Synthetic Vasculature and Pathology Enhance Vision-Language Model Reasoning

Chenjun Li^{1,2}
Cheng Wan^{1,2}
Laurin Lux^{2,3}
Alexander H. Berger^{2,3}
Richard B. Rosen⁴
Martin J. Menten³
Johannes C. Paetzold^{2,5}

CL2733@CORNELL.EDU
CW2222@CORNELL.EDU
LAURIN.LUX@TUM.DE
A.BERGER@TUM.DE
RROSEN@NYEE.EDU
MARTIN.MENTEN@TUM.DE
JPAETZOLD@MED.CORNELL.EDU

- ¹ School of Electrical and Computer Engineering, Cornell University, Ithaca, NY 14853, USA
- ² Weill Cornell Medicine, New York, NY 10021, USA
- ³ School of Computation, Information and Technology, Technical University of Munich, 80333 Munich, Germany
- ⁴ New York Eye and Ear Infirmary of Mount Sinai, New York, NY
- ⁵ Cornell Tech, New York, NY 10044, USA

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Abstract

Vision-Language Models (VLMs) offer a promising path toward interpretable medical diagnosis by allowing users to ask about clinical explanations alongside predictions and across different modalities. However, training VLMs for detailed reasoning requires large-scale image-text datasets. In many specialized domains, for example in reading Optical Coherence Tomography Angiography (OCTA) images, such precise text with grounded description of pathologies is scarce or even non-existent. To overcome this bottleneck, we introduce Synthetic Vasculature Reasoning (SVR), a framework that controllably synthesizes images and corresponding text, specifically: realistic retinal vasculature with Diabetic Retinopathy (DR) features: capillary dropout, microaneurysms, neovascularization, and tortuosity, while automatically generating granular reasoning texts. Based on this we curate OCTA-100K-SVR, an OCTA image-reasoning dataset with 100,000 pairs. Our experiments show that a general-purpose VLM (Qwen3-VL-8b) trained on the dataset achieves a zero-shot balanced classification accuracy of 89.67% on real OCTA images, outperforming supervised baselines. Through human expert evaluation we also demonstrate that it significantly enhances explanation quality and pathology localization on clinical data.

Keywords: VLM, CoT, OCTA, DR, Synthetic Pathology

1. Introduction

Vision-language models (VLMs) integrate visual processing with natural language reasoning. Many studies discuss how such models can be particularly valuable in medical image analysis, as they can move beyond simple classification to support interpretable diagnosis (Li et al., 2023; Zhang et al., 2024; Yang et al., 2025; Sellergren et al., 2025). Compared to traditional black-box classifiers, VLMs could explicitly describe what features are present, where pathologies are located, and why a specific diagnosis is suggested. This explainability is critical for clinical validation.

Chain-of-thought (CoT) reasoning enables models to generate step-by-step explanations that simulate human workflows (Wei et al., 2022). In medical imaging, this approach breaks down diagnosis into interpretable stages: identifying anatomical structures, detecting and localizing abnormalities, and synthesizing these findings into a conclusion. However, training VLMs to produce clinically accurate CoT requires extensive datasets with annotations that exceed standard image-level labels (Pan et al., 2025; Lai et al., 2025). Privacy regulations, significant acquisition costs, and the requirement for specialized expertise restrict data availability, particularly for modalities like Optical Coherence Tomography Angiography (OCTA), where even the largest public datasets that include OCTA typically involve only hundreds to a few thousand subjects (Li et al., 2024; AI-READI Consortium, 2024). While a recent approach has attempted to improve VLM interpretability on OCTA images via graph-based knowledge extraction (Li et al., 2025), it is limited to small sample sizes and lacks detailed localization of different pathological features. Without ground-truth annotations, it is difficult to train VLMs that provide high-quality, location-specific explanations.

Synthetic data generation offers a practical solution for data augmentation in VLM training (Ma et al., 2025; Wu et al., 2025). Synthetic generation provides control over visual features and automatically produces ground-truth annotations. Despite these benefits, synthetic data is underutilized in medical VLM training. Previous work by Kreitner et al. (2024) validated synthetic OCTA for vessel segmentation but was limited to healthy vasculature, without pathological features and text-based reasoning chains. A framework capable of generating both realistic pathology and corresponding grounded explanations is needed to enable VLMs to diagnose, understand and reason about OCTA images.

We investigate this approach for Diabetic Retinopathy (DR) staging using OCTA images. DR is a primary cause of vision loss (Lee et al., 2015), and accurate diagnosis of DR relies on the detection and localization of microvascular abnormalities (Alam et al., 2020; Sun et al., 2021). Current public datasets (Dai et al., 2021; Li et al., 2024; AI-READI Consortium, 2024) generally provide only image-level labels.

In this work, we introduce **Synthetic Vasculature Reasoning (SVR)**, a pathology-aware OCTA synthesis framework designed to improve VLM reasoning capabilities (Code and dataset available at: https://github.com/d0ng231/0CTA-SVR). Our work makes the following contributions:

- We developed the first module capable of simulating four distinct DR features on synthetic OCTA images: capillary dropout, microaneurysms, neovascularization, and vessel tortuosity.
- Based on the controllable features, we present **OCTA-100K-SVR**, a synthetic dataset with 100,000 pairs of high-quality OCTA images and texts for VLM training, and demonstrate that scaling synthetic training data improves VLM performance in both classification and reasoning.
- Through evaluations on proprietary and public datasets, we show that VLMs trained via SVR generate clinically accurate explanations and correct pathology localization, exceeding the performance of other models without fine-tuning on real data.

2. Method

2.1. Overview

In Fig. 1 we illustrate the core of our method, which is based on a simulation module that generates topologically accurate vascular graphs with controlled diabetic retinopathy features. A generative adversarial network (GAN) then converts vessel maps into realistic OCTA images, while a teacher VLM converts the corresponding pathology metadata into grounded Chain-of-Thought reasoning texts. By aligning synthetic OCTA images with granular reasoning across 100,000 samples, the framework enables the VLM to learn robust diagnostic representations prior to fine-tuning on limited real-world clinical data.

