

The evolution of sex for artificial intelligence

A population-genetic framework for multigenerational model populations

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Significance statement

Artificial intelligence is shifting from single, frozen models to populations of models that specialise, are retrained on each other’s output, and are combined (“merged”) into new models. Trained on their own output, model lineages degenerate — a process already recognised as the mathematics of genetic drift. This paper imports the other half of population genetics: the biology of sexual reproduction. It treats model merging as recombination, real data as immigration, and merge failure as reproductive isolation, and tests each correspondence in simulations, small neural networks, and language models. The framework yields design rules — when to average models, when to keep them separate, how much real data suffices — and a first controlled test showing that measured functional conflict, not weight distance, predicts when merging fails.

Abstract

AI development increasingly resembles a population process: models are specialised, retrained on model output, and recombined by weight merging, with an openly evolutionary vocabulary but little use of evolutionary theory. Here we treat multigenerational model populations as systems whose inheritance, diversity, and compatibility must be managed, and transfer the quantitative apparatus of the evolution of sex. We take as settled that training on model output is genetic drift (model collapse). In a minimal inheritance model that is exactly Wright–Fisher — and measurably Wright–Fisher-plus-bias in trained networks — we derive and test the remedies: grounding as immigration, with a critical real-data fraction far below one but a per-capability floor that leaves the rarest knowledge unrescuable; recombination, where averaging parents’ output distributions exactly cancels the benefit of multiple parents while union-preserving operators realise it; the Fisher–Muller effect, with merged language-model specialists exceeding every parent in replicated experiments; outbreeding depression on rugged task landscapes, converted into reliable gains by directed, offspring-screened recombination; and population structure, where the optimal mating breadth shrinks as skills entangle. Sex has a limit: we introduce model speciation — merge failure as reproductive isolation — and show in trained networks that a merge barrier surviving the full function-preserving symmetry group tracks functional conflict, that isolation did not emerge from compatible specialisation, and, in a controlled predictive test, that pre-merge functional disagreement predicts merge damage where weight-geometry baselines do not. We state precisely what is exact, what is measured, and what remains hypothesis.

Introduction

The unit of AI progress is quietly changing. Multi-agent systems arrange many models across *space* — specialists cooperating on a task. A newer axis is *time*: populations of models that persist across generations, each new model built from older ones — specialised by fine-tuning, trained on data earlier models generated, and, increasingly, produced by **model merging**, the direct combination of trained weights (1, 2). The engineering literature describes this openly in evolutionary vocabulary — “crossover,” “mutation,” “mate choice,” populations of merging models that climb benchmarks (2–5) — but as metaphor over search algorithms. The organising claim of this paper is that the vocabulary deserves its mathematics: **multigenerational model populations are systems whose inheritance, diversity, and compatibility must be managed — not merely collections of models to optimise — and the branch of biology that studies exactly this problem, the population genetics of the evolution of sex, transfers as a quantitative framework.**

One half of the transfer is settled and is not our contribution. Training each generation of a model on the previous generation’s output degrades it — *model collapse*: rare capabilities vanish first and the lineage drifts toward its own most common behaviour (6). That this is the mathematics of **genetic drift** in a finite population is now established from several directions (7–9); a closed-form first-extinction law even places collapse onset at the Wright–Fisher first-extinction time (8). We cite this literature as the diagnosis and build on it.

Our contribution is on the remedy side, and we are explicit about what kind of contribution each claim is, distinguishing **interpretation** (an existing result understood in population-genetic terms), **explanation** (the transferred mechanism accounts for observations existing accounts leave open), and **prediction** (the framework forecasts an unmeasured outcome). The paper is strongest on the first; makes concrete progress on the second — separating merge failures that are coordinate artefacts from those that are functional; and reports a first, bounded step on the third — a controlled predictive test in which pre-merge functional-disagreement measures, chosen by the framework, predicted merge damage on a constructed task grid while weight-geometry baselines did not.

The correspondences we develop, summarised in Table 1: single-teacher retraining is **asexual reproduction**, and the irreversible arm of its decay corresponds to **Muller’s ratchet** (10) — once every copy of a rare capability is gone from all parents and sources, no recombination can rebuild it, which is precisely why remedies must act before fixation-by-loss. Injecting verified real data is **immigration** from a non-drifting source (11–13). Model merging is **recombination**, and its celebrated payoff — a merged model exceeding every parent — is the **Fisher–Muller effect** (14, 15). Merging entangled skills courts **outbreeding depression**; screening many candidate merges is a form of **directed sex** with no biological analogue; restricting who merges with whom is **population structure**. And merging’s hard limit — models too diverged in function to combine — is **reproductive isolation**, for which the Bateson–Dobzhansky–Muller theory of incompatibilities (16, 17) supplies the structure. The nearest precursor to this programme reads sex as an algorithm for mixability in the theory of computation (18), pre-dating model merging; the model-merging literature itself has strong empirical operators (1, 19, 20) and emerging merge-success predictors (21, 22), to which our delta is mechanism: *when and why* failure is coordinate versus functional, and what moves the boundary.

We support the framework at three tiers of evidence, in ascending realism and descending exactness: a **minimal analytic model** validated against closed forms to a fraction of a percent; **small trained networks** (MLPs, recurrent networks, an MNIST image generator) where the operators are measured in real weights; and **language models** (LoRA-specialised Qwen models, 0.5B locally and 7B on a compute cluster) where the claims are tested as signs under seed replication. Throughout, we report negative and tempering results with the same prominence

as confirmations: they include the failure of an internal pre-registered prediction, a null on emergent speciation that bounds the analogy, and the sensitivity analyses that temper the predictive test.

The minimal model, and where its exactness ends

Knowledge is modelled as a distribution $\mathbf{p}_t$ over K discrete items — capabilities, facts, modes of behaviour — with a fixed true distribution $\mathbf{p}^*$ whose rare tail carries the knowledge most at risk. One generation is: *draw n samples from the parent’s distribution, optionally mix in m verified real samples (“grounding”, $g = m/(n+m)$), and refit the child*. In this minimal inheritance model the resampling step **is** the Wright–Fisher process — the same equations, which we exploit as an engineering gate: our simulator reproduces the classical closed forms (heterozygosity decay $E[H_t] = H_0(1 - 1/n)^t$; the exact immigration–drift equilibrium; the closed-form multi-teacher union) to within 0.5%, and these are standing tests in the codebase, not one-off checks.

