Comparing Clinical and General LLMs on Knowledge Boundaries and Robustness

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Abstract

Recent studies demonstrate that large language models often encode correct answers internally even when their outputs are incorrect, and that lightweight probes can recover these latent signals. This work extends such analyses to compare general-purpose and biomedical domain–specialized models. Across circular, logistic, and MLP probes, both models exhibit low probe accuracy on internal and external knowledge, but strong error-detection performance in deeper layers. The key difference lies in stability: probe performance in the biomedical model is markedly more variable, with nearly double the standard deviation in error detector F1 compared to the general model (e.g., 0.0742 vs. 0.0510 for circular probes). An isotropy analysis provides a complementary explanation. The general model displays higher anisotropy (baseline similarity = 0.4667), producing stable, linearly separable correctness signals, whereas the biomedical model exhibits greater isotropy (baseline similarity = 0.3737), coinciding with noisier probe behavior. These findings suggest that domain-specific finetuning does not destroy or add probe-accessible knowledge, but rather reorganizes representational geometry in ways that reduce the stability of error-detection signals. The results here indicate that increased isotropy may undermine robustness in self-monitoring.[1]

1 Introduction

Large language models (LLMs) have rapidly advanced the state of the art across a wide range of tasks. However, their tendency to produce "hallucinations", plausible but factually incorrect statements, raises serious concerns about reliability, especially in high-stakes domains such as medicine. Empirical studies show that exposing an LLM to new factual information during supervised fine-tuning slows learning and *increases* the tendency to hallucinate: fine-tuning examples introducing new knowledge are learned more slowly than those consistent with pre-existing knowledge, and once they are learned the model's hallucination rate grows roughly linearly with the proportion of new facts in the fine-tuning data [1]. Moreover, head-to-head comparisons on medical question-answering find that domain-adapted LLMs rarely outperform their general-purpose counterparts; medical models win in only about 12 % of test cases and are significantly worse in more than one-third [2]. These findings suggest that most factual knowledge is acquired during pre-training and that naïvely fine-tuning on biomedical corpora may actually degrade factuality [1].

To mitigate hallucinations, a complementary line of work probes a model's *hidden activations* to understand what it "knows" [3, 4]. Early results showed that a simple classifier trained on hidden activations can tell whether a statement is true or false with 71–83 % accuracy, outperforming probability-based heuristics [5]. More recent work on three-digit addition demonstrated that *lightweight probes* can decode both the model's prediction and the correct answer from hidden

[1] Code will be released at `https://github.com/PlaceholderRepoName`

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states, regardless of whether the output is right; these probes can also predict whether the output is correct with over 90 % accuracy and can guide selective re-prompting [6]. Visualizations of hidden representations on true/false datasets reveal clear linear structure, and difference-in-mean probes generalize across datasets while causally influencing the model's answer [7]. Despite these insights, existing studies focus on general-domain models and simple arithmetic or binary truth tasks; it is unclear whether similar signals exist in medical models or for long-tail biomedical knowledge.

Two factors make the biomedical setting particularly challenging. First, *biomedical knowledge is long-tailed*: many facts appear in only a handful of documents. A model's ability to answer a fact-based question correlates strongly with how many pre-training documents mention the subject and object [8]. Even after applying knowledge-editing methods, performance on long-tail biomedical facts remains markedly worse than on high-frequency facts, partly because biomedical triples often exhibit one-to-many relations [9]. Second, *hallucination detection is under-explored in medicine*. The MedHallu benchmark shows that state-of-the-art models struggle to identify hallucinated answers in PubMedQA; even GPT-4o achieves an F1 as low as 0.625 on the hardest category [10]. Intriguingly, hallucinations that are semantically closer to the ground truth are the most difficult to detect [10], and general-purpose models outperform fine-tuned medical models on this task [10]. These observations suggest that domain-specific fine-tuning reorganizes internal representations in ways that may make self-monitoring less robust.

