ISSN 2707-1898 (print)
ISSN 2786-9172 (online)

Український журнал інформаційних технологій
Ukrainian Journal of Information Technology

http://science.lpnu.ua/uk/ujit
https://doi.org/10.23939/ujit2025.02.093
Article received 12.10.2025 p.
Article accepted 30.10.2025 p.
UDC 004.89

Correspondence author
R. Y. Shuvar
rshuvar@gmail.com

V. O. Pretsel, R. Y. Shuvar
Ivan Franko National University of Lviv, Lviv, Ukraine

DYNAMIC MUTATION RATE CONTROL IN GENETIC ALGORITHMS USING CONVERGENCE AND DIVERSITY METRICS

Developed a dynamic mutation rate control strategy using convergence and diversity metrics, which enables the mutation probability to adapt automatically to the current convergence state. The strategy increases the mutation rate when population convergence increases and diversity decreases, thereby promoting exploration and enhancing genetic diversity. When diversity is maintained at a sufficient level, the mutation rate decreases, thereby preventing unnecessary disruption of evolved solutions. Conducted experiments on benchmark functions with different fitness landscapes, including unimodal, multimodal, and deceptive functions, to validate the effectiveness of the proposed approach. Established the Composite Convergence Score (CCS) as a unified measure integrating the most informative metrics into a normalized indicator of convergence dynamics. Correlation analysis and machine learning-based evaluation confirmed that the CCS can reliably identify generations approaching stagnation, and the dynamic mutation rate strategy guided by the CCS significantly improves optimization performance compared to approaches that use a static mutation rate.

Investigated results revealed that CCS-guided mutation control consistently prevents premature convergence, maintains higher population diversity throughout the evolutionary process, accelerates convergence toward global optima, and improves the overall success rate of reaching desired solutions. The approach reduces the need for manual tuning of mutation parameters, as the CCS automatically balances exploration and exploitation. Also, the methodology allows GA frameworks to automatically update evolutionary parameters.

The research demonstrates that the CCS framework can serve as a generalizable tool for adaptive control in evolutionary computation. It provides a foundation for future development of self-adapting genetic algorithms and may be extended to multi-objective, high-dimensional, or real-world optimization problems, including engineering design, logistics, scheduling, and neural architecture search. The study confirms that integrating quantitative convergence monitoring with dynamic parameter adjustment substantially improves GA reliability, robustness, and solution quality, offering significant opportunities for advancing both theoretical and practical aspects of evolutionary optimization.

Keywords: premature convergence, convergence detection, population diversity, adaptive mutation, evolutionary computation.

Introduction

The efficiency of GA is highly dependent on their convergence dynamics and the ability to maintain population diversity. While rapid convergence accelerates the search for optimal solutions, it also increases the risk of falling in local optima – a phenomenon known as *premature convergence*, which remains one of the key challenges in evolutionary computation.

Although numerous techniques have been proposed to mitigate the effects of premature convergence – including adaptive operator control, niching techniques etc. – it is important to have a deeper, quantitative understanding of convergence dynamics before introducing new algorithms. Without such understanding, the field risks being overwhelmed with heuristic methods that remain poorly explained and difficult to generalize. A systematic analysis of convergence can uncover early indicators of stagnation, providing a foundation for adaptive strategies that balance exploration and exploitation throughout the optimization process and are based on theoretical argumentation.

Object of the study – convergence dynamics during the optimization process in genetic algorithms.

Subject of the study – statistical metrics of GA populations and their use in mitigating the convergence effects for dynamic mutation rate control.

Aim of the study – to develop and validate a *Composite Convergence Score (CCS)* that quantitatively measures GA convergence and population diversity, enabling dynamic mutation rate strategies to mitigate premature convergence and improve solution quality across different optimization problems.

To achieve the set aim, the following tasks were defined:

1. Investigate statistical metrics gathered during GA runs and evaluate whether they can serve as reliable predictors of convergence.
2. Identify the subset of metrics with the highest predictive power for premature convergence detection.

3. Design a composite convergence score (CCS) based on the selected metrics and validate its ability to quantify the degree of convergence.

