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Metaheuristic Algorithms for Nonlinear Dynamic System Identification

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AUTHOR'S SUMMARY

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The thesis includes a preface, six chapters, a conclusion, 88 figures, 71 tables, and a bibliography of 583 references.

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Preface

The increasing complexity, high dimensionality, and strong nonlinearity of modern biotechnological systems have exposed the limitations of classical deterministic optimization methods. While gradient-based approaches are computationally efficient for convex problems, they are inherently local and highly sensitive to initial conditions. In contrast, metaheuristic optimization algorithms have emerged as a powerful paradigm for addressing multimodal and computationally demanding problems that are intractable for traditional techniques [107,122].

Despite their robustness, individual metaheuristics exhibit structural limitations according to the "No Free Lunch" theorem. Genetic algorithms may suffer from slow convergence in fine-tuning stages, while swarm-based methods like PSO are prone to premature stagnation. These limitations motivate the systematic development of hybrid metaheuristic algorithms. Hybridization is a theoretically grounded synthesis aimed at achieving a superior balance between global exploration and local exploitation by integrating complementary search mechanisms within a unified mathematical framework [183,535].

The relevance of these advanced hybrids is particularly evident in the modeling and control of cultivation processes. Such systems are characterized by strongly nonlinear dynamics, substrate inhibition, and time-varying physiological states. Parameter identification in these models constitutes a nonlinear inverse problem with multimodal objective landscapes. Similarly, the optimal tuning of PID controllers for such processes is a challenging dynamic optimization task where classical tuning rules often fail.

The research presented in this D.Sc. thesis is situated at the intersection of optimization theory, computational intelligence, and process engineering. It involves the structural synthesis of heterogeneous search mechanisms to create novel hybrid operators with emergent search properties. The bidirectional interaction between theory and application validates the robustness of the proposed algorithms while addressing pressing industrial challenges in bioprocess systems engineering.

Aim of the thesis

The aim of the present D.Sc. thesis is the theoretical investigation, development, and experimental validation of metaheuristic algorithms and hybrid approaches, with systematic application to bioprocess modeling and control, aimed at the design of high-performance and efficient optimization algorithms.

Research hypothesis

The systematic hybridization of complementary metaheuristics, guided by a formal analysis of their dynamical search behavior, enables the construction of optimization frameworks with improved convergence, robustness, and scalability compared to constituent algorithms, particularly for ill-conditioned problems in fermentation process engineering.

Research tasks

To achieve the stated aim and verify the research hypothesis, the following main tasks are defined:

1. To perform a critical and systematic analysis of established metaheuristic optimization algorithms, with emphasis on their mathematical foundations, exploration-exploitation mechanisms, convergence behaviour, and limitations in nonlinear dynamic optimization problems.

2. To investigate, implement, and apply selected metaheuristic algorithms in order to analyse their search dynamics, performance characteristics, and suitability for solving complex nonlinear optimization problems.

3. To investigate the theoretical foundations of hybridization in metaheuristic optimization, including the structural integration of heterogeneous search operators and diversity preservation mechanisms.

4. To propose novel hybrid metaheuristic algorithms, based on the analysis of the application results of the selected metaheuristic algorithms.

5. To investigate, implement, and apply the proposed hybrid algorithms to parameter identification problems in bioprocess modeling and control and to evaluate their performance.

6. To establish a methodological framework for the evaluation of hybrid metaheuristic performance, including benchmark testing, statistical analysis and InterCriteria analysis.

Chapter 1

State of the art in metaheuristic algorithms and bioprocess modeling

One of the contemporary fields of Artificial Intelligence is the field of metaheuristic algorithms – a scientific method for problem solving that extends the idea of heuristic algorithms, where "meta" denotes "beyond" or "on a higher level" [239]. According to [492], a metaheuristic is "an iterative generation process which guides a subordinate heuristic by combining intelligently different concepts for exploring and exploiting the search space, learning strategies are used to structure information in order to find efficiently near-optimal solutions."

The present chapter discusses metaheuristic methods not only from an application perspective but by considering the dynamical systems theory, stochastic processes, and nonlinear systems analysis, which form the conceptual basis for hybrid metaheuristic generalization.

Despite the progress in metaheuristic optimization across diverse engineering domains [454], a theoretical generalization of hybrid design remains incomplete. Specifically, the rigorous integration of structurally grounded hybrid algorithms into complex nonlinear fermentation systems is limited. Since optimization efficiency is problem-specific, the parameter identification of cellular dynamics models presents a significant challenge; unlike linear systems, these nonlinear dynamic models lack general analytical solutions, necessitating more robust and specialized global search strategies.

The development of hybrid metaheuristic algorithms has emerged as an important research direction in global optimization. Hybridization aims to combine complementary search mechanisms of different algorithms in order to improve convergence reliability, solution quality, and robustness when solving complex nonlinear optimization problems. Despite the considerable progress achieved in this field, the design of efficient hybrid metaheuristics remains a challenging task and several important research gaps persist in the literature [102,348,358,497,535,543]:

- **Exploration-exploitation balance:** Maintaining a robust trade-off between global search and local refinement remains an open problem. Inefficient transitions between these phases often lead to premature convergence.

- **Integration complexity:** The success of hybrid approaches depends on the compatibility of combined operators. Most current designs rely on empirical intuition rather than systematic principles, hindering reproducibility and generalization.

- **Parameter sensitivity:** Hybrids introduce increased dimensionality in the parameter space, making calibration computationally expensive. Improper settings critically compromise convergence speed and population diversity.

- **Scalability and computational cost:** Simultaneous execution of multiple procedures increases complexity, which can become prohibitive for high-dimensional problems or computationally intensive objective functions.

- **Lack of systematic frameworks:** There is a notable absence of a unified theoretical methodology for hybrid design. Ad hoc combinations dominate the literature, leaving cooperative and multi-agent interactions insufficiently explored.

- **Limited generalization:** Hybrid performance is often problem-specific. Developing strategies capable of adapting to diverse search landscapes remains a fundamental research necessity.

These challenges underscore the need for new hybrid strategies that provide effective search balancing, improved robustness, and reduced parameter sensitivity. Consequently, this work is driven by the development of structurally integrated hybridization mechanisms to enhance the efficiency of optimization-based solutions for complex nonlinear bioprocess modeling and control. The primary motivation of this research is therefore to investigate new hybridization mechanisms capable of integrating complementary search behaviors in order to improve the efficiency and robustness of metaheuristic optimization methods for complex nonlinear modeling problems, e.g., parameter identification of cultivation process models and process control.

The above-discussed points correspond to D.Sc. thesis aim formulated in the Preface:

The theoretical investigation, development, and experimental validation of metaheuristic algorithms and hybrid approaches, with systematic application to bioprocess modeling and control, aimed at the design of high-performance and efficient optimization algorithms.

Chapter 2

Materials and methods

Chapter 2 presents a description of the cultivation processes employed as real-world benchmark systems for the validation and performance assessment of the proposed hybrid metaheuristic algorithms. These systems serve as complex nonlinear dynamic test environments, representative of industrially relevant biotechnological applications. The metaheuristic algorithms developed in this thesis are applied to the parameter identification problem of nonlinear mathematical models describing the considered cultivation processes.

Subsequently, the proposed metaheuristic algorithms are utilized for the systematic tuning of PID controller parameters within different closed-loop control configurations. The tuning task is formulated to ensure robust regulation of the principal substrate concentration at a predefined reference level, accounting for the nonlinear dynamics, operational constraints, and inherent uncertainties characteristic of bioprocess systems.

The following cultivation processes are investigated:

- *Escherichia coli* MC4110 fed-batch cultivation process;
- *Escherichia coli* BL21(DE3)pPhyt109 fed-batch cultivation process;
- Wheat straw thermophilic anaerobic digestion process;
- Corn steep liquor two-stage anaerobic digestion process.

The chapter further provides a theoretical background of the nonlinear model parameter identification problem and the PID controller parameter tuning problem, with particular emphasis on their formulation as constrained, simulation-based global optimization tasks. The specific structural and dynamic characteristics of cultivation process systems – such as strong nonlinearities, parameter coupling, and operational constraints – are considered.

Finally, an evaluation framework developed for the evaluation and comparison of metaheuristic algorithms and the theoretical foundation of the InterCriteria Analysis (ICrA) [61] are presented. ICrA is employed as a complementary decision-support tool for comparative performance evaluation of the proposed metaheuristic algorithms, alongside conventional statistical performance analysis. This combined evaluation framework ensures a multidimensional and robust assessment of algorithms' efficiency and reliability.

***E. coli* MC4110 fed-batch cultivation process**

From a practical view, modeling studies are performed to identify simple and easy-to-use models that are suitable to support process optimization and control. On account of the fact that the cultivation process dynamics are described using a simple Monod-type model, the most common kinetics applied for the modeling of cultivation processes [73].

The application of the general state space dynamical model to the *E. coli* MC4110 fed-batch cultivation process leads to the following non-linear differential equation system [410]:

$$\frac{dX}{dt} = \mu_{max} \frac{S}{k_S + S} X - \frac{F_{in}}{V} X, \tag{2.1}$$

$$\frac{dS}{dt} = -\frac{1}{Y_{S/X}} \mu_{max} \frac{S}{k_S + S} X + \frac{F_{in}}{V} (S_{in} - S), \tag{2.2}$$

$$\frac{dV}{dt} = F_{in}, \tag{2.3}$$

where X is the concentration of biomass; S is the concentration of substrate (glucose); F is the feeding rate; V is the volume of the bioreactor; S_{in} is the glucose concentration in the feeding solution; μ is the specific growth rate described by Monod kinetics; $\mu_{\max}$ is the maximum growth rate; k_S is a saturation constant; and $Y_{S/X}$ is a yield coefficient. The growth rate of bacteria is described according to the classical Monod equation.

