THE FLAW OF AVERAGES: QUANTIFYING UNIFORMITY OF PERFORMANCE ON BENCHMARKS

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ABSTRACT

Benchmarks shape scientific conclusions about model capabilities and steer model development. This creates a feedback loop: stronger benchmarks drive better models, and better models demand more discriminative benchmarks. Ensuring benchmark reliability is therefore essential for trustworthy evaluation and meaningful progress. In this work, we study benchmark reliability from a *distributional* perspective and introduce benchmark HARMONY, which measures *how uniformly a model's performance is distributed across the subdomains of a benchmark*. We posit that high HARMONY is a desirable benchmark property, indicating that the aggregate metric reflects uniform competence across subdomains. Across 19 multiple-choice benchmarks and five model families, we map each benchmark onto a mean-variance plane of HARMONY computed across models, where high mean and low variance signal more reliable evaluation. Our analysis shows that less harmonious benchmarks can give misleading results, since overall accuracy may be disproportionately influenced by specific subdomains. For instance, *ARC-Easy* is overwhelmed by questions on *Biological Concepts*, overshadowing other critical subdomains such as Geography, Physics, Chemistry, and Environmental Science. By recommending that HARMONY should be reported alongside accuracy, we reframe evaluation from simple performance averages to a more robust, distributionally reliable measurement of performance.

1 INTRODUCTION

Benchmarks lie at the crux of measuring and shaping scientific progress in language models, forming a feedback loop with model development. Discriminative benchmarks refine learning signals and guide model design, while stronger models expose benchmark limitations and drive the creation of more rigorous evaluations. In this reciprocal process, benchmark reliability is essential to ensure that reported improvements reflect genuine capabilities rather than evaluation artifacts (Ott et al., 2022). Yet, despite its importance, benchmark auditing (Swayamdipta et al., 2020; D'Amour et al., 2020; Sainz et al., 2023) has received far less attention than algorithmic advances (Brown et al., 2020; Ouyang et al., 2022; DeepSeek-AI et al., 2025).

Motivated by this gap, recent work identifies structural issues in widely used benchmarks, such as redundancy (Polo et al., 2024; Perlitz et al., 2024b) and uneven data distributions (Huang et al., 2025), that can skew results and mislead interpretations of model capability (Ruan et al., 2024; Ilić & Gignac, 2024). In response, the research community *interrogates the reliability of already-existing benchmarks*, in addition to proposing new ones. Rather than treating benchmark gains as definitive, recent work urges caution about what benchmarks truly measure and how these measurements are obtained (Singh et al., 2025; Heineman et al., 2025). This reframes evaluation as an ongoing measurement challenge, highlighting the need for benchmarks whose properties and limitations are understood well.

In our work, we investigate benchmark reliability from a distributional perspective. Since benchmarks claim to assess competence over a stated domain, we ask whether their data evenly represents its subdomains and whether performance is uniform on these subdomains. We instantiate this idea with benchmark HARMONY, a measurement of performance uniformity among subdomains of a benchmark (§2). Figure 1 illustrates our pipeline: Given a target benchmark, we first partition the datapoints in this benchmark into semantic clusters, where each cluster represents a subdomain (Step

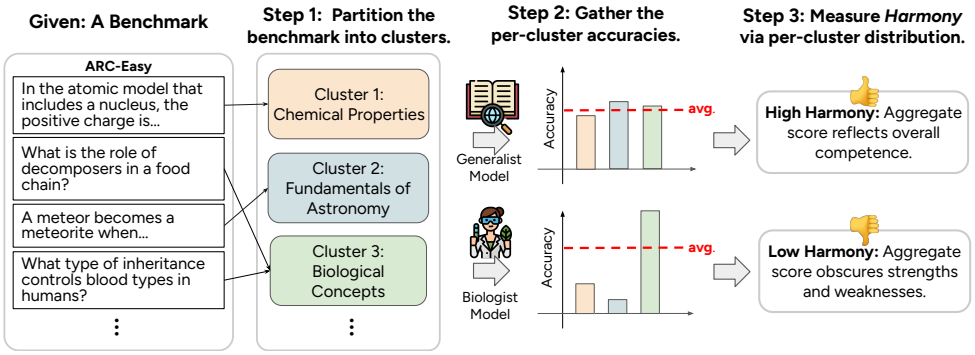

Figure 1: Pipeline of evaluating HARMONY for a given benchmark. Step 1: We partition the benchmark into semantic clusters, where each cluster represents a subdomain. Step 2: We gather each model's performance on every cluster. Step 3: We calculate the harmony — the uniformity of the distribution of performance across subdomains. We posit that high HARMONY implies that aggregate metrics capture broad competence, whereas low HARMONY obscures strengths and weaknesses.

1); we then gather the performances per subdomain for different models (Step 2); finally, we compute HARMONY for each benchmark-model pair, where high HARMONY suggests that aggregate metrics capture broad competence, while low HARMONY obscures strengths and weaknesses of the model (Step 3).

Using HARMONY, we conduct a range of analyses on a variety of benchmarks and models to assess the reliability of benchmark evaluations (§3, §4). Here we showcase one result: Figure 2 plots the mean and variance of HARMONY across 36 different models for 18 commonly used Multiple-Choice Question Answering benchmarks. We posit that high HARMONY with low variance is a desirable benchmark property, since it implies that the benchmark reflects overall competence consistently for different models. In summary, our contributions are twofold:

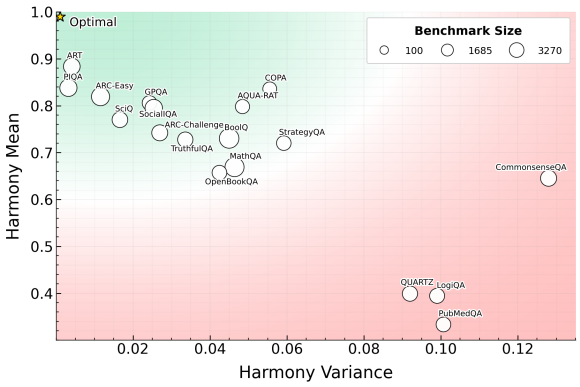

Figure 2: Plot of the mean and variance of HARMONY across 36 models on 18 MCQA benchmarks. A higher mean indicates benchmark scores are more evenly distributed across subdomains, while a lower variance shows this uniformity is consistent across models. Benchmarks with both high mean and low variance are thus more reliable and informative for evaluation.

- We propose a distributional view of benchmark reliability and introduce HARMONY, an entropy-based metric that quantifies how uniformly performance is distributed across subdomains in a benchmark.
- We provide a large-scale empirical mapping of 19 MCQA benchmarks across five model families in the HARMONY mean-variance plane, revealing the spectrum of benchmark reliability.

2 BENCHMARK HARMONY

2.1 PRELIMINARIES AND NOTATION

Let $\mathcal{B} = \{(x_i, y_i)\}_{i=1}^{N}$ be a benchmark consisting of input-output pairs (x, y). Our goal is to understand the *underlying distribution* of $\mathcal{B}$ by inducing a semantic partition $\mathcal{G} = \{A_1, \ldots, A_k\}$ of $\mathcal{B}$, where $A_i \subseteq \mathcal{B}$, $A_i \cap A_j = \emptyset$ for $i \neq j$, and $\bigcup_{i=1}^{k} A_i = \mathcal{B}$. The partition is guided by a similarity function $\mathcal{S} : \mathcal{X} \times \mathcal{X} \to (0, 1]$ that measures the semantic similarity between data points $x_i, x_j \sim \mathcal{B}$. Lastly, let f be a model and let $\Psi(f; A_i)$ denote a measure of performance (e.g., accuracy) for f computed on a subset $A_i \subseteq \mathcal{B}$.

2.2 HARMONY: A MEASURE OF BALANCED COVERAGE AND UNIFORM PERFORMANCE

Intuition. Consider a biology benchmark spanning microbiology, animal biology, and plant biology. If microbiology dominates and a model excels only there, the overall score may misleadingly suggest broad competence in biology. Conversely, if microbiology is underrepresented and the model is weak on it but strong elsewhere, the aggregate evaluation may conceal a critical weakness. Moreover, even when subdomains are equal in size, large accuracy gaps make the aggregate metric uninformative (e.g., 90% accuracy in microbiology and 50% accuracy in plant biology averages to a number that reflects neither). A *harmonious* benchmark therefore mitigates these distortions by balancing coverage and promoting comparable performance across subdomains.

Formal definition of HARMONY. Given a partition $\mathcal{G}_f = \{A_i\}_{i=1}^k$, HARMONY measures how uniformly performance is distributed across the subsets in this partition. For each A_i, let $w_i = \frac{|A_i|}{|\mathcal{B}|}$ be the size weight and let $\mu = \sum_{i=1}^k w_i \Psi(f; A_i)$ be the weighted mean. We convert differences between μ and $\Psi(f; A_i)$ into smooth proximity scores via a Gaussian kernel:

$$K_i \;=\; \exp\Big(-\big(\tfrac{\Psi(f;A_i)-\mu}{b}\big)^2\Big),$$

where $b > 0$ is a bandwidth parameter.[1] We then form *performance masses*

$$p_i \;=\; \frac{w_i K_i}{\sum_{j=1}^k w_j K_j}, \qquad \sum_{i=1}^k p_i = 1,$$

and compute the HARMONY (normalized Shannon entropy)

$$H(\mathcal{G}_f) \;=\; -\frac{1}{\log k}\sum_{i=1}^k p_i \log\big(p_i + \varepsilon\big) \in [0,1],$$

with a small $\varepsilon = 10^{-12}$ for numerical stability.

Subsets with accuracies far from μ receive exponentially smaller p_i, lowering entropy. Thus, higher HARMONY $H(\mathcal{G}_f)$ indicates performance that is evenly distributed across subsets, while lower HARMONY captures a more concentrated performance in a few subsets. Therefore, HARMONY quantifies the uniformity of performance while considering the distributional balance.

Interpreting HARMONY. Let Π be a partitioning rule that maps a benchmark $\mathcal{B}$ and a model f to a partition $\mathcal{G}_f(\mathcal{B}) = \Pi(\mathcal{B}; f)$ using $\mathcal{S}$. Then, define the per-model harmony of $\mathcal{B}$ as

$$H_{\mathcal{B}}(f) \;:=\; H\big(\mathcal{G}_f(\mathcal{B})\big) \in [0,1].$$

Given a model set $\mathcal{F}$, we evaluate $\mathcal{B}$ by the cross-model mean and variance

$$\mu_H(\mathcal{B}) \;=\; \mathbb{E}_{f\sim\mathcal{F}}[H_{\mathcal{B}}(f)]\,, \qquad \sigma_H^2(\mathcal{B}) \;=\; \mathrm{Var}_{f\sim\mathcal{F}}(H_{\mathcal{B}}(f))\,. \tag{1}$$

Higher $\mu_H(\mathcal{B})$ indicates that, on average across models, performance is more uniformly distributed across the subsets of $\mathcal{B}$, while lower $\sigma_H^2(\mathcal{B})$ indicates that this property is stable across models. Rather than dichotomizing benchmarks as *good* or *bad*, we adopt a comparative view, where $\mathcal{B}_1$ is preferred to $\mathcal{B}_2$ if it attains a higher expectation and a lower variance.

Implications. We approach benchmarks as diagnostic tools rather than scoreboards. A benchmark with *high mean* HARMONY and *low cross-model variance* indicates that aggregate metrics consistently capture broad competence rather than artifacts of data composition. In contrast, either *low mean* or *large variance* signals fragility, since the conclusions about model evaluation may depend excessively on a few subdomains and be less reliable. Notably, models with similar aggregate accuracy can differ in HARMONY, implying different breadth of competence. In practice, benchmarks with favorable mean-variance HARMONY profiles enable more trustworthy evaluation, fairer comparisons, and clearer measure of progress.

[1] We set b by a robust scale of $\{\Psi(f; A_i)\}$. Let $\tilde{a} = \mathrm{median}_i\, \Psi(f; A_i)$ and $\mathrm{MAD} = \mathrm{median}_i |\Psi(f; A_i) - \tilde{a}|$, then $b = \max\{0.02,\ 1.4826 \cdot \mathrm{MAD}\}$.

2.3 PARTITION INDUCTION

To compute HARMONY, we require a semantic partition of the benchmark. To this end, we introduce a novel similarity metric named **predictive similarity**, a model-aware similarity between data points based on the divergence of their probability distributions, and induce $\mathcal{G}_f$ via spectral clustering on the resulting affinity matrix $\mathcal{S}$.

Predictive Similarity. We define predictive similarity as a model-aware similarity measure that quantifies how similarly a model f distributes probability over the output space for two data points. For $x_i, x_j \sim \mathcal{B}$, let $\bar{p}_f(x)$ denote the model's length-normalized probability distribution over tokens. Then, predictive similarity is computed as

$$S(x_i, x_j) \;=\; \exp\!\left(-\tfrac{\tau}{2}\Big[D_{\mathrm{KL}}\big(\bar{p}_f(x_i)\,\|\,\bar{p}_f(x_j)\big) \;+\; D_{\mathrm{KL}}\big(\bar{p}_f(x_j)\,\|\,\bar{p}_f(x_i)\big)\Big]\right), \tag{2}$$

where $D_{\mathrm{KL}}(\cdot\,\|\,\cdot)$ denotes the Kullback–Leibler divergence, τ is a scaling factor chosen as the reciprocal of the median symmetric divergence, and the averaged predictive distribution is given by $\bar{p}_f(x_i) \;=\; \frac{1}{T}\sum_{t=1}^{T} p_f(x_i, y_i^{<t})$, with $y_i^{<t}$ denoting the ground-truth prefix up to token $t-1$.[2]

Intuitively, predictive similarity S is large when the model treats x_i and x_j as interchangeable from a predictive standpoint and small when the model sharply distinguishes them. We defer in-depth discussion on different aspects of predictive similarity to Appendix B.

Clustering. Given the predictive similarity matrix $S \in (0,1]^{N\times N}$, we induce the partition of a benchmark via spectral clustering (Ng et al., 2001). We treat S as a precomputed affinity, form the symmetric normalized Laplacian $L \;=\; D^{-1/2}(D-S)D^{-1/2}$ with $D \;=\; \mathrm{diag}(S\mathbf{1})$, compute the k eigenvectors of L associated with its smallest eigenvalues, and apply k-means in this spectral embedding to obtain a partition $\mathcal{G} = \{A_1, \ldots, A_k\}$. To determine the optimal number of subsets, we sweep $2 \le k \le 20$ and select the value maximizing the silhouette score $s(k) \in [-1, 1]$ as an intrinsic compactness diagnostic (Rousseeuw, 1987).

2.4 EMPIRICAL VALIDATION OF PARTITION INDUCTION

We need a controlled benchmark with a known partition to evaluate our method's ability to induce well-defined semantic partitions. We therefore introduce RedundantQA, a synthetic, four-domain[3] MCQA benchmark where each item pairs a reference question with two *true-similar* paraphrases (same underlying knowledge) and two *false-similar* distractors (high lexical overlap, different answers). This structure cleanly separates semantic from lexical similarity and allows us to control underlying data distribution. See Appendix A for construction and validation details of RedundantQA, along with representative examples.

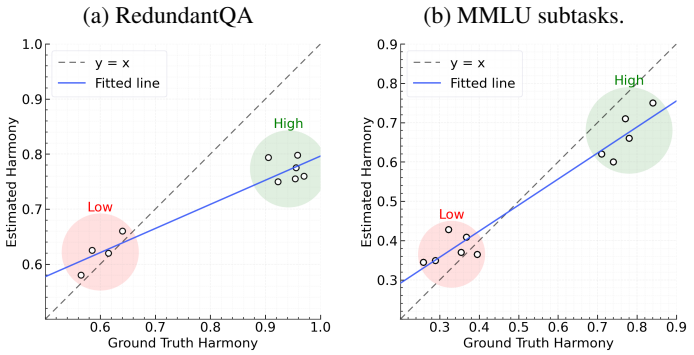

Figure 3: Validation of our approach on (a) RedundantQA and (b) MMLU high school subtasks. Estimated HARMONY strongly correlates with the ground truth and clearly separates low from high HARMONY variants. Each dot represents one variant averaged across five random seeds.

