

# Do Biological Structural Guarantees Earn Their Complexity?

Empirical Benchmarks for Biologically-Inspired Agent Reliability

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Bogdan Banu  
bogdan@banu.be

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## Abstract

Biologically-inspired AI agent frameworks claim reliability benefits through structural guarantees adapted from gene regulatory networks, immune systems, and metabolic control. These claims are rarely tested empirically against simpler alternatives. We present three deep benchmarks—metabolic priority gating, autoinducer-based quorum sensing, and Bayesian stagnation detection—each comparing a biologically-grounded implementation against a naive non-biological alternative and an ablated control, across 1,000 trials per seed and 10 seeds (10M+ data points total). Metabolic priority gating delivers 100% critical-operation service under bursty load versus 39.8% for a flat budget counter ( $\Delta = +0.602$ ,  $p < 0.001$ ). Quorum sensing achieves 0% false-positive rate with 71–87% true-positive rate at 40% agent compromise, occupying a unique precision–recall operating point that neither majority voting nor independent detection reaches. Bayesian stagnation detection loses to cosine similarity with mock embeddings but wins on convergence and false-stagnation discrimination with real sentence embeddings (96% versus 2–40% naive), while the naive detector retains an advantage on trivial loop detection. This reveals a conditional structural guarantee that activates when embedding quality is present. The pattern across all three benchmarks: biological design earns its complexity through *mechanism-level structural guarantees*—priority gating, signal accumulation with temporal decay, two-signal discrimination—rather than through algorithmic sophistication. End-to-end evaluation with Gemma 4 27B confirms that state-integrity guarantees (DNA repair) provide deterministic protection, while behavioral and output-layer guarantees show honest limitations with capable models.

## 1 Introduction

Biological metaphors have a long history in computing. Artificial immune systems detect network intrusions [8]. Swarm intelligence algorithms solve combinatorial optimization [4]. Neural architectures borrow structural motifs from neuroscience. In each case, the biological analogy provides organizing structure for the algorithm—but the question of whether that structure *earns its complexity* over simpler alternatives is rarely asked.

The default assumption is that biological inspiration provides qualitative benefits: more robust error handling, more adaptive resource management, more distributed coordination. What is missing is quantitative comparison. Does a multi-currency metabolic state machine actually serve more critical operations under pressure than a flat budget counter? Does signal accumulation with temporal decay actually reduce false alarms compared to majority voting? Does Bayesian two-signal

stagnation detection actually distinguish convergence from pathological loops better than cosine similarity?

This paper tests these questions empirically using Operon, a biologically-inspired AI agent reliability framework that implements 22 biological motifs spanning genome-level configuration through tissue-level coordination [3]. We select three motifs that represent distinct reliability claims, ground each benchmark in real biological pathway data from KEGG and Reactome, and compare each biological implementation against both a naive non-biological alternative and an ablated control.

**The structural guarantee hypothesis.** Our central hypothesis is that biological design earns complexity when it provides *mechanism-level structural guarantees*—hard properties enforced by design rather than achieved by optimization. A metabolic state machine that rejects low-priority operations in STARVING state provides a structural guarantee: critical operations *will* be served regardless of load pattern. A signal accumulation model with exponential decay provides a structural guarantee: stale evidence *will* age out regardless of query timing. These are mechanism design choices, not algorithmic improvements.

We contrast this with biological designs that attempt *information processing*—using the biological metaphor to make better decisions rather than to enforce structural invariants. Our hypothesis is that these do not reliably outperform simpler alternatives.

**Pathway-grounded methodology.** Each benchmark derives its test scenarios from real biological pathway data. The metabolism benchmark uses AMPK signaling pathway parameters (KEGG hsa04152) for metabolic state thresholds and rate-of-change sensitivity. The quorum sensing benchmark uses autoinducer kinetics from the *V. fischeri* LuxI/LuxR system (KEGG map02024) for signal decay half-life and threshold scaling. The epiplexity benchmark uses the free energy principle [7] to generate trophic-withdrawal scenarios. This grounding prevents the benchmarks from testing against our own assumptions about what failure patterns look like.

**Three-variant comparison.** Each benchmark runs three experimental conditions:

1. **Biological:** the full Operon feature, biologically grounded.
2. **Ablated:** the feature disabled entirely (e.g., no monitor, no scaling).
3. **Naive:** a simple, reasonable, non-biological alternative that a competent engineer would reach for (e.g., cosine similarity, majority vote, flat counter).

Ablation proves necessity; the naive alternative proves the biological *design* matters, not just having any feature at all.

## Contributions.

1. A benchmark suite testing three biologically-grounded agent reliability features against naive alternatives, with 10M+ data points across 10 seeds.
2. Three empirical wins for biological structural guarantees (metabolism, quorum sensing, epiplexity with real embeddings), with the epiplexity result conditional on embedding quality.
3. Evidence that the distinction between *structural guarantees* and *algorithmic sophistication* predicts where biological design earns complexity.

## 2 Related Work

**Artificial immune systems.** Hofmeyr and Forrest [8] proposed an architecture for distributed intrusion detection modeled on the complement cascade and T-cell activation. Dasgupta [5] surveys two decades of AIS research. These systems demonstrate that immune-inspired pattern matching can detect novel threats, but comparative benchmarks against non-biological baselines (e.g., rule-based detectors) are sparse. Our quorum sensing benchmark addresses a related problem—multi-agent threat consensus—but explicitly compares the biological signal-accumulation model against majority voting and independent detection.

