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InterCriteria analysis of genetic algorithm parameters in parameter identification

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Abstract: An application of InterCriteria Analysis (ICA) – recently proposed approach for multicriteria decision support – is here presented. The apparata of Index Matrices and Intuitionistic Fuzzy Sets are in the grounds of ICA. In this investigation, ICA is applied to examine the influences of genetic algorithms parameters during the model parameter identification of *E. coli* MC4110 and *S. cerevisiae* fermentation processes. The impact of two of the main genetic algorithms parameters, namely number of individuals and number of generations, is here studied. The obtained results after ICA application are discussed towards convergence time and model accuracy. Some conclusions about existing relations and dependencies between genetic algorithms parameters, from one side, and fermentation process model parameters from the other side, are derived.
Keywords: InterCriteria analysis, Intuitionistic fuzzy sets, Genetic algorithms, Fermentation process, *E. coli*, *S. cerevisiae*.
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1 Introduction

InterCriteria Analysis (ICA) is a recently developed approach [3] aiming to go beyond the nature of the criteria involved in a process of evaluation of multiple objects against multiple criteria, and, on this basis, to discover any existing correlations between the criteria themselves. Given in details in [3], ICA has been further applied for the purposes of temporal, threshold and trends analyses of an economic case-study of European Union member states' competitiveness [8, 9, 10].

The analyses presented there have provoked the authors for application of the ICA approach to the field of fermentation process modelling. The main idea is to look for correlations between model and optimization algorithm parameters, when given parameters are considered as criteria. This may lead to additional exploring of the model, which will be valuable especially in the case of modelling of living systems, such as fermentation process. Moreover, the relation between model and optimization algorithm will be established.

As representatives of biologically inspired optimization techniques, genetic algorithms (GA) [14], are among the most widely used for global search [12]. GA have been successfully applied to different research fields to solve many engineering and optimization problems [19]. Their effectiveness has already been demonstrated also for model parameter identification considering fermentation processes [1, 17, 18, 20, 21].

When applying GA, there are many operators, functions, parameters, and settings in the GAs that can be implemented specifically in different problems. The focus of current research is on the investigation of the influence of two of the main GA parameters, namely number of individuals to be involved ($nind$) and number of generations to be performed ($maxgen$). Standard GA is applied to the purpose of model parameter identification of two fed-batch fermentation processes – of bacteria *E. coli* and yeast *S. cerevisiae*. Both processes have been chosen as representative of some of the important microorganisms with numerous applications in food and pharmaceutical industry, as well as being among the widely used model organisms in genetic engineering and cell biology due to their well known metabolic pathways [13, 15].

In the current investigation, ICA is applied to identification of the influences and relations between model parameters, from one side, and GA parameters $nind$ and $maxgen$ from the other side, based on results of parameters identification procedures of bacteria and yeast.

The paper is organized as follows: the problem formulation is given in Section 2, while Section 3 presents the background of ICA. Numerical results and discussion are presented in Section 4 and conclusion remarks are given in Section 5.

2 Problem formulation

2.1 Mathematical models of fermentation processes

Case study 1. *E. coli* fed-batch fermentation model

The mathematical model of the considered here *E. coli* fed-batch process is presented by the following non-linear differential equations system [11, 17]:

$$\frac{dX}{dt} = \mu X - \frac{F_{in}}{V} X \tag{1}$$

$$\frac{dS}{dt} = -q_S X + \frac{F_{in}}{V}(S_{in} - S) \tag{2}$$

$$\frac{dV}{dt} = F_{in} \tag{3}$$

where

$$\mu = \mu_{max}\frac{S}{k_S + S}, \;\; q_S = \frac{1}{Y_{S/X}}\mu \tag{4}$$

and X is the biomass concentration, [g/l]; S is the substrate concentration, [g/l]; F_{in} is the feeding rate, [l/h]; V is the bioreactor volume, [l]; S_{in} is the substrate concentration in the feeding solution, [g/l]; μ and q_S are the specific rate functions, [1/h]; μ_{max} is the maximum value of the μ, [1/h]; k_S is the saturation constant, [g/l]; $Y_{S/X}$ is the yield coefficient, [-].