We propose a lightweight, unified framework for biomedical *knowledge probing and error detection*. Given a triple template $T(s, r)$, we first perform *external probing*: we ask the LLM to predict the object o and record its top-k outputs. We then perform *internal probing* on the residual-stream hidden states at the final subject token to decode both (a) the model's predicted object and (b) a proxy for the ground-truth object. Building on prior work that trains simple probes to decode answers from hidden states and detect arithmetic errors [5, 6, 11], we design logistic and MLP probes that predict whether the model's answer is correct. We test this framework across base and medical LLMs (Mistral-7B, Llama-3, BioMistral) [12, 13, 14, 15], and we explicitly evaluate long-tail triples where subjects and objects co-occur infrequently [8, 9]. Our probing approach also connects to mechanistic interpretability: by inspecting linear directions in the hidden state, we shed light on how models encode biomedical relations [7, 5, 16].

Motivated by these gaps, we ask: *Do biomedical domain–adapted LLMs differ from general LLMs in how they internally represent and monitor factual knowledge?* We adapt the probing framework for arithmetic errors [6] to biomedical knowledge triples $\langle s, r, o \rangle$ and make three main contributions:

1. **Cross-domain probing.** We design simple circular, logistic, and MLP probes that decode both the model's prediction and the correct object from hidden states at each layer. We find that, while both general and biomedical models encode latent knowledge, probes on biomedical models show much higher variance in detecting errors.

2. **Error detection and geometry.** We train lightweight classifiers to flag mismatches between predicted and ground-truth objects and analyze the geometry of hidden activations. Our results indicate that general models have more structured representations that support stable error detection, whereas biomedical models have more uniform representations, making error detection noisier.

3. **Implications for safety.** We argue that the altered representational geometry in domain-adapted models may weaken their ability to self-monitor. Lightweight probes offer a low-overhead tool for real-time error detection and highlight potential risks when deploying domain-adapted LLMs in medical settings.

2 Method

We study biomedical triples $\langle s, r, o \rangle$ with a simple prompt $T(s, r)$ and use the residual–stream vector at layer l for the last subject token, $\mathbf{x}_l \in \mathbb{R}^d$. On the same $\mathbf{x}_l$ we train two decoders: an *internal* decoder that predicts the ground-truth object o (what the model "knows") and an *external* decoder that predicts the model's own output $f_\theta(s, r)$ (what the model will "say"), following the compact probing setup of Sun, Stolfo & Sachan [6]. We then turn these signals into a lightweight correctness score.

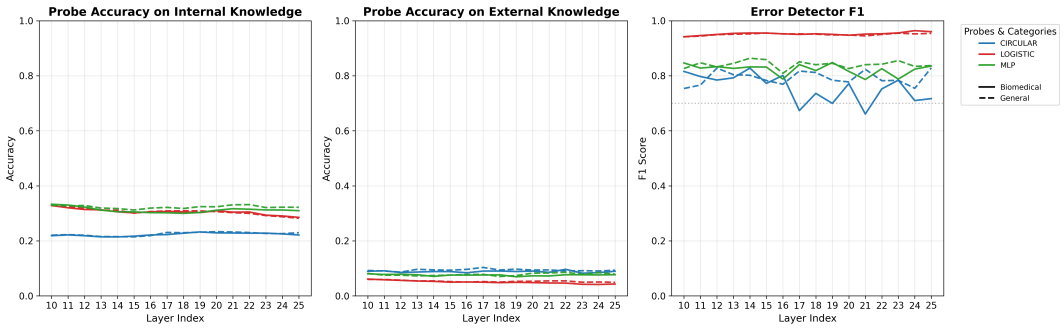

Figure 1: Layer-wise probe performance on general models (solid) and biomedical models (dashed). Left, internal Acc@10. Center, external Acc@10. Right, error-detector F1. Biomedical models exhibit notably higher variability in error detection at later layers despite similar average recall.