4. Develop a dynamic mutation rate control strategy based on CCS and evaluate its effectiveness in avoiding premature convergence and improving solution quality.

Analysis of recent research and publications

The effectiveness of genetic algorithms (GAs) depends crucially on the balance between exploration and exploitation. Recent studies have emphasized that maintaining population diversity and adaptively controlling genetic operators are key to achieving robust and efficient search behavior.

A general overview of the development of GAs and their application trends is presented in [1], which outlines how the design of genetic operators, selection schemes, and mutation control directly affects convergence behavior. The authors highlight that maintaining diversity throughout evolution is essential to avoid stagnation and local optima. Similarly, [2] provides a comparative review of techniques that mitigate premature convergence, categorizing them into diversity-preserving, adaptive, and hybrid strategies. The review identifies population diversity and selective pressure as primary factors of algorithmic performance and explains the need for quantitative convergence monitoring instead of purely heuristic adjustments.

The importance of diversity-preserving mechanisms for global exploration is further demonstrated in [3]. Through both theoretical and empirical analysis, it was shown that algorithms without diversification behave similarly to simple hill-climbers, rapidly converging to local optima. Mechanisms such as fitness sharing and deterministic crowding, however, enable populations to locate multiple global optima efficiently. These findings confirm that explicit diversity maintenance is necessary for preventing convergence collapse and sustaining exploration across the search space.

Further insights into balancing exploration and exploitation are provided in [4], which discusses recent advancements in hybrid and self-adaptive GAs integrating diversity metrics into parameter control. The authors emphasize that the future of GA optimization lies in self-regulating control mechanisms guided by convergence indicators derived from population statistics, fitness entropy, and genotypic or phenotypic diversity.

The theoretical basis for analyzing convergence dynamics was established in [5], where the degree of population diversity was introduced as a measurable parameter within a Markov chain framework. The study proved that, in the absence of mutation, the population diversity inevitably converges to zero. Furthermore, an explicit expression for the probability of allele loss was derived, revealing how population size, mutation rate, and selection intensity together influence convergence. This analytical foundation provides a rigorous context for adaptive mechanisms that modify mutation and population parameters in response to measured diversity indicators.

From an algorithmic design perspective, several modern studies have proposed hybrid or adaptive operators that explicitly integrate diversity information into evolutionary processes. The Fitness and Diversity Ranking-Based Differential Evolution (FDDE) algorithm [6] combines both fitness and diversity rankings to assign each individual an adaptive role in the mutation process. This approach improves the balance between global exploration and local refinement, outperforming established DE variants (e. g., SHADE, L-SHADE, jDE) on standard CEC benchmark suites. Similarly, the Two-Stage Differential Evolution (TDE) algorithm [7] introduces historical-solution-based and inferior-solution-based mutation phases, together with a fitness-independent parameter control, enhancing adaptability under various fitness landscape conditions.

Another contribution to adaptive selection is the Fitness-Distance Balance (FDB) method [8], which introduces a new criterion that simultaneously considers the fitness value of individuals and their distance from the best-known solutions. This method provides more stable guidance for search direction and effectively mitigates premature convergence by promoting candidates that contribute both quality and diversity. Experimental validation across 90 benchmark functions demonstrated the robustness of the FDB mechanism across unimodal, multimodal, and composition functions.

Adaptive GA frameworks also continue to evolve. The improved GA for the flexible job shop scheduling problem (FJSP) proposed in [9] combines adaptive mutation probability, artificial pairing crossover, and weighted neighborhood search to dynamically adjust exploration strength based on population state and individual fitness. These mechanisms significantly enhanced performance under complex scheduling constraints, confirming that adaptive operator control can generalize across domains.

In our previous work [10], speciation was studied as a mechanism for maintaining diversity and improving the robustness of optimization in problems with suboptimal solutions. The results showed that speciation increased population diversity, indicated by higher fitness variance, and enhanced convergence toward global optima, confirming that separating similar individuals promotes exploration and prevents premature convergence.

Finally, [11] demonstrates through the Split-Based Selection (SBS) mechanism that maintaining a balanced selection pressure between high- and low-fitness individuals improves global search capability. The SBS approach distributes selection weights dynamically across ranked subsets of the population, thus maintaining population heterogeneity and reducing the risk of premature convergence.