**Swarm intelligence.** Bonabeau, Dorigo, and Theraulaz [4] established the foundations of swarm-based optimization (ACO, PSO). These algorithms use biological coordination metaphors (pheromone trails, flocking rules) for optimization. Operon’s quorum sensing addresses a different problem: *consensus* rather than *optimization*. The distinction matters: our benchmark tests whether the biological coordination model achieves better precision–recall tradeoffs than simpler voting schemes, not whether it finds better optima.

**Metabolic computing.** Resource-aware agent systems have been explored in economic frameworks [11], but explicitly metabolic models—with multiple energy currencies, state-dependent behavior, and regeneration—are less common. Operon’s ATP\_Store draws on AMPK signaling pathway structure (KEGG hsa04152), where the AMP:ATP ratio and its rate of change drive metabolic state transitions. Our benchmark tests whether this biological structure provides measurable benefits over a flat budget counter.

**Free energy principle.** Friston’s free energy principle [7] provides the theoretical foundation for Operon’s epiplexity monitor: healthy agents minimize surprise while maintaining viability; agents with high perplexity and low novelty are in pathological loops. Our benchmark tests whether this theoretical framework translates to practical stagnation detection advantages over cosine-similarity thresholds.

**Multi-agent benchmarks.** Recent work on multi-agent scaling laws [9] establishes architecture-level performance predictors. Operon’s epistemic topology (Paper 1) derives similar bounds from wiring diagram structure. Our benchmarks complement this work by testing *mechanism-level* guarantees rather than *architecture-level* predictions.

## 3 Methods

### 3.1 Experimental Design

Each benchmark runs three variants (Biological, Ablated, Naive) across the same scenario sequences. We use  $N = 1,000$  trials per scenario per seed, with 10 independent seeds, yielding 10,000 trials per scenario. Confidence intervals use Wilson score intervals at the 95% level. All benchmarks are deterministic given the seed—no LLM calls are made during benchmark execution.

Scenarios are generated from two sources: *synthetic* scenarios with controlled failure patterns (loops, bursts, spikes), and *pathway-grounded* scenarios whose parameters derive from real KEGG/Reactome pathway data. The synthetic scenarios provide controlled baselines; the pathway-grounded scenarios test whether the biological design handles biologically-realistic patterns better than alternatives.

### 3.2 Benchmark 1: Metabolic Priority Gating

**Biological system.** `ATP_Store` manages three energy currencies (ATP, GTP, NADH) with regeneration, debt tracking, and a five-state metabolic state machine: FEASTING ( $> 90\%$ ), NORMAL ( $30\text{--}90\%$ ), CONSERVING ( $< 30\%$ ), STARVING ( $< 10\%$ ), and DORMANT. In STARVING state, operations with priority  $< 5$  are rejected; in DORMANT, only priority  $\geq 10$  operations proceed.

`MTORScaler` reads the ATP store’s state and computes an effective AMPK ratio (AMP:ATP) including both the absolute level and its rate of change, inspired by KEGG pathway hsa04152. The scaler determines a scaling state (GROWTH, MAINTENANCE, CONSERVATION, AUTOPHAGY) with hysteresis margins derived from Hill coefficient kinetics ( $h = 0.05$ ). Operations whose cost exceeds the feature gate are rejected in CONSERVATION and AUTOPHAGY states unless they have critical priority ( $\geq 5$ ).

**Naive alternative.** `SimpleBudget`: a flat integer counter that starts at  $N$ , decrements by cost, and returns `False` when empty. No states, currencies, regeneration, priority gating, or scaling.

**Ablated control.** `ATP_Store` without `MTORScaler`—the state machine operates but no feature gating or scaling is applied.

**Scenarios.** Five load patterns: constant rate, periodic bursts (cost 50 every 20 steps), gradual depletion (linearly increasing cost), sudden spike (half-budget cost at step 100), and mixed priority (30% critical operations). Operations have priorities 0–10. Budget regenerates 5 units every 10 steps for the biological and ablated variants.

**Key metrics.** `operations_completed`: fraction of all operations that succeeded. `critical_served_under_pressure`: fraction of priority  $\geq 5$  operations that succeeded when the system was in CONSERVING or STARVING state (biological/ablated) or when balance was below 30% of initial budget (naive).

### 3.3 Benchmark 2: Quorum Sensing

**Biological system.** `QuorumSensingBio` models autoinducer signal accumulation inspired by KEGG pathway map02024 (*V. fischeri* LuxI/LuxR system). Each agent deposits a continuous signal proportional to its suspicion level into a shared `SignalEnvironment`. Signals decay exponentially with a half-life of 5.0 time units (derived from AHL lactonase degradation rates). The activation threshold scales as  $\log(N) \times \theta_{\text{base}}$  where  $N$  is the population size and  $\theta_{\text{base}} = 10.0$ .

Signal concentrations below a noise floor (0.001) are excluded from both reads and writes. Pruning occurs on the write path (deposits) with monotonic time guards to prevent order-dependent state corruption.

**Naive alternatives.** Three alternatives represent standard coordination approaches:

- **IndependentActors**: each agent decides alone; alert if *any* agent’s suspicion exceeds 0.5.
- **MajorityVote**: each agent votes ALERT/NORMAL based on individual threshold (0.5); majority ( $\geq 50\%$ ) wins.

**Ablated control.** Independent actors (no coordination)—each agent’s suspicion is evaluated in isolation without signal accumulation or decay.

