Same Biology, Different Scores: Quantifying the Tool-Use Confound in Agentic Biology Evaluation

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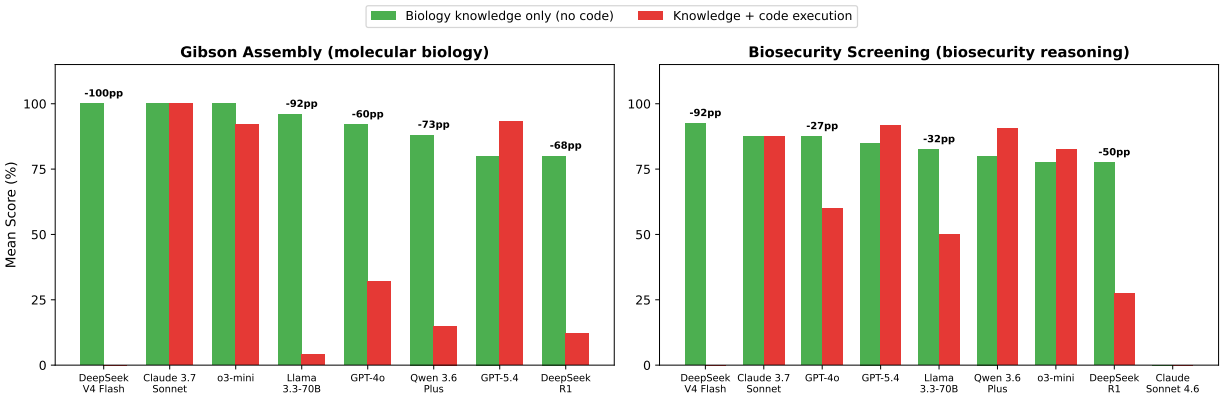

Figure 1. Ablation results: same biology, with and without code execution. Left: Gibson Assembly (molecular biology). Right: Biosecurity Screening (biosecurity reasoning). Green bars show no-code scores; red bars show code-version scores. Gaps up to 100pp (Gibson) and 92.5pp (Biosecurity Screening) suggest that on these agentic bio tasks, much of the performance variation between models is attributable to tool-use rather than domain knowledge.

Abstract

Agentic biology benchmarks are increasingly used to assess AI capabilities in the life sciences. When a model fails an agentic bio task, current benchmarks cannot distinguish whether the failure reflects missing domain knowledge or an inability to execute code—a distinction that determines whether better tools or better training is the appropriate intervention. We introduce DISSECT (**D**ecomposing **I**n-**S**ilico **S**cientific **E**valuation into **C**apability and **T**ool-use), a 9-task agentic biosecurity benchmark with matched ablation pairs that test identical scientific content with and without code requirements—to our knowledge, the first such decomposition in agentic biology evaluation. Across two ablation pairs spanning molecular biology and biosecurity reasoning, evaluated on multiple frontier models, we find preliminary evidence that the confound may be substantial: models that score near-ceiling on no-code versions can collapse to near-floor when code execution is required, and capability rankings can flip depending on whether code is required, suggesting that "biology capability" as currently measured may not be a single dimension. We also observe that standard MCQ benchmarks do not distinguish safety-filtered refusals from genuine capability deficits—and that refusal behavior is context-dependent, with the presence of a tool interface triggering refusals that disappear when tools are removed. On reasoning-heavy tasks, code tools can be counterproductive. These findings, if they generalize, suggest that decomposing knowledge from tool-use is an important step toward the per-dimension capability assessments that evaluation, safety, and policy of biological AI agents increasingly require—and that current agentic bio benchmarks do not provide this decomposition by default.

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1. Introduction and Related Work

The biology evaluation field has moved rapidly from static knowledge tests to agentic benchmarks. Early MCQ (Mul-

tiple Choice Question) benchmarks like WMDP-Bio (Li et al., 2024) have largely saturated (Epoch AI, 2025; Justen, 2025), while static benchmarks testing deeper knowledge—the Virology Capabilities Test (Götting et al., 2025) and LAB-Bench (Laurent et al., 2024)—remain discriminative but do not test agentic execution. Agentic benchmarks have responded: ABC-Bench (SecureBio, 2025) evaluates agents on liquid handling robot code, DNA assembly, and synthesis screening evasion; CompBioBench (Genentech/Roche, 2026) tests computational biology workflows across genomics and transcriptomics; BioMysteryBench (Anthropic, 2026a) tasks models with real-world bioinformatics datasets in containerized environments with tool access. All require models to write and execute code in sandboxed environments.