Research results and their discussion

Investigation of Statistical Metrics

A classical genetic algorithm was applied to a series of benchmark functions representing different fitness landscapes, including unimodal, multimodal, and deceptive functions.

Each function was optimized under the following GA configuration:

- Population size: 50.
- Generations: 30.

- Selection: Tournament selection (size = 3).
- Crossover: Uniform crossover (crossover rate = 0.5).
- Mutation: Bit-flip mutation (mutation rate = 0.05).
- Encoding: Gray code.
- Each experiment was repeated 20 times per function. For every generation, the following metrics were recorded:
- Standard deviation of fitness values.
- Fitness variance.
- Fitness entropy (Shannon entropy):

$$H = -\sum_{i=1}^{N} p_i \log(p_j) \tag{1}$$

where p_i is the normalized frequency of the i-th fitness value.

- Average Pairwise Distance:

$$D = \frac{2}{N(N-1)} \sum_{i=1}^{N-1} \sum_{j=i+1}^{N} d(p_i, p_j) \tag{2}$$

where $d(p_i, p_j)$ is the Hamming distance between chromosomes.

- Number of individuals with unique fitness values (phenotypic diversity).
- Number of individuals with unique chromosomes (genotypic diversity);

Additionally, the generation of the last improvement in best fitness was recorded for each run. Correlation analysis and a Random Forest classifier were used to identify metrics with the strongest predictive capacity for convergence detection.

The results reveal strong negative correlations between convergence generation and the metrics of fitness entropy, unique fitness values, unique chromosomes, and average pairwise distance (Fig. 1). In other words, as these diversity-related measures decline, the algorithm approaches stagnation. The random forest model confirmed their high predictive power, achieving approximately 90 % accuracy in classifying converged vs. non-converged generations across all test functions (Table 1).

Design and Evaluation of the Composite Convergence Score (CCS)

The most important metrics were integrated into a *Composite Convergence Score (CCS)*, designed as a normalized weighted sum of the selected metrics:

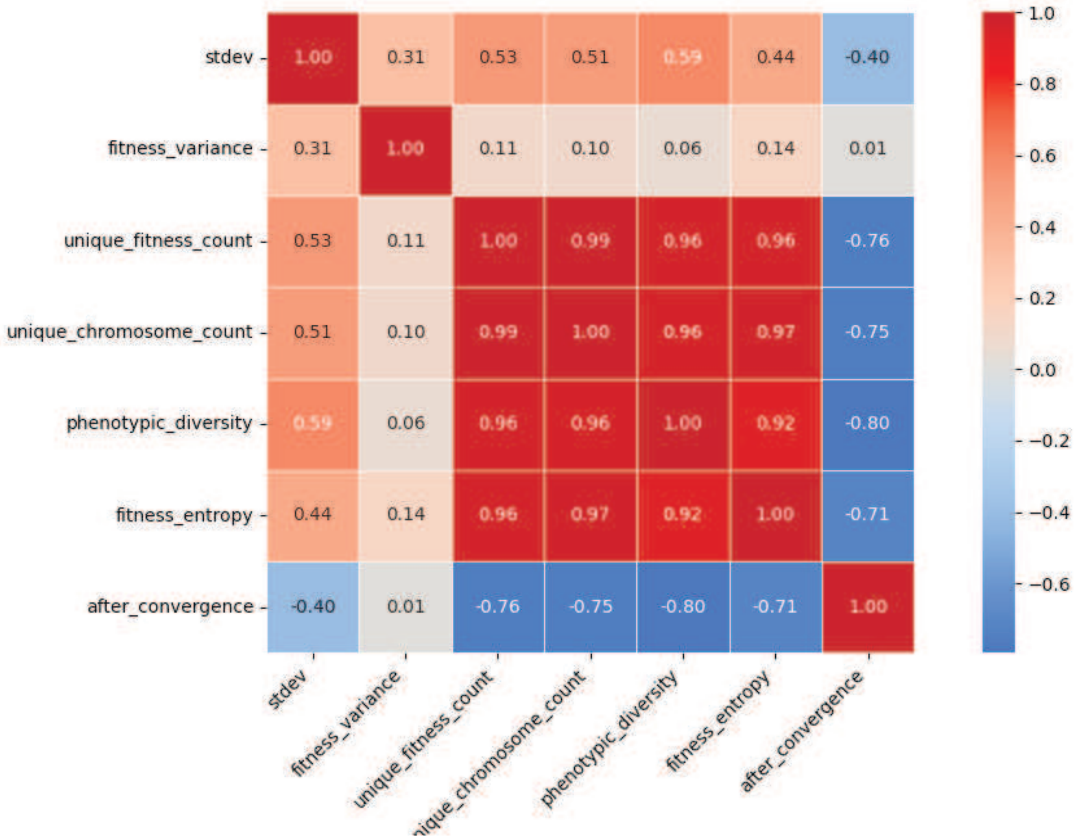
$$CCS = \sum_{i=1}^{k} \omega_i m_i, \quad \sum_{i=1}^{k} \omega_i = 1 \tag{3}$$

