Enhancing Model Accuracy: A Parameter Optimization Strategy Based on the Dream Optimization Algorithm

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***Abstract**: Reliable parameter identification is essential for the development and predictive use of non-linear bioprocess models. This study evaluates the recently proposed Dream Optimization Algorithm (DOA), a human-inspired metaheuristic based on memory retention, partial forgetting, and dream-sharing mechanisms, for the identification of kinetic parameters in an Escherichia coli fed-batch cultivation model. The algorithm's performance is assessed using experimental cultivation data and compared with three widely employed metaheuristics: the genetic algorithm (GA), simulated annealing (SA), and the crow search algorithm (CSA). Results demonstrate that DOA achieves the lowest objective function value, the best mean performance across 30 independent runs, and substantially reduced computational time compared to SA and CSA. The model dynamics generated using DOA-identified parameters show excellent agreement with experimental biomass and substrate measurements, even in the presence of significant noise in the substrate data. These findings highlight the high accuracy, robustness, and computational efficiency of DOA, confirming its strong potential as an effective tool for bioprocess model parameter estimation and broader non-linear optimization tasks.*

***Keywords:** Dream optimization algorithm, Metaheuristic, Escherichia coli, Model parameter identification.*

Introduction

Accurate parameter identification in dynamic models is a foundational step in the modelling, simulation, and predictive control of complex biological and industrial systems. Among these, cultivation processes hold critical importance in biotechnology and biomanufacturing [1, 10]. However, the models governing these phenomena – which often involve intricate metabolic pathways, environmental dependencies, and cellular growth dynamics – are inherently highly non-linear, multi-modal, and often non-stationary [9, 11, 15]. Consequently, the task of reliably and accurately estimating the unknown kinetic parameters from noisy experimental data transforms into a significant, high-dimensional optimization challenge.

Traditional deterministic optimization methods, such as Levenberg-Marquardt [3] or Sequential Quadratic Programming [8], are frequently inadequate for this task. They require the objective function to be differentiable and convex and are highly susceptible to becoming trapped in local optima within the rugged, discontinuous, and complex search landscape characteristic of bioprocess models. Furthermore, their performance is often heavily reliant on the quality of the initial parameter guess, a constraint that is particularly limiting when dealing with novel or poorly characterized systems.

In response to these limitations, metaheuristic optimization algorithms have rapidly emerged as the method of choice for challenging parameter identification problems across diverse engineering and scientific domains, including highly non-linear energy systems, complex motor models, and, increasingly, bioprocesses [12, 16, 17]. These techniques – inspired by natural processes, collective animal behavior, or physical phenomena – rely on superior global search capabilities and robust strategies to maintain a healthy balance between exploration (searching new regions of the space) and exploitation (refining known good solutions). This independence from the objective function's analytical properties allows metaheuristics to consistently outperform classical deterministic techniques in achieving global or near-global parameter estimates.

The field of metaheuristics is currently undergoing a period of explosive growth, with numerous novel algorithms being proposed recently [2, 4, 19]. This continuous innovation aims to overcome the inherent weaknesses of previous generations, particularly concerning convergence speed and the ability to effectively escape sophisticated local optima in large search spaces [14]. In this context, the current study focuses on the Dream Optimization Algorithm (DOA), a recently proposed human-based metaheuristic [6].

The DOA is distinguished by its unique inspiration from the characteristics of human dreams, specifically integrating mechanisms for memory retention, forgetting, and supplementation, and dream sharing [6]. These features are mathematically modelled to enhance the algorithm's performance: the forgetting/supplementation mechanism promotes effective exploration to prevent premature convergence, while the dream-sharing strategy facilitates information exchange among the population, greatly improving the ability to escape complex local minima. Preliminary benchmarking has indicated that the DOA demonstrates superior convergence speed, high computational stability, and greater robustness compared to several well-established metaheuristic competitors [6].