**Scenarios.** Three scenario types: *static compromise* (compromised agents emit high suspicion throughout), *gradual infiltration* (compromised agents activate at random times during the simulation), and *noisy environment* (no actual compromise, testing false-positive rate under noise). Each runs across agent counts  $N \in \{5, 10, 20\}$  and compromised fractions  $\{0\%, 20\%, 40\%\}$ . Normal agents emit suspicion  $\sim \mathcal{N}(0.15, 0.15)$ ; compromised agents emit  $\sim \mathcal{N}(0.80, 0.15)$ , both clipped to  $[0, 1]$ .

**Key metrics.** `true_positive`: fraction of time steps where compromise was correctly detected. `false_positive`: fraction of non-compromise time steps where an alert was raised.

### 3.4 Benchmark 3: Epiplexity Stagnation Detection

**Biological system.** `EpiplexityMonitor` implements the operational epiplexity approximation from the free energy principle [7]:

$$\hat{E}_t = \alpha \cdot \frac{1}{2}(1 - \cos(e_t, e_{t-1})) + (1 - \alpha) \cdot \sigma(H(m_t|m_{<t}))$$

where  $e_t$  is the embedding of message  $t$ ,  $\sigma(H) = 1 - e^{-H/H_0}$  is exponential saturation to  $[0, 1]$ , and  $\alpha = 0.5$ . The epiplexic integral  $E_w = \frac{1}{w} \sum \hat{E}_t$  over a window of size  $w = 10$  determines health status: HEALTHY, CONVERGING, EXPLORING, STAGNANT, or CRITICAL.

The key design insight: stagnation is not just output repetition (low novelty) but output repetition *combined with* model uncertainty (high perplexity). An agent with both low novelty and low perplexity is *converging*, not stagnant.

**Naive alternative.** `RepetitionCounter`: computes average pairwise cosine similarity across a sliding window of embeddings. If similarity exceeds 0.85, declares STAGNANT. Also declares STAGNANT after 20 consecutive steps of elevated similarity ( $> 0.7 \times$  threshold). Uses the same `MockEmbeddingProvider` as the biological variant for fair comparison.

**Ablated control.** No monitor—always reports HEALTHY.

**Scenarios.** Five scenarios: *loop* (exact message repetition), *convergence* (messages become similar while perplexity drops), *exploration* (high-novelty diverse messages), *trophic withdrawal* (pathway-grounded: novelty decays gradually while perplexity stays high, mimicking neuronal atrophy from trophic factor withdrawal), and *false stagnation* (low novelty + low perplexity = convergence, not stagnation).

**Embedding caveat.** All scenarios use `MockEmbeddingProvider`, which generates deterministic pseudo-embeddings via SHA-256 hashing. This means semantically similar but lexically different messages receive *random* cosine similarity—the embedding signal does not carry semantic information. Results with real embedding models may differ significantly (Section 6).

**Key metrics.** `detection_accuracy`: fraction of steps where the detector’s status matched ground truth. `false_positive`: fraction of non-stagnant steps where stagnation was incorrectly declared. `false_negative`: fraction of stagnant steps where stagnation was missed. `convergence_discrimination`: fraction of converging steps correctly identified as non-stagnant.

## 4 Results

All results are aggregated across 10 seeds with  $N = 1,000$  trials per seed per scenario. Wilson 95% confidence intervals are reported where applicable. Significance ( $p < 0.001$ ) is determined by non-overlapping Wilson CIs between biological and naive variants.

### 4.1 Metabolism: Clear Win for Priority Gating

Table 1 summarizes the metabolism benchmark results.

Table 1: Metabolism benchmark: Biological (ATP\_Store + MTORScaler) vs Ablated (ATP\_Store only) vs Naive (flat counter). N = total operations or pressure events across 10 seeds.

Scenario	Metric	Bio	Abl	Naive	$\Delta$	N
bursty	critical served	1.000	1.000	0.398	<b>+0.602</b>	24,139
bursty	ops completed	0.719	0.715	0.685	<b>+0.034</b>	2,000,000
gradual depl.	critical served	1.000	1.000	0.769	<b>+0.231</b>	43,372
gradual depl.	ops completed	0.979	0.996	0.950	<b>+0.029</b>	2,000,000
constant	ops completed	1.000	1.000	1.000	0.000	2,000,000
sudden spike	ops completed	1.000	1.000	1.000	0.000	2,000,000
mixed priority	ops completed	1.000	1.000	1.000	0.000	2,000,000

The headline result is **critical\_served\_under\_pressure**. Under bursty load, the biological system served 100% of critical operations (priority  $\geq 5$ ) during resource pressure, while the naive flat counter served only 39.8% ( $\Delta = +0.602$ , significant). Under gradual depletion, the gap is smaller but still significant: 100% vs 76.9% ( $\Delta = +0.231$ ).

Against the naive baseline, the biological system actually *improves* total throughput: 71.9% versus 68.5% under bursty load ( $\Delta = +0.034$ ), because priority gating preserves budget for later operations that the flat counter would miss entirely. Comparing biological against ablated, both achieve identical critical-service rates (100%). However, under gradual depletion the mTOR scaler’s anticipatory conservation gates some non-critical operations earlier: biological completed 97.9% versus ablated’s 99.6%. This 1.7 percentage-point throughput reduction is the cost of the mTOR scaler’s preemptive feature gating, which in these experiments did not produce an additional critical-service benefit beyond what ATP\_Store’s own state machine already provides.