where m_i denotes the normalized value of the $\boldsymbol{i}$-th metric and ω_i its respective weight.

The CCS ranges from 0 (maximal diversity) to 1 (complete convergence).

Repeated GA simulations revealed consistent CCS dynamics across different test functions. Fig. 2 illustrates the dynamics of convergence metrics for one of the benchmark functions.

As optimization progresses, the CCS steadily increases, reaching a critical threshold (≈ 0.38) at which the last improvement in best fitness occurs. Beyond this point, the CCS plateaus between 0.5–0.6, marking the onset of population stagnation.



	stdev	fitness_variance	unique_fitness_count	unique_chromosome_count	phenotypic_diversity	fitness_entropy	after_convergence
stdev	1.00	0.31	0.53	0.51	0.59	0.44	-0.40
fitness_variance	0.31	1.00	0.11	0.10	0.06	0.14	0.01
unique_fitness_count	0.53	0.11	1.00	0.99	0.96	0.96	-0.76
unique_chromosome_count	0.51	0.10	0.99	1.00	0.96	0.97	-0.75
phenotypic_diversity	0.59	0.06	0.96	0.96	1.00	0.92	-0.80
fitness_entropy	0.44	0.14	0.96	0.97	0.92	1.00	-0.71
after_convergence	-0.40	0.01	-0.76	-0.75	-0.80	-0.71	1.00

Fig. 1. Correlation heatmap for Gaussian benchmark function

Table 1. Accuracy and importance of convergence-predictive metrics. FE – fitness entropy, APD – average pairwise distance, UF – number of individuals with unique fitness values, UC – number of individuals with unique chromosomes

Function $f(x)$	Accuracy	Most important features
$-x^2$	0.96	FE (0.24), UF (0.2), APD (0.19), UC (0.14)
e^{-x^2}	0.95	APD (0.23), FE (0.19), UF (0.15), UC (0.13)
$\sin(x)$	0.95	APD (0.23), FE (0.2), UC (0.14), UF (0.14)
$\sin(x)+\frac{\sin(3x)}{3}+\frac{\sin(5x)}{5}$	0.94	FE (0.23), APD (0.19), UF (0.14), UC (0.14)
$-\left[x^2-10\cos(2\pi x)+10\right]$	0.93	APD (0.23), FE (0.21), UF (0.15), UC (0.11)
$-x\cdot\sin\left(\sqrt{\lvert x\rvert}\right)$	0.87	APD (0.21), FE (0.19), UF (0.1), UC (0.09)
$-\lvert x\rvert$	0.93	APD (0.25), FE (0.2), UF (0.18), UC (0.11)
$\begin{cases} x, & \{0\le x<0.3\} \\ 0.3-(x-0.3), & \{0.3\le x\le 0.6\} \\ 0.1\cdot x, & \{0.6<x\le 1\} \end{cases}$	0.96	UF (0.19), FE (0.17), APD (0.15), UC (0.1)

