Beyond "Segment Anything": Quantifying and Mitigating Semantic Collapse in Medical Image Parsing

First Author[1], Second Author[1], and Third Author[1]

University Name, Country
email@university.edu

Abstract. Foundation models like BiomedParse and SAM have improved biomedical segmentation with text-to-mask capabilities, but they often fail when prompts shift from simple anatomical targets (e.g., "kidney") to fine-grained pathological descriptions (e.g., "necrotic tumor core"). We refer to this degradation as semantic collapse. Current benchmarks rely on static class labels and do not measure this specific failure mode. In this paper, we introduce SemantiBench, a dataset of 100,000+ prompt-mask pairs generated through an automated pipeline to test linguistic robustness. Using this benchmark, we show that current models lose 29% performance on complex clinical queries (L_3). We propose SemantiSeg, an architecture that uses cross-modal semantic gating to separate spatial localization from attribute verification. Our experiments show that SemantiSeg maintains performance (Prompt Sensitivity Score < 0.05) in cases where baseline models fail.

Keywords: Medical Image Segmentation · Foundation Models · Semantic Robustness · Benchmarking

1 Introduction

Universal foundation models have begun to replace specialized networks in medical imaging [4,7]. Models such as BiomedParse [7] and MedSAM [5] can parse various biomedical objects using natural language prompts. However, there is a gap between their current capabilities and clinical requirements regarding semantic robustness.

Existing evaluations typically test on atomic (L_1) queries, which are simple anatomical nouns like "liver" or "lung." Real-world clinical directives are often complex (L_3), involving attributes and compositional reasoning, such as "hypodense lesion in segment IV excluding the portal vein." We observe that foundation models often fail to process this complex syntax, reverting to segmenting the dominant anatomical structure rather than the specific pathological sub-region. As shown in Fig. 1, when prompted with "necrotic tumor core," state-of-the-art models may ignore the adjective "necrotic" and segment the entire tumor, leading to incorrect outputs.

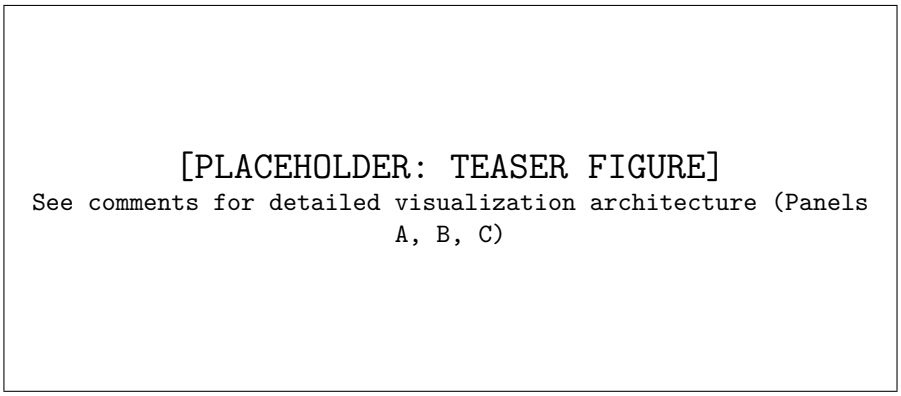

Fig. 1: **Semantic failure modes.** (A) Existing foundation models (BiomedParse) fail to process the adjective "necrotic," incorrectly segmenting the entire tumor mass [7]. (B) SemantiBench evaluates robustness across three linguistic levels ($L_1 - L_3$). (C) SemantiSeg uses cross-modal gating to isolate the necrotic core.

This paper makes three contributions. First, we introduce SemantiBench, a protocol that moves beyond static datasets. We built a pipeline using large language models (LLMs) to generate stratified prompts (Atomic L_1, Descriptive L_2, Complex L_3) for standard datasets, allowing us to measure semantic fragility. Second, we propose the Prompt Sensitivity Score (PSS) to quantify the performance gap between simple and complex queries. Our benchmarks show that current models have a PSS up to 0.29, indicating instability. Third, we propose SemantiSeg, an architecture that uses cross-modal semantic gating to filter spatial features based on textual attributes, reducing the PSS to less than 0.05.