Probing Internal and External Knowledge. Both decoders share the same readouts and differ only by their target label. We consider K candidate objects and use three lightweight probes in one pass over $\mathbf{x}_l$: *circular* projects with $(\mathbf{w}_1, \mathbf{w}_2)$, reads an angle $\theta = atan2(\mathbf{w}_2^\top \mathbf{x}_l, \mathbf{w}_1^\top \mathbf{x}_l)$, then predicts $\hat{k} = \lfloor (\theta/2\pi)\, K \rfloor$; *logistic* computes logits $\mathbf{z} = \mathbf{W}\mathbf{x}_l + \mathbf{b}$ and predicts $\hat{k} = \arg\max_i z_i$; *MLP* computes $\mathbf{h} = \mathrm{ReLU}(\mathbf{W}_1\mathbf{x}_l + \mathbf{b}_1)$, then $\mathbf{z} = \mathbf{W}_2\mathbf{h} + \mathbf{b}_2$, and predicts $\hat{k} = \arg\max_i z_i$. Internal accuracy is the accuracy of decoders trained to recover o; external accuracy is the accuracy of decoders trained to recover $f_\theta(s, r)$.

Probing for Error Detection. We detect erroneous biomedical triples using three lightweight probes that analyze hidden activations: (1) *Logistic Regression* provides interpretable linear error detection, (2) *Circular MLP* captures non-linear geometric patterns in embedding space, and (3) *Joint Circular Error Detector* compares internal vs. external knowledge representations through angular differences. The circular approach maps activations to angles $\theta = \mathrm{atan2}(w_1^\top x, w_2^\top x)$ and flags errors when angular discrepancies exceed learned thresholds, achieving high accuracy while preserving semantic relationships in the embedding space.

3 Experiment

We probe knowledge and error signals in six large language models (three general-purpose models and their biomedical adaptations) across three datasets.

Language Models. We compare three open-source bases, Gemma-2-9B [17], Llama-3-8B [13], and MISTRAL-7B-INSTRUCT-V0.1 [12], with their corresponding biomedical variants (Meditron3-Gemma2-9B [18], MMed-Llama-3-8B [19], and BioMistral-7B [14]). This pairing isolates the effect of medical finetuning, which may not reliably improve recall or reduce hallucinations [2, 1].

Datasets and Prompts. We employ three relation-based datasets. The first is MedLAMA, which contains UMLS triples from Meng et al. [20] to probe general knowledge; we mark triples with fewer than ten PubMed co-occurrences as long-tail, following Kandpal et al. [8] and Yi et al. [9]. The second is a set of drug–symptom pairs from Berkowitz et al. [21] comprising 165 positive controls and 234 negative controls to assess pharmacovigilance. The third is a collection of drug–drug interactions extracted from SemMedDB [22]. For each relation (for example, "may treat"), we define a simple template such as "[X] might treat [Y]" to prompt the models, and Appendix 1 provides the full list.

Evaluation Metric. We evaluate how well the model accesses stored knowledge using Accuracy@K metrics (Acc@1, Acc@5, Acc@10). For each triple $\langle s, r, o \rangle$, we query the model with a relation template and compute Acc@10 as the fraction of cases where the gold object o appears among the top-10 predictions. For error detection, we label a prediction correct if the top-ranked object matches o and incorrect otherwise, train lightweight probes on hidden states to predict correctness, and report F1 scores, with labels following the missing-from-top-10 criterion [20]. To locate where knowledge becomes accessible, we truncate the model at layers $L \in 10, \ldots, 25$, extract residual streams at the final subject token, train probes at each layer, and identify the optimal depth that maximizes validation performance. Finally, we detect retrieval failures—cases where the model internally encodes the

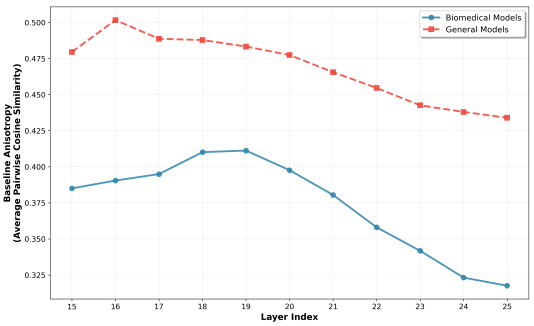

Figure 2: Baseline anisotropy across layers. General models (red) show higher anisotropy. Biomedical models (blue) are more isotropic. Lower anisotropy coincides with more volatile error-detection signals.

correct knowledge but fails to produce it among the top-10 predictions—by training a probe to predict such failures and reporting F1 scores.

