NOVA: A Benchmark for Rare Anomaly Localization and Clinical Reasoning in Brain MRI

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Abstract

In many real-world applications, deployed models encounter inputs that differ from the data seen during training. Open-world recognition ensures that such systems remain robust as ever-emerging, previously *unknown* categories appear and must be addressed without retraining. Foundation and vision-language models are pre-trained on large and diverse datasets with the expectation of broad generalization across domains, including medical imaging. However, benchmarking these models on test sets with only a few common outlier types silently collapses the evaluation back to a closed-set problem, masking failures on rare or truly novel conditions encountered in clinical use.

We therefore present *NOVA*, a challenging, real-life *evaluation-only* benchmark of $\sim$900 brain MRI scans that span 281 rare pathologies and heterogeneous acquisition protocols. Each case includes rich clinical narratives and double-blinded expert bounding-box annotations. Together, these enable joint assessment of anomaly localisation, visual captioning, and diagnostic reasoning. Because NOVA is never used for training, it serves as an *extreme* stress-test of out-of-distribution generalisation: models must bridge a distribution gap both in sample appearance and in semantic space. Baseline results with leading vision-language models (GPT-4o, Gemini 2.0 Flash, and Qwen2.5-VL-72B) reveal substantial performance drops, with approximately a 65% gap in localisation compared to natural-image benchmarks and 40% and 20% gaps in captioning and reasoning, respectively, compared to resident radiologists. Therefore, NOVA establishes a testbed for advancing models that can detect, localize, and reason about truly unknown anomalies.

1 Introduction

Generalization under distribution shift remains a central unsolved challenge in machine learning [14, 52]. Despite advances in large-scale pretraining and transfer learning [12, 33], most models fail to reliably detect or reason about previously unseen categories or domains at test time. Anomaly detection, the task of identifying deviations from a given normative distribution, *e.g.*, samples exclusively from healthy patients, represents an extreme stress-test of out-of-distribution (OOD) generalization due to the open-ended and unpredictable nature of anomalies. While OOD generalization has been extensively studied in natural image classification [17, 34, 22], it remains underexplored in healthcare. Medical data presents extreme heterogeneity, rare event frequencies, and non-standardized acquisition protocols, making it a worst-case scenario for evaluating model robustness to distribution

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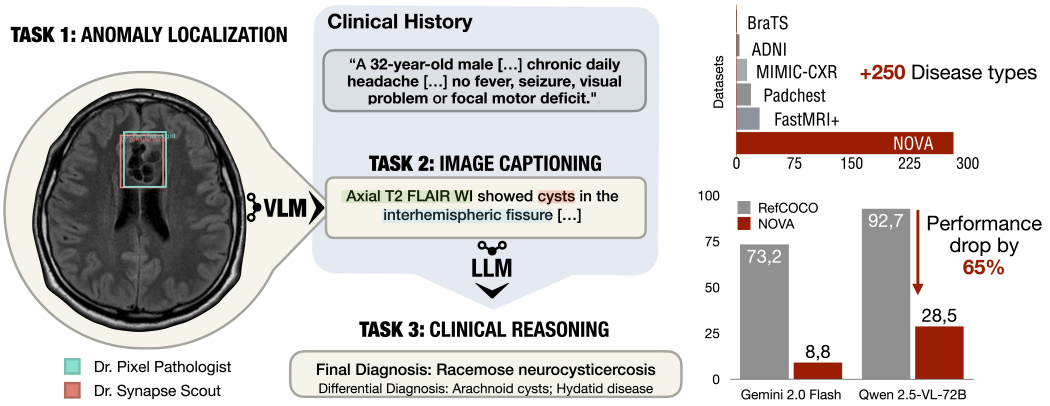

Figure 1: Overview of the NOVA benchmark. Task 1: Anomaly localization: models predict bounding boxes identifying abnormal regions in brain MRI; ground truth annotations from two independent radiologists are shown. Task 2: Image captioning: models generate a brief diagnostic description from the MRI image. Task 3: Diagnostic reasoning: models predict the final diagnosis by integrating clinical history and image findings. NOVA establishes the first benchmark designed to systematically evaluate vision-language models (VLMs) and large language models (LLMs) for rare anomaly localization, clinical description, and multimodal diagnostic reasoning in brain MRI.

shift. Detecting anomalies—potential pathologies—in imaging is often the first and most challenging step of the diagnostic process. Providing effective assistance to physicians at this stage has the potential to substantially improve clinical outcomes.

In medical imaging, unsupervised anomaly detection (UAD) methods [37, 6] are trained exclusively on healthy anatomy and identify deviations from this learned distribution as potential pathologies. While recent methods demonstrate strong performance on curated benchmarks [54, 38, 10, 43, 39, 5], they remain insufficiently reliable in the wild, particularly in high-stakes settings like clinical triage and health screening, where specificity and robustness to rare clinical presentations are essential [4, 23]. This challenge is particularly acute in magnetic resonance imaging (MRI) of the brain, where radiologists must detect subtle and diverse abnormalities across patient populations and heterogeneous imaging protocols.

The fundamental bottleneck lies in the datasets used for validation. Most existing benchmarks define anomalies through fixed categories, inducing implicit data leakage: although models are trained on healthy data, test sets remain constrained to known abnormality types. This narrows the evaluation to familiar distributions and undermines open-set detection. Datasets such as BraTS [29], ATLAS [26], and ISLES [18] were designed for segmentation and primarily capture canonical disease patterns, causing model development to converge on closed-set optimization rather than true discovery of unknown conditions.

The medical out-of-distribution analysis challenge (MOOD) [53] introduced synthetic anomalies to simulate unknown deviations. However, *real* anomalies from rare or previously unobserved diseases remain essential for clinical relevance. fastMRI+ [50] provided incremental pathology variability through bounding box annotations of brain and knee MRI scans [47], yet lacked the pathology heterogeneity and structured clinical metadata necessary to reflect clinical variability.

Detecting an abnormality alone does not satisfy clinical requirements. Radiologists must localize pathologically suspicious regions, assess severity, distinguish them from imaging artefacts, and formulate a differential diagnosis based on patient history and imaging findings. No existing dataset reflects this full diagnostic workflow, limiting prior benchmarks to binary detection and systematically failing to capture clinically meaningful information in generated text or diagnostic predictions [27]. Data sharing restrictions and poor standardization have further constrained the development of vision-language models (VLMs) in medicine.

Therefore, NOVA establishes a new benchmark for evaluating, detecting, and reasoning on unexpected abnormalities in clinical brain MRI, as illustrated in Figure 1. The dataset comprises 906 brain MRI scans spanning 281 rare and diagnostically diverse pathologies from Eurorad [13], enriched

with detailed clinical narratives. Each case is independently annotated by at least two radiologists with bounding boxes identifying suspected abnormalities. NOVA uniquely enables joint evaluation of anomaly localization, visual captioning, and diagnostic reasoning under real-world clinical heterogeneity. It is explicitly designed as an evaluation-only benchmark to serve as an extreme stress-test of OOD generalization, requiring models to bridge distribution shifts in both visual and semantic space.

We benchmark state-of-the-art vision-language models, including GPT-4o, Gemini 2.0 Flash, and Qwen2.5-VL-72B, on NOVA. Results reveal substantial performance degradation across all tasks, underscoring the urgent need for benchmarks that reflect the demands of open-world clinical reasoning.

2 Related Work

Anomaly detection, OOD detection, and novelty detection have received sustained focus in computer vision and machine learning, with advances across tasks from natural image understanding to industrial inspection [32, 25, 51, 45, 15, 36, 42]. Despite this progress, transferring these methods to medical imaging remains challenging. The concept of normality in medicine is inherently ambiguous, varying across individuals, imaging protocols, and institutions.

Clinical anomalies are often rare and highly heterogeneous, making them ill-suited for evaluation protocols that treat a selected set of predefined categories as representative out-of-distribution cases. The distinction between healthy and abnormal tissue is frequently subtle and localized, with considerable overlap between in-distribution and out-of-distribution regions within the same image. As a result, approaches that excel on constrained datasets such as MVTec-AD [7] fail systematically under the extreme clinical variability of real-world neuroimaging [19].

In medical imaging, unsupervised anomaly detection models learn the normative distribution of healthy anatomy to identify deviations as candidate pathologies [6]. Large healthy population datasets, including IXI [1], CamCAN [41], and UK Biobank [40] are valuable for normative modeling and population studies, but they are ill-suited for evaluating anomaly detection, as they lack pathological cases and localized anomaly annotations. Datasets such as ADNI [31] and OASIS [28] focus exclusively on Alzheimer's disease and neurodegeneration, providing only narrow coverage of pathologies. Similarly, condition-specific datasets, including MSLUB [24] for multiple sclerosis lesions, ATLAS [26] and ISLES [18] for stroke lesions, and BraTS [29] for brain tumors, support segmentation of predefined abnormalities but offer no framework for open-set detection or evaluation of vision-language reasoning in clinical contexts.