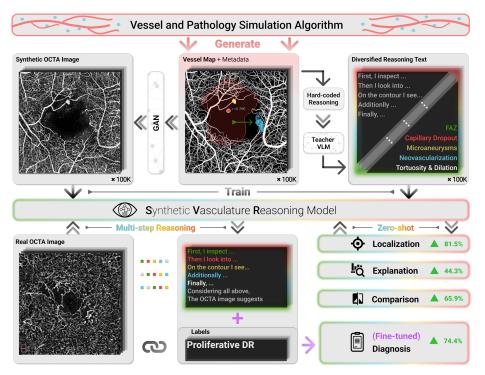


Figure 1: Overview of the Synthetic Vasculature Reasoning Framework. The pipeline begins with the simulation of vessels and pathology. In this way we generate ground-truth vessel maps with and without various DR hallmarks (detailed in Sec. 2.2 and Fig. 2). These maps are then used for: (1) visual synthesis, where a pretrained GAN from Kreitner et al. (2024) converts maps into realistic synthetic OCTA images, and (2) text generation, where structured pathology metadata is converted into diversified Chain-of-Thought reasoning text using GPT-5 (OpenAI, 2025) (see Pseudo code 1 for more details). On these image-text pairs we can fine-tune VLMs which are capable of multiple tasks including disease staging, locating pathological features, and explaining their reasoning. The marked improvements in localization, explanation, comparison and diagnosis are based on expert evaluation (see Sec. 4).

2.2. Synthetic Vessel Growth and Pathology

Synthetic OCTA generation pipeline. We build on the statistical angiogenesis simulator of Kreitner et al. (2024), which itself adapts the space–colonization model of Rauch and Harders (2021). In brief, the retinal vasculature is represented as a forest of rooted 3D binary trees growing in a normalized box $\Omega = [0,1] \times [0,1] \times [0,h_z]$, where the lateral coordinates $(x,y) \in [0,1]^2$ correspond, after global scaling, to a 3×3 mm² macular crop and h_z denotes the normalized slab thickness in the axial (z) direction. Arterial and venous trees are grown in two successive layers that together form the superficial and deep vascular complexes, driven by randomly sampled oxygen sinks and CO_2 sources. Growth follows local attraction cones and Murray's law–based bifurcation rules, producing capillary beds and major vessels. After growth, the vessel graph is voxelized into a 3D volume, projected to an en-face map, and passed through a GAN-based contrast adaptation module to produce realistic synthetic OCTA images.

To increase variability in viewpoint and morphology, we add a random shift and jitter of the foveal avascular zone (FAZ) within the normalized image plane before projection. All variables and parameters of the growth model are described in Appendix A.

Pathology-aware graph augmentation. Going beyond previous works which have been focused on healthy vessel graph generation (Menten et al., 2022; Kreitner et al., 2024; Wittmann et al., 2024; Prabhakar et al., 2024), we introduce a pathology module that operates directly on the 3D tree representation. For each synthetic sample we first use the base simulator to complete the growth of arterial and venous forests, and then apply a sequence of pathology-specific graph remodeling operations that are clinically motivated by the four defining pathologies of DR that show in OCTA images of the retinal vasculature (Kaizu et al., 2017; Alam et al., 2020; Sun et al., 2021) (See Fig. 2). Although the vasculature is simulated in 3D with nodes $\mathbf{x} = (x, y, z)$, all pathology fields are parameterized in the normalized en-face plane using the lateral coordinates $\tilde{\mathbf{x}} = (x, y) \in [0, 1]^2$.

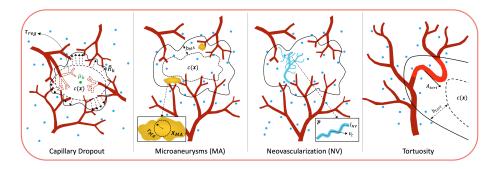


Figure 2: Illustration of the synthesized DR pathologies. DR cases show four main pathologies in OCTA images, which we implement in our vessel synthesis model: (1) capillary dropout, (2) microaneurysms (MA), (3) neovascularization (NV), and (4) increased tortuosity along dropout borders. Comprehensive mathematical description of the algorithms is provided in Appendix A. Afterwards, the generated (pathology-including) vessel maps are fed to the GAN.

Capillary dropout. We first sample n non-perfusion regions around the FAZ. For a region centered at μ_k , its boundary \tilde{R}_k is modeled as an irregular ellipse modulated with a series of angular harmonics and a smooth spatial noise field. We then define a continuous dropout field $c(\mathbf{x}) \in [0,1]$ that encodes how deep the regression should be at each location. Terminal vessel segments (capillaries) inside high- $c(\mathbf{x})$ areas (with threshold τ_{reg}) are stochastically pruned, with sampling weights that favor small-radius vessels and locations close to the lesion core. In addition, surviving vessels inside dropout regions undergo mild elongation and dilation to mimic remodeling at the borders of ischemic zones. The full definition of $c(\mathbf{x})$ and the pruning/remodeling rules is provided in Appendix A.2.

Microaneurysms (MA). Microaneurysms are modeled as short bulbous side branches that bud from existing vessels near dropout borders. For each arterial segment whose endpoint lies in a specified band b_{MA} of the dropout field, we sample a Bernoulli trial whose success probability is modulated by both the global dropout severity and the local value of $c(\mathbf{x})$, making microaneurysms more likely (but not guaranteed) near more severe dropout. Successful trials spawn a small perpendicular branch of length proportional to the simulator step size and with a radius r_{MA} drawn from a clinically plausible range (typically $20-80\,\mu m$). Additional child nodes around the MA center \mathbf{x}_{MA} create irregular cluster-like shapes. All MA segments are stored explicitly in the graph and exported as part of the pathology metadata (see Appendix A.3).

Neovascularization (NV). Neovascularization is implemented as fine, tortuous sprouts that grow from arterial tips adjacent to dropout regions. We identify leaf tips in the 2D projection and, for a subset selected according to a global NV severity parameter, simulate short polylines \mathbf{p} of effective length $l_{\rm NV}$ that extend away from the parent vessel, where $l_{\rm NV}$ corresponds to a small number of growth iterations per tuft. The step direction \mathbf{v}_t at each growth step t combines the previous direction, a weak radial component relative to the nearest dropout center, and a small swirling field with random jitter, producing tuft-like shapes. We also spawn side branches along the main sprout to obtain clinically realistic NV shapes. A detailed description of the polyline construction and radius profiles is given in Appendix A.4.

Tortuosity along dropout borders. Finally, we increase vessel tortuosity in a narrow band b_{tort} around the dropout border. For arterial segments whose endpoints lie in this band, we jitter node positions in the direction perpendicular to the local vessel tangent by a small, zero-mean random offset whose amplitude A_{tort} is proportional to a tortuosity gain parameter. This preserves global connectivity and the FAZ geometry while increasing local curvature, producing the characteristic curling of vessels along non-perfusion borders. The exact definition of the tortuosity band and jitter distribution is provided in Appendix A.5.