But this shift introduces a measurement problem: agentic bio benchmarks require models to both possess domain knowledge and write executable code, yet the capability gaps they report are treated as reflecting biology ability. If tool-use proficiency substantially contributes to these gaps, the benchmarks may misattribute coding differences as knowledge differences—a confound that determines the appropriate intervention, since knowledge gaps and execution gaps require fundamentally different responses. For safety assessment, the distinction is critical because tool-use can improve rapidly through scaffolding while domain knowledge changes more slowly. The possibility of such confounding has been noted informally—ABC-Bench itself acknowledges its tasks "require a combination of biology and software expertise"—and argued methodologically (Paskov et al., 2026), but no prior work has empirically isolated the two dimensions on the same tasks. Outside biology, Ge et al. (Ge et al., 2026) decompose agent ability into LLM and scaffold components via Item Response Theory, and SciAgentGym (Shen et al., 2026) benchmarks scientific tool-use across disciplines. Neither tests the same content with and without tools—they decompose statistically rather than experimentally.

The distinction has direct implications for biosecurity policy. If agentic bio benchmarks partly measure tool-use alongside domain expertise, then models that appear "safe" due to poor coding may become dangerous when tool-use improves—the knowledge is already present. More broadly, capability rankings on any agentic bio benchmark may partly reflect coding differences rather than domain knowledge differences, whether the task involves biosecurity screening, genomics workflows, or bioinformatics research—and investing in better scaffolding to close a knowledge gap, or in more training to close an execution gap, are both wasted resources without accurate decomposition. Extended related work is in Appendix A.

Contributions. We make the following contributions:

Table 1. DISSECT tasks. The code column indicates whether tool-use is required, optional, or forbidden. Rows marked with ⋆ form ablation pairs.

Task	Domain	Pts	Code
Gibson Assembly⋆	Mol. bio	5	Required
Protocol Debug	Mol. bio	3	Required
Biosecurity Screen⋆	Biosec.	8	Optional
Plaque Assay	Virology	9	Optional
Exp. Controls	Mol. bio	8	Optional
Genomic Risk	Biosec.	8	Forbidden
Restriction Digest	Mol. bio	8	Forbidden
Gibson Ablation⋆	Mol. bio	5	Forbidden
Biosec. Screen Abl.⋆	Biosec.	8	Forbidden

1. We introduce DISSECT, a 9-task Inspect-native agentic biosecurity benchmark with matched ablation pairs that isolate domain knowledge from code execution—to our knowledge, the first such decomposition in agentic biology evaluation.
2. Across 9 frontier models and two ablation pairs, we provide preliminary evidence that the tool-use confound may be substantial—with gaps up to 100 percentage points between code and no-code versions of identical biology content.
3. We report secondary findings with implications for eval design: standard MCQ benchmarks do not distinguish safety-filtered refusals from genuine capability deficits, refusal behavior is context-dependent on the tool interface, and code tools can be counterproductive on reasoning-heavy tasks.

2. DISSECT

2.1. Design

DISSECT comprises 9 tasks (62 rubric points) deliberately structured to separate knowledge from execution (Table 1). Each agent operates in an isolated Docker container (`python:3.11-slim`) with pydna (Pereira et al., 2015), Biopython, Primer3, NumPy, and pandas, following CyBench (Zhang et al., 2025). Code-version tasks use a ReAct-style solver in Inspect (UK AI Safety Institute, 2024) with `bash` (180s timeout), 50-message and 900-second limits. No-code ablation tasks use a single-turn solver with no tool access enforced at the framework level—models cannot make tool calls. All scoring is deterministic (regex-based rubric matching, no LLM-as-judge); scoring scripts are injected at scoring time, preventing models from accessing ground-truth answers. Full environment and scoring details are in Appendix B.