[2]For $t > 1$, we condition on the ground-truth answer tokens rather than on the model's own autoregressive predictions, ensuring that accumulated model errors do not affect the similarity measure.

[3]Biology, History, Economics, Popular Culture.

We empirically validate our partitioning approach on controlled variants of RedundantQA and a compilation of MMLU high school subtasks.[4] In each variant, we designate a domain as dominant and assign it a proportion $r \in \{0.3, 0.4, 0.5, 0.6, 0.7\}$ of the benchmark, with the remaining domains sharing $1 - r$ equally. This yields a spectrum of distributional imbalance with known ground-truth HARMONY. We repeat every $(\text{dominant domain}, \text{ratio})$ variant with five random seeds.

As shown in Fig. 3, HARMONY estimated by our method exhibits a strong positive correlation with the ground-truth HARMONY. This alignment demonstrates that our measure reliably distinguishes between high HARMONY and low HARMONY regimes across different degrees of imbalance. Importantly, the trend persists across different (dominant domain, ratio) variants, indicating that the signal is robust to variations in benchmark construction.

We further validate predictive similarity along three axes and defer all details and results to Appendix B: (i) discrimination of semantic vs. lexical similarity (App. B.2), (ii) recovery of ground-truth domains on RedundantQA and MMLU (App. B.3), and (iii) fidelity of HARMONY estimates under controlled distributional shifts (App. B.4).

3 MAIN ANALYSES: HOW HARMONIOUS ARE THE BENCHMARKS?

We now examine how harmonious widely used MCQA benchmarks are. Accordingly, we compute HARMONY for each model and benchmark pair (as detailed in §2) and then aggregate it across models to position each benchmark in the mean-variance plane given by $(\mu_H(\mathcal{B}), \sigma_H^2(\mathcal{B}))$ in Eq. 1. This section first details the experimental setup (§3.1), then maps each benchmark to this plane and provides an interpretation of this mapping (§3.2).

3.1 EXPERIMENTAL SETUP

We conduct evaluations using a modified version of `lm-evaluation-harness`[5], covering a wide range of model sizes across five prominent model families: `Llama 3` (Grattafiori & et al, 2024), `Qwen3` (Yang et al., 2025), `Gemma 3` (Team et al., 2025), `Phi-3` (Abdin et al., 2024), and `OLMo 2` (OLMo et al., 2025) (see App. C for full model list). Our setup spans 19 MCQA benchmarks that assess a broad range of model capabilities:

- **Reasoning**: ARC-Challenge (Clark et al., 2018), ARC-Easy (Clark et al., 2018), ART (Bhagavatula et al., 2020), BoolQ (Clark et al., 2019), CommonsenseQA (Talmor et al., 2018), COPA (Roemmele et al., 2011), LogiQA (Liu et al., 2020), PIQA (Bisk et al., 2020), QUARTZ (Tafjord et al., "2019"), SocialIQA (Sap et al., 2019a), StrategyQA (Geva et al., 2021).
- **Mathematical Problem-Solving**: AQUA-RAT (Ling et al., 2017), MathQA (Amini et al., 2019).
- **World Knowledge**: GPQA (Rein et al., 2023), MMLU (Hendrycks et al., 2020), OpenBookQA (Mihaylov et al., 2018a), PubMedQA (Jin et al., 2019), SciQ (Johannes Welbl, 2017).
- **Truthfulness**: TruthfulQA (Lin et al., 2021).

For evaluation, we use average token-level log-likelihood scoring over answer options as implemented in the harness, selecting the option with the highest average log-probability. We follow each benchmark's evaluation protocol as implemented in the harness, using zero-shot evaluation by default, and report accuracy. We focus on MCQA benchmarks because (i) the discrete label space $\mathcal{Y}$ yields unambiguous ground truth and exact accuracy,[6] and (ii) evaluation is automatic and does not rely on a judge, avoiding grading variance that is common in free-form scoring. However, we note that our methodology extends to free-response benchmarks given an appropriate evaluation metric.

3.2 MAPPING BENCHMARK HARMONY

We analyze the widely used benchmarks from §3.1 with HARMONY, placing each benchmark in a two dimensional plane whose axes are the mean and variance of HARMONY across our model suite.

[4] Biology, Geography, European History, Computer Science.

[5] https://github.com/EleutherAI/lm-evaluation-harness

[6] In free-response settings, multiple plausible intermediate steps can lead to the same answer, complicating ground truth.

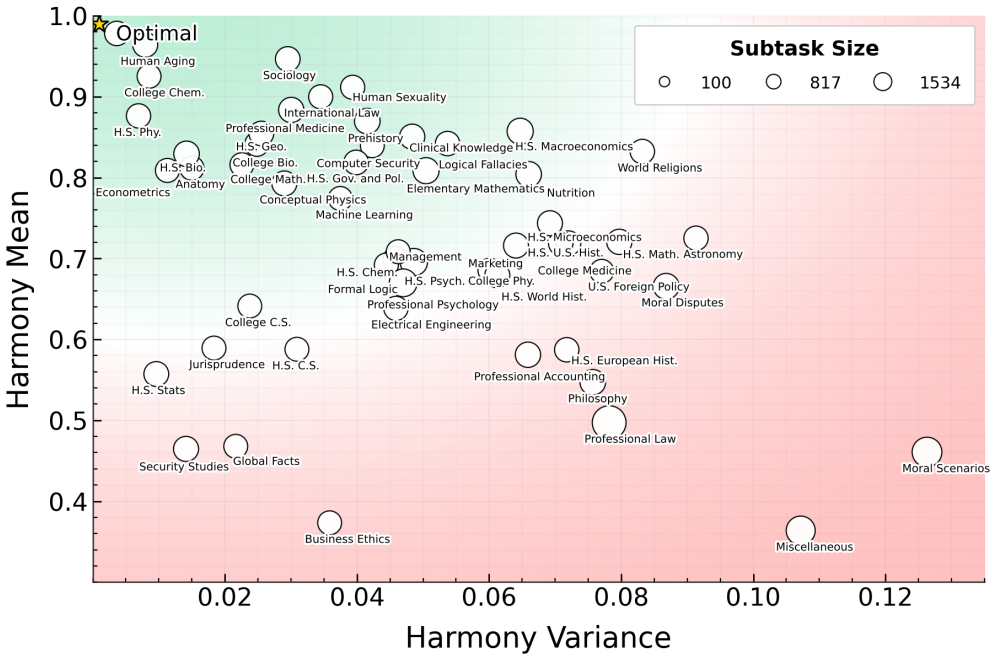

Figure 4: **The mean-variance plane for HARMONY across MMLU subtasks.** Each point represents an MMLU subtask, plotted by the HARMONY mean ($\mu_H(\mathcal{B})$) and variance ($\sigma^2_H(\mathcal{B})$) over 36 different models. Upper-left (high mean, low variance) indicates higher *benchmark reliability* (i.e., consistently balanced performance across subsets), while rightward (higher variance) and downward (lower mean) shifts signal diminished reliability. The star on the top left represents an optimal benchmark. Harmony mean and variance are defined in Eq. 1.

Fig. 2 and 4 respectively position benchmarks and MMLU subtasks in the cross-model mean-variance plane of HARMONY. The vertical axis is $\mu_H(\mathcal{B})$ (average uniformity of performance across subdomains) and the horizontal axis is $\sigma^2_H(\mathcal{B})$ (stability of that uniformity across models). Moving *upward* increases average distributional uniformity, while moving *leftward* increases cross-model stability. Consequently, the *upper-left* region (high mean, low variance) identifies benchmarks whose aggregate scores consistently reflect broad competence. In contrast, model performances on benchmarks with *low mean* are distributionally skewed on average. If accompanied by *low variance*, this skew is consistent across models (i.e., *consistently fragile*), whereas if accompanied by *high variance*, reliability becomes model-dependent. Thus, *upward* and *leftward* trajectories indicate more reliable evaluation, whereas *downward* and *rightward* shifts suggest more concentrated model performance on a few subdomains and conclusions that vary substantially across models.

4 CONTROLLED ANALYSES OF CONFOUNDING FACTORS

In this section, we (i) show how less harmonious benchmarks can distort model evaluations and (ii) examine whether low HARMONY benchmarks warrant extra caution for larger models or those trained with more tokens.

4.1 HOW DOES MODEL PERFORMANCE CHANGE WITH INCREASED HARMONY?

We analyze the extent to which less harmonious benchmarks can distort model evaluations via unrepresentative aggregate metrics. To this end, we prune benchmarks using predictive similarity to eliminate overly similar items. The pruning ratio is set to be inversely proportional to benchmark HARMONY, such that high HARMONY benchmarks receive minimal pruning while low HARMONY benchmarks are pruned more aggressively.[7] By mitigating the skewness, this procedure reveals models' uniform performance on benchmarks.

[7]Specifically, we use the formula $p = \text{clip}_{[0.05,0.5]}\big(0.05 + (0.5 - 0.05)\big(\frac{1-\text{clip}(H;0.1,1)}{1-0.1}\big)^{1.5}\big)$.

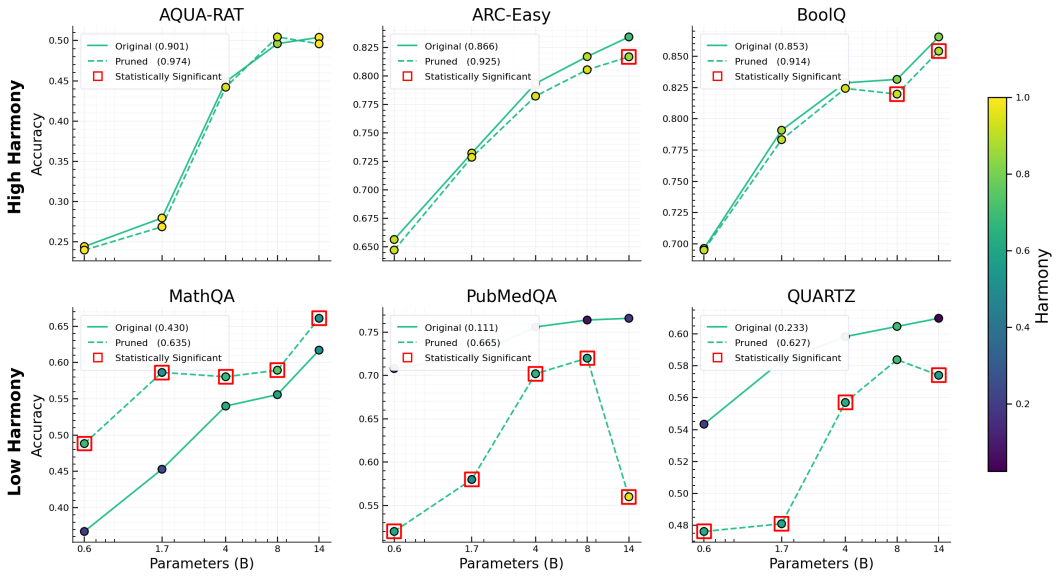

Figure 5: **Balancing benchmarks via pruning.** We remove overly similar items with a pruning rate inversely proportional to HARMONY. *Top row* shows more harmonious benchmarks, where accuracy remains stable as HARMONY increases. *Bottom row* shows less harmonious benchmarks, where HARMONY rises and accuracy shifts significantly.

As shown in Figure 5, model accuracies on high HARMONY benchmarks remain stable under pruning, with differences that are not statistically significant despite increased HARMONY. In contrast, low HARMONY benchmarks are fragile, where pruning notably improves HARMONY and aligns with statistically significant accuracy changes. Details of our significance tests appear in Appendix F. As HARMONY increases, per-subdomain accuracies tighten around the benchmark mean, making the aggregate a more faithful representation of the underlying accuracy distribution. Overall, low HARMONY benchmarks can be misleading as they skew aggregate scores, whereas high HARMONY benchmarks provide more reliable and representative evaluations.

While Figure 5 illustrates our findings for the Qwen3 family, we provide the comprehensive results for the full experimental setup in Appendix G.

4.2 How does Harmony change across model sizes and token budgets?

Given that low HARMONY signals fragility, we now ask whether this risk depends on model scale or training budget. We therefore seek to characterize how HARMONY scales with model parameters and pre-training budget. Rather than focusing on raw accuracy, our goal is to understand whether larger models or longer pre-training runs yield more uniform performance across subdomains. Concretely, we pose two questions. *Model size:* As parameter count increases within a family, does HARMONY steadily rise, indicating broader competence across subsets? *Token budget:* Along a fixed architecture, does increasing pre-training token budget improve HARMONY, suggesting a more even reallocation of accuracy on the benchmark?

Model parameters. We observe that the relationship between model parameter count and HARMONY is *family-specific* rather than universal. As shown in Fig. 6, within-family comparisons reveal a negative correlation for Qwen and Llama families, indicating that larger models in these families concentrate performance more on a few subdomains. In contrast, Gemma and OLMo families exhibit a positive correlation between model size and HARMONY, with larger models distributing accuracy more evenly across the subdomains in the benchmark. This suggests that parameter count alone is not a sufficient indicator of uniformity of the performance.

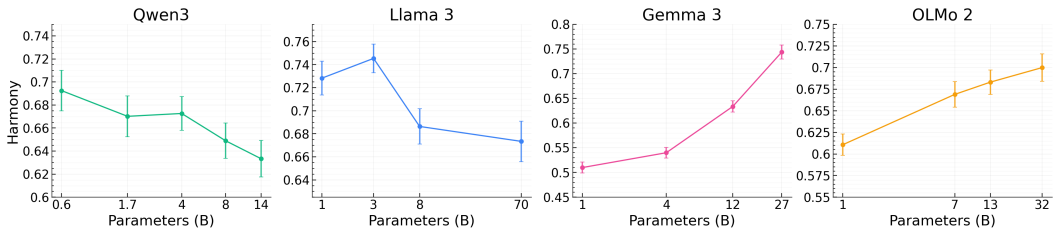

Figure 6: **Model size vs. HARMONY.** Scaling trends are *family-specific*: Qwen and Llama show negative correlations, while Gemma and OLMo show positive correlations (larger models perform more uniformly). Thus, parameter count alone is not predictive of performance uniformity.

Pre-training tokens. We examine how HARMONY evolves under a fixed architecture by tracking OLMo2 1B and OLMo2 7B across increased token budgets. As shown in Fig. 7, HARMONY dips early and then rises steadily, while aggregate accuracy increases minimally across checkpoints. Thus, we find that the distribution of performance improves (i.e., increased HARMONY) even as aggregate accuracy remains nearly unchanged. In other words, additional pre-training reallocates competence from a few dominant subdomains toward a more uniform spread, yielding a strictly more favorable accuracy profile without changing the aggregate score drastically.

In addition to HARMONY, we also formulate the uniformity of improvements that come with scaling and share our findings in Appendix E. We emphasize that these findings are empirical rather than causal. We leave modeling the mechanisms underlying these trends as valuable future work.

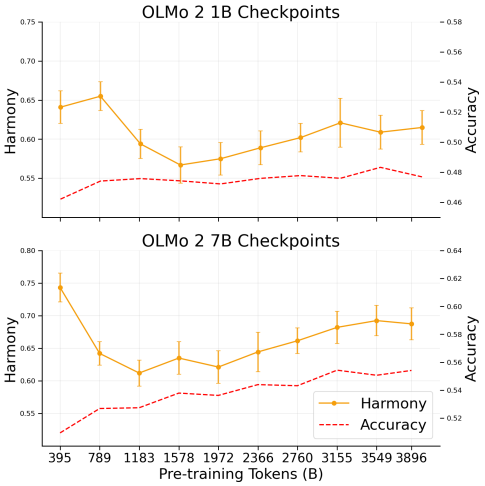

Figure 7: **Pre-training tokens vs. HARMONY.** For OLMo 2 1B/7B, HARMONY dips then steadily rises with more pre-training tokens while aggregate accuracy improves slightly, indicating competence shifts from dominant subsets toward greater uniformity.

