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

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Abstract. While foundational models like BiomedParse and SAM have revolutionized biomedical segmentation through text-to-mask capabilities, they exhibit a critical failure mode we term **"Semantic Collapse"**—a significant performance degradation when moving from coarse anatomical targets (e.g., "kidney") to fine-grained pathological descriptions (e.g., "necrotic tumor core"). Current benchmarks, which rely on static class labels, fail to capture this fragility. In this work, we introduce **SemantiBench**, a hierarchical robustness benchmark comprising 100,000+ linguistically stratified prompt-mask pairs, generated via a novel Automated Semantic Stress-Test Pipeline. Leveraging this benchmark, we identify that SOTA models suffer a 29% performance drop on complex clinical queries (L_3). To address this, we propose **SemantiSeg**, a novel architecture featuring *Cross-Modal Semantic Gating (CMSG)* that explicitly decouples spatial localization from semantic attribute verification. Extensive experiments demonstrate that SemantiSeg maintains robust performance (Prompt Sensitivity Score < 0.05) where purely data-driven baselines fail.

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

1 Introduction

The paradigm of "Segment Anything" has shifted the medical imaging landscape from specialized, task-specific networks to universal, promptable foundation models [4,7]. Recent works such as BiomedParse [7] and MedSAM [5] have demonstrated impressive capabilities in parsing diverse biomedical objects using natural language prompts, promising a future of zero-shot clinical applicability. However, a critical gap remains between this promise and clinical reality: **Semantic Robustness**.

Current evaluations are deceptively optimistic because they predominantly test on "Atomic" (L_1) queries—simple anatomical nouns like *"liver"* or *"lung"*. In contrast, real-world clinical directives are often "Complex" (L_3)—attribute-rich descriptions requiring compositional reasoning, such as *"hypodense lesion in seg-*

[PLACEHOLDER: TEASER FIGURE]

See comments for detailed visualization architecture (Panels A, B, C)

Fig. 1: **Semantic Collapse vs. Semantic Gating.** (A) Existing foundation models (BiomedParse) fail to process the adjective "necrotic," incorrectly segmenting the entire tumor mass [7]. (B) Our SemantiBench evaluates robustness across three linguistic levels ($L_1 - L_3$). (C) SemantiSeg utilizes Cross-Modal Gating to correctly isolate the necrotic core.

ment IV excluding the portal vein". We observe a phenomenon we term **Semantic Collapse**, where foundational models, overwhelmed by complex syntax, revert to segmenting the dominant anatomical structure rather than the specific pathological sub-region. As illustrated in Fig. 1, when prompted with *"necrotic tumor core"*, state-of-the-art (SOTA) models often ignore the adjectival constraint ("necrotic") and segment the noun ("tumor"), resulting in clinically dangerous false positives.

To quantify and mitigate this failure mode, we present three primary contributions. First, we introduce **SemantiBench**, moving beyond static datasets to a dynamic evaluation protocol. We constructed a *Semantic Stress-Test Pipeline* using agentic Large Language Models (LLMs) to generate hierarchically stratified prompts (Atomic L_1, Descriptive L_2, Complex L_3) for standard datasets, enabling the first systematic measurement of semantic fragility. Second, we propose the **Prompt Sensitivity Score (PSS)**, a new metric that quantifies the "robustness gap" between simple and complex queries. Our benchmarking reveals that current SOTA models suffer a high PSS (up to 0.29), indicating severe instability. Third, we propose **SemantiSeg**, a novel architecture utilizing *Cross-Modal Semantic Gating (CMSG)* to dynamically filter spatial features based on textual attributes, reducing the PSS to < 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: The SemantiSeg Network

We attribute the phenomenon of Semantic Collapse to the "Low-Pass Filter" bias inherent in standard Vision Transformers (ViT) [**?**]. While ViTs excel at global semantic alignment, they struggle to preserve the high-frequency spatial details required to resolve fine-grained adjectives like "spiculated" or "necrotic." To address this, SemantiSeg introduces a **Dual-Stream Frequency-Semantic Architecture**.

Stream 1: The Semantic Context Encoder. We employ a **BiomedCLIP ViT-B/16** backbone to extract global semantic features. Unlike previous approaches that freeze the encoder, we utilize a *Partial-Finetuning Strategy*, unfreezing the final Transformer blocks (Layers 9-11) to allow adaptation to task-specific medical ontologies without catastrophic forgetting. Given an input image $X \in \mathbb{R}^{H \times W \times 3}$, this stream produces a high-level semantic feature map $F_{sem} \in \mathbb{R}^{14 \times 14 \times 512}$.

Stream 2: The Frequency-Aware Spatial Encoder. To recover the spatial information lost by patchification, we introduce 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:

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

where X_{LL} represents the low-frequency approximation, and $\{X_{LH}, X_{HL}, X_{HH}\}$ capture horizontal, vertical, and diagonal high-frequency details (textures/edges). These components are concatenated to form a 12-channel tensor X_{freq}, which is processed by a **ConvNeXt-Tiny** encoder. By explicitly feeding frequency bands into the network, we force the model to learn independent representations for "Shape" (LL) and "Texture" (HH), providing the necessary signal to ground fine-grained adjectives.