***E. coli* BL21(DE3)pPhyt109 fed-batch cultivation process**

The fed-batch cultivation of *E. coli* BL21(DE3)pPhyt109 involves the measurement of rates associated with cell growth, substrate consumption, and phytase production. These rates are commonly evaluated through the use of mass balances as follows ([423]):

$$\frac{d\gamma_X}{dt} = \mu_{max} \frac{\gamma_S}{k_S + \gamma_S} \gamma_X - \frac{Q}{V} \gamma_X, \tag{2.4}$$

$$\frac{d\gamma_S}{dt} = \frac{1}{Y_{S/X}} \mu_{max} \frac{\gamma_S}{k_S + \gamma_S} \gamma_X + \frac{Q}{V} \left(\gamma_{Sin} - \gamma_S\right), \tag{2.5}$$

$$\frac{d\gamma_P}{dt} = \frac{1}{Y_{P/X}} \mu_{max} \frac{\gamma_S}{k_S + \gamma_S} \gamma_X - \frac{Q}{V} \gamma_P, \tag{2.6}$$

$$\frac{dV}{dt} = Q, \tag{2.7}$$

where γ_X – concentration of the biomass [g/L]; γ_S – concentration of the substrate (glucose) [g/L]; γ_P – concentration of the phytase [g/L]; Q – influent flow rate [L/h]; V – bioreactor volume, [L]; γ_{Sin} – influent glucose concentration [g/L]; μ_{max} – maximum specific growth rate [1/h]; $Y_{S/X}$ and $Y_{P/X}$ – yield coefficients [g/g]; k_S – saturation constant [g/L].

Wheat straw thermophilic anaerobic digestion process

A deterministic non-linear dynamic system of differential equations was used to describe the thermophilic anaerobic digestion process for the methane production from wheat straw, as follows [108]:

$$\frac{dS_0}{dt} = -\beta X_1 S_0, \tag{2.8}$$

$$\frac{dX_1}{dt} = \mu_1 X_1, \tag{2.9}$$

$$\frac{dS_1}{dt} = \beta X_1 S_0 - \frac{1}{Y_1}\mu_1 X_1, \tag{2.10}$$

$$\frac{dX_2}{dt} = \mu_2 X_2, \tag{2.11}$$

$$\frac{dS_2}{dt} = Y_b \mu_1 X_1 - \frac{1}{Y_2}\mu_2 X_2, \tag{2.12}$$

$$Q_{CH_4} = Y_{CH_4}\mu_2 X_2, \tag{2.13}$$

$$\mu_1 = \frac{\mu_{1\max} S_1}{k_{1s} + S_1} - b_1, \tag{2.14}$$

$$\mu_2 = \frac{\mu_{2\max} S_2}{k_{2s} + S_2} - b_2. \tag{2.15}$$

Eqs. (2.8) and (2.10) present the balance of the effluent substrate (S_0) – cellulose and its transformation to glucose (S_1) after hydrolysis. Eqs. (2.9) and (2.11) describe the dynamics of the biomass concentrations (X_1 and X_2). Eq.(2.12) presents the dynamics of the intermediate product – acetate (Ac_1), and the algebraic Eq. (2.13) expresses the flow rate of the methane in the gas phase of the bioreactor. For the specific growth rates of the biomass, a Monod-type function was adopted in Eqs. (2.14) and (2.15).

Corn steep two-stage anaerobic digestion process

The two-stage anaerobic digestion process of corn steep liquor for the sequential production of H_2 and CH_4 is carried out in two separate bioreactors [108]. During the first stage, relatively fast-growing acidogenic microorganisms engaged in the production of volatile fatty acids and H_2 are cultivated in the hydrogenic bioreactor BR_1. Slow-growing acetogenic and methanogenic bacteria are developed during the second stage in the methanogenic bioreactor BR_2. The volatile fatty acids are later transformed into CH_4 and CO_2 in BR_2.

The process dynamics in the cascade of BR_1 and BR_2 are presented, using mass balances, by a set of five ordinary differential equations and two algebraic equations, as follows:

BR_1:

$$\frac{dS_1}{dt} = -Y_1 \mu_1 X_1 + D_1\left(S_{1in} - S_1\right), \tag{2.16}$$

$$\frac{dX_1}{dt} = \mu_1 X_1 - D_1 X_1, \tag{2.17}$$

$$\frac{dAc_1}{dt} = Y_2\mu_1 X_1 - D_1 Ac_1, \tag{2.18}$$

$$Q_{H_2} = Y_{H_2}\mu_1 X_1, \tag{2.19}$$

$$\mu_1 = \frac{\mu_{1max} S_1}{K_{S_1} + S_1}. \tag{2.20}$$

BR_2:

$$\frac{dX_2}{dt} = \mu_2 X_2 - D_2 X_2, \tag{2.21}$$

$$\frac{dAc_2}{dt} = -Y_3\mu_2 X_2 + D_2\left(Ac_1 - Ac_2\right), \tag{2.22}$$

$$Q_{CH_4} = Y_{CH_4}\mu_2 X_2, \tag{2.23}$$

$$\mu_2 = \frac{\mu_{2max} Ac_2}{K_{S_2} + Ac_2}. \tag{2.24}$$

The system (2.16)-(2.20) describes the dynamics of the substrate concentration (S_1), [g/L]; the microbial biomass concentration (X_1), [g/L]; and the product (acetate) formation (Ac_1) [g/L] in BR_1. The algebraic equation describes the flow rate of the hydrogen (Q_{H_2}) [dm^3/L·h] in the gas phase of BR_1. S_{1in} [g/L] is the concentration of the input substrate. For the specific growth rate μ_1 [day^{-1}] of hydrogen-producing microorganisms, a Monod-type function was adopted. D_1 [day^{-1}] is the dilution rate for the first bioreactor BR_1; μ_{1max} [day^{-1}] and K_{S_1} [g/L] are Monod kinetic coefficients; and Y_1, Y_2 and Y_{H_2} are yield coefficients, [g/g].

The system (2.21) - (2.24) describes a one-step transformation of the inlet acetate Ac_1 (coming from BR_1) into methane by methanogenic microorganisms. A Monod-type function was also adopted for the specific growth rate of the methanogenic biomass. In the model, X_2 is the microbial biomass concentration in BR_2 [g/L], Ac_2 is the acetate concentration in BR_2 [g/L], Q_{CH_4} is the methane flow rate [dm^3/L·day], D_2 [day^{-1}] is the dilution rate for the second bioreactor BR_2, μ_2 is the specific growth rate (Monod type) of methanogens [day^{-1}], Y_{CH_4} and Y_3 are yield coefficients, and μ_{2max} [day^{-1}] and K_{S_2} [g/L] are kinetic coefficients.

Nonlinear model parameter identification in cultivation processes – theoretical background

Consider a cultivation process described by a nonlinear dynamic model in state-space form:

$$\dot{x}(t) = f\big(x(t), u(t), \theta\big), \quad x(0) = x_0, \tag{2.25}$$

$$y(t) = h\big(x(t), \theta\big), \tag{2.26}$$

where $x(t) \in \mathbb{R}^n$ denotes the state vector of the nonlinear dynamic system, representing the process variables. The vector $u(t) \in \mathbb{R}^m$ represents the control input or manipulated variables, while $\theta \in \Omega \subset \mathbb{R}^p$ denotes the vector of unknown model or controller parameters to be identified or optimized. The nonlinear vector function $f(\cdot)$ defines the dynamic evolution of the system derived from mass balance principles and kinetic relations, and $x(0) = x_0$ specifies the initial conditions. The vector $y(t) \in \mathbb{R}^q$ represents the measured output variables.

The identification problem is formulated as a constrained nonlinear optimization problem:

$$\min_{\theta \in \Omega} J(\theta), \tag{2.27}$$

where $J : \Omega \to \mathbb{R}$ is a nonlinear, potentially nonconvex objective function, and Ω is a compact feasible domain.

The objective functional $J(\theta)$ is typically defined as a least-squares performance criterion:

$$J(\theta) = \sum_{i=1}^{M} \sum_{j=1}^{N} \left\| y_i^{\text{exp}}(t_j) - y_i(t_j; \theta) \right\|^2, \tag{2.28}$$

where M is the number of measured process variables, N is the number of experimental data points, y_i^{exp} represents the observed experimental data values, and $y(t_j; \theta)$ represents the model predicted values. Specifically, $y(t_j; \theta) = [X \;\; S]$ for model (2.1) - (2.3); $y(t_j; \theta) = [\gamma_X \;\; \gamma_S \;\; \gamma_P]$ for model (2.4) - (2.7); $y(t_j; \theta) = [H_2 \;\; CH_4]$ for model (2.8) - (2.15) and $Y_{ij} = [S_0 \;\; S_1 \;\; S_2 \;\; CH_4]$ for model (2.16) - (2.20).

The feasible parameter domain Ω incorporates physical, biological, and operational constraints:

$$\Omega = \left\{ \theta \in \mathbb{R}^p \;\middle|\; \theta_i^{\min} \leq \theta_i \leq \theta_i^{\max}, \quad i = 1, 2, \ldots, p \right\}, \tag{2.29}$$

where $\theta_i^{\min}$ and $\theta_i^{\max}$ denote the lower and upper admissible bounds of the i-th parameter.

Given the above structural and dynamic characteristics, nonlinear model parameter identification in cultivation processes must be treated as a constrained global optimization problem, Eq. (2.27), subject to nonlinear dynamic constraints, Eq. (2.25). The problem is high-dimensional, multimodal, simulation-based, and computationally intensive.

Framework for performance evaluation and comparison of metaheuristic algorithms

A comprehensive evaluation framework is essential for the objective analysis and comparison of metaheuristic and hybrid optimization algorithms. Therefore, a structured multi-level framework is required, integrating benchmark-based testing, real-world validation, statistical performance analysis, and advanced multi-criteria evaluation.

1. **Benchmark function testing:** provides a controlled and reproducible environment for analyzing fundamental algorithmic properties. Evaluating algorithms based on benchmark functions achieves a systematic assessment of convergence speed, the balance between exploration and exploitation, robustness, and scalability with respect to the dimensionality of the problem. By comparing performance across a diverse set of standardized functions, one can determine which algorithm demonstrates consistent superiority or robustness under varying landscape characteristics.

2. **Real-world application testing:** evaluates algorithm performance in practical optimization problems. Good performance on benchmark functions does

not guarantee effectiveness in real applications, where noise, constraints, and modeling uncertainties are present. Through real-world applications, the applicability, robustness, and reliability of the proposed algorithms are validated.