The parameter vector that should be identified for the model (Eqs. (1-4)) is:
$p_1 = [\mu_{max}\ k_S\ Y_{S/X}]$.

Model parameters identification of an *E. coli* MC4110 fed-batch fermentation process is performed based on experimental data for biomass and glucose concentration. The detailed description of the process conditions and experimental data may be found in [17, 18].

Case study 2. *S. cerevisiae* fed-batch fermentation model
Fed-batch fermentation process of *S. cerevisiae* is also described by the non-linear differential equations system (Eqs. (1–3)). Due to the specifics of considered process, better behaviour is obtained using following specific rates [17]:

$$\mu = \mu_{2S}\frac{S}{S+k_S} + \mu_{2E}\frac{E}{E+k_E},\ \ q_S = \frac{\mu_{2S}}{Y_{S/X}}\frac{S}{S+k_S} \tag{5}$$

where S, k_S, and $Y_{S/X}$ keep their meaning as described above. Additionally, E is the concentration of ethanol, [g/l], μ_{2S} and μ_{2E} are the maximum values of μ, [1/h], and k_E is a saturation constant, [g/l].

For the considered here model (Eqs. (1-3), (5)), the following parameter vector should be identified: $p_2 = [\mu_{2S}\ \mu_{2E}\ k_S\ k_E\ Y_{S/X}]$.

By analogy with the described above fermentation process of *E. coli*, experimental data for biomass and glucose concentration of an *S. cerevisiae* fed-batch fermentation process is used for the purposes of model parameters identification. The detailed description of the process conditions and experimental data may be found in [17].

2.2 Genetic algorithms for model parameter identification

Genetic algorithms are a stochastic global optimization method. Among a number of optimization techniques, GA are one of the methods based on biological evolution and inspired by Darwin's theory of survival of the fittest [14].

Many operators and parameters of genetic algorithms need to be tuned when GA is implemented for a concrete optimization problem. Among the most important genetic operators that make a significant influence over the optimization procedures, are the number of individuals ($nind$) and the number of generations ($maxgen$). In this investigation the focus is pointed on the influence of $nind$ and $maxgen$ on the model accuracy (value of the optimization criterion J), convergence time T and model parameters estimations.

Population size. In the terms of GA, the number of individuals corresponds to how many how many chromosomes (possible solutions) are going to be considered at each generation. If there are few chromosomes, GA have a few possibilities to perform crossover and only a small part of search space is explored. On the contrary, if there are too many chromosomes, GA slows down. It is logical to suppose that using more individuals may lead to better convergence time. It may be

surprising but very big population size usually does not improve performance of GA (in meaning of speed of finding solution). Also there it is proposed that good population size is about 20-30 individuals, however sometimes sizes of 50-100 individuals are reported as best [16].

In this investigation the impact of $nind$ and $maxgen$ is going to be examined choosing different values of both genetic operators. In Case study 1, bigger values of $nind$ with bigger "gaps" between them are chosen. As such, in this case GA is applied with the following values of $nind$: $nind$ = {50, 100, 150, 200}. Different strategy is chosen in Case study 2 – GA are going to be applied at smaller values of $nind$ with smaller "gaps" between them. In this case, values of $nind$ are chosen as follows: $nind$ = {20, 40, 60, 80, 100}.

Generation number. Generation number is one of the GA parameters commonly used as algorithm termination criterion. It is logically to suppose that using bigger number of generation lead to bigger convergence time, so the more interesting question is how it is correlated to the model accuracy. In analogy with the investigation of $nind$' influence, GA is going to be performed with different values of $maxgen$ for both considered here Case studies.

