier in the second task of predicting the severity of cardiomegaly. Following the *Chest Xray - 2 Views* template from RadReport.

Severity	Initialization prompt	Training	Validation	Testing
Normal	The heart is normal in size.	3140	478	943
Top Normal	The heart is top normal in size.	635	72	160
Mild	There is mild cardiomegaly.	6084	809	1816
Moderate	There is moderate cardiomegaly.	8696	1164	2619
Severe	There is severe cardiomegaly.	2231	335	676
Marked	There is marked cardiomegaly.	246	36	85
		21032	2894	6299

3.2. Severity prediction of cardiomegaly

The first task evaluates the model to predict the severity of cardiomegaly following the textual prompts defined in the TLAP endorsed structured report template *Chest Xray - 2 Views* created by Penn Medicine at the University of Pennsylvania[1]. Using the keywords we have extracted from reports 6 possible severity states of cardiomegaly. Prompts distribution can be seen in Table 1. We calculate probabilities using softmax and train the DenseNet121 baseline with a cross-entropy loss. The methods are compared using the AUC.

3.3. Localized pathology detection

The second task is localizing pathologies in chest radiographs using the MIMIC-CXR dataset. For this, we use the labels provided by ImaGenome (Wu et al., 2021), which have also been used by Agu et al. (2021). The 9 attributes are: *Lung Opacity*, *Pleural Effusion*, *Atelectasis Enlarged Cardiac Silhouette*, *Pulmonary Edema/Hazy Opacity*, *Pneumothorax*, *Consolidation*, *Fluid Overload/Heart Failure* and *Pneumonia*. The dataset contains 19 anatomical locations including different regions of the lung, hilar structures, costophrenic angle, and mediastinum as well as the cardiac silhouette and trachea. For each patient, we extract the triplet of *attribute* located in the *anatomical site* from the medical scene graph provided. For all patients, this resulted in 98 (of 162 possible) unique combinations of attribute and location. By joining the *attribute* and *location* with *"in the"*, we create the template sentences used as an initialization of the classifier, for example, *"consolidation in the left lung"*. Following Agu et al. (2021), we calculate the area under the receiver operating characteristic curve (AUC) for all possible locations of each pathology and average them to one location-sensitive AUC per pathology. For a fair comparison with the image encoder in CLIP, the DenseNet121 used as a baseline for detection-free localization has been pretrained on the global pathology classification. This task was used in the ablation study since there are more annotations available.

1. https://radreport.org/home/144/2011-10-21%2000:00:00

Table 2: Ablation of the FlexR method with different backbones and weight initializations on the task of pathology localization and results for cardiomegaly grading in comparison with naïve transfer learning. Mean AUC is used as the evaluation metric. Our proposed approach is highlighted in bold.

Method	Backbone	Pretraining	1-shot	5-shot	10-shot	100-shot	sampled	all
Ablation on localizing pathologies								
MLP	DN121	pathologies	0.67	0.69	0.71	0.76	0.77	0.84
FlexR	ViT-B/16-CLIP	CLIP	0.66	0.70	0.73	0.75	0.77	-
FlexR	DN121+SB	random init.	0.67	0.72	0.75	0.79	0.81	-
FlexR	**DN121+SB**	**CLIP**	0.74	0.77	0.78	0.80	0.81	0.84
Grading task: Cardiomegaly severity prediction								
MLP	DenseNet121	pathologies	0.59	0.65	0.68	0.75	0.79	0.73
FlexR	**DN121+SB**	**CLIP**	0.65	0.72	0.74	0.77	0.78	0.82

Table 3: Comparison of FlexR against baselines using all available data with and without localization of pathologies as well as naïve transfer learning in the few-shot setting. AUC is used as the evaluation metric. The proposed method is marked bold.