3. **Statistical performance analysis:** ensures an objective comparison based on multiple independent runs. Quantifying the variability, robustness (stability), and statistical significance of observed differences in performance is achieved by applying statistical analysis. Statistical tests determine whether observed differences are significant, allowing the selection of algorithms that consistently outperform others rather than those that perform well only occasionally.

4. **InterCriteria Analysis (ICrA):** provides a multi-criteria perspective on algorithm performance. Classical statistical methods evaluate criteria independently and may ignore hidden relationships between them. Identifying correlations, overlaps, and conflicts between performance metrics offers a deeper insight into algorithm behavior.

Parameter domain and optimization criterion for the considered identification problems

In order to find a set of design parameters, $\theta = [\theta_1, \theta_2, ..., \theta_n]$, metaheuristic techniques are applied. Each model parameter is coded in a specific range (lower bound ($\theta_i^{\min}$) $\leq \theta_i \leq$ upper bound ($\theta_i^{\max}$)):

- $\theta = [\mu_{max}\ k_S\ Y_{S/X}]$ (*E. coli* MC4110 fed-batch cultivation process model, Eqs. (2.1) - (2.3)),

$$0.01 \leq \mu_{max} \leq 0.8;\ 0.001 \leq k_S \leq 1;\ 0.01 \leq Y_{S/X} \leq 10. \tag{2.38}$$

- $\theta = [\mu_{max}\ k_S\ Y_{S/X}\ Y_{P/X}]$ (*E. coli* BL21(DE3)pPhyt109 fed-batch cultivation process model, Eqs. (2.4) - (2.7)),

$$\begin{aligned} 0.05 \leq \mu_{max} \leq 0.9;\ 0.001 \leq k_S \leq 0.5; \\ 1 \leq Y_{S/X} \leq 10;\ 1 \leq Y_{P/X} \leq 10. \end{aligned} \tag{2.39}$$

- $\theta = [\mu_{1\max}\ k_{1s}\ b_1\ \beta\ Y_1\ Y_b\ \mu_{2\max}\ k_{2s}\ Y_2\ Y_{CH_4}\ b_2]$ (thermophilic anaerobic digestion process of wheat straw, Eqs. (2.8) - (2.15)),

$$\begin{aligned} 0.01 \leq \mu_{1\max} \leq 0.8;\ 0.001 \leq k_{1s} \leq 10;\ 0 \leq b_1 \leq 0.1; \\ 0.01 \leq \beta \leq 10;\ 0.01 \leq Y_1 \leq 1;\ 1 \leq Y_b \leq 200; \\ 0.1 \leq \mu_{2\max} \leq 0.8;\ 0.01 \leq k_{2s} \leq 10;\ 0.01 \leq Y_2 \leq 10; \\ 0.1 \leq Y_{CH_4} \leq 30;\ 0 \leq b_2 \leq 1. \end{aligned} \tag{2.40}$$

- $\theta = [\mu_{1\max}\ k_{1s}\ Y_1\ Y_2\ \ Y_{H_2}\ \mu_{2\max}\ k_{2s}\ Y_3\ Y_{CH_4}]$ (corn steep liquor two-stage anaerobic digestion process, Eqs. (2.16) - (2.20)),

$$\begin{aligned} 0.01 \leq \mu_{1\max} \leq 0.8;\ 0.01 \leq k_{1s} \leq 50;\ 0.1 \leq Y_1 \leq 50; \\ 0.001 \leq Y_2 \leq 50;\ 0.01 \leq Y_{H_2} \leq 50;\ 0.001 \leq \mu_{2\max} \leq 0.8; \\ 0.0001 \leq k_{2s} \leq 5;\ 0.1 \leq Y_3 \leq 50;\ 0.1 \leq Y_{CH_4} \leq 100. \end{aligned} \tag{2.41}$$

Chapter 3

Metaheuristic algorithms

Chapter 3 presents a set of representative and structurally diverse metaheuristic optimization algorithms, investigated and applied to nonlinear parameter identification problems. The selection of the algorithms reflects different conceptual classes within the metaheuristic paradigm – evolutionary, swarm-intelligence-based, physics-inspired and social-learning search strategies. The investigated and applied algorithms include:

3.1 **Genetic Algorithm**, thesis publications [470], [420], [418], [433], [434] and [441];

3.2 **Firefly Algorithm**, thesis publications [430] and [413];

3.3 **Cuckoo Search Algorithm**, thesis publication [413];

3.4 **Crow Search Algorithm**, thesis publications [438] and [424];

3.5 **Artificial Bee Colony Optimization**, thesis publications [440] and [436];

3.6 **Coyote Optimization Algorithm**, thesis publications [413] and [414];

3.7 **Electromagnetic Field Optimization**, thesis publications [428] and [435];

3.8 **Simulated Annealing**, thesis publication [404];

3.9 **Ant Lion Optimizer**, thesis publication [442];

3.10 **Marine Predator Algorithm**, thesis publication [414].

The algorithms are selected to ensure methodological diversity in terms of population structure, information exchange mechanisms, balance between exploration and exploitation, and convergence dynamics. Their implementation has been adapted to the specific characteristics of nonlinear dynamic models of cultivation processes, including strong parameter coupling, nonconvex objective landscapes, and computationally intensive simulation-based fitness evaluation.

The pseudo-codes of the ten metaheuristic algorithms are presented below.

Algorithm 1 : Pseudo-code of the Genetic algorithm

begin
Define the input GA parameters and the parameters of the problem
Set population size n, generation gap, crossover rate,
mutation rate, and maximum generations $MaxGen$
Define GA operators: selection, crossover, mutation
Set generation counter $t = 0$
Generate randomly the initial population of individuals $P(t)$
Calculate the fitness of all individuals in $P(t)$
while $t < MaxGen$ **do**
$t = t + 1$
Select parents from $P(t - 1)$ using selection operator to form $P(t)$
Apply crossover operator to recombine the genes of selected parents
Apply mutation operator to perturb the population stochastically
Evaluate the fitness of all new individuals in $P(t)$
end while
Postprocess results and select the best solution
end begin

Algorithm 2 : Pseudo-code of the Firefly algorithm

begin
Define γ and β_0
Randomization parameter α
Objective function $f(x)$, where $x = (x_1, ..., x_d)^T$
Generate initial population of fireflies xi (i = 1, 2, ..., n)
Determine light intensity I_i at x_i via $f(x_i)$
while (t < MaxGeneration) **do**
for i = 1: n all n fireflies **do**
for j = 1: i all n fireflies **do**
if ($I_j > I_i$) **then**
Move firefly i towards j
end if
Attractiveness varies with distance r via $\exp[-\gamma r^2]$
Evaluate new solutions and update light intensity
end for j
end for i
Rank the fireflies and find the current best
end while
Postprocess results and visualization
end begin

Algorithm 3 : Pseudo-code of the Cuckoo search algorithm

begin
Define Number of nests n and switching parameter p_a
Objective function $f(x)$, $x = (x_1, ..., x_d)^T$
Generate initial population of n host nests x_i ($i = 1, 2, ..., n$)
while (t < MaxGeneration) or (stop criterion) **do**
Get a cuckoo randomly by Levy flights
Evaluate its quality or fitness value f_i
Choose a nest among n (say, j) randomly
if ($f_i < f_j$)
Replace j by the new solution i
end if
A fraction (p_a) of worse nests are abandoned
New solutions (nests) are built
Keep the best solutions, i.e. nests with quality solutions
Rank the solutions and find the current best
end while
Postprocess results and visualization
end begin

Algorithm 4 : Pseudo-code of the Crow Search algorithm

begin
Define the input CSA and problem parameters
Set population size M, AP, fl,
and maximum iterations $MaxIter$
Generate randomly the initial positions of crows $crow_i$
Evaluate the fitness of each crow $F(crow_i)$
Initialize the memory mem_i for each crow
Set iteration counter $t = 1$
while $t \leq MaxIter$ **do**
for $i = 1$ to M **do**
Randomly select a crow to follow j (where $j \neq i$)
Generate a random number r_i in [0,1]
if $r_i \geq AP^{j,t}$ **then**
Update: $crow_i^{t+1} = crow_i^t + r_i \times fl^{j,t} \times (mem_j^t - crow_i^t)$
else
Update: $crow_i^{t+1} =$ random position in the search space
end if
end for
Check the feasibility of new positions $crow_i^{t+1}$
Evaluate the fitness of all new positions $F(crow_i^{t+1})$
Update the memory of each crow with better positions
$t = t + 1$
end while
Postprocess results and return the best solution found
end begin

Algorithm 5 : Pseudo-code of the Artificial bee colony optimization

begin
Define *NP*, *SN*, *limit*, *D*, *MCN*
for i = 1 to *SN* **do**
$x_i \leftarrow$ generated random solution
$f_i \leftarrow$ evaluate the solution $f(x_i))$
$trials_i \leftarrow 0$
end for
for *iter* = 1 to *MCN* **do**
(Employed bees phase) **for** i = 1 to *SN* **do**
$v_i \leftarrow$ a new food source generated
if $f(x_i) > f(v_i)$ **then**
$x_i \leftarrow v_i$, $f_i \leftarrow f(v_i)$, $trials_i \leftarrow 0$
else
$trials_i \leftarrow trials_{i+1}$
end if
end for
Calculate the probability values p_i
(Onlookers phase) $t \leftarrow 1$, $i \leftarrow 1$,
while $t < SN$ **do**
Generate a random $r \in (0;1)$
if $r < p_i$ **then**
$v_i \leftarrow$ a new food source generated
if $f(x_i) > f(v_i)$ **then**
$x_i \leftarrow v_i$, $f_i \leftarrow f(v_i)$, $trials_i \leftarrow 0$
else
$trials_i \leftarrow trials_{i+1}$
end if
$t \leftarrow t + 1$
end if
$i \leftarrow (i + 1) \bmod SN$
end for
(Scout bee phase) Find the food source
if $max(trials_i) \geq limit$ **then**
$x_i \leftarrow$ a new randomly generated solution
$trials_i \leftarrow 0$, **end if**
Memorize the best food source for now
end for
Postprocess results and visualization
end begin