Experiment Results. Figure 1 reports layer-wise curves. Mean internal and external $\mathrm{Acc@10}$ are comparably low for the general and biomedical models, indicating that finetuning does not add or remove probe-accessible knowledge. The key difference is stability: the biomedical model exhibits substantially larger layer-to-layer variance in error-detector F1, especially in deeper layers (Table 2; e.g., circular probes $\mathrm{SD} = 0.053$ vs. 0.027).

To explain this variability, we analyze representation geometry. Following Ethayarajh [23], we compute the cosine similarity between random directions and layer-averaged representations and use the resulting baseline as an anisotropy score. The general model is more anisotropic (0.608) than the biomedical model (0.354). Intuitively, higher anisotropy concentrates activations along a few dominant directions, yielding more consistent, linearly separable probe directions across layers. Lower anisotropy (i.e., greater isotropy) disperses activations, which makes the induced error signals noisier and less stable over depth. Taken together, these results support a causal interpretation: reduced anisotropy can drive greater across-layer variation in both error detection and prediction. This, in turn, suggests that finetuning primarily reorganizes, rather than expands, probe-accessible knowledge, and that such reorganization may undermine self-monitoring robustness, in line with reports that certain finetuning regimes exacerbate hallucinations.

4 Limitations and Conclusion

Our results show that general-purpose and biomedical LLMs contain similar amounts of probe-accessible knowledge, but their internal error-detection signals differ sharply in stability: across circular, logistic, and MLP probes, the biomedical model has nearly twice the across-layer standard deviation in error-detector F1 compared to the general model (Table 2). An isotropy analysis indicates a plausible mechanism: domain-specific fine-tuning reduces anisotropy, yielding more isotropic representations that are less amenable to simple linear separation of correct vs. incorrect states. Practically, this implies that fine-tuning reorganizes internal geometry without adding new knowledge and can make self-monitoring less reliable, consistent with reports that instruction tuning increases hallucination rates [1, 2]. As a simple diagnostic, we propose measuring the variability of internal error-detection signals to assess robustness. More broadly, our unified probing and error-detection framework links mechanistic interpretability to safety: by extracting both predicted and ground-truth objects from hidden states, lightweight probes act as oracles that anticipate hallucinations and, when plugged into re-prompting or abstention pipelines, improve reliability with minimal overhead. Although we focus on biomedical facts, the approach generalizes to other domains with long-tail knowledge and high-stakes decisions. Future work should study cross-model prediction [24], explore unsupervised clustering for richer error signals, and test whether stronger probes or representation editing can mitigate the variability introduced by domain-specific fine-tuning.

References

[1] Z. Gekhman, G. Yona, R. Aharoni, M. Eyal, A. Feder, R. Reichart & J. Herzig. "Does Fine-Tuning LLMs on New Knowledge Encourage Hallucinations?" In: *Proceedings of the 2024 Conference on Empirical Methods in Natural Language Processing*(. 2024), pp. 7765–7784.

[2] D. Jeong, S. Garg, Z. C. Lipton & M. Oberst. "Medical Adaptation of Large Language and Vision-Language Models: Are We Making Progress?" In: *Proceedings of the 2024 Conference on Empirical Methods in Natural Language Processing*(. 2024), pp. 12143–12170.

[3] Z. Gekhman, E. B. David, H. Orgad, E. Ofek, Y. Belinkov, I. Szpektor, J. Herzig & R. Reichart. "Inside-out: Hidden factual knowledge in llms". In: *arXiv preprint arXiv:2503.15299* ((2025)).