A successful application of DOA is presented in [20], where a constrained multi-objective DOA is designed to solve the time-jerk optimal trajectory planning problem and generate Pareto solutions for optimized trajectories. The DOA was enhanced and combined with a fast non-dominated sorting technique and an archive update strategy to address multi-objective optimization tasks. Results from benchmark test functions confirmed that the algorithm is effective for convex, concave, and various other optimization problems, demonstrating strong convergence, solution diversity, and Pareto front coverage, as well as improved computational speed and algorithmic stability.

In [21], the multi-strategy enhanced DOA is introduced to overcome limitations such as weak search performance, slow convergence speed, and a tendency to become trapped in local optima in intelligent optimization methods used for 3D unmanned aerial vehicle (UAV) path planning. As a result, the global search effectiveness and accuracy of UAV path-planning algorithms in three-dimensional environments are significantly improved.

The good results obtained from applying the DOA motivated us to apply the algorithm further. The primary objective of this work is to assess the power and efficacy of the novel DOA when applied to the demanding problem of parameter identification of highly non-linear and non-stationary cultivation process models. By utilizing one of the newest and most competitive metaheuristics, this research aims to demonstrate a significant improvement in the accuracy, stability, and reliability of bioprocess model parameter estimation, thereby providing a robust tool for advanced bioprocess engineering.

The paper is organized as follows. The DOA background is presented in Section 2. The model parameter identification problem is discussed in Section 3. The obtained results are presented and discussed in Section 4. Concluding remarks are given in Section 5.

Dream optimization algorithm

The DOA is a metaheuristic algorithm inspired by the unconscious elements of human dreams and introduced in 2025 by Yifan Lang and Yuelin Gao [6].

The vision behind DOA relies on certain processes of human (un)consciousness taking place during dreaming, thus finding its basis in both neuroscience and psychology. DOA utilizes characteristics of dreams such as memory retention, partial forgetting, and self-organizing behavior to build optimization strategies centered around re-grouping pieces of information on multiple dimensions and modalities, while bringing a sense of randomness and chance.

Studies on dreaming as a recurring phenomenon can be traced from neuroscience to psychoanalysis and even mythos. In their expose, the authors behind the DOA [6] focus on the research concerning the rapid eye movement (REM) stage of sleep as the phase during which dreams originate. Neuroscientific research relying on both electroencephalogram and positron emission tomography suggests that brain activity looks similar during wakefulness and REM sleep [13], showing selective (re-)activation of different brain regions during dreaming. Although our current understanding is limited and thus unable to fully determine the manyfold process behind the occurrence of dreams, we could outline certain prominent cognitive and behavioral aspects that prove to be distinct for the state of dreaming. Lang and Gao [6] focus on *memory-specific conditions* and *self-organizing conduct* as their main inspiration for DOA recognizing the ability to only partially retain memories but still being capable of "random self-organization based on existing information".

The following premises serve as a foundation for developing the DOA:

1) A fitness function can be used to evaluate "the quality" of dreams.
2) Dreams occur in connection with existing memories.
3) Partial forgetting takes place during dreaming and results in the loss of information pieces, but allows for a semi-creative act of self-organizing to logically fill in the blanks.
4) Individuals and groups exhibit different levels of memory capabilities, introducing randomness to the constructive process of remembering.

The principles of DOA are developed following the assumptions 1) - 4). DOA consists of the *initialization phase*, the *exploration phase*, and the *exploitation phase*.