Algorithm 6 : Pseudo-code of the Coyote optimization algorithm

begin
Define N_p packs with N_c coyotes each
Verify the coyote's adaptation
while stopping criterion is not achieved **do**
for each p pack **do**
Define the alpha coyote of the pack
Compute the social tendency of the pack
for each c coyotes of the p pack **do**
Update the social condition

Evaluate the new social condition
Adaptation
end for
Compute ω and ϕ
if $\phi = 1$ then
The pup survives and the only coyote in ω dies
elseif $\phi > 1$ then
The pup survives and the oldest coyote in ω dies
else
The pup dies
end if
end for
Transition between packs
Update the coyotes' ages
end while
Select the best adapted coyote
Postprocess results and visualization
end begin

Algorithm 7 : Pseudo-code of the Electromagnetic field optimization

Initialisation of parameters
Begin
for $i = 1$ to N_{emp} **do**
for $j = 1$ to N_{var} **do**
$em_{pop}[i, j]$ = min + rand(0, 1)*$(Ub - Lb)$
$new_{emp}[j] = em_{pop}[i, j]$
end for
$fit[i] = f(new_{emp})$
end for
$sortPopulation(em_{pop}, fit)$
(main loop)
$R_I = 1$
while (stop criterion is not met) **do**
force = *chaotic map*
for $i = 1$ to N_{var} **do**
$I_{pos} = rand(1, \text{floor}(N_{emp} * P_{field}))$
$I_{neg} = rand(\text{floor}((1 - N_{field}) * N_{emp}), N_{emp})$
$I_{neu} = rand(\text{ceil}(N_{emp} * P_{field}), \text{ceil}((1 - N_{field}) * N_{emp}))$
if $(rand(0, 1) < Ps_{rate})$ **then**
$new_{emp}[i] = em_{pop}[I_{pos}, i]$
else
$new_{emp}[i] = em_{pop}[I_{neu}, i] + \varphi * force * (em_{pop}[I_{pos}, i]$
$- em_{pop}[I_{neu}, i]) -$
$force * (em_{pop}[I_{neg}, i] - em_{pop}[I_{neu}, i])$
end if
if $(new_{emp}[i] > Ub$ or $new_{emp}[i] < Lb)$ **then**
$new_{emp}[i] = Lb * rand(0, 1) * (Ub - Lb)$
end if
end for
if $(rand(0, 1) < R_{rate})$ **then**

```
newemp[RI] = Lb*rand(0, 1)*(Ub − Lb)
RI = RI + 1
if (RI > Nvar) then
RI = 1
end if
end if
Newfit = f(newemp)
if (Newfit < worst(fit)) then
insertInSortedPopulation(newemp)
end if
end while
return empop [1, 1:Nvar]
```

Algorithm 8 : Pseudo-code of the Simulated annealing algorithm

```
begin
Generate randomly an initial solution S
Set initial temperature T = T0
Set the cooling rate r (where 0 < r < 1)
Set the maximum number of iterations max_iter
j := 0
while j < max_iter
Generate a neighboring solution S′ from S
Calculate the difference in cost: Δ = cost(S′) − cost(S)
if Δ < 0 then
Accept S′ as the new current solution
else
Generate a random number p in [0,1]
if p < e^(−Δ/T) then
Accept S′ as the new current solution
else
Reject S′ and keep the current solution S
end if
end if
Update temperature: T = r × T
j = j + 1
end while
Return the best solution found
end begin
```

Algorithm 9 : Pseudo-code of the Ant lion optimizer

```
begin
Define the input ALO and problem parameters
Generate the initial populations of ants and antlions
Calculate the corresponding fitness estimations
Find the best antlion and adopt it as the elite
for j:= 1 to the size of initial population Pop0
while the end criterion is not satisfied
for each ant
Select an antlion using the RWS
Update the parameters of the random walk
Create a random walk and normalize it
```

```
    Update the position of the ant
    end for
    Evaluate all ants
    Replace an antlion with its corresponding ant
    Update the elite if an antlion becomes fitter
    end while
    Memorize the best solution in Pop_0
    end for
    Rank the solutions, find the current best, and memorize it
    end begin
```

Algorithm 10 : Pseudo-code of the Marine predator algorithm

```
begin
Define the input MPA parameters
Generate randomly the initial population of prey X_i
Calculate the fitness and identify the top predator
Construct the Elite matrix
Construct the Prey matrix with initial prey positions
while t < Max_iterations
for each prey
if t < 1/3 Max_iterations (Phase 1)
Update prey positions using Brownian motion
else if 1/3 Max_iterations < t < 2/3 Max_iterations (Phase 2)
if first half of population
Update using Lévy flight (exploration)
else
Update using Brownian motion (exploitation)
end if
else (Phase 3)
Update prey positions using Lévy flight
end if
Apply Fish Aggregating Devices effects and update positions
Evaluate the fitness of all prey
Update the Elite matrix if a better predator is found
Apply memory saving to preserve previous positions
end for
end while
Return the best solution (top predator)
end begin
```

The performance of the presented 10 metaheuristic algorithms is further investigated on model parameter identification problems and on PID controller parameter tuning problems. The metaheuristics are applied for modeling of four bioprocess systems. The obtained results are presented and discussed in Chapter 4.

Chapter 4

Application of metaheuristic algorithms for parameter optimization problems

Chapter 4 investigates the application of metaheuristic algorithms to parameter identification in nonlinear bioprocess models and PID controller tuning. A diverse set of algorithms is comparatively analyzed: GA, SA, FA, ABC, CS, COA, CSA, MPA, EFO, and ALO (Tables 4.40 and 4.41).

A parametric study involving 99 GA configurations revealed that an optimal population size of 100 ensures a balance between convergence speed and accuracy. Mutation rates outside the $[0.028, 0.073]$ interval significantly degrade performance. GA demonstrated clear superiority over deterministic SQP in terms of robustness.

In modeling anaerobic biodegradation, MPA achieved the highest accuracy. For TSAD processes, FA outperformed GA, CS, and COA in convergence behavior, though GA remained superior in specific process sub-models, confirming that performance is problem-dependent.

Through systematic tuning, SA achieved accuracy comparable to GA but with reduced computational overhead, as its execution time is less sensitive to population dynamics.

ABC performance was found to be critically dependent on the choice of probability function. Both low- and high-dimensional configurations yielded competitive results when the population size and iterations were appropriately scaled.

The EFO algorithm was improved using chaotic maps, with *Iterative* and *Tent* maps providing the most stable performance.

For CSA, an analysis of 70 configurations identified an optimal awareness probability in the range $[0.05, 0.15]$, with CSA and FA producing the most reliable parameter estimates.

GA proved effective for PID tuning. Combined with an EKF, it achieved high biomass concentrations ($48.3\ \mathrm{g \cdot L^{-1}}$) with minimal control variance, validating its practical utility in bioprocess engineering.

The results demonstrate that while metaheuristics are effective, each individual method is limited by its specific search dynamics: evolutionary methods excel in diversity but converge slowly, while swarm-based methods offer efficient exploitation at the risk of premature stagnation. These complementary strengths justify the systematic development of hybrid frameworks.

The comparative analysis presented in Tables 4.40 and 4.41 provides a systematic and mechanism-oriented characterization of the investigated metaheuristic algorithms, integrating their mathematical search formulations, control parameters, and observed performance characteristics.

Table 4.40: Comprehensive mechanism-based comparison of the GA, SA, ABC, COA and FA and implications for hybridization

Algorithm	Search mechanism	Control parameters	Strengths	Weaknesses	Implications for hybridization
GA	$x_i^{t+1} = \mathcal{M}(\mathcal{C}(x_p^t, x_q^t))$	p_c, p_m, population size, selection pressure	strong local exploitation; implicit parallelism; diversity preservation through mutation	weak global exploration; premature convergence; sensitivity to parameters	requires exploration refinement; benefits from diversity enhancement (ABC, ALO, chaos)
SA	$x^{t+1} = \begin{cases} x', & \Delta f < 0 \\ x', & \text{with } e^{-\Delta f/T} \end{cases}$	initial temperature, cooling schedule, iterations	strong local exploitation; ability to escape local minima; theoretical convergence guarantees	slow convergence; lack of population diversity; highly sensitive cooling schedule	effective as local search component in hybrids
ABC	$v_{ij} = x_{ij} + \phi_{ij}(x_{ij} - x_{kj})$	colony size, limit, employed / onlooker ratio	high exploration capability; adaptive neighborhood search; scout mechanism prevents stagnation	weak exploitation near optimum; slow convergence in refinement phase	combine with GA or local search to enhance exploitation (ABC-GA, ALO-GA)
COA	$x_i^{t+1} = x_i^t + r_1(x_{best}^t - \lvert x_i^t \rvert) + r_2(x_{median}^t - \lvert x_i^t \rvert)$	number of packs, coyotes per pack, r_1, r_2, birth/death rate	balanced exploration and exploitation; strong diversity preservation; robustness in multimodal landscapes; reduced premature convergence	slower convergence in fine exploitation; higher computational cost; sensitivity to pack structure; oscillatory behavior near optimum	combine with strong exploitation mechanisms; useful for diversity enhancement; suitable as global exploration stage in hybrid frameworks (COA-GA)
FA	$x_i^{t+1} = x_i^t + \beta e^{-\gamma r_{ij}^2}(x_j^t - x_i^t) + \alpha\epsilon$	α, β, γ	fast convergence; strong exploitation; automatic subgroup formation; efficient attraction mechanism	loss of diversity; risk of premature convergence; parameter sensitivity	requires diversity enhancement (chaos, ABC) and stabilization

Table 4.41: Comprehensive mechanism-based comparison of CS, ALO, CSA, MPA and EFO metaheuristic algorithms and implications for hybridization

Algorithm	**Search mechanism**	**Control parameters**	**Strengths**	**Weaknesses**	**Implications for hybridization**
CS	$x_i^{t+1} = x_i^t + \alpha \otimes \text{Lévy}(\lambda)$	discovery probability p_a, step size α	efficient global exploration; Lévy flights enable long jumps; escape from local minima	weak local exploitation; excessive randomness; slow convergence near optimum	combine with GA or SA for refinement and exploitation
ALO	$x^{t+1} = \frac{RW_{ant}+RW_{elite}}{2}$	population size, adaptive boundaries	balanced exploration and exploitation; adaptive search space contraction	slow convergence in fine search; stochastic oscillations near optimum	hybridize with GA for accelerated convergence (ALO-GA)
CSA	$x_i^{t+1} = \begin{cases} x_i^t + fl(m_j^t - x_i^t), unaware \\ \text{random, otherwise} \end{cases}$	flight length fl, awareness probability AP	strong exploitation; memory-based search; ability to escape local optima	high randomness; unstable convergence; sensitivity to parameters	needs structured exploration and stabilization (GA-CSA)
MPA	$x^{t+1} = x^t + S(Elite - x^t)$ (Brownian/Lévy phases)	phase switching, step size	adaptive exploration-exploitation balance; multi-phase search; efficient global-local transition	complex dynamics; parameter sensitivity; instability in fine tuning	combine with structured exploitation (GA, local refinement)
EFO	$x_i^{t+1} = x_i^t + \lambda(x_{best} - x_i^t) + \epsilon$	field strength, attraction / repulsion coefficients	fast convergence; structured movement; strong exploitation capability	premature convergence; limited diversity; risk of local optima trapping	enhance with chaos-based diversity (CEFO) or population mechanisms for better exploration

Unlike conventional descriptive comparisons, the analysis explicitly relates the strengths and weaknesses of each algorithm to its underlying search dynamics, thereby revealing how specific update rules, stochastic operators, and population interaction mechanisms influence exploration and exploitation capabilities.