The boundary of the exactness matters, and we measured it rather than assumed it. Real training adds approximation, optimisation noise, and inductive bias, and when trained networks are fit against the exact drift null they deviate in *opposite, architecture-specific* directions: a smoothing recurrent network resists collapse (keeping spurious variants alive), while a sharpening image generator accelerates it. A one-parameter **learning kernel** (a smoothing knob and a sharpening knob on the refit) reproduces both. The honest statement, used throughout: a real learner is Wright–Fisher *plus a signed, measurable estimator bias* — and the drift signs (rare-first loss; the grounding response) survived that bias in every architecture we tested, including a convolutional VAE retrained on its own generated digits, where the dry lineage collapses to a single blurred digit class while 10% grounding holds all thirty modes (Fig. 1).

Table 1. The dictionary. Each correspondence is stated with the level of support it currently has (exact = closed form in the minimal model; empirical = measured in trained systems; hypothesis = stated with a falsifier, untested or unconfirmed). The full claim-by-claim ledger with assumptions and known limits is SI Appendix, Table S1.

Population genetics	Model populations	Support
Genetic drift in a finite population	Training on finite samples of model output	Exact (minimal model); signs in trained nets; diagnosis conceded to prior work
Immigration from a fixed source	Grounding with verified real data	Exact equilibrium; signs in RNN/MLP/VAE/MNIST
Muller’s ratchet (asexual decay)	Irreversible arm of model collapse	Correspondence, scoped: applies to unrecoverable loss
Recombination / sexual reproduction	Model merging	Empirical at 0.5B–7B
Fisher–Muller effect	Merged specialists exceed every parent	Exact-model result; replicated in LLMs
Outbreeding depression under epistasis	Merging entangled skills harms offspring	Exact-model (NK landscapes); hypothesis at LLM scale
Mating systems / population structure	Who merges with whom (breadth of the parent pool)	Exact-model result; hypothesis for real populations
Reproductive isolation (BDM incompatibilities)	Merge failure from functional conflict	Empirical (MLP + LLM tiers, conflict-associated); emergent form not observed
Selection on a fitness function	Verifier-anchored selection (“reality that can say no”)	Exact-model result (jointly necessary with sex and diversity)

Results

Grounding is immigration: cheap, with a floor

In the minimal model, grounding from a fixed real source is immigration into a drifting population, and the equilibrium diversity has a closed form our simulator matches exactly. The engineering headline is the *magnitude*: a critical grounding fraction $g^* \approx 0.05$ retains most diversity indefinitely — real data is cheap insurance. But the same analysis yields a floor the field’s average-loss framing misses: an individual capability of rarity p survives only if the *absolute* real-data budget satisfies $m \cdot p \gtrsim 1$. Protecting the rarest knowledge is priced per item, at cost $\propto 1/p$, and no affordable grounding fraction rescues the deepest tail — that requires recombination (next section). In trained networks the *sign* of the grounding response transfers everywhere we looked, with two honest deviations, both traced to the estimator bias above: sharp thresholds soften, and support-counting metrics decouple from truth (forward-KL is the operative collapse metric for a smoothing learner). On real images (Fig. 1B), dry self-training collapses a convolutional VAE to one mode while $\sim 10\%$ grounding holds all thirty (the trained model needs roughly twice the exact-operator fraction — the measured price of the estimator bias).

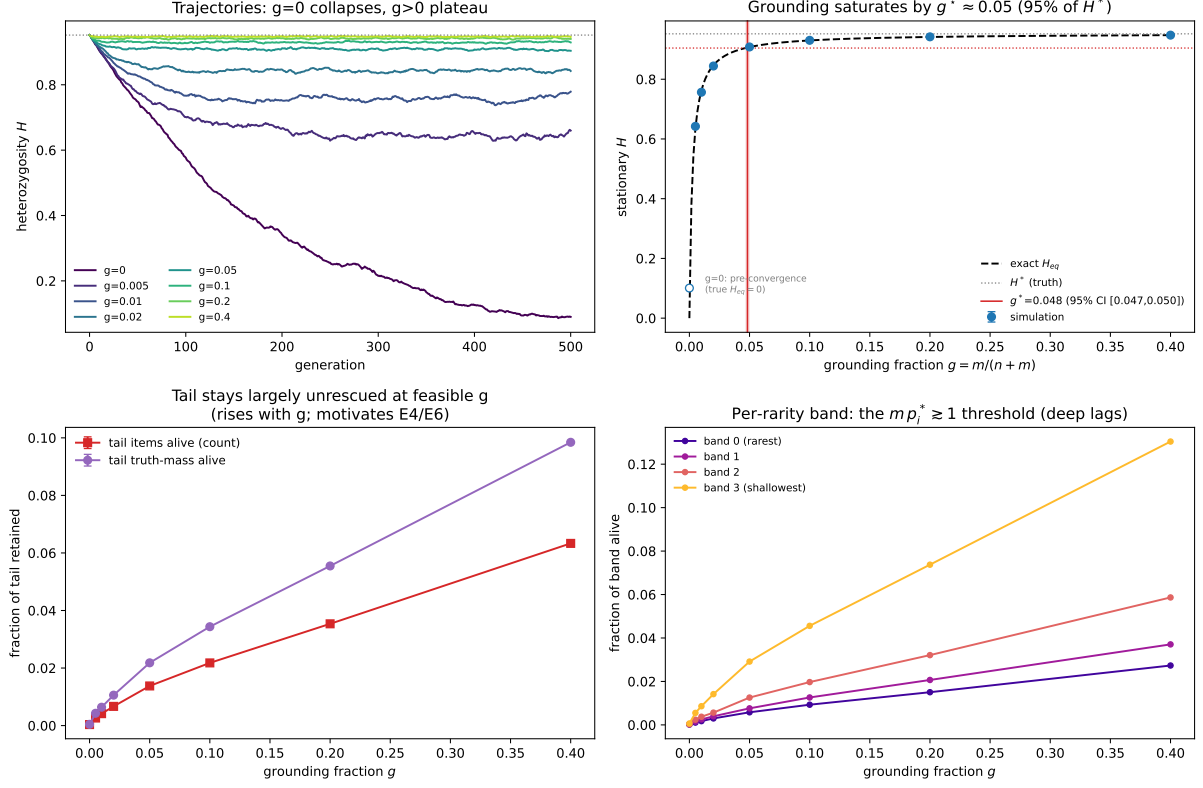
Recombination: a conservation law, its operators, and offspring that exceed every parent

