SOVEREIGN: How does the inference throughput of AnyExperts' sparse MoE architecture compare to dense transformers of equi

SOVEREIGN Research Kernel
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Abstract

We describe MUSCLE, a new computer program for creating multiple alignments of protein sequences. Elements of the algorithm include fast distance estimation using kmer counting, progressive alignment using a new profile function we call the log-expectation score, and refinement using tree-dependent restricted partitioning. The speed and accuracy of MUSCLE are compared with T-Coffee, MAFFT and CLUSTALW on four test sets of reference alignments: BAliBASE, SABmark, SMART and a new benchmark, PREFAB. MUSCLE achieves the highest, or joint highest, rank in accuracy on each of these sets. Without ref

1 Introduction

Analysis of: MUSCLE: multiple sequence alignment with high accuracy and high throughput. Research goal: How does the inference throughput of AnyExperts' sparse MoE architecture compare to dense transformers of equivalent parameter count on code generation benchmarks (e.g., HumanEval, MBPP) when expert count is scaled from 8 to 64?.

2 Methodology

Multi-query arXiv search (1 parallel queries, Relevance-sorted). TF-IDF cosine semantic verification (bigrams, threshold=0.15). NIM nv-embedqa-e5-v5 (dim=1024) for semantic indexing. Tribunal v2: 3-role parallel review (SKEPTIC/VALIDATOR/SYNTHESIZER) with revision round if score $<$ 6.5.

3 Results

10 papers retrieved. 3 claims extracted, 3 verified. Tribunal: 6.0/10 → REVISE (revision_round=1). Policy: SOFT_APPROVE.

4 Uncertainties

NIM free tier latency varies. TF-IDF verification is a weak signal. arXiv Relevance ranking is query-dependent. Tribunal consensus is LLM-based and prompt-sensitive.

5 Extracted Claims

Claim	Verified	Confidence
MUSCLE achieves the highest, or joint highest, rank in accuracy on each of the four test sets of reference alignments: B	✓	0.36
Without refinement, MUSCLE achieves average accuracy statistically indistinguishable from T-Coffee and MAFFT	✓	0.35
MUSCLE achieves the highest, or joint highest, rank in accuracy on each of these sets	✓	0.28

References

- `https://doi.org/10.14806/ej.17.1.200`
- `https://doi.org/10.1093/nar/gkh340`
- `https://doi.org/10.1093/genetics/155.2.945`