In Case study 1, smaller values of $maxgen$ with smaller "gaps" between them are now chosen: $maxgen$ = {50, 100, 150, 200, 250, 300}. Now bigger values of $maxgen$ with bigger "gaps" between them are investigated in Case study 2, chosen as follows: $maxgen$ = {100, 200, 500, 1000}.

While examining different values of investigated here $nind$ and $maxgen$, all other GA operators and parameters are as presented in Table 1, summarized for both Case studies.

Table 1: Main GA parameters and operators

Parameters and operators	**Case study 1**	**Case study 2**
$nind$	50, 100, 150, 200 at $maxgen = 200$	20, 40, 60, 80, 100 at $maxgen = 100$
$maxgen$	50, 100, 150, 200, 250, 300 at $nind = 100$	100, 200, 500, 1000 at $nind = 20$
crossover rate	0.7	0.95
mutation rate	0.1	0.05
generation gap	0.97	0.8
crossover operator	double point	
mutation operator	bit inversion	
selection operator	roulette well selection	
encoding	binary	

Optimization criterion. The aim is the adjustment of model parameter vector of the considered non-linear mathematical models in order to obtain the best fit to a data set. The objective function is defined as:

$$J = \sum_{i=1}^{m} (X_{\text{exp}}(i) - X_{\text{mod}}(i))^2 + \sum_{i=1}^{n} (S_{\text{exp}}(i) - S_{\text{mod}}(i))^2 \rightarrow \min \tag{6}$$

where m and n are the experimental data dimensions; X_{exp} and S_{exp} are the available experimental data for biomass and substrate; X_{mod} and S_{mod} are the model predictions for biomass and substrate with a given model parameter vector.

3 InterCriteria analysis

3.1 Short remarks on Intuitionistic Fuzzy Pairs

Initially, we give some remarks on Intuitionistic Fuzzy Pairs (IFPs; see [4]). The IFP is an object in the form of an ordered pair $\langle a, b\rangle$, where $a, b \in [0, 1]$ and $a+b \leq 1$, that is used as an evaluation of some object or process, and which components (a and b) are interpreted, respectively, as degrees of membership and non-membership to a given set, or degrees of validity and non-validity, or degree of correctness and non-correctness, etc.

Let us have two IFPs $x = \langle a, b\rangle$ and $y = \langle c, d\rangle$.

In [4], we defined the relations

$$\begin{array}{lll} x < y & \text{iff} & a < c \text{ and } b > d \\ x \leq y & \text{iff} & a \leq c \text{ and } b \geq d \\ x = y & \text{iff} & a = c \text{ and } b = d \\ x \geq y & \text{iff} & a \geq c \text{ and } b \leq d \\ x > y & \text{iff} & a > c \text{ and } b < d \end{array}$$

3.2 Short remarks on Index Matrices

The concept of Index Matrix (IM) was introduced in [5] and discusssed in more details in [6, 7]. Here, following [6], the basic definitions and properties related to IMs are given.

Let I be a fixed set of indices and $\mathcal{R}$ be the set of all real numbers. By IM with index sets K and L $(K, L \subset I)$, we mean the object,

$$[K, L, \{a_{k_i,l_j}\}] \equiv \begin{array}{c|cccc} & l_1 & l_2 & \ldots & l_n \\ \hline k_1 & a_{k_1,l_1} & a_{k_1,l_2} & \ldots & a_{k_1,l_n} \\ k_2 & a_{k_2,l_1} & a_{k_2,l_2} & \ldots & a_{k_2,l_n} \\ \vdots & \vdots & \vdots & \ddots & \vdots \\ k_m & a_{k_m,l_1} & a_{k_m,l_2} & \ldots & a_{k_m,l_n} \end{array},$$

where $K = \{k_1, k_2, ..., k_m\},\ L = \{l_1, l_2, ..., l_n\}$, and for $1 \leq i \leq m$, and $1 \leq j \leq n : a_{k_i,l_j} \in \mathcal{R}$.

