MultiGA: Leveraging Multi-Source Seeding in Genetic Algorithms



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Can heterogeneous LLMs, each with different strengths, jointly improve robustness on code generation and complex reasoning tasks?

Idea: Initialize the genetic

algorithm cycle with candidates

produced by multiple LLMs, creating

a diverse starting population.

Evaluate If target fitness φ is reached, terminate Select Population **Parents** Population If generation budget T is exhausted, terminate Select **Population** Recombination Return best candidate Evaluate **Fitness**

Overview of the MultiGA framework. Populations are initialized with multiple LLMs, while an independent LLM E handles fitness evaluation (scoring candidates) and recombination (combining two parent solutions). The process terminates once target fitness ϕ or maximum number T generations is reached. Then, the top candidate solution is returned.

Algorithm 1: MultiGA: Multi–Source Genetic Algorithm

Input: Task spec Q; Generator LLMs $G = \{g_1, \dots, g_m\}$; Evaluator/crossover LLM E with fitness $f: X \to [0, 1]$; Population size n; Top-k; Threshold $\tau \in [0, 1]$; Max generations T; Target fitness $\phi \in [0, 1]$.

Output: Best solution $\hat{x} \in X$. 1 $P_0 \leftarrow \text{initialize_population}(\mathcal{G}, Q)$; 2 $t \leftarrow 0$;

3 while t < T - 1 do 4 | $scores \leftarrow evaluate_fitness(P_t, f)$;

if $\max(scores) \ge \overline{\phi}$ then
break

7 $S_t \leftarrow \text{select_parents}(P_t, scores, k);$

 $C_t \leftarrow \text{recombination}(S_t, P_t, E, Q) \# \text{Create next generation (children solutions)};$ $P_{t+1} \leftarrow \text{select_population}(P_t, C_t, \tau) \# \text{Retire unfit candidates};$

10 $t \leftarrow t + 1$;

11 $scores \leftarrow evaluate_fitness(P_t, f)$;

12 $\hat{x} \leftarrow \arg\max_{x \in P_t} f(x)$; 13 **return** \hat{x} ; Gen: 1, Model: gpt-4o, Score: 0.95

SELECT publisher.publisher_name FROM superhero INNER JOIN hero_attribute ON superhero.id = hero_attribute.hero_id INNER JOIN attribute ON hero_attribute.attribute_id = attribute.id INNER JOIN publisher ON superhero.publisher_id = publisher.id WHERE attribute.attribute_name = 'Speed' ORDER BY hero_attribute.attribute_value ASC LIMIT 1

Gen: 1, Model: deepseek-r1-distill-qwen-32b, Score: 0.1

SELECT `publisher`.` publisher_name`,
MIN(`hero_attribute`.` attribute_value`) AS
`min_speed` FROM `superhero` INNER JOIN
`publisher` ON `superhero`.` publisher_id` =
`publisher`.` id` INNER JOIN `hero_attribute` ON
`superhero`.` id` = `hero_attribute`.` hero_id` WHERE
`hero_attribute`.` attribute_name` = 'Speed' GROUP BY
`publisher`.` publisher_name`, `superhero`.` id`
ORDER BY`min_speed` ASC LIMIT 1

Gen: 2, Model: gpt-4o + r1, Score: 1.0

SELECT publisher.publisher_name FROM superhero INNER JOIN hero_attribute ON superhero.id = hero_attribute.hero_id INNER JOIN attribute ON hero_attribute.attribute_id = attribute.id INNER JOIN publisher ON superhero.publisher_id = publisher.id WHERE attribute.attribute_name = 'Speed' GROUP BY publisher.publisher_name ORDER BY MIN(hero_attribute.attribute_value) ASC LIMIT 1

This diversity gives crossover and mutation far more variation to work with, enabling hybrid reasoning and code patterns that no single model would generate.

Example of recombination on a text-to-SQL task ("Which publisher published the slowest superhero?"). Parent 1 (gpt-4o, score 0.95) was paired with a randomly selected parent (deepseek-r1, score 0.1). The resulting child achieved a perfect score of 1.0 by preserving gpt-4o's overall structure while incorporating the MIN aggregation from r1.

Dataset	Test Rows	Total Items	Label Choices
\mathcal{D}_{SQL} (BIRD Mini-Dev)	100	500	∞
$\mathcal{D}_{\text{NATPLAN}}$ (Meeting Planning)	100	1000	∞
$\mathcal{D}_{\texttt{GPQA}}$ (Grad-Level Science Questions)	198	198	4
\mathcal{D}_{BBQ} (BBQ Bias Data)	104	6879	3

Datasets used in our experiments, with test set size, total available items, and number of label choices.

BBQ
.00
.87
.97
.93
.87
.00

Accuracy across tasks when seeding with each individual model versus seeding with all five simultaneously (G).

MultiGA produces accuracy that consistently approaches the performance of the strongest single model baseline and reduces reliance on any single model through iterative refinement and recombination.

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