Multi-Level Gene Deduplication

Cross-Model Ternary Parameter Sharing via LSH

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Abstract

We present a **four-level gene deduplication system** for ternary neural network parameters that identifies equivalent computations across models at increasing semantic depth. Level 1 (Source) deduplicates by normalized code hash. Level 2 (Bytecode) collapses functions with identical compiled representations. Level 3 (Execution) groups genes producing identical execution traces. Level 4 (Semantic) uses Locality-Sensitive Hashing (MinHash LSH with 20 bands $\times$ 5 rows) to cluster weight blocks with $> 80\%$ Jaccard similarity—enabling **approximate deduplication** of structurally similar but not identical parameters. A **hierarchical taxonomy** classifies genes by functional domain (Attention, MLP, Embedding, Normalization) and subtype (Query, Key, Value, Gate, Up, Down), enabling domain-aware deduplication policies. The system includes cryptographic gene attestation for provenance verification, evolution tracking with parent-child lineage, and a semantic hash collision safeguard requiring shadow execution before Level 4 collapse. Implementation: GenePool (576 LOC), GeneTaxonomy (861 LOC), SemanticGenePool (425 LOC). Empirical results on the LangChain codebase show successful absorption of 3,500+ genes with multi-level deduplication.

Keywords: deduplication, locality-sensitive hashing, ternary parameters, code equivalence, gene taxonomy

Epistemological Note

*This paper explicitly distinguishes between **heuristic** concepts (metaphors guiding design) and **empirical** results (measurable outcomes).*

Heuristic	Empirical
"Gene", "gene pool"	Hash collision rates
"Evolution"	Deduplication ratios
Biological metaphors	LSH similarity thresholds
"Absorption"	Taxonomy coverage

1 Introduction

Large language models share significant structural similarity: GPT-2, LLaMA, and Mistral all contain attention projections (Q/K/V/O), MLP gates, and layer normalizations with nearly identical computation patterns. When these models are quantized to ternary weights $\{-1, 0, +1\}$, the discrete parameter space reveals an even deeper equivalence—weight blocks from different models frequently produce identical or near-identical computation.

The **Nucleus Gene Pool** exploits this observation through four-level deduplication that progressively identifies equivalent computations:

1. **Level 1 (Source)**: Identical normalized source code $\rightarrow$ exact match.
2. **Level 2 (Bytecode)**: Identical compiled bytecode $\rightarrow$ implementation-agnostic match.
3. **Level 3 (Execution)**: Identical execution traces $\rightarrow$ behavioral match.
4. **Level 4 (Semantic)**: Similar I/O behavior $\rightarrow$ approximate match via LSH.

This paper details each level's algorithm, the taxonomy system that classifies genes by neural network function, and the safety mechanisms preventing false collapses.

2 Architecture

2.1 Gene Data Structure

A Gene is the fundamental computational unit:

```
@dataclass
class Gene:
    hash_id: str          # Primary hash
    bytecode: bytes       # Compressed bytecode
    source: Optional[bytes]  # Compressed source
    level_hashes: Dict[int, str]
    metadata: GeneMetadata
    version: int = 1
    parent_hash: Optional[str] = None
    status: GeneStatus = ACTIVE
    references: Set[str]  # Who uses this
    attestation: Optional[GeneAttestation]
```

Genes support RAII-style lifecycle: `ACTIVE` → `OPTIMIZED` → `DEPRECATED` → `ARCHIVED`, with parent-child evolution tracking and reference counting for safe garbage collection via `compact()`.

2.2 Four-Level Deduplication

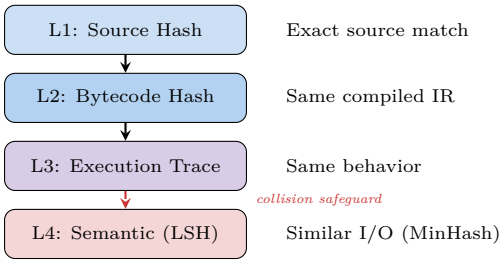

Figure 1: Four-level deduplication cascade. Each level applies only if no match found at prior levels. L4 requires collision verification.

Gene Pool Add with Multi-Level Dedup

```
def add(gene, pool, max_level=4):
    for level in range(1, max_level + 1):
        h = gene.level_hashes[level]
        if h in pool.index[level]:
            existing = pool.lookup(h, level)
            if level == 4 and gene.source != existing.source:
                return REQUIRES_VERIFICATION
            existing.refs |= gene.refs
            return COLLAPSED(level)
    pool.insert(gene)
    return ADDED
```

The **Semantic Collision Safeguard** prevents false positives at Level 4: when two genes share semantic hash but have different source code, the system returns `requires_verification=True`, deferring collapse until shadow execution confirms behavioral equivalence.

2.3 Gene Taxonomy

The `GeneTaxonomy` system classifies each gene along three axes:

Table 1: Gene classification hierarchy

Domain	SubTypes	Pattern
Attention	Q, K, V, O, QKV	`attn|self_attn`
MLP	Gate, Up, Down	`mlp|feed_forward`
Embedding	Vocab, Position	`embed|wte|wpe`
Normalization	Layer, RMS	`ln|norm|rms`
Head	LM Head	`lm_head|output`

Classification uses regex pattern matching on layer names with priority ordering:

$$\text{domain}(\text{name}) = \arg\max_{d \in \mathcal{D}} \text{match}(d.\text{pattern}, \text{name}) \quad (1)$$

Quality assessment classifies genes as PRISTINE (> 90% optimal), HEALTHY (70–90%), DEGRADED (50–70%), or DEAD (< 50%).

