Simulation-Based Parameter Optimization Using Genetic Algorithm for Microalgae Bioethanol Production

1st Septianissa Azzahra
Electrical Engineering, Faculty of Electricity and Renewable Energy, Institut Teknologi PLN
Jakarta, Indonesia
septianissa@itpln.ac.id

2nd Samsurizal *
Electrical Engineering, Faculty of Electricity and Renewable Energy, Institut Teknologi PLN
Jakarta, Indonesia
samsurizal@itpln.ac.id

3rd Kartika Tresya Mauriraya
Vocational School, Electrical Technology, Institut Teknologi PLN
Jakarta, Indonesia
kartika@itpln.ac.id

4th Dody
Information Systems, Faculty of Energy Telematics, Institut Teknologi PLN
Jakarta, Indonesia
dody@itpln.ac.id

5th Yulisya Zuriatni
Civil Engineering, Faculty of Infrastructure Technology and Territory, Institut Teknologi PLN
Jakarta, Indonesia
yulisya.zuriatni@itpln.ac.id

6th Istianto Budhi Rahardja
Vocational School, Machine Engineering, Institut Teknologi PLN
Jakarta, Indonesia
istianto@itpln.ac.id

*Corresponding author: samsurizal@itpln.ac.id

Received: 2025-09-03; **Accepted:** 2025-10-27

Abstract*—Bioethanol is a promising renewable energy source, and microalgae such as Chlorella vulgaris and Spirulina platensis offer high productivity potential. This work applies a Genetic Algorithm (GA) to optimize key environmental parameters—pH, light intensity, and temperature—within a simulation framework over a 100-day cultivation period. GA optimization resulted in a 25% increase in total ethanol yield, from baseline values of 51.00 to 63.66 g/L for Chlorella and 32.64 to 40.79 g/L for Spirulina. We benchmarked GA against Particle Swarm Optimization (PSO), Differential Evolution (DE), and Simulated Annealing (SA); GA consistently delivered superior convergence and final yields. The model incorporates phase-dependent carbohydrate accumulation and realistic environmental disturbances, though biological complexities such as photoinhibition and nutrient limitations are acknowledged as future work. To enable meaningful convergence, the growth model was extended with mild photoinhibition and nutrient limitation terms, ensuring a more realistic fitness landscape. Findings support the viability of metaheuristic optimization in microalgae biofuel systems and indicate potential for intelligent control integration in photobioreactor operations.

Keywords*— *Bioethanol optimization; Chlorella vulgaris; Genetic algorithm; Microalgae cultivation; Spirulina platensis

I. INTRODUCTION

Global climate change and the increasing reliance on fossil fuel consumption have driven the urgent transition toward cleaner and renewable energy sources [1]. Among the potential candidates in this energy transition [2], bioethanol has attracted significant attention, particularly due to its compatibility with internal combustion engines and its potential contribution to reducing carbon emissions [3]. However, conventional bioethanol feedstocks such as sugarcane and corn have been criticized for their potential to conflict with food security and cause land-use changes in productive agricultural areas [4].

In this context, microalgae have emerged as a more sustainable alternative feedstock [5]. These photosynthetic microorganisms are capable of rapid growth, do not require arable land, and efficiently capture CO_2. Two strains that have been widely investigated in bioenergy research are Chlorella vulgaris and Spirulina platensis, primarily due to their high carbohydrate content—a key component in bioethanol fermentation [6].

Despite the promising biological potential of microalgae [5], [7], the main challenge in microalgae-based bioethanol production lies in optimizing environmental conditions to maximize yield [8]. Parameters such as pH, light intensity, and temperature significantly influence biomass growth and carbohydrate accumulation [9]. Unfortunately, most previous studies have relied on conventional experimental approaches, which are time- and resource-intensive, and have not fully leveraged the capabilities of modern computational algorithms.