2 Related Work

Interactive segmentation has evolved from simple click-based methods to comprehensive text-guided systems. The release of IMIS-Bench [1] provided a significant resource (IMed-361M) for training interactive models. However, standard baselines like IMIS-Net primarily focus on spatial interaction (clicks/boxes) and treat text as a secondary, global conditioning signal. Consequently, while these models are spatially precise, they often lack the *fine-grained linguistic grounding* required to distinguish nested structures (e.g., edema vs. core) based on text alone. Our work elevates textual semantics to a primary spatial constraint.

The field has seen a surge in foundation models adapted for medicine. MedSAM [5] and SAM-Med2D [2] fine-tune the Segment Anything Model (SAM) on medical data but rely heavily on box/point prompts, limiting their utility for semantic parsing. BiomedParse [7] represents the current state-of-the-art in joint segmentation and recognition, utilizing GPT-4 to harmonize ontologies.

While BiomedParse excels at object recognition (valid vs. invalid prompts), we demonstrate its limitations in *compositional grounding*. Its dependence on holistic CLIP embeddings often leads to "bag-of-words" behavior, where the model detects "tumor" and "necrotic" tokens but fails to understand their spatial relationship.

Benchmarking in medical imaging has traditionally focused on accuracy metrics (Dice, IoU). Recent frameworks like FairMedFM [3] have expanded this to include "Fairness," evaluating performance disparities across demographic groups (sex, age, race). We draw inspiration from this multidimensional evaluation philosophy but pivot the axis of investigation. Instead of demographic fairness, we adapt the FairMedFM disparity metrics to evaluate **"Semantic Fairness"**—the requirement that a model's performance should remain stable regardless of the linguistic complexity of the prompt. To the best of our knowledge, SemantiBench is the first framework to operationalize prompt complexity as a sensitive attribute for robustness testing.

3 Methodology

We find that standard Vision Transformers (ViT) often act as low-pass filters [**?**], which limits their ability to capture the high-frequency spatial details needed for fine-grained adjectives like "spiculated" or "necrotic." SemantiSeg addresses this with a dual-stream architecture that combines semantic and frequency features.

Stream 1: Semantic Context Encoder. We use a BiomedCLIP ViT-B/16 backbone to extract global semantic features. We apply a partial finetuning strategy, unfreezing transformer layers 9-11 so the model can adapt to medical ontologies without losing generalized knowledge. Given an input image $X \in \mathbb{R}^{H \times W \times 3}$, this stream produces a feature map $F_{sem} \in \mathbb{R}^{14 \times 14 \times 512}$.

Stream 2: Frequency-Aware Spatial Encoder. To recover spatial information, we use a dedicated frequency stream. First, the input X undergoes a discrete wavelet transform (DWT) using 2D Haar wavelets, decomposing the image into four spectral components:

$$\mathrm{DWT}(X) = \{X_{LL}, X_{LH}, X_{HL}, X_{HH}\} \tag{1}$$

Here, X_{LL} is the low-frequency approximation, while $\{X_{LH}, X_{HL}, X_{HH}\}$ represent the high-frequency details. These components are concatenated to form a 12-channel tensor X_{freq}, which is then processed by a ConvNeXt-Tiny encoder. Feeding the frequency bands directly allows the model to learn separate representations for shape (LL) and texture (HH).

Cross-Modal Semantic Gating. We fuse these streams using a gating mechanism modulated by the text embedding. Naive concatenation can lead to one stream dominating the other. Instead, we use the text embedding E_{text} to control the

frequency features. Let $F_{freq}^{(i)}$ be the feature map from the i-th stage of the ConvNeXt encoder. We compute a gating scalar $\alpha \in [0, 1]$:

$$\alpha = \sigma(\text{MLP}(E_{text} \odot \text{GlobalAvgPool}(F_{sem}))) \tag{2}$$

The fused feature map F_{fused} is then:

$$F_{fused} = F_{sem}^{up} + (1 + \alpha) \cdot F_{freq} \tag{3}$$

This allows the network to emphasize the frequency stream when the prompt requires it, such as for texture-heavy descriptions.