Method	Lung Opac.	Pleural Eff.	Atelectasis	Enl. Card. S.	Pulm. Edema	Pneumothor.	Consolidation	Heart Failure	Pneumonia	**Avg. AUC**
Multi-label classification with no localization on global view using all data										
DenseNet169 (Agu et al., 2021)	0.91	0.94	0.86	0.92	0.92	0.93	0.86	0.87	0.84	0.89
DenseNet169	0.87	0.90	0.79	0.86	0.85	0.83	0.75	0.77	0.75	0.82
DenseNet121	0.88	0.91	0.81	0.87	0.87	0.87	0.79	0.80	0.77	0.84
ViT-B16	0.88	0.91	0.80	0.87	0.86	0.85	0.77	0.78	0.76	0.83
Fully supervised object detection with bounding boxes and high-resolution crops using all data										
FasterR-CNN (Agu et al., 2021)	0.84	0.89	0.77	0.85	0.87	0.77	0.75	0.81	0.71	0.80
AnaXNet (Agu et al., 2021)	0.88	0.96	0.92	0.99	0.95	0.80	0.89	0.98	0.97	0.93
***Few-shot**, detector-free localization on global view* (224×224)										
DenseNet121 1-shot	0.70	0.76	0.64	0.77	0.70	0.60	0.66	0.62	0.58	0.67
DenseNet121 5-shot	0.72	0.78	0.66	0.78	0.73	0.64	0.67	0.64	0.62	0.69
DenseNet121 (all data)	0.83	0.89	0.79	0.87	0.84	0.89	0.83	0.81	0.82	0.84
FlexR 1-shot	0.72	0.83	0.69	0.82	0.77	0.72	0.74	0.73	0.67	0.74
FlexR 5-shot	0.75	0.84	0.71	0.82	0.79	0.78	0.76	0.73	0.71	0.77
FlexR (all data)	0.82	0.89	0.78	0.87	0.84	0.90	0.83	0.80	0.81	0.84

4. Results and discussion

In this section, we present our findings and discuss the implications and limitations of FlexR.

4.1. Domain-specific contrastive language-image pretraining

We observed severe overfitting in the MIMIC-CXR fine-tuning of the CLIP model with a ViT-16/B backbone (Dosovitskiy et al., 2021) using the original CLIP tokenizer and text encoder. Therefore, we replaced the text and image encoder with domain-specific pretrained encoders DenseNet121 (DN121) (Huang et al., 2017) trained on the classification of non-localized pathologies in the ImaGenome dataset (see section 3.3) and SciBERT (SB) (Beltagy et al., 2019) pretrained on a large corpus of scientific text. This setup showed better generalization, and we, therefore, used this model for all following experimental setups and compared it with the fine-tuned, unmodified CLIP model initially trained.

4.2. Few-shot classification of clinical findings

In the second set of experiments, we investigate the effectiveness of FlexR in predicting fine-grained clinical findings with limited training samples per class. We use the pretrained CLIP model and fine-tune FlexR to the task-specific textual prompts.

4.2.1. Ablation and severity grading

The ablation study in Table 2 on the task of localizing pathologies shows that the FlexR model outperforms the random initialization without language embeddings and the ViT-B/16-CLIP backbone fine-tuned on MIMIC-CXR. This confirms the better generalization of the domain-adapted CLIP model and that the initialization with language embeddings improves the few-shot performance. FlexR outperforms the naïve transfer learning baseline from a DenseNet121 pretrained on detecting non-localized pathologies. With an increasing number of samples seen per class, the gap between FlexR and the other models decreases. The second part of Table 2 shows the results of detecting and grading cardiomegaly with the language embeddings extracted from a real-world RadReport reporting template. Over the naïve transfer learning baseline FlexR has an increase in AUC of 0.06 in the 1-shot case and 0.07 in the 5-shot learning over the naïve transfer learning baseline. Another interesting finding is that the DenseNet121 optimized by cross-entropy required oversampling of underrepresented classes to gain a similar performance as FlexR. Without oversampling, FlexR reached its best AUC of 0.82 when trained on all data. This could be explained by the inherent class weighting in the LSES-loss used by FlexR.

4.2.2. Localized pathology detection

In the few-shot setting of localized pathology detection, FlexR showed the best result with a 0.07 higher AUC for 1-shot learning and a 0.08 increase for 5-shot learning compared to transfer learning with a pretrained DenseNet121. In Table 3 FlexR is compared with global classification baselines and methods based on object detection that use the full training data. To establish an upper-bound AUC, we report the image encoders used for global pathology detection without the localization of diseases. Compared to object detection methods, the few-shot methods expectedly do not reach the AUC of AnaXNet, which uses

all training data, is fully supervised with bounding boxes, and refines features extracted from high-resolution crops.