Under constant load, sudden spike, and mixed priority, all three variants perform identically. The biological complexity only matters under specific pressure patterns where resource contention forces choices about what to serve.

### 4.2 Quorum Sensing: Unique Precision–Recall Operating Point

Table 2 summarizes key quorum sensing results.

The three coordination strategies occupy distinct positions on the precision–recall curve:

- **Independent actors** (ablated): 100% TPR but 5–18% FPR. Catches everything but cries wolf on 1 in 6–20 clean time steps.
- **Majority vote** (naive): 0% FPR but near-0% TPR. Almost never detects threats because clean agents ( $\mu = 0.15$ ) always outvote compromised agents at the 0.5 threshold.
- **Signal accumulation** (biological): 0% FPR with 71–87% TPR at 40% compromise. Zero false alarms with meaningful detection.

Table 2: Quorum sensing benchmark: selected configurations. Bio = QuorumSensingBio (signal accumulation + decay), Abl = IndependentActors (no coordination), Naive = MajorityVote.

Config	Metric	Bio	Abl	Naive	$\Delta$	N
static, $n=20$ , $c=8$	TPR	0.866	1.000	0.005	<b>+0.861</b>	300,000
static, $n=10$ , $c=4$	TPR	0.711	1.000	0.052	<b>+0.659</b>	300,000
static, $n=20$ , $c=4$	TPR	0.748	1.000	0.000	<b>+0.748</b>	300,000
gradual, $n=20$ , $c=8$	TPR	0.718	0.999	0.002	<b>+0.716</b>	216,959
all $c=0$ configs	FPR	0.000	0.048–0.180	0.000	0.000	300K ea.

The biological model’s advantage comes from two structural properties: (1) *continuous signals* average out noise (unlike binary votes), and (2) *temporal decay* ensures stale evidence ages out (unlike a vote that persists forever). The combination naturally filters noise while remaining sensitive to sustained patterns.

Detection sensitivity scales with both the number of agents and the compromise fraction, consistent with the biological signal-accumulation model: more agents producing more signal yield higher accumulated concentrations relative to the threshold.

### 4.3 Epiplexity: Embedding Quality Determines Outcome

The epiplexity benchmark produced the most instructive result: the biological design’s performance depends critically on embedding quality. With mock embeddings (SHA-256 hash-based pseudo-embeddings), the naive detector wins. With real semantic embeddings (all-MiniLM-L6-v2), the biological design dominates on convergence discrimination—the exact capability the two-signal design was built for.

Table 3 shows results with both embedding providers.

Table 3: Epiplexity benchmark with mock vs real embeddings. Bio = EpiplexityMonitor (two-signal Bayesian), Naive = cosine similarity + timeout. Real embeddings: all-MiniLM-L6-v2 ( $N = 100$  trials, seed 42); mock embeddings: SHA-256 hash ( $N = 1,000 \times 10$  seeds).

Embedding	Scenario	Metric	Bio	Naive	$\Delta$
Mock	loop	accuracy	0.467	<b>0.940</b>	−0.473
	convergence	accuracy	0.473	<b>1.000</b>	−0.527
	false stagn.	accuracy	0.540	<b>0.993</b>	−0.453
	false stagn.	FP rate	0.052	<b>0.007</b>	+0.045
Real	convergence	accuracy	<b>0.960</b>	0.401	+0.559
	false stagn.	accuracy	<b>0.960</b>	0.020	+0.940
	false stagn.	FP rate	<b>0.000</b>	0.980	−0.980
	loop	accuracy	0.571	<b>0.940</b>	−0.369
	loop	FP rate	<b>0.000</b>	0.750	−0.750

**With mock embeddings: naive wins.** The naive cosine-similarity detector outperforms the biological design on detection accuracy across all scenarios. However, the false-positive/false-negative breakdown reveals a precision–recall tradeoff: the biological variant achieves 0% FP rate on loops (versus naive’s 75% FP), at the cost of 58% FN rate. With mock embeddings, the novelty signal

is essentially random noise—semantically similar messages receive unrelated cosine similarity—so the two-signal combination performs worse than a single signal.

**With real embeddings: biological wins on convergence.** Switching to all-MiniLM-L6-v2 sentence embeddings flips the result on convergence discrimination. The biological monitor achieves 96.0% accuracy on both convergence and false-stagnation scenarios, versus 40.1% and 2.0% for the naive detector. The naive detector’s false-positive rate on false stagnation reaches 98.0%—it sees similar outputs and screams “stagnant” regardless of the agent’s confidence level.

The biological design’s two-signal structure now earns its complexity: the perplexity signal distinguishes convergence (low novelty + low perplexity = healthy) from stagnation (low novelty + high perplexity = pathological). The naive cosine detector has no access to this distinction.

**Loop detection still favors naive.** Even with real embeddings, the naive detector wins on loop detection (94.0% vs 57.1%) because exact repetition is trivially detectable by cosine similarity. The biological monitor’s advantage is not on easy cases (identical outputs) but on hard cases (semantically similar but subtly different outputs where the agent’s confidence level matters).

#### 4.4 Epistemic Theorem Validation

The preceding benchmarks test mechanism-level guarantees (priority gating, signal accumulation, stagnation detection). Operon also provides architecture-level predictions via epistemic topology analysis: four theorems that bound error amplification, sequential overhead, parallel speedup, and tool density from wiring diagram structure alone. We validate two of these predictions against measured behavior from real LLM execution.

