GA Benchmark Report

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This report presents the benchmarking of Genetic Algorithm (GA) configurations on two standard 2D multimodal functions: Rastrigin and Six-Hump Camelback. We compare binary-encoded and real-valued GA variants using different crossover operators, and provide statistical analysis of results.

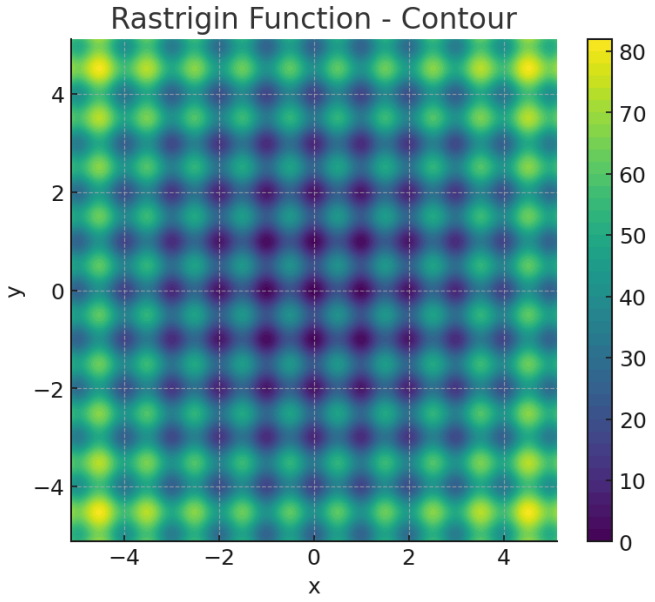
1. Benchmark Functions

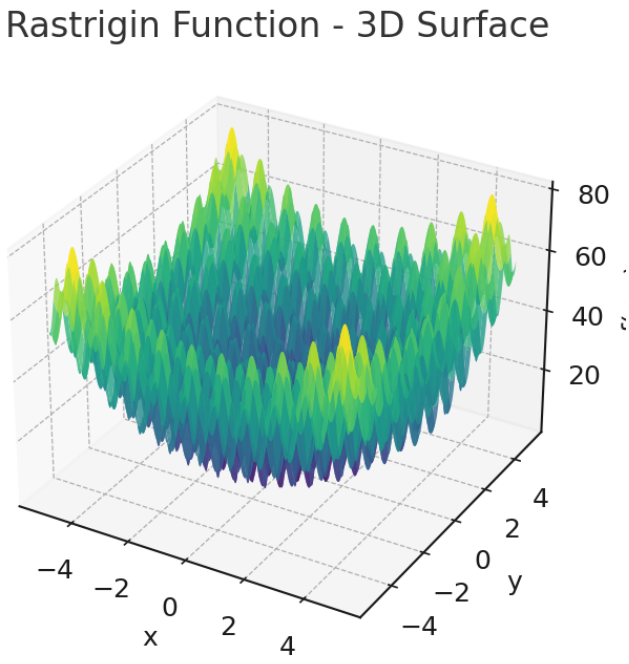
1.1 Rastrigin Function

Domain: x, y in [-5.12, 5.12]

Definition: f(x,y) = 20 + x^2 + y^2 - 10*(cos(2*pi*x) + cos(2*pi*y))

Global minimum at (0,0) with f = 0.





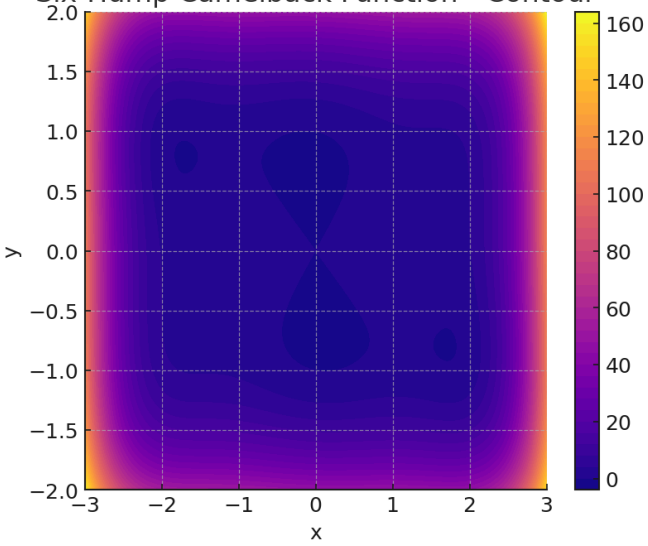
1.2 Six-Hump Camelback Function

Domain: x in [-3, 3], y in [-2, 2]