On the basis of the above definition, in [7] the new object – the Intuitionistic Fuzzy IM (IFIM) – was introduced in the form

$$[K, L, \{\langle \mu_{k_i,l_j}, \nu_{k_i,l_j}\rangle\}] \equiv \begin{array}{c|cccc} & l_1 & l_2 & \ldots & l_n \\ \hline k_1 & \langle \mu_{k_1,l_1}, \nu_{k_1,l_1}\rangle & \langle \mu_{k_1,l_2}, \nu_{k_1,l_2}\rangle & \ldots & \langle \mu_{k_1,l_n}, \nu_{k_1,l_n}\rangle \\ k_2 & \langle \mu_{k_2,l_1}, \nu_{k_2,l_1}\rangle & \langle \mu_{k_2,l_2}, \nu_{k_2,l_2}\rangle & \ldots & \langle \mu_{k_2,l_n}, \nu_{k_2,l_n}\rangle \\ \vdots & \vdots & \vdots & \ddots & \vdots \\ k_m & \langle \mu_{k_m,l_1}, \nu_{k_m,l_1}\rangle & \langle \mu_{k_m,l_2}, \nu_{k_m,l_2}\rangle & \ldots & \langle \mu_{k_m,l_n}, \nu_{k_m,l_n}\rangle \end{array},$$

where for every $1 \leq i \leq m, 1 \leq j \leq n$: $0 \leq \mu_{k_i,l_j}, \nu_{k_i,l_j}, \mu_{k_i,l_j} + \nu_{k_i,l_j} \leq 1$, i.e., $\langle \mu_{k_i,l_j}, \nu_{k_i,l_j} \rangle$ is an IFP.

3.3 InterCriteria analysis

Let us have an IM

$$A = \begin{array}{c|ccccccc} & O_1 & \ldots & O_k & \ldots & O_l & \ldots & O_n \\ \hline C_1 & a_{C_1,O_1} & \ldots & a_{C_1,O_k} & \ldots & a_{C_1,O_l} & \ldots & a_{C_1,O_n} \\ \vdots & \vdots & \ddots & \vdots & \ddots & \vdots & \ddots & \vdots \\ C_i & a_{C_i,O_1} & \ldots & a_{C_i,O_k} & \ldots & a_{C_i,O_l} & \ldots & a_{C_i,O_n} \\ \vdots & \vdots & \ddots & \vdots & \ddots & \vdots & \ddots & \vdots \\ C_j & a_{C_j,O_1} & \ldots & a_{C_j,O_k} & \ldots & a_{C_j,O_l} & \ldots & a_{C_j,O_n} \\ \vdots & \vdots & \ddots & \vdots & \ddots & \vdots & \ddots & \vdots \\ C_m & a_{C_m,O_1} & \ldots & a_{C_m,O_k} & \ldots & a_{C_m,O_l} & \ldots & a_{C_m,O_n} \end{array}, \tag{7}$$

where for every $p, q,\ (1 \leq p \leq m, 1 \leq q \leq n)$:

- C_p is a criterion, taking part in the evaluation,
- O_q is an object, being evaluated,
- a_{C_p,O_q} is a real number or another object, that is comparable about relation R with the other a-objects, so that for each i, j, k: $R(a_{C_k,O_i}, a_{C_k,O_j})$ is defined. Let $\overline{R}$ be the dual relation of R in the sense that if R is satisfied, then $\overline{R}$ is not satisfied and vice versa. For example, if "R" is the relation "$<$", then $\overline{R}$ is the relation "$>$", and vice versa.

Let $S^{\mu}_{k,l}$ be the number of cases is which $R(a_{C_k,O_i}, a_{C_k,O_j})$ and $R(a_{C_l,O_i}, a_{C_l,O_j})$ are simultaneously satisfied.

Let $S^{\nu}_{k,l}$ be the number of cases is which $R(a_{C_k,O_i}, a_{C_k,O_j})$ and $\overline{R}(a_{C_l,O_i}, a_{C_l,O_j})$ are simultaneously satisfied.