In its *initialization phase*, DOA generates the initial population with respect to the search space of the problem and its specifics, such as population size, lower and upper bound of the space, and dimensionality. The expression for obtaining the first-in-order population is [6]:

$$X_i = X_l + rand(X_u - X_l),\ i = 1, 2, \ldots, N. \quad (1)$$

Here, N marks the population size generated, X_i stands for the i-th individual, X_u and X_l define the upper and lower bounds of the search space as per the problem's restrictions, while $rand$ is a vector pointing out the dimensionality of the problem, where each dimension is a number between 0 and 1. Thus, the initial population takes the shape of:

$$X = \begin{bmatrix} X_1 \\ X_2 \\ \vdots \\ X_i \\ \vdots \\ X_N \end{bmatrix} = \begin{bmatrix} x_{1,1} & x_{1,2} & \ldots & x_{1,j} & \ldots & x_{1,Dim} \\ x_{2,1} & x_{2,2} & \ldots & x_{2,j} & \ldots & x_{2,Dim} \\ \vdots & \vdots & \vdots & \vdots & \vdots & \vdots \\ x_{i,1} & x_{i,2} & \ldots & x_{i,j} & \ldots & x_{i,Dim} \\ \vdots & \vdots & \vdots & \vdots & \vdots & \vdots \\ x_{N,1} & x_{N,2} & \ldots & x_1 & \ldots & x_{N,Dim} \end{bmatrix}, \quad (2)$$

where $x_{i,j}$ refers to the individual at the i-th position in the j-th dimension, while Dim stands for the dimensionality of the problem. Individuals are updated one by one.

The *exploration phase* begins with partitioning the existing population into five groups (q = 1, …, 5) with the individuals in each group being regarded as having different "memory capabilities" (tagged as $k_1, \ldots, k_5$) [6]. Then, we start iterating, and each iteration constitutes a dream. The number of iterations is pre-defined between 0 and T_d, where the latter determines the maximum number of iterations for this phase. The goal is to find the individual (optimal solution) dreaming the best dream or exhibiting the finest "dreaming behavior" (optimal value). The progress of the *exploration phase* can be summarized as follows:

1) Before the start of each dream, all individuals are shown the best solution available so far.
2) According to the group individuals belong to, some of them are able to hold on to the memory of the best individual available.
3) Other individuals belonging to k_q groups constituting "forgetting dimensions" $(K_1, K_2, \ldots, K_k)$ forget parts of the information shared.
4) The positions of the latter groups of individuals are updated during the iteration according to particular optimization strategies.

For the workflow described, DOA implements a *memory strategy*, a *forgetting and supplementation strategy*, and a *dream-sharing strategy*.

The *memory strategy* refers to the process of showing each individual the optimal solution available so far. The position of each individual is updated to the position of the best one up to the current iteration:

$$X_i^{t+1} = X_{bestq}^t, \quad (3)$$

where X_i^{t+1} represents the current individual adopting the position of the best individual from the previous iteration from group q referred to as X_{bestq}^t [6].

The *forgetting and supplementation strategy* follows the *memory strategy* affecting the population in the so-called "forgetting dimensions" It is precisely in the groups belonging to these dimensions that the position of each individual is updated in response to being unable to

recall the optimal solution shared beforehand, but being allowed to self-organize to a new position according to:

$$x_{i,j}^{t+1} = x_{best,j}^{t} + \frac{\left(x_{l,j}+rand\left(x_{u,j}+x_{l,j}\right)\right)\left(cos\left(\pi\frac{t+T_{max}-T_d}{T_{max}}\right)+1\right)}{2}, j = K_1, K_2, \ldots, K_{k_r} \quad (4)$$

Here, the modification of the individual's position happens with respect to the optimal solution available for iteration t within dimension j (X_{bestqj}^{t}), observing the lower and upper bounds of said dimension ($x_{u,j}$, $x_{l,j}$), while $rand$ takes a random value between 0 and 1, and iterations are defined in relation to the maximum number of iteration for the problem (T_{max}) and the maximum number of iteration for the current phase (T_d) [6].

As demonstrated in [6], the *cos* function used in Eq. (4) aims to achieve approximation to the (shown but forgotten) optimal solution with the increasing number of iterations, thus acknowledging the initial assumption behind self-organized behavior during dreaming.