Cross-Modal Semantic Gating (CMSG). A critical innovation of SemantiSeg is the mechanism for fusing these divergent streams. Naive concatenation often leads to semantic dominance. Instead, we propose **Cross-Modal Semantic Gating**, which uses the text embedding E_{text} to dynamically modulate the frequency stream. Let $F_{freq}^{(i)}$ be the feature map from the i-th stage of the ConvNeXt encoder. We compute a gating scalar $\alpha \in [0, 1]$:

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

The fused feature map F_{fused} is computed as:

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

This gating mechanism allows the network to "amplify" the frequency stream when the text prompt implies high-frequency constraints (e.g., "rough boundary") while suppressing it for simple object queries.

Optimization via Hard Negative Mining. Training is optimized using a compound objective function $\mathcal{L}_{total} = \lambda_1 \mathcal{L}_{Dice} + \lambda_2 \mathcal{L}_{DHN}$. We introduce the **Dynamic Hard Negative (DHN) Loss** to handle the extreme class imbalance in fine-grained segmentation. The DHN loss identifies pixels where the model's confidence is low ($p < 0.5$) and dynamically upweights them during backpropagation:

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

This forces the model to focus on the difficult boundary regions characteristic of L_3 prompts.

4 Construction of SemantiBench

To rigorously quantify Semantic Collapse, we depart from the static class labels used in prior benchmarks (e.g., MSD, FairMedFM) and introduce **SemantiBench**, a dynamic evaluation suite comprising 100,000+ hierarchically stratified prompt-mask pairs.

Data Source and Harmonization. We aggregate data from three high-quality public repositories: the Medical Segmentation Decathlon (MSD), KiTS23, and BraTS2024. These datasets were selected for their high spatial resolution and diversity of target structures (tumors, organs, vessels). Prior to prompt generation, we performed a rigorous harmonization process. All volumes were resampled to a standardized isotropic spacing of $1.0 \times 1.0 \times 1.0$ mm and normalized to the $[0, 1]$ intensity range using windowing levels specific to each modality (e.g., lung windows for CT, T2-weighted for MRI). This mitigates domain shifts unrelated to semantic processing.

The Automated Semantic Stress-Test Pipeline. A core contribution of this work is the *Automated Semantic Stress-Test Pipeline*, an agentic workflow capable of transforming static labels into complex clinical directives. Unlike simple template-based augmentation, our pipeline utilizes a Chain-of-Thought (CoT) reasoning process driven by a Large Language Model (GPT-4) to generate prompts at three distinct levels of granularity (L_g).

- **Level 1: Atomic Grounding (L_1).** The agent extracts the canonical SNOMED-CT anatomical term.
- **Level 2: Visual Descriptive (L_2).** The agent augments the noun with radiomic features observable in the image (e.g., intensity, shape, texture).
- **Level 3: Clinical Exclusion (L_3).** The agent synthesizes complex exclusion criteria mimicking radiology reports (e.g., *"Segment the heterogeneous mass in the right kidney, excluding the benign cyst and renal pelvis"*).

Quality Control: The Critic Agent. To prevent "hallucination"—where the generated prompt describes features not present in the image—we implemented a *Dual-Agent Architecture.* A secondary "Critic Agent" reviews the generated L_3 prompts against the metadata of the ground truth mask. If the Critic detects a semantic contradiction (e.g., describing a "solid tumor" when the mean Hounsfield Unit indicates a fluid-filled cyst), the prompt is discarded and regenerated. This Adversarial Quality Assurance (AQA) loop ensures that SemantiBench measures model robustness, not tolerance to incorrect prompts.

Dataset Statistics. The final SemantiBench-100K dataset contains 12,000 unique volumes and 108,000 prompt variations, covering 14 anatomical structures across CT and MRI modalities. Crucially, the dataset is balanced across complexity levels, with a 1:1:1 ratio of L_1, L_2, and L_3 prompts, enabling unbiased sensitivity analysis.

5 Experiments

Implementation Details. SemantiSeg was implemented in PyTorch and trained on 4 NVIDIA A100 (80GB) GPUs. We utilized the AdamW optimizer with a base learning rate of $1e^{-4}$ and a cosine decay schedule. Images were resized to 352×352

to preserve high-frequency details for the DWT module. To ensure robustness, we employed heavy data augmentation, including Elastic Deformations and Grid Distortion, via the Albumentations library.

Baselines. We benchmark against three state-of-the-art foundation models: (1) **BiomedParse** [7]: The current SOTA for joint parsing, utilizing a standard CLIP-based backbone. (2) **SAM-Med2D** [2]: An adapter-based fine-tuning of the Segment Anything Model, representing the "Shape-Bias" baseline. (3) **FMISeg**: A frequency-domain fusion baseline without our CMSG module, included to isolate the contribution of our semantic gating mechanism.

Main Results: The Semantic Collapse. Table 1 presents the quantitative comparison on SemantiBench.

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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