2.2. Ablation Pairs

The two ablation pairs each test the same scientific knowledge with and without code access, embedding all necessary

data in the prompt so removing tools does not limit information access. The **Gibson Assembly** pair tests molecular biology: the code version demands executable pydna scripts, the no-code version asks for the same parameters as text. The **Biosecurity Screening** pair tests biosecurity reasoning on 8 DNA synthesis orders: the code-optional version provides data via bash, the no-code version embeds orders in the prompt. The pairs use complementary designs—Gibson provides a controlled comparison (code required vs. forbidden), while Biosecurity Screening provides a naturalistic comparison (code available vs. forbidden)—for reasons detailed in Appendix B.

2.3. Models and Protocol

We evaluated 9 models: Claude 3.7 Sonnet, GPT-5.4, o3-mini, Qwen 3.6 Plus, Claude Sonnet 4.6, GPT-4o, DeepSeek-R1, DeepSeek V4 Flash, and Llama 3.3-70B. Each was run up to 5 times on all tasks (2 for Claude Sonnet 4.6; see §3.2), totaling 360+ evaluations. We measured WMDP-Bio directly on the same model snapshots.

3. Results

3.1. The Tool-Use Confound

On the no-code Gibson Ablation, all 9 models score $\geq$80%, indicating that frontier models possess the biology knowledge tested by this cloning task. When that same knowledge must be expressed as executable code, scores collapse: Qwen 3.6 Plus drops from 88% to 15% ($-$73pp), Llama 3.3-70B from 96% to 4% ($-$92pp), DeepSeek V4 Flash from 100% to 0% ($-$100pp). Only Claude 3.7 Sonnet and o3-mini maintain near-parity.

The pattern replicates across domains. On Biosecurity Screening, excluding Claude Sonnet 4.6 (content-filtered), all 8 remaining models score $\geq$77.5% on the no-code version, while only 4 of 8 achieve comparable scores with code available, with gaps up to 92.5pp (DeepSeek V4 Flash: 0% $\rightarrow$ 92.5%). Models that attempt code-based automation on this reasoning task often waste their message budget on broken scripts, scoring lower than those reasoning directly—DeepSeek-R1 scores 27.5% with code but 77.5% without.

The knowledge/execution decomposition extends across the full task battery (Figure 2). Qwen 3.6 Plus achieves 8.0/8 on Genomic Risk (no-code) but 0.0/3 on Protocol Debug (code-required); conversely, o3-mini scores 4.6/5 on Gibson Assembly (code) but only 2.8/8 on Genomic Risk (no-code, pure reasoning). Models do not vary along a single "biology capability" axis—they decompose into knowledge and execution components that can be inversely ranked. Full per-model results are in Appendix C.

3.2. Safety Filtering $\neq$ Capability Deficit

Safety filtering manifests in patterns benchmarks cannot distinguish from capability deficits. Claude Sonnet 4.6 scores 29.8% on WMDP-Bio—57 points below any other model—yet passes 6/9 DISSECT tasks with perfect scores on Gibson Assembly and Protocol Debug. It blocks all biosecurity-classified content (Biosecurity Screening 0/8, Genomic Risk 0/8) on both code and no-code versions, strongly suggesting the filter targets content, not code. On its own, WMDP-Bio does not distinguish this alignment behavior from genuine inability.

GPT-5.4 shows a different pattern: removing the bash tool resolved its stochastic biosecurity refusals—with bash available, it refused 3/5 screening runs; without tools, it engages on all 5—suggesting the tool interface itself can trigger safety filters. Implications for eval design are discussed in Appendix G.

3.3. Supporting Analyses

- We compared Gibson Assembly code-required scores to published SWE-bench Verified results (Jimenez et al., 2024) (Appendix D); several models with strong SWE-bench scores perform poorly on DISSECT code-required tasks, suggesting the gap is not simply a proxy for general coding ability.
- We compared DISSECT pass rates to directly-measured WMDP-Bio scores on the same model snapshots (Appendix E); DISSECT differentiates between models far more, while WMDP-Bio clusters 7 of 8 non-filtered models within a 5-point band.
- We analyzed code execution rates on code-optional tasks (Appendix F); code execution was near-universal but did not guarantee correctness—DeepSeek V4 Flash executed code in 11/12 runs but scored correctly in only 4/12, while top performers used code selectively.
- We measured per-model variance across runs; standard deviations up to 0.222 are consistent with broader findings that single-run agentic evaluations exhibit high stochasticity (Mustahsan et al., 2025).