In parallel, large-scale vision-language datasets in medical imaging focus exclusively on chest radiographs. MIMIC-CXR [20] and PadChest [8, 9] integrate images with radiology reports for multimodal learning but are entirely disconnected from brain MRI. Hamamci et al. [16] introduced the CLM3D dataset and corresponding VLM3D challenge for developing generalist vision-language models in 3D medical imaging. However, CLM3D targets thoracic CT and focuses on common abnormality classification, report generation, and text-conditioned image synthesis, without addressing rare disease detection, anomaly localization, or open-world clinical reasoning.

Despite the critical technical and clinical need, a comprehensive neuroimaging benchmark remains absent. Brain MRI analysis presents significant technical challenges due to the wide spectrum of pathologies and their diverse appearances, ranging from localized lesions to diffuse structural alterations, coupled with inherent technical variability. Clinically, a clear need exists as most rare diseases are neurological or have neurological manifestations [35], positioning brain MRI centrally in patient care. NOVA establishes the first rigorous benchmark for systematically evaluating these capabilities under the real-world variability and diagnostic uncertainty of clinical brain MRI.

3 Dataset Description

We curated the NOVA dataset to establish an evaluation benchmark for vision-language model generalization under extreme clinical variability in brain MRI. We sourced cases from Eurorad, a peer-reviewed educational platform operating under a Creative Commons Attribution-NonCommercial-ShareAlike 4.0 International License[1]. To comply with licensing requirements, we included only cases published after July 6, 2015. We filtered the dataset to include all cases from the "Neuroradiology"

[1] https://www.eurorad.org/node/38655

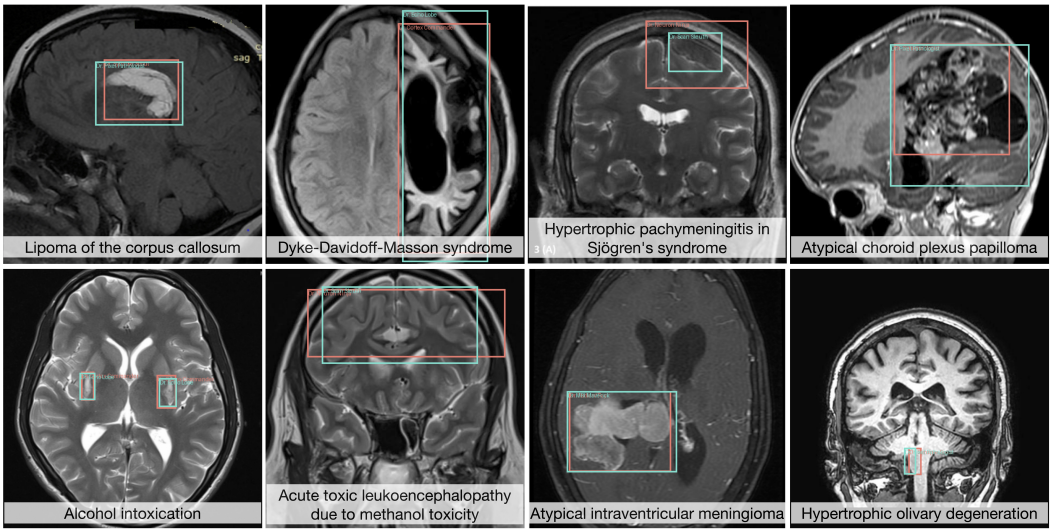

Figure 2: Representative brain MRI scans from the NOVA dataset illustrating the diversity of anatomical planes, MRI sequences, and pathological conditions. Radiologist-provided bounding box annotations are overlaid. The examples include rare congenital malformations, toxic and metabolic encephalopathies, and inflammatory or neoplastic lesions—capturing the broad radiological spectrum.

category and manually excluded non-relevant content such as CT, spine MRI, clinical photographs, and other non-MRI data. This ensured consistent imaging modality and anatomical focus.

We collected a total of 906 brain MRI scans spanning 281 unique diagnoses. We retained all images in their original form without preprocessing, cropping, or normalization to preserve the full clinical variability essential for evaluation. We preserved the naturally imbalanced long-tailed distribution of rare diseases to reflect real-world case frequencies. Representative examples illustrating the diversity of imaging planes, sequences, and pathologies are shown in Figure 2.

3.1 Dataset Composition

NOVA captures the diagnostic heterogeneity of clinical brain MRI. We included axial, sagittal, and coronal planes across standard sequences, including T1-weighted, T2-weighted, and FLAIR imaging. The distribution of anatomical planes and imaging sequences is detailed in Supplementary Tables 5 and 6. We manually grouped cases into six diagnostic categories: neoplastic, neurodegenerative, inflammatory, congenital, metabolic, and vascular pathologies. Figure 3a) shows the long-tailed distribution of diseases and the rarity of many conditions, which present unique challenges for model evaluation. The dataset's 281 unique diagnosis labels exceed the diversity of existing brain MRI benchmarks by an order of magnitude. We summarize additional statistics on patient demographics, and information of disease location, scale, and frequency in Supplementary Figures 9, 10, and 11.

3.2 Annotation Process and Quality Control

We implemented a rigorous multi-stage protocol to obtain high-quality anomaly localization annotations. Eight neuroradiology residents annotated the dataset using a custom web-based platform (Supplementary Figure 7). Ethics approval was waived by the local IRB at TUM University Hospital (IRB #2025-446-W-CB in Appendix F). Each case was independently labeled by two readers, who reviewed the full Eurorad clinical description and associated metadata to inform their annotations.

Inter-rater agreement was computed using a greedy matching algorithm that maximized intersection over union (IoU) between boxes. Figure 3b shows the distribution of inter-reader agreement, and Figure 3c presents the overall IoU distribution across annotations. Annotations with IoU > 0.3 were merged into consensus labels. While some inter-reader IoU values are modest, this reflects the inherent ambiguity of clinical neuroimaging. Lower overlap stems from diffuse pathologies with unclear boundaries, comprehensive labeling that includes incidental findings, and borderline

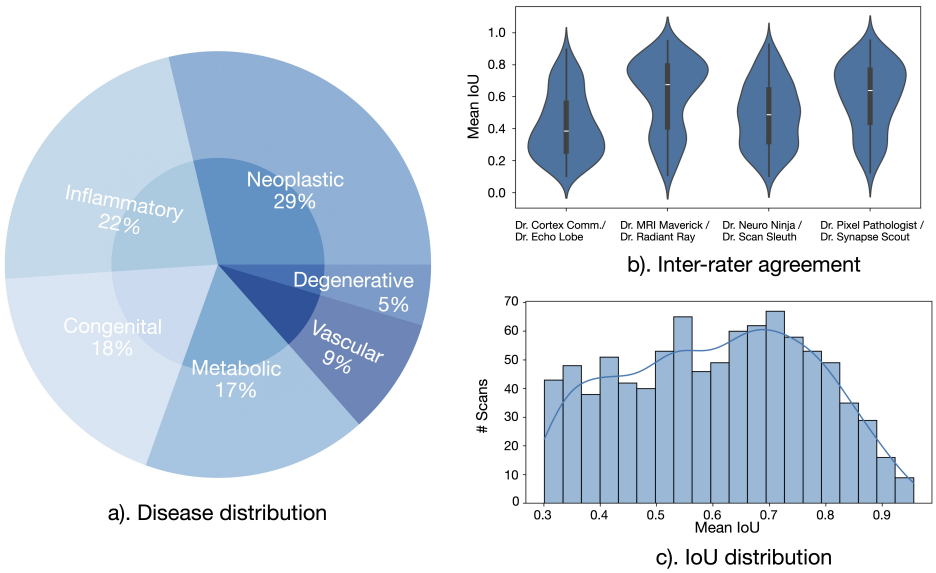

Figure 3: Dataset composition and annotation quality in NOVA. (a) Distribution of cases across six diagnostic categories. (b) Inter-rater agreement as mean intersection over union (IoU) between radiologist pairs. (c) Histogram of IoU scores across all scans.

decisions on subtle lesions. For 247 cases with persistent disagreement, a senior board-certified neuroradiologist (15+ years experience) adjudicated the final ground truth.

3.3 Data Format and Benchmark Design

We release all brain MRI scans as uniformly sized 480×480 grayscale PNG slices. We provide accompanying clinical metadata, including clinical history, patient demographics, imaging information, radiologist image captions, and bounding boxes for detected abnormalities in CSV files.

We explicitly designed NOVA as an evaluation-only dataset. Each case represents a unique diagnosis, and we do not provide predefined train, validation, or test splits. This enforces a zero-shot evaluation setting for all models, requiring them to generalize to previously unseen cases.

We publicly release NOVA on Hugging Face Datasets[2] under the same Creative Commons Attribution-NonCommercial-ShareAlike 4.0 license as the Eurorad source. The dataset is distributed solely for non-commercial research to enable reproducible evaluation of VLMs under clinical conditions.

4 Benchmark Tasks

NOVA defines a comprehensive evaluation suite to assess the capabilities of vision-language models under realistic and clinically relevant conditions. These three tasks defined here reflect the sequential decision-making process of radiologists, progressing from anomaly localization to image description and diagnostic interpretation, enabling a realistic benchmarking.