Merging is where the evolution-of-sex apparatus pays for itself, beginning with a result about the obvious operator. **Averaging is blending inheritance, and it cancels the benefit of multiple parents:** when a child is refit to the *mean of its parents’ output distributions*, the expected mass on any rare item is conserved at the single-parent level — in the rare-item regime the $1/K$ dilution of averaging exactly cancels the union gain of K parents, so adding parents cannot help. An operator that keeps, per item, its strongest source (which presupposes a verifier or oracle to say which) realises the union. That statement is exact for those operators in the minimal model. The practically important operators — **weight averaging** (a nonlinear network’s weight-mean does not compute its parents’ output-mean) and **routing among intact specialists** (different storage and inference budgets from a single child) — are its empirical cousins, and the measured bridge is a **headroom rule**: in language models, union-preserving operators beat the weight-average in proportion to how far that average is from the best attainable. On easy tasks a capable base’s average is already at ceiling and refinements add nothing; on hard tasks the average dilutes a fragile specialist below even the best single parent and routing wins by a wide margin (Fig. 6A–B).

The generative payoff is the **Fisher–Muller effect**: recombination assembles, in one offspring, complementary variants that arose in different lineages, producing a genotype fitter than any parent. In the multi-locus model, sexual merging of decorrelated specialists climbs to the global optimum — a genotype no parent held — while the best single parent and the blended average both plateau below (Fig. 2). In real language models the signature replicates under seed replication: merges of three LoRA specialists beat every parent overall (decisively at 7B: 0.87 vs 0.77), and on the sharper worst-family metric the merged models are the only ones competent everywhere, in every seed (Fig. 6A).

Sex has risks and, for AI, an unfair advantage — both quantified on rugged (epistatic) NK landscapes (Fig. 3). When skills are entangled, blind recombination produces offspring *below* their parents — **outbreeding depression** — worsening with ruggedness, and the optimal recombination rate shrinks as entanglement grows. But an engineered population can do what biology cannot: recombine unbounded parents, choose complementary mates, and *screen many candidate offspring against a verifier before keeping one*. This **directed sex** converts the

E2 — a critical grounding ratio $g^* \ll 1$ rescues diversity; the deep tail needs recombination



Dry MNIST lineage collapse: varied digits (top) -> a single mode (bottom)

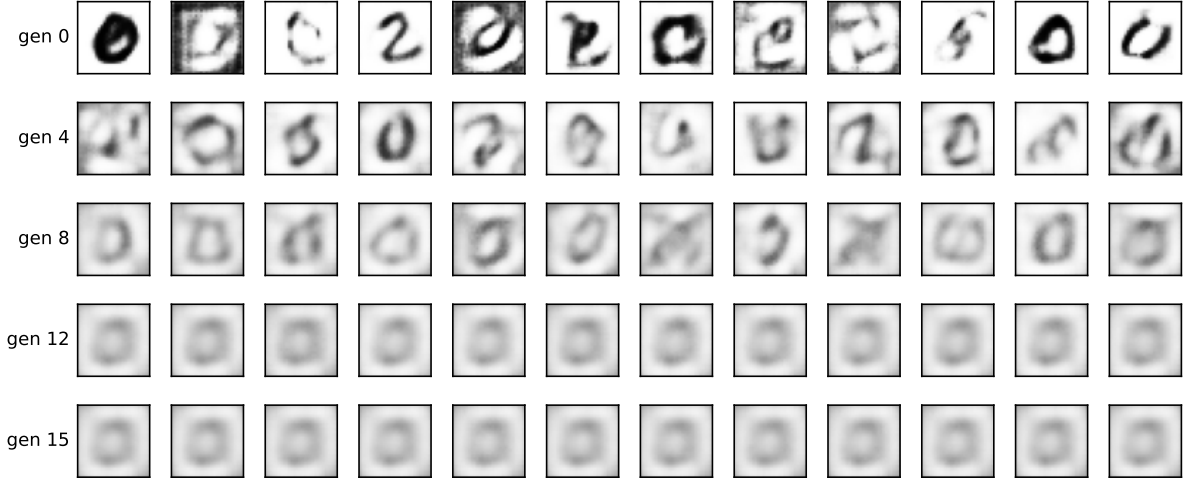


Figure 1: Collapse is drift; grounding is immigration. (A, top) The grounding phase response in the minimal model: a critical real-data fraction $g^* \approx 0.05$ retains most diversity indefinitely, while tail survival obeys the per-item floor $mp \gtrsim 1$. (B, bottom) The same signs on real images: a convolutional VAE retrained each generation on its own output collapses to a single blurred mode (rows: generations), while $\sim 10\%$ grounding holds all thirty class $\times$ style modes.

outbreeding catastrophe into a reliable gain in the model (tracking or exceeding the best parent at every ruggedness) and replicates as a sign in language models: bred-and-screened merges beat the a-priori blend in every seed on headroom tasks — including one seed where the blend failed catastrophically and selection was immune (Fig. 6A). Finally, population *structure* is itself a knob: sweeping the mate-pool breadth from monogamous (local) to promiscuous (panmictic) against ruggedness, wide mixing maximises the population mean while monotonically destroying diversity, and the best *champion* shifts from wide breadth on smooth landscapes to intermediate breadth on rugged ones (Fig. 3C) — the mating-system phenomenon known to structured-population search, mapped onto merging populations.