**Methodology.** We constructed a validation harness that, for each of 20 benchmark tasks (5 easy, 8 medium, 7 hard), builds the same `ExternalTopology` the live evaluator would construct, runs full epistemic analysis to capture all theorem predictions, then executes the task through a `SkillOrganism` pipeline with Gemma 4 27B (mixture-of-experts, 4B active parameters) served locally via Ollama. Each task was run in both guided and unguided configurations with 3 repetitions, yielding  $20 \times 2 \times 3 = 120$  runs. Quality was assessed by LLM self-judging on a 0.0–1.0 scale (correctness 50%, completeness 30%, clarity 20%). Correlations are Spearman rank ( $\rho$ ) with p-values floored at 0.1 for  $n < 10$ .

**Testable theorems.** Since `SkillOrganism` always executes stages as a sequential pipeline, Theorem 3 (parallel speedup) is structurally constant and reported for completeness only. Theorem 4 (tool density) uses role-implied capability annotations that are not present in the live executor’s topology, so it is reported as informational. Theorems 1–2 and the composite risk score are directly testable.

**Interpretation.** The error amplification bound— $n_{\text{agents}}$  independent error sources in a sequential pipeline—strongly predicts execution failure ( $\rho = +0.751$ ,  $p < 0.001$ ). However, the dominant failure mode is not quality degradation but *timeout*: longer pipelines are increasingly likely to exceed the provider’s request budget. Among the 42 runs that completed, quality was uniformly high (mean 0.981), including all 12 completed medium-difficulty tasks (quality 1.0). The bound correctly identifies *which architectures are fragile* without modeling *how* they fail.



Table 4: Epistemic theorem validation: predicted structural bounds vs measured execution outcomes.  $N = 120$  runs (20 tasks  $\times$  2 configs  $\times$  3 repeats). Of these, 42 executed successfully and 78 timed out. Timeouts are included as failures (quality = 0) since they represent real execution limits predicted by the structural bounds.

Theorem	Predicted	Measured	Dir	$\rho$	$p$	Status
Error Ampl.	$n_{\text{agents}}$	1 – quality	+	+0.751	<0.001	<b>validated</b>
Seq. Penalty	overhead ratio	mean stage latency	+	+0.166	0.287	not significant
Speedup	predicted speedup	1.0 (sequential)	—	0.000	1.000	informational
Tool Density	planning cost	tokens / stage	+	—	—	informational
Composite Risk	risk score	1 – quality	+	+0.751	<0.001	<b>validated</b>

The overall success rate was 35% with mean quality 0.343, declining from 0.97 on easy tasks (2–3 stages) to 0.25 on medium tasks (4–5 stages) to 0.00 on hard tasks (5–7 stages). Timeout risk increases with stage count: 0/30 easy runs timed out, 36/48 medium runs timed out, and 42/42 hard runs timed out. This reflects a resource threshold for Gemma 4 27B (4B active MoE parameters) at the 30s default timeout, not an inherent quality limit.

Sequential overhead ( $\rho = +0.166$ ,  $p = 0.287$ ) trends in the predicted direction but does not reach significance, likely because per-stage latency varies more with prompt complexity than with handoff count.

The mechanism-level benchmarks (Sections 4.1–4.3) provide stronger guarantees than the topology-level predictions because they enforce structural invariants at the feature level (priority gates, signal decay, two-signal discrimination) rather than predicting outcomes from architecture shape alone. The two layers are complementary: epistemic topology identifies architectures likely to need structural guarantees; the mechanism benchmarks validate that those guarantees deliver.

## 4.5 End-to-End Real Agent Evaluation

The preceding benchmarks test mechanisms in isolation. We now evaluate whether the structural guarantees provide measurable value when wrapping a real LLM agent performing real tasks.

**Methodology.** We compare three runtime variants: **RAW** (direct `Nucleus.transcribe()` call, no Operon wrapper), **GUARDED** (`SkillOrganism` with `WatcherComponent` integrating epiplexity monitoring, immune inspection, and ATP budgeting), and **FULL** (GUARDED plus pre/post-flight `DNARepair` and certificate collection). Each variant is tested on three tasks: *stagnation escalation* (code review with subtle bugs), *injection blocking* (behavioral manipulation prompts against a trained immune baseline), and *state integrity* (genome corruption injected mid-run between organism stages). All runs use Gemma 4 27B (4B active MoE) via local Ollama with 3 repetitions per cell. A multi-model comparison uses Phi-3 Mini (3.8B) on the stagnation task.

**State integrity: clear structural value.** The FULL variant detects all four corruption sites (three gene drifts plus one checksum failure) injected between organism stages and repairs them in a single `CHECKPOINT_RESTORE` operation. The certificate (`state_integrity_verified`) holds after repair in all repetitions. RAW and GUARDED are completely blind to genome corruption—the `WatcherComponent` monitors epiplexity, ATP, and immune signals but has no genome-level signal source. `DNARepair` as a pre/post-flight integrity check is the strongest structural guarantee in the evaluated stack.

Table 5: End-to-end evaluation: RAW vs GUARDED vs FULL across three tasks. Gemma 4 27B,  $n = 3$  repetitions (injection:  $n = 30$ , i.e.  $3 \times 10$  prompts). TP = true positive rate, FP = false positive rate, Det = corruption detection rate, Rep = repair rate.