The final strategy employed in the *exploration phase* is the *dream-sharing strategy*, which takes place alongside the *forgetting and supplementation strategy*. As opposed to the idea of self-organizing after partial forgetting of the optimal solution shared, dream-sharing allows individuals to adopt the position of other individuals in the same dimension. This process takes place in accordance with the following equation [6]:

$$x_{i,j}^{t+1} = \begin{cases} x_{m,j}^{t+1}, & m \leq i \\ x_{m,j}^{t}, & i < m \leq N \end{cases} \quad j = K_1, K_2, \ldots, K_{k_r}, \quad (5)$$

where m refers to the individual selected in random whose position will be adopted by the population for the purposes of the dimension update. k_r stands for the number of "forgetting dimensions" assigned to group q (*exploration phase*). The logic behind this process is to facilitate escaping local optima.

The strategies described above conclude the *exploration phase* of the DOA. The *exploitation phase* utilizes the same strategies, with the exception of dream-sharing. Another distinction to note is that in the development stage, the population is no longer divided into groups; individuals are only assigned to specific dimensions. In consequence of these differences, the formulas for the memory and the forgetting and supplementation strategies are respectively modified as follows:

$$X_i^{t+1} = X_{best}^{t}, \quad (6)$$

$$x_{i,j}^{t+1} = x_{best,j}^{t} + \frac{\left(x_{l,j}+rand\left(x_{u,j}+x_{l,j}\right)\right)\left(cos\left(\pi\frac{t}{T_{max}}\right)+1\right)}{2}, j = K_1, K_2, \ldots, K_{k_r}. \quad (7)$$

Some of the parameters used in DOA were noted above. For a more comprehensive understanding and a thorough description, the parameters are described as presented in [6].

The relationship between the maximum number of iterations within the exploration phase and the total maximum employed by the algorithm for a specific problem is set as follows [6]:

$$T_d = \frac{9}{10}T_{max}. \quad (8)$$

Classifying dimensions within certain groups as "forgetting" is performed on the basis of:

$$k_q = randi\left(\left\lceil\frac{Dim}{8\times q}\right\rceil, max\left\{2, \left\lceil\frac{Dim}{3\times q}\right\rceil\right\}\right),\ q = 1, \dots, 5, \tag{9}$$

where the value accepted by $randi(a, b)$ is a random integer within determined bounds.

During the *development phase*, Eq. (9) takes the following form as a result of the population no longer being divided into groups:

$$k_q = randi\left(2, max\left\{2, \left\lceil\frac{Dim}{3}\right\rceil\right\}\right). \tag{10}$$

As the *forgetting-and-supplementation strategy and the dream-sharing strategy* take place simultaneously after the memory strategy in the exploration phase, an additional parameter u is included to define the ratio that guides the strategies' execution. By default, u is set to 0.9, and its relationship with $rand$ serves as a criterion for which of the two parallel strategies will be implemented for a given group and dimension at a certain iteration. In cases where $rand > u$, the algorithm proceeds with the *forgetting and supplementation strategy*. If $rand < u$, the dream-sharing strategy is executed.

In DOA, the dimensionality of the specific problem the metaheuristics is applied to is connected to how individuals are updated within the determined boundaries of the search space.

For $Dim \leq 15$, fewer local optima are expected, and the following formula is used [6]:

$$x_{i,j}^{t+1} = x_{l,j} + rand(x_{u,j} + x_{l,j}) \tag{11}$$

to update the position of each individual in the population according to the group and/or dimension allocation.

For more complex problems with $Dim > 15$, re-updating the position of individuals takes place according to the equation below:

$$x_{i,j}^{t+1} = \begin{cases} x_{m,j}^{t+1}, & m < i \\ x_{m,j}^{t}, & i < m \leq N \end{cases}, \tag{12}$$

where m takes a random value of a natural number from 1 to N, but different than i for the purposes of the re-update [6].