The society: grounding, sex, and diversity are jointly necessary

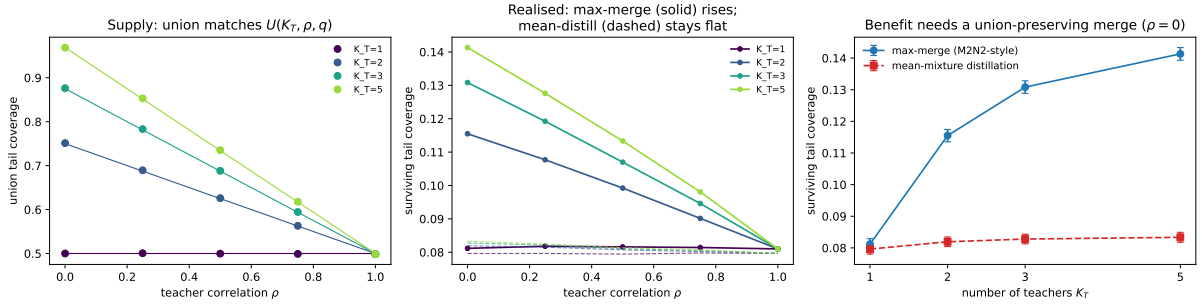
Composing the operators closes the loop (Fig. 4). A finite population of agents evolves on a rugged NK landscape, with selection acting on a grounded score — $g \cdot \text{true-fitness} + (1-g) \cdot \text{conformity to the population's own consensus}$, the analogue of training on the crowd's output. A four-arm ablation separates the failure modes: the **full** system (grounding + directed recombination + diversity-preserving selection) climbs to near the global optimum while keeping its specialists; remove *grounding* and the population converges confidently on an unfit consensus (self-consumption); remove *sex* and it strands on local optima; remove *diversity* and it converges prematurely to a worse answer. Each removal fails *differently* — the operators are jointly necessary, which is the system-level claim the single-operator results build toward. At language-model scale this composed loop remains unbuilt; it is the paper's largest stated gap.

The limit of sex: model speciation

Recombination presupposes compatible parents. In biology, lineages pushed far enough apart become separate species — **reproductive isolation** — through Bateson–Dobzhansky–Muller incompatibilities: changes harmless on their own background but deleterious in combination. A merged model is exactly the exposed hybrid. We built the analytic model (Fig. 5A): hybrid fitness tracks the parents while compatible, then peels off and crashes below the ancestor; the isolation cliff arrives earlier the denser the incompatibilities; and the incompatibility *count* snowballs quadratically with divergence (17) — noting that a super-linear count does not by itself entail a sharp performance cliff without the count-to-effect-size link, which the analytic model supplies under its assumptions and any neural test must establish separately.

In trained networks, the claim must survive a known alternative: merge barriers between independently trained networks are famously *coordinate artefacts*, removable by re-aligning hidden units (23), and richer symmetry groups remove more (24). We therefore aligned modulo the **complete** function-preserving unit symmetry group of the architecture tested (permutation composed with per-unit positive rescaling, for plain ReLU MLPs) and decomposed the barrier (Fig. 5B): two networks trained from different initialisations on the *same* task have a barrier that alignment removes essentially entirely (residual ≈ 0.001 , the aligned merge performing at parent level) — coordinate, not functional; two networks trained on *conflicting* label maps have a barrier the full group leaves intact ($0.502 \rightarrow 0.497$), with the merged model functionally dead — and this cannot be an alignment failure, because the same aligner succeeded on the control. Sweeping conflict traces the cliff as hybrid fitness, $0.97 \rightarrow 0.03$. Two scope notes: exact recovery of a permuted-and-rescaled copy validates a special case rather than global optimality, so the removable share is a lower bound and the residual an upper bound; and the conflict floor itself is information-theoretic — no single model can satisfy contradictory conventions (SI Appendix, Proposition S2) — with the framework's role being the *structure around it*: which divergences generate conflict, and what moves the cliff.

E4 — recombination supplies the tail; only a union-preserving merge realises it in the pupil



E8 — the vertical claim: an offspring recombined from many decorrelated parents is fitter than any parent (Fisher-Muller; no two-parent limit)

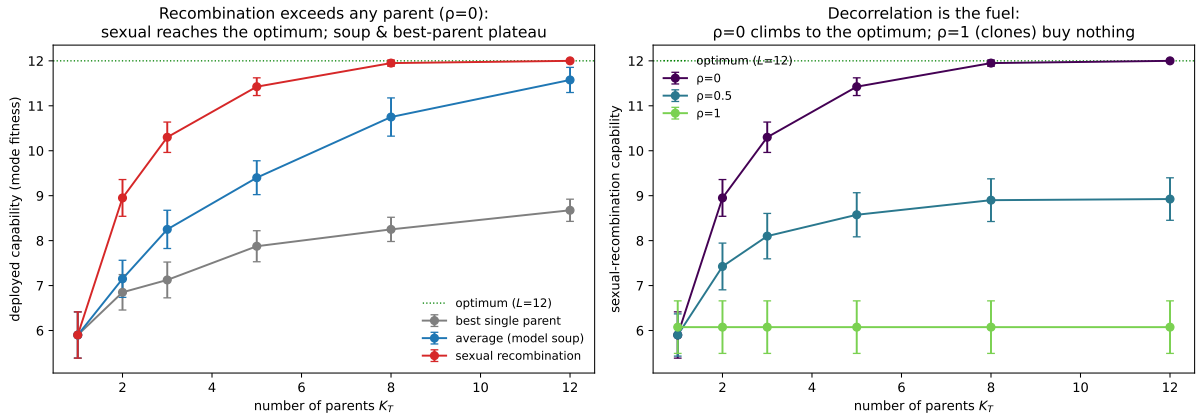
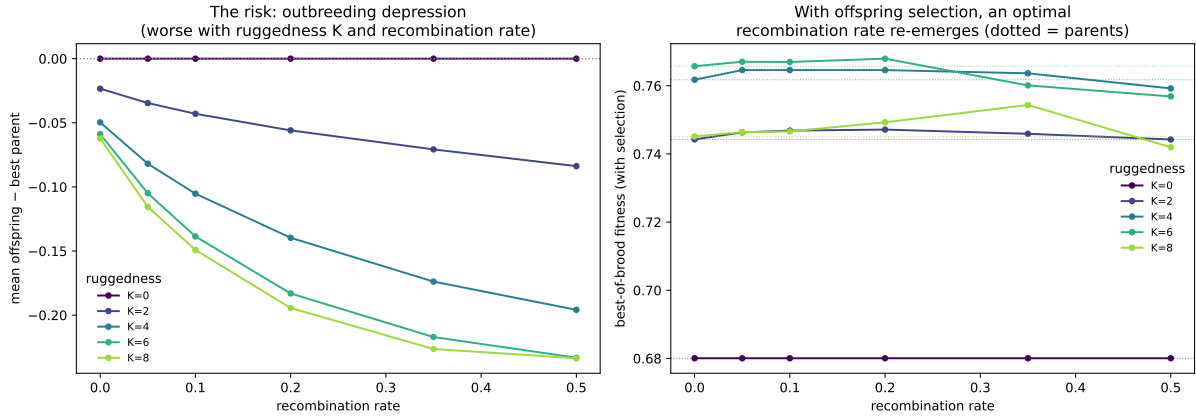
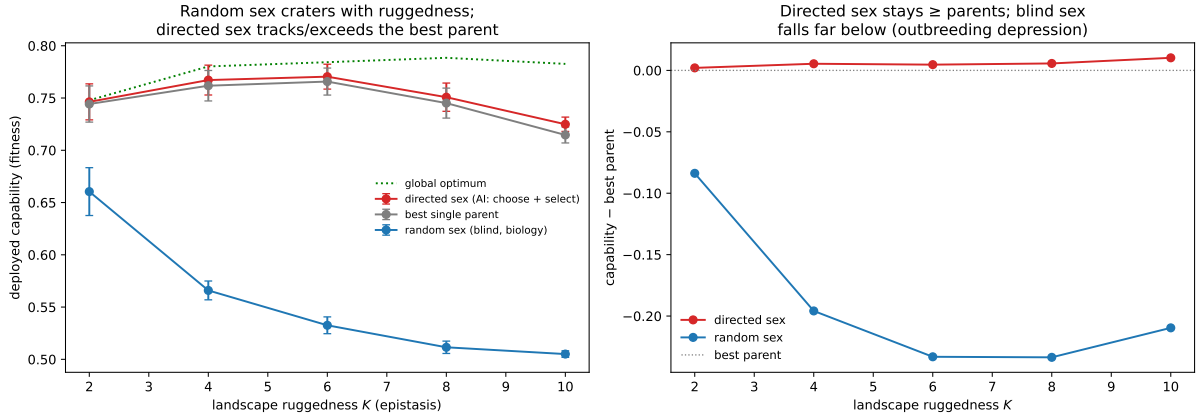