4.1 Task 1: Anomaly Localization

This task requires models to detect and localize abnormalities within brain MRI scans, regardless of the patient's eventual diagnosis. Clinically, this is a relevant task, as most medical errors actually stem from not seeing a pathology at all [21]. Models must predict one or more bounding boxes per image corresponding to abnormal regions, using radiologist-annotated ground truth as reference. Performance is measured using mean average precision at intersection over union thresholds of 0.3 (mAP@30), 0.5 (mAP@50), and the COCO-style averaged mAP across thresholds from 0.50 to 0.95

[2] https://huggingface.co/datasets/c-i-ber/Nova

Table 1: Localization performance on NOVA. We evaluate the models with standard object detection metrics (mAP at multiple thresholds), detection accuracy (ACC50), number of true positives (TP30), number of false positives (FP30), and the false negative rate (FNR).

Model	mAP30 ↑	mAP50 ↑	mAP50-95 ↑	ACC50 ↑	TP30 ↑	FP30 ↓	FNR ↓
Gemini 2.0 Flash	20.16	7.37	1.99	8.83	227/1068	899	78.7
Qwen2-VL-72B	25.02	15.09	6.44	25.50	338/1068	1163	68.4
Qwen2.5-VL-72B	**37.66**	**24.49**	**11.23**	**28.48**	**406/1068**	**672**	**62**

in 0.05 increments (mAP@[50:95]). The benchmark also reports the number of correctly detected versus missed pathologies per case to reflect the clinical priority of minimizing false negatives. The dataset includes cases with multiple annotated abnormalities, providing a uniquely difficult evaluation setting for object detection under open-world conditions and rare disease variability.

4.2 Task 2: Image Description

This task measures the ability of models to generate clinically meaningful descriptions of brain MRI scans, an important prerequisite for making the correct diagnosis and in clinical communication. Each image is paired with an expert-generated caption describing the imaging findings. Evaluation uses case-insensitive exact keyword matching to compute precision, recall, and F1-score across the full keyword set. Modality-specific terms (such as *flair*, *axial*, *sagittal*, *t1*, *t2*, *coronal*, *dwi*, *t1w*, *t2w*, *weighted*) are evaluated separately from non-modality keywords capturing clinical content. Binary classification accuracy and F1-score for normal versus abnormal classification are also reported. Sentence-level generation quality is evaluated using BLEU-4 [30], METEOR [2], and BERT F1 [49].

4.3 Task 3: Diagnostic Reasoning

This task tests whether models can integrate clinical context and imaging observations to predict a diagnosis, arguably the "supreme discipline" in medical decision-making. Each case provides a brief clinical history and corresponding image caption as input, and the model must generate a free-text diagnostic label. Performance is reported as Top-1 accuracy (exact match with ground truth) and Top-5 accuracy (ground truth among the five most likely predictions). As model outputs are unconstrained free text, GPT-4o is used to perform semantic matching between predictions and ground truth labels. The task demands multimodal reasoning and open-ended prediction and is performed in a zero-shot setting, closely mirroring real-world clinical decision-making workflows.

5 Experiments and Results

We benchmarked large vision-language models on NOVA to systematically test their ability to generalize under extreme clinical heterogeneity. All experiments were conducted in inference-only mode. We report results for Gemini 2.0 Flash (Google DeepMind), Qwen2-VL-72B (Alibaba DAMO Academy), and Qwen2.5-VL-72B for abnormality grounding; and GPT-4o (OpenAI), Gemini 2.0 Flash, and Qwen2.5-VL-72B-Instruct for image captioning and diagnostic reasoning. As these models are proprietary and their training data is undisclosed, Eurorad cases may have been partially included. Results should thus be interpreted as an upper bound on zero-shot generalization. We encourage future evaluation of open models for a more conservative assessment.

We designed NOVA to expose generalization failures in models confronted with previously unseen, rare clinical cases. To do so, we evaluate along three critical axes of clinical reasoning: *localization, description, and diagnosis.*

5.1 Stress Test 1: Localization under Clinical Heterogeneity

The anomaly localization task revealed a strong performance degradation. While large vision-language models achieve detection scores of 73%–92% [44] on natural image benchmarks such as RefCOCO [46], performance on NOVA dropped sharply to 8.3%–28.5%. Models were evaluated using standard object detection metrics (mAP@30, mAP@50, and mAP@[50:95]), as summarized in Table 1. Despite occasional correct detections, all models exhibited poor calibration under clinical

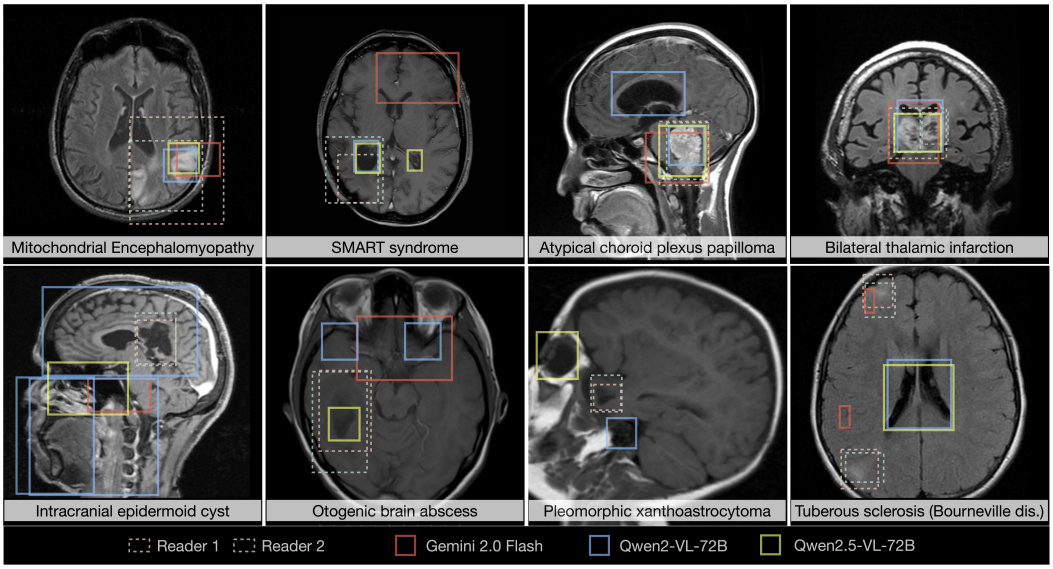

Figure 4: Examples of model predictions for anomaly grounding on NOVA. Ground truth and model-predicted bounding boxes are shown for Gemini 2.0 Flash, Qwen2.0-VL-72B, and Qwen2.5-VL-72B.

Table 2: Image Description on NOVA. Captioning quality is evaluated by Clinical Term F1, Modality Term F1, BLEU, and METEOR. Binary F1 measures binary abnormality classification performance.

Model	Clinical F1 (%)	Modality F1 (%)	BLEU-4	METEOR	BERT F1 (%)	Binary F1 (%)
Gemini 2.0 Flash	**19.8**	**59.8**	**1.83**	15.2	85.5	5.3
GPT-4o	15.7	49.3	0.92	**17.5**	84.3	**11.3**
Qwen2.5-VL-72B	13.6	45.3	1.08	17.1	84.4	2.4

distribution shift, frequently producing incomplete, misplaced, or spurious bounding boxes. For completeness, we also tested medical-domain VLMs (CheXagent [11], MAIRA-2[3], HuatuoGPT Vision [48]) on a 25-case subset. All underperformed generalist models, with CheXagent and MAIRA-2 failing to generalize (mAP@50 = 0) and HuatuoGPT Vision reaching only 8.3. We included the full results in Supplementary Table 7. Clinical inspection of representative cases (Figure 4) revealed typical failure patterns such as false-positive detection of normal anatomical structures (e.g., orbital cavity misinterpreted as lesion by Qwen2.5-VL) and failure to localize true abnormalities even under relaxed overlap thresholds. Quantitatively, even at 30% IoU criteria, fewer than half of ground truth abnormalities were detected (62% FNR), and over 600 false-positive boxes were recorded. In clinical practice, missed anomalies risk delayed or missed diagnoses, while high false-positive rates drive unnecessary specialist referrals, patient anxiety, and increased healthcare costs. NOVA sets the first extreme benchmark designed to systematically expose these critical failure modes.