[4] H. Orgad, M. Toker, Z. Gekhman, R. Reichart, I. Szpektor, H. Kotek & Y. Belinkov. "LLMs Know More Than They Show: On the Intrinsic Representation of LLM Hallucinations". In: *The Thirteenth International Conference on Learning Representations*.

[5] A. Azaria & T. Mitchell. "The Internal State of an LLM Knows When It's Lying". In: *Findings of the Association for Computational Linguistics: EMNLP 2023*(. 2023), pp. 967–976.

[6] Y. Sun, A. Stolfo & M. Sachan. "Probing for Arithmetic Errors in Language Models". In: *arXiv preprint arXiv:2507.12379* ((2025)).

[7] S. Marks & M. Tegmark. "The Geometry of Truth: Emergent Linear Structure in Large Language Model Representations of True/False Datasets". In: *First Conference on Language Modeling*.

[8] N. Kandpal, H. Deng, A. Roberts, E. Wallace & C. Raffel. "Large language models struggle to learn long-tail knowledge". In: *Proceedings of the 40th International Conference on Machine Learning*(. 2023), pp. 15696–15707.

[9] X. Yi, J. Lever, K. Bryson & Z. Meng. "Can We Edit LLMs for Long-Tail Biomedical Knowledge?" In: *arXiv preprint arXiv:2504.10421* ((2025)).

[10] S. Pandit, J. Xu, J. Hong, Z. Wang, T. Chen, K. Xu & Y. Ding. "Medhallu: A comprehensive benchmark for detecting medical hallucinations in large language models". In: *arXiv preprint arXiv:2502.14302* ((2025)).

[11] A. Shrivastava & A. Holtzman. "Linearly Decoding Refused Knowledge in Aligned Language Models". In: *arXiv preprint arXiv:2507.00239* ((2025)).

[12] A. Q. Jiang et al. *Mistral 7B*(. 2023). arXiv: 2310.06825 [cs.CL]. URL: https://arxiv.org/abs/2310.06825.

[13] Meta AI. *Introducing Meta Llama 3: The most capable openly available LLM to date*. https://ai.meta.com/blog/meta-llama-3/. Accessed: 2025-08-21(. 2024).

[14] Y. Labrak, A. Bazoge, E. Morin, P.-a. Gourraud, M. Rouvier & R. Dufour. "BioMistral: A Collection of Open-Source Pretrained Large Language Models for Medical Domains". In: *62th Annual Meeting of the Association for Computational Linguistics (ACL'24)*(. 2024).

[15] M. S. Ankit Pal. *OpenBioLLMs: Advancing Open-Source Large Language Models for Healthcare and Life Sciences*. https://huggingface.co/aaditya/OpenBioLLM-Llama3-70B(. 2024).

[16] M. Beigi, Y. Shen, R. Yang, Z. Lin, Q. Wang, A. Mohan, J. He, M. Jin, C.-T. Lu & L. Huang. "InternalInspector I2: Robust Confidence Estimation in LLMs through Internal States". In: *Findings of the Association for Computational Linguistics: EMNLP 2024*(. 2024), pp. 12847–12865.

[17] G. Team, M. Riviere, S. Pathak, P. G. Sessa, C. Hardin, S. Bhupatiraju, L. Hussenot, T. Mesnard, B. Shahriari, A. Ramé, et al. "Gemma 2: Improving open language models at a practical size". In: *arXiv preprint arXiv:2408.00118* ((2024)).

[18] OpenMeditron Initiative. *Meditron-3 (Gemma2-9B): A Clinical Medicine–Specialized LLM*. https://huggingface.co/OpenMeditron/Meditron3-Gemma2-9B. Model Card; fine-tuned from google/gemma-2-9b(. 2025).

[19] P. Qiu, C. Wu, X. Zhang, W. Lin, H. Wang, Y. Zhang, Y. Wang & W. Xie. *Towards Building Multilingual Language Model for Medicine*(. 2024). arXiv: 2402.13963 [cs.CL].

