Automated Design Competition at GECCO 2025

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Results

To avoid duplication of slides from the previous year, this section has been skipped.

See the full 2024 presentation first at https://www.framsticks.com/files/presentations/

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Submissions

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Results

2024:

- TryBestEA
- CaSPO ("Cascaded Structure and Parameter Optimization Based on Prior Knowledge")
- AdaptMut+Diversity ← 2024 winner, becomes the baseline for 2025

Submissions

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2024:

- TryBestEA
- CaSPO ("Cascaded Structure and Parameter Optimization Based on Prior Knowledge")
- AdaptMut+Diversity ← 2024 winner, becomes the baseline for 2025

2025:

GP-GOMEA-Island-Mut

Submission: AdaptMut+Diversity

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Result

2024 winner, becomes the baseline for 2025

This submission uses the **f0** encoding, but other encodings can be used as well.

Two mechanisms introduced aimed at promoting explorative capabilities:

- Adaptive mutation strength the mutation strength (i.e., the number of mutation operations applied to a genotype) is adjusted during evolution. Starts from mutation strength = 1.0. If the maximal fitness of the population has not changed by more than 1% for the last 4 generations, the mutation strength is multiplied by 1.1. Otherwise, it is multiplied by 0.9. Mutation strength is limited to the range [1, 5]. The motivation was to help the algorithm escape the local optima.

Submission: GP-GOMEA-Island-Mut

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- This submission uses the **f1** encoding represented as a Genetic Programming (GP) tree
- There are 10 islands (populations), 30 individuals each.
- Genotypes in the initial island populations are randomly generated as f1 genotypes using the Framsticks library function:
 getRandomGenotype(initial_genotype="X", parts_min=20,
 parts_max=30, neurons_min=6, neurons_max=8, iter_max=100,
 return_even_if_failed=True).
- Processing each population see the next slide.

Submission: GP-GOMEA-Island-Mut

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Islands (populations) are processed sequentially, each undergoing the following steps:

- Genotypes are converted from f1 to GP trees (in normal Polish notation, NPN).
- Linkage tree is built using hierarchical clustering.
- Gene-pool Optimal Mixing (GOM) is performed. Each genotype undergoes GOM.
- In the GOM operator, the shorter genotype is padded with special symbols at the end, and mixing is performed. After that, the special symbols are filtered out.
- Genotypes are converted from GP trees (NPN) to f1 for evaluation.
- When stagnation is detected (best fitness in the population not improving for 2 generations), mutation is performed (on the entire population with probability of 80%). The default, native f1 mutation operator is used.
- If the similarity of any two populations is above 0.8, one of them is reinitialized randomly. Similarity is estimated using the identity of genotypes and the Jaccard index: intersection over union $=\frac{|\text{unique genotypes, the same in each population}|}{|\text{unique genotypes in merged both populations}|}$.
- If the uniqueness of the population = $\frac{\text{number of unique genotypes}}{\text{population size}}$ is below 0.2, individuals from other islands migrate to it (25% random originals stay, the remaining 75% is migrated as random genotypes from random islands).

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Best solutions

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Distance:

https://www.framsticks.com/files/varia/automated-design-competition-2025-best-distance.mp4

Tall runners:

https://www.framsticks.com/files/varia/automated-design-competition-2025-best-tall-runners.mp4

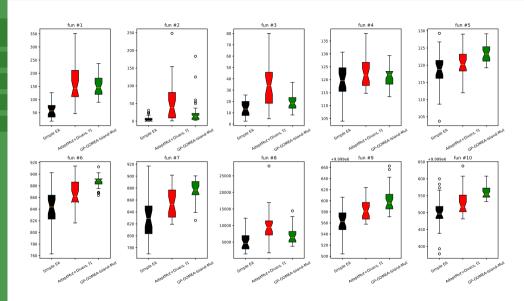
Individual benchmark tasks

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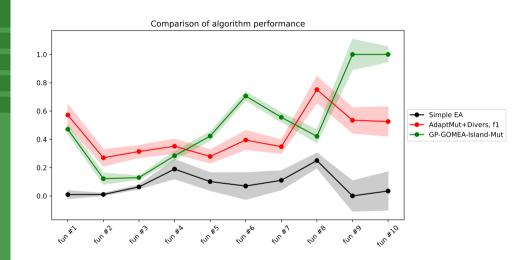
Averaged normalized performance

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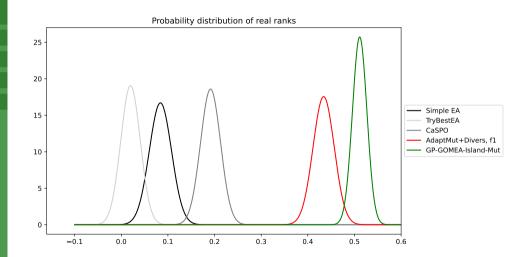
Aggregated performance

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Best algorithm: winning in the "f1 genetic encoding" category

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The 2025 submission outperformed the 2024 winner when evaluated using the **f1** genetic encoding.

However, the 2024 winner remains unchallenged when used with the ${\bf f0}$ genetic representation!

Aggregated performance

Including the 2024 winner that uses the better-performing encoding

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