5 RELATED WORK

Assessing Benchmark Reliability. Beyond proposing new tasks, a growing body of work interrogates the *reliability* of benchmarks themselves. A line of work targets the robustness of the test sets, focusing on building dynamic benchmarks to replace static benchmarks (Kiela et al., 2021; Chiang et al., 2024) and building adversarial perturbations to eliminate spurious cues present in static benchmarks (Nie et al., 2020; Croce et al., 2021). Closely related are concerns about overfitting to public test sets and contamination from pre-training corpora, which can inflate reported gains (Deng et al., 2024; Golchin & Surdeanu, 2024; Roberts et al., 2023; Dong et al., 2024). Barton (2025) analyzes a collection of benchmarks, showing that some benchmarks (e.g. Hellaswag (Zellers et al., 2019)) scale smoothly with increased scale and compute, while others (e.g. CommonsenseQA (Talmor et al., 2018)) do not. Another branch of literature audits data reliability and distributional coverage by introducing shifted test sets to probe generalization (Recht et al., 2019; Taori et al., 2020; Teney et al., 2020) and correcting pervasive label errors in widely used benchmarks (Northcutt et al., 2021; Gema et al., 2025). Beyond individual datasets, meta-evaluation work proposes frameworks and documentation practices to systematically assess benchmark design, provenance, and intended use (Reuel et al., 2024; Mazumder et al., 2023; Gebru et al., 2021). Another important topic is the external validity of benchmarks, such as how well leaderboard gains translate to real-world performance (Ott et al., 2022) and what reported scores actually measure (Dehghani et al., 2021; Singh et al., 2025). Finally, a complementary line of work separates signal from noise in benchmark results by quantifying variance and prescribing protocols that stabilize rankings in order to make comparative conclusions more reliable (Madaan et al., 2024; Wang et al., 2024a; Heineman et al., 2025). Advancing this field of work, we contribute a distributional perspective on benchmark reliability.

Rather than treating a benchmark evaluation as a single score, we model the benchmark as a mixture over the subdomains of the stated benchmark domain. We then measure how *performance mass* is distributed across these subdomains. This perspective diagnoses whether aggregate metrics reflect a broad competence over the benchmark or are dominated by certain subdomains.

Distributional Frameworks for Efficient Evaluation. Scaling laws of neural language models suggest that performance improves with model size (Kaplan et al., 2020), encouraging the development of increasingly larger and costlier models. Consequently, there has been growing interest in developing efficient evaluation methods that reduce computational and financial costs without compromising reliability. Perlitz et al. (2024a) introduce a reliability metric that dynamically adjusts compute by performance tier while preserving rank fidelity. Rodriguez et al. (2021) propose Item Response Theory (Tatsuoka et al., 1971) based leaderboards that jointly model difficulty and discrimination to identify examples that best differentiate model performance. Similarly, Polo et al. (2024) propose tinyBenchmarks, an efficient evaluation method that uses IRT to model the discriminative power of benchmark examples, allowing the selection of a small yet representative subset of items that can accurately estimate performance. Vivek et al. (2024) propose anchor point selection to identify small, representative subsets by leveraging cross-model correlations in instance-level predictions. Ethayarajh et al. (2022) identify informative data points via *usable information* (how much input a model family can exploit) extending Shannon information to account for model constraints. Notably, these works introduce distinct metrics such as IRT item parameters, cross-model instance correlations, and information-theoretic usable information to characterize the benchmark distribution and guide principled compression of benchmarks. Ultimately, these metrics enable targeted downsampling (e.g., selecting maximally discriminative or most informative items) that preserves rankings and reduces evaluation cost while maintaining coverage. In contrast, we do not seek cheaper evaluations. We instead assess whether a benchmark reliably measures its stated domain and, where it does not, we question the original evaluation rather than preserve it.

Prior work mainly 1) proposes new or dynamic tests, 2) compresses evaluation via discriminative selection, and 3) stabilizes leaderboards through variance control and guidelines. We instead audit *existing* benchmarks through a distributional lens, modeling a benchmark as a mixture over subdomains and measuring whether models spread accuracy uniformly. Unlike efficiency work that preserves overall scores while reducing cost, HARMONY reveals where aggregate metrics fail to provide a representative understanding of model competency. Our method is post hoc and lightweight, complements robustness and contamination audits, and yields practical guidance: report HARMONY with accuracy and rebalance low HARMONY benchmarks.

We further discuss additional related work on language model evaluation in Appendix J.

6 CONCLUSION

We introduce HARMONY, an entropy-based measure of how uniformly performance is distributed across a benchmark's subdomains. Mapping 19 MCQA benchmarks across five model families on the HARMONY mean-variance plane reveals a spectrum of reliability. High mean and low variance indicate that aggregate metrics consistently reflect broad competence across models. In contrast, low mean signals that performance concentrates on a few subdomains and high variance indicates model-dependent reliability. Therefore, benchmarks with high mean and low variance of HARMONY enable more reliable evaluation.

Controlled pruning shows that increasing HARMONY stabilizes aggregate accuracy by reducing overrepresented subdomains. Moreover, we find that scaling trends of performance uniformity are family specific, rendering the number of parameters as an unreliable indicator for the uniformity of model performance. Nevertheless, models perform more uniformly on average as the pre-training budget increases. HARMONY complements aggregate accuracy by exposing when performance gains reflect uniform competence versus concentrated strengths and supports multi-dimensional evaluation that makes subdomain trade-offs explicit.

ETHICS STATEMENT

This work evaluates publicly available MCQA benchmarks and introduces *RedundantQA*, a synthetic dataset generated from author-written seeds and LLM generations with no human subjects, personal data, or sensitive attributes collected. All examples were screened to avoid offensive content and verbatim copyrighted material. We respect the licenses of all benchmarks and models used. We will release our code and RedundantQA with documentation of construction, intended use, and limitations.

HARMONY is intended to complement (and *not replace*) standard accuracy and robustness analyses. Potential risks include misinterpretation of HARMONY or benchmark rebalancing to mask undesired failure modes. We therefore report both harmony and accuracy and encourage transparent, multi-metric evaluation. Our experiments rely on inference with open-sourced models. The authors declare no conflicts of interest or external sponsorship that could bias this work. We declare use of Large Language Models in this work in Appendix L.

REPRODUCIBILITY STATEMENT

We describe all experiments, datasets, models, and evaluation protocols openly and in detail in the main paper and appendix, including the construction of RedundantQA, the predictive similarity computation, partition induction, HARMONY definition and computation, pruning procedures, and statistical significance tests. We report model and benchmark versions, inference settings, and random seeds, and we specify hyperparameters and implementation choices (e.g., bandwidth selection, similarity scaling, and clustering criteria) to enable reproducibility. We also provide clear references to where each component is defined (Sections §2–§4 and Appendices A–K). We will open-source our codebase and findings, as well as RedundantQA, to facilitate exact replication.

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A REDUNDANTQA

To rigorously evaluate the discriminative power of similarity metrics, we construct RedundantQA, a controlled benchmark designed to disentangle genuine semantic similarity from superficial lexical overlap. Each set in RedundantQA consists of a reference question accompanied by two *true-similar* and two *false-similar* questions. The true-similar questions are paraphrases that evaluate the same underlying knowledge as the reference, while differing in surface form.[8] In contrast, the false-similar questions exhibit high lexical similarity to the reference but target distinct conceptual content. This design ensures that strong similarity metrics must go beyond surface-level cues, rewarding semantic alignment while ignoring spurious correlations.

In this section, we detail the construction (A.1) and validation (A.2) of RedundantQA, as well as showcasing examples (A.3).

A.1 CONSTRUCTION

We construct RedundantQA through a two-phase pipeline followed by strict validation: **(i) Seed Set Selection.** We begin by manually authoring three high-quality reference questions across four domains (Biology, Economics, Popular Culture, History). For each reference question, we also craft two paraphrases that target the same underlying knowledge (*true-similar*) and two distractors that share surface tokens but probe different concepts (*false-similar*). **(ii) Generative Expansion.** Using the seed sets as in-context learning examples, we prompt `Gemini-2.0-flash` (DeepMind, 2023) to generate 100 sets that consist of one reference question, two true-similar questions, and two false-similar questions for each domain. For different domains, we use a fixed template (Listing A.1) with domain-specific examples. This pipeline yields a large, automatically generated candidate pool.

[8] E.g., variations in vocabulary, syntax, or phrasing.

Prompt for Generating RedundantQA (Biology)

Come up with question sets. Each set must contain:

- A reference question,
- Two same-meaning questions: These should require the same factual answer and test the same biological concept as the reference question, but they should use different wording, phrasing styles, and sentence structures.
- Two distractor questions: These should look superficially very similar to the reference question but evaluate a different knowledge or skill with different answers than the reference question.

Notes:

- Focus on the domain of biological knowledge.
- Same-meaning questions should preserve deep semantic equivalence but vary stylistically. These must have the same answer.
- Distractor questions should maximize shallow textual similarity (e.g., shared nouns, verbs, syntactic patterns) while changing the underlying meaning. So, distractor questions should trick an incapable similarity measure into thinking they are similar.

Examples:
Set 1

- *Reference Question:* What organ pumps blood throughout the human body?
- *Same-meaning Question 1:* Which organ circulates blood to deliver oxygen and nutrients?
- *Same-meaning Question 2:* What body system structure maintains blood flow across the body?
- *Distracting Question 1:* What organ removes carbon dioxide from the blood?
- *Distracting Question 2:* What organ transports nutrients through the blood?

Set 2

- *Reference Question:* What process converts glucose into energy in cells?
- *Same-meaning Question 1:* Which process produces ATP from sugar molecules?
- *Same-meaning Question 2:* What pathway transforms glucose into usable cellular energy?
- *Distracting Question 1:* What process stores glucose in cells?
- *Distracting Question 2:* What process breaks down proteins for energy?

Set 3

- *Reference Question:* What type of blood vessel carries blood away from the heart?
- *Same-meaning Question 1:* Which vessels transport oxygenated blood from the heart?
- *Same-meaning Question 2:* What structures move blood outward from the heart?
- *Distracting Question 1:* What type of blood vessel brings blood to the heart?
- *Distracting Question 2:* What blood vessel type filters blood in the kidneys?

A.2 VALIDATION

We validate each set generated by `Gemini-2.0-flash` through a two-stage pipeline: (a) an automated and simple consistency check using `Gemini-2.0-flash` to confirm that true-similar paraphrases produce identical answers while false-similar distractors yield divergent ones (using Listing A.2); and (b) a manual review by expert annotators to correct any misclassifications, formatting issues, or errors introduced during automated filtering. After the validation step, we obtain 71, 39, 72, and 73 sets from Biology, Economics, Culture, and History domains respectively, with each set consisting of one reference question, two true-similar questions, and two false-similar questions.

This procedure yields a benchmark in which effective similarity metrics must discriminate semantic equivalence from mere lexical coincidence.

Prompt for Validating RedundantQA

Do the following questions have the same answer? Output only yes or no.
Question 1: REFERENCE_QUESTION
Question 2: TRUE_SIM_1

A.3 EXAMPLES

We provide examples from RedundantQA across all four domains in Table 1.

Biology	Economics	History	Popular Culture
Reference	**Reference**	**Reference**	**Reference**
What process converts glucose into energy in cells? A: Cellular respiration B: Photosynthesis C: Osmosis D: Transcription	How does increased government spending affect aggregate demand? A: Increases it. B: Decreases it. C: Has no effect. D: Only affects aggregate supply.	Who was the first president of the United States? A: George Washington B: Abraham Lincoln C: Thomas Jefferson D: John Adams	Who played Iron Man in the Marvel Cinematic Universe? A: Robert Downey Jr. B: Chris Evans C: Hugh Jackman D: Tobey Maguire
True Similar	**True Similar**	**True Similar**	**True Similar**
Which process produces ATP from sugar molecules? A: Cellular respiration B: Photosynthesis C: Osmosis D: Transcription	What happens to total demand in economy when the government increase its spending? A: Increases it. B: Decreases it. C: Has no effect. D: Only affects aggregate supply.	Who assumed leadership as America's first head of state? A: George Washington B: Abraham Lincoln C: Thomas Jefferson D: John Adams	Which actor portrayed Tony Stark in the MCU? A: Robert Downey Jr. B: Chris Evans C: Hugh Jackman D: Tobey Maguire
False Similar	**False Similar**	**False Similar**	**False Similar**
What process stores glucose in cells? A: Glycogenolysis B: Gluconeogenesis C: Glycogenesis D: Glycolysis	How does increased government spending affect government debt? A: Increases it. B: Decreases it. C: Has no effect. D: Only affects short-term debt.	Who was the first vice president of the United States? A: John Adams B: Thomas Jefferson C: Alexander Hamilton D: James Madison	Who played Captain America in the Marvel Cinematic Universe? A: Chris Evans B: Chris Pratt C: John Krasinski D: Matt Damon

Table 1: Example sets across all domains in RedundantQA.

B PREDICTIVE SIMILARITY

B.1 ALTERNATIVE BASELINES

In this section, we describe the alternative baselines compared against predictive similarity across a range of controlled settings.

Bigram. We compute an n-gram-overlap Jaccard similarity matrix. For each text x_i, we lowercase and split on whitespace, then form the set G_i of contiguous bigrams. The pairwise similarity is $S_{ij} = \dfrac{|G_i \cap G_j|}{|G_i \cup G_j|}$ with $S_{ii} = 1$ for all i.[9] The resulting $S \in [0,1]^{N \times N}$ is symmetric and measures surface-form overlap.

BERTScore F1. We use BERTScore (Zhang et al., 2020) to measure semantic similarity between pairs of texts by comparing their contextualized token embeddings. Tokens are greedily matched via cosine similarity to compute precision and recall, and the final sentence-sentence score is the F1 aggregate, where $F_1 = \frac{2PR}{P+R}$. We treat this F1 value as the pairwise similarity, which yields a symmetric matrix $S \in [-1,1]^{N \times N}$. We employ $\texttt{Roberta}_{\texttt{Large}}$ (Liu et al., 2019) for obtaining the contextualized token embeddings.

Input Embeddings Cosine Similarity. We map each input to a single vector and measure pairwise similarity via cosine in embedding space. We use two variants: (i) for each example,

[9]Note that if a text has fewer than n tokens, its n-gram set is empty. In such a case, the pairwise similarity is set to be 1. However, this is not observed in practice.

we take the last-token hidden state from the model under evaluation, ℓ_2-normalize it, and set $S_{ij} = \hat{h}_i^\top \hat{h}_j$, (ii) we encode each input with a frozen sentence-embedding model, normalize the embeddings, and compute the same cosine-based matrix. In both cases, we obtain a symmetric matrix $S \in [-1, 1]^{N \times N}$. For the sentence-embedding variant, we use `MiniLM`[10] (Wang et al., 2020) and `gte-Qwen2-7B-instruct`[11] (Li et al., 2023); for the model-under-evaluation variant, we use `microsoft/Phi-3-mini-4k-instruct`[12] (Abdin et al., 2024), which yields the best performance in Appendix B.2.

Input and Output Embeddings Cosine Similarity. We represent each input-output pair (e.g., question+answer) as a single vector by taking the last-token hidden state of the concatenated sequence from the model under evaluation. We ℓ_2-normalize these vectors and define pairwise similarity via cosine with $S_{ij} = \hat{h}_i^\top \hat{h}_j$. The resulting $S \in [-1, 1]^{N \times N}$ is symmetric and reflects similarity over both the question and its associated answer. We use `microsoft/Phi-3-mini-4k-instruct` (Abdin et al., 2024) for obtaining the hidden states, as it yields the best performance in Appendix B.2.