[20] Z. Meng, F. Liu, E. Shareghi, Y. Su, C. Collins & N. Collier. "Rewire-then-Probe: A Contrastive Recipe for Probing Biomedical Knowledge of Pre-trained Language Models". In: *Proceedings of the 60th Annual Meeting of the Association for Computational Linguistics (Volume 1: Long Papers)*(. 2022), pp. 4798–4810.

[21] J. Berkowitz, D. Weissenbacher, A. Srinivasan, N. A. Friedrich, J. M. A. Cortina, S. Kivelson, G. G. Hernandez & N. P. Tatonetti. "Probing Large Language Model Hidden States for Adverse Drug Reaction Knowledge". In: *International Conference on Artificial Intelligence in Medicine*. Springer(. 2025), pp. 55–64.

[22] H. Kilicoglu, D. Shin, M. Fiszman, G. Rosemblat & T. C. Rindflesch. "SemMedDB: a PubMed-scale repository of biomedical semantic predications". In: *Bioinformatics* 28.23 ((2012)), pp. 3158–3160.

[23] K. Ethayarajh. "How Contextual are Contextualized Word Representations? Comparing the Geometry of BERT, ELMo, and GPT-2 Embeddings". In: *Proceedings of the 2019 Conference on Empirical Methods in Natural Language Processing and the 9th International Joint Conference on Natural Language Processing (EMNLP-IJCNLP)*(. 2019), pp. 55–65.

[24] J. Gallifant, S. Chen, K. Sasse, H. Aerts, T. Hartvigsen & D. S. Bitterman. "Sparse autoencoder features for classifications and transferability". In: *arXiv preprint arXiv:2502.11367* ((2025)).

[25] D. Chanin, A. Hunter & O.-M. Camburu. "Identifying Linear Relational Concepts in Large Language Models". In: *Proceedings of the 2024 Conference of the North American Chapter of the Association for Computational Linguistics: Human Language Technologies (Volume 1: Long Papers)*(. 2024), pp. 1524–1535.

A Related Work

Long-Tail Biomedical Knowledge Biomedical knowledge exhibits a long-tailed distribution: many subject–object pairs appear in only a few training documents. LLMs' ability to answer fact-based questions correlates strongly with the number of documents containing the subject and object [8]. Kandpal et al. [8] demonstrated that even very large models struggle to learn rare facts and require orders of magnitude more parameters to match performance on questions with little pre-training support. Knowledge editing can inject rare facts into LLMs, but Yi et al. [9] found that edited models still perform worse on long-tail biomedical knowledge than on high-frequency knowledge and that one-to-many relations limit the effectiveness of editing. Our evaluation therefore stratifies probes by knowledge popularity to assess whether internal error signals differ between common and rare facts.

Mechanistic Interpretability Mechanistic interpretability (MI) aims to identify and understand the circuits and directions in neural networks that implement high-level functions. Studies have shown that hidden activations encode truthfulness signals that can be isolated by linear probes [7]. The linear classifiers on hidden activations can detect when a language model is lying [5] and that concept directions found via linear relational embeddings can causally steer model outputs [25]. Our work builds on these insights by applying MI tools to domain-adapted biomedical models and analyzing how fine-tuning affects the geometry of internal representations.

Error Detection in LLMs Detecting hallucinations is essential for trustworthy deployment. Azaria & Mitchell [5] trained a classifier on hidden activations to distinguish true from false statements and demonstrated that internal states provide more reliable confidence estimates than softmax probabilities. Many subsequent works explore probability-based or consistency-based detectors, but general-purpose LLMs still struggle on medical hallucination benchmarks. The MedHallu dataset showed that even GPT-4o achieves only moderate F1 scores and that hallucinations close to the truth are hardest to detect [10]. Our probes build on this literature by comparing logistic, circular, and MLP probes for binary error detection and by analyzing how probe performance varies across domains and layers.