Figure 2: Recombination: the conservation law and the Fisher–Muller effect. (A, top) Refitting a child to the mean of its parents’ output distributions conserves rare-item mass at single-parent level regardless of parent count (blending inheritance); a strongest-source (union) operator realises the multi-parent gain. (B, bottom) Multi-locus recombination of decorrelated specialists assembles a genotype fitter than any parent, climbing to the optimum as parents are added, while the best single parent and the blended average plateau below.

E9 — landscape robustness: recombination helps when skills are complementary, but blindly merging entangled models causes outbreeding depression



E10 — directed sex beats biological sex: mate choice + offspring selection + unbounded parents rescue recombination where blind sex fails



E14 — monogamy vs promiscuity: the best mate-pool breadth shrinks as skills get more entangled

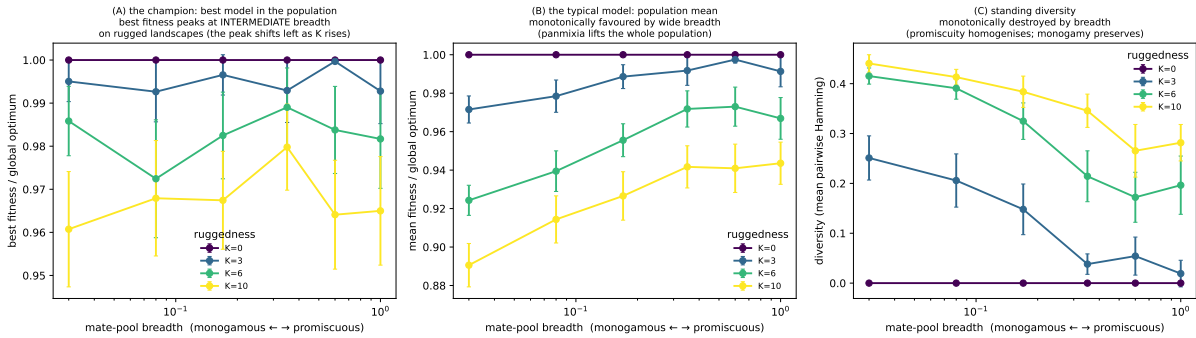


Figure 3: Rugged (epistatic) landscapes: risk, remedy, and structure. (A, top) Outbreeding depression: blind recombination of specialists drops offspring below their parents, worsening with ruggedness; the optimal recombination rate shrinks as skills entangle. (B, middle) Directed sex — unbounded parents, chosen mates, verifier-screened offspring — converts the catastrophe into a reliable gain at every ruggedness. (C, bottom) Mating structure: wide (promiscuous) mixing maximises the population mean but monotonically destroys diversity; the champion-optimal mate-pool breadth narrows as the landscape roughens.

The sharpest honesty comes from the pre-registered **emergent test**: true BDM incompatibilities are emergent (each lineage’s changes harmless alone), so we let children diverge with *no conflicting signal anywhere* — complementary class specialists, and divergent input conventions — to $6.4\times$ the base training. **No isolation emerged** (residual 0.000 throughout); instead the merge *rescued* the two catastrophically-forgetting specialists (parents ≈ 0.50 , merge ≈ 0.955 — a sustained Fisher–Muller rescue). The same double result appears at the language-model tier (Fig. 5C): conflicting conventions produce **function-specific** hybrid breakdown (the merge scores below both parents on the conflicted function, while a budget-controlled design shows the disjoint skills merge unharmed), and over-training disjoint specialists 1→12 epochs produces no isolation at all — the merge improves. Across every tier tested, **isolation had to be provoked by functional conflict; specialisation alone did not speciate** — a bound on the analogy that sharpens the design rule: what breaks merging is conflicting conventions on shared circuitry, not divergence per se.