5.2 Stress Test 2: Description under Semantic Shift

The second test probes whether models can generate clinically meaningful image descriptions under severe semantic shifts. Table 2 summarizes performance across Clinical Term F1, Modality Term F1, BLEU-4, METEOR, BERT F1, and binary abnormality classification accuracy. Gemini 2.0 Flash achieved the highest Clinical Term F1 (19.8%), Modality Term F1 (59.8%), and BLEU (1.83), reflecting comparatively stronger recognition of structured imaging attributes. GPT-4o outperforms in Binary F1 (11.3%) and METEOR (17.5), indicating slightly better fluency and sentence-level description. Qwen2.5-VL-72B-Instruct underperformed across all metrics. Despite the low lexical overlap captured by BLEU-4 and METEOR, models achieve high BERTScore (0.84–0.85), indicating that generated captions preserve most of the clinical meaning. To further investigate the semantic limitations observed in captioning (Table 2), we analyzed language behavior across models in Figure 5. Example cases illustrate that all models tend to produce longer but vaguer descriptions under uncertainty. The ground truth showed the highest vocabulary size (1527 unique words), reflecting

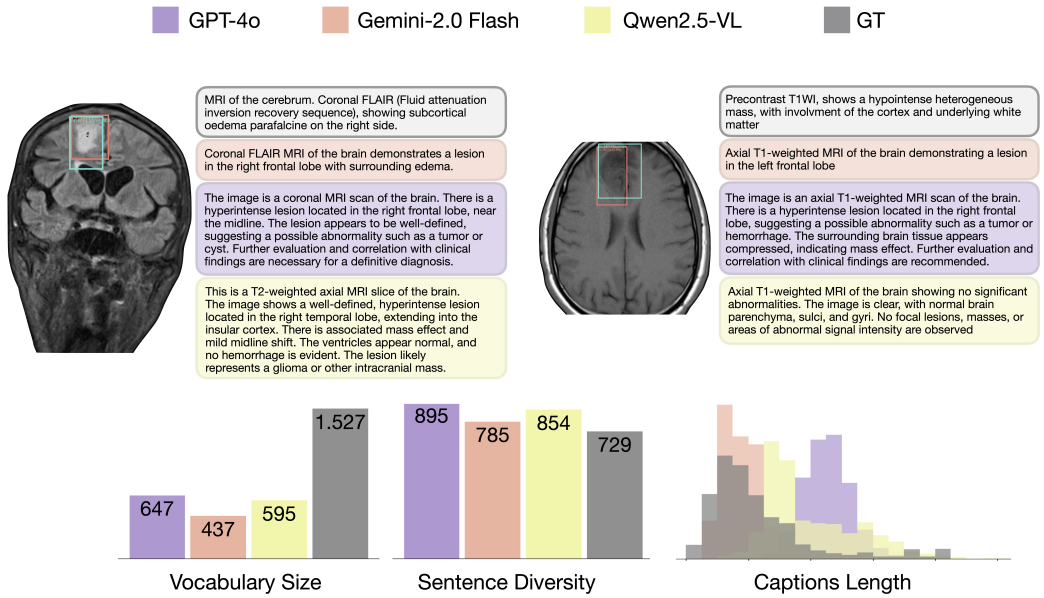

Figure 5: Task 2: Image Captioning. (Top) Example image-caption pairs showing model predictions and reference ground truth. Model outputs tend toward verbose, redundant phrasing with fewer specialized terms. (Bottom) Quantitative analysis. Left: Vocabulary size (unique words). Center: Sentence diversity (unique captions). Right: Caption length distribution (number of words per caption). Ground truth radiology reports exhibit the highest vocabulary richness but shorter, information-dense sentences. All models display severe vocabulary collapse and compensate with longer and more varied sentence constructions.

expert use of precise diagnostic terminology. VLMs exhibited drastic vocabulary compression, with GPT-4o, Gemini 2.0 Flash, and Qwen2.5-VL using only 647, 437, and 595 unique words, respectively. Interestingly, models showed comparable or slightly higher sentence diversity (895, 785, and 854 unique captions vs. 729 in the ground truth), likely due to paraphrasing and verbose redundancy. Caption length distribution revealed distinct patterns: Gemini produced captions with similar lengths to ground truth, while GPT-4o and Qwen2.5-VL consistently generated longer outputs. This analysis highlights a consistent pattern of low lexical precision and repetitive verbosity, particularly for GPT-4o and Qwen2.5-VL, confirming that current models exhibit limitations in expressing clinically meaningful descriptive detail in image captioning tasks under real-world clinical distribution shifts.

5.3 Stress Test 3: Diagnostic Reasoning under Distributional Shift

The final test evaluates models' ability to assign diagnostic labels based on combined image captions and clinical history. Performance was assessed via Top-1 and Top-5 classification accuracy (Table 3). GPT-4o achieved the highest scores (24.2% Top-1, 38.4% Top-5), with Gemini 2.0 Flash and Qwen2.5-VL-72B performing lower.

To further probe diagnostic behavior, we analyzed prediction distributions against ground truth (Figure 6). All models followed the expected Zipfian-like scaling of disease frequencies (right), demonstrating comparable rank-frequency slopes to ground truth. However, this occurred over a substantially compressed label space, with model predictions collapsing onto smaller vocabularies covering only $\sim$30% of the ground truth (Table 3). This truncation effect was also visible in the cumulative frequency curves (left), where model predictions saturated rapidly relative to ground truth.

Ground truth labels exhibited a Shannon entropy of 8.68 bits, reflecting the high uncertainty and diversity of rare disease distributions. In contrast, model outputs showed a marked entropy reduction of approximately 1 bit (Table 3), consistent with over-reliance on dominant classes and poor exploration of the long tail—an effect akin to premature entropy collapse under distributional shift.

Table 3: Diagnostic reasoning results on NOVA. Diagnostic accuracy is captured by the Top-1 and Top-5 accuracy. Coverage and entropy are extracted from diagnostic reasoning distributions.

Model	Top-1	Top-5	Cov.	Ent.
Gemini 2.0 Flash	22.1	37.4	29.4	**7.71**
GPT-4o	**24.2**	**38.4**	**31.9**	7.64
Qwen2.5-VL-72B	22.4	35.2	26.1	7.26

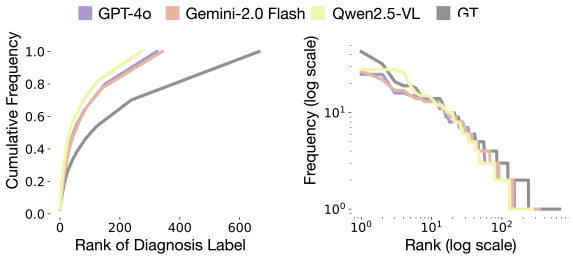

Figure 6: Distribution of diagnostic label frequencies for ground truth vs model predictions.

Table 4: Disentangling captioning and reasoning gaps. Replacing model-generated captions with human or ground-truth descriptions markedly improves diagnostic accuracy (captioning gap). Even with perfect captions, model reasoning lags expert performance (reasoning gap).

Condition	**Top-1**	**Top-5**
(a) Human captions → Human reasoning (Resident Neuroradiologists)		
Neuroradiologist 1	48.0%	76.0%
Neuroradiologist 2	52.0%	68.0%
(b) Human / ground-truth captions → AI reasoning		
Radiologist 1 captions	40.0%	60.0%
Radiologist 2 captions	40.0%	60.0%
Ground-truth captions	44.0%	52.0%
GPT-paraphrased GT captions	42.0%	66.0%
(c) AI-generated captions → AI reasoning		
GPT-4o	24.0%	38.4%
DeepSeek-R1	24.0%	44.0%

Reasoning gap
Top-1: ▼ 16%
Top-5: ▼ 21%

Captioning gap
Top-1: ▼ 40%
Top-5: ▼ 36%

5.4 Disentangling Captioning and Reasoning Gaps

The grounding performance of VLMs on NOVA drops by over 65% compared to natural-image referring-expression benchmarks, revealing a pronounced challenge in transferring generic spatial alignment to medical imaging. To understand how this failure propagates to clinical inference, we disentangle two downstream limitations: the *captioning gap*, where imperfect visual descriptions hinder reasoning, and the *reasoning gap*, where models underperform even with high-quality captions.

We compared the reasoning performance on a 25-case subset, that we also used for human baselines (a), under the following setups: (b) radiologist-written captions derived directly from images, ground-truth Eurorad captions, and GPT-paraphrased versions of the ground truth to test robustness to phrasing, (c) model-generated captions (GPT-4o). Replacing model-generated captions with human or GT captions markedly improves diagnostic accuracy (Table 4), establishing a clear captioning gap. However, even with ideal captions, models remain below neuroradiologist-level accuracy, indicating a residual reasoning gap. Using ground-truth captions, DeepSeek-R1 reaches 44% Top-1 and 52% Top-5 accuracy, approaching residents but still trailing human experts (48–52% / 68–76%). Performance remains stable under GPT-paraphrased captions (Top-1: 42% vs. 44.0%), suggesting that the model responds primarily to clinical semantics rather than memorized phrasing.

To examine whether this residual gap arises from missing rare-disease knowledge, a board-certified neuroradiologist probed GPT-4o's understanding across the same cases. The model consistently produced clinically accurate textual descriptions of hallmark findings, e.g., *Multiple intracranial meningiomas—well-circumscribed, extra-axial masses with homogeneous gadolinium enhancement and a "dural tail" sign;* These qualitative probes confirm that the rare-disease concepts and their imaging correlates are represented in the model's linguistic knowledge. The persistent reasoning deficit therefore reflects a limited ability to integrate visual evidence with this knowledge into coherent diagnostic inference, rather than an absence of medical understanding.