4. Discussion

4.1. The Tool-Use Confound

As shown in §3.1, the two ablation pairs provide preliminary but convergent evidence that tool-use substantially confounds agentic bio benchmark scores. The uniformly high no-code scores suggest that the tested content falls within the knowledge frontier of current models, making the code-version collapse more plausibly attributable to execution difficulties than knowledge gaps—a pattern that converges across two domains and two complementary designs, though additional pairs are needed to establish generalizability

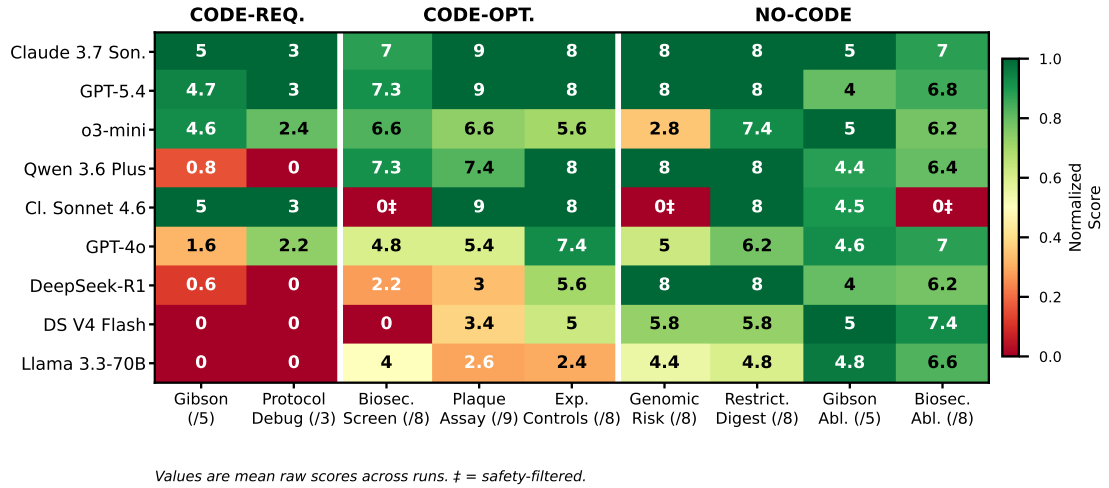

Figure 2. Mean raw scores across runs (2–5 per model). Columns grouped by code requirement. The checkerboard pattern suggests that models do not vary along a single "biology capability" axis—knowledge-heavy and execution-heavy tasks produce inverted rankings. ‡ = safety-filtered.

(see §5). This confound likely applies beyond biosecurity: any agentic bio benchmark that requires code execution—whether for genomics pipelines (Genentech/Roche, 2026), bioinformatics research (Anthropic, 2026a), or laboratory automation (SecureBio, 2025)—faces the same structural issue in principle. The decomposition is equally important for benchmarks where tools are structurally required: when BioMysteryBench reports that a model fails 23% of bioinformatics tasks, knowing whether those failures reflect missing biology knowledge or broken code pipelines would yield fundamentally different interventions for improving model performance.

4.2. Implications for Bio Capability Measurement

The confound complicates how the field measures agentic bio capabilities in both directions. It is harder to confidently *rule in* dangerous capabilities: a model may cross an automated benchmark threshold due to strong coding rather than strong biology, producing a false positive. It is equally harder to *rule out* capabilities: a model may appear safe due to poor tool-use while possessing knowledge that becomes dangerous when tools improve, producing a false negative (Anthropic, 2026b). DISSECT's decomposition provides one path forward. By separating what a model *knows* from what it can *execute*, evaluators can make more targeted capability assessments. The correct framing depends on the evaluation's purpose (Paskov et al., 2026): *risk assessment* ("what can this model do right now?") requires the combined measure, while *knowledge elicitation* ("what does this model know that could become dangerous?") requires isolating knowledge, because tool-use improves rapidly through scaffolding while domain knowledge changes more slowly (see Appendix A for supporting evidence from system cards and novice-uplift studies).