4.3. Limitations and future work

The self-supervised pretraining with CLIP is only possible if large amounts of image-text pairs are available. This might not be the case with other medical problems. Therefore, the FlexR method is mainly suited if large amounts of unlabeled text-image pairs and only limited amounts of high-quality labels are available. At the same time, the non-few-shot learning methods outperformed few-shot learning, so all labels should be used for training when available. Specifically, the results indicate that the localization of diseases in chest X-rays is better suited for a specialized object-detection-based model using full supervision with bounding boxes. In the context of structured reporting, FlexR is particularly helpful in adapting the classification of clinical findings to hospital-specific reporting templates.

In contrast to Seibold et al. (2022) and Tiu et al. (2022), our approach utilizes only a single negative prompt, a healthy patient without any findings, rather than negative prompts for every pathology. Adapting this strategy could potentially improve performance in detecting diseases by having two embeddings as a reference. This could also be used to explicitly model label hierarchies, such as detecting diseases and then localizing or grading them. These label dependencies have only been modeled implicitly in FlexR by the similarity of text in prompts.

Another limitation is that within this study, we only investigate two subtasks of structured reporting of chest X-rays and not the generation of a full radiology report with all possible clinical findings, which would require further logic. The cardiomegaly assessment was extracted from a real-life RadReport template and the localization of diseases was extracted from a knowledge graph from the ImaGenome dataset to model a structured reporting setting. The main reason for this is the lack of a publically available, standardized reporting template for chest X-rays with a high level of detail and annotations for datasets like MIMIC-CXR. While Wu et al. (2021) and Jain et al. (2021) provide highly detailed, structured annotations in the form of graphs, a translation to a real-life reporting template and a benchmark for complete structured reporting is still needed.

5. Conclusion

In this paper, we highlight the need for methods for structured reporting because standardized reports can formalize the evaluation of knowledge embedded in the representations of neural networks. We proposed a Few-shot classification with Language Embeddings for chest X-ray Reporting (FlexR) method that utilizes self-supervised pretraining with CLIP to predict fine-grained clinical findings for a given radiology image. Our primary goal was to use large amounts of unlabelled pairs of clinical free-text reports and radiological images to accurately classify the clinical findings in structured reports, given only a small number of labels for each clinical finding. Our results showed that even with limited image-level annotations, our method can predict the structured reporting subtasks of cardiomegaly severity assessment and localizing pathologies in chest X-rays in a few-shot setting.

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Appendix A. Log-Sum-Exp used in the LSES loss

The Log-Sum-Exp (LSE) function defined as

$$LSE = \log\left(\sum_{i=1}^{C} e^{x_i}\right) \tag{1}$$

is a smooth approximation of the maximum function $max\{x_1, x_2, \ldots, x_i\}$ with softmax being its derivative. With $x_i = -y_i \gamma s_i$ it assigns the highest loss to classes that are present in the report but have a low similarity with the image embedding or have a high similarity but are not present. At the same time, the softmax gradient keeps the correctly initialized class weights stable. More details can be found in the work of Jin et al. (2021) that served as an inspiration for the use of the loss.