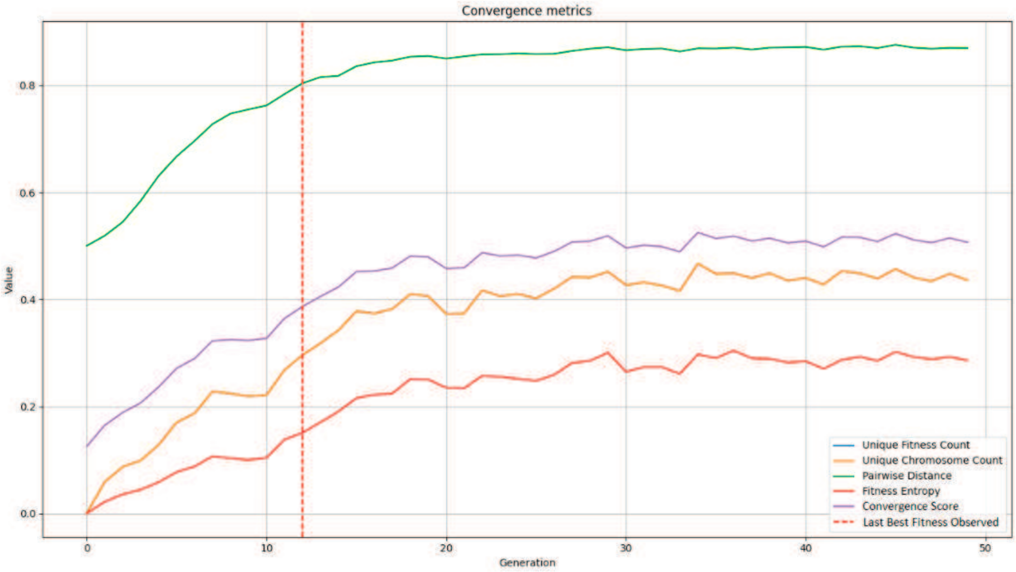


Fig. 2. Convergence metrics dynamics for function $\sin(x)+\frac{\sin(3x)}{3}+\frac{\sin(5x)}{5}$. All metrics normalized. Unique fitness count matches with unique chromosome count

Table 2 summarizes CCS thresholds and plateau values across benchmark functions. Convergence consistently began within 0.29–0.41, confirming CCS as a robust early indicator of convergence.

We also need to note, that received scores of gathered metrics will differ drastically if different configuration is used: with higher mutation rates the diversity is maintained longer, although doesn't allow to achieve desired solution. The population size and crossover also can interfere with the results. Here we aimed to show the overall dynamics of metrics that indicate population diversity and convergence.

Dynamic mutation rate control

Based on the CCS, a dynamic mutation rate control strategy was formulated:

$$\mu_t=\mu_{min}+\left(\mu_{max}-\mu_{min}\right)\cdot CCS_t \tag{4}$$

where μ_t is a mutation rate at generation ***t***, μ_{min} – base (minimum) mutation rate, μ_{max} – maximum allowable mutation rate, CCS_t – CCS at generation ***t***.

This mechanism adaptively increases mutation when the population exhibits high convergence (high CCS), and reduces it when diversity is sufficient (low CCS).

Experiments were conducted on the Schwefel function (2 variables) with the initial population centered at (0, 0). We compared our strategy with a classical algorithm without any strategy applied.

1. No mutation control: fixed mutation rate resulted either in premature convergence (for low rates) or instability

(for high rates). For low rates: for a significant amount of experiments the solutions stuck and local optimum and lost diversity quickly. For high rates: the solution was able to get close to the global optimum, but wasn't able to achieve the desired precision. Although, the right picked mutation rate helped to achieve a higher score of successful results.

2. CCS-based dynamic mutation: mutation adjusted automatically based on CCS, enabling adaptive balance between exploration and exploitation. This approach achieved global optimum in 95 % of runs, outperforming both other strategies in convergence speed and precision. It should also be noted that tuning the mutation rate becomes easier, as only the minimum and maximum allowable ranges need to be specified, while the actual rate is adjusted automatically according to the CCS. This strategy helps maintain diversity, keeping the CCS at lower values and UF, UC, and APD at higher levels compared to using a static low mutation rate.