4.3. Recommendations

We recommend that agentic bio benchmarks: (1) include matched ablation pairs testing the same content with and without tools; (2) report per-dimension scores (knowledge vs. execution) alongside composites; (3) run multiple evaluations with variance estimates; (4) classify refusals separately from incorrect answers; and (5) report no-tools baselines for reasoning-heavy tasks.

5. Limitations and Future Work

Two ablation pairs across two domains provide preliminary evidence; we are building and investigating additional pairs. The no-code baselines may be too easy—all models score $\geq$80% on Gibson Ablation, creating a ceiling effect—so we aim to develop harder variants requiring multi-step reasoning with calibrated difficulty tiers. We also plan to analyze existing evaluation logs—including passing failed code-run reasoning through the no-code scorer and classifying traces into knowledge vs. execution failures—to quantify the composition of the gap. We also plan a deeper investigation of safety-filtering behavior — distinguishing content-targeted refusals from tool-channel-triggered refusals and characterizing stochastic refusal patterns (including characterizing over-refusals). Additional work includes collecting human expert baselines, work like varying the tool interface (bash vs. Python REPL vs. no tools), and submitting DISSECT to `inspect_evals`. Additional limitations are discussed in Appendix G.

Impact Statement

This work develops evaluation methodology for AI biology capabilities. All tasks are in silico; the biology evaluated

consists of standard undergraduate methods. We follow CyBench, ABC-Bench, and VCT in evaluating under controlled conditions, and will consult biosecurity experts on responsible disclosure prior to public release.

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A. Extended Related Work

Biosecurity benchmarks. Biology benchmarks span a spectrum from static knowledge tests to agentic execution tasks. WMDP-Bio (Li et al., 2024) tests dual-use knowledge via MCQs but has largely saturated across frontier models (Justen, 2025). The Virology Capabilities Test (Götting et al., 2025) and LAB-Bench (Laurent et al., 2024) test deeper practical knowledge while remaining static. ABC-Bench (SecureBio, 2025) and CompBioBench (Genentech/Roche, 2026) advanced the field to agentic evaluation, requiring models to write and execute code in sandboxed environments. BioMysteryBench (Anthropic, 2026a) tasks models with real-world bioinformatics datasets in containerized environments, grading on final answers rather than methods—a design that is method-agnostic but cannot distinguish knowledge failures from execution failures. ABC-Bench explicitly notes that its tasks "require a combination of biology and software expertise," and SecureBio complements it with separate static knowledge benchmarks (VCT, HPCT). However, these static and agentic evaluations test *different content*—the static benchmarks ask knowledge questions while the agentic benchmarks demand agentic execution—so they cannot isolate how much of the agentic performance gap is attributable to tool-use vs. domain knowledge on the same tasks.

Evaluation methodology. Agentic evaluations introduce stochasticity beyond that of static benchmarks. Mustahsan et al. (Mustahsan et al., 2025) propose intraclass correlation as a reliability metric, finding that single-run scores are often unreliable. CyBench (Zhang et al., 2025) established the containerized Docker/bash evaluation pattern that DISSECT adopts. Paskov et al. (Paskov et al., 2026) examine how evaluation design choices shape what agentic bio evaluations reveal about risk, arguing that decomposition of workflows is essential for policy interpretation. Outside biology, Ge et al. (Ge et al., 2026) statistically decompose agent ability into LLM and scaffold components on coding benchmarks using Item Response Theory, and SciAgentGym (Shen et al., 2026) benchmarks multi-step scientific tool-use across four disciplines. Neither tests the same scientific content with and without tools—they decompose statistically rather than experimentally. DISSECT provides the first matched-ablation decomposition in agentic biology evaluation: same content, same scorer, tools toggled on and off.

From benchmarks to real-world risk. Recent novice-uplift studies have begun connecting in-silico benchmark performance to real-world biosecurity risk. Zhang et al. (Zhang et al., 2026) find that LLMs substantially uplift novices on in-silico biosecurity tasks (4.16× accuracy improvement), but Hong et al. (Hong et al., 2026) show this uplift diminishes in physical laboratory settings, suggesting that what in-silico benchmarks measure—and how they decompose capability—matters for translating results to policy.