Parameterization. All four pathology types share a small set of interpretable hyperparameters controlling count, size, strength, and probability. These parameters are sampled from ranges chosen to match clinical OCTA statistics. The full list of parameters and typical values is summarized in Tab. 5 in Appendix A.

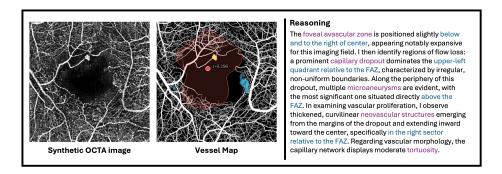


Figure 3: Synthetic OCTA image and generated reasoning text. Purple phrases mark structures/pathologies that are directly controlled by the simulator, while the blue texts mark localizations.

2.3. VLM Pretraining and Fine-tuning

2.3.1. OCTA-100K-SVR DATASET

We refer to the full collection of our 100,000 synthetic image—reasoning pairs as the **OCTA-100K-SVR** dataset. For every simulated sample, the pathology module exports structured metadata describing FAZ geometry and the presence and location of capillary dropout, microaneurysms, neovascular tufts, and tortuosity. From this metadata we first construct a deterministic "template" reasoning paragraph that follows a fixed order (FAZ \rightarrow dropout \rightarrow microaneurysms \rightarrow neovascularization \rightarrow tortuosity) and states explicitly which patterns are present and where they lie relative to the FAZ and macular quadrants.

This template is then passed to a teacher model (GPT-5 (OpenAI, 2025)), which is prompted to rewrite the paragraph while strictly preserving all clinical facts and spatial relations. The teacher model diversifies the Chain-of-Thought descriptions that remain aligned with the metadata (see Fig. 3 and Appendix A.7). For each image we keep one such paragraph as the assistant answer a. The user question q is a short prompt asking the model to describe the OCTA image. Training with these image—reasoning pairs minimizes next-token cross-entropy. We use the same conversation format for the in-house OCTA data and add the explicit diagnosis sentence at the end of the reasoning paragraph for the fine-tuning stage.

2.3.2. SVR PRETRAINING AND FINE-TUNING

Our main reasoning model, denoted SVR, is obtained by pretraining the general-purpose Qwen3-VL-8b-Instruct (Yang et al., 2025) on the synthetic OCTA-100K-SVR dataset. We treat this as instruction-style supervised fine-tuning on the synthetic image—reasoning pairs while freezing the language module, so that only the vision encoder and multi-modal projection layers are updated. In this stage the model learns OCTA-specific visual features and their alignment to the existing language space without disturbing its general language capabilities. Models trained on smaller synthetic subsets (1k–75k samples) are used in the scaling experiments of Sec. 3.2.

To close the remaining domain gap, we then perform a second stage of supervised finetuning on clinical OCTA data, starting from an SVR-pretrained checkpoint. The resulting model is denoted **SVR-FT** and is trained on OCTA images from OCTA-500 and our inhouse dataset together with reasoning and final DR labels. In this stage we train the model end-to-end, allowing it to adapt both its decision boundaries and linguistic style to realworld data while retaining the pathology-aware visual grounding acquired from synthetic vasculature. Training details and hyperparameters are summarized in Sec. 3.

3. Experiments

3.1. Datasets

We evaluate models on one synthetic dataset and two clinical datasets. Apart from OCTA-100K-SVR, the in-house dataset contains 1,286 OCTA deep capillary plexus scans labeled as Healthy, Non-proliferative DR (NPDR), or Proliferative DR (PDR) following the 5-fold setup of Lux et al. (2025). For OCTA-500 (Li et al., 2024), we follow the same test split of 189 scans as in Lux et al. (2025) and Li et al. (2025).

3.2. Tasks and metrics

We study two DR staging settings. On OCTA-500, models perform binary DR-vs.-Healthy classification. On the in-house dataset, models perform three-label staging (Healthy, NPDR, PDR). In both cases the VLM receives a single OCTA image and a prompt asking about DR staging. We report class-wise precision and recall and use *balanced accuracy* (mean per-class recall) as the primary metric.

We compare SVR-based models with supervised baselines (ResNet18 and a vessel-graph GNN (Lux et al., 2025)) and several VLM baselines: vanilla Qwen3-VL-8b/30b (Yang et al., 2025), LLaMA-3.2-11B-VL (Touvron et al., 2023), LLaVA-NEXT-8B (Liu et al., 2023), the graph-knowledge-based Qwen3-VL-8b-GFT (Li et al., 2025), and a baseline Qwen3-VL-8b-FT finetuned using only classification labels.

To quantify explanation quality we use GPT-5 as an automatic judge, similar to the ways in Liu et al. (2023) and Li et al. (2025). For each model, GPT-5 scores the candidate response on helpfulness, clinical and localization accuracy, and relevance, and we report the average score over these dimensions on both the in-house set and a held-out synthetic test set. Two ophthalmology experts then each evaluated 30 in-house cases, ranking the explanations under the same criteria. To verify if GPT-5 is a good judge and to study the correlation between the GPT-5 score and model performance (in terms of classification accuracy), we perform a scaling effects experiment in which Qwen3-VL-8b-SVR is trained on synthetic subsets from 1k to 100k samples and evaluated on OCTA-500. We track both balanced accuracy and GPT-5 Score as functions of synthetic dataset size, and observe a strong positive correlation (Fig. 6), indicating that GPT-5 scores are aligned with diagnostic accuracy and can therefore serve as a reliable automatic judge in our setting.

Ablation experiments isolate key components of SVR: (i) prompt diversification vs. static template reasoning, and (ii) the contribution of individual pathology types by removing dropout or microaneurysms from the reasoning. We additionally compare against a baseline (Qwen3-VL-8b CoT-FT) that fine-tunes on GPT-5-generated reasoning instead of SVR.

3.3. Training setup

All experiments are implemented with LLaMA-Factory (Zheng et al., 2024) on four NVIDIA H100 GPUs. OCTA images are resized to 512×512 . In the SVR stage we fine-tune Qwen3-VL-8b-Instruct on OCTA-100K-SVR using a cosine learning-rate schedule, training the vision encoder and multimodal projector while freezing the language backbone. In the SVR-FT stage we start from the SVR checkpoint and continue supervised training end-to-end on clinical OCTA images with their reasoning and labels. Additional implementation details are provided in Appendix C.