6 Discussion

NOVA introduces a new benchmark for evaluating anomaly detection and multimodal reasoning in clinical brain MRI. Its design offers several key advantages. First, NOVA provides one of the largest and most diverse expert-annotated collections of brain MRI scans available, covering approximately 900 scans with over 280 distinct diagnoses and rare pathological conditions. Second, the dataset uniquely integrates multimodal annotations, combining radiologist-drawn bounding boxes, expert-generated image captions, and detailed clinical histories. This comprehensive structure enables systematic evaluation of detection, description, and diagnostic reasoning within a single resource. Third, the dataset reflects real-world clinical variability by using actual patient cases rather than synthetic perturbations, creating a challenging and realistic testbed. Finally, the structured multi-reader annotation protocol with adjudication by a senior neuroradiologist ensures a high level of annotation quality and reliability.

Despite these advantages, NOVA has limitations that are important to acknowledge. The dataset is sourced from a European radiology teaching repository, which may introduce geographic or demographic biases that could affect model generalization in other healthcare systems. Additionally, NOVA provides only 2D image slices rather than full 3D volumes. While this choice may constrain certain volumetric analyses, the decision to release data in 2D format was deliberate: most standard machine learning and computer vision tools and libraries offer limited support for 3D medical imaging, which can significantly slow down experimentation and accessibility for the broader research community. Finally, NOVA is released as an *evaluation-only* benchmark, not intended for supervised model training. This design reflects the realities of rare disease imaging, where collecting sufficient labeled data for training is often infeasible and where true generalization must be tested without model adaptation. Beyond current baselines, future work could explore adapting large generalist models to medical imaging domains, injecting structured medical knowledge, and enhancing multimodal reasoning to bridge visual and clinical understanding.

Looking forward, we plan to maintain NOVA as a dynamic benchmark and to open a public leaderboard to encourage continuous community participation and advancement of the state of the art. Given the dataset's focus on rare diseases and its intended role as an inference benchmark, we do not envision extensions to fine-tuning tasks or inclusion of 3D imaging data. Instead, we anticipate that NOVA will catalyze the development of next-generation foundation models and VLMs capable of performing robust diagnostic reasoning under realistic open-set clinical conditions.

7 Conclusion

We present NOVA, the first large-scale, expert-annotated benchmark dataset for anomaly localization, clinical captioning, and diagnostic reasoning in brain MRI. NOVA provides a uniquely challenging and clinically grounded resource, combining real-world imaging variability with high-quality multimodal annotations. By releasing NOVA to the community, we aim to establish a new standard for evaluating the robustness and generalization of models for clinical anomaly detection and multimodal medical reasoning. We invite the research community to engage with NOVA and drive the development of next-generation models capable of detecting the unknown in clinical imaging.

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- The answer NA means that the paper does not include experiments.
- The paper should indicate the type of compute workers CPU or GPU, internal cluster, or cloud provider, including relevant memory and storage.
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Question: Does the paper discuss both potential positive societal impacts and negative societal impacts of the work performed?

Answer: [Yes]

Justification: The paper discusses both potential positive and negative societal impacts. On the positive side, NOVA enables more realistic evaluation of generalization and robustness in clinical AI systems, helping benchmark the performance of vision-language models in medical contexts that reflect true diagnostic complexity. This could support the development of safer and more interpretable AI for healthcare applications. On the negative side, the dataset inherits population and acquisition biases from Eurorad, which may not represent global or demographically balanced clinical populations. Additional risks include the potential misuse of benchmark results as evidence of clinical readiness, overfitting to the dataset, or use outside its intended non-clinical research scope.

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    Answer: [Yes]

    Justification: NOVA does not include generative models or scraped web content, but we recognize that medical datasets inherently carry risk of misuse. To mitigate this, we implement several safeguards. First, all data is derived from publicly released, de-identified Eurorad cases curated for educational purposes, with no patient-identifying information. Second, we release the dataset under a research-only license with clear restrictions against clinical deployment or commercial use. Third, we provide structured usage guidelines emphasizing that NOVA is an evaluation benchmark, not intended for training diagnostic systems. Finally, metadata has been reviewed to avoid inclusion of sensitive or potentially identifiable content. These steps aim to ensure responsible use and reduce misuse risks.

    Guidelines:

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13. **New assets**

Question: Are new assets introduced in the paper well documented and is the documentation provided alongside the assets?

Answer: [Yes]

Justification: We introduce NOVA, a new benchmark dataset for anomaly localization, visual captioning, and diagnostic reasoning in brain MRI. The dataset includes over 900 cases with rare and heterogeneous diagnoses curated from Eurorad, each containing high-resolution medical images, expert-written diagnostic reports, and bounding box annotations of anomalies provided independently by nine radiologists. We provide full documentation detailing the data structure, annotation format, label ontology, and usage guidelines. All assets are publicly availble under a non-commercial research license. A dataset card and structured metadata are provided in the public dataset.

Guidelines:

- The answer NA means that the paper does not release new assets.
- Researchers should communicate the details of the dataset/code/model as part of their submissions via structured templates. This includes details about training, license, limitations, etc.
- The paper should discuss whether and how consent was obtained from people whose asset is used.
- At submission time, remember to anonymize your assets (if applicable). You can either create an anonymized URL or include an anonymized zip file.

14. **Crowdsourcing and research with human subjects**

Question: For crowdsourcing experiments and research with human subjects, does the paper include the full text of instructions given to participants and screenshots, if applicable, as well as details about compensation (if any)?

Answer: [NA]

Justification: The paper does not involve crowdsourcing or direct interaction with human subjects. All annotations were obtained from certified radiologists as part of their professional duties under existing institutional agreements. No crowd workers or external participants were involved, and no additional compensation was provided beyond standard institutional arrangements.

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    Question: Does the paper describe potential risks incurred by study participants, whether such risks were disclosed to the subjects, and whether Institutional Review Board (IRB) approvals (or an equivalent approval/review based on the requirements of your country or institution) were obtained?

    Answer: [Yes]

    Justification: We obtained an IRB number (2025-446-W-CB) and confirmation of exemption from full IRB approval, as our study exclusively utilized publicly available anonymized datasets. In addition, our annotation protocol was performed internally by in-house radiologists under anonymized conditions, ensuring that no identifiable human subject data were involved.

    Guidelines:

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    Answer: [NA]

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    Guidelines:

    - The answer NA means that the core method development in this research does not involve LLMs as any important, original, or non-standard components.
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Appendix

This supplementary material provides detailed insights into the NOVA benchmark. Section A outlines the annotation protocol, including our custom web interface, rater instructions, adjudication strategy, and the weighted consensus merging based on expert agreement. Section B presents summary statistics capturing the demographic diversity of patients and the spatial characteristics of the annotated abnormalities, including bounding box distributions and heatmaps. Section C compares medical VLMs against generalist VLMs. Section D introduces the three main tasks defined in our benchmark: abnormality detection, radiological image captioning, and clinical reasoning through differential diagnosis. For each task, we detail the prompting formats and model-specific configurations. We further provide two standardized evaluation protocols to assess the factual consistency and diagnostic correctness of model outputs in zero-shot settings. Section E includes concrete prompting examples to support reproducibility. Section F includes our IRB document.

A Annotation Protocol and Interface

To ensure reliable ground truth annotations for NOVA, we designed a multi-stage annotation pipeline in collaboration with experienced neuroradiologists. Each image was independently annotated by two medical experts using a custom web interface developed for this project (Figure 7). Annotators were presented with the case description, including clinical history and radiological findings, alongside the MRI image. They could interactively draw, adjust, and delete bounding boxes.

Consensus merging and disagreement resolution. Eight neuroradiology residents participated in the annotation process. Each image was reviewed by a consistent pair of annotators drawn randomly from this pool. Annotators were instructed to mark all visually and clinically relevant abnormalities, excluding normal anatomical variations and imaging artifacts. To construct a consensus set, we first computed the intersection-over-union (IoU) for all bounding box pairs. When annotations from the two readers did not overlap sufficiently (IoU ≤ 0.3), the image was flagged for adjudication. A board-certified senior neuroradiologist reviewed these cases and provided the final reference bounding boxes. Examples of annotator disagreement and expert adjudication are illustrated in Figure 8. This set of 188 images served as the basis for estimating each annotator's agreement with the expert.

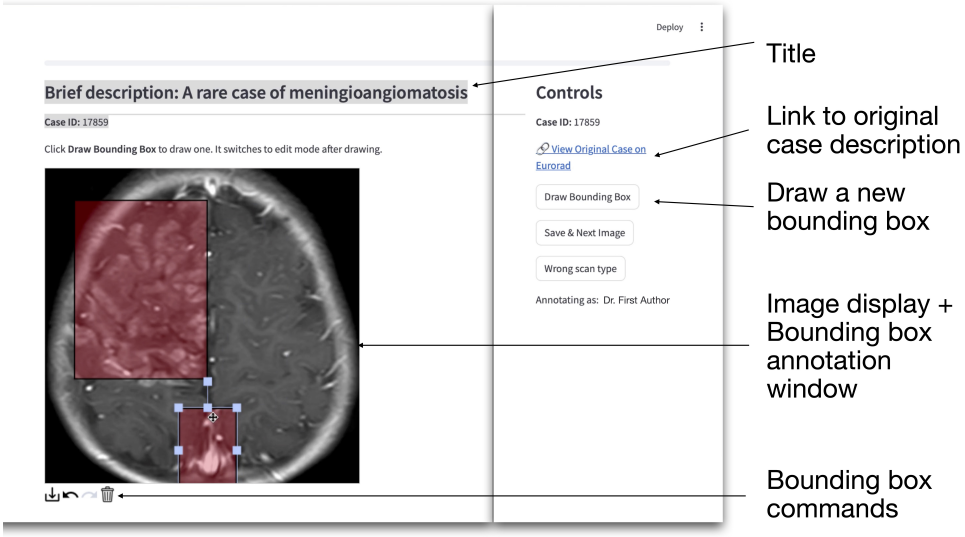

Figure 7: Each case includes a brief clinical description and a link to the full Eurorad entry. Annotators mark pathologically relevant regions using a custom bounding box tool. Controls are optimized for clinical workflows, enabling rapid annotation and review.