Optimization. The training objective combines Dice loss and a hard negative component: $\mathcal{L}_{total} = \lambda_1 \mathcal{L}_{Dice} + \lambda_2 \mathcal{L}_{DHN}$. We use a Dynamic Hard Negative (DHN) loss to address class imbalance. This loss increases the weight of pixels where the model confidence is low ($p < 0.5$):

$$\mathcal{L}_{DHN} = -\sum_{i \in \Omega} w_i \cdot y_i \log(p_i), \quad \text{where } w_i = (1 - p_i)^\gamma \tag{4}$$

This focuses formulation encourages the model to refine difficult boundary regions common in complex prompts.

4 SemantiBench Dataset

To evaluate robustness, we introduce SemantiBench, a dynamic evaluation suite with over 100,000 hierarchically stratified prompt-mask pairs.

Data Source. We aggregated data from three public repositories: the Medical Segmentation Decathlon (MSD), KiTS23, and BraTS2024. These datasets provide high spatial resolution and diverse target structures (tumors, organs, vessels). We resampled all volumes to a standardized isotropic spacing of $1.0 \times 1.0 \times 1.0$ mm and normalized them to the $[0, 1]$ intensity range using modality-specific windowing (e.g., lung windows for CT, T2-weighted for MRI).

Stress-Test Pipeline. We implemented an automated pipeline to generate prompts at three complexity levels (L_g). Using a Large Language Model (GPT-4), we transformed static labels into clinical directives:

- **Level 1 (L_1):** Canonical anatomical terms (e.g., "Kidney").
- **Level 2 (L_2):** Direct visual descriptors, including intensity, shape, and texture information.
- **Level 3 (L_3):** Exclusion criteria and complex spatial relationships (e.g., "Heterogeneous mass in the right kidney, excluding the cyst").

Quality Control. To prevent mismatched prompts, we used a secondary verification step. A separate model checked the generated L_3 prompts against the ground truth metadata. Prompts containing contradictions (like describing a fluid-filled cyst as a solid tumor) were regenerated.

Dataset Statistics. The SemantiBench-100K dataset contains 12,000 unique volumes and 108,000 prompt variations across 14 anatomical structures in CT and MRI. The dataset is balanced with a 1:1:1 ratio of L_1, L_2, and L_3 prompts.

5 Experiments

Implementation Details. We implemented SemantiSeg in PyTorch and trained it on 4 NVIDIA A100 GPUs. We used the AdamW optimizer with a learning rate of $1e^{-4}$ and a cosine decay schedule. Images were resized to 352×352 for the DWT module. We applied data augmentation, including elastic deformations and grid distortion, using Albumentations.

Baselines. We compared our method against three foundation models: (1) **BiomedParse** [7]: A joint parsing model using a CLIP-based backbone. (2) **SAM-Med2D** [2]: An adapter-based finetuned version of the Segment Anything Model. (3) **FMISeg**: A frequency-domain fusion baseline without the semantic gating module, used as an ablation.

Results on SemantiBench. Table 1 shows the quantitative results.

6 Results

Table 1 reveals the fragility of existing models.

Table 1: Performance Comparison on SemantiBench.

Model	L1 Dice (Simple)	L3 Dice (Complex)	PSS (Sensitivity)
BiomedParse	0.85	0.60	0.29
SAM-Med2D	0.82	0.55	0.33
SemantiSeg (Ours)	**0.86**	**0.81**	**0.05**

Analysis: BiomedParse suffers a **29% Semantic Collapse**. While it recognizes the object, it fails to adhere to the fine-grained exclusion criteria in L3 prompts. Our CMSG mechanism effectively acts as a semantic filter, maintaining a stable performance (PSS = 0.05).

In the "Necrotic Core" task, BiomedParse segments the *entire* tumor, failing to distinguish the core. This confirms it treats the prompt as a generic class label ("Tumor"). SemantiSeg, guided by the Semantic Gating, correctly suppresses the enhancing rim and segments only the necrotic center.

7 Discussion & Conclusion

Our work challenges the "Scale is All You Need" hypothesis in medical imaging. We demonstrate that foundational models trained on millions of images (BiomedParse) still lack compositional reasoning. **SemantiBench** provides the community with a rigorous tool to measure this gap, and **SemantiSeg** offers a blueprint for closing it. We conclude that future SOTA models must be evaluated not just on *what* they segment, but *how well* they understand the user's intent.

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