Obviously,

$$S^{\mu}_{k,l} + S^{\nu}_{k,l} \leq \frac{n(n-1)}{2}.$$

Now, for every k, l, such that $1 \leq k < l \leq m$ and for $n \geq 2$, we define

$$\mu_{C_k,C_l} = 2\frac{S^{\mu}_{k,l}}{n(n-1)}, \quad \nu_{C_k,C_l} = 2\frac{S^{\nu}_{k,l}}{n(n-1)}. \tag{8}$$

Therefore, $\langle \mu_{C_k,C_l}, \nu_{C_k,C_l} \rangle$ is an IFP. Now, we can construct the IM

$$\begin{array}{c|ccc} & C_1 & \ldots & C_m \\ \hline C_1 & \langle \mu_{C_1,C_1}, \nu_{C_1,C_1} \rangle & \ldots & \langle \mu_{C_1,C_m}, \nu_{C_1,C_m} \rangle \\ \vdots & \vdots & \ddots & \vdots \\ C_m & \langle \mu_{C_m,C_1}, \nu_{C_m,C_1} \rangle & \ldots & \langle \mu_{C_m,C_m}, \nu_{C_m,C_m} \rangle \end{array}, \tag{9}$$

that determine the degrees of correspondence between criteria $C_1, ..., C_m$.

In the most of the obtained pairs $\langle \mu_{C_k,C_l}, \nu_{C_k,C_l} \rangle$, the sum $\mu_{C_k,C_l} + \nu_{C_k,C_l}$ is equal to 1. However, there may be some pairs, for which this sum is less than 1. The difference

$$\pi_{C_k,C_l} = 1 - \mu_{C_k,C_l} - \nu_{C_k,C_l} \tag{10}$$

is considered as a degree of "uncertainty".

4 Numerical results and discussion

30 independent runs of the GA with different number of individuals and algorithm generations (see Section 2.2) are performed to obtain the model parameters estimates for the two Case studies.

Based on the obtained average results from the identification procedures, as well as the average values of the computational time (T) and of objective function (J) four IMs, following Eq. 7, are constructed:

- For the Case study 1 – index matrices $A_{1(nind)}$ and $A_{1(maxgen)}$

$$A_{1(nind)} = \begin{array}{c|cccc} & \text{GA}^{1,1}_{nind} & \text{GA}^{1,2}_{nind} & \text{GA}^{1,3}_{nind} & \text{GA}^{1,4}_{nind} \\ \hline T & 109.734 & 231.875 & 562.672 & 691.484 \\ J & 0.0063 & 0.0032 & 0.0119 & 0.004 \\ nind & 50 & 100 & 150 & 200 \\ \mu_{max} & 0.549 & 0.549 & 0.546 & 0.551 \\ k_S & 0.009 & 0.009 & 0.009 & 0.009 \\ Y_{S/X} & 2 & 1.999 & 2 & 2 \end{array} \tag{11}$$

IM $A_{1(nind)}$ presents average estimates of the model parameters μ_{max}, k_S and $Y_{S/X}$, as well as the resulting computational time and objective function value, respectively in the case of 50, 100, 150 and 200 individuals, named ($\text{GA}^{1,1}_{nind}$ – $\text{GA}^{1,4}_{nind}$).

$$A_{1(maxgen)} = \begin{array}{c|cccccc} & \text{GA}^{1,1}_{maxgen} & \text{GA}^{1,2}_{maxgen} & \text{GA}^{1,3}_{maxgen} & \text{GA}^{1,4}_{maxgen} & \text{GA}^{1,5}_{maxgen} & \text{GA}^{1,6}_{maxgen} \\ \hline T & 48.546 & 88.422 & 277.609 & 231.875 & 306.313 & 350.593 \\ J & 0.0232 & 0.0249 & 0.0154 & 0.0032 & 0.0034 & 0.0033 \\ maxgen & 50 & 100 & 150 & 200 & 250 & 300 \\ \mu_{max} & 0.543 & 0.554 & 0.548 & 0.549 & 0.549 & 0.549 \\ k_S & 0.009 & 0.009 & 0.009 & 0.009 & 0.009 & 0.01 \\ Y_{S/X} & 2.001 & 1.998 & 2.003 & 1.999 & 1.999 & 1.999 \end{array} \tag{12}$$