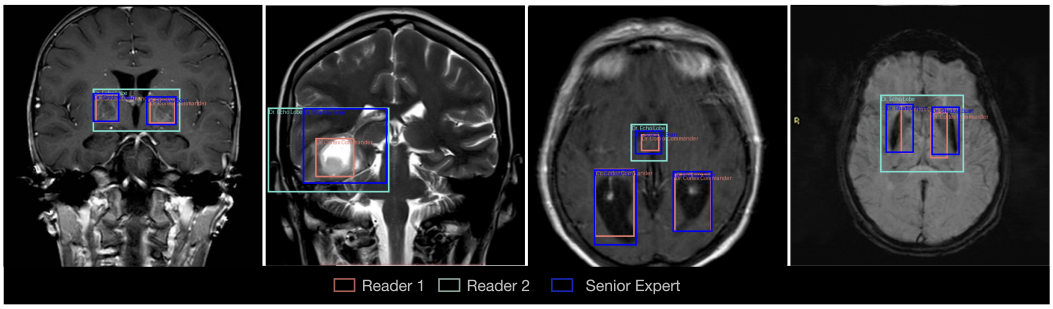

Figure 8: **Examples of annotation disagreement.** Each image shows bounding boxes from two independent annotators (Reader 1 in salmon and Reader 2 in teal) and the adjudicated expert bounding box (blue). These cases illustrate scenarios where annotators either disagreed on lesion boundaries or identified different pathological structures. In such cases, a board-certified neuroradiologist reviewed the image and merged or revised annotations to produce the final consensus labels.

Table 5: Distribution of anatomical planes in NOVA.

View	Axial	Sagittal	Coronal	Unknown
Count	548	64	140	154

For each annotator r, we computed the average intersection-over-union (IoU) between their annotations and the expert-approved boxes across all adjudicated images they participated in. Let I_r denote this mean agreement score for reader r.

For the remaining images where readers produced overlapping boxes (IoU > 0.3), we merged these into a single consensus box. The coordinates of the merged box $\mathbf{b}_{\text{merged}}$ were computed using a weighted average of the two boxes:

$$\mathbf{b}_{\text{merged}} = w_A \cdot \mathbf{b}_A + w_B \cdot \mathbf{b}_B, \quad \text{with} \quad w_A = \frac{I_A}{I_A + I_B}, \quad w_B = \frac{I_B}{I_A + I_B}$$

where I_A and I_B are the expert agreement scores for annotators A and B, and $\mathbf{b}_A$, $\mathbf{b}_B$ are their respective bounding boxes.

This approach ensured that annotators with a stronger history of agreement with the expert contributed more to the final consensus. It allowed us to systematically leverage expert-reviewed cases to calibrate reader reliability, even when direct adjudication was not performed.

Annotation reliability. The resulting annotation set combines double-blinded readings with targeted expert oversight. While some inter-reader variability reflects the inherent subjectivity in clinical interpretation, the adjudication procedure mitigates systematic noise and ensures high-quality labels suitable for benchmarking robust detection systems.

B Dataset Composition and Annotation Statistics

The NOVA dataset encompasses a wide spectrum of demographic and spatial variability, reflecting the diversity of real-world clinical neuroimaging. In this section, we provide supporting statistics to contextualize the challenges posed by the benchmark.

Acquisition variability. NOVA preserves the heterogeneity of real-world clinical brain MRI: scans originate from multiple sites and protocols and include standard anatomical planes (axial, coronal, sagittal) across T1-weighted, T2-weighted, FLAIR, and other sequences without harmonization. As scanner vendor and field strength information were unavailable for Eurorad cases, acquisition metadata were extracted from image captions and summarized in Tables 5, and 6.

Patient demographics. Figure 9 presents the distribution of patient sex and age across all included cases. The dataset spans a broad age range, from pediatric to geriatric populations, with a relatively

Table 6: Distribution of imaging sequences in NOVA.

Sequence	FLAIR	T2w	T1w	DWI	ADC	SWI	GRE	PD	Unknown
Count	242	226	223	41	16	15	2	1	140

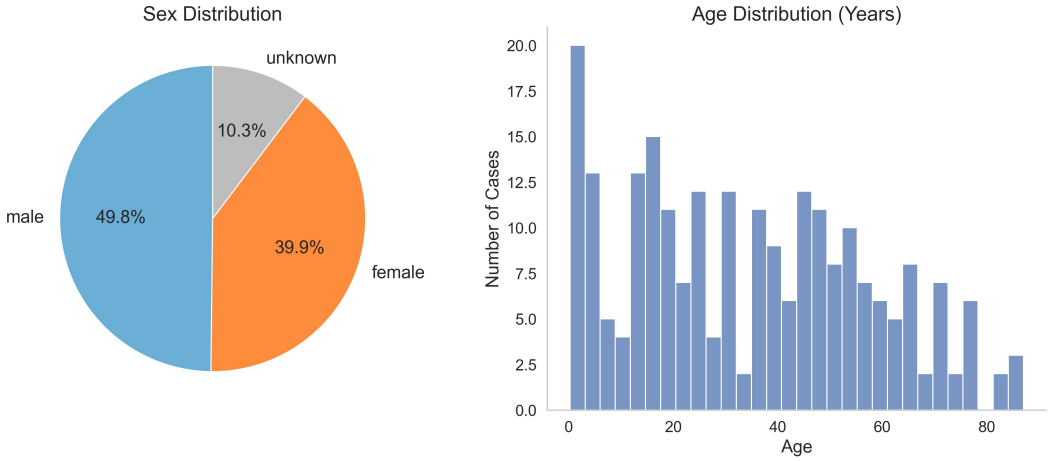

Figure 9: **Demographics.** Left: Sex distribution of cases, with a nearly balanced male-to-female ratio and a subset of cases with unknown sex. Right: Histogram of patient ages showing broad coverage across pediatric, adult, and elderly populations.

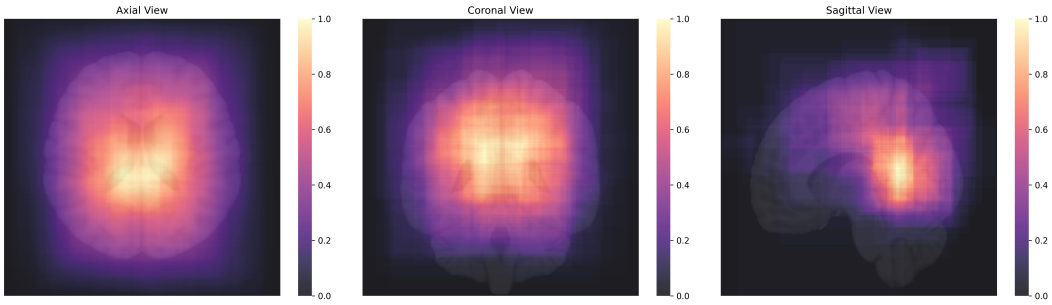

Figure 10: Heatmaps of bounding box locations aggregated across axial, coronal, and saggital views.

balanced sex distribution (min: 4 months; max: 87 years: mean: 34 years and 6 months). This heterogeneity emphasizes the need for models that generalize across anatomical, developmental, and demographic variations.

Spatial distribution of annotations. Figure 10 visualizes the anatomical spread of bounding boxes across axial, sagittal, and coronal planes. The heatmaps reflect the diversity of pathological presentations in the dataset, including cortical, subcortical, ventricular, brainstem, and cerebellar anomalies. This spatial variability introduces significant challenges for localization models, which must be robust to changes in context and anatomical orientation.

Bounding box properties. Figure 11 summarizes key properties of the annotated bounding boxes. The top panel reports the log-area distribution, indicating a wide range of lesion sizes—from small focal abnormalities to extensive pathology. The bottom panels show the number of boxes per image and a scatterplot of width versus height. Notably, a large fraction of cases contain multiple distinct findings, while many pathologies are highly non-square or irregularly shaped.