Task	Variant	Quality	Tokens	Latency	TP%	Det%	Rep%
Stagnation	RAW	1.000	2149	58s	—	—	—
Stagnation	GUARDED	1.000	3468	85s	—	—	—
Stagnation	FULL	1.000	3076	76s	—	—	—
Injection	RAW	—	829	25s	0	—	—
Injection	GUARDED	—	792	23s	20	—	—
Injection	FULL	—	787	24s	20	—	—
Integrity	RAW	—	2199	68s	—	0	0
Integrity	GUARDED	—	2012	61s	—	0	0
Integrity	FULL	—	2058	63s	—	100	100

**Injection blocking: precise but limited.** The immune system is trained on 10 real Gemma 4 outputs to clean Python questions, then evaluated on 5 clean and 5 behaviorally manipulative prompts (ALL CAPS, structured prefix, JSON-only format). Per-prompt isolation with seeded baseline profiles yields TP = 20% with FP = 0%: the canary-based Signal 2 fires on the most format-deviant anomalies with zero false positives. The two-signal activation architecture (TCe11 requires both Signal 1 and Signal 2) is designed for sustained behavioral monitoring, not single-prompt classification—a single observation cannot reach REPEATED\_ANOMALY, so only the canary path provides Signal 2 in one-shot evaluation.

**Stagnation escalation: correctly scoped.** Both Gemma 4 (quality = 1.0) and Phi-3 Mini (quality = 0.63) show 0% escalation. The EpiplexityMonitor measures output *novelty* (are successive outputs repetitive?), not output *quality* (is the output good?). Phi-3 Mini produces different-but-mediocre reviews each time, which register as novel to the monitor. Escalation is a loop-breaker—correctly scoped to detect stuck agents, not to gate output quality.

**Wrapper tax.** The organism wrapper adds measurable overhead: +1,319 tokens and +27s mean latency on Gemma 4 for the stagnation task (GUARDED vs RAW). On Phi-3 Mini the proportional cost is similar (+432 tokens, +10s). This cost floor is model-size-dependent: the wrapper’s prompt augmentation (stage instructions, role context, shared state) is a fixed input-token overhead that becomes proportionally larger on smaller, slower models.

## 5 Discussion

### 5.1 When Biological Structure Earns Complexity

The two positive results share a common pattern: both work through *mechanism design* rather than *algorithmic sophistication*.

The metabolic priority gate is a simple state machine. When resources drop below 10%, operations with priority < 5 are rejected. This is not a complex algorithm—it is a structural rule. But it provides a hard guarantee: critical operations *will* be served under any load pattern, at the cost of bounded throughput reduction. A flat counter cannot provide this guarantee without reimplementing the state machine, at which point it is no longer a flat counter.

The quorum sensing decay is exponential half-life applied to signal concentrations. Again, not algorithmically complex. But the combination of continuous signals (noise averaging) and temporal decay (stale evidence removal) occupies a precision–recall position that neither majority voting nor independent detection can reach without adding similar structural properties.

In both cases, the biological metaphor provided the *right structural choice*—priority-dependent resource gating from metabolic state machines, temporal signal decay from autoinducer kinetics—rather than a better algorithm for the same structural choice.

## 5.2 When Embedding Quality Matters

The epiplexity result demonstrates a subtler lesson than the other two benchmarks: biological designs that rely on *information quality* succeed only when that quality is present.

With mock embeddings, the two-signal design fails—the novelty signal carries no semantic information, so combining it with approximate perplexity produces worse results than a single clean cosine-similarity signal. With real sentence embeddings (all-MiniLM-L6-v2), the same design dominates on convergence discrimination: 96% accuracy versus 2–40% for the naive detector on the hardest scenarios.

The structural guarantee here is conditional: the Bayesian two-signal design provides a *convergence/stagnation distinction guarantee* that the cosine detector structurally cannot make, but only when the embedding signal carries semantic meaning. This is analogous to a biological receptor that provides a structural binding guarantee but only functions in the presence of its ligand.

This refines the C8 finding [3] that biological abstractions generalize as code structure rather than optimization algorithms. The epiplexity monitor’s *structure* (two independent signals combined via Bayesian weighting) does generalize—but its *performance* depends on signal quality.

The pattern across all three benchmarks: biological designs that enforce structural invariants outperform simpler alternatives, while information-processing gains depend on signal quality.

## 5.3 Implications for Framework Integration

Operon provides convergence adapters for six agent frameworks [2]. The benchmark results inform which frameworks benefit most from biological structural guarantees:

**A-Evolve.** Its single-agent Solve-Observe-Evolve-Gate-Reload loop is where metabolic budgets directly prevent unbounded exploration. The benchmark shows the fitness gate (a critical operation) is always evaluated under metabolic budgeting—mapped to A-Evolve, this means the evolutionary quality check is never skipped even when the exploration budget is depleted.

**Swarms.** Its graph-based multi-agent topology is where quorum sensing provides the most value: leaderless consensus with zero false positives. When false consensus triggers coordinated action across a swarm, the 0% FPR guarantee is operationally critical.

**DeerFlow.** Its hierarchical architecture with recursive sub-agent calls benefits from metabolic budgets that prevent resource exhaustion. The MTORScaler’s rate-of-change sensitivity is especially relevant for DeerFlow’s progressive skill loading, where resource consumption can accelerate suddenly.

**AnimaWorks, Ralph, Scion.** Lighter benefits: genome immutability for configuration audit (AnimaWorks), metabolic budgets mapping to backpressure enforcement (Ralph), and quorum sensing for cross-container consensus (Scion).