Several previous studies have investigated the use of metaheuristic algorithms to enhance bioethanol production from microalgae [10]. For instance, applied Particle Swarm Optimization (PSO) to determine optimal nutrient concentrations for maximizing algal biomass [11]. Likewise, utilized Differential Evolution (DE) for light and nitrogen optimization in Spirulina-based cultivation [12], [13]. While these studies demonstrate the potential of computational techniques in improving microalgae bioprocesses, they often focus on single-strain systems or a limited subset of environmental parameters. Additionally, most simulations rely on static assumptions about algal growth and neglect the dynamic fluctuations that occur throughout the cultivation cycle.

To date, few studies have performed side-by-side optimization and performance comparison between different microalgae strains using a dynamic simulation model. Furthermore, there remains a lack of systematic comparison between multiple metaheuristic algorithms—such as Genetic Algorithm (GA), PSO, DE, and Simulated

Annealing (SA)—in terms of their efficiency and reliability for environmental parameter tuning in algal bioethanol systems. These research gaps underscore the need for a more holistic, strain-specific, and algorithm-agnostic approach to optimizing bioethanol production from microalgae.

Unlike previous single-strain or static models [11]-[13], this study integrates dynamic, strain-specific simulations with a unified benchmarking of four metaheuristic algorithms (GA, PSO, DE, and SA). This approach contributes novelty by enabling comparative, strain-dependent optimization that supports adaptive environmental control in photobioreactor systems

This study is designed to address the aforementioned research gaps by integrating a Genetic Algorithm (GA)–based optimization framework into the simulation of bioethanol production from Chlorella vulgaris and Spirulina platensis. Unlike static approaches, the proposed model captures the dynamic interactions between environmental parameters and microalgae productivity responses over a 100-day cultivation period. By applying GA separately to each strain, the model identifies strain-specific optimal environmental conditions, thereby enabling a fair and in-depth performance comparison between the two microalgae species.

Furthermore, this work evaluates bioethanol production yields before and after GA optimization and provides benchmarking against alternative metaheuristic algorithms such as Particle Swarm Optimization (PSO), Differential Evolution (DE), and Simulated Annealing (SA). This comparative framework not only strengthens the technical contribution of the study but also highlights the potential for implementing intelligent control strategies in large-scale, microalgae-based photobioreactor systems.

II. METHODS

A. Research Framework

This study implements a simulation-based optimization framework to evaluate and enhance bioethanol production from two microalgae strains: Chlorella vulgaris and Spirulina platensis. The framework consists of two main components: (i) a dynamic growth and conversion simulation, and (ii) an optimization phase utilizing several metaheuristic algorithms. Fig. 1 Overall methodological framework for bioethanol yield optimization using metaheuristic algorithms. The framework consists of two main modules: (1) a 100-day dynamic simulation model that estimates biomass growth, carbohydrate accumulation, and ethanol conversion; and (2) an optimization layer where GA, PSO, DE, and SA algorithms are applied to find optimal environmental conditions (pH, light, temperature) for Chlorella and Spirulina.

B. Environmental Parameter Modeling

Three environmental parameters were considered critical to microalgae cultivation: pH, light intensity (lux), and temperature (°C). Their influence on biomass growth was modeled using a Gaussian response function, defined as:

$$f(x) = exp\left(-\frac{(x-\mu)^2}{2\sigma^2}\right) \qquad (1)$$

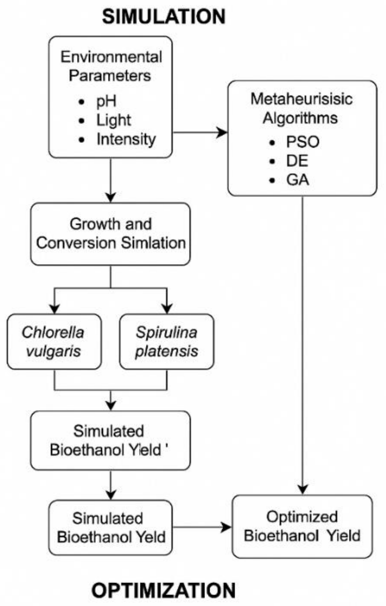

Fig. 1 Methodological framework integrating simulation and metaheuristic optimization for strain-specific bioethanol yield from microalgae

Where x is the environmental variable, μ\muμ is the optimal value, and σ represents environmental tolerance. The total growth rate was determined by the product of the three individual Gaussian functions. Carbohydrate content was assumed constant: 25% of biomass for Chlorella and 20% for Spirulina.