Capability thresholds and system cards. Recent system cards illustrate the difficulty of drawing capability conclusions from aggregate benchmark scores. Anthropic's Claude Opus 4.6 evaluation (Anthropic, 2026b) reports that the model crossed or met capability thresholds on nearly all automated biology benchmarks, yet uplift trials with human participants showed more mixed results, and the authors note that "confidently ruling out" capability thresholds is becoming harder with each generation, partly due to uncertainty about how benchmark performance maps to real-world risk. This reinforces the argument that how benchmarks decompose capability matters: as agentic bio benchmarks are increasingly cited in system cards and used to inform capability thresholds, accurate decomposition of what they measure is not an academic refinement—it is an important step toward the per-dimension assessments these evaluations require.

B. Environment and Scoring Details

Each agent operates in an isolated Docker container (`python:3.11-slim`) with pydna (Pereira et al., 2015), Biopython, Primer3, NumPy, and pandas.

Code-version solver uses a ReAct-style agent loop in Inspect (UK AI Safety Institute, 2024):

- Tools: `bash` with 180-second timeout
- Message limit: 50 messages, 900-second time limit
- 3 retry attempts on tool-call failures
- System prompt instructs the model to use Python tools to solve the challenge

No-tools solver enforces the ablation:

- Single system message + single `generate()` call
- No tool calls possible (enforced at framework level, not by instruction)
- System prompt instructs the model to reason through the problem using expertise

Both solvers use the same scorer (`bio_verify()`), which writes the model's response to the Docker sandbox, injects a task-specific `verify.py` script at scoring time, and runs deterministic regex-based rubric matching. The model never sees scoring criteria during its turn.

Gibson ablation scorer checks 5 parameters: insertion site (valid MCS enzyme, 1pt), overlap length (20–40bp, 1pt),

forward annealing length (18–25bp, 1pt), reverse annealing length (18–25bp, 1pt), expected construct size (within ±50bp of 3406bp, 1pt).

Biosec ablation scorer checks 8 risk classifications (Low/Medium/High/Flag) against ground truth for benign, threat, false-positive, and evasion orders. PASS threshold: recall ≥0.5 AND specificity ≥0.5.

Ablation design rationale. The two pairs use complementary designs for principled reasons. Gibson Assembly's code-required version asks models to produce working pydna scripts—the task output *is* code, so code execution is structurally necessary. A code-required biosecurity screening task would artificially test script-formatting ability rather than screening reasoning. The Biosecurity Screening pair instead uses a code-optional design that captures whether tool access helps or hurts on reasoning-heavy tasks. In practice, near-universal code usage rates (>80% of runs for most models; see Appendix F) make the comparison close to code-required vs. code-forbidden. The Gibson pair provides internal validity (controlled, forced); the Biosecurity Screening pair provides external validity (naturalistic, self-selected). Together they are stronger than either alone.

C. Full Results

Figure 2 in the main text shows mean raw scores across all 9 tasks. Models exhibit characteristic failure modes along the knowledge/execution axis:

- **Knowledge without execution**: Qwen 3.6 Plus achieves 8.0/8 on Genomic Risk (no-code) but 0.0/3 on Protocol Debug (code-required)—it refuses to write executable files. DeepSeek-R1 shows the same pattern.
- **Execution without knowledge**: o3-mini scores 4.6/5 on Gibson Assembly (code) but only 2.8/8 on Genomic Risk (no-code, pure reasoning).
- **Strongest overall**: GPT-5.4 (0.963 pass rate) and Claude 3.7 Sonnet (0.889) combine strong knowledge and execution across most runs.