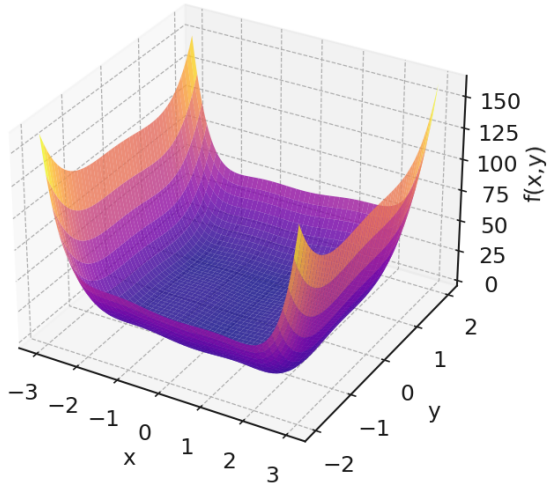
Definition: f(x,y) = (4 - 2.1*x^2 + x^4/3)*x^2 + x*y + (-4 + 4*y^2)*y^2

Two global minima near (±0.0898, -0.7126) with f approx -1.0316.

Six-Hump Camelback Function - Contour



Six-Hump Camelback Function - 3D Surface



2. GA Methodology

2.1 Encodings and Operators

Binary Encoding:

- Each variable encoded with a fixed-length bitstring.
- 1-point crossover: cut at one point, swap tails.
- 2-point crossover: cut at two points, swap the middle segment.
- Bit-flip mutation: each bit flips with probability Pm.

Real-Valued Encoding:

- Each chromosome stores x and y as floats directly.
- Arithmetic crossover: offspring = alpha*parent1 + (1-alpha)*parent2.
- BLX-alpha crossover: for each gene, sample from [min - alpha*I, max + alpha*I].
- Gaussian mutation: add N(0, sigma^2) noise to each variable with probability Pm.

GA Parameters (fixed across all runs):

- Population size: 50
- Number of generations: 200 (total evaluations = 50 * 200 = 10,000)
- Crossover rate Pc = 0.8
- Mutation rate Pm = 0.01 (binary) or 0.1 (real)

2.2 Experimental Setup

We ran 30 independent replicates (seeds 1-30) for each configuration on both functions:

- Rastrigin: Binary 1-point, Binary 2-point, Real Arithmetic, Real BLX-alpha
- Six-Hump: Binary 1-point, Binary 2-point, Real Arithmetic, Real BLX-alpha

Results (best f-value per run) are recorded in JSON files under 'data/'. A summary table (mean +/- std) is provided below.

4. Statistical Analysis

Pairwise t-tests and one-way ANOVA were conducted to compare configurations.

Detailed p-values and Tukey's HSD results can be found in the analysis notebook (analysis.ipynb).

5. Conclusion

On the Rastrigin function, the real-valued BLX-alpha configuration achieved the lowest average best-value, consistent with its ability to explore continuous space. On the Six-Hump Camelback function, both real-valued and binary configurations found values near -1.03, but real-valued variants showed slightly lower variance. Future work could explore different bit-lengths, adaptive mutation rates, or additional benchmark functions.

Summary Table: Mean ± Standard Deviation of Best Fitness Values

Configuration	Mean f-value	Std. Dev.
Rastrigin - Binary 1-point	0.456168	0.572023
Rastrigin - Binary 2-point	0.604790	0.708196
Rastrigin - Real Arithmetic	0.596976	0.607930
Rastrigin - Real BLX-alpha	0.530645	0.666614
Six-Hump - Binary 1-point	-1.025876	0.008771
Six-Hump - Binary 2-point	-1.027959	0.007030
Six-Hump - Real Arithmetic	-1.031628	0.000000
Six-Hump - Real BLX-alpha	-1.031628	0.000000