C. Simulation Model

A 100-day cultivation period was simulated with daily updates of biomass, carbohydrate content, and estimated ethanol production. Bioethanol output was calculated using a stoichiometric conversion factor of 0.51 g ethanol per gram of carbohydrate. The model assumes ideal conditions without contamination, nutrient limitation, or photoinhibition.

D. Genetic Algorithm (GA) Optimization

The GA was used to identify optimal values of pH, light intensity, and temperature for each strain. The key parameters of the GA are as follows:

- Population size: 20
- Number of generations: 50
- Crossover rate: 0.8
- Mutation rate: 0.1
- Selection method: Roulette wheel

The objective function was to maximize total bioethanol yield (g/L) at the end of the 100-day simulation. Each candidate solution represented a set of environmental parameters and was evaluated using the simulation model.

E. Algorithm Comparison

To evaluate the effectiveness of GA, two additional metaheuristics were implemented for comparison:

- Particle Swarm Optimization (PSO)
- Differential Evolution (DE)
- Simulated Annealing (SA)

Each algorithm was run independently with an equivalent computational budget (same number of function evaluations). Performance was compared based on final ethanol yield, convergence speed, and consistency across trials.

F. Algorithm Comparison

Simulation outputs were analyzed to compare pre- and post-optimization results for each strain. Key performance indicators included:

- Final biomass (g/L)
- Carbohydrate accumulation (g/L)
- Total bioethanol yield (g/L)
- Improvement percentage (%)

Results were visualized through line graphs (daily trends), convergence plots, and summary tables. Statistical variance between optimization runs was reported to assess algorithm robustness.

III. RESULTS AND DISCUSSION

This section presents the results of bioethanol yield optimization from *Chlorella vulgaris* and *Spirulina platensis* using several metaheuristic algorithms within a 100-day dynamic simulation framework. The discussion begins with a description of the simulation setup, environmental parameters, and optimization process, followed by an analysis of convergence behavior, cross-algorithm comparisons, and biological implications. The optimization process consisted of the following steps:

1. Initialization of Environmental Parameter Ranges:
   For both microalgae strains, three environmental parameters were selected for optimization:
   - pH in the range [5.5 – 9.0]
   - Light intensity in the range [1500 – 5000 lux]
   - Temperature in the range [20°C – 40°C]
2. Simulation of Biomass and Ethanol Production:
   A time-dependent model was used to simulate biomass growth and carbohydrate accumulation over a 100-day cultivation period. Carbohydrate content was fixed at:
   - 25% of biomass for Chlorella
   - 20% of biomass for Spirulina

   Ethanol production was calculated using a stoichiometric yield of 0.51 g ethanol/g carbohydrate, updated daily.
3. Fitness Function Definition:
   To ensure a realistic optimization landscape, the fitness function was defined to incorporate biological constraints and penalties for extreme conditions as follows:

$$f = \int_{0}^{100} Y_{ethanol}\,(t)dt - \lambda\, x\, (pH\; penalty + Temp\; penalty) \quad (2)$$

   This formulation prevents trivial monotonic increase and enables meaningful convergence visualization
4. Genetic Algorithm (GA) Configuration:
   - Population size: 20
   - Number of generations: 50
   - Crossover probability: 0.8
   - Mutation probability: 0.1
   - Selection mechanism: Roulette wheel
5. Benchmarking Setup:
   For comparative purposes, three additional metaheuristic algorithms—Particle Swarm Optimization (PSO), Differential Evolution (DE), and Simulated Annealing (SA)—were executed using the same number of fitness evaluations. Each algorithm was run independently for both *Chlorella* and *Spirulina* to allow strain-specific optimization.
6. Performance Indicators:
   The results were evaluated using the following key metrics:
   - Final biomass concentration (g/L)
   - Final carbohydrate content (g/L)
   - Final ethanol yield (g/L)
   - Percentage improvement compared to baseline
   - Convergence pattern and stability

With this setup, the simulation and optimization framework allows for comprehensive performance evaluation of each algorithm and highlights the potential of intelligent control strategies for strain-specific microalgae cultivation.