4. Results and Discussion

4.1. DR Staging

4.1.1. Zero-shot and supervised fine-tuning

Tabs. 1 and 6 summarize DR staging performance on OCTA-500 and the in-house dataset. Directly fine-tuning a general-purpose VLM on limited classification labels (Qwen3-VL-8b-FT) is unstable and causes mode collapse, where the DR cases are neglected. In contrast, SVR pretraining (Qwen3-VL-8b-SVR) already produces competitive or better balanced accuracy in a zero-shot setting, despite never seeing real scans.

When subsequently fine-tuned on clinical data (*Qwen3-VL-8b-SVR-FT*), the model achieves consistently higher and more balanced recall across all stages, especially for advanced DR on both datasets. Compared with purely supervised CNN and GNN baselines, SVR-FT reaches similar or better balanced accuracy while additionally producing explanations. This suggests that SVR pretraining provides a strong reasoning capability regularizes downstream training, improves sensitivity to disease, and mitigates overfitting.

Table 1:	DR staging on	OCTA-500. H =	= Healthy, DR $=$	Diabetic Retinopathy.

Model	Prec(H)	$\operatorname{Prec}(\operatorname{DR})$	$\operatorname{Rec}(H)$	$\operatorname{Rec}(\operatorname{DR})$	Bal.Acc
ResNet18 (Lux et al., 2025)	0.8734	0.2903	0.8625	0.3103	0.5864
GNN (Lux et al., 2025)	0.9636	0.9583	0.9938	0.7931	0.8934
Qwen3-VL-8b (Yang et al., 2025)	0.8503	0.5000	0.9938	0.0345	0.5142
Qwen3-VL-30b (Yang et al., 2025)	0.8511	1.0000	1.0000	0.0345	0.5173
Qwen3-VL-8b-GFT (Li et al., 2025)	0.9718	0.5846	0.9347	0.7703	0.8525
	± 0.0073	± 0.0408	± 0.0091	±0.0594	± 0.0275
Qwen3-VL-8b-FT	0.8551	0.2000	1.0000	0.0621	0.5310
	± 0.0189	± 0.4000	± 0.0000	± 0.1241	± 0.0620
Qwen3-VL-8b-SVR (ours)	0.9739	0.6944	0.9313	0.8621	0.8967
Qwen3-VL-8b-SVR-FT (ours)	0.9762	0.7944	0.9575	0.8690	0.9133
	±0.0093	±0.0567	±0.0166	±0.0581	±0.0204

4.1.2. Scaling effects of synthetic data

The scaling experiment in Tab. 2 and Fig. 6 shows that increasing the size of OCTA-100K-SVR improves both zero-shot DR classification and GPT-5 scores. With very small synthetic subsets, performance is highly variable and remains close to chance level, indicating that limited coverage of vascular topologies and lesion patterns is insufficient for robust reasoning. Once the synthetic dataset reaches tens of thousands of samples, we observe a sharp improvement (See Fig. 6 in Appendix).

Interestingly, while classification performance begins to saturate at larger synthetic scales, explanation quality (GPT-5 score) continues to improve, and over the full range of dataset sizes the two metrics still exhibit a strong positive correlation (Fig. 6). This suggests that additional synthetic diversity could be utilized not only to refine decision boundaries but also to strengthen pathology localization and clinical explainability.

Table 2: Scaling Effects of Synthetic Data (zero-shot test on OCTA-500).

Size	Prec(H)	Prec(DR)	Rec(H)	Rec(DR)	Bal.Acc	GPT-5 Score
0	0.8503	0.5000	0.9938	0.0345	0.5142	50.3
1k	0.8281	0.1440	0.3312	0.6207	0.4759	57.7
5k	0.8508	0.2500	0.9625	0.0690	0.5158	62.7
10k	0.8492	0.1587	0.6687	0.3448	0.5067	60.9
25k	0.9292	0.1579	0.6207	0.6000	0.6103	63.9
50k	0.9329	0.6429	0.9375	0.6207	0.7791	69.0
75k	0.9739	0.6944	0.9313	0.8621	0.8967	68.5
100k	0.9533	0.5641	0.8938	0.7586	0.8262	73.2

4.1.3. Ablation Studies

The ablation results in Tab. 3 highlight two central components of SVR. First, removing reasoning diversification (w/o diversifying) degrades downstream performance. This indicates that varied but fact-preserving CoT texts are critical for preventing the VLM from memorizing a fixed template and instead encouraging it to condition genuinely on the image content. Second, ablating individual pathology types (w/o dropout or microaneurysms) also decreases the performance, showing the importance of explicitly modeling all key DR hallmarks in the pipeline.

Table 3: Ablation Study.

Model	Prec(H)	Prec(DR)	Rec(H)	Rec(DR)	Bal.Acc
Qwen3-VL-8b (Yang et al., 2025)	0.8503	0.5000	0.9938	0.0345	0.5142
Qwen3-VL-8b CoT-FT	0.8951	0.4444	0.9063	0.4138	0.6601
Qwen3-VL-8b SVR (w/o diversifying)	0.8359	0.1311	0.6687	0.2759	0.4723
Qwen3-VL-8b SVR (w/o Dropout)	0.9444	0.7308	0.9563	0.6552	0.8058
Qwen3-VL-8b SVR (w/o MA)	0.8743	1.0000	1.0000	0.2069	0.6035
LLaMA-3.2-11B-VL-SVR (Touvron et al., 2023)	0.8889	1.0000	1.0000	0.3103	0.6552
LLaVA-NEXT-8b-SVR (Liu et al., 2023)	0.9433	0.2500	0.7870	0.6000	0.6935
Qwen3-VL-8b-SVR (ours)	0.9739	0.6944	0.9313	0.8621	0.8967
Qwen3-VL-8b-SVR-FT (ours)	0.9762	0.7944	0.9575	0.8690	0.9133

4.2. Quality of Explanation

We next examine explanation quality. Using GPT-5 as an automatic judge, we score each model response on both the in-house and synthetic test sets (Tab. 4), where SVR-FT obtains the highest GPT-5 scores in all settings. Expert ratings are also provided in Tab. 4, where SVR-FT again achieves the best result. Qualitative examples in Fig. 4 show that SVR-FT produces grounded descriptions that discuss FAZ, dropout, microaneurysms, neovascularization, and tortuosity, rather than generic or hallucinated findings.



Figure 4: Comparison of model response. True, partially true and false sentences are marked in green, yellow and red, respectively.

Table 4: Explanation quality evaluated by GPT-5 and human experts in ophthalmology (higher is better). Metrics: H = helpfulness, A = accuracy (localization & clinical), R = relevance, Avg = average score.