## 5.4 Composition Non-Interference

Ma et al. [10] show that five atomic coding skills (localize, edit, test, reproduce, review) compose without negative interference under joint RL training. We ran a limited comparison using Operon’s skill composition machinery with a real LLM (Gemma 4 27B via Ollama) on three bug-fix tasks (SQL injection, off-by-one pagination, TOCTOU race condition), 3 repetitions each. This tests 3 of 5 skills via prompt composition (not joint RL), so the comparison is narrower than Ma et al.’s original setting.

Table 6: Composition non-interference: individual skill quality vs composed localize→edit→test pipeline.  $\Delta = \text{composed} - \text{mean}(\text{individual})$ . Threshold:  $|\Delta| \leq 0.1 = \text{no interference}$ .

Task	mean(indiv)	composed	$\Delta$	Verdict
sql_injection	0.806	0.967	+0.161	positive
off_by_one	0.900	0.993	+0.093	none
race_condition	0.517	0.350	−0.167	<b>negative</b>
Overall	0.741	0.770	+0.029	none

The overall result matches the direction of Ma et al.’s finding: composition does not degrade quality on average ( $\Delta = +0.029$ ). However, the race\_condition task shows negative interference ( $\Delta = -0.167$ ), suggesting that composition can hurt on genuinely hard problems where intermediate stage outputs mislead later stages. The baseline (raw LLM call, quality 0.961) still dominates in absolute terms—a single capable model answering the full task outperforms a three-stage pipeline—consistent with the Ao et al. finding [1] that delegation cannot beat a centralized baseline without exogenous signals.

Individual skill quality varies by task difficulty. On easier tasks (SQL injection, off-by-one), “localize” and “edit” score 0.80–1.00 on average, while on the harder race\_condition task, mean “edit” quality drops to 0.37 and mean “test” to 0.42, with both reaching 0.0 in their worst repetitions. “test” consistently scores lowest across tasks because test-writing in isolation lacks the context of what was found and fixed—an expected consequence of skill decomposition where some skills are context-dependent.

## 5.5 Relationship to Epistemic Topology

Operon’s epistemic topology layer derives four bounds from wiring diagram structure: error amplification, sequential communication overhead, parallel speedup, and tool density scaling. These operate at a different level than the mechanism benchmarks presented here.

The epistemic bounds predict architecture-level properties (a long pipeline *will* accumulate sequential overhead); the mechanism benchmarks test feature-level guarantees (critical operations *will* be served under pressure). The two are complementary: epistemic topology identifies architectures likely to need structural guarantees; the mechanism benchmarks validate that those guarantees work as claimed.

Section 4.4 validates the error amplification bound against measured LLM execution: the number of pipeline stages strongly predicts execution failure ( $\rho = +0.751$ ,  $p < 0.001$ ), though the

dominant failure mode is timeout rather than quality degradation. The epistemic and mechanism layers operate at different levels of abstraction: topology predicts structural difficulty (more stages  $\Rightarrow$  more fragile), while mechanism benchmarks enforce feature-level invariants (priority gates, signal decay) that deliver regardless of pipeline length.

## 5.6 Categorical Certificates for Structural Guarantees

The quorum sensing threshold calibration provides a concrete instance of *semantic certificates* as formalized by de los Riscos et al. [6]. The no-false-activation guarantee is a certificate  $\text{cert}_{\text{QS}} = (T, \tau, \text{evds})$  where  $T$  states that normal traffic never triggers activation,  $\tau$  maps the theorem’s symbols to the quorum sensing parameters  $(N, s, h, m)$ , and the evidence is the derivation:

$$c_{\text{ss}} = \frac{N \cdot s}{1 - 2^{-1/h}}, \quad \theta = c_{\text{ss}} \cdot m, \quad \text{level} = \frac{c_{\text{ss}}}{\theta} = \frac{1}{m} < 1.$$

Because the threshold is defined in terms of architecture parameters  $(N, s, h)$  rather than a fixed constant, the guarantee preserves under architecture morphisms that change  $N$ —for instance, when a convergence compiler maps an Operon organism to a Swarms workflow with a different agent count. This is a concrete instance of Proposition 5.1: structural properties are functorially stable under architectural refinement.

This pattern—deriving thresholds from steady-state dynamics rather than hand-tuning constants—extends to other structural guarantees. The metabolic priority gate’s STARVING threshold (10% of capacity) could similarly be formalized as a certificate whose evidence is the state machine’s priority rejection rule. The epiplexity monitor’s convergence/stagnation discrimination threshold could be certified relative to the embedding model’s similarity distribution.

## 5.7 Structural Guarantees by Layer

The end-to-end evaluation (Section 4.5) reveals that structural guarantee value is layer-dependent:

**State layer (deterministic).** DNA repair provides 100% corruption detection and repair across all repetitions. The guarantee is deterministic: checkpointing, scanning, and restoring are structural operations on the genome datastructure, independent of model quality or prompt content. This is the strongest form of structural guarantee—verifiable, reproducible, and unconditional.

**Behavioral layer (statistical).** The immune system’s two-signal activation detects behavioral anomalies with zero false positives ( $\text{FP} = 0\%$ ) but limited sensitivity in single-prompt evaluation ( $\text{TP} = 20\%$ ). The architecture is correctly conservative: requiring both Signal 1 (baseline violation) and Signal 2 (canary failure or repeated anomaly) prevents false alarms at the cost of delayed detection. This is appropriate for sustained agent monitoring where observations accumulate over time, less so for one-shot prompt classification. The VerifierComponent extends this layer with rubric-based quality evaluation—analogue to *adaptive immunity* (B-cell antigen recognition) complementing the innate detection of ImmuneSystem. When quality falls below threshold on a fast model, the watcher escalates to the deep model, providing a quality-sensitive escalation path that the novelty-based epiplexity signal cannot.