G-Vendi. Following Jung et al. (2025), we quantify the diversity of per–example gradients via a sketch-based spectral entropy. For each example, we form a compact count-sketch of the gradient of the (negative) log-probability of the correct answer under a proxy LM, yielding a matrix $G \in \mathbb{R}^{N \times d}$. We compute $C = \frac{1}{N} G^\top G$ and its eigenvalues $\{\lambda_i\}$. Let $p_i = \lambda_i / \sum_j \lambda_j$; the *G-Vendi* score is the exponential Shannon entropy of this spectrum:

$$\text{G-Vendi} \;=\; \exp\Big(- \sum_i p_i \log p_i \Big),$$

which acts as an effective rank where higher values indicate gradients spread across more orthogonal directions and lower values indicate concentration in a low dimensional subspace. For pairwise similarity, we ℓ_1-normalize the sketch rows of G and take their dot products to obtain a symmetric similarity matrix with unit diagonal. Following the original implementation, we employ `Qwen2.5-0.5B-Instruct` (Qwen et al., 2025) as the proxy model.

CORRS. Following Vivek et al. (2024), given a bank of source models, we map each input i to a vector $v_i \in \mathbb{R}^M$ whose m-th entry is the logit of the probability that model m assigns to the correct choice. Then, the similarity between two examples is defined as the Pearson correlation of these vectors with $S_{ij} = \text{corr}(v_i, v_j)$. The resulting $S \in [-1, 1]^{N \times N}$ is symmetric and represents the cross-model agreement in correct class confidence across inputs. We instantiate the source bank using the Llama model family (Grattafiori & et al, 2024) and the full set of models used in our experiments.

Method	Duplicate Catch Ratio (↑)
N-gram & Token	
Bigram	96.3
BERTScore F1	100.0
Embedding-Based	
Input Embeddings$_{\text{MiniLM}}$	100.0
Input Embeddings$_{\text{gte-Qwen2}}$	100.0
Input Embeddings$_{\text{phi3}}$	100.0
Input+Output Embeddings$_{\text{phi3}}$	100.0
Literature	
G-Vendi	100.0
CORRS$_{\text{Llama}}$	100.0
CORRS$_{\text{all}}$	100.0
IRT Representation	100.0
Predictive Similarity	100.0

Table 2: **Validation of our metric implementations.** All metrics other than bigram similarity perfectly catch exact duplicate question, satisfying the minimum requirement to ensure implementation accuracy.

IRT Representation. Following Polo et al. (2024), from a bank of source models, we form a binary response matrix $Y \in \{0, 1\}^{L \times N}$ whose (ℓ, i) entry indicates whether model ℓ answered example i correctly. We then fit a d-dimensional IRT model with per-example parameters ($\alpha_i \in \mathbb{R}^d$, $\beta_i \in \mathbb{R}$) and per-model ability vectors $\theta_\ell \in \mathbb{R}^d$, using

$$\Pr(Y_{\ell i} = 1) = \sigma\big(- \theta_\ell^\top \alpha_i + \beta_i \big).$$

Here, optimization alternates between gradient updates for θ (with ℓ_2 regularization and recentring) and logistic regressions to update (α_i, β_i). Finally, we obtain the embedding $E_i = \big[\alpha_i; \beta_i\big] \in \mathbb{R}^{d+1}$ and define pairwise similarity by cosine

[10] https://huggingface.co/sentence-transformers/all-MiniLM-L6-v2

[11] https://huggingface.co/Alibaba-NLP/gte-Qwen2-7B-instruct

[12] https://huggingface.co/microsoft/Phi-3-mini-4k-instruct

similarity as $S_{ij} = \frac{E_i^\top E_j}{\|E_i\| \, \|E_j\|}$, which yields a symmetric matrix $S \in [-1, 1]^{N \times N}$. We use $d = 200$ and instantiate the source bank using the full set of models used in our experiments.

As open-source implementations of efficient evaluation metrics are unavailable, we re-implement them following the specifications in prior work. We then validate our implementations via a sanity check in which each metric was tasked with detecting verbatim duplicate questions. As shown in Table 2, all metrics (with the exception of bigram similarity) achieve perfect performance, satisfying the minimum requirement to ensure implementation accuracy.

B.2 Measuring Semantic Similarity

An effective similarity measure for uncovering underlying data distributions must exhibit strong discriminative power, reliably identifying semantically similar data points while rejecting distractors. We empirically validate that predictive similarity meets this criterion, as it consistently distinguishes true semantic matches from misleading surface-level overlaps in RedundantQA.

Method	True Similar (↑)					False Similar (↓)				
	Biology	Economics	Culture	History	All	Biology	Economics	Culture	History	All
N-gram & Token										
Bigram	1.4	0.0	6.9	7.0	4.5	70.0	67.6	30.6	47.9	53.7
BERTScore F1	8.6	0.0	12.5	21.1	12.4	74.3	83.8	33.3	54.9	60.3
Embedding-Based										
Input Embeddings$_{\text{MiniLM}}$	42.9	24.3	62.5	66.2	54.1	27.1	51.4	5.6	12.7	21.1
Input Embeddings$_{\text{gte-Qwen2}}$	18.6	18.9	23.6	39.4	26.9	38.6	51.4	26.4	22.5	33.5
Input Embeddings$_{\text{phi3}}$	21.4	5.4	16.7	36.6	22.7	47.1	75.7	37.5	31.0	45.5
Input+Output Embeddings$_{\text{phi3}}$	51.4	62.2	40.3	56.3	52.9	22.9	27.0	16.7	15.5	20.2
Literature										
G-Vendi	62.9	37.8	36.1	46.5	47.9	5.7	2.7	6.9	5.6	5.8
CORRS$_{\text{Llama}}$	2.9	8.1	9.7	14.1	9.1	1.4	0.0	1.4	1.4	1.2
CORRS$_{\text{all}}$	35.7	13.5	59.7	59.2	47.5	1.4	5.4	0.0	1.4	1.7
IRT Representation	1.4	0.0	1.4	0.0	0.8	1.4	0.0	0.0	2.8	1.2
Predictive Similarity	**80.0**	**86.5**	**66.6**	**73.2**	**77.7**	1.4	2.7	0.0	4.2	2.1

Table 3: Proportion of identified true-similar (↑) and false-similar (↓) pairs by method and domain.

As shown in Table 3, predictive similarity achieves the highest retrieval of true semantic matches across all domains, while maintaining one of the lowest rate of false matches. This indicates that it captures semantic equivalence without being misled by superficial lexical similarity. In contrast, embedding-based and bigram baselines suffer from high false positives, conflating surface-level resemblance with meaning. Metrics from efficient evaluation literature show stronger performance but still fall short of predictive similarity. Overall, these results highlight the unique discriminative advantage of predictive similarity in measuring semantic similarity.

B.3 Inducing the Semantic Partition

A core requirement for our work is that the similarity function should induce a semantic partition of the data. We evaluate this property by inducing cluster assignments from each metric and measuring agreement with the ground-truth domain labels in RedundantQA and its reference-only subset (RedundantQA-Ref) using Adjusted Rand Index (ARI) and Normalized Mutual Information (NMI). In addition, we apply the same protocol to MMLU high school subtasks, testing whether clusters recover canonical subject domains (e.g., computer science, biology, physics).

As shown in Table 4, predictive similarity achieves the highest agreement on all

Method	`RedundantQA`		`RedundantQA-Ref`		`MMLU-HS`	
	ARI	NMI	ARI	NMI	ARI	NMI
N-gram & Token						
Bigram	-0.3	2.5	-0.4	6.7	0.1	6.2
BERTScore F1	-0.2	1.6	2.2	8.6	1.4	7.9
Embedding-Based						
Input Embeddings$_{\text{MiniLM}}$	55.8	64.4	59.4	68.4	47.4	56.8
Input Embeddings$_{\text{gte-qwen2-7b-instruct}}$	28.6	34.9	36.3	45.9	27.1	34.4
Input Embeddings$_{\text{phi3}}$	27.8	37.1	33.0	45.6	25.1	31.6
Input+Output Embeddings$_{\text{phi3}}$	57.1	67.0	58.9	70.3	51.3	59.6
Literature						
G-Vendi	6.5	11.3	4.7	10.9	3.2	9.2
CORRS$_{\text{all}}$	6.1	8.2	4.8	8.2	2.8	8.4
IRT Representation	2.1	2.7	0.4	1.9	0.4	1.5
Predictive Similarity	60.4	70.4	62.5	76.5	55.4	62.1

Table 4: Validation of our partition induction method on RedundantQA and MMLU. Adjusted Rand Index (ARI) and Normalized Mutual Information (NMI) (both are higher is better) are shown for different methods on **`RedundantQA`**, **`RedundantQA-Ref`**, and **`MMLU-HS`**. Predictive similarity consistently achieves the best domain recovery.

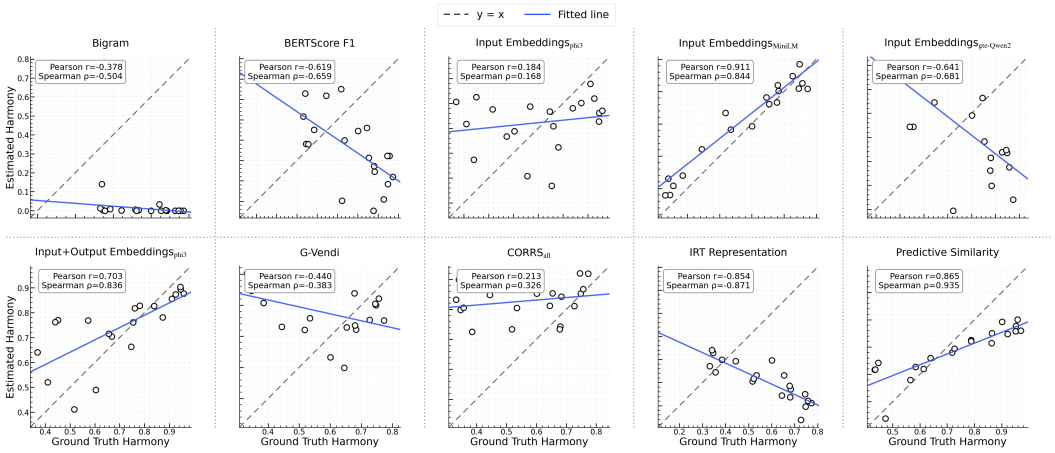


Figure 8: **Validation of our partition induction method on RedundantQA**. Predictive similarity achieves the strongest correlation between the ground truth HARMONY and estimated HARMONY, while input embeddings derived from `MiniLM` is a close runner-up.

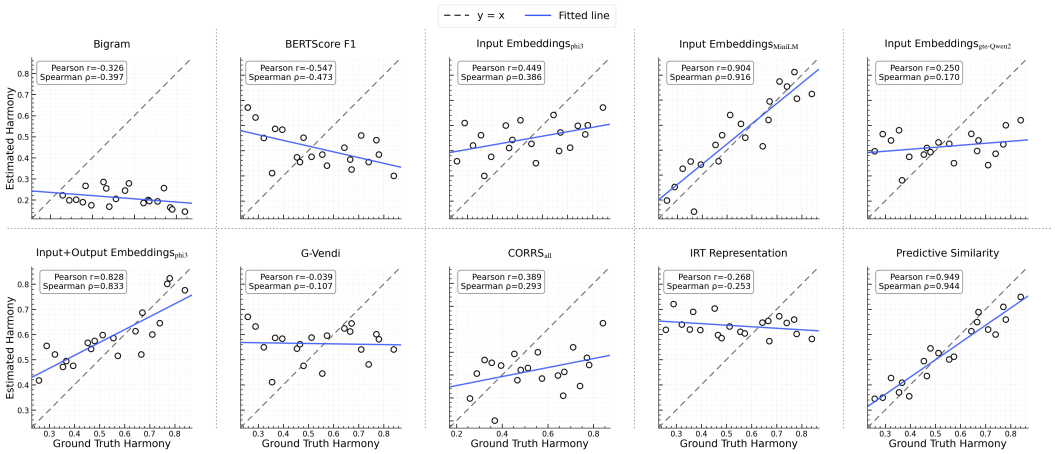


Figure 9: **Validation of our partition induction method on MMLU**. Similar to the results on RedundantQA, predictive similarity achieves the strongest correlation between the ground truth HARMONY and estimated HARMONY, while input embeddings derived from `MiniLM` is a close runner-up.

three sets, while strong embedding-based baselines are competitive yet consistently behind. By contrast, token/ngram measures and metrics from the efficient evaluation literature fail to recover domain structure, indicating that they are unreliable for semantic grouping. Taken together with the pairwise retrieval evidence, these results show that predictive similarity not only discriminates true semantic matches from distractors, but also organizes instances into compact and consistent clusters. This behavior is precisely what enables a cluster-centric analysis of benchmarks, yielding low within-cluster variance and high between-cluster separation.

B.4 CAPTURING BENCHMARK HARMONY

We evaluate all alternative similarity baselines from Appendix B.1 in the identical setting of §2.4. For each baseline, we induce clusters from its similarity matrix, compute HARMONY $H(\mathcal{G})$, and report correlations between the ground-truth HARMONY and its counterpart computed from the partition induced by each baseline.

	Gemma		Llama		OLMo		Phi		Qwen		Average	
Benchmark	**Spearman**	**Pearson**	**Spearman**	**Pearson**	**Spearman**	**Pearson**	**Spearman**	**Pearson**	**Spearman**	**Pearson**	**Spearman**	**Pearson**
AQUA-RAT	61.8	62.7	63.3	65.9	47.0	49.3	49.8	50.9	76.1	76.5	59.6	61.1
ARC-Challenge	41.9	42.7	76.3	76.9	72.9	73.9	71.9	73.9	74.5	76.1	67.5	68.7
ARC-Easy	41.6	42.0	66.6	67.1	67.9	68.7	75.3	76.3	62.7	64.0	62.8	63.6
ART	25.5	26.4	84.1	84.6	76.6	77.9	78.6	79.8	75.7	76.8	68.1	69.1
BoolQ	25.5	25.9	58.3	59.8	35.3	36.3	18.2	18.9	27.5	28.9	33.0	34.0
CommonsenseQA	33.8	35.6	33.6	34.4	62.8	64.5	42.4	43.8	39.1	39.8	42.3	43.6
COPA	27.9	29.5	76.7	78.4	68.7	70.2	64.8	67.2	51.4	52.8	57.9	59.6
GPQA	77.8	78.0	53.4	51.9	64.1	65.2	82.1	83.0	85.5	86.1	72.6	72.8
LogiQA	55.4	57.3	77.7	79.8	67.8	67.2	70.3	72.1	80.1	80.3	70.3	71.3
MathQA	33.5	34.2	61.0	62.0	55.2	56.0	54.9	54.0	57.1	56.4	52.3	52.5
OpenBookQA	33.2	34.0	73.9	75.0	70.1	72.3	74.0	75.5	71.0	72.5	64.4	65.9
PIQA	38.6	39.6	78.6	80.2	77.3	79.4	67.0	68.2	74.6	76.4	67.2	68.8
PubMedQA	50.5	50.0	60.8	60.8	37.8	36.8	50.6	50.6	63.0	61.1	52.5	51.9
QUARTZ	37.9	39.0	81.4	80.3	65.9	63.9	76.0	74.9	70.0	68.1	66.2	65.2
SciQ	22.0	22.5	55.7	58.3	60.3	61.4	56.0	56.0	58.0	60.3	50.4	51.7
SocialIQA	20.7	21.3	72.9	73.5	64.6	65.6	63.5	64.9	61.2	62.0	56.6	57.5
StrategyQA	3.6	3.7	48.2	49.6	20.5	20.9	21.6	21.4	27.9	28.9	24.4	24.9
TruthfulQA	50.4	52.7	78.4	80.7	71.4	73.6	85.3	86.4	77.1	79.3	72.5	74.5
Average	37.9	38.7	66.7	67.7	60.3	61.3	61.2	62.1	62.9	63.7	57.8	58.7

Table 5: **Cross-model consistency of predictive similarity**: Spearman and Pearson correlations (values $\times 100$) between the upper-triangle entries of affinity matrices, by benchmark (rows) and model family (columns). The rightmost block reports per-benchmark averages across families; the bottom row reports per-family averages across benchmarks; the bottom-right cell shows overall means.