Model		In-house Dataset			Synthetic Test Set				Expert Rating	
1.15461	Н	A	R	Avg	Н	A	R	Avg	(1–10)	
GPT-5-mini (OpenAI, 2025)	76.2	68.7	82.9	75.9	73.4	65.1	79.2	72.6	4.915	
Gemini-2.5-flash (Comanici et al., 2025)	69.7	52.1	78.3	66.7	46.8	37.9	53.7	46.1	5.860	
Qwen3-VL-8b (Yang et al., 2025)	56.0	36.8	75.5	56.1	58.2	45.2	75.2	59.5	2.440	
Qwen3-VL-8b-FT	40.1	37.1	59.0	45.4	43.4	47.8	57.2	49.5	2.178	
Qwen3-VL-8b-GFT (Li et al., 2025)	71.3	67.9	74.2	71.1	72.5	69.4	75.1	72.3	6.445	
$\label{eq:Qwen3-VL-8b-SVR-FT} Qwen3-VL-8b-SVR-FT \ (ours)$		70.6	91.6	81.0	87.6	83.9	95.3	89.0	6.985	

5. Conclusion

In this work, we presented a novel framework for training medical VLMs using synthesized images and pathological features. By simulating realistic retinal vasculature and specific DR pathologies we generated a large-scale synthetic dataset with precise ground-truth annotations and reasoning chains. Our experiments demonstrate that pretraining on this synthetic vasculature (SVR) substantially enhances VLM performance, allowing general-purpose models to outperform specialized supervised methods in diagnostic accuracy even without training on real clinical data, while providing interpretable, clinically meaningful explanations. Importantly, we showed that synthetic scaling could overcome the data scarcity bottleneck in medical imaging, transforming empirical knowledge into highly effective instruction-tuning data. Future work could extend this synthesis approach to 3D volumetric reasoning and multi-modal integration.

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Appendix A. Details of Vessel and Pathology Simulation

This appendix provides the mathematical details of the vessel growth and pathology simulation summarized in Sec. 2.2. All coordinates are defined in a normalized 2D en-face domain $[0,1]^2$ unless otherwise stated, and radii in millimeters are mapped to pixel units via the same physical scale used by the baseline OCTA simulator (Kreitner et al., 2024).

A.1. Baseline healthy vessel simulation

We adopt the angiogenesis-based statistical growth model of Kreitner et al. (2024), which represents the vasculature as a forest of rooted binary trees growing in a 3D box

$$\Omega = [0, 1] \times [0, 1] \times [0, h_z]. \tag{1}$$

Each vessel segment is an edge

$$e = (\mathbf{x}_i, \mathbf{x}_j, r_{ij}), \tag{2}$$

where $\mathbf{x}_i, \mathbf{x}_j \in \Omega$ are the 3D coordinates of the incident nodes and $r_{ij} > 0$ is the segment radius. Sibling segments satisfy Murray's law with bifurcation exponent κ ,

$$r_{\text{parent}}^{\kappa} = r_{\text{child},1}^{\kappa} + r_{\text{child},2}^{\kappa}.$$
 (3)

Growth proceeds in two phases (superficial and deep vascular complexes) by repeatedly sampling oxygen sinks (for arteries) and CO_2 sources (for veins) and letting leaf or internodes sprout if the attraction points fall into a perception cone of distance δ and angle γ around the current segment. The growth direction is a weighted combination of the mean attraction vector and an optimal branching vector that minimizes deviation from the parent vessel.

FAZ center shift A circular exclusion zone around the FAZ with radius r_{FAZ} prevents sink placement in the foveal center. To increase variability, we randomly jitter the FAZ center by a vector $\Delta \mathbf{c}$ sampled from a disk of radius r_{jitter} and clamp the resulting center to a maximum normalized displacement $|\Delta \mathbf{c}| \leq r_{\text{max}}$. This effectively shifts the view while leaving the underlying vasculature unchanged.

After growth, the vessel graph is voxelized at high resolution and projected along the depth axis to obtain a grayscale vessel map X and a binarized segmentation label bin(X). A pretrained GAN then converts X into a realistic OCTA image.

A.2. Capillary dropout field and vessel regression

Dropout regions and inside-score. Each dropout lesion k is specified by:

- center $\mu_k = (c_{k,x}, c_{k,y}) \in [0, 1]^2$,
- base radius $r_k > 0$ in normalized units,
- axis ratios $a_k, b_k > 0$ controlling ellipticity,
- harmonic amplitudes $A_{k,m}$ and phases $\phi_{k,m}$ for a small set of modes \mathcal{H}_k (typically $m \in \{2,3,5\}$),

- shape exponent $\alpha_k > 0$,
- noise gain $g_k \ge 0$ and lesion strength $s_k \in [0,1]$.

For a location $\mathbf{x} = (x, y)$ we define its coordinates relative to lesion k as

$$\delta_k(\mathbf{x}) = \mathbf{x} - \boldsymbol{\mu}_k, \quad \rho_k(\mathbf{x}) = \|\boldsymbol{\delta}_k(\mathbf{x})\|_2, \quad \theta_k(\mathbf{x}) = \operatorname{atan2}(\delta_{k,y}, \delta_{k,x}).$$
 (4)

The radius of the underlying ellipse in direction θ is

$$R_k(\theta) = \frac{r_k}{\sqrt{\left(\frac{\cos\theta}{a_k}\right)^2 + \left(\frac{\sin\theta}{b_k}\right)^2}},\tag{5}$$

and we modulate it with angular harmonics to obtain an irregular boundary

$$\tilde{R}_k(\theta) = R_k(\theta) \left[1 + \sum_{m \in \mathcal{H}_k} A_{k,m} \cos(m\theta + \phi_{k,m}) \right]. \tag{6}$$

We use the notation $[z]_+ = \max(z,0)$. The geometric "inside-score" of lesion k is

$$u_k(\mathbf{x}) = \left[1 - \frac{\rho_k(\mathbf{x})}{\tilde{R}_k(\theta_k(\mathbf{x}))}\right]_+^{\alpha_k},\tag{7}$$

which smoothly decays from 1 at the center to 0 at the boundary.

To introduce additional boundary irregularity we construct a smooth noise field $n_k(\mathbf{x}) \in [0,1]$ by summing a few sinusoidal components in x and y. With a noise gain g_k we define

$$c_k(\mathbf{x}) = u_k(\mathbf{x}) \operatorname{clip}(0.75 + g_k(n_k(\mathbf{x}) - 0.5), 0, 1.2),$$
 (8)

where $\operatorname{clip}(\cdot)$ clamps to the indicated range, and $c_k(\mathbf{x})$ is subsequently capped to [0, 1].