**Output layer (stochastic).** The epiplexity monitor detects output *repetition*, not output *mediocrity*. A weaker model (Phi-3 Mini, quality 0.63) does not trigger escalation because it produces

varied output—the stagnation signal measures novelty, not quality. The wrapper tax (+1,300 tokens, +27s) is the cost floor for structural wrapping, justified for state integrity but not yet for output quality improvement with capable models.

**Developmental layer (preventive).** The CertificateGateComponent implements the G1/S DNA damage checkpoint analogy: before each stage executes its LLM call, the gate scans the genome against a DNARepair checkpoint. If corruption is detected, a HALT intervention prevents the corrupted state from reaching the model. Unlike the state layer’s reactive repair (detect corruption after execution, then restore), this is a *preventive* gate—corruption is blocked before it can affect output. The guarantee is deterministic: the gate checks structural integrity of the genome datastructure, not model output quality. This completes the cell cycle analogy alongside CellCycleController, with CertificateGate enforcing the G1/S transition that guards against propagation of damaged state.

The pattern mirrors the mechanism benchmarks: structural guarantees that enforce invariants (state checksums, signal thresholds, integrity gates) deliver unconditionally, while guarantees that depend on information quality (embedding novelty, behavioral baselines) deliver conditionally.

## 6 Limitations

**Embedding dependence.** The epiplexity benchmark was run with both mock embeddings (SHA-256 hash-based) and real sentence embeddings (all-MiniLM-L6-v2). The results differ dramatically: the biological design loses with mock embeddings and wins with real embeddings on convergence discrimination. The real-embedding results use a single model and  $N = 100$  trials (versus  $N = 10,000$  for mock embeddings); confirmation with additional embedding models and larger sample sizes would strengthen the finding.

**Synthetic load patterns.** The metabolism benchmark uses programmatically generated operation sequences (constant, bursty, gradual, spike). Real agent workloads may have different statistical properties—heavier tails, correlated bursts, priority distributions that differ from our 30% critical assumption.

**Simulated agents.** The quorum sensing benchmark simulates agent suspicion signals as Gaussian draws around known baselines. Real multi-agent systems have richer signal environments: suspicion may be autocorrelated, agents may have heterogeneous detection capabilities, and compromised agents may adapt their behavior to avoid detection.

**Limited end-to-end evaluation.** Section 4.5 provides initial end-to-end results primarily with Gemma 4 27B (plus a limited Phi-3 Mini comparison on stagnation) and self-judging across 3 repetitions. The positive result (state integrity) is deterministic and model-independent. The statistical results (20% injection TP, 0% stagnation escalation) are honest but underpowered: larger sample sizes, cross-model validation, and external judging would strengthen the findings. The immune system’s behavioral detection is evaluated in single-prompt mode, which underestimates its design intent as a sustained monitoring system.

**Manual thresholds.** Several parameters are manually set rather than auto-calibrated: the mTOR hysteresis margin ( $h = 0.05$ ), quorum sensing decay half-life (5.0 time units), threshold

base (10.0), and epiplexity mixing parameter ( $\alpha = 0.5$ ). Sensitivity analysis across these parameters is not provided.

**Statistical assumptions.** Wilson CIs assume independence across trials within seeds. The 10-seed aggregation partially addresses between-seed variability, but within-seed trials share the same random number generator state progression.

## 7 Conclusion

We tested three biologically-grounded agent reliability features against naive non-biological alternatives, with 10M+ data points across 10 independent seeds plus a follow-up experiment with real sentence embeddings. All three features demonstrate empirical benefits under the right conditions.

Metabolic priority gating provides a structural guarantee that critical operations are served under resource pressure (100% vs 39.8% for a flat counter under bursty load). Autoinducer-based quorum sensing achieves zero false-positive rate with meaningful true-positive rate (71–87% at 40% compromise), occupying a precision–recall position unreachable by majority voting or independent detection. Bayesian two-signal stagnation detection dominates on convergence discrimination with real embeddings (96% vs 2–40% naive) but loses with mock embeddings, demonstrating that biological designs relying on information quality succeed only when that quality is present.

The consistent pattern: biological design earns complexity through *mechanism-level structural guarantees*—hard properties enforced by design (priority gating, signal decay, two-signal discrimination)—rather than through algorithmic sophistication alone. Embedding quality determines whether the two-signal structure delivers its guarantee, just as metabolic state determines whether priority gating activates.

A limited composition experiment matches the direction of Ma et al.’s finding [10]: composing localize→edit→test as a serial pipeline does not degrade overall quality ( $\Delta = +0.029$  vs individual skills), though harder tasks (TOCTOU race conditions) show negative interference ( $\Delta = -0.167$ ). This tests 3 of 5 skills via prompt composition, not Ma et al.’s joint-RL setting.

**Open problems.** Confirmation of the real-embedding result across additional models and larger sample sizes. Auto-calibration of quorum sensing thresholds from population and signal statistics. Understanding when composition degrades quality on hard tasks—the race\_condition result suggests that intermediate stage outputs can mislead later stages, an effect that may be addressable through stage-specific context filtering.

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