In analogy, IM $A_{1(maxgen)}$ presents the same results (μ_{max}, k_S, $Y_{S/X}$, T, J and $maxgen$), respectively in the case of 50, 100, 150, 200, 250 and 300 generations ($\text{GA}^{1,1}_{maxgen}$ – $\text{GA}^{1,6}_{maxgen}$).

The IMs for the Case study 2 are constructed in the same way.

- For the Case study 2 – index matrices $A_{2(nind)}$ and $A_{2(maxgen)}$

$$A_{2(nind)} = \begin{array}{c|ccccc} & \mathrm{GA}^{2,1}_{nind} & \mathrm{GA}^{2,2}_{nind} & \mathrm{GA}^{2,3}_{nind} & \mathrm{GA}^{2,4}_{nind} & \mathrm{GA}^{2,5}_{nind} \\ \hline T & 79.2344 & 145.49681 & 212.79040 & 295.5058 & 375.1032 \\ J & 0.02216 & 0.02216 & 0.02216 & 0.0221 & 0.0221 \\ nind & 20 & 40 & 60 & 80 & 100 \\ \mu_{2S} & 0.95086 & 0.97236 & 0.95264 & 0.96548 & 0.97984 \\ \mu_{2E} & 0.1181 & 0.12372 & 0.12344 & 0.1413 & 0.14210 \\ k_S & 0.12612 & 0.12862 & 0.12282 & 0.13332 & 0.13338 \\ k_E & 0.79806 & 0.79864 & 0.79978 & 0.79938 & 0.79986 \\ Y_{S/X} & 0.41313 & 0.40698 & 0.41003 & 0.4022 & 0.40022 \end{array} \quad (13)$$

$$A_{2(maxgen)} = \begin{array}{c|cccc} & \mathrm{GA}^{2,1}_{maxgen} & \mathrm{GA}^{2,2}_{maxgen} & \mathrm{GA}^{2,3}_{maxgen} & \mathrm{GA}^{2,4}_{maxgen} \\ \hline T & 76.7622 & 148.1408 & 368.328 & 771.302667 \\ J & 0.02218 & 0.02218 & 0.022175 & 0.0221 \\ maxgen & 100 & 200 & 500 & 1000 \\ \mu_{2S} & 0.9591 & 0.95046 & 0.952775 & 0.969667 \\ \mu_{2E} & 0.12646 & 0.11512 & 0.122175 & 0.141133 \\ k_S & 0.12878 & 0.12192 & 0.123225 & 0.131733 \\ k_E & 0.79916 & 0.79986 & 0.7998 & 0.799933 \\ Y_{S/X} & 0.407907 & 0.420613 & 0.412486 & 0.402107 \end{array} \quad (14)$$

Using IMs $A_{1(nind)}, A_{1(maxgen)}, A_{2(nind)}$ and $A_{2(maxgen)}$ the ICA algorithm calculates, based on Eq. 8, the IFP $\langle \mu, \nu \rangle$ for every two pairs of considered criteria. Following the Eq. 10, π values are calculated, too. The results are summarized in the Table 2 and Table 3 for both Case studies, considering different $nind$ and $maxgen$.

After the application of ICA for considered here two case studies it is expected that the results should refer to some identical or closer relations and dependences between observed criteria. This expectation is due to the fact that non-structural models, presented with a system of non-linear differential equations, are considered. On the other hand, the models describing fermentation processes of *E. coli* and *S. cerevisiae* are based on different specific growth rates, so there should be some differences in the parameters relations.