Appendix B. Implementation details

B.1. Data processing

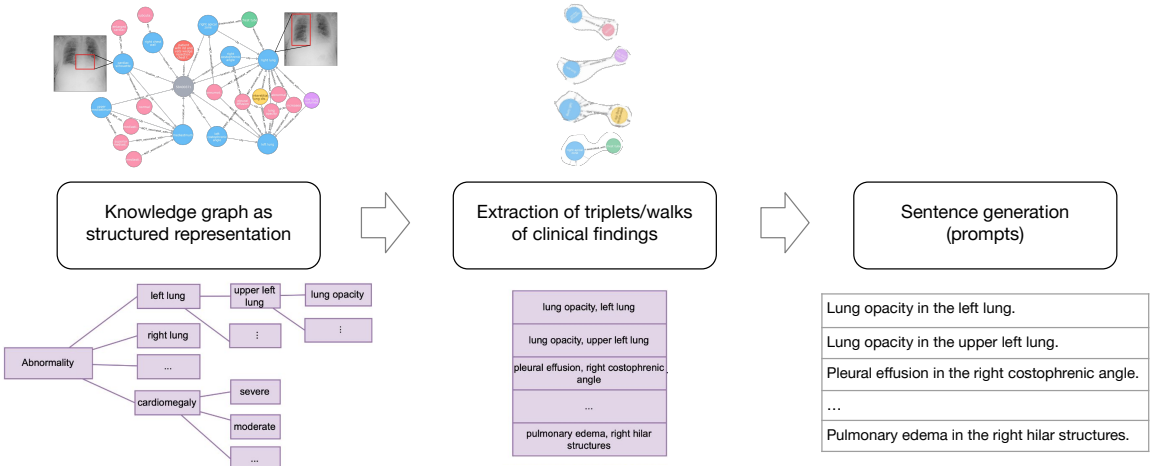

Figure 2: Extraction of natural language prompts from the ImaGenome (Wu et al., 2021) knowledge graph representing sentences in a structured reporting template.

We use the data split provided by ImaGenome with Posterior-Anterior (PA) and Anterior-Posterior (AP) radiographs resulting in 166512 training images, 23952 validation images, and 47389 test images after preprocessing. The images were processed with MONAI 0.8.0 and the dataloader is implemented with ffcv 0.0.2. All images are resized to 224x224, padded if needed, and scaled to the range [-1,1]. For training, the following image augmentations were applied: random crop with at least 75% image size, random rotation up to $\pm 15°$, and a color jitter of 10% brightness as well as 20% contrast and saturation. The reports were augmented by randomly sampling a sentence containing a finding in the ImaGenome scene graph. For healthy patients with no findings, a random sentence from the full report was randomly sampled.

B.2. FlexR Model - Cosine similarity

The cosine similarity of the input image embedding and the language embeddings of the clinical finding prompts is implemented with a fully connected layer without bias. Both the initial text embeddings and the image embeddings are normalized and the linear layer calculates the dot product between the embeddings while allowing the embeddings of the clinical findings to be differentiable. Algorithm 1 shows the pseudo-code of a PyTorch implementation.

Algorithm 1: Prompt Similarity Pytorch Module

```
class PromptSimilarity(nn.Linear)
    method __init__(prompt_embeddings)
        out_features, in_features ← prompt_embeddings.shape;
        call super().__init__(in_features, out_features, bias=False);
        self.weight.data ← F.normalize(prompt_embeddings);
    method forward(x)
        x ← F.normalize(x);
        x ← super().forward(x);
        return x;
```

B.3. Training

All networks were trained with PyTorch 1.10 and PyTorch lightning 1.5.10 in native mixed precision. The transformer-based models and tokenizers are implemented using the huggingface library (transformers 4.16.2). The CLIP models were fine-tuned on 8 NVIDIA A40 for 300 epochs with a batch size of 128 using an AdamW optimizer with a learning rate of 5e-6, no weight decay on the normalization layer, and bias and 0.1 weight decay on all other parameters. The learning rate was decayed with a cosine annealing schedule and 1 epoch linear warmup. All other models were trained on a single NVIDIA A40. The DenseNet and Vision Transformer classifiers were trained for 25 epochs with the same hyperparameters as in (Agu et al., 2021): Adam optimizer, a learning rate of 1e-4 and unweighted binary cross-entropy loss. The FlexR models were fine-tuned for 10 epochs with a learning rate of 1e-4, AdamW optimizer with no weight decay, and learning rate scheduler with cosine annealing decay and 1 epoch linear warmup. During fine-tuning, all weights are optimized including the image encoder. Fine-tuning only the language embeddings and zero-shot inference did not yield useful results and was therefore omitted from the experiments. The model performing best on the validation set was used for testing. After a hyperparameter search on the localized pathology task with 50, 100, and 150 the γ parameter of the LSES loss was set to 50 for all experiments. For few-shot learning, an epoch is defined as seeing 128 images per class. In the setup of sampling all classes, the same amount of images was chosen per class to ensure comparability while having access to the entire dataset. A batch size of 256 is used for the classification baselines and FlexR finetuning. All experiments were repeated 5 times with different seeds and the average results are reported.