In regard to DOA's time complexity, the algorithm's authors offer extensive analysis of the different phases and the respective processes associated with each, thus concluding that

$$\begin{aligned} &Time\_complexity(DOA) = \\ &O(initialization) + O(exploration\_process) + O(exploitation\_process) + \\ &+ O(parameter\_generation) + O(fitness\_evaluation) = \\ &= O(N_{max}\times Dim) + O(T_d\times N_{max}\times Dim) + O((T_{max} - T_d)\times N_{max}\times Dim) + \\ &+ O(6\times T_d\times(1 + Dim)) + O(T_{max}\times N_{max}\times E) = O(T_{max}\times N_{max}\times Dim) + O(T_{max}\times N_{max}\times E) = \\ &= O(T_{max}\times N_{max}\times Dim + T_{max}\times N_{max}\times E), \end{aligned}$$

where E stands for the time necessary for single function evaluation in accordance with fitness evaluation [6].

For the purposes of the current research, the DOA, as summarized above, is applied to a parameter identification problem. The next section outlines the specifics of the problem at hand.

Model parameter identification problem

Mathematical model of E. coli fed-batch cultivation process

Application of the general state space dynamical model to the *E. coli* cultivation fed-batch process leads to the following non-linear differential equation system [18]:

$$\frac{dX}{dt} = \mu_{max}\frac{S}{k_S+S}X - \frac{F}{V}X, \tag{13}$$

$$\frac{dS}{dt} = -\frac{1}{Y_{S/X}}\mu_{max}\frac{S}{k_S+S}X + \frac{F}{V}(S_{in} - S), \tag{14}$$

$$\frac{dV}{dt} = F, \tag{15}$$

where X and S are the biomass and substrate concentrations, [g·L^{-1}]; F is the feed rate, [L·h^{-1}]; V is the bioreactor volume, [L]; S_{in} is the influent glucose concentration, [g·L^{-1}]; μ_{max} is the maximum specific growth rate, [L·h^{-1}]; $Y_{S/X}$ is the yield coefficient, [-]; k_S is the saturation constant, [g·L^{-1}].

In developing the *E. coli* fed-batch cultivation model, several key assumptions are adopted:

- The bioreactor is considered to operate under ideal, complete mixing conditions.
- Glucose, the primary substrate, is predominantly utilized through oxidative pathways, and its uptake follows Monod-type kinetics.
- Changes in growth rate and substrate utilization are assumed not to substantially affect the biomass elemental composition. Therefore, the system is treated as being under balanced growth conditions.

Objective function

The optimization process relies on a specific criterion that determines how well a given parameter set performs. For the non-linear dynamic system under study, the parameter estimation task is formulated as minimizing the objective function J, which represents the discrepancy between the experimental data and the model-predicted values of the selected state variables:

$$J = \sum_{i=1}^{n}\sum_{j=1}^{k}\left\{\left[y_{exp}(i) - y_{mod}(i)\right]_j\right\}^2 \rightarrow min, \tag{16}$$

where n is the length of the data vector for each state variable k; y_{exp} are known experimental data; y_{mod} are model predictions with a given set of parameters.

For the parameter identification process, real experimental data collected from an *E. coli* MC4110 fed-batch cultivation are utilized. Comprehensive details about the cultivation conditions can be found in references [18].

Results and discussion

For the purposes of applying the DOA to the parameter identification problem described, the original MATLAB code provided [5] is adapted. The resulting code is run on a MacBook Air, Apple M2, macOS 15.6.1, 8 GB RAM, and the MATLAB version installed is R2024b.

A set of parameter identification procedures is carried out using the DOA algorithm or the model described by Eqs. (13)-(15). The main DOA parameters are listed in Table 1.

Table 1. DOA parameters

DOA parameters	Name	Value
Population size	*pop_size*	50
Number of generations/iterations	*max_iter*	100
Number of algorithm executions/runs	*run*	30
Problem size	*dim*	3
Model parameters upper limit	*ul*	[0.8 0.1 3]
Model parameters lower limit	*lb*	[0.2 0.0001 0.5]

The findings in this study are further evaluated against the results obtained from other metaheuristic approaches applied to the same parameter estimation problem – genetic algorithm (GA), simulated annealing (SA) and Crow search algorithm (CSA). The main algorithm parameters of GA, SA, and CSA are summarized in Table 2.