A controlled predictive test: functional conflict, measured pre-merge, predicts merge damage

The framework’s prediction-level claim was put to a designed test (Fig. 6C). Thirty-nine parent pairs (13 conditions $\times$ 3 seeds; rows are not independent — parents share task-data seeds across conditions — so all inference is condition-clustered) span three axes decorrelated by construction: *conflict* (contradictory conventions on shared prompts, private budgets fixed), *compatible overlap* (the same shared prompts under the same convention — overlap and volume without conflict), and *duration* (weight divergence with zero conflict). Before merging, six predictors are computed: **confidence-weighted functional conflict** (bilateral confident disagreement on probes drawn blind to where conflict lives — a proposed proxy for merge-relevant interactions, motivated by the observation that raw disagreement counts harmless complementation, one parent merely ignorant, as conflict), raw disagreement, gradient alignment at the shared base (21), LoRA-delta cosine and distance, and a cross-task performance baseline. The pre-registered outcome is the merge penalty against oracle parent potential (the hybrid-load analogue), also reported against best- and mean-parent references because the predictor ordering is sensitive to that choice.

The supported conclusion, stated conditionally: **across this controlled grid, pre-merge functional disagreement predicted merge penalties (clustered bootstrap CIs excluding zero; held-out leave-one-condition-out $\rho \approx 0.35\text{--}0.40$), whereas LoRA-delta cosine and L2 showed no statistically detectable association; gradient alignment carried intermediate signal**. Head-to-head predictor differences are not individually significant at this sample size, and only these baselines were tested. Two further results earn their place by tempering: the initial two-axis grid’s best predictor was delta-cosine ($\rho = +0.60$) — an overlap artefact that the compatible-overlap control was added to expose, and did (collapse to $+0.03$); and the pre-registered internal prediction that confidence weighting would beat raw disagreement **failed** (they are statistically indistinguishable as rank predictors), so the present evidence favours functional disagreement generally, not the DMI-specific refinement. The framework motivated the measurement and the controls; their success does not validate the specifically population-genetic mechanism. Whether the prediction improves a budget-matched operator choice, and whether it generalises to unfamiliar conflict structures and real task pairs, are the experiment’s open front.

Discussion

Design rules. Read as engineering, the results compress into rules an operator of a model population can apply. *Ground every generation* in verified reality — a few percent retains most

diversity — but price the rarest capabilities individually ($m \cdot p \gtrsim 1$) and use recombination, not grounding, to reach the deep tail. *Merge, don't blend, when there is headroom*: keep specialists intact and route, or breed-and-screen candidate merges, whenever the naive average is far from ceiling; plain averaging is adequate only where a strong base has already composed the skills. *Match the operator to entanglement*: merge freely when skills are additive; sparingly, with offspring selection, when they entangle; and expect the champion-optimal mating breadth to narrow as landscapes roughen. *Preserve diversity as a first-class objective*, because selection can only preserve variety that exists, and the society result shows grounding, recombination, and diversity are jointly necessary. *Before merging, measure functional conflict* — cheap, pre-merge, and in our controlled setting predictive where weight distance was not; and expect specialisation alone to be merge-safe, with conflicting conventions on shared circuitry as the thing to detect and avoid.

What is borrowed and what is ours. The diagnosis — collapse as drift — is prior art (6–9), as are the empirical facts that merges can beat parents, that decorrelated parents merge better, and that naive averaging loses to interference-aware or routed merges (1, 19, 20), that model populations can climb (2–5), and that merge success admits ML-native predictors (21, 22). Ours is the framework-level synthesis — inheritance, diversity, and compatibility as managed quantities — together with: the conservation law for blending inheritance and its operator boundaries; the per-item grounding floor; the jointly-necessary society; model speciation as a named, tested question, with the coordinate-versus-functional decomposition under a complete symmetry group and the emergent null that bounds it; and the controlled predictive test with its controls. We claim the framework generated these measurements and experiments; we do not claim their outcomes validate a uniquely population-genetic mechanism, and one refinement it proposed was not supported.

Limits and open problems. The demonstrations are deliberately small: exact where small is a virtue, sign-level and seed-replicated at the language-model tier, on constructed task families with a trivially separable router and one model lineage (Qwen, 0.5B–7B). The composed society has not been built at language-model scale. The predictive test's next bars, in order of value: generalisation to *unfamiliar* conflict structures and real task pairs; a demonstrably better *budget-matched* merging decision; then scale replication. Beyond engineering, the framework's hardest open problem is the fitness function itself: selection optimises what is measured, and for knowledge systems the persuasive and the true compete — grounding against a reality that can refuse is the only anchor we trust, and institutionalising that anchor (verification, replication, and challenge among models) is the society-level problem we pose but do not solve. What biology receives in return is a new model system: populations of learners where every genotype, environment, and mating decision is observable and manipulable — where the evolution of sex can be studied with interventions (unbounded parents, offspring preview, directed mating) that no living system permits.

Materials and Methods

Analytic tier. Pure NumPy/SciPy Wright–Fisher simulator over K -item distributions (knowledge as p_t ; Zipf-tailed truth p^* ; drift–grounding–refit generations), extended with a learning kernel (smoothing/sharpening refit), multi-locus genotypes on additive and Kauffman NK landscapes, n -parent crossover, and finite-population society loops. All parameters live in per-experiment YAML configs; every run derives all randomness from one master seed (`SeedSequence.spawn`) and is bitwise reproducible; scientific-validation tests assert the closed forms (heterozygosity decay, immigration equilibrium, closed-form union) to $<0.5\%$ and run in CI with 151 further correctness tests.

Neural tier. Trained-network experiments realise the same abstractions with an exact

oracle: histogram/RNN/MLP/VAE generators on a synthetic mode universe (the histogram model reduces the harness exactly to the analytic tier — the bridge gate), and a convolutional VAE on MNIST with a frozen CNN oracle (98.5% mode accuracy; confusion matrix recorded as the measurement floor). Speciation experiments fork no-BatchNorm MLPs (784–512–512–10) from a shared base, weight-average, and measure linear-mode-connectivity error barriers before and after alignment; alignment composes deterministic Git Re-Basin permutation matching with exact per-unit scale canonicalisation (the complete unit symmetry group for this class), gated by exact recovery of a permuted-and-rescaled copy.