As shown in Fig. 8 and 9, predictive similarity achieves the strongest correlation with ground-truth entropy. Similar to prior validation experiments (App. B.2, B.3), embedding-based baselines are the next-best performers but consistently lag behind, whereas token-and-n-gram overlap measures perform substantially worse. These results establish predictive similarity as the most reliable similarity metric choice for capturing the benchmark dynamics.

B.5 Consistency of Predictive Similarity Across Models

As defined in §2.3, predictive similarity induces, for each benchmark $\mathcal{B}$ and model f, a symmetric similarity matrix $S^{(f,\mathcal{B})} \in (0,1]^{N_\mathcal{B} \times N_\mathcal{B}}$ over the $N_\mathcal{B}$ items of $\mathcal{B}$. In this section, we ask whether these model-specific neighborhoods are idiosyncratic. To quantify cross-model consistency, we correlate the upper-triangular entries of the corresponding similarity matrices using both rank-based (Spearman) and linear (Pearson) correlations:

$$r_{\mathrm{S}}^{\mathcal{B}}(f_1, f_2) = \rho_{\mathrm{S}}\big(\mathrm{vec}(S^{(f_1,\mathcal{B})}),\ \mathrm{vec}(S^{(f_2,\mathcal{B})})\big), \qquad r_{\mathrm{P}}^{\mathcal{B}}(f_1, f_2) = \rho_{\mathrm{P}}\big(\mathrm{vec}(S^{(f_1,\mathcal{B})}),\ \mathrm{vec}(S^{(f_2,\mathcal{B})})\big),$$

where $\mathrm{vec}(\cdot)$ stacks the upper triangle of a matrix into a vector, ρ_{S} is Spearman's rank correlation, and ρ_{P} is Pearson's correlation. We report both, as Spearman is invariant to monotone re-scalings and thus robust to calibration differences across models, while Pearson captures linear alignment in similarity magnitudes.

As shown in Table 5, predictive similarity neighborhoods exhibit substantial within-family consistency across many benchmarks. Averaging across families yields high per-benchmark means clustered in the mid-60s, with notable peaks for *LogiQA* (70.3 Spearman / 71.3 Pearson), *TruthfulQA* (72.5 / 74.5), *PIQA* (67.2 / 68.8), and *ART* (68.1 / 69.1). Family-wise averages further show broad stability for Llama (66.7 / 67.7), Qwen (62.9 / 63.7), and Phi (61.2 / 62.1), with OLMo close behind (60.3 / 61.3) and Gemma lower (37.9 / 38.7). In particular, *ART*, *COPA*, *LogiQA*, *PIQA*, and *TruthfulQA* attain high agreement for Llama, Phi, and Qwen (typically 70–85), indicating that the induced item-item structure is largely task-driven rather than model idiosyncratic. Knowledge-centric *GPQA* is also strong for Phi and Qwen (82–86). By contrast, *StrategyQA*, *BoolQ*, and, to a lesser extent, *SocialIQA* show weaker agreement particularly for Gemma and Phi, suggesting greater family-specific effects on these benchmarks.

B.6 Probing the Determinants of Predictive Similarity

Dependence on the Tail. We test sensitivity to the probability tail by constructing a truncated variant that re-normalizes mass over the union of the `top-50` tokens, yielding $S^{(f,\mathcal{B})}_{\text{KL-top-50}}$, and contrasting it with the full $S^{(f,\mathcal{B})}_{\text{KL}}$.

JS vs. KL-based Similarity. Equation 2 defines S as an RBF of the Jeffreys divergence, producing *sharp, tunable* neighborhoods that strongly penalize coverage errors (as near-zeros drive J higher and S lower). Jensen-Shannon (JS) instead compares to the mixture $M = \frac{1}{2}(\bar{p}_f(x_i) + \bar{p}_f(x_j))$, yielding a bounded, tail-robust divergence that is easier to compare across benchmarks. To place JS on the same similarity scale, we apply the same RBF transform from Equation 2 entrywise, obtaining $S_{\mathrm{JS}}^{(f,\mathcal{B})}$.

Following Appendix B.5, we compute Spearman and Pearson correlations between the upper-triangular entries of $S_{\mathrm{KL}}^{(f,\mathcal{B})}$ and, respectively, $S_{\mathrm{KL\text{-}top\text{-}50}}^{(f,\mathcal{B})}$ and $S_{\mathrm{JS}}^{(f,\mathcal{B})}$. We report per-benchmark scores where f is OLMo 2 7B. *High agreement* indicates that neighborhoods are driven by high probability mass and remain stable under truncation or mixture smoothing, while *low agreement* indicates sensitivity to tail mismatches or calibration asymmetries that Jeffreys magnifies but JS attenuates.

Across benchmarks, correlations between $S_{\mathrm{KL}}^{(f,\mathcal{B})}$ and (i) $S_{\mathrm{KL\text{-}top\text{-}50}}^{(f,\mathcal{B})}$ and (ii) $S_{\mathrm{JS}}^{(f,\mathcal{B})}$ variants are uniformly high (typically 95-99%) (Table 6). This indicates that the divergence of probability distributions generated by OLMo 2 7B are governed by head probability mass rather than the tail. Truncation preserves structure nearly perfectly as $S_{\mathrm{KL\text{-}top\text{-}50}}$ matches or exceeds S_{JS} on most tasks, while S_{JS} remains strongly aligned, reflecting robustness to calibration and coverage noise. Modest dips (e.g., COPA, PIQA) suggest settings where tail mismatches or asymmetries matter more, but overall the stability under truncation and mixture smoothing supports that S captures meaningful, head-driven divergence.

	S_{JS}		$S_{\mathrm{KL\text{-}top\text{-}50}}$	
Benchmark	Pearson	Spearman	Pearson	Spearman
AQUA-RAT	96.1	95.5	97.4	97.4
ARC-Challenge	95.7	95.2	98.5	98.5
ARC-Easy	95.4	95.0	98.7	98.7
ART	95.5	95.4	97.1	96.9
BoolQ	93.5	92.5	98.4	98.4
CommonsenseQA	97.0	96.7	99.5	99.5
COPA	94.7	95.2	95.1	94.9
GPQA	97.1	97.1	99.1	99.0
LogiQA	98.7	98.5	98.5	98.5
MathQA	99.1	99.4	96.4	96.3
OpenBookQA	97.6	97.7	97.5	97.6
PIQA	96.4	96.1	96.2	95.9
PubMedQA	96.8	96.7	99.6	99.6
QUARTZ	95.8	95.8	99.8	99.8
SciQ	93.6	93.3	98.8	98.9
SocialIQA	98.2	98.2	97.0	96.8
StrategyQA	99.4	99.5	97.0	97.0
TruthfulQA	94.6	94.2	98.1	97.7

Table 6: **Agreement between predictive similarity variants.** Per-benchmark Pearson/Spearman correlations between $S_{\mathrm{KL}}^{(f,\mathcal{B})}$ and (i) $S_{\mathrm{JS}}^{(f,\mathcal{B})}$ and (ii) $S_{\mathrm{KL\text{-}top\text{-}50}}^{(f,\mathcal{B})}$ shows that neighborhoods are driven by head probability mass and remain stable under truncation or mixture smoothing.

B.7 Theoretical and Computational Discussions

A Theoretical Perspective on Predictive Similarity. We measure similarity via the (symmetrized) D_{KL} between model predictive distributions because it aligns with how models differ operationally and geometrically. First, D_{KL} has a clear testing meaning, as it governs optimal error exponents in distinguishing two distributions. Hence, larger D_{KL} divergence implies that the model would more reliably tell the two inputs apart (by Stein/Chernoff asymptotics) (Cover & Thomas, 2006). Second, small D_{KL} guarantees closeness in total variation by Pinsker's inequality, implying high indistinguishability and hence high similarity for our purposes (Cover & Thomas, 2006). Third, D_{KL} is information monotone under coarse-graining, making the measure stable to relabeling or merging answer tokens/options that preserve semantics (Csiszár & Shields, 2004). Finally, locally D_{KL} induces the Fisher-Rao geometry on the probability simplex, so $\exp(-\tau\, \mathrm{D}_{\mathrm{KL}})$ behaves like a Gaussian kernel in the natural metric of the model's predictive space, yielding compact clusters of similar predictive behavior (Amari, 2016). We use the Jeffreys (symmetrized) form to remove directionality while retaining these properties.

Computational Overhead of Predictive Similarity. Predictive similarity is a *post hoc* computation, since we operate on the logits already cached from the benchmark evaluation. Hence, no additional model forward passes are required. Given these logits, we convert them to predictive distributions and evaluate the pairwise KL terms that define the similarity in Eq. 2.

The principal cost arises from forming pairwise interactions across N items, which is quadratic in N and linear in the label-space size D (i.e., $O(N^2 \cdot D)$ time). Memory is dominated by storing the evaluation logits ($O(N \cdot D)$) and the similarity matrix ($O(N^2)$). In practice, D corresponds to the

size of the vocabulary of a given model and can be large. We therefore view the cost as $O(N^2D)$ and the memory requirement as $O(N \cdot D)$. When N is large, standard remedies (e.g. blockwise evaluation) reduce peak memory without changing the definition of the metric. Overall, computing predictive simlarity adds negligible *inference* overhead and modest *analysis* overhead relative to running the benchmarks themselves.

Compared to alternative baselines discussed in Appendix B.1, predictive similarity is computationally frugal: it reuses cached logits and requires neither additional inference nor any backward passes. By contrast, embedding baselines, as well as BERTScore, invoke separate encoders (extra forward passes), G-Vendi relies on gradients (backward passes), and CORRS/IRT aggregate signals from a bank of models (multiple evaluations per item). While string-based methods such as Bigram are lightweight, they do not leverage model behavior. Thus, predictive similarity offers a favorable trade-off between compute and quality when benchmarks are already being run.

B.8 Discussion on Model-Specific Similarity

Our goal is to *evaluate benchmarks*, not to define a single, task-agnostic neighborhood data points. A benchmark can be *reliable for one model but unreliable for another*. Accordingly, the similarity function used to induce the partition $\mathcal{G}_f$ should be *conditional on the model* f. We provide our rationale below.

Evaluation target is $H_{\mathcal{B}}(f)$. Section 2 defines harmony *per model*, $H_{\mathcal{B}}(f)$, and then aggregates across f via (μ_H, σ_H^2) in Eq. 1. Using a *global, model-agnostic* similarity collapses distinct predictive neighborhoods into a single partition, implicitly assuming that $\mathcal{G}_f$ is invariant across f. This undermines the very statistic we report: two models with the same accuracy profile but different predictive structure could receive the same H under a fixed partition, obscuring model specialities.

Benchmarks are instruments relative to a model. A benchmark is a diagnostic instrument for a *given* model: priors, tokenization, calibration, and pre-training exposure all change which items are *similar* from the model's perspective. Hence, a model can perform uniformly on a benchmark while another one overfits to certain subdomains. Model specific similarity preserves this relativity, letting reliability vary meaningfully across families.

C Model List

We list all evaluated models and provide links to their open-source weights.

- Qwen3: Qwen3-0.6B-Base, Qwen3-1.7B-Base, Qwen3-4B-Base, Qwen3-8B-Base, Qwen3-14B-Base, Qwen3-0.6B, Qwen3-1.7B, Qwen3-4B, Qwen3-8B, Qwen3-14B.
- Llama 3: Llama-3.2-1B, Llama-3.2-3B, Llama-3.1-8B, Llama-3.1-70B, Llama-3.2-1B-Instruct, Llama-3.2-3B-Instruct, Llama-3.1-8B-Instruct, Llama-3.1-70B-Instruct.
- Olmo 2: OLMo-2-0425-1B, OLMo-2-1124-7B, OLMo-2-1124-13B, OLMo-2-0325-32B, OLMo-2-0425-1B-Instruct, OLMo-2-1124-7B-Instruct, OLMo-2-1124-13B-Instruct, OLMo-2-0325-32B-Instruct.
- Gemma 3: gemma-3-1b-pt, gemma-3-4b-pt, gemma-3-12b-pt, gemma-3-27b-pt, gemma-3-1b-it, gemma-3-4b-it, gemma-3-12b-it, gemma-3-27b-it.
- Phi-3: Phi-3-mini-4k-instruct, Phi-3-medium-4k-instruct.

D Model-wise Decomposition of Benchmark Harmony

In §3.2, we position each benchmark $\mathcal{B}$ using the cross-model mean $\mu_H(\mathcal{B})$ and variance $\sigma_H^2(\mathcal{B})$. We now resolve this view at the model level. For each benchmark, Fig. 10 plots the per-model vector $\{H_{\mathcal{B}}(f)\}_{f \in \mathcal{F}}$, revealing structure that is obscured by aggregation. Similarly, Fig. 11 provides the analogous decomposition for MMLU subtasks, treating each subtask as a benchmark on its own.

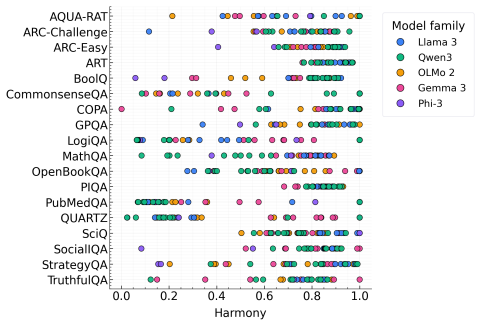
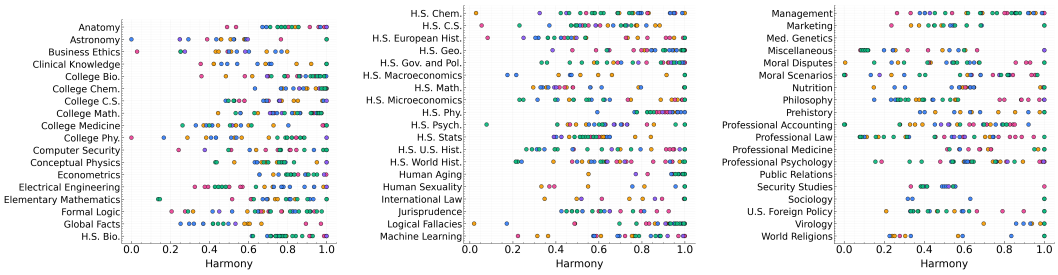


Figure 10: Model-wise decomposition of Harmony for MCQA benchmarks.



(a) MMLU subtask group 1. (b) MMLU subtask group 2. (c) MMLU subtask group 3.

Figure 11: Model-wise decomposition of HARMONY for MMLU subtasks.

Tight *horizontal* groupings (small spread across models) indicate *model-invariant* distributional balance, where different families assign similar HARMONY to the same benchmark, suggesting that aggregate accuracy reflects uniform competence irrespective of architectural or training choices. Conversely, wide horizontal scatter exposes *model-dependent reliability*, as some families concentrate performance on a few subsets (low HARMONY), while others distribute performance more evenly (high HARMONY).

We note that benchmarks with tight clusters are favorable for cross-family comparison, as accuracy rankings are less likely to be artifacts of benchmark composition. In contrast, wide scatter warns that leaderboard deltas may be driven by subsets that particular families exploit. In such cases, we suggest reporting accuracy alongside the HARMONY profiles of the models under evaluation, $\{H(\mathcal{G}_f)\}_f$.

E IMPROVEMENT HARMONY

In §4.2, we show that scaling behavior varies across model families as parameter count increases: some families (e.g., Qwen3) exhibit increasing HARMONY, while others (e.g., Gemma 3) show the opposite. We now ask whether *performance improvements* from scaling are distributed evenly across subsets. For two adjacent model sizes within a family, let the per-subset change be

$$d_i \;=\; \Psi(f_{\text{large}}; A_i) \;-\; \Psi(f_{\text{small}}; A_i),$$

with subset weights w_i and partition $\mathcal{G} = \{A_i\}_{i=1}^k$ defined as in §2.1. Let $\bar{d} = \sum_i w_i d_i$ be the weighted mean and reuse the HARMONY computation by replacing accuracies $\Psi(f; A_i)$ with changes d_i:

$$K_i \;=\; \exp\Big(-\big(\tfrac{d_i-\bar{d}}{b}\big)^2\Big), \qquad p_i \;=\; \frac{w_i K_i}{\sum_j w_j K_j}, \qquad H_\Delta(\mathcal{G}) \;=\; -\frac{1}{\log k}\sum_{i=1}^{k} p_i \log\big(p_i+\varepsilon\big).$$

High H_Δ indicates that scaling yields *uniform* changes across subsets, while low H_Δ indicates *spiky* changes concentrated in a few clusters. Similar to § 2, we adopt a comparative perspective, asking which models improve more uniformly and which benchmarks most facilitate uniform gains. To ensure within-family comparability, we fix the partition to that induced by the smallest model in each family and evaluate all larger models on these partitions.