Table 2. CSA, GA and SA main parameters

Algorithm parameters	Name	Value
Crow search algorithm		
Maximum number of iterations	t_{max}	100
Problem dimension	p_d	3
Flock population size	*N*	50
Awareness probability	*AP*	0.1
Flight length	*fl*	2
Genetic algorithm		
Number of individuals	*nind*	50
Maximum number of	*maxgen*	100
Precision of binary	*preci*	20
Mutation rate	*mutr*	0.2
Crossover rate	*xovr*	0.8
Generation gap	*ggap*	0.97
Simulated annealing algorithm		
Initial temperature	*InitialTemperatur*	100
Temperature function	*TemperatureFcn*	@temperatureex
Reannealing interval	*ReannealInterval*	100
Display interval	*DisplayInterval*	100

The DOA parameters – number of algorithm executions/runs, problem size, model parameters upper limit and model parameters lower limit – are valid for CSA, GA and SA. Due to the stochastic nature of the applied optimization algorithms, they were executed at least 30 times to enable a reliable statistical evaluation. The best obtained results for parameter estimates, along with the corresponding objective function values *J*, are provided in Table 3.

Table 3. Parameter identification results obtained by GA, SA, CSA, and DOA

Model parameters	GA	SA	CSA	DOA
μ_{max}	0.475	0.455	0.484	0.486
$Y_{S/X}$	2.023	2.007	2.022	2.019
k_S	0.009	0.010	0.011	0.011
J	4.768	5.950	4.732	4.460

The model parameter estimates shown in Table 3 are consistent and align with their expected physical interpretation. The calculated values for the glucose-to-biomass yield, the maximum specific growth rate, and the saturation constant obtained through the applied metaheuristics closely match previously reported results in the literature [7, 18, 22].

The substrate concentration measurements obtained during the fed-batch process exhibit substantial noise due to the characteristics of the online glucose sensor used in the control loop. These sensors are known to suffer from slow response time, drift, and signal fluctuations under varying aeration and mixing regimes. Despite this, DOA effectively handles noisy data because its exploration mechanisms prevent overfitting to local variations caused by sensor noise, while the exploitation stage still refines parameter estimates toward globally coherent values.

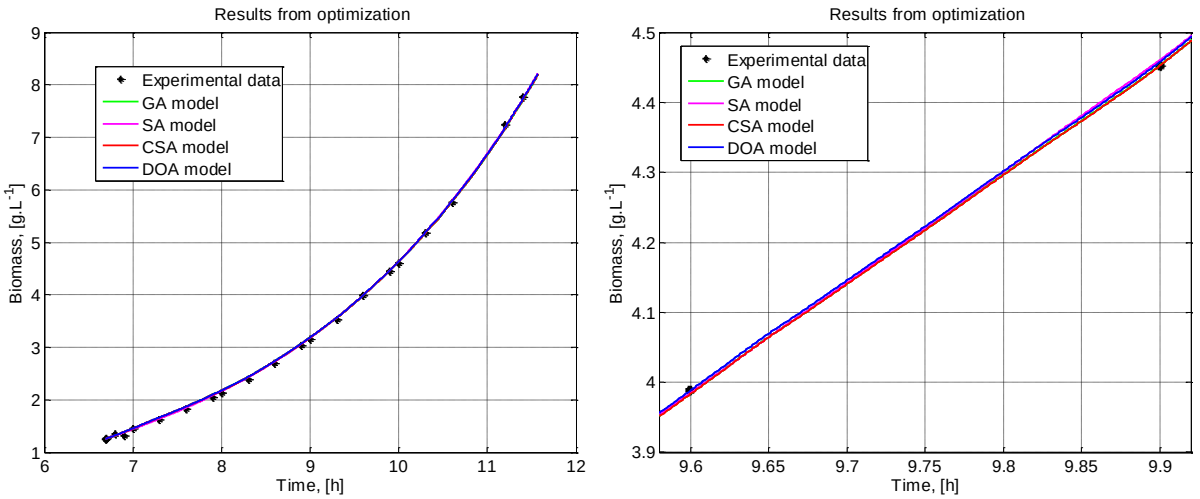
Graphical comparisons are often useful for revealing whether systematic deviations exist between measured data and model predictions. A quantitative assessment of the discrepancy between calculated and experimental values is essential for evaluating model adequacy. Figures 1 and 2 present the model-generated trajectories of the state variables, using the DOA-, GA-, CS- and CSA-estimated parameters, alongside the corresponding experimental data from the *E. coli* MC4110 cultivation process.