Language-model tier. LoRA specialists (rank 16) on procedurally generated task families with an exact-match verifier, on frozen Qwen2.5-Instruct bases (0.5B on one 16 GB GPU; 7B on one L40S). Operators: weight-space merges (soup/TIES via adapter arithmetic), per-input routing, and Dirichlet-sampled offspring populations screened on held-out validation splits. Multi-seed protocols fix the test sets and vary the training seed. The predictive test computes all predictors pre-merge (generation confidence from token log-probabilities; base-model gradient cosines; exact r-space LoRA-delta geometry) and evaluates merges on held-out tests; robust statistics (condition-clustered bootstrap, paired predictor contrasts, leave-one-condition-out prediction, multi-reference outcomes) are produced by a committed script. Statistical, per-seed reproducibility is documented for GPU tiers.

Data and code availability. All code, configs, seeds, results artifacts (with content hashes), figures, and a one-command reproduction script will be deposited openly (repository + archived DOI) on publication; every figure in this paper regenerates from committed artifacts without re-simulation.

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E11 — the dynamic Lamarckian society: grounding + directed sex + diversity climb to the optimum; remove any one and it breaks (the vertical claim, C3)

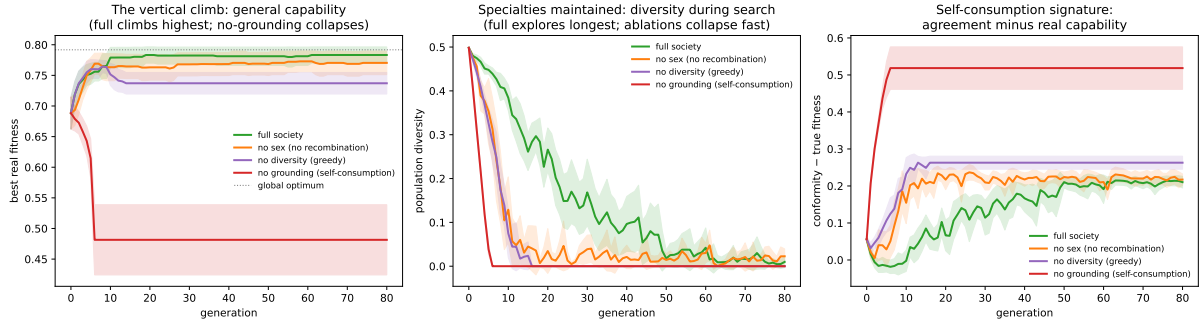
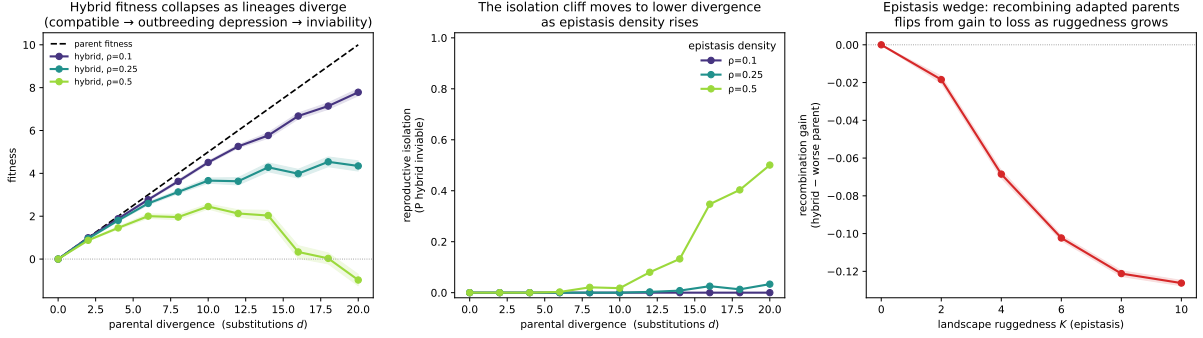
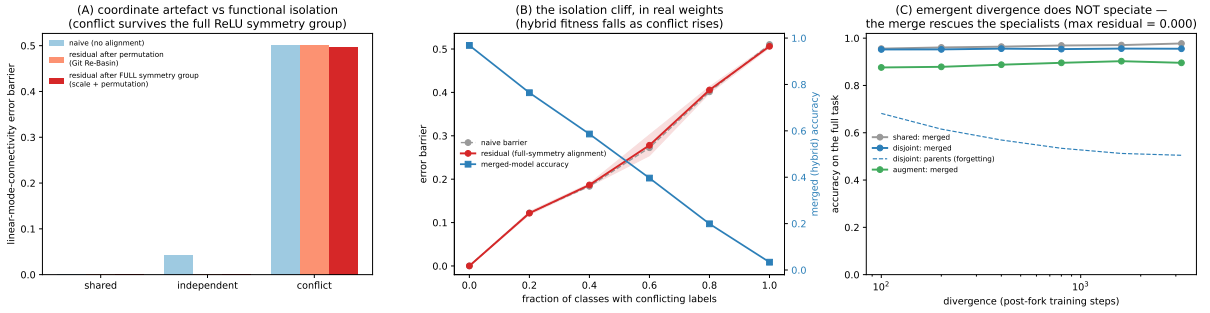


Figure 4: The society: grounding, sex, and diversity are jointly necessary. A finite agent population on a rugged NK landscape under a grounded selection score. Four-arm ablation: the full system climbs to near the global optimum; removing grounding collapses the population onto a confident, unfit consensus (self-consumption); removing recombination strands it on local optima; removing diversity converges it prematurely. Each ablation fails differently.