B Experiments Compute Resources

All experiments were conducted on 4 NVIDIA H100 GPUs. Probe training and evaluation completed within approximately one day of wall-clock time.

C Prompt Templates and Layerwise Stability

This appendix documents (i) the minimal natural-language templates we use to render (s, r, o) tuples into prompts for extracting layer representations $\mathbf{x}\ell$, and (ii) the layerwise stability of three probe

Relation	Manual Prompt
may treat	[X] might treat [Y].
may prevent	[X] might prevent [Y].
adverse drug effect	The adverse effect of [X] is [Y].
interacts with	The [X] interacts with [Y].

Table 1: Templates $T(s, r)$ used to elicit $\mathbf{x}_l$. Here [X] is the subject s and [Y] is the object o.

Probe	Metric	Bio s.d.	Gen s.d.	Ratio
Circular	Acc@10	0.00730	0.00796	0.917
Circular	External_Acc@10	0.00441	0.00553	0.797
Circular	F1 (err. det.)	0.05287	0.02725	**1.940**
Logistic	Acc@10	0.00959	0.01311	0.732
Logistic	External_Acc@10	0.00460	0.00295	1.561
Logistic	F1 (err. det.)	0.00504	0.00353	**1.427**
MLP	Acc@10	0.00727	0.00477	1.526
MLP	External_Acc@10	0.00268	0.00473	0.567
MLP	F1 (err. det.)	0.01994	0.01292	**1.543**

Table 2: Across-layer standard deviations (s.d.) of probe metrics. Bio = biomedical model; Gen = general model. Larger s.d. indicates less stability across layers.

families. In Table 1, `[X]` is the subject s and `[Y]` is the object o; instantiating $T(s, r)$ yields the input from which we read $\mathbf{x}\ell$. Table 2 reports the standard deviation across layers for each metric; larger values indicate less stable signals over depth. Notably, error-detection F1 varies substantially more in the biomedical model.

D Additional Layer-wise Results by Co-occurrence

We stratify (s, o) pairs by corpus co-occurrence into four buckets (low to high frequency): ≤ 10, $(10, 100]$, $(100, 1000]$, and > 1000. For each bucket we plot layer-wise probe accuracy on internal and external knowledge (left/center) and error-detector F1 (right) for circular, logistic, and MLP probes. Across buckets, knowledge readout remains low while error detection strengthens with depth; the biomedical model shows consistently higher across-layer variability, especially in later layers.

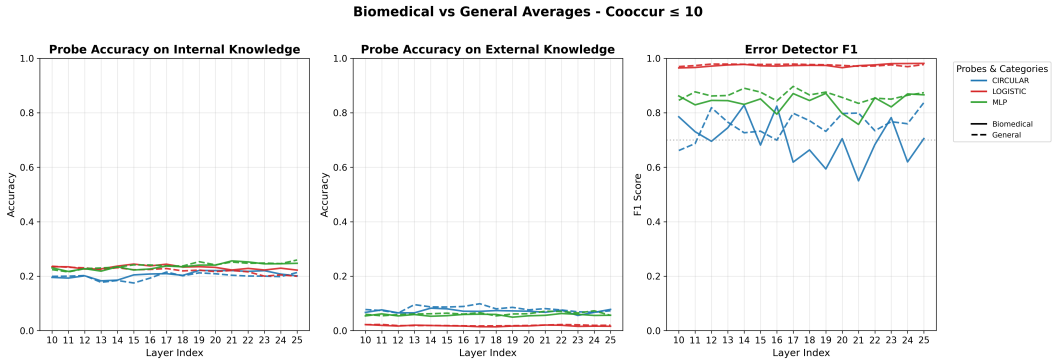

Figure 3: Layer-wise probe performance for low-frequency pairs (**co-occurrence** ≤ 10). Error detection is strong in deeper layers, with notably higher variability for the biomedical model (solid)