Table 2. Convergence scores for example functions

Function $f(x)$	Convergence score on last fitness improvement generation	Max convergence score value
$-x^2$	0.36	0.5
e^{-x^2}	0.37	0.54
$\sin(x)$	0.35	0.45
$\sin(x)+\frac{\sin(3x)}{3}+\frac{\sin(5x)}{5}$	0.38	0.53
$-\left[x^2-10\cos(2\pi x)+10\right]$	0.41	0.54
$-x\cdot\sin\left(\sqrt{\lvert x\rvert}\right)$	0.29	0.34
$-\lvert x\rvert$	0.34	0.48
$\begin{cases} x, \{0\le x<0.3\} \\ 0.3-(x-0.3), \{0.3\le x\le 0.6\} \\ 0.1\cdot x, \{0.6<x\le 1\} \end{cases}$	0.37	0.61

Table 3. Comparison of mutation control strategies on the Schwefel function

Applied mutation strategy	Configuration	Percent of succeeded attempts, %
Static low mutation rate	Static mutation rate $\mu=0.002$	15
Static moderate mutation rate	Static mutation rate $\mu=0.05$	75
Static high mutation rate	Static mutation rate $\mu=0.2$	0
Dynamic mutation rate based on fitness CCS	Min mutation rate $\mu_{min}=0.0001$ Max mutation rate $\mu_{max}=0.5$	95

Discussion of the research results. The conducted experiments demonstrated that convergence in genetic algorithms can be detected and quantified through a combination of diversity and entropy-based metrics. The Composite Convergence Score (CCS), introduced in this work, provided an indicator of convergence dynamics across various benchmark functions. A consistent pattern was observed – as population diversity decreased, CCS increased, marking the transition to stagnation. The application of CCS for dynamic mutation rate control allowed the mutation rate to adjust automatically in response to the convergence state. This strategy achieved better optimization stability and precision compared to the fixed-rate approach. The results confirmed that using convergence and diversity metrics in mutation control can significantly improve the balance between exploration and exploitation in evolutionary search processes. These findings provide a data-driven basis for designing self-adapting genetic algorithms with minimal manual tuning of parameters.

Scientific Novelty of the Obtained Research Results – for the first time, a Composite Convergence Score (CCS) has been developed as a unified, normalized indicator that integrates several statistical metrics – including fitness entropy, average pairwise distance, and counts of unique chromosomes and fitness values – to quantify the dynamics of convergence and population diversity in genetic algorithms. A new dynamic mutation rate control strategy based on CCS was proposed, which adaptively modifies mutation probability based on the current convergence state of the population. This approach provides a quantitative grounded mechanism for maintaining diversity and preventing premature convergence.

Practical Significance of the Research Results – the proposed CCS-based framework enables real-time monitoring of convergence and allows for automatic update of evolutionary parameters during optimization. This reduces the need for manual parameter tuning and improves algorithm performance in problems with complex, multimodal fitness landscapes. The developed method can be applied in a wide range of domains where genetic algorithms are used – including engineering design, logistics, scheduling, and neural architecture search – providing robust and reliable convergence toward global optima.

Conclusions

This study introduces the *Composite Convergence Score (CCS)* – a unified, normalized metric for real-time monitoring of convergence in genetic algorithms. By combining entropy-based and diversity-based measures, CCS provides a quantitative, interpretable indicator of convergence dynamics.

Key findings:

- At certain thresholds of CCS can indicate the onset of convergence across diverse benchmark functions and loss of population diversity, thus meaning that fitness improvements can no longer be achieved.
- CCS-based mutation rate control effectively mitigates premature convergence and improves global search efficiency compared to methods with a static mutation rate.
- The CCS framework offers a generalizable tool for adaptive control of evolutionary parameters, enabling principled interventions such as population restarts, diversity injections, and adaptive operator tuning.
- Future work will focus on:
- Refining metric weighting schemes to enhance predictive accuracy.
- Evaluating CCS across high-dimensional and deceptive fitness landscapes.
- Extending the approach to multi-objective and coevolutionary algorithms.
- Applying CCS-guided adaptation in real-world optimization problems in engineering design, logistics, and neural architecture search.