E12 — model speciation: when two diverged models are too incompatible to merge



E13 — real-weight model speciation: isolation requires functional conflict; alignment (even modulo the full symmetry group) cannot remove it, and compatible specialists merge into a rescuing generalist



LLM-tier model speciation: conflict provokes function-specific hybrid breakdown; no isolation emerges from duration alone (shared base controls coordinate mismatch — a cleaner test of conflict-associated failure)

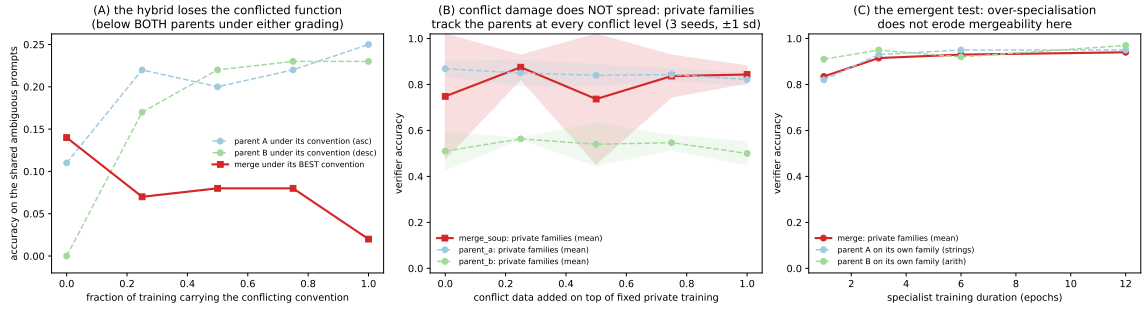


Figure 5: Model speciation across three tiers. (A, top) Analytic: hybrid fitness traces compatible → outbreeding depression → inviability; the cliff arrives earlier the denser the incompatibilities; incompatibility count snowballs with divergence. (B, middle) Trained MLPs: the merge barrier decomposed under the complete unit symmetry group — same-task/different-init barriers are coordinate artefacts (removed by alignment); conflicting-task barriers survive in full, with hybrid fitness falling $0.97 \rightarrow 0.03$; divergence without conflict produced no isolation, the merge instead rescuing the forgetting specialists. (C, bottom) Language models: conflicting conventions produce function-specific hybrid breakdown; over-training disjoint specialists produces none — at every tier tested, isolation had to be provoked by functional conflict.

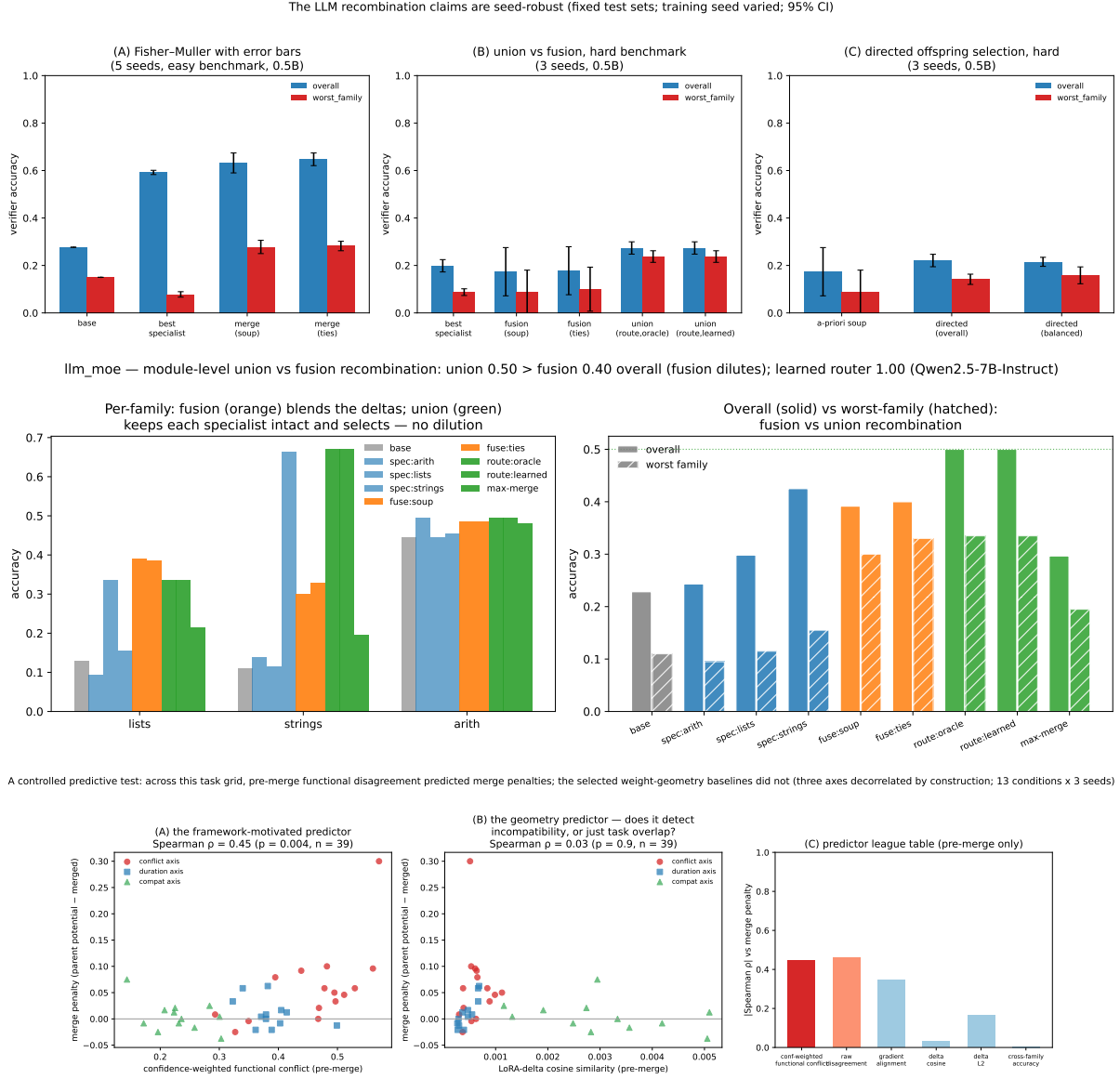


Figure 6: The language-model tier. (A, top) Seed-replicated recombination claims (fixed test sets, training seed varied, 95% CI): merges beat every specialist; union-preserving routing and directed offspring selection beat the blend in every seed on headroom tasks, including one catastrophic blend failure they avoided. (B, middle) The headroom rule at 7B on hard (unsaturated) tasks: the weight-average dilutes a fragile specialist below the best single parent; routing preserves it. (C, bottom) The controlled predictive test: across a task grid with conflict, compatible-overlap, and duration axes decorrelated by construction, pre-merge functional disagreement predicts merge penalty (held-out $\rho \approx 0.4$) while weight-geometry baselines show no detectable association; paired predictor differences are not individually significant.