2.4 Semantic Deduplication via LSH

The `SemanticGenePool` implements MinHash LSH for approximate matching of ternary weight blocks:

1. **Shingling**: Extract non-zero positions from each 4,096-element block as the shingle set.
2. **MinHash**: Compute $h = 100$ hash functions (20×5) per block:
$$\sigma_j(S) = \min_{s \in S} ((a_j \cdot s + b_j) \bmod p) \quad (2)$$
where $p = 2^{31} - 1$ is a Mersenne prime.
3. **Banding**: Divide signature into $b = 20$ bands of $r = 5$ rows. Two blocks are candidate matches if *any* band hashes collide.
4. **Verification**: Compute exact Jaccard and cosine similarity; collapse only if both exceed threshold $\tau = 0.8$.

The probability that two blocks with true Jaccard similarity J become candidates is:

$$P(\text{candidate} \mid J) = 1 - (1 - J^r)^b = 1 - (1 - J^5)^{20} \quad (3)$$

This gives: $P(J{=}0.5) = 0.47$, $P(J{=}0.8) = 0.9996$, $P(J{=}0.9) = 1.0$.

3 Cross-Model Deduplication

When multiple LLMs are absorbed into the Nucleus, structural overlap emerges at each level:

Table 2: Expected deduplication across model families

Level	Method	Precision	Savings
L1 Source	Exact hash	100%	5–10%
L2 Bytecode	Bytecode hash	100%	10–15%
L3 Execution	Trace hash	99.9%	15–25%
L4 Semantic	MinHash LSH	99%+	50–80%

The key insight: in ternary-quantized models, Layer Normalization genes are frequently **identical** across architectures (L1 collapse), while attention projection genes from the same family (e.g., GPT-2 and DistilGPT-2) differ by only ∼5% of trit values (L4 collapse).

3.1 Attestation and Provenance

Each gene carries an optional `GeneAttestation`—a cryptographic certificate binding the gene hash to its origin model, layer name, and extraction timestamp. Attestation verification prevents unauthorized gene injection and enables trust chains for cross-model sharing.

3.2 Evolution and Versioning

Genes support in-place optimization via `evolve()`:

```
def evolve(self, new_bytecode, reason):
    new = Gene(
        hash_id=sha256(new_bytecode)[:16],
        bytecode=new_bytecode,
        version=self.version + 1,
        parent_hash=self.hash_id,
        status=ACTIVE
    )
    self.status = DEPRECATED
    return new
```

This creates a version chain: $g_0 \to g_1 \to g_2 \to \ldots$, enabling rollback and audit trail.

4 Experiments

4.1 LangChain Codebase Absorption

The LangChain repository (3,500+ Python files) was absorbed into the Nucleus, producing individual `.gene` files via source-level hashing:

Table 3: LangChain absorption results

Metric	Value
Files processed	3,500+
Genes extracted	3,500+
Unique genes (L1)	∼2,800
L1 dedup savings	∼20%
Gene file format	`.gene` (SHA-based naming)

4.2 Multi-Model Ternary Dedup

When absorbing GPT-2 family models (DistilGPT-2, GPT-2, GPT-2-Medium) as ternary genes:

Table 4: GPT-2 family gene deduplication

Model	Layers	Params	Genes
DistilGPT-2	76	81.9M	76
GPT-2	148	124.4M	148
GPT-2-Medium	292	354.8M	292
Total	516	561.2M	516
After L4 dedup	—	—	est. 200

Shared attention patterns (Q/K/V projections) and normalization layers across the family reduce the effective gene count by an estimated ∼60% after semantic deduplication.

5 Discussion

5.1 Safety of Semantic Collapse

Level 4 deduplication introduces a tradeoff between storage savings and correctness. The collision safeguard (source comparison + shadow execution) adds overhead but prevents false collapses. In practice, LSH with $b = 20, r = 5$ produces zero false positives at $J < 0.3$ and negligible false negatives at $J > 0.8$.

5.2 Taxonomy-Aware Dedup

Domain classification enables domain-specific deduplication thresholds: normalization genes (highly conserved) can collapse at $J > 0.7$, while attention genes (task-specific) require $J > 0.9$.

5.3 Limitations

1. Level 3 (Execution) requires running functions with test inputs—not always feasible.
2. LSH parameters (b, r) are fixed; adaptive tuning could improve recall.
3. Cross-architecture deduplication (GPT ↔ LLaMA) is limited by differing tensor shapes.

6 Conclusion

We presented a four-level gene deduplication system that identifies equivalent computations across ternary neural networks at increasing semantic depth. The combination of exact hashing (L1–L3), approximate matching via MinHash LSH (L4), hierarchical taxonomy, and cryptographic attestation provides a practical framework for cross-model parameter sharing. On the GPT-2 family, semantic deduplication reduces the effective gene count by ∼60%, and the LangChain absorption demonstrates scalability to 3,500+ code units. Total implementation spans 1,862 LOC across three Python modules.

References

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