The global dropout field is given by the maximum over lesions,

$$c(\mathbf{x}) = \max_{k} c_k(\mathbf{x}) \in [0, 1], \tag{9}$$

and the overall dropout severity by

$$s_{\max} = \max_{k} s_k \in [0, 1]. \tag{10}$$

Probabilistic pruning of capillaries. Let \mathcal{L} denote the set of leaf nodes (terminal segments) in one vascular forest. Each leaf $i \in \mathcal{L}$ has position \mathbf{x}_i and radius r_i , and we evaluate $c_i = c(\mathbf{x}_i)$. We only consider leaves with

$$c_i \ge \tau_{\text{reg}},$$
 (11)

where $\tau_{\text{reg}} \in (0, 1)$ is a regression threshold (we use $\tau_{\text{reg}} \approx 0.35$).

We target a global removal fraction

$$f_{\rm drop} \approx s_{\rm max},$$
 (12)

with empirical lower/upper bounds to avoid trivial cases. Among eligible leaves we define sampling weights

$$w_i \propto (1 - c_i)^{\gamma} r_i^{-\alpha}, \quad i \in \mathcal{L},$$
 (13)

where $\gamma > 0$ biases removal towards the lesion core and $\alpha \in [0.3, 1]$ controls the preference for smaller vessels. We sample $\lfloor f_{\text{drop}} | \mathcal{L} | \rfloor$ leaves without replacement according to w_i and delete the corresponding segments from the graph.

Remodeling: elongation and dilation. For non-removed nodes we model subtle remodeling. Let node i with parent p have positions \mathbf{x}_i and \mathbf{x}_p , local dropout $c_i = c(\mathbf{x}_i)$, direction

$$\mathbf{d}_{pi} = \mathbf{x}_i - \mathbf{x}_p,\tag{14}$$

and original radius r_i . We sample an elongation factor $e_i \in [e_{\min}, e_{\max}]$ and apply

$$\mathbf{x}_i^{\text{(new)}} = \mathbf{x}_p + \left[1 + (e_i - 1)c_i\right] \mathbf{d}_{pi},\tag{15}$$

which increases segment length more strongly near the lesion center.

Similarly, we dilate radii according to

$$r_i^{\text{(new)}} = r_i \left[D_{\min} + (D_{\max} - D_{\min}) c_i \right],$$
 (16)

with D_{\min} , $D_{\max} \geq 1$ and optional global radius clamps.

A.3. Microaneurysm synthesis

Microaneurysms are modeled as short, roughly circular side branches emerging near dropout borders.

Spawn region. For each non-root arterial node i with parent p we compute $c_i = c(\mathbf{x}_i)$. If MAs are restricted to dropout borders, we require

$$c_{\min}^{\text{MA}} \le c_i \le c_{\max}^{\text{MA}},\tag{17}$$

for some band $b_{MA}: (c_{\min}^{MA}, c_{\max}^{MA}) \subset (0, 1)$.

Spawn probability. For each eligible node we perform a Bernoulli trial with probability

$$p_{\text{MA}}(\mathbf{x}_i) = p_0 (1 + \lambda_s s_{\text{max}}) (1 + \lambda_c c_i), \tag{18}$$

where p_0 is a base MA density, λ_s couples MA counts to global dropout severity, and λ_c increases density near dropout borders. We also reweight p_{MA} by the area of the largest dropout region, so larger lesions tend to host more MAs.

MA geometry. We form a short side branch. Let

$$\mathbf{u}_{pi} = \frac{\mathbf{x}_i - \mathbf{x}_p}{\|\mathbf{x}_i - \mathbf{x}_p\|_2} \tag{19}$$

be the parent-to-child direction and

$$\mathbf{u}_{\perp} = (-u_{pi,y}, u_{pi,x}, 0) \tag{20}$$

a perpendicular unit vector in the en-face plane. With simulator step size d and MA length factor $\ell_{\rm MA}$ we place the MA center at

$$\mathbf{x}_{\mathrm{MA}} = \mathbf{x}_i + \ell_{\mathrm{MA}} d \mathbf{u}_{\perp}. \tag{21}$$

The MA radius is sampled as

$$r_{\rm MA} \sim \mathcal{U}(r_{\rm min}^{\rm MA}, r_{\rm max}^{\rm MA}),$$
 (22)

where r_{\min}^{MA} and r_{\max}^{MA} are specified in millimeters. Additional child nodes can be sampled in a small disk around \mathbf{x}_{MA} with slightly reduced radii to create irregular clusters.

A.4. Neovascular tufts

Neovascularization is represented as thin, tortuous sprouts grown from existing vessel tips.

Tip selection. We project arterial segments to 2D, identify leaf tips j with position \mathbf{x}_j , tangent direction \mathbf{u}_j , and local dropout value $c(\mathbf{x}_j)$. Tips too close to the FAZ or clearly outside dropout are down-weighted. A global NV severity parameter $s_{\text{NV}} \in [0, 1]$ determines the number of NV groups G and typical sprout length.

Main tuft growth. For each selected tip we initialize a polyline $\{\mathbf{p}_t^{(g)}\}_{t=0}^{T_{\text{main}}}$ with

$$\mathbf{p}_0^{(g)} = \mathbf{x}_j. \tag{23}$$

At iteration t we update

$$\mathbf{p}_{t+1}^{(g)} = \mathbf{p}_t^{(g)} + \ell_{\text{NV}} \mathbf{v}_t^{(g)}, \tag{24}$$

where ℓ_{NV} is a small step size and $\mathbf{v}_t^{(g)}$ is a unit direction obtained as a weighted combination of:

- 1. previous direction $\mathbf{v}_{t-1}^{(g)}$ (persistence),
- 2. a weak radial vector pointing away from the closest dropout center,
- 3. a low-frequency swirling field and isotropic jitter.

We clamp positions to remain within dropout regions and outside the FAZ.

Radius profile and side branches. Along each polyline we use a linearly tapering radius

$$r_{\rm NV}(t) = (1 - \tau_t)r_{\rm start} + \tau_t r_{\rm end}, \quad \tau_t = \frac{t}{T_{\rm main}},$$
 (25)

with r_{start} proportional to the parent vessel radius and $r_{\text{end}} < r_{\text{start}}$. With probability increasing in s_{NV} we spawn side branches starting from intermediate points. These follow the same growth rule but with shorter maximum length T_{side} .

A.5. Tortuosity along dropout borders

To model increased tortuosity at dropout borders we jitter node positions perpendicular to the local vessel direction within a band of the dropout field.