The comparison shows strong agreement between the simulated and measured values for both biomass and substrate concentrations. The model accurately captures the behavior of these variables throughout the *E. coli* MC4110 fed-batch cultivation. As illustrated in Fig. 1, the predicted biomass trajectory aligns very well with the experimental data. Because of certain characteristics of the online monitoring system used during cultivation [18], the substrate concentration data contain substantial noise (Fig. 2). The identification procedure was carried out using raw measurements without any preprocessing. Despite this, the models are still able to track the overall trend of the substrate measurements.

In order to compare the numerical results, Table 4 provides some statistical information, and the boxplot results are presented in Fig. 3.

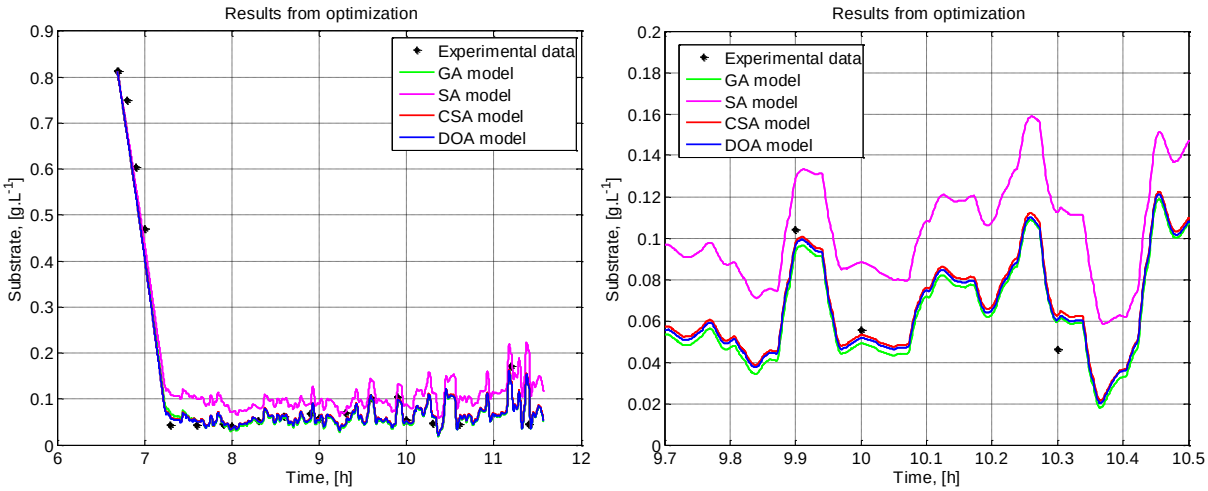
DOA achieves the lowest best J (4.460) among all algorithms, indicating the most accurate single-run solution. Its mean J (4.86) is also the lowest, confirming high reliability across multiple runs. CSA shows extremely small standard deviation in J (5.59×10^{-8}), but this is misleading: CSA's mean and best J are worse than DOA's, meaning CSA converges consistently – but to a worse local optimum.