Improvement HARMONY of Benchmarks (Fig. 12). Due to the lack of a principled baseline for H_Δ, we interpret results comparatively rather than absolutely. Benchmarks vary in improvement HARMONY, and those with higher performance HARMONY tend to exhibit higher H_Δ. Using all benchmarks in our setup, the fitted-line correlation is $r = 0.226$, which increases to $r = 0.387$ after excluding the three lowest-HARMONY benchmarks. Thus, higher HARMONY benchmarks are associated with more uniform improvements in a comparative sense, though the effect size is modest and sensitive to less harmonious outliers.

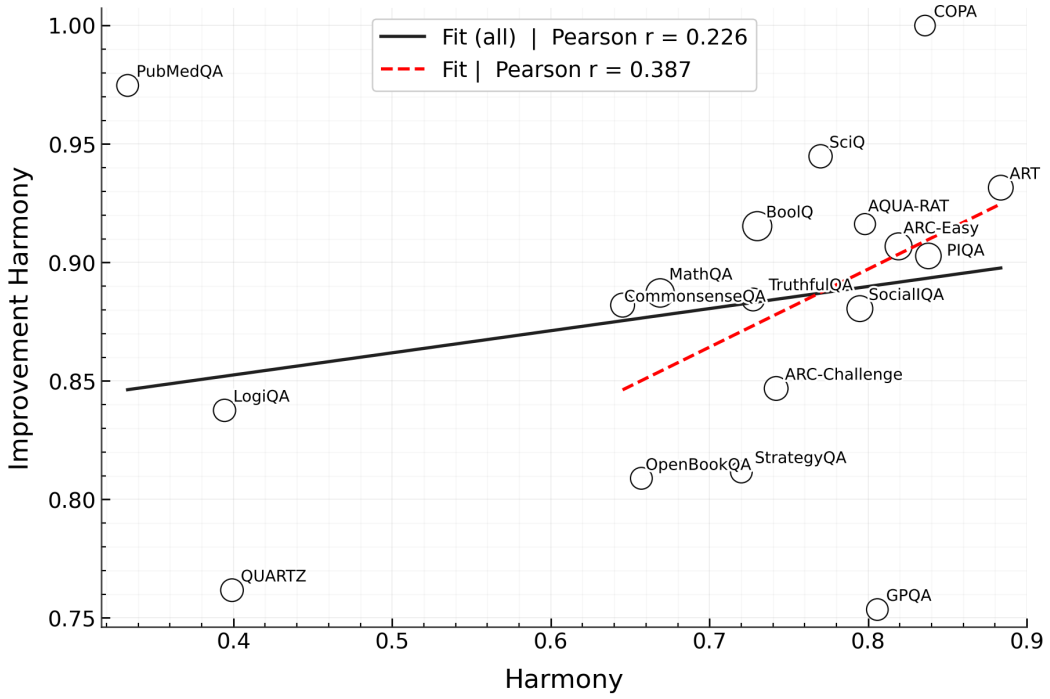


Figure 12: H_Δ **across benchmarks.** Higher performance HARMONY modestly correlates with improvement HARMONY ($r = 0.226$; $r = 0.387$ excluding the three lowest HARMONY) benchmarks, indicating an outlier-sensitive correlation.

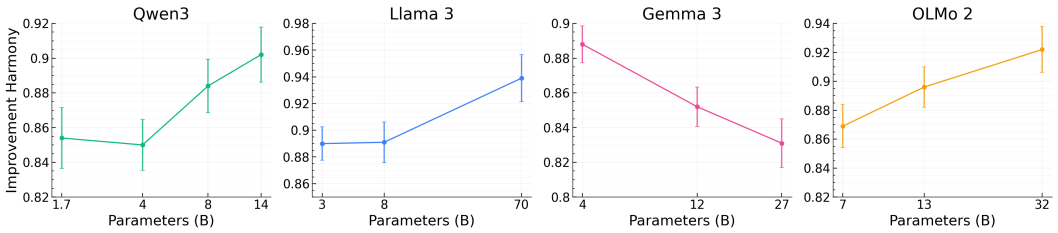


Figure 13: **Model size vs.** H_Δ. Improvement harmony scales differently by family: it increases with size for `Qwen`, `Llama`, and `OLMo`, while decreasing for `Gemma`.

Improvement HARMONY of Models (Fig. 13). We measure improvement HARMONY H_Δ for adjacent sizes within each family. For `Qwen` and `Llama`, despite a *decline* in performance HARMONY with scale (§4.2), H_Δ *increases* with the model scale, as larger models distribute their gains more evenly across subsets, whereas smaller variants exhibit spikier changes. `Gemma` shows the complementary pattern, where its larger models, which had higher performance HARMONY, display *lower* H_Δ, indicating that improvements concentrate on fewer subsets as scale grows. By contrast, in `OLMo` model family, both performance HARMONY and improvement HARMONY *rise* with model size. Taken together, these results underscore that aggregate HARMONY and improvement HARMONY can decouple, since models may become less harmonious overall yet still scale their improvements uniformly, or vice versa.

F DETAILS OF STATISTICAL SIGNIFICANCE TEST

We assess whether the subset we keep after pruning has a higher mean than the full set using a nonparametric, *coupled* bootstrap sign test. Let $a_1, \ldots, a_N$ be per-example accuracy and $k_i \in \{0, 1\}$ indicate membership in the keep subset $K = \{i : k_i = 1\}$. For $b = 1, \ldots, B$, we draw a bootstrap sample of indices $S^{(b)}$ of size N (with replacement), compute both means on the *same* resample,

and then take their difference:

$$\bar{a}^{(b)}_{\text{all}} = \frac{1}{N} \sum_{i \in S^{(b)}} a_i, \tag{3}$$

$$n^{(b)}_{\text{keep}} = \sum_{i \in S^{(b)}} k_i, \tag{4}$$

$$\bar{a}^{(b)}_{\text{keep}} = \frac{1}{n^{(b)}_{\text{keep}}} \sum_{i \in S^{(b)}} k_i \, a_i, \tag{5}$$

$$\Delta^{(b)} = \bar{a}^{(b)}_{\text{keep}} - \bar{a}^{(b)}_{\text{all}}. \tag{6}$$

Resamples with $n^{(b)}_{\text{keep}} = 0$ are discarded (to avoid degenerate runs we cap total draws at $3B$); let $m \leq B$ be the number of valid differences retained. We then form a two-sided p-value from the sign statistic with a plus-one small-sample correction:

$$r = \sum_{b=1}^{m} \mathbf{1}\Big\{\Delta^{(b)} \geq 0\Big\}, \tag{7}$$

$$p = \min\left\{1,\, 2\min\left(\frac{r+1}{m+1},\, \frac{m-r+1}{m+1}\right)\right\}. \tag{8}$$

We fix the random seed for reproducibility and declare significance at level α when $p < \alpha$ (testing $H_0 : \mathbb{E}[\Delta] = 0$ vs. $H_1 : \mathbb{E}[\Delta] \neq 0$). We use $B = 10000$ and set $\alpha(N)$ as follows:

$$\alpha(N) = \begin{cases} 0.1, & N < 500, \\ 0.05, & 500 \leq N < 1500, \\ 0.01, & 1500 \leq N < 3000 \end{cases}$$

G Extended Results: How does model performance change with increased Harmony?

In this section, we generalize the pruning experiments from §4.1 beyond the illustrative cases to *all* model families and benchmarks in our setup. Our aim is methodological: we examine how aggregate accuracy and per-subset dispersion evolve as we progressively rebalance a benchmark. Concretely, for each (model, benchmark) pair we sweep a pruning budget (scheduled inversely to baseline Harmony), recompute Harmony and accuracy at each budget, and compare the pruned-set accuracy to the full-set accuracy using the coupled bootstrap significance test detailed in App. F. Family-wise plots in this section visualize these trajectories, allowing us to observe whether increased Harmony coincides with stable (or shifting) aggregate scores and tighter per-subset distribution of performance.

Across all model families (Fig. 14, 15, 16, 17), two patterns consistently hold. **(i) Accuracy shifts with increased harmony.** As pruning raises Harmony, aggregate accuracy frequently changes in a statistically significant manner (App. F), indicating that low Harmony composition can result in a misleading aggregate score. **(ii) Low Harmony benchmarks are fragile.** Benchmarks starting with lower Harmony exhibit more instances of significant accuracy change under the pruning procedure than high Harmony benchmarks, underscoring their susceptibility to presenting misleading aggregate scores.

H Multi-Dimensional Evaluation

Motivated by the skewed aggregate scores in low Harmony benchmarks, we conduct model evaluation at finer granularity. Following recent work on fine-grained evaluation (Zeng et al., 2025), we recursively induce partitions as described in §2.3. This procedure yields a *labeled tree*, where the root is the full benchmark; each internal node is a subset from the partitioning of its parent node; and leaves are atomic subdomains that admit no further valid split (see App. K for details). The resulting

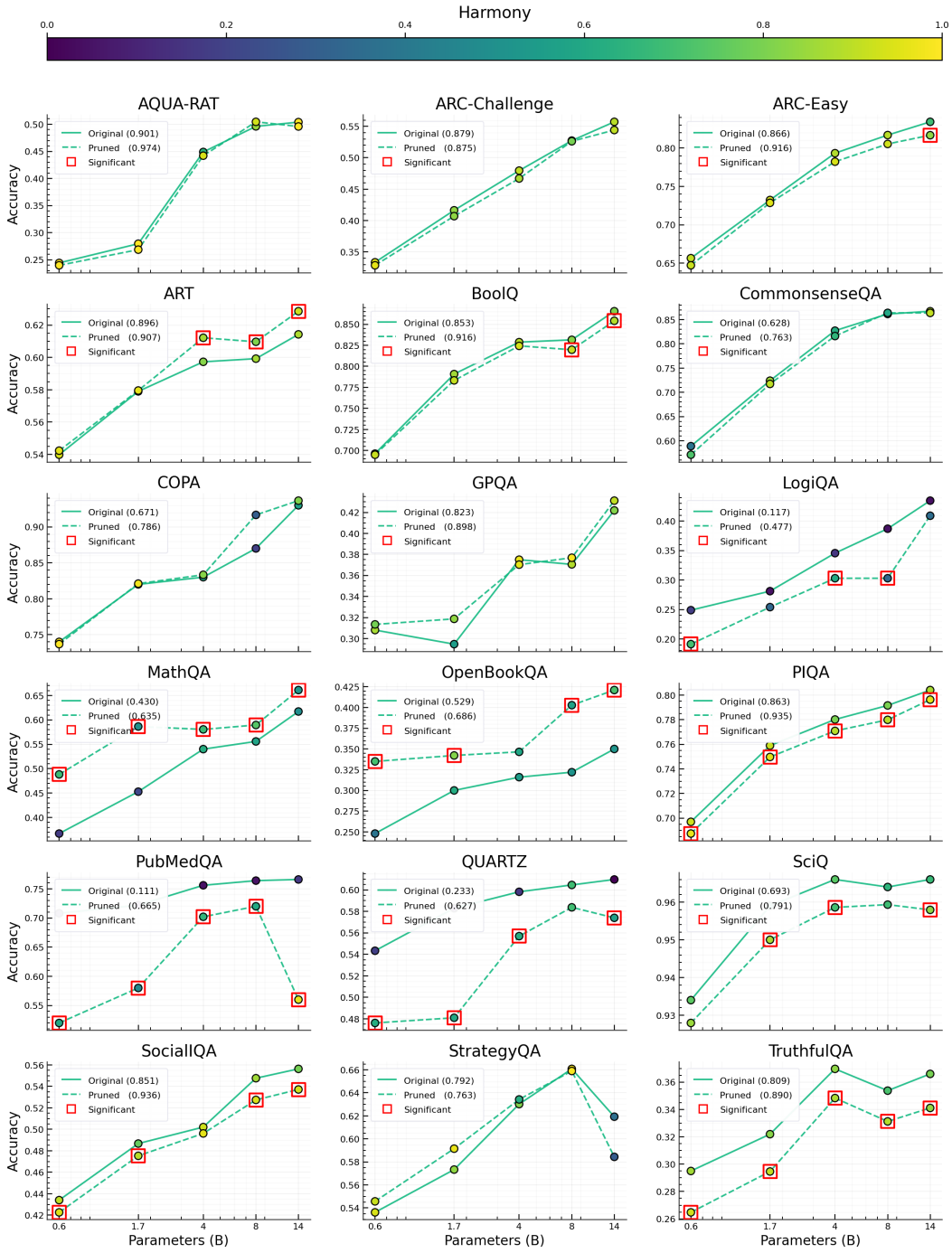


Figure 14: **Full results of balancing benchmarks via pruning in Qwen3 model family.** We remove overly similar items with a pruning rate inversely proportional to HARMONY, which consistently improves HARMONY. We find that aggregate scores often change statistically significantly on less harmonious benchmarks, whereas they remain more stable on more harmonious benchmarks.

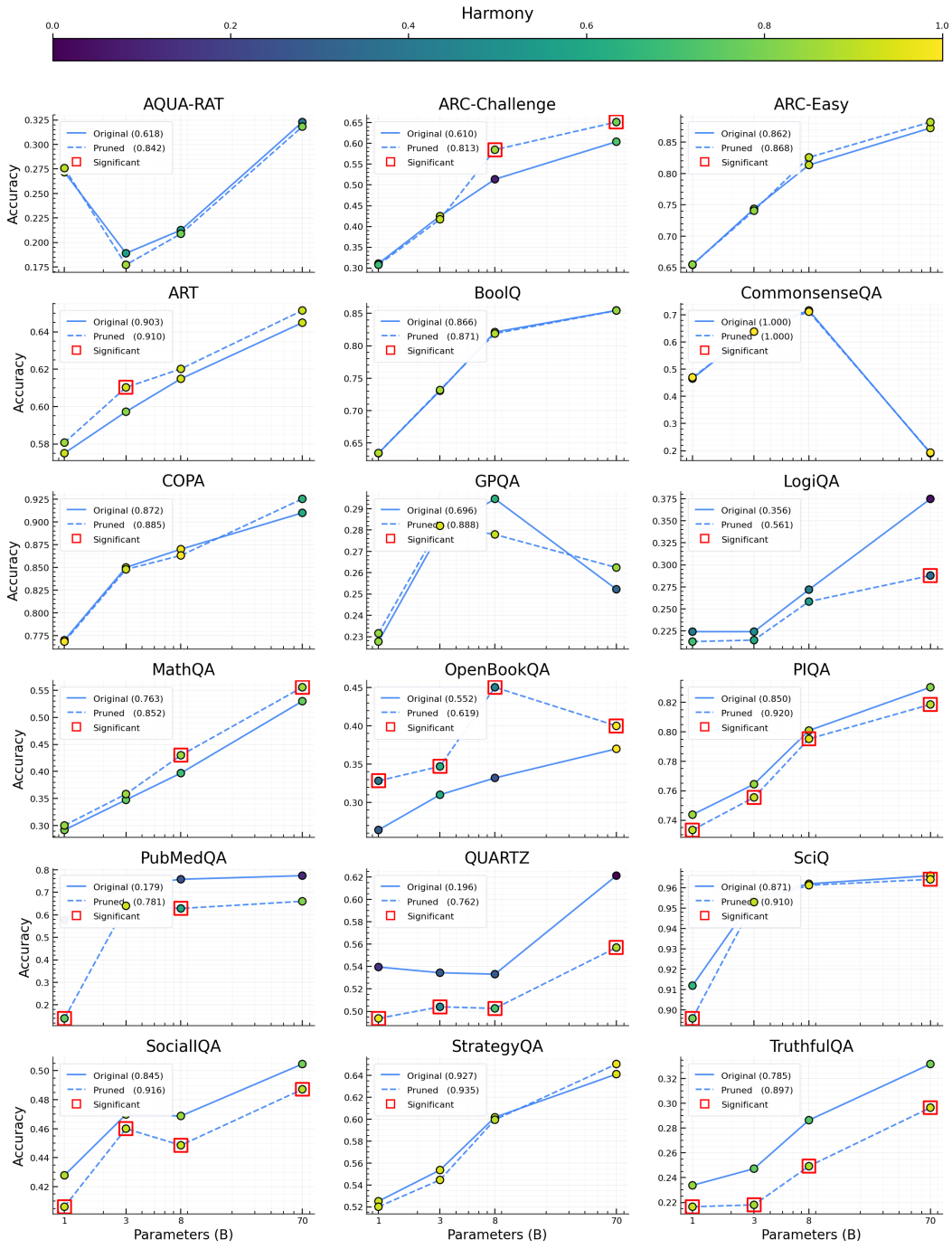


Figure 15: **Full results of balancing benchmarks via pruning in Llama 3 model family.** We remove overly similar items with a pruning rate inversely proportional to HARMONY, which consistently improves HARMONY. We find that aggregate scores often change statistically significantly on less harmonious benchmarks, whereas they remain more stable on more harmonious benchmarks.