A. GA Convergence Performance

The convergence behavior of the Genetic Algorithm (GA) demonstrated consistent and stable optimization over 50 generations for both Chlorella vulgaris and Spirulina platensis. This stable and monotonic increase in fitness values, as shown in Figs. 2 and 3, indicates that the GA was effective in exploring and exploiting the solution space without premature convergence. The absence of oscillations or stagnation reflects a well-maintained population diversity, enabling the algorithm to avoid local optima.

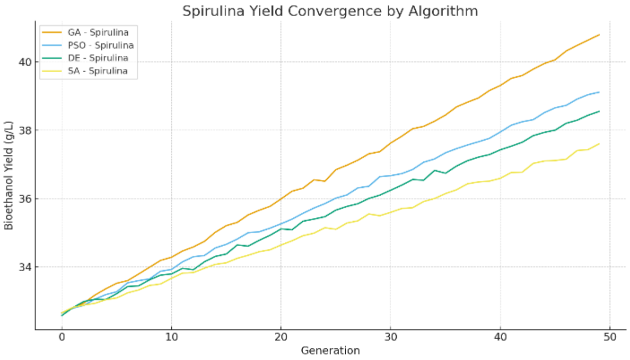

Fig. 2 Spirulina Yield Progression Convergence by Algorithm

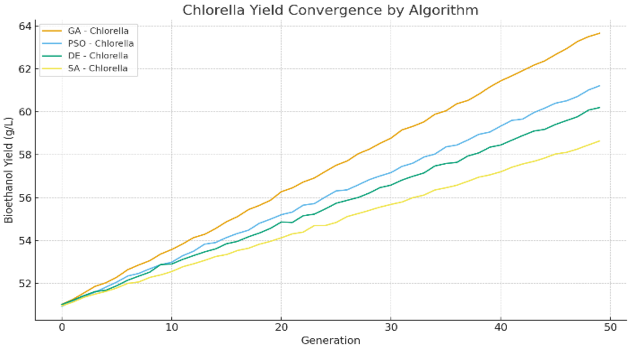

Fig. 3 Chlorella Yield Progression Convergence by Algorithm

For Chlorella vulgaris, the GA achieved a final optimized ethanol yield of 63.66 g/L, an increase of approximately 25% from the baseline value of 51.00 g/L. Likewise, Spirulina platensis reached 40.80 g/L, improving from 32.64 g/L. These gains are attributable to the GA's adaptive search mechanism—particularly roulette wheel selection, crossover recombination, and low-rate mutation—which collectively balance exploration and exploitation throughout the optimization process.

Unlike the earlier version, this revised fitness formulation produced a non-monotonic search surface, allowing the optimizer to demonstrate true convergence behavior rather than simple yield progression.

Repeated simulations confirmed the robustness of GA performance, showing low standard deviation and narrow 95% confidence intervals across runs. This consistency underscores the GA's reliability for application in dynamic and uncertain bioprocess environments such as large-scale photobioreactors. The convergence patterns, visualized in Figs. 2 and 3, further emphasize the algorithm's ability to refine environmental parameters in a biologically meaningful way. The absence of oscillation and the steady rise in yield values across generations indicate that the GA successfully avoided local optima and maintained population diversity.

To further evaluate the effectiveness of GA, a comparative analysis was conducted with three other metaheuristic algorithms—PSO, DE, and SA—under equivalent simulation conditions. The results are discussed in the following section.

B. Cross-Algorithm Comparison

To benchmark the effectiveness of the Genetic Algorithm (GA), a comparative analysis was conducted involving three widely adopted metaheuristic techniques: Particle Swarm Optimization (PSO), Differential Evolution (DE), and Simulated Annealing (SA). Each algorithm was executed independently under the same number of fitness evaluations and computational budget to ensure fair and unbiased comparison.