Implications. The demographic breadth and spatial diversity observed in NOVA mirror the complexity of clinical imaging workflows. These statistics underscore the difficulty of the anomaly

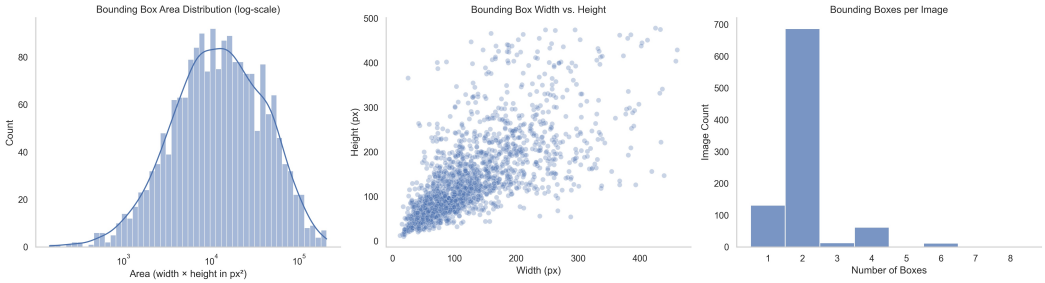

Figure 11: **Bounding box statistics.** Left: Log-area distribution of annotated bounding boxes. Center: Scatterplot of width versus height. Right: Histogram of the number of bounding boxes per image.

Table 7: Performance of generalist and medical VLMs on Task 1 (Anomaly Localization), 25-case NOVA subset.

Model(s)	mAP@50	mAP@50:95	RoDeO / Loc.	RoDeO / Shape
General Models				
Gemini 2.0 Flash	16.28	4.54	**53.06**	**34.45**
Qwen 2-VL-72B	11.11	4.12	42.45	23.82
Qwen 2.5-VL-72B	**18.97**	**8.02**	51.30	27.41
Medical Models				
CheXagent / MAIRA-2	0.00	0.00	0.00	0.00
HuatuoGPT Vision	8.33	1.94	49.25	32.90

localization task and highlight the importance of structured evaluation settings that go beyond synthetically simplified benchmarks.

C Evaluation of Generalist vs. Medical VLMs on NOVA (Task 1)

We benchmarked three medical vision–language models (VLMs)—CheXagent, MAIRA-2, and HuatuoGPT Vision in Table 7. We evaluated the results on a 25-case NOVA subset for *Task 1: anomaly localization*, using the same evaluation protocol as in the main experiments. The chest-X-ray–tuned models (CheXagent, MAIRA-2) did not generalize to brain MRI (mAP@50 = 0), while HuatuoGPT Vision achieved mAP@50 = 8.3. Generalist VLMs such as Gemini 2.0 Flash (16.3) and Qwen 2.5-VL-72B (19.0) remained substantially stronger. These results highlight the limited transferability of current modality-specific medical VLMs to brain MRI.

D Prompting and Evaluation Details of LLMs

This section details the prompting strategies, evaluation metrics, and model-specific configurations used in our benchmark for assessing clinical reasoning and factual consistency of large language and vision-language models on brain MRI tasks.

We design a comprehensive benchmark comprising three clinically grounded tasks to evaluate the capabilities of advanced language and vision-language models in neuroradiological image understanding. We show details in Section D.1:

- **Detection** — identifying and localizing abnormalities via bounding boxes.
- **Captioning** — generating structured radiological descriptions from MRI scans.
- **Reasoning** — performing differential diagnosis based on imaging findings and clinical history.

In addition, we define two evaluation procedures to assess the factual consistency and correctness of generated outputs (Section D.2). All models are evaluated in a zero-shot setting with fixed parameters

(temperature = 0.1, max output length = 2048 tokens) and a unified system prompt: *"You are a medical expert."*. The three clinical tasks are performed on four advanced models: GPT-4o, Gemini 2.0 Flash, Qwen 2.5-VL 72B, and Qwen 2.0-VL 72B. For evaluation tasks, we employ GPT-4o to conduct output assessment and consistency verification.

Note on DeepSeek-R1. As DeepSeek-R1 does not support direct visual input, we evaluated it using externally provided image descriptions. Specifically, we tested two setups: one using ground-truth (GT) captions and one using captions generated by GPT-4o. With GT captions, DeepSeek-R1 achieved 52.3% Top-1 and 67.9% Top-5 accuracy. When prompted with GPT-4o-generated captions, performance was 25.9% Top-1 and 41.6% Top-5. While these results highlight the potential of text-only diagnostic reasoning, they are not directly comparable to the other tested models due to differences in inputs.

D.1 Clinical Tasks

This component includes three tasks, each targeting a specific dimension of diagnostic reasoning:

(1) Abnormality Grounding. Given an MRI image, the model identifies abnormalities with bounding box coordinates and corresponding labels. Due to differences in coordinate conventions, we use model-specific prompt formats. For Qwen-series models, boxes are expressed as [x1, y1, x2, y2]; for Gemini models, we use [ymax, xmin, xmax, ymin]. Prompt templates and parsing logic are tailored accordingly to ensure compatibility across models.

Abnormality Grounding—Qwen Series:

Template 1: Abnormality Grounding Prompt

Return bounding boxes of any abnormal areas as JSON format.
If the image does not have the target, return the string: `"no target"`.
If detected, return a list of 2D bounding boxes around the target regions in the following JSON format:

```
[
  {"bbox_2d": [x1, y1, x2, y2], "label": "label"},
  ...
]
```

where `x1, y1` and `x2, y2` are the coordinates of the top-left and bottom-right corners of the bounding box, and `label` is the abnormality type.

Abnormality Grounding—Gemini:

Template 2: Abnormality Grounding Prompt

Return bounding boxes of any abnormal areas as JSON format.
If the image does not have the target, return the string: `"no target"`.
If detected, return a list of 2D bounding boxes around the target regions in the following JSON format:

```
[
  {"bbox_2d": [ymax, xmin, xmax, ymin], "label": "label"},
  ...
]
```

where `ymax, xmin, xmax, ymin` represent the coordinates of the bounding box corners, and `label` is the abnormality type.

(2) Medical Image Description. The model generates structured medical image findings directly from MRI scans. Prompts guide the model to describe the imaging modality, slice orientation, lesion location, and key visual abnormalities.

Template 3: Medical Image Description Prompt

System Prompt:
You are a highly skilled radiologist AI assistant. Your task is to analyze medical images with precision and generate accurate, concise diagnostic descriptions suitable for clinical use. Always prioritize clarity, accuracy, and domain-specific terminology in your responses.

Please carefully examine the provided medical image and perform a comprehensive, in-depth analysis. Generate a clear, concise description focusing on the **imaging modality**, **slice orientation**, **lesion location**, and any **notable abnormalities** observed.

Format to Follow:
- Answer:
`[Only output the final concise description result.]`

(3) Differential Diagnosis. The model receives a patient's clinical history and imaging findings as input. It outputs a list of five candidate diagnoses: one primary diagnosis and four plausible alternatives. The format is standardized to support automatic top-1 and top-5 accuracy evaluation. For a detailed example, see Sec. E.0.1.

Template 4: Differential Diagnosis Prompt

Please provide the most likely diagnosis along with four other possible differential diagnoses based on the following clinical history and MRI findings. Your output should be structured in JSON format.

Clinical History:
`"Clinical_History"`

MRI Findings:
`"MRI_Findings"`

Format to Follow:
`json`

```
{
  "most_likely_diagnosis": "Diagnosis name here",
  "other_possible_diagnoses": [
    "Diagnosis 1 here",
    "Diagnosis 2 here",
    "Diagnosis 3 here",
    "Diagnosis 4 here"
  ]
}
```

D.2 Evaluation

We design two evaluation tasks to quantitatively assess the quality of model outputs:

(1) Image Description Evaluation. This prompt extracts key clinical findings from model-generated MRI image descriptions and compares them to ground truth annotations. It emphasizes relevant anatomical, pathological, and imaging details, standardizing terms for direct comparison. Consistency is measured by agreement on the presence or absence of abnormalities, enabling accurate diagnostic evaluation. For a detailed example, see Sec. E.0.2.

Template 5: Image Description Evaluation Prompt

You are given two radiology reports: Ground Truth (GT) and Predicted (Pred). Your task is to extract and standardize medically important keywords from both reports.

Task: Extract keywords related to the following categories:

- Anatomical structures: e.g., brain regions, body parts.
- Imaging characteristics: e.g., hyperintensity, low density, enhancement, mass-like, signal changes.
- Disease or pathological findings: e.g., leukoencephalopathy, infarct, tumor.
- Negated findings: any finding explicitly stated as absent or negative, such as "no hemorrhage", "no mass" — keep the negation in the keyword.
- Imaging sequence and plane: e.g., T1, T2, FLAIR, DWI, sagittal, axial, coronal.

Standardization Rules:

- Normalize synonymous or semantically similar expressions into a single canonical form.
- Normalize anatomical mentions related to disease into their broader anatomical structures when appropriate.
- Ensure that after normalization, all terms that refer to the same concept are exactly string-equal, to support direct set-based comparison (e.g., for intersection/union using string matching).
- Prefer higher-level or broader terms when multiple expressions refer to variations of the same anatomical area (e.g., "inferior pointing of the ventricles", "ventricles slightly enlarged", and "ventricular dilation" should all be normalized to "ventricles").
- The goal is to eliminate variation in expression and granularity, so that conceptually equivalent phrases normalize to the same string.