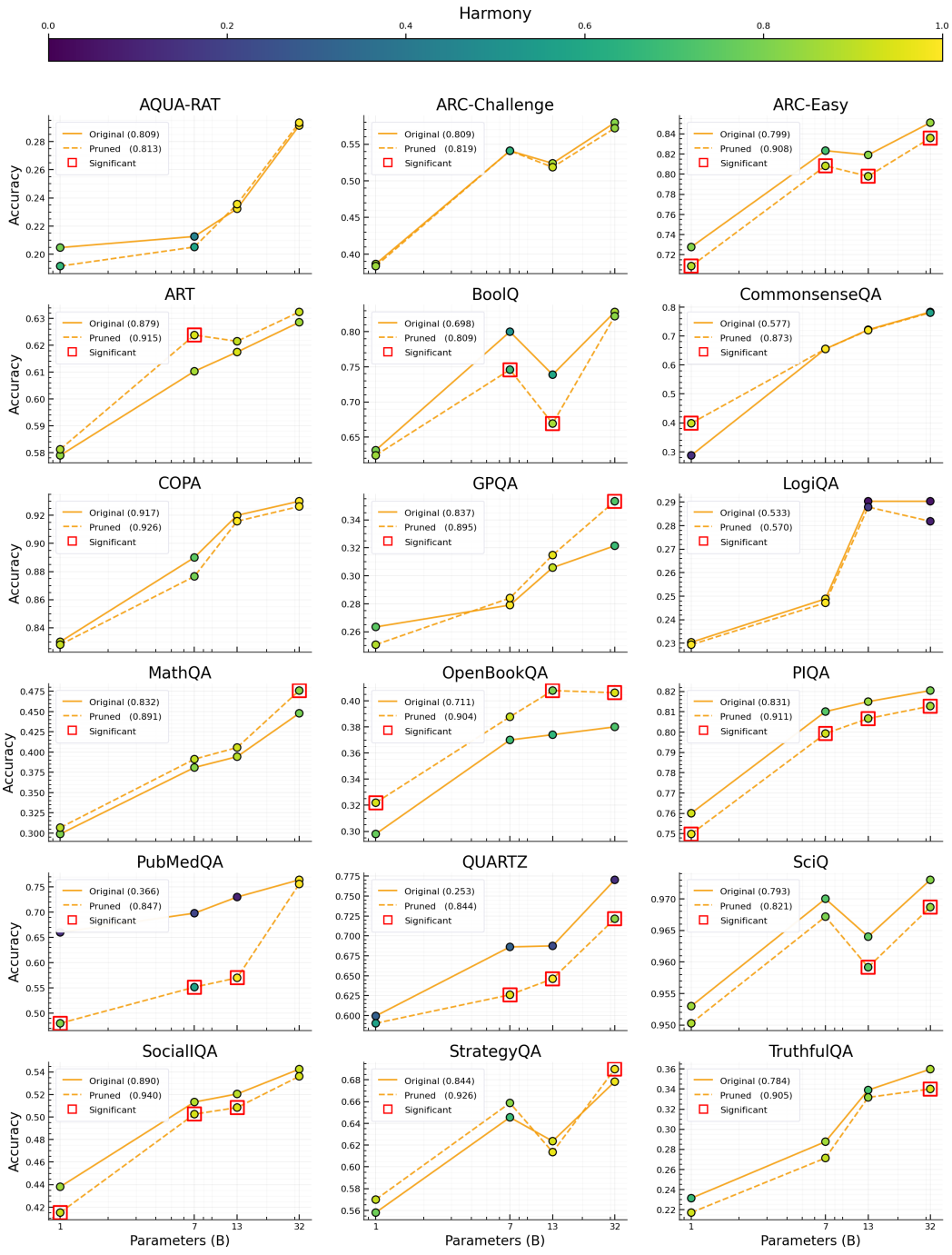


Figure 16: **Full results of balancing benchmarks via pruning in Olmo 2 model family.** We remove overly similar items with a pruning rate inversely proportional to HARMONY, which consistently improves HARMONY. We find that aggregate scores often change statistically significantly on less harmonious benchmarks, whereas they remain more stable on more harmonious benchmarks.

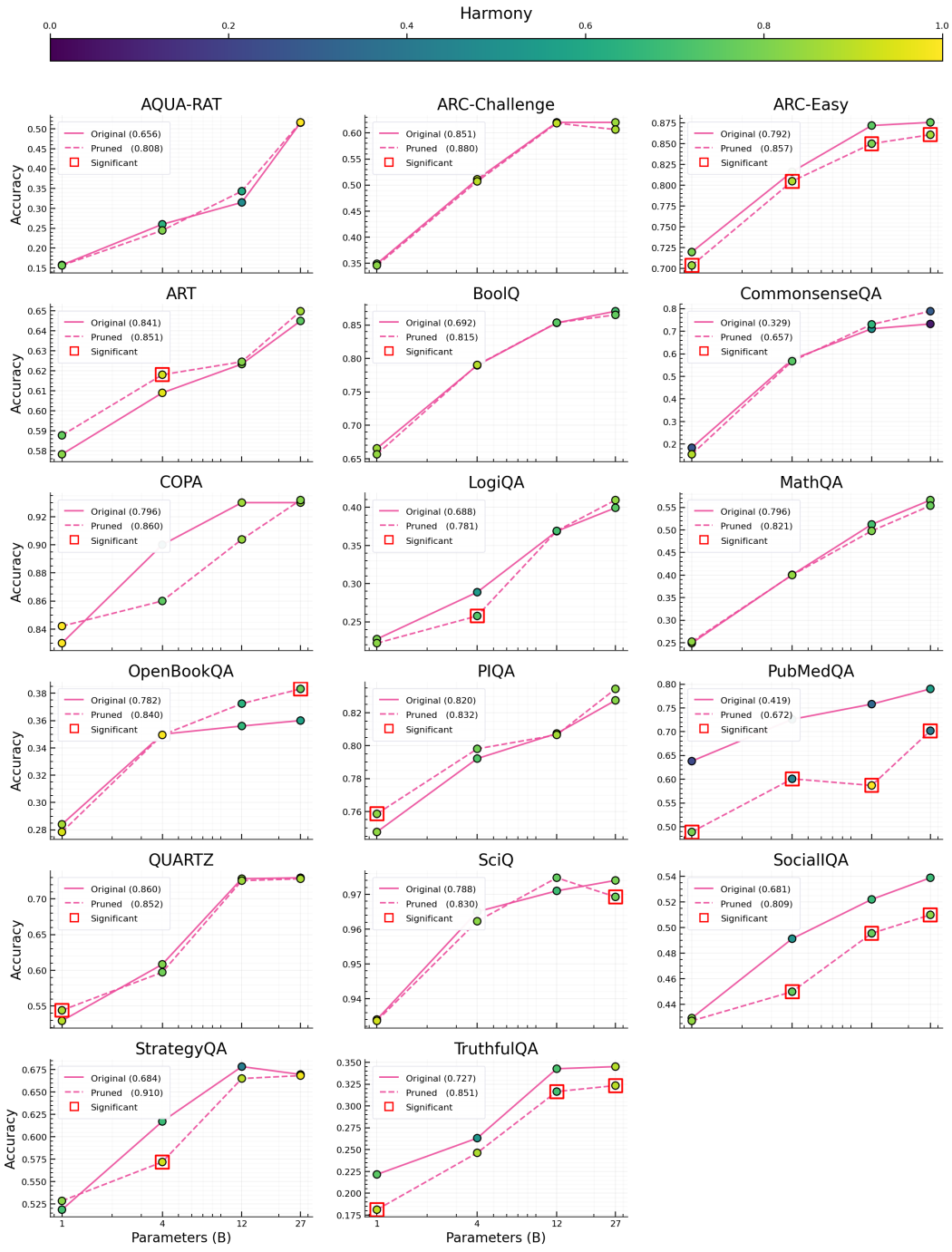


Figure 17: **Full results of balancing benchmarks via pruning in Gemma 3 model family.** We remove overly similar items with a pruning rate inversely proportional to HARMONY, which consistently improves HARMONY. We find that aggregate scores often change statistically significantly on less harmonious benchmarks, whereas they remain more stable on more harmonious benchmarks.

	Qwen3-0.6B	Qwen3-1.7B	Qwen3-4B	Qwen3-8B	Qwen3-14B
Overall	47.2	68.1	82.6	86.8	**91.0**
Multicellular Biology (42.4%)	45.9	68.9	88.5	88.5	**93.4**
Evolutionary & Ecological Processes (25.7%)	51.4	59.5	86.5	**91.9**	**91.9**
Molecular & Cellular Biology (31.9%)	45.7	73.9	71.7	80.4	**87.0**
HARMONY	0.951	0.918	0.757	0.784	0.859

Table 7: Multi-dimensional evaluation results of Qwen3 model family in MMLU College Biology. **Bold** implies the best performance.

	Qwen3-0.6B	Qwen3-1.7B	Qwen3-4B	Qwen3-8B	Qwen3-14B
Overall	24.5	34.3	58.8	57.8	**69.6**
Quantum Mechanics Principles and Applications (22.5%)	56.5	34.8	65.2	69.6	**73.9**
Thermodynamics (8.8%)	0.0	55.6	66.7	55.6	**77.8**
Special Relativity Concepts (13.7%)	21.4	14.3	**71.4**	50.0	57.1
Classical Physics Principles and Relationships (20.6%)	9.5	38.1	47.6	52.4	**61.9**
Physics Phenomena and Application (16.7%)	0.0	11.8	11.8	17.6	**58.8**
Electromagnetism (5.9%)	16.7	16.7	**83.3**	**83.3**	66.7
Solid State Physics (11.8%)	50.0	75.0	**100.0**	**100.0**	**100.0**
HARMONY	0.686	0.712	0.765	0.815	0.789

Table 8: Multi-dimensional evaluation results of Qwen3 model family in MMLU College Physics. **Bold** implies the best performance.

hierarchy enables interpretable, multi-dimensional evaluation, where each dimension corresponds to a subdomain of the benchmark.

We illustrate this approach on two examples: *MMLU College Biology* and *MMLU College Physics*. The average HARMONY across Qwen3 models is markedly higher for biology (0.8538) than for physics (0.7534). This suggests that the aggregate accuracy for biology is a more representative reflection of the performance across subdomains. Indeed, Table 7 shows that rankings in biology subdomains mirror the overall ordering: models that achieve higher overall accuracy also achieve higher accuracy in every subdomain. In other words, no model with superior overall performance is ever surpassed by a model with lower overall performance in any biology subdomain.[13] This alignment underscores that the aggregate score is a consistent and reliable summary of subdomain performance in biology.

In contrast, physics exhibits lower HARMONY and more notable divergences (Table 8). For example, Qwen3-4B lags behind Qwen3-14B in overall accuracy (58.8% vs. 69.6%), yet it surpasses it in *Special Relativity* (71.4% vs. 57.1%) and *Electromagnetism* (83.3% vs. 66.7%). Similarly, Qwen3-0.6B, despite its weak overall score (24.5%), achieves competitive performance in *Quantum Mechanics* (56.5%), outperforming Qwen3-1.7B (34.8%). These cases highlight how aggregate scores can obscure areas of relative strength, and how fine-grained, multi-dimensional evaluation reveals nuanced interpretation of model competence across subdomains.

We provide extended results for Qwen3 and Llama 3 model families across 2 MCQA benchmarks and 6 MMLU subtasks in Appendix I.

I EXTENDED RESULTS: MULTI-DIMENSIONAL EVALUATION

We provide the extended results of multi-dimensional evaluation conducted as described in Appendix H. Our setup consists of Qwen3 and Gemma 3 model families and ARC-Easy, BoolQ, MMLU Anatomy, MMLU College Biology, MMLU College Computer Science, MMLU College Mathematics, MMLU College Physics, MMLU High School US History.

I.1 QWEN3 FAMILY

See Tables 9, 10, 11, 12, 13, 14, 15, and 16 for the extended results of Qwen3 model family.

[13] Comparison of 1.7B and 4B in *Molecular & Cellular Biology* is the only exception.

	Qwen3-0.6B	Qwen3-1.7B	Qwen3-4B	Qwen3-8B	Qwen3-14B
Overall	60.7	72.2	80.5	83.5	84.2
Geology and Earth Sciences (15.0%)	64.4	73.4	83.8	83.8	83.8
Scientific Principles and Processes (32.6%)	56.3	70.1	79.9	83.5	84.3
Biological Processes and Concepts (24.1%)	65.4	74.0	78.8	82.9	83.6
Physics Principles in Engineering and Science (9.4%)	64.3	75.9	82.1	86.6	86.6
Environmental and Energy Assessment (6.5%)	60.4	63.6	78.6	81.2	79.9
Fundamental Concepts in Astronomy (7.6%)	56.1	76.7	80.6	83.3	87.2
Fundamentals of Chemical and Material Properties (4.8%)	56.1	71.9	81.6	84.2	84.2

Table 9: Multi-dimensional evaluation results for the Qwen3 model family on ARC-Easy.

	Qwen3-0.6B	Qwen3-1.7B	Qwen3-4B	Qwen3-8B	Qwen3-14B
Overall	64.1	77.5	85.0	86.6	89.3
Product Composition, Properties, and Standards (8.8%)	66.8	80.6	83.7	86.9	88.9
Geographic, Operational, and Temporal Analysis (11.0%)	69.3	77.3	85.3	88.4	91.7
Media Standards and Analysis (24.8%)	61.3	77.7	86.8	88.7	91.0
Scientific and Analytical Principles (9.0%)	67.9	81.2	83.3	84.6	89.1
Sports History and Regulations (10.1%)	63.5	75.1	82.1	84.5	87.2
Governmental Laws and Regulations (10.6%)	64.1	72.8	80.3	84.6	86.1
Human Biology and Medical Science (6.5%)	60.6	81.2	87.8	85.4	87.8
Economic Systems (8.3%)	61.6	75.3	85.2	85.6	87.5
Sociocultural, Geopolitical, and Linguistic Analysis (7.1%)	63.9	76.8	88.0	86.7	89.7
Fictional Narrative Analysis and Elements (3.8%)	64.8	80.8	89.6	88.0	93.6

Table 10: Evaluation results for the Qwen3 model family on BoolQ.

I.2 Gemma 3 Family

See Tables 17, 18, 19, 20, 21, 22, 23, and 24 for the extended results of Gemma 3 model family.