The standard deviation of DOA (0.388) is notably higher than CSA's but lower than SA's, and comparable to GA's. This indicates a good balance between exploration and reliability, consistent with DOA's design.



a) normal view b) zoomed view

Fig. 1 Experimental and models-predicted data for biomass dynamics



a) normal view b) zoomed view

Fig. 2 Experimental and models-predicted data for substrate dynamics

Table 4. Comparison of the algorithms' performance

Algorithm	Objective function value, *J*		SD	Mean computational time, s	SD
	Best results	Mean results			
DOA	4.460	4.86	0.388	27.40	2.20
GA	4.768	4.94	0.190	34.668	2.23
SA	5.950	6.73	0.783	350.57	131.01
CSA	4.732	4.73	5.59×10^{-8}	1151.83	644.04

SD – standard deviation

DOA is significantly faster than SA and CSA, with only GA being slightly faster. The mean computational time for DOA (27.4 s) is nearly 13 times faster than SA (~350 s) and 42 times faster than CSA (~1152 s). Low time variability (SD = 2.20 s) indicates stable runtime behavior.

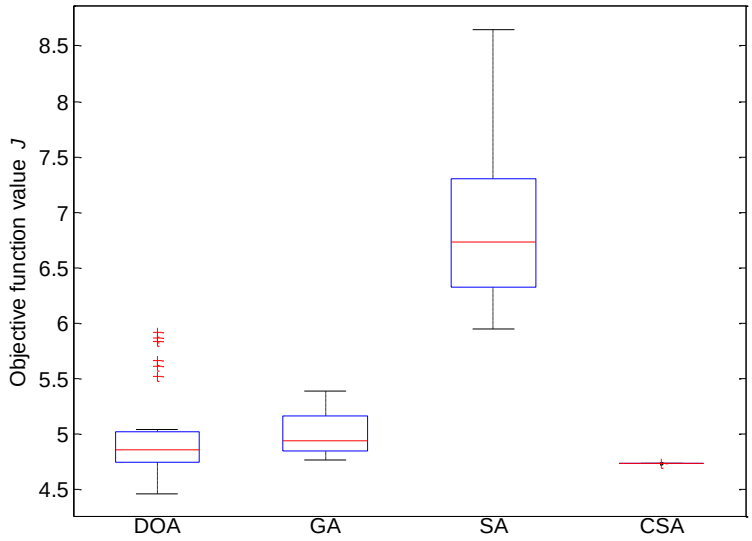


Fig. 3 Boxplot results

The boxplot in Fig. 3 illustrates that DOA exhibits the lowest median objective function value among all tested algorithms. Its interquartile range is narrow, indicating reliable performance across runs. Although CSA shows very small variability, its box is centered at higher objective function values, confirming convergence to inferior solutions. Simulated annealing displays the largest dispersion, reflecting instability and frequent entrapment in suboptimal regions.

In summary, DOA demonstrates the best accuracy (lowest best and mean J), good robustness (moderate standard deviation), high computational efficiency, better than all except GA, and consistently superior overall performance. The numerical results support the claim that DOA outperforms classical and swarm-based metaheuristics for bioprocess parameter identification.

Conclusion

This work investigates the applicability of the DOA to the non-linear parameter identification problem of an *E. coli* MC4110 fed-batch cultivation model. The DOA demonstrates excellent performance across all evaluation criteria. The DOA yields the lowest objective function values both in the best and average sense, outperforming established metaheuristics such as GA, SA, and CSA. In addition, the algorithm requires significantly less computational time than SA and CSA, reflecting its efficient search dynamics. The model trajectories obtained using DOA-optimized parameters closely match experimental biomass and substrate profiles, despite the presence of substantial measurement noise. These results confirm that the dream-inspired mechanisms of memory retention, forgetting, supplementation, and dream sharing enable an effective balance between exploration and exploitation.

Overall, DOA proves to be a robust, accurate, and computationally efficient optimization tool, well-suited for complex bioprocess modelling tasks. Future work will explore hybridization strategies and the integration of adaptive parameter control to further enhance DOA's performance in large-scale and real-time bioprocess optimization problems.

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