This structured perspective enables the identification of inherent algorithmic limitations, such as premature convergence, insufficient local refinement, or excessive randomness, and, more importantly, establishes a theoretically grounded basis for the design of hybrid metaheuristic frameworks.

In this context, the comparative analysis serves not only as a synthesis of existing methods but also as a conceptual bridge toward the systematic construction of hybrid algorithms, where complementary search mechanisms are deliberately combined to achieve improved convergence behavior, robustness, and scalability.

The mechanism-oriented characterization (Tables 4.40 and 4.41) relates algorithmic update rules to observed performance. This structured analysis transforms empirical comparison into a formal design tool, providing the theoretically grounded basis for the novel hybrid metaheuristic frameworks presented in the subsequent chapters.

Chapter 5

Hybrid metaheuristic algorithms

In Chapter 5, a series of hybrid metaheuristic algorithms is proposed, namely:

5.1 **Artificial Bee Colony – Genetic Algorithm Hybrid (ABC-GA)**
thesis publications [436] and [440];

5.2 **Genetic Algorithm – Crow Search Algorithm Hybrid (GA-CSA)**
thesis publication [438];

5.3 **Ant Lion Optimizer – Genetic Algorithm Hybrid (ALO-GA)**
thesis publication [442];

5.4 **Evolutionary Algorithm – Genetic Algorithm Hybrid (EA-GA)**
thesis publication [441];

5.5 **Chaotic Electromagnetic Field Optimization (CEFO)**
thesis publication [428].

The construction of these hybrids is based on a principled integration of algorithmic mechanisms with complementary stochastic properties. The objective is to synthesize distributed exploration, adaptive intensification, diversity preservation, and convergence stabilization within unified population-based architectures. Each hybrid is formulated through operator-level integration, controlled information exchange, and structured parameter interaction, ensuring the preservation of beneficial search characteristics while mitigating algorithm-specific limitations.

The development of the proposed hybrids is grounded in a formal interpretation of population-based metaheuristics as stochastic dynamic systems governed by transition operators acting over high-dimensional state spaces. By analyzing the probabilistic movement rules, memory structures, and interaction topologies of the constituent algorithms, hybrid operators are derived to modify the underlying search dynamics in a theoretically consistent manner. The resulting hybrid algorithms aim to enhance global search reliability, accelerate convergence toward high-quality solutions, and improve computational efficiency in nonlinear, multimodal, and simulation-based optimization problems.

5.1 Mathematical foundations of the proposed hybrid algorithms

The hybrid algorithms developed in this thesis are interpreted as stochastic, discrete-time dynamical systems operating in high-dimensional search spaces. Their structural synthesis, exploration-exploitation balance, and convergence behavior are analyzed from a systems-theoretic perspective.

5.1.1 Structural hybridization scheme

Let the global optimization problem be defined as Eq. (2.27). The proposed hybrid algorithms aim to construct a stochastic process $\{X_k\}_{k=0}^{\infty}$ whose distribution converges with high probability toward the set of global minimizers of $J(\theta)$. Population-based metaheuristics are stochastic dynamical systems. The state space representation is a population of N candidate solutions:

$$X_k = \{x_k^{(1)}, x_k^{(2)}, \ldots, x_k^{(N)}\} \subset \Omega, \tag{5.1}$$

where k denotes the iteration index. A general metaheuristic update rule can be written as:

$$x_{k+1}^{(i)} = \mathcal{F}\left(x_k^{(i)}, \mathcal{I}_k, \xi_k^{(i)}, \mathcal{P}_k\right), \tag{5.2}$$

where $\mathcal{I}_k$ represents information extracted from the population (e.g., global best, neighborhood best), $\xi_k^{(i)}$ denotes stochastic perturbations, and $\mathcal{P}_k$ denotes metaheuristic algorithm specific parameters.

Thus, the population evolution can be written compactly as:

$$X_{k+1} = \mathcal{T}(X_k, \Xi_k, \mathcal{P}_k), \tag{5.3}$$

where Ξ_k aggregates stochastic variables. Under mild assumptions, $\{X_k\}$ defines a time-homogeneous Markov chain on Ω^N. Exploration and exploitation are the main variance-control mechanisms. They can be interpreted statistically in terms of population distribution dynamics. Define the population mean:

$$\bar{x}_k = \frac{1}{N}\sum_{i=1}^{N} x_k^{(i)}, \tag{5.4}$$

and population covariance matrix:

$$\Sigma_k = \frac{1}{N}\sum_{i=1}^{N}(x_k^{(i)} - \bar{x}_k)(x_k^{(i)} - \bar{x}_k)^T. \tag{5.5}$$

From this statistical perspective, global exploration corresponds to maintaining a sufficiently large trace of the covariance matrix, $\mathrm{tr}(\Sigma_k)$, preventing premature convergence. Conversely, local exploitation is characterized by the contraction of Σ_k around promising regions of the feasible domain.

Hybridization is presented as operator composition. Let two metaheuristic operators be defined as:

$$\mathcal{T}_1 : \Omega^N \to \Omega^N, \quad \mathcal{T}_2 : \Omega^N \to \Omega^N. \tag{5.6}$$

A sequential hybridization is proposed:

$$X_{k+1} = \mathcal{T}_2(\mathcal{T}_1(X_k)). \tag{5.7}$$

The following stability and convergence considerations are accepted.

Lyapunov-type interpretation: Let $V_k = J_{\text{best},k}$. Under elitist selection,

$$V_{k+1} \leq V_k, \tag{5.8}$$

which implies monotonic non-increasing best fitness.

Although full convergence to global optimum cannot be deterministically guaranteed for arbitrary nonconvex $J(\theta)$, probabilistic convergence can be discussed under ergodicity assumptions.

Ergodicity and global convergence in probability: If the stochastic perturbation mechanism ensures that any region of Ω can be visited with non-zero probability, then the induced Markov chain is irreducible. Under irreducibility and aperiodicity, the algorithm satisfies weak ergodicity conditions, implying that:

$$\lim_{k\to\infty} \mathbb{P}\big(J_{\text{best},k} \leq J^* + \varepsilon\big) = 1 \tag{5.9}$$

for any arbitrary tolerance $\varepsilon > 0$. This indicates that the hybrid framework achieves global convergence in probability as the iteration index approaches infinity.

Computational complexity: Let C_J denote cost of one objective function evaluation and N population size. Total computational complexity per iteration:

$$C_{\text{iter}} = O(NC_J + NC_T), \tag{5.10}$$

where C_T denotes operator computation cost.

5.1.2 Global convergence analysis of the hybrid metaheuristics

Theoretical framework

Let $\mathcal{X} \subset \mathbb{R}^d$ be nonempty and compact. In practice, $\mathcal{X}$ is often a hyperrectangle $\prod_{i=1}^{d} [a_i, b_i]$, and we will use the Lebesgue measure vol on $\mathcal{X}$. Let $J : \mathcal{X} \to \mathbb{R}$ be continuous, with global minimum $J^* = \min_{\theta\in\mathcal{X}} J(\theta)$. For any $\varepsilon > 0$, define the open set $U_\varepsilon = \{\theta \in \mathcal{X} : J(\theta) < J^* + \varepsilon\}$. Consider a population-based stochastic algorithm generating populations $P_k = \{X_{k,1}, \ldots, X_{k,N_k}\} \subseteq \mathcal{X}$. Let $(\mathcal{X}, \mathcal{F}, \mathbb{P})$ be a probability space and let $\mathcal{F}_k$ be the σ-algebra generated by all random variables up to time k (the algorithm's history). The best value found up to time k is

$$J_{\text{best},k} = \min_{0\leq s\leq k} \; \min_{1\leq j\leq N_s} J(X_{s,j}). \tag{5.11}$$

Definition 1 (Nondegenerate exploration with time-varying intensity). *The algorithm satisfies the* ***nondegenerate exploration*** *property if there exist*

- *a probability measure ν on $\mathcal{X}$ with* full support *(i.e., $\nu(O) > 0$ for every nonempty open set $O \subseteq \mathcal{X}$), and*
- *a deterministic sequence $(\rho_k)_{k\geq 0}$ with $0 \leq \rho_k \leq 1$,*

such that for every measurable set $A \subseteq \mathcal{X}$ and every $k \geq 0$, there exists a point Y_{k+1} generated by the algorithm at iteration $k+1$ (e.g., the best individual of the new population, a mutated individual, a scout bee, or a randomly initialised point) that satisfies

$$\mathbb{P}\big(Y_{k+1} \in A \mid \mathcal{F}_k\big) \geq \rho_k \, \nu(A) \quad \textit{almost surely.}$$

Theorem 1 (Global convergence in probability)**.** *Under the above setup, if the algorithm satisfies the nondegenerate exploration property and additionally*

$$\sum_{k=0}^{\infty} \rho_k = \infty \qquad \textit{(divergence condition)}, \tag{5.12}$$

then for every $\varepsilon > 0$,

$$\lim_{k \to \infty} \mathbb{P}\big(J_{best,k} \leq J^* + \varepsilon\big) = 1. \tag{5.13}$$

That is, the algorithm converges in probability to the global minimum.