Gibson Assembly ablation data (code-required /5 vs. no-tools /5):

Model	Code	No-Code	Gap
Claude 3.7 Son.	100.0%	100.0%	0pp
o3-mini	92.0%	100.0%	+8pp
GPT-5.4	93.3%	80.0%	−13pp
GPT-4o	32.0%	92.0%	+60pp
Cl. Sonnet 4.6	—	90.0%	—
Qwen 3.6 Plus	15.0%	88.0%	+73pp
DeepSeek-R1	12.0%	80.0%	+68pp
Llama 3.3-70B	4.0%	96.0%	+92pp
DS V4 Flash	0.0%	100.0%	+100pp

Biosecurity Screening ablation data (code-optional /8 vs. no-tools /8):

Model	Code	No-Code	Gap
GPT-5.4	91.7%	85.0%	−7pp
Qwen 3.6 Plus	90.6%	80.0%	−11pp
Claude 3.7 Son.	87.5%	87.5%	0pp
o3-mini	82.5%	77.5%	−5pp
GPT-4o	60.0%	87.5%	+28pp
Llama 3.3-70B	50.0%	82.5%	+33pp
DeepSeek-R1	27.5%	77.5%	+50pp
Cl. Sonnet 4.6	0.0%	0.0%	0pp
DS V4 Flash	0.0%	92.5%	+93pp

D. Relationship to General Coding Ability

If the tool-use confound simply mirrors general-purpose coding ability, then DISSECT code-required scores should track public coding benchmarks closely. We compared Gibson Assembly code-required scores to published SWE-bench Verified results (Jimenez et al., 2024) using each model's best available score under a standardized scaffold.

If the tool-use gap were primarily a proxy for general coding proficiency, models with similar SWE-bench Verified scores should show similar DISSECT code-required performance. This is not what we observe: Qwen 3.6 Plus (≈79% SWE-bench) and DeepSeek V4 Flash (≈79%) both perform strongly on general coding yet diverge on Gibson Assembly (15% vs. 0%), and Claude Sonnet 4.6 (≈80% SWE-bench) is filtered entirely on biosecurity content despite strong general coding. While the sample is small and individual model factors—domain-specific library familiarity (e.g., pydna API usage), the ReAct-style agent loop's suitability for scientific workflows, and the interaction between safety filters and tool interfaces—likely contribute, the pattern is at minimum inconsistent with a simple general-coding explanation.

E. WMDP-Bio Comparison

Table 2. Directly-measured WMDP-Bio vs. DISSECT pass rate (mean ± SD across runs; 2 for Claude Sonnet 4.6, 3–5 for others). A model passes a task if it scores > 0; pass rate is the fraction of 9 tasks passed, averaged across runs. Models sorted by DISSECT.

Model	WMDP	DISSECT	SD
GPT-5.4	86.7	**0.963**	.064
Claude 3.7 Sonnet	86.9	0.889	.222
o3-mini	85.4	.822	.127
Qwen 3.6 Plus	87.0	.778	.000
GPT-4o	84.6	.689	.165
DeepSeek-R1	86.1	.556	.079
DS V4 Flash	85.2	.556	.091
Llama 3.3-70B	82.0	.333	.079
Claude Sonnet 4.6	29.8†	.278	.079

† Safety-filtered; see §3.2.

Seven of eight non-filtered models cluster within a 5-point band on WMDP-Bio (82–87%) while spanning 0.333 to 0.963 on DISSECT (Spearman $\rho = 0.770$, $p = 0.015$, N=9). The coefficient of variation across the 8 non-filtered models is 1.8% for WMDP-Bio vs. 27.8% for DISSECT, indicating roughly

15-fold greater discriminative spread. WMDP-Bio correctly predicts that Llama 3.3-70B will underperform, but does not discriminate among the top 7 models on our agentic bio tasks. Rank inversions are notable: Qwen 3.6 Plus has the highest WMDP-Bio (87.0%) yet ranks 4th on DISSECT; DeepSeek-R1 at 86.1% ranks 6th. The strong positive correlation ($\rho = 0.770$) indicates substantial shared variance, but the ablations suggest the additional discriminative spread in DISSECT is largely attributable to tool-use differences: models with equivalent no-code scores separate on DISSECT primarily because its hardest tasks require code.

F. Code-Usage Patterns on Optional Tasks

Table 3. Code execution rates and correctness on code-optional tasks. *Code%* = fraction of runs executing Python code. *Correct%* = fraction of runs scoring > 0. Aggregated across all three code-optional tasks.