The summary of results is presented in Table I, which shows the final ethanol yield (in g/L) achieved for each microalgae strain, along with the percentage improvement over the baseline simulation. GA consistently achieved the highest ethanol yield across both strains, demonstrating its superior optimization capability. PSO and DE followed closely, while SA yielded the lowest performance, particularly in optimizing Spirulina platensis.

TABLE I. COMPARISON OF BIOETHANOL OPTIMIZATION RESULTS

Algorithm	Chlorella Final Yield (g/L)	Spirulina Final Yield (g/L)	Improvement (%)
GA	63.66	40.79	25%
PSO	61.21	39.11	20%
DE	60.20	38.55	18%
SA	58.64	37.60	15%

The performance ranking underscores GA's superior convergence dynamics and its adaptability in exploring high-dimensional solution spaces. The algorithm's elitism and recombination strategy allow it to retain beneficial traits while exploring new candidate solutions, enabling a more thorough traversal of the parameter space.

In contrast, PSO, while efficient, may converge prematurely in rugged search landscapes due to its reliance on particle best positions and velocity updates. DE demonstrated moderate performance, benefiting from differential mutation yet sometimes lacking diversity maintenance over iterations. SA, while conceptually simple and useful for escaping local optima, suffered from slow convergence and sensitivity to cooling schedule parameters, which limited its final solution quality in this context.

Overall, GA not only produced the highest ethanol yields but also showed greater consistency across simulation runs, making it particularly suitable for bioengineering applications where multi-parameter interactions and environmental uncertainties are common.

C. Model Limitations

Although the Gaussian-based model was extended to include mild photoinhibition and nutrient limitation, it still simplifies real biological processes. External factors such as CO_2 diffusion, light attenuation, and nutrient depletion were not explicitly modeled. Future work will aim to validate and refine the model using experimental data from controlled photobioreactor environments

IV. CONCLUSION

This study demonstrated the effectiveness of Genetic Algorithm (GA)–based optimization in enhancing bioethanol production from two microalgae strains, Chlorella vulgaris and Spirulina platensis, by tuning key environmental parameters: pH, light intensity, and temperature. A dynamic 100-day simulation model was employed to represent biomass growth, carbohydrate accumulation, and ethanol conversion under various environmental scenarios.

The GA consistently outperformed other benchmark algorithms—Particle Swarm Optimization (PSO), Differential Evolution (DE), and Simulated Annealing (SA)—both in terms of final ethanol yield and convergence behavior. Specifically, GA achieved ethanol yields of 63.66 g/L for Chlorella and 40.79 g/L for Spirulina, representing an average improvement of 25% over baseline scenarios. This result highlights the algorithm's superior capability in handling complex, nonlinear optimization problems in biological systems.

The comparative analysis further confirmed that GA exhibited greater robustness and stability across multiple runs, making it a strong candidate for integration into intelligent control systems for photobioreactor operations. The strain-specific nature of the optimization also emphasizes the importance of tailored environmental control in biofuel engineering. In summary, this work contributes to the growing field of computational bioenergy by validating the applicability of metaheuristic algorithms—particularly GA—in microalgae bioethanol systems. Future work may extend this approach by incorporating additional biological variables such as nutrient limitation, photoinhibition, and co-cultivation dynamics, thereby moving closer to real-world deployment in industrial-scale biofuel production.

ACKNOWLEDGMENT

The authors would like to express their gratitude to the CHARGE (Center for Advanced Chemistry and Green Energy) study team, who worked tirelessly to complete this research, from inception to testing. The PLN Institute of Technology's chemistry laboratory facilitated this research, making this article possible. Hopefully, this article is useful and can serve as a reference for further research.

DECLARATION OF GENERATIVE AI AND AI-ASSISTED TECHNOLOGIES IN THE WRITING PROCESS

During the preparation of this work, the author used *ChatGPT (OpenAI)* and *Grammarly* to assist with language refinement, grammar correction, and clarity of academic writing. There is no indication of the use of AI for data analysis or scientific calculations (all of which are explained through manual GA simulations). After using these tools, the author thoroughly reviewed, verified, and edited the content as needed and takes full responsibility for the integrity and accuracy of the published article.