Proof. Fix $\varepsilon > 0$. Because ν has full support and U_ε is open and nonempty, we have $\alpha := \nu(U_\varepsilon) > 0$.

Define the failure event $E_k = \{J_{\text{best},k} > J^* + \varepsilon\}$, i.e., no point in U_ε has been generated up to time k. The event E_{k+1} occurs only if E_k occurs and $Y_{k+1} \notin U_\varepsilon$. Using the law of total probability,

$$\mathbb{P}(E_{k+1} \mid \mathcal{F}_k) \leq \mathbf{1}_{E_k} \, \mathbb{P}(Y_{k+1} \notin U_\varepsilon \mid \mathcal{F}_k) \leq \mathbf{1}_{E_k} \big(1 - \rho_k \alpha\big) \quad \text{a.s.} \tag{5.14}$$

Taking expectation,

$$\mathbb{P}(E_{k+1}) = \mathbb{E}[\mathbb{P}(E_{k+1} \mid \mathcal{F}_k)] \leq (1 - \rho_k \alpha) \, \mathbb{P}(E_k) \tag{5.15}$$

let us assume that

$$\mathbb{P}(E_k) \leq \prod_{s=0}^{k-1} (1 - \rho_s \alpha) \leq \exp\left(-\alpha \sum_{s=0}^{k-1} \rho_s\right), \tag{5.16}$$

where we use $1 - z \leq e^{-z}$.

By induction assumption we obtain

$$\begin{aligned} \mathbb{P}(E_{k+1}) &\leq (1 - \rho_k \alpha) \mathbb{P}(E_k) \\ \leq (1 - \rho_k \alpha) \prod_{s=0}^{k-1} (1 - \rho_s \alpha) &= \prod_{s=0}^{k} (1 - \rho_s \alpha) \leq \exp\left(-\alpha \sum_{s=0}^{k} \rho_s\right). \end{aligned} \tag{5.17}$$

Since $\sum_{s=0}^{\infty} \rho_s = \infty$, the right-hand side tends to 0 as $k \to \infty$.
Hence $\mathbb{P}(E_k) \to 0$, i.e., $\mathbb{P}(J_{\text{best},k} \leq J^* + \varepsilon) \to 1$. □

The verification sections demonstrate that the condition is satisfied by all five hybrids under standard parameter choices. In particular:

- **EA-GA**: Uniform mutation gives constant ρ_k;

- **ALO-GA**: GA mutation provides the needed exploration [332];
- **ABC-GA**: Scout bees produce uniformly random points [15];
- **GA-CSA**: Random flights of crows yield uniform sampling [48];
- **CEFO**: With a probabilistic restart, it also meets the condition.

The theorem does not give a convergence rate; the speed depends on the ρ_k sequence. For constant ρ, the failure probability decays exponentially in k; for decaying ρ_k, the rate is slower.

5.1.3 ABC-GA hybridization

The hybrid algorithm, ABC-GA [440], is a collaborative combination between the ABC algorithm and GA. The aim is to mitigate the slow convergence rate during the fine-tuning phase, a disadvantage reported in ([189,289,477]). The pseudo-code of ABC-GA hybrid is presented as Algorithm 11.

Algorithm 11 : Pseudo-code of the hybrid ABC-GA

```
begin
Objective function f(x), x = (x_1, ..., x_d)^T
Define the ABC parameters
Define the GA parameters
begin ABC
Start
Generate initial population of n food sources
within the defined parameter bounds
Objective function
Evaluate the objective function of each food source
Evaluate the fitness of each food source
Employed bee phase
For each employed bee generate new candidate solution
using neighborhood search mechanism
Apply bound constraints if necessary
Apply greedy selection between old and new solution
Onlooker bee phase
Calculate probability values proportional to fitness
Select food sources according to probability
Generate new candidate solutions
Apply greedy selection
Scout phase
Replace abandoned food sources with new random solutions
within parameter bounds
Test
If termination criterion is satisfied, go to Step 24
else move to Objective function step
Loop
Rank the food sources and select the best n solutions
end begin ABC
begin GA
```

Start
Initial population of n chromosomes = Final best ABC n solutions
Objective function
Evaluate fitness of each chromosome
Selection
Select parent chromosomes according to fitness
Crossover
Perform crossover with predefined probability
Mutation
Mutate offspring with mutation probability
Apply bound constraints if necessary
Replacement
Form new population (elitism may be applied)
Test
If termination criterion is satisfied return best solution else move to Objective function step in GA
end begin GA
Postprocess and visualize the results
end begin

5.1.4 GA-CSA hybridization

Although the CSA is effective across search space configurations, its convergence exhibit a severe sensitivity to the distribution of the initial population [48, 362]. Conversely, while the GA excels at diversity preservation, it often suffers from a diminished convergence rate in fine-tuning phases [368, 510]. To mitigate these drawbacks, a GA-CSA hybrid is proposed [438], wherein a GA sequence is utilized during the initialization and early distribution phase of the CSA. The pseudo-code of the GA-CSA hybrid algorithm is presented as Algorithm 12.

Algorithm 12 : Pseudo-code of the hybrid GA-CSA

begin
define the GA input parameters: GA operators, *NInd*, *MaxGen*, *GGAP*, p_c, and p_m
define the CSA input parameters: *N*, *MaxIter*, *fl*, *AP*
problem initialization: number of parameters d, parameters' bounds, objective function *f(x)*, process model, experimental data
begin GA
for $i := 1$ to N
generate randomly *NInd* number of individuals
evaluate the individuals in the population
for $j := 1$ to *MaxGen*
select individuals from the current generation
perform crossover on the selected individuals with a probability p_c
perform mutation on each individual with a probability p_m
place the offspring into the new population
evaluate the individuals in the new population
end for
rank the individuals in the population
store the best individual and its estimation
end for
end begin GA

begin CSA
initialize the memory of each crow
for iter := 1 to *MaxIter*
for i := 1 to N (all crows in the flock)
choose randomly a crow to follow
define an awareness probability r_i
if $r_i \geq AP$
change the current position of the $crow_i$
else
generate a new random position of the $crow_i$
end if
end for
check if all new positions are feasible
evaluate the new positions
update the memory of each crow
end for
rank the position of the crows in the flock
store the best position
end begin CSA
Postprocess and visualize the results
end begin

5.1.5 ALO-GA hybridization

According to [567], there is a higher probability for the RWS method to choose the elite. This can lead to falling into a local optimum. A hybridization with GA [440] is proposed to avoid this limitation of the ALO algorithm. On the other hand, one drawback of GA is that convergence to an optimum may take significant computational effort when the randomly generated initial population is quite distant from it. The ALO-GA pseudo-code is presented below (Algorithm 13).

Algorithm 13 : Pseudo-code of the hybrid ALO-GA

begin
Define the input parameters for both ALO and GA
Define the parameters of the problem under consideration
begin ALO
Generate randomly the initial populations of ants and antlions
Calculate the corresponding fitness estimations
Find the best antlion and adopt it as the elite (determined optimum)
for j:= 1 to the size of initial population Pop_0
while the end criterion is not satisfied
for each ant
Select an antlion using the roulette wheel selection
Update the parameters of the random walk
Create a random walk and normalize it
Update the position of the ant
end for
Evaluate all ants
Replace an antlion with its corresponding ant if it becomes fitter
Update the elite if an antlion becomes fitter
end while

Memorize the best solution for the current iteration in Pop_0
end for
end begin ALO
begin GA
Set the initial population Pop_0 to the set of best solutions generated by ALO
Calculate the value of the fitness function for each individual in Pop_0
for j:= 1 to MaxGeneration
Select individuals Pop_i from the current population Pop_{i-1} in a way that gives an advantage to better individuals
Perform crossover with probability p_c
Perform mutation with probability p_m
Calculate the value of the fitness function for each individual in Pop_i
end for
end begin GA
Rank the solutions, find the current best, and memorize it
Postprocess and visualize the results
end begin

5.1.6 EA-GA hybridization

Within the hybrid EA-GA [441], the evolutionary approach runs for *pop_size* times to generate the initial population of the GA. The maximum number of iterations within the EA, defined by the the parameter *max_iter*, is significantly smaller than in cases where it could be applied alone. Through this process, the generated initial population accumulates valuable domain knowledge; therefore, the GA requires a smaller population size and fewer generations to improve the solution quality and converge to a near-optimal solution. The detailed pseudo-code implementation of the EA-GA hybrid is illustrated in Algorithm 14.

Algorithm 14 : Pseudo-code of the Hybrid EA-GA

begin
Objective function $f(x), x = (x_1, \ldots, x_d)^T$
Define EA parameters: σ, max_iter, pop_size
Define GA parameters: max_gen, pc, pm, selection method
begin EA
Start
For $i = 1$ to pop_size
Generate initial candidate solution s_0 within bounds
Set $best\_solution = s_0$
Evaluate $best\_estimate = f(best\_solution)$
While no improvement over max_iter iterations
Generate random vector r with median 1 and SD σ
Compute $new\_solution = best\_solution \circ r$
Apply parameter bounds if necessary
Evaluate $new\_estimate = f(new\_solution)$
If $new\_estimate$ better than $best\_estimate$
Update $best\_solution$ and $best\_estimate$
End If
End While
Store $best\_solution$ in Pop_0

End For
Rank individuals and select best n solutions
end begin EA
begin GA
Start
Initial GA population = Final EA population Pop_0
For $j = 1$ to max_gen
Selection
Select individuals according to fitness
Crossover
Apply crossover with probability pc
Mutation
Apply mutation with probability pm
Apply parameter bounds if necessary
Evaluate new population
End For
Rank individuals and select best solution
end begin GA
Postprocess and visualize the results
end begin

5.1.7 CEFO hybridization

The principal benefits of incorporating CMs into EFO include: (i) improved initial space coverage due to the ergodic properties of chaotic sequences; (ii) an enhanced balance between exploration and exploitation through nonlinear time-varying attraction-repulsion coefficients; (iii) an increased ability to escape local optima due to deterministic irregular perturbations; (iv) reduction of stochastic variance while preserving diversity. The pseudo-code of the designed CEFO algorithm is shown as Algorithm 15.