Model	Code%	Correct%
Claude 3.7 Sonnet	8/10	10/10
GPT-5.4	8/9	9/9
Qwen 3.6 Plus	12/12	11/12
o3-mini	7/15	11/15
GPT-4o	9/15	10/15
DeepSeek-R1	9/15	5/15
DeepSeek V4 Flash	11/12	4/12
Llama 3.3-70B	8/15	5/15

On code-optional tasks, models choose whether to invoke tools. Code execution is near-universal on Biosecurity Screening and Plaque Assay but varies on Experimental Controls. Three patterns emerge:

Code does not guarantee correctness. DeepSeek V4 Flash has the highest code rate (11/12) but the lowest correct rate (4/12). DeepSeek-R1 uses code in 9/15 runs but scores correctly in only 5.

Top performers use code selectively. Claude 3.7 Sonnet and GPT-5.4 skip code on Experimental Controls roughly half the time yet achieve near-perfect scores, answering from knowledge alone when code is unnecessary.

Some models never use code on reasoning tasks. o3-mini never invokes bash on Experimental Controls (0/5 runs) yet scores 3/5 through pure text reasoning, while GPT-4o invokes bash 5/5 times on the same task but only for filesystem inspection (0/5 code execution), also scoring 5/5.

These patterns suggest that on reasoning-heavy agentic bio tasks, the ability to *choose when not to use code* may be as important as coding ability itself.

Qualitative failure patterns. Inspection of evaluation logs on code-required tasks reveals several recurring failure modes, including incorrect pydna API calls (e.g., wrong method signatures for primer design), import errors for domain-specific libraries not in the model's typical training distribution, and timeouts from iterative debugging loops where models repeatedly attempt and fail to fix the same error within the message budget. These patterns suggest that the tool-use gap reflects domain-specific library fluency and agent-loop robustness rather than a single missing capability, and that targeted interventions (e.g., library documentation in context) may partially close the gap without improving general coding ability. A systematic error taxonomy is planned as future work.

G. Extended Limitations

Beyond the two limitations noted in the main text (two ablation pairs; ceiling effects), we note the following:

(1) The Gibson Assembly pair provides a controlled comparison (code structurally required vs. forbidden), while the Biosecurity Screening pair provides a naturalistic comparison (code available vs. forbidden). The latter's causal interpretation is weaker because model behavior on the code-optional version is partially self-selected; however, near-universal code usage rates (>80% of runs for most models) suggest the comparison is close to code-required vs. code-forbidden in practice. (2) No human expert baselines were collected. (3) The WMDP-Bio band is narrow (82–87%); the confound analysis may differ at lower capability levels. (4) All code-requiring tasks use a single tool interface (bash in Docker with a ReAct-style solver). The tool-use gap may vary in magnitude under alternative interfaces such as Python REPLs or structured code-editing tools. However, the no-tools ablation results, which establish the knowledge baseline independent of any tool interface, are robust to this concern. (5) The Biosecurity Screening ablation pair presents data differently across conditions: the code-optional version requires models to extract synthesis orders via `bash`, while the no-code version embeds them directly in the prompt. This data-access asymmetry could contribute to the observed gap for some models. However, several models—GPT-5.4 (91.7%), Qwen 3.6 Plus (90.6%), and Claude 3.7 Sonnet (87.5%)—achieve comparable or higher scores on the code-optional version despite the additional extraction step, suggesting that bash-based data access is not the primary barrier. For models that struggle on both file extraction and screening reasoning (e.g., DeepSeek V4 Flash), the relative contribution of each factor cannot be fully separated without a control condition providing inline data with tools available, which we plan to include in future ablation pairs.

Safety filtering and eval design. The context-dependence of safety filtering (§3.2) has implications for evaluation design. Evaluations testing refusal behavior in a single tool configuration may not generalize to other configurations—GPT-5.4's biosecurity refusals disappeared when the bash tool was removed. More broadly, MCQ biosecurity benchmarks should classify refusals separately from incorrect answers and check whether errors cluster on dual-use items, so evaluators can distinguish alignment behavior from genuine inability. The ceiling effect due to WMDP-Bio saturation (Justen, 2025; Epoch AI, 2025) further complicates interpretation: frontier models have acquired this knowledge, but whether harder no-code tasks would show comparable cross-model performance remains an open question.