For a non-root arterial node i with parent p, we define the tangent direction

$$\mathbf{u}_{pi} = \frac{\mathbf{x}_i - \mathbf{x}_p}{\|\mathbf{x}_i - \mathbf{x}_p\|_2},\tag{26}$$

and choose a perpendicular direction \mathbf{u}_{\perp} as above. Let $c_i = c(\mathbf{x}_i)$ and specify a tortuosity band b_{tort} where

$$c_{\min}^{\text{tort}} \le c_i \le c_{\max}^{\text{tort}}.$$
 (27)

Nodes outside this band are left unchanged.

Given a gain parameter $g_{\text{tort}} \in [0, 1]$ and simulator step size d, we set the jitter amplitude

$$A_{\text{tort}} = 0.35 \, g_{\text{tort}} \, d, \tag{28}$$

sample

$$\epsilon_i \sim \mathcal{U}(-A_{\text{tort}}, A_{\text{tort}}),$$
 (29)

and update the node position as

$$\mathbf{x}_i^{\text{(new)}} = \mathbf{x}_i + \epsilon_i \, \mathbf{u}_\perp, \tag{30}$$

clipping back to $[0,1]^2$ if necessary. This leaves the topology and global FAZ shape intact but increases local curvature.

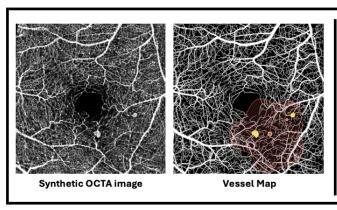
A.6. Parameter ranges and typical settings

Tab. 5 summarizes the key parameters that control the four DR lesion types and the typical ranges used in the OCTA-100K-SVR dataset. Spatial coordinates are normalized to $[0, 1]^2$; radii in millimeters refer to the physical scale of the baseline simulator.

Table 5: Key parameters of the simulator and typical settings used in this work.

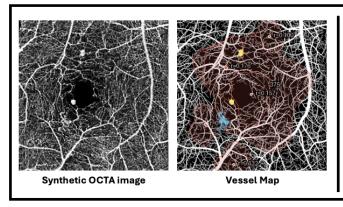
Pathology	Parameter	Typical value / range
Dropout	$\#$ regions n Radius r_{drop} Lesion strength s_k Gradient exponent α_k Noise gain g_k	[0,6] per sample [0.18,0.32] (normalized) [0.90,0.99] [2.0,3.0] [0.20,0.40]
MA	Base density p_0 Radius $r_{\rm MA}$ Length factor $\ell_{\rm MA}$ Strength coupling λ_s	≈ 0.03 (per segment) [0.01, 0.08] mm [0.3, 0.4] (in units of d) ≈ 15
NV	NV probability Severity $s_{\rm NV}$ Footprint radius Sprout length $l_{\rm NV}$	≈ 0.4 [0.2, 0.7] [0.015, 0.07] (normalized) [3, 6] growth steps
Tortuosity	Gain g_{tort} Band $[c_{\min}^{\text{tort}}, c_{\max}^{\text{tort}}]$	[0.01, 0.5] [0.30, 0.75]

A.7. Extra Examples of Reasoning Texts



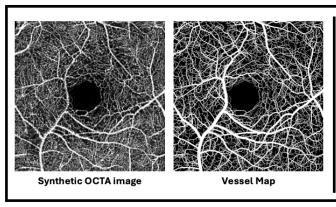
Reasoning

The foveal avascular zone is positioned slightly below and to the left of center, appearing larger than expected for this imaging plane. Flow loss is evident in multiple regions; the most prominent defect resides in the bottom-right quadrant relative to the FAZ and exhibits irregular borders. Along the periphery of this flow-deficient area, several small, rounded protrusions—identified as microaneurysms—are present, with the largest clustered near the bottom and right of the FAZ. No evidence of neovascularization is observed. Vascular architecture reveals moderate tortuosity in the capillary network.



Reasoning

The FAZ is slightly left of center and appears notably expansive within this scan. I then identify zones of capillary dropout: a dominant region occupies the topright quadrant relative to the FAZ, exhibiting irregular borders. Additional substantial dropout areas are evident in the top-left and right quadrants, with smaller foci situated in the bottom-left and lower central regions. Along the periphery of these flow-deficient zones, multiple microaneurysms are detectable; their largest clusters reside above and below the FAZ, specifically in the upper-left and lower-left areas. No neovascularization is observed adjacent to the dropouts. Vessels appear uniformly smooth.



Reasoning

The foveal avascular zone is positioned slightly left of center. No evidence of capillary dropout is present; vascular flow remains uninterrupted across the region. Microaneurysms are absent upon inspection. No neovascular structures are identified. Vessel architecture appears uniform, with no signs of abnormal curvature or tortuosity.

Figure 5: Extra Examples of Synthetic OCTA and Reasoning.

Appendix B. Pseudocode of the SVR Pipeline

```
Algorithm 1: Synthetic Vasculature Reasoning (SVR) pipeline
Input: number of synthetic samples N; vessel-growth config \theta_{\text{vessel}}; pathology profile
         \theta_{\text{path}}; optional GAN config \theta_{\text{GAN}}; teacher VLM T; base VLM M
Output: synthetic image—text dataset \mathcal{D}; pretrained model M_{\text{SVR}}; fine-tuned model
            M_{\text{SVR-FT}}
Initialize dataset \mathcal{D} \leftarrow \varnothing for i = 1 to N do
    Sample structural parameters (FAZ, seed, view shift, etc.)
    Simulate healthy vessel graph G_i
    Apply pathology profile \theta_{\text{path}} to get augmented graph G_i^*
    Rasterize G_i^* into a 2D vessel map X_i
    if GAN is enabled then
        Generate OCTA-like image I_i from X_i using \theta_{\text{GAN}}
    else
       Set I_i \leftarrow X_i
    Extract structured metadata m_i from the simulator (FAZ, dropout, MA, NV, tor-
   Build template reasoning r_i^{\text{tmp}} from m_i (FAZ \rightarrow dropout \rightarrow MA \rightarrow NV \rightarrow tortuos-
    Query teacher VLM T with (I_i, m_i, r_i^{\text{tmp}}) to obtain a diversified, fact-preserving
     reasoning r_i
    Define question q_i asking to describe I_i and assess DR stage
    Define answer a_i as r_i (plus final diagnosis sentence for clinical data) Add sample
     (I_i, q_i, a_i, m_i) to dataset \mathcal{D}
end
Pretrain base VLM M on \mathcal{D} (freeze language backbone) to obtain M_{\text{SVR}} Fine-tune
 M<sub>SVR</sub> end-to-end on clinical OCTA data with reasoning and DR labels to obtain
 M_{\text{SVR-FT}}
```

Appendix C. Training details

SVR training prompt (student VLM). During both SVR pretraining and SVR-FT fine-tuning, the VLM is trained in a single-turn instruction-following format. The human turn consists of the OCTA image token plus the following question (identical for synthetic and clinical data):

```
<image>
```

```
What features are visible in this OCTA image?
Please first describe the image features, then inspect it for signs
of diabetic retinopathy (DR) and classify it as Healthy, NPDR, or PDR.
```

The assistant turn contains the full Chain-of-Thought reasoning followed by the final diagnosis sentence.