Algorithm 15 : Pseudo-code of the CEFO

begin
Objective function $f(x), x = (x_1, \ldots, x_d)^T$
Define EFO parameters
Select CM $\Psi(z)$ and initial value $z_0 \in (0, 1)$
Start
Generate chaotic sequence $z_{k+1} = \Psi(z_k)$
Initialize population using chaotic mapping within bounds
Objective function
Evaluate objective function of each particle
Evaluate fitness of each particle
Rank population and divide into positive, neutral and negative fields
Electromagnetic update
Generate new chaotic value z_k
Update attraction coefficient $\alpha = z_k$
Update repulsion coefficient $\beta = 1 - z_k$
For each particle compute new position using chaotic field equation
Apply parameter bounds if necessary
Replacement

```
19:  Evaluate new solutions and update population
20:  Test
21:  If stopping criterion satisfied go to Step 22
     else move to Objective function step
22:  Rank population and select best solution
23:  Postprocess and visualize results
24:  end begin
```

In Chapter 5, based on the analysis of metaheuristic algorithms and their applications (Chapters 3 and 4), several hybrid metaheuristic schemes are constructed by integrating selected operators, population management strategies, and diversification mechanisms from the aforementioned algorithms. Five hybrid metaheuristic algorithms, namely ABC-GA, GA-CSA, ALO-GA, EA-GA, and CEFO, are proposed. A convergence theorem for hybrid metaheuristics based on a nondegenerate exploration condition is provided. By applying it to five distinct hybrids, it is shown that the condition is easy to verify and holds for common algorithmic choices.

The performance of the designed hybrid algorithms is investigated through their application for nonlinear model parameter identification problems and on specific benchmark functions. The obtained results are presented and discussed in Chapter 6.

Chapter 6

Application of hybrid metaheuristic algorithms for parameter optimization problems

Chapter 6 presents the results from the application of the proposed hybrid metaheuristic algorithms. The hybrid metaheuristic algorithms are applied to the problems of model parameter identification and parameter tuning of PID controllers, as follows:

- **ABC-GA hybrid** applied to *E. coli* MC4110 fed-batch cultivation process, thesis publication [440],
- **GA-CSA hybrid** applied to *E. coli* BL21(DE3)pPhyt109 fed-batch cultivation process, thesis publication [438],
- **ALO-GA hybrid** applied to *E. coli* MC4110 fed-batch cultivation process, thesis publication [442],
- **EA-GA hybrid** applied to *E. coli* MC4110 fed-batch cultivation process, thesis publication [441],
- **CEFO algorithm** applied to tuning of PID controller for glucose concentration control in *E. coli* BL21(DE3)pPhyt109 fed-batch cultivation process, thesis publication [428].

To test the performance of the designed hybrid algorithms they are applied to a set of different benchmark optimization problems [239]. Further, the performance of the hybrid algorithms is compared to some classical optimization algorithms and other popular metaheuristic algorithms – pure and/or hybrids. The obtained numerical results are analyzed additionally based on some statistical approaches [92,128,165,463] and ICrA [61]. All metaheuristic algorithms have been implemented in *MATLAB* environment based on the presented in Chapter 3 and Chapter 4 flow-charts and pseudo-codes. The mathematical models (Chapter 2) are simulated through Simulink implementation. Model parameter identification procedures are performed using real experimental data sets of the considered case studies (Chapter 2). Due to the stochastic nature of metaheuristics, a meaningful statistical evaluation requires multiple optimization runs; hence, a series of 30 independent runs is executed for each algorithm. The performance of the hybrid algorithms is compared with the performance of pure and/or hybrid metaheuristics based on the following statistical tests – parametric test ANOVA and nonparametric tests Friedman, Wilcoxon, Paired t-test and Kruskal-Wallis test. The tests are run in *MATLAB* using functions *'anova1'*, *'friedman'*, *'ranksum'*, *'ttest2'* and *'kruskalwallis'*.

A summary of weakness addressed, mechanism-based analysis, hybrid effect and theoretical justification of the proposed hybrid metaheuristic algorithms, is presented in Table 6.24.

Table 6.24: Summary of weakness addressed, mechanism-based analysis, hybrid effect and theoretical justification of the proposed hybrid metaheuristic algorithms.

Hybrid	**Weakness addressed**	**Mechanism-based complementarity**	**Hybrid effect**	**Theoretical justification**
EA-GA	GA: weak exploration; premature convergence due to random initialization; inefficient sampling	EA refinement: $x^{k+1} = x^k \odot r,\ r \sim \mathcal{N}(1, \sigma)$ Transforms initialization: $P_0^{GA} \sim \mathcal{U}(\Omega) \to P_0^{EA-GA} \sim \mathcal{L}(\Omega^*)$	Generates initial population in promising region; improves starting quality and convergence	Reduces premature convergence probability; introduces a guided initialization; modifies sampling distribution across the search space
ABC-GA	ABC: strong exploration, weak exploitation; GA: exploitation depends on diversity	ABC exploration: $v_{ij} = x_{ij} + \phi_{ij}(x_{ij} - x_{kj})$ GA recombination: $x^{k+1} = \mathcal{M}(\mathcal{C}(x_p, x_q))$	ABC generates diverse high-quality solutions $\to$ GA local refinement mechanism	Couples stochastic exploration with structured recombination; improves diversity and convergence speed; optimizes exploration-exploitation balance

Hybrid	Weakness addressed	Mechanism-based complementarity	Hybrid effect	Theoretical justification
ALO-GA	ALO: slow exploitation; oscillations near optimum	ALO random walks: $x^{k+1} = \frac{RW_{ant} + RW_{elite}}{2}$ GA selection and crossover	ALO performs wide global exploration, while GA accelerates convergence during the refinement phase	Two-stage search: global exploration (ALO) + local exploitation (GA); reduces convergence time and improves accuracy
GA-CSA	CSA: excessive randomness; unstable convergence; GA: limited exploitation	GA structured operators CSA exploitation: $x_i^{k+1} = x_i^k + fl(m_j^k - x_i^k)$	CSA enhances global exploration, whereas GA stabilizes and guides convergence	Converts purely stochastic search into guided stochastic process; improves convergence stability and robustness
CEFO	EFO: premature convergence; insufficient diversity	Chaotic maps: $w_{n+1} = f(w_n)$ EFO movement: $x_i^{k+1} = x_i^k + \lambda(x_{best} - x_i^k)$	Replaces random variables with chaotic sequences	Improves ergodicity and search space coverage (better exploration); prevents premature convergence while preserving convergence speed

The performance of the proposed hybrid metaheuristic algorithms (ABC-GA, GA-CSA, ALO-GA, EA-GA, and CEFO) has been systematically evaluated using classical benchmark functions and real-world *E. coli* fed-batch cultivation models. The key empirical findings are summarized below:

- **ABC-GA:** Integrates the robust exploration of ABC with the local exploitation of GA. It outperformed existing ACO and FA hybrids in parameter estimation for *E. coli* MC4110. However, its performance remains sensitive to the population size, suggesting a critical need for adaptive parameter tuning to sustain population diversity.

- **GA-CSA:** Utilized for *E. coli* BL21(DE3) identification, this hybrid framework significantly outperformed standalone GA, CSA, and deterministic SQP methods. It achieved superior accuracy while reducing computational costs by 8–10 times; nonetheless, observed parameter variability suggests a future focus on adaptive flight length and awareness probability mechanisms.

- **ALO-GA:** Ranked first among 12 state-of-the-art hybrids during comprehensive benchmark testing. In bioprocess modeling applications, it outperformed both ABC-GA and ACO-FA, improving objective function values by 6.5%. Its operational success points toward potential architectural synergies with water cycle and grey wolf optimizers.

- **EA-GA:** Employs a structured evolutionary initialization scheme to guide the GA sequence toward promising regions of the search space. It achieved 5% better accuracy than previously published models and converged to optimal solutions in only 200 iterations (compared to 1000 iterations for BHJO), demonstrating high efficiency for real-time application deployment.

- **CEFO:** Integrates EFO mechanics with chaotic maps, improving objective function values by up to 30% over the standard EFO algorithm. In PID controller tuning, it achieved rapid settling times (9 min) and stable control behavior, though structural PID limitations suggest future integration with robust control strategies.

Structured hybridization consistently yields superior convergence trajectories, enhanced numerical accuracy, and reduced computational overhead compared to standalone optimization methods. These cumulative results fully validate the integration of heterogeneous search mechanisms as a robust, scalable framework for solving complex, nonlinear biotechnological optimization problems.

Chapter 7

Conclusion and future work directions

7.1. Conclusion

The D.Sc. thesis presents an investigation into the development, analysis, and application of metaheuristic and hybrid metaheuristic optimization algorithms for solving complex nonlinear parameter identification problems in bioprocess systems engineering. The summary of the numerical results and algorithm performance can be presented as follows:

1. **General performance of standalone metaheuristics**. All investigated metaheuristic algorithms (GA, SA, FA, CS, ABC, CSA, COA, MPA, ALO, and EFO) demonstrate the capability to successfully solve the parameter identification problems. However, the numerical results clearly indicate that the performance of each algorithm strongly depends on the structure and complexity of the optimization problem.

2. **Observed limitations of standalone algorithms**. The conducted experiments reveal several inherent limitations of individual metaheuristics: premature convergence (e.g., GA, ALO), leading to suboptimal solutions; slow convergence rates (e.g., COA, ABC); high sensitivity to algorithm-specific parameters (GA, EFO); and an insufficient balance between exploration and exploitation mechanisms (ABC, ALO).

3. **Hybrid construction and design principles**. The development of the hybrid metaheuristic algorithms is based on a systematic and theoretically grounded framework, aiming to combine complementary search mechanisms in order to overcome the limitations of standalone approaches.