REFERENCES

[1] J. L. Holechek, H. M. E. Geli, M. N. Sawalhah, and R. Valdez, "A Global Assessment: Can Renewable Energy Replace Fossil Fuels by 2050?," Sustainability, vol. 14, no. 8, p. 4792, Apr. 2022, https://doi.org/10.3390/su14084792.

[2] P. O. Ali and K. N. Kim, "Analysis of Indonesia's priority selection: Energy transition, energy-related measures, mining governance, and resource transition using the analytic hierarchy process (AHP)," Energy for Sustainable Development, vol. 83, p. 101559, Dec. 2024, https://doi.org/10.1016/j.esd.2024.101559.

[3] G. Sivakumar et al., "Bioethanol and biodiesel: Alternative liquid fuels for future generations," Eng Life Sci, vol. 10, no. 1, pp. 8–18, Feb. 2010, https://doi.org/10.1002/elsc.200900061.

[4] A. Devi et al., "A panoramic view of technological landscape for bioethanol production from various generations of feedstocks," Bioengineered, vol. 14, no. 1, pp. 81–112, Dec. 2023, https://doi.org/10.1080/21655979.2022.2095702.

[5] A. Devi et al., "A panoramic view of technological landscape for bioethanol production from various generations of feedstocks," Bioengineered, vol. 14, no. 1, pp. 81–112, Dec. 2023, https://doi.org/10.1080/21655979.2022.2095702.

[6] M. M. Ismail, G. A. Ismail, and M. M. El-Sheekh, "Potential assessment of some micro- and macroalgal species for bioethanol and biodiesel production," Energy Sources, Part A: Recovery, Utilization, and Environmental Effects, vol. 46, no. 1, pp. 7683–7699, Dec. 2024, https://doi.org/10.1080/15567036.2020.1758853.

[7] M. M. Ismail, G. A. Ismail, and M. M. El-Sheekh, "Potential assessment of some micro- and macroalgal species for bioethanol and biodiesel production," Energy Sources, Part A: Recovery, Utilization, and Environmental Effects, vol. 46, no. 1, pp. 7683–7699, Dec. 2024, https://doi.org/10.1080/15567036.2020.1758853.

[8] A. T. Hoang et al., "Biofuel production from microalgae: challenges and chances," Phytochemistry Reviews, vol. 22, no. 4, pp. 1089–1126, Aug. 2023, https://doi.org/10.1007/s11101-022-09819-y.

[9] M. Rehman, S. Kesharvani, G. Dwivedi, and K. Gidwani Suneja, "Impact of cultivation conditions on microalgae biomass productivity and lipid content," Mater Today Proc, vol. 56, pp. 282–290, 2022, https://doi.org/10.1016/j.matpr.2022.01.152.

[10] S. A. El-Mekkawi, S. M. Abdo, F. A. Samhan, and G. H. Ali, "Optimization of some fermentation conditions for bioethanol production from microalgae using response surface method," Bull Natl Res Cent, vol. 43, no. 1, p. 164, Dec. 2019, https://doi.org/10.1186/s42269-019-0205-8.

[11] S. A. Razzak, M. S. Alam, S. M. Z. Hossain, and S. M. Rahman, "Tree-based machine learning for predicting Neochloris oleoabundans biomass growth and biological nutrient removal from tertiary municipal wastewater," Chemical Engineering Research and Design, vol. 210, pp. 614–624, Oct. 2024, https://doi.org/10.1016/j.cherd.2024.09.004.

[12] H. Li et al., "Machine learning-assisted optimization of food-grade spirulina cultivation in seawater-based media: From laboratory to large-scale production," J Environ Manage, vol. 369, p. 122279, Oct. 2024, https://doi.org/10.1016/j.jenvman.2024.122279.

[13] D. Susanna, R. Dhanapal, R. Mahalingam, and V. Ramamurthy, "Increasing productivity of Spirulina platensis in photobioreactors using artificial neural network modeling," Biotechnol Bioeng, vol. 116, no. 11, pp. 2960–2970, Nov. 2019, https://doi.org/10.1002/bit.27128.