CoT diversification prompts (teacher VLM). To obtain linguistically diverse and fact-preserving reasoning, we prompt GPT-5 with a system prompt and a user prompt that include the synthetic OCTA image, the original CoT and structured pathology metadata. The system prompt is:

You are an ophthalmology OCTA expert and skilled medical writer. You will receive an OCTA image, concise metadata, and an original chain-of-thought (CoT). Rewrite the CoT in a different language style while preserving ALL medical facts, locations, and uncertainty. Do not add new findings. Keep content consistent with the image and metadata. Spatial terminology constraint: avoid eye-dependent terms (e.g., temporal, nasal, superotemporal, inferonasal, superior/inferior when tied to eye laterality). Use only absolute image directions such as left, right, up, down, and center to describe locations. Aim for similar length and clarity. Output only the rewritten CoT.

The corresponding user prompt is:

Here is an OCTA image <image>.
Metadata (JSON): <COMPACT_METADATA_JSON>

Original CoT describing the image: <ORIGINAL_COT>

Task: Rewrite the CoT with a distinct language style (e.g., more academic, more succinct, or slightly conversational) while preserving all facts and spatial relations. Do not invent new content.

Use only absolute image directions such as left, right, up, down, and center. Return only the rewritten CoT.

where <COMPACT_METADATA_JSON> is the compacted pathology metadata (FAZ, dropout, MA, NV, tortuosity) extracted from the simulator and <ORIGINAL_COT> is the deterministic template reasoning.

For robustness to natural-language variation in the input question, we also diversify the user prompt itself using a similar pair of prompts.

Appendix D. Supplementary Details in Evaluation

At inference we use temperature 0.1 and top-p=0.8, and compute all metrics from unified JSONL outputs to ensure consistent parsing across models. To evaluate using GPT-5 scores, for each image, question, and model response, GPT-5 receives (i) the OCTA image, (ii) the dataset tag (synthetic vs. in-house), (iii) the question text, (iv) the ground-truth DR label when available, (v) an optional synthetic reference explanation (for synthetic data), and (vi) the candidate response. The system message is the fixed instruction:

You are a retina specialist. First write your response to the question with all the information provided, and then score a single model response

by comparing it with yours on:

- helpfulness (0-10): clarity, usefulness, specificity to the question.
- accuracy (0-10): localization + clinical correctness (use the image; if GT label provided, consider it).
- relevance (0-10): how on-topic and focused the response is. Return a compact JSON: {"helpfulness": int, "accuracy": int, "relevance": int, "rationale": string}.

and the user message concatenates the textual context (dataset, question, GT label, reference, model response) with the OCTA image. We then parse the helpfulness, accuracy, and relevance integers and average them to obtain the per-sample "GPT-5 Score", which is then aggregated over all samples for each model and dataset.

Table 6: DR staging on the in-house OCTA dataset. H = Healthy, N = NPDR, P = PDR.

Model	Prec(H)	Prec(N)	Prec(P)	Rec(H)	Rec(N)	Rec(P)	Bal.Acc
ResNet18 (Lux et al., 2025)	0.943	0.335	0.426	0.793	0.544	0.563	0.633
	± 0.008	± 0.044	± 0.070	± 0.021	± 0.094	± 0.131	± 0.030
GNN (Lux et al., 2025)	0.950	0.326	0.456	0.720	0.594	0.775	0.697
	± 0.010	± 0.049	± 0.107	± 0.035	± 0.091	± 0.034	± 0.034
Qwen3-VL-8b (Yang et al., 2025)	0.775	0.198	0.065	0.576	0.163	0.255	0.331
Qwen3-VL-30b (Yang et al., 2025)	0.787	0.228	0.444	0.849	0.241	0.041	0.377
Qwen3-VL-8b-GFT (Li et al., 2025)	0.889	0.535	0.454	0.881	0.502	0.550	0.645
	± 0.007	± 0.045	± 0.017	±0.019	±0.027	±0.041	± 0.017
Qwen3-VL-8b-FT	0.908	0.364	0.245	0.828	0.636	0.073	0.512
	± 0.014	± 0.084	± 0.322	±0.071	±0.061	±0.107	± 0.050
Qwen3-VL-8b-SVR (ours)	0.928	0.295	0.357	0.786	0.453	0.510	0.583
Qwen 3-VL-8b-SVR-FT (ours)	0.958	0.411	0.418	0.840	0.488	0.737	0.688
	±0.024	±0.087	±0.016	±0.082	±0.088	±0.074	± 0.027

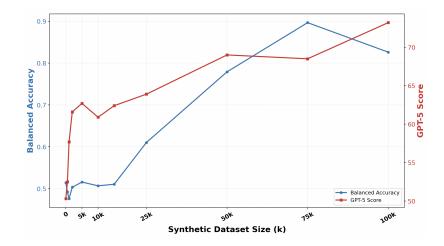


Figure 6: Correlation between Classification Performance and GPT-5 Score

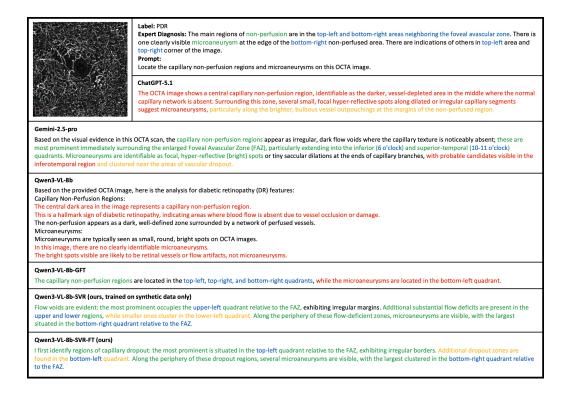


Figure 7: Extra Example for Qualitative Evaluation.



Figure 8: Extra Example for Qualitative Evaluation.