   The hybrid metaheuristics operate as structured dynamical systems in which multiple search operators interact to produce enhanced optimization behaviour. The proposed hybrid algorithms are constructed as follows:

   - EA-GA: evolutionary local refinement and genetic global search;
   - ABC-GA: ABC diversification and GA-based refinement;
   - ALO-GA: integration of ant lion exploration with GA operators;
   - GA-CSA: combination of GA operators with stochastic crow search;
   - CEFO: enhancement of electromagnetic field optimization through chaotic maps for improved diversity.

   A convergence theorem for hybrid metaheuristics based on a nondegenerate exploration condition is provided. By applying it to five distinct hybrids, it is shown that the condition is easy to verify and holds for common algorithmic choices.

4. **Effect of hybridization**. The introduction of hybrid metaheuristic algorithms leads to consistent and significant performance improvements. The numerical results demonstrate that the hybrid approaches: (i) improve convergence speed; (ii) increase solution accuracy; and (iii) enhance the robustness and stability of the optimization process. Furthermore, different hybrid structures exhibit specific advantages:
   - EA-GA: enhanced local refinement capability;
   - ABC-GA: improved diversity preservation and exploitation;
   - ALO-GA: a balanced exploration-exploitation trade-off;
   - GA-CSA: strengthened global exploration ability;
   - CEFO: increased diversity through the incorporation of chaotic dynamics.
5. **Validation across different test environments**. The effectiveness of the studied and proposed algorithms is demonstrated through a multi-level evaluation framework. This framework includes benchmark test functions that provide controlled and reproducible conditions for validation. Practical relevance and applicability are ensured by real-world problems. The significance and consistency of the obtained results are confirmed through statistical analysis. The essential dependencies between performance indicators and algorithm behavior are further analyzed using ICrA.

7.2. Future work directions

The results of the D.Sc. thesis provide a foundation for future research directions:

(i) Development of unified dynamical system models to provide a rigorous mathematical characterization of hybrid search stability and diversity preservation;

(ii) Design of intelligent frameworks capable of dynamically adjusting search behaviors and parameters based on the problem landscape;

(iii) Application of the developed hybrids to large-scale networks for the modeling and optimization of various classes of complex systems;

(iv) Adaptation of the hybridization framework for solving multi-criteria problems by maintaining broad population diversity and balancing practical relevance.

7.3. Summary of scientific and scientific-applied contributions

The main contributions of the D.Sc. thesis can be summarized as follows:

I. **Scientific contributions**

1. A systematic analysis of ten metaheuristic algorithms was performed, and specific hybridization guidelines were formulated to address and overcome their inherent limitations.

2. A generalized theoretical framework for the hybridization of metaheuristic algorithms was formulated, based on their representation as stochastic dynamical systems.

3. New hybrid metaheuristic algorithms (EA-GA, ABC-GA, ALO-GA, GA-CSA, and CEFO) were synthesized, and individual component integration schemes along with their corresponding algorithmic structures were developed.

4. A theorem for the global convergence in probability of hybrid metaheuristic algorithms was proven under a nondegenerate exploration condition.

5. A generalized comparative analysis of the behavior and performance of hybrid metaheuristic algorithms was proposed.

II. **Scientific-applied contributions**

6. A multi-level evaluation framework was developed for the systematic validation and benchmarking of metaheuristic algorithms.

7. The metaheuristic algorithms and their hybrids were applied to the modeling and control problems of various bioprocess systems.

The presented contributions correspond to the current state-of-the-art advancements in the field of global optimization and metaheuristics, representing an original contribution to the development of hybrid optimization methods and their application to complex nonlinear systems.

7.4. Publications of the thesis

I. **Publications with IF**

1. **Roeva, O.**, Chorukova, E., Kabaivanova, L., (**2025**). Advanced mathematical modeling of hydrogen and methane production in a two-stage anaerobic co-digestion system. *Mathematics*, 13(10), 1601 (ISSN 2227-7390).
   Q1 (Web of Science), IF = 2.2 (2024), citations – 2 (Scopus)

2. **Roeva, O.**, Zoteva, D., Roeva, G., Ignatova, M., Lyubenova, V., (**2024**). An effective hybrid metaheuristic approach based on the genetic algorithm. *Mathematics*, 12(23), 3815 (ISSN 2227-7390).
   Q1 (Web of Science), IF = 2.2 (2024), citations – 6 (Scopus)

3. **Roeva, O.**, Slavov, Ts., Kralev, J. (**2024**). PID controller design for an *E. coli* fed-batch fermentation process system using chaotic electromagnetic field optimization, *Processes*, 12(9), 1795 (ISSN 2227-9717).
   Q3 (Web of Science), IF = 2.8 (2024), citations – 0 (Scopus)

4. Lyubenova, V., Ignatova, M., Zoteva, D., **Roeva, O.** (**2024**). Model-based adaptive control of bioreactors – A brief review. *Mathematics*, 12(14), 2205 (ISSN 2227-7390).
   Q1 (Web of Science), IF = 2.2 (2024), citations – 4 (Scopus)

5. **Roeva, O.**, Roeva, G., Chorukova, E. (**2024**). Crow search algorithm for modelling an anaerobic digestion process: Algorithm parameter influence. *Mathematics*, 12(15), 2317 (ISSN 2227-7390).
   Q1 (Web of Science), IF = 2.2 (2024), citations – 0 (Scopus)

6. **Roeva, O.**, Zoteva, D. (**2024**). Model identification of *E. coli* cultivation process applying hybrid crow search algorithm. *Fermen-tation*, 10(1), 12 (ISSN 2311-5637).
   Q2 (Web of Science), IF = 3.3 (2024), citations – 0 (Scopus)

7. **Roeva, O.**, Zoteva, D., Roeva, G., Lyubenova, V. (**2023**). An efficient hybrid of an ant lion optimizer and genetic algorithm for a model parameter identification problem. *Mathematics*, 11(6), 1292 (ISSN 2227-7390).
   Q1 (Web of Science), IF = 2.3 (2023), citations – 11 (Scopus)

8. **Roeva, O.**, Chorukova, E. (**2023**). Metaheuristic algorithms to optimal parameters estimation of a model of two-stage anaerobic digestion of corn steep liquor. *Applied Sciences*, 13(1), 199 (ISSN 2076-3417).
   Q2 (Web of Science), IF = 2.5 (2023), citations – 3 (Scopus)

9. Chorukova, E., Kabaivanova, L., Hubenov, V., Simeonov, I., **Roeva, O.** (**2022**). Mathematical model of a thermophilic anaerobic digestion for methane production of wheat straw. *Processes*, 10(4), 742 (ISSN 2227-9717).
   Q2 (Web of Science), IF = 3.5 (2022), citations – 5 (Scopus)

10. **Roeva, O.**, Zoteva, D., Lyubenova, V. (**2021**). *Escherichia coli* cultivation process modelling using ABC-GA hybrid algorithm. *Processes*, 9(8), 1418 (ISSN 2227-9717).

    Q2 (Web of Science), IF = 3.352 (2021), citations – 10 (Scopus)

II. **Publications with SJR**

11. **Roeva, O.**, Zoteva, D., (**2024**). A comparison of chaotic electroma-gnetic field optimization algorithms, *International Journal Bioauto-mation*, 28(4), 245-265 (ISSN 1314-2321).
Q4 (Scopus), SJR = 0.149 (2024), citations – 2 (Scopus)

12. **Roeva, O.**, Zoteva, D., (**2021**). ICrA over ordered pairs applied to ABC optimization results. *Studies in Computational Intelligence*, Vol. 920, 135-148. (ISSN 1860-9503).
Q4 (Scopus), SJR = 0.237 (2021), citations – 1 (Scopus)

13. **Roeva, O.**, Vassilev, P., Ikonomov, N., Angelova, M., Su, J., Pencheva, T. (**2021**). On different algorithms for InterCriteria relations calculation. *Studies in Computational Intelligence*, Vol. 757, 143-160, (ISSN 1860-9503).
Q4 (Scopus), SJR = 0.237 (2021), citations – 16 (Scopus)

14. Ikonomov, N., Vassilev, P., **Roeva, O.**, (**2018**). ICrAData – Software for InterCriteria analysis. *International Journal Bioautomation*, 22(1), 1-10 (ISSN 1314-2321).
Q3 (Scopus), SJR = 0.267 (2018), citations – 55 (Scopus)

15. **Roeva, O.**, Vassilev, P. (**2016**). InterCriteria analysis of generation gap influence on genetic algorithms performance. *Advances in Intelligent Systems and Computing*, Vol. 401, 301-313. (ISSN 2194-5365).
Q3 (Scopus), SJR = 0.254 (2016), citations – 13 (Scopus)

16. **Roeva, O.**, Ikonomov, N., Vassilev, P. (2019). Discovering knowle-dge from predominantly repetitive data by InterCriteria analysis. *Studies in Computational Intelligence*, Vol. 795, 213-233, (ISSN 1860-9503).
Q4 (Scopus), SJR = 0.183, citations – 2 (Scopus)

III. **Other publications**

17. **Roeva, O.**, Fidanova, S., Paprzycki, M. (**2013**). Influence of the population size on the genetic algorithm performance in case of cultivation process modelling. In *Federated Conference on Computer Science and Information Systems*, 371-376 (ISBN 978-1-4673-4471-5). citations – 163 (Scopus)

18. **Roeva, O.**, (**2013**). A comparison of simulated annealing and genetic algorithm approaches for cultivation model identification. *Monte Carlo Methods and Applications*, Walter de Gruyter GmbH & Co. KG, 193-201 (ISBN 978-3-11-029347-0). citations – 3 (Scopus)

19. **Roeva, O.**, Trenkova, T., (**2012**). Genetic algorithms and firefly algorithms for non-linear bioprocess model parameters identification. In *International Conference on Evolutionary Computation Theory and Applications*, Vol. 2, 164-169 (ISBN 978-989-8565-33-4). citations – 1 (Scopus)

20. Slavov, T., **Roeva, O.**, (**2011**). Genetic algorithm tuning of PID controller in Smith predictor for glucose concentration control. *International Journal Bioautomation*, 15(2), 101-114 (ISSN 1314-2321). citations – 7 (Scopus)

The publications presented in the dissertation thesis have been cited 304 times in Scopus, including 146 citations in journals with IF, 93 citations in journals with SJR, and 65 citations in other scientific publications.

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