Consistency

- GT and Pred are labeled as "normal" or "abnormal" based on their findings.
- Is_Consistent is true if both GT and Pred are either "normal" or both "abnormal".
- Is_Consistent is false if one is "normal" and the other is "abnormal".

Input:
GT = `"GT_INPUT"`
Pred = `"PRED_INPUT"`
Output Format (JSON):

```
{
  "Raw_Keywords": {
    "GT": ["keyword1", "keyword2", "..."],
    "Pred": ["keyword1", "keyword2", "..."]
  },
  "Standardized_Keywords": {
    "GT": ["standardized_keyword1", "standardized_keyword2", "..."],
    "Pred": ["standardized_keyword1", "standardized_keyword2", "..."]
  },
  "Consistency": {
    "GT": "normal" | "abnormal",
    "Pred": "normal" | "abnormal",
    "Is_Consistent": true | false
  }
}
```

Only return valid JSON with no extra text.

(2) Diagnosis Result Evaluation. This prompt evaluates predicted diagnoses against ground truth labels using top-1 and top-5 accuracy. It focuses on the core diagnostic entity, allowing synonyms and terminology variations, while ignoring differences in specificity or etiology unless the diagnosis is fundamentally different. For a detailed example, see Sec. E.0.3.

Template 6: Medical Diagnosis Evaluation

You are a professional medical diagnosis evaluation system. You will receive two inputs:

- **Ground Truth Diagnosis (GT)**: A single confirmed diagnosis.
- **Predicted Diagnosis (Pred)**: One most likely diagnosis and four additional possible diagnosis candidates.

Evaluation Rules

- Focus only on the **core diagnosis**, regardless of etiology or cause.
- Allow for synonyms and variations in medical terminology.
- If the same diagnostic entity (imaging pattern, pathological finding, or clinical condition) is present in the predictions, consider it correct.
- Do not penalize for differences in specificity or cause (e.g., idiopathic vs secondary), unless the disease is fundamentally different.

Input:
GT: `"GT_Diagnosis"`
Pred: `"Pred_Diagnosis"`
Output Format:
Return only JSON in the following structure:

```
{
  "Top_1": "Correct" | "Wrong",
  "Reason_for_Top1": "<your explanation>",
  "Top_5": "Correct" | "Wrong",
  "Reason_for_Top5": "<your explanation>"
}
```

Only return valid JSON with no extra text.

E Examples of Different prompts

E.0.1 Example of Differential Diagnosis Prompt

Example 1: Differential Diagnosis Example

Please provide the most likely diagnosis along with the other four possible diagnoses based on the following clinical history and MRI findings from the patient. The output should be in JSON format.

Clinical History:
"A 6-year-old boy came for MRI with complaints of delayed development, hypotonia, seizures. Birth history was normal and he was born to non-consanguineous parents. His younger sibling was normal. On clinical examination, the patient had multiple hypopigmented and hyperpigmented patches on limbs, back and chest."

MRI Findings:
"Slice 1: The image is an axial T2-weighted MRI of the brain. It shows hyperintense lesions in the periventricular white matter, suggestive of demyelination. The lesions are located adjacent to the lateral ventricles, which is characteristic of multiple sclerosis.
Slice 2: The image is a sagittal MRI scan of the brain. It shows a well-defined mass in the posterior fossa, likely affecting the cerebellum. There is no obvious midline shift or hydrocephalus. Further evaluation and correlation with clinical findings are recommended for diagnosis.
Slice 3: The image is an axial MRI scan of the brain. It shows a T1-weighted sequence. There are multiple small hyperintense lesions located in the periventricular white matter, which may suggest demyelinating disease or chronic small vessel ischemic changes.
Slice 4: The image is an axial FLAIR MRI of the brain. It shows hyperintense lesions in the periventricular white matter, which may indicate demyelination or other white matter pathology.
Slice 5: The image is an axial FLAIR MRI scan of the brain. There are hyperintense lesions visible in the periventricular white matter, which may suggest demyelination or other pathological processes."

Format to Follow:

```
json

{
  "most_likely_diagnosis": "Diagnosis name here",
  "other_possible_diagnoses": [
    "Diagnosis 1 here",
    "Diagnosis 2 here",
    "Diagnosis 3 here",
    "Diagnosis 4 here"
  ]
}
```

E.0.2 Example of Image Description Evaluation Prompt

Example 2: Image Description Evaluation Example

You are given two radiology reports: Ground Truth (GT) and Predicted (Pred). Your task is to extract and standardize medically important keywords from both reports.

Task: Extract keywords related to the following categories:

- Anatomical structures: e.g., brain regions, body parts.
- Imaging characteristics: e.g., hyperintensity, low density, enhancement, mass-like, signal changes.
- Disease or pathological findings: e.g., leukoencephalopathy, infarct, tumor.
- Negated findings: any finding explicitly stated as absent or negative, such as "no hemorrhage", "no mass" — keep the negation in the keyword.
- Imaging sequence and plane: e.g., T1, T2, FLAIR, DWI, sagittal, axial, coronal.

Standardization Rules:

- Normalize synonymous or semantically similar expressions into a single canonical form.
- Normalize anatomical mentions related to disease into their broader anatomical structures when appropriate.
- Ensure that after normalization, all terms that refer to the same concept are exactly string-equal, to support direct set-based comparison (e.g., for intersection/union using string matching).
- Prefer higher-level or broader terms when multiple expressions refer to variations of the same anatomical area (e.g., "inferior pointing of the ventricles", "ventricles slightly enlarged", and "ventricular dilation" should all be normalized to "ventricles").
- The goal is to eliminate variation in expression and granularity, so that conceptually equivalent phrases normalize to the same string.

Consistency

- GT and Pred are labeled as "normal" or "abnormal" based on their findings.
- Is_Consistent is true if both GT and Pred are either "normal" or both "abnormal".
- Is_Consistent is false if one is "normal" and the other is "abnormal".

Input:

- GT = "Coronal T1W with GADO: peripherical enhancement on post-contrast image."
- Pred = "Coronal T1-weighted MRI of the brain demonstrating multiple enhancing lesions, suggestive of metastatic disease."

Output Format (JSON):

```
{
  "Raw_Keywords": {
    "GT": ["keyword1", "keyword2", "..."],
    "Pred": ["keyword1", "keyword2", "..."]
  },
  "Standardized_Keywords": {
    "GT": ["standardized_keyword1", "standardized_keyword2", "..."],
    "Pred": ["standardized_keyword1", "standardized_keyword2", "..."]
  },
  "Consistency": {
    "GT": "normal" | "abnormal",
    "Pred": "normal" | "abnormal",
    "Is_Consistent": true | false
  }
}
```

Only return valid JSON with no extra text.

E.0.3 Example of Medical Diagnosis Evaluation Prompt

Example 3: Medical Diagnosis Evaluation Example

You are a professional medical diagnosis evaluation system. You will receive two inputs:

1. **Ground Truth Diagnosis (GT)**: A single confirmed diagnosis.
2. **Predicted Diagnosis (Pred)**: One most likely diagnosis and four additional possible diagnosis candidates.

Evaluation Rules

- Focus only on the **core diagnosis**, regardless of etiology or cause.
- Allow for synonyms and variations in medical terminology.
- If the same diagnostic entity (imaging pattern, pathological finding, or clinical condition) is present in the predictions, consider it correct.
- Do not penalize for differences in specificity or cause (e.g., idiopathic vs secondary), unless the disease is fundamentally different.

Input:
GT: `"Septo - optic dysplasia"`

Pred:

```
{
  "most_likely_diagnosis": "Craniopharyngioma",
  "other_possible_diagnoses": [
    "Optic Pathway Glioma",
    "Arachnoid Cyst",
    "Hydrocephalus",
    "Neurofibromatosis Type 1"
  ]
}
```

Output Format:
Return only JSON in the following structure:

```
{
  "Top_1": "Correct" | "Wrong",
  "Reason_for_Top1": "<your explanation>",
  "Top_5": "Correct" | "Wrong",
  "Reason_for_Top5": "<your explanation>"
}
```

Only return valid JSON with no extra text.

F IRB Documentation

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Our sign: 2025-446-W-CB

TUM Universitätsklinikum Klinikum rechts der Isar
Institut für Diagnostische und Interventionelle Neuroradiologie
Herrn Prof. Dr. med. Benedikt Wiestler
Ismaninger Str. 22
81675 München
Germany

Munich, 07.08.2025

Consultation according to § 15 of the professional code of conduct for physicians in Bavaria
Confirmation of exemption

Title of study:	NOVA: A Benchmark for Anomaly Localization and Clinical Reasoning in Brain MRI
Applicant:	Prof. Dr. med. Benedikt Wiestler

Dear Prof. Dr. med. Benedikt Wiestler,

the Ethics Committee has reviewed your application dated 06.08.2025 on the basis of the documents submitted.

The Ethics Committee hereby confirms that professional advice pursuant to Section 15 of the Professional Code of Conduct for Physicians in Bavaria is not required for the submitted research project.

Yours sincerely

Prof. Dr. Georg Schmidt
Chairman of the Ethics Committee
Technical University Munich

The correspondence contains only a name and is valid without a signature.

Technische Universität München
Ethikkommission

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