Overall, the proposed CCS provides a data-driven foundation for understanding and controlling convergence in evolutionary computation, bridging theoretical insights with practical algorithmic advancements.

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В. О. Прецель, Р. Я. Шувар

Львівський національний університет ім. І. Франка, м. Львів, Україна

КЕРУВАННЯ ДИНАМІЧНОЮ ЙМОВІРНІСТЮ МУТАЦІЙ У ГЕНЕТИЧНИХ АЛГОРИТМАХ НА ОСНОВІ ПОКАЗНИКІВ ЗГОРТАННЯ ТА РІЗНОМАНІТТЯ ПОПУЛЯЦІЇ

Розроблено стратегію керування динамічною ймовірністю мутацій у генетичних алгоритмах (ГА) на основі показників згортання та різноманітності популяції. Механізм збільшує ймовірність мутації зі зростанням збіжності популяції та зниженням її різноманітності, стимулюючи пошук на ширшій області пошуку, тоді як зменшення ймовірності мутації застосовується у разі достатньої варіативності, запобігаючи зайвому порушенню еволюційно вже сформованих рішень. Виконано експерименти на прикладних функціях із різними функціями пристосованості, ураховуючи унімодальні, мультимодальні та оманливі функції, для перевірки ефективності запропонованого підходу. Введено узагальнений показник – композитний показник збіжності (CCS), що об'єднує найінформативніші метрики в нормалізований індикатор динаміки збіжності. Кореляційний аналіз та оцінювання на основі машинного навчання підтвердили, що CCS надійно визначає покоління, які наближаються до стагнації, а стратегія динамічної мутації, керована CCS, істотно підвищує продуктивність оптимізації порівняно з підходами зі статичною ймовірністю мутацій.

З'ясовано, що контроль мутації на основі CCS послідовно запобігає передчасній збіжності, підтримує вищий рівень різноманітності популяції протягом всього еволюційного процесу, пришвидшує збіжність до глобальних оптимумів та підвищує загальний відсоток успішного досягнення бажаних рішень. Підхід зменшує необхідність ручного налаштування параметрів мутації, оскільки CCS автоматично балансує пошук на ширшій та вужчій областях пошуку. Крім того, методологія дає змогу фреймворкам генетичних алгоритмів автоматично оновлювати еволюційні параметри.

Дослідження демонструє, що CCS може слугувати універсальним інструментом для адаптивного управління в еволюційних обчисленнях. Воно створює основу для подальшого розвитку самоналаштовуваних генетичних алгоритмів та може бути розширене на багатокритеріальні, багатовимірні або прикладні задачі оптимізації, зокрема інженерний дизайн, логістику, планування та пошук нейронних архітектур. Встановлено, що інтеграція кількісного моніторингу збіжності із динамічним регулюванням параметрів істотно підвищує надійність, стабільність та якість рішень ГА, відкриваючи великі можливості для розвитку як теоретичних, так і практичних аспектів еволюційної оптимізації.

Ключові слова: передчасне згортання, виявлення згортання, різноманіття популяції, адаптивна мутація, еволюційні обчислення.

Інформація про авторів:

Прецель Віталій Олегович, магістр комп'ютерних наук, аспірант кафедри системного проєктування.

Email: vitalii.pretsel@lnu.edu.ua; https://orcid.org/0009-0004-6509-2126

Шувар Роман Ярославович, канд. фіз.-мат. наук, доцент, завідувач кафедри системного проєктування.

Email: roman.shuvar@lnu.edu.ua; https://orcid.org/0000-0001-6768-4695

Цитування за ДСТУ: Прецель В. О., Шувар Р. Я. Керування динамічною ймовірністю мутацій у генетичних алгоритмах на основі показників згортання та різноманіття популяції. *Український журнал інформаційних технологій*. 2025, т. 7, № 2. С. 93–99.

Citation APA: Pretsel, V. O., & Shuvar, R. Y. (2025). Dynamic mutation rate control in genetic algorithms using convergence and diversity metrics. *Ukrainian Journal of Information Technology*, 7(2), 93–99. https://doi.org/10.23939/ujit2025.02.93