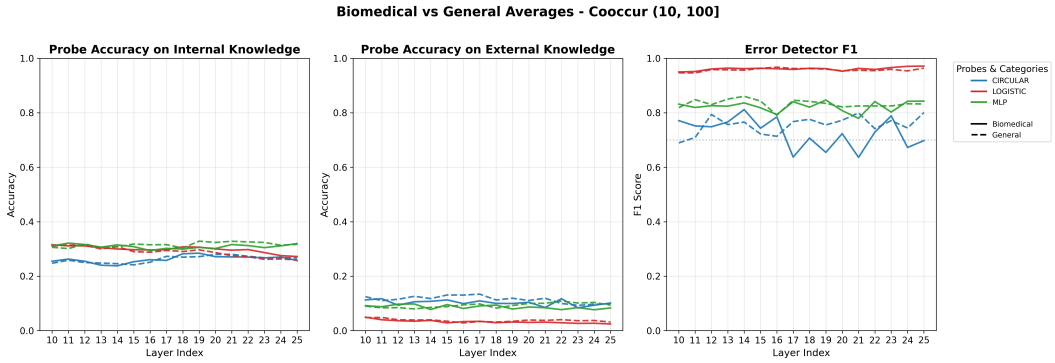

Figure 4: Layer-wise probe performance for **(10, 100]** co-occurrence. The stability gap persists:

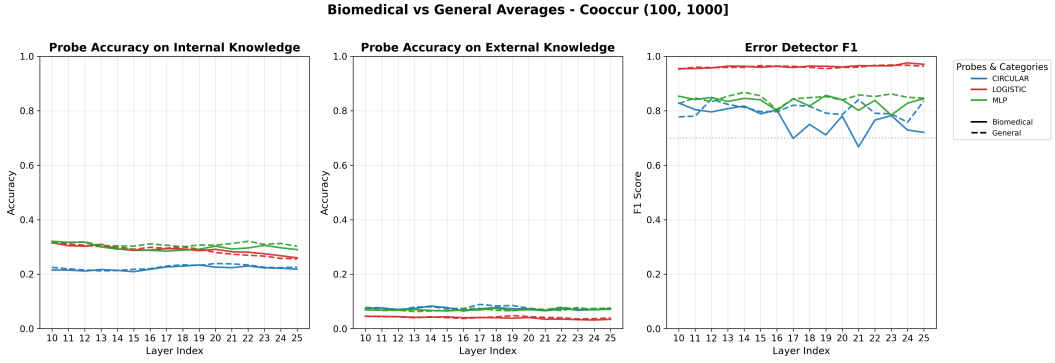

Figure 5: Layer-wise probe performance for **(100, 1000]** co-occurrence. General model (dashed)

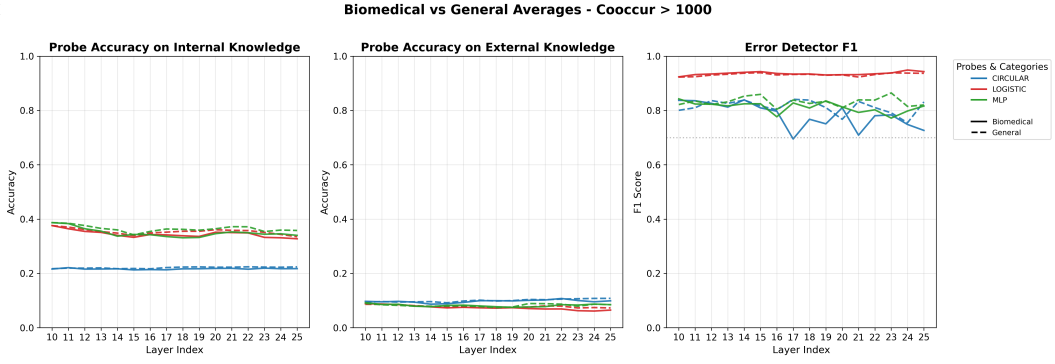

Figure 6: Layer-wise probe performance for high-frequency pairs (**co-occurrence** >1000). Trends hold with slightly smoother curves; biomedical error-detection variability remains elevated at later layers.

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