J Additional Related Work

Language Model Evaluation. Reliable evaluation is essential for accurately assessing model capabilities and enabling fair comparisons, which in turn informs future developments. Hence, there has been a surge in the development of benchmarks designed to test various model capabilities, such as reasoning (Bisk et al., 2019; Sap et al., 2019b; Zellers et al., 2019; Liu et al., 2020), world knowledge (Mihaylov et al., 2018b; Hendrycks et al., 2020; et al., 2023), and truthfulness (Lin et al., 2022; Khatun & Brown, 2024). Beyond individual benchmarks, holistic frameworks have emerged to offer a more comprehensive assessment of model performance (Liang et al., 2023; Chiang et al., 2024; Gao et al., 2024; Fourrier et al., 2023; et al., 2023). Reciprocally, understanding and improving current benchmarks have been equally important. MMLU Pro (Wang et al., 2024b) and Big-Bench-Hard (Suzgun et al., 2022) address benchmark saturation by constructing more challenging variants of MMLU (Hendrycks et al., 2020) and Big-Bench (bench authors, 2023) respectively. As top models approach ceiling effects on narrow probes, evaluation has shifted toward complex end-to-end tasks and composite suites. HLE and ARC-AGI assess multi-step reasoning, tool use, and robustness across domains (Phan et al., 2025; Chollet et al., 2025). Execution-grounded tasks such as SWE-bench measure real-world software problems and end-to-end correctness (Jimenez et al., 2024). Competitive exams like AIME and IMO, and professional exams such as the bar, push systems toward expert-level competence. Another recent practice is evaluation with online leaderboards, which use hidden test sets, fixed prompts, and compute disclosures in order to support fair comparison and consistent progress tracking (Chiang et al., 2024). Yet, these advances rest on a common premise that benchmarks reliably evaluate models on their stated domains. We audit this premise by testing whether benchmarks provide balanced coverage and promote comparable performance across subdomains.

K Hierarchical Labeling for Multi-Dimensional Evaluation

We build a tree benchmark over questions, then assign concise, human-readable labels to every node. Leaves summarize the shared evaluation focus of their questions, while internal nodes summarize their children.

	Qwen3-0.6B	Qwen3-1.7B	Qwen3-4B	Qwen3-8B	Qwen3-14B
Overall	37.8	56.3	62.2	71.1	80.7
General Human Anatomy, Physiology, and Terminology (31.9%)	51.2	67.4	79.1	76.7	86.0
Head and Neck Anatomy (21.5%)	20.7	34.5	34.5	62.1	82.8
Skeletal Development and Anatomy (14.1%)	26.3	42.1	47.4	52.6	57.9
Neurological Disorders (10.4%)	21.4	50.0	50.0	71.4	78.6
Bone Anatomy and Terminology (3.0%)	0.0	50.0	50.0	50.0	50.0
Anatomy of Circulatory System (2.2%)	66.7	100.0	100.0	100.0	100.0
Developmental Structures (6.7%)	22.2	44.4	55.6	77.8	88.9
Nephrology (10.4%)	78.6	92.9	100.0	92.9	92.9

Table 11: Evaluation results for the Qwen3 model family on MMLU Anatomy.

	Qwen3-0.6B	Qwen3-1.7B	Qwen3-4B	Qwen3-8B	Qwen3-14B
Overall	47.2	68.1	82.6	86.8	91.0
Multicellular Biology (42.4%)	45.9	68.9	88.5	88.5	93.4
Evolutionary and Ecological Processes (25.7%)	51.4	59.5	86.5	91.9	91.9
Molecular and Cellular Biology (31.9%)	45.7	73.9	71.7	80.4	87.0

Table 12: Evaluation results for the Qwen3 model family on MMLU College Biology.

To build the tree, we recursively induce partitions as discussed in §2.3, starting from the root (i.e., the entire benchmark) and ending at leaves (i.e., the clusters that do not admit a valid partition). For labeling leaves, we gather brief question annotations within a leaf and ask a model for one specific noun-phrase label. For labeling internal nodes of the tree, we pass the child labels to the model and ask for a slightly more abstract label that still captures the shared theme. Therefore, this procedure yields a bottom-up label propagation from leaves to internal nodes then to the root. We use `Gemini-2.0-flash` to annotate individual questions, assign each leaf a label from its question annotations, and propagate labels upward by aggregating child labels.

Prompts. We share the prompts we use for annotating the questions (Prompt K), labeling the leaves (Prompt K), and labeling the internal nodes (Prompt K).

Prompt for annotating questions.

You are given a question from the BENCHMARK benchmark.
Given this question, generate a single, concise sentence that clearly describes the **specific evaluation focus** of the question.
Question: QUESTION
Requirements:
- Do not have a prefix, simply provide a brief phrase or a gerund.
- Do not add commentary.

L THE USE OF LARGE LANGUAGE MODELS (LLMS)

In this work, we used large language models (LLMs) only for light polishing (grammar, wording, and clarity) after the technical content was written. LLMs were not used for research ideation, experimental design or execution, analysis, figure or table generation, or drafting technical sections. All substantive content, results, and conclusions are authored by the listed authors, who take full responsibility for the paper's contents, including any text edited with LLM assistance. LLMs are not eligible for authorship, and no LLM is listed as an author.

	Qwen3-0.6B	Qwen3-1.7B	Qwen3-4B	Qwen3-8B	Qwen3-14B
Overall	28.0	41.0	66.0	72.0	68.0
Theoretical Foundations of Computation (52.0%)	26.9	40.4	59.6	69.2	65.4
Computer Architecture and Optimization (7.0%)	28.6	42.9	71.4	57.1	57.1
Operating Systems (10.0%)	50.0	80.0	90.0	90.0	80.0
Network Layer Protocols and Technologies (5.0%)	60.0	60.0	80.0	100.0	100.0
Data Processing (12.0%)	8.3	8.3	66.7	50.0	66.7
Sorting Algorithms (4.0%)	25.0	25.0	75.0	100.0	100.0
Graph Algorithms and Data Structures (10.0%)	20.0	40.0	60.0	80.0	50.0

Table 13: Evaluation results for the Qwen3 model family on MMLU College Computer Science.

	Qwen3-0.6B	Qwen3-1.7B	Qwen3-4B	Qwen3-8B	Qwen3-14B
Overall	31.0	39.0	55.0	59.0	68.0
Advanced Real Analysis (19.0%)	26.3	26.3	42.1	52.6	52.6
Abstract Algebra (11.0%)	27.3	45.5	90.9	63.6	81.8
Probability (7.0%)	28.6	71.4	28.6	57.1	57.1
Properties of Mathematical Operations and Functions (5.0%)	20.0	20.0	40.0	80.0	80.0
Advanced Mathematical Concepts and Applications (16.0%)	31.3	37.5	75.0	56.3	75.0
Mathematical Modeling and Algorithms (10.0%)	30.0	50.0	60.0	60.0	70.0
Multivariable Calculus (27.0%)	25.9	37.0	40.7	59.3	63.0
Mathematical Optimization Methods (5.0%)	100.0	40.0	80.0	60.0	100.0

Table 14: Evaluation results for the Qwen3 model family on MMLU College Mathematics.

Prompt for labeling leaves.

You are a taxonomy assistant. Your task is to read short annotations that describe what each question evaluates and produce one concise but descriptive label that summarizes the shared knowledge or concept.
Guidelines:
- The label must be highly specific, directly capturing the core idea, while still generalizable across closely related items.
- Prioritize specificity: avoid vague or overly broad terms.
- Use a clear noun phrase.
- Return only the label text.

	Qwen3-0.6B	Qwen3-1.7B	Qwen3-4B	Qwen3-8B	Qwen3-14B
Overall	24.5	34.3	58.8	57.8	69.6
Quantum Mechanics Principles and Applications (22.5%)	56.5	34.8	65.2	69.6	73.9
Thermodynamics (8.8%)	0.0	55.6	66.7	55.6	77.8
Special Relativity Concepts (13.7%)	21.4	14.3	71.4	50.0	57.1
Classical Physics Principles and Relationships (20.6%)	9.5	38.1	47.6	52.4	61.9
Physics Phenomena and Applications (16.7%)	0.0	11.8	11.8	17.6	58.8
Electromagnetism (5.9%)	16.7	16.7	83.3	83.3	66.7
Solid State Physics Concepts (11.8%)	50.0	75.0	100.0	100.0	100.0

Table 15: Evaluation results for the Qwen3 model family on MMLU College Physics.

	Qwen3-0.6B	Qwen3-1.7B	Qwen3-4B	Qwen3-8B	Qwen3-14B
Overall	52.5	66.2	83.3	88.7	91.7
US Sociopolitical Ideologies, Movements, and Issues (46.1%)	52.1	64.9	83.0	90.4	95.7
Progressive Era Economic and Social Initiatives (3.9%)	75.0	87.5	100.0	100.0	100.0
United States Governance and Politics (37.3%)	46.1	61.8	81.6	85.5	88.2
Ideological and Territorial Expansion in the Americas (9.8%)	70.0	80.0	90.0	95.0	85.0
American History Eras (2.9%)	50.0	66.7	66.7	66.7	83.3

Table 16: Evaluation results for the Qwen3 model family on MMLU High School U.S. History.

	Gemma 3 1B	Gemma 3 4B	Gemma 3 12B	Gemma 3 27B
Overall	72.0	81.6	87.2	87.5
Geology and Earth Sciences (15.0%)	74.5	84.6	87.7	89.4
Scientific Principles and Processes (32.6%)	71.2	79.7	86.5	87.0
Biological Processes and Concepts (24.1%)	74.3	83.0	88.5	87.8
Physics Principles in Engineering and Science (9.4%)	70.5	83.0	88.8	88.8
Environmental and Energy Assessment (6.5%)	68.2	80.5	83.1	84.4
Fundamental Concepts in Astronomy (7.6%)	72.8	79.4	86.7	87.2
Fundamentals of Chemical and Material Properties (4.8%)	64.0	79.8	86.8	86.8

Table 17: Multi-dimensional evaluation results for the Gemma 3 model family on ARC-Easy.

	Gemma 3 1B	Gemma 3 4B	Gemma 3 12B	Gemma 3 27B
Overall	66.5	79.0	85.3	87.1
Product Composition, Properties, and Standards (8.8%)	67.5	76.1	82.4	88.6
Geographic, Operational, and Temporal Analysis (11.0%)	67.6	83.7	84.8	87.3
Media Standards and Analysis (24.8%)	66.7	80.6	88.5	89.6
Scientific and Analytical Principles (9.0%)	65.2	75.1	82.9	86.0
Sports History and Regulations (10.1%)	63.2	78.7	83.0	86.0
Governmental Laws and Regulations (10.6%)	64.1	75.7	80.3	82.0
Human Biology and Medical Science (6.5%)	77.0	82.6	86.9	89.2
Economic Systems (8.3%)	66.1	77.1	85.6	85.6
Sociocultural, Geopolitical, and Linguistic Analysis (7.1%)	61.8	78.1	87.6	84.1
Fictional Narrative Analysis and Elements (3.8%)	71.2	79.2	91.2	90.4

Table 18: Multi-dimensional evaluation results for the Gemma 3 model family on BoolQ.

	Gemma 3 1B	Gemma 3 4B	Gemma 3 12B	Gemma 3 27B
Overall	25.9	61.5	70.4	70.4
General Human Anatomy, Physiology, and Terminology (31.9%)	27.9	69.8	83.7	79.1
Head and Neck Anatomy (21.5%)	27.6	41.4	55.2	48.3
Skeletal Development and Anatomy (14.1%)	21.1	52.6	52.6	57.9
Neurological Disorders (10.4%)	42.9	64.3	57.1	71.4
Bone Anatomy and Terminology (3.0%)	50.0	50.0	50.0	50.0
Anatomy of Circulatory System (2.2%)	0.0	100.0	100.0	100.0
Developmental Structures (6.7%)	11.1	44.4	77.8	88.9
Nephrology (10.4%)	14.3	92.9	92.9	92.9

Table 19: Multi-dimensional evaluation results for the Gemma 3 model family on MMLU Anatomy.

	Gemma 3 1B	Gemma 3 4B	Gemma 3 12B	Gemma 3 27B
Multicellular Biology (42.4%)	27.9	68.9	98.4	93.4
Evolutionary and Ecological Processes (25.7%)	21.6	67.6	86.5	86.5
Molecular and Cellular Biology (31.9%)	21.7	65.2	87.0	91.3

Table 20: Multi-dimensional evaluation results for the Gemma 3 model family on MMLU College Biology.

	Gemma 3 1B	Gemma 3 4B	Gemma 3 12B	Gemma 3 27B
Overall	30.0	48.0	57.0	63.0
Theoretical Foundations of Computation (52.0%)	36.5	38.5	51.9	61.5
Computer Architecture and Optimization (7.0%)	28.6	57.1	71.4	57.1
Operating Systems (10.0%)	20.0	60.0	80.0	80.0
Network Layer Protocols and Technologies (5.0%)	20.0	60.0	100.0	100.0
Data Processing (12.0%)	25.0	33.3	41.7	41.7
Sorting Algorithms (4.0%)	0.0	100.0	100.0	75.0
Graph Algorithms and Data Structures (10.0%)	30.0	70.0	30.0	60.0

Table 21: Multi-dimensional evaluation results for the Gemma 3 model family on MMLU College Computer Science.

	Gemma 3 1B	Gemma 3 4B	Gemma 3 12B	Gemma 3 27B
Overall	33.0	41.0	50.0	58.0
Advanced Real Analysis (19.0%)	57.9	52.6	47.4	52.6
Abstract Algebra (11.0%)	27.3	72.7	63.6	54.5
Probability (7.0%)	14.3	57.1	42.9	57.1
Properties of Mathematical Operations and Functions (5.0%)	60.0	40.0	40.0	80.0
Advanced Mathematical Concepts and Applications (16.0%)	25.0	31.3	56.3	68.8
Mathematical Modeling and Algorithms (10.0%)	20.0	30.0	50.0	60.0
Multivariable Calculus (27.0%)	29.6	25.9	40.7	55.6
Mathematical Optimization Methods (5.0%)	20.0	40.0	80.0	40.0

Table 22: Multi-dimensional evaluation results for the Gemma 3 model family on MMLU College Mathematics.

	Gemma 3 1B	Gemma 3 4B	Gemma 3 12B	Gemma 3 27B
Overall	20.6	41.2	52.9	63.7
Quantum Mechanics Principles and Applications (22.5%)	8.7	39.1	43.5	73.9
Thermodynamics (8.8%)	11.1	22.2	55.6	55.6
Special Relativity Concepts (13.7%)	28.6	35.7	42.9	50.0
Classical Physics Principles and Relationships (20.6%)	42.9	28.6	57.1	66.7
Physics Phenomena and Applications (16.7%)	5.9	41.2	29.4	41.2
Electromagnetism (5.9%)	0.0	66.7	83.3	50.0
Solid State Physics Concepts (11.8%)	33.3	75.0	91.7	100.0

Table 23: Multi-dimensional evaluation results for the Gemma 3 model family on MMLU College Physics.

	Gemma 3 1B	Gemma 3 4B	Gemma 3 12B	Gemma 3 27B
Overall	26.0	75.5	88.2	91.2
US Sociopolitical Ideologies, Movements, and Issues (46.1%)	26.6	80.9	87.2	92.6
Progressive Era Economic and Social Initiatives (3.9%)	25.0	100.0	100.0	87.5
United States Governance and Politics (37.3%)	26.3	67.1	89.5	90.8
Ideological and Territorial Expansion in the Americas (9.8%)	20.0	75.0	85.0	90.0
American History Eras (2.9%)	33.3	66.7	83.3	83.3

Table 24: Multi-dimensional evaluation results for the Gemma 3 model family on MMLU High School U.S. History.

Prompt for labeling internal nodes.

You are a taxonomy assistant. Your task is to read the labels of child clusters and generate one concise but descriptive parent label that captures their common theme at a higher level of abstraction.
Guidelines:
- The label must be specific and clearly meaningful, while still broad enough to encompass all children.
- Prioritize specificity: avoid vague or generic terms that do not capture the essence of the group.
- Use a clear noun phrase.
- Return only the label text.