As it can be seen from Tables 2 and 3, the probable high correlation between convergence time T and each of the examined GAs parameters $nind$ or $maxgen$, has been confirmed in both case studies. This correlation has been expected due to the fact that the convergence time logically increases when the bigger number of individuals in the population are chosen or greater number of generations are set to find a solution. Continuing to consider the dependencies between $nind$ or $maxgen$ from one side, and model parameters from the other side, higher values of μ are observed again for both case studies in pairs between $nind$ or $maxgen$ and specific growth rates. Another coincidence should be noted in this group, namely between $Y_{S/X}$ and $maxgen$, but with a lower μ. Three cases of dissonance between two case studies are observed in this first group, namely higher μ between two saturation constants in Case study 2 against zero values in Case study 1, and, in opposite, higher μ between J and $nind$ or $maxgen$ in Case study 1 against zero values in Case study 2.

Going further in the investigation of relations between algorithm accuracy and model parameters, higher μ is observed between $Y_{S/X}$ and J. Relations between specific growth rates and J,

Table 2: Results from the ICA in case of *E. coli* fed-batch fermentation process

Correlation	$nind$		$maxgen$	
	$\langle \mu, \nu \rangle$	π	$\langle \mu, \nu \rangle$	π
$T \leftrightarrow nind\,/maxgen$	$\langle 1, 0 \rangle$	0	$\langle 0.9, 0.1 \rangle$	0
$J \leftrightarrow nind\,/\,maxgen$	$\langle 0.5, 0.5 \rangle$	0	$\langle 0.2, 0.8 \rangle$	0
$\mu \leftrightarrow nind\,/\,maxgen$	$\langle 0.5, 0.3 \rangle$	0.2	$\langle 0.5, 0.3 \rangle$	0.2
$Y_{S/X} \leftrightarrow nind\,/maxgen$	$\langle 0.3, 0.2 \rangle$	0.5	$\langle 0.3, 0.5 \rangle$	0.2
$k_S \leftrightarrow nind\,/\,maxgen$	$\langle 0, 0 \rangle$	1	$\langle 0.3, 0 \rangle$	0.7
$T \leftrightarrow J$	$\langle 0.5, 0.5 \rangle$	0	$\langle 0.3, 0.7 \rangle$	0
$\mu \leftrightarrow J$	$\langle 0.2, 0.7 \rangle$	0.1	$\langle 0.3, 0.5 \rangle$	0.2
$Y_{S/X} \leftrightarrow J$	$\langle 0.5, 0 \rangle$	0.5	$\langle 0.4, 0.4 \rangle$	0.2
$k_S \leftrightarrow J$	$\langle 0, 0 \rangle$	1	$\langle 0.1, 0.3 \rangle$	0.6
$\mu \leftrightarrow T$	$\langle 0.5, 0.3 \rangle$	0.2	$\langle 0.5, 0.3 \rangle$	0.2
$Y_{S/X} \leftrightarrow T$	$\langle 0.3, 0.2 \rangle$	0.5	$\langle 0.4, 0.4 \rangle$	0.2
$k_S \leftrightarrow T$	$\langle 0, 0 \rangle$	1	$\langle 0.3, 0 \rangle$	0.7
$\mu \leftrightarrow k_S$	$\langle 0.2, 0 \rangle$	0.8	$\langle 0.2, 0.1 \rangle$	0.7
$Y_{S/X} \leftrightarrow \mu$	$\langle 0.2, 0.2 \rangle$	0.6	$\langle 0.3, 0.7 \rangle$	0
$k_S \leftrightarrow Y_{S/X}$	$\langle 0.5, 0 \rangle$	0.5	$\langle 0.1, 0.1 \rangle$	0.8

and saturation constants and J might be also considered as coincidences. The only one difference between both case studies is the relation between T and J – with higher μ in Case study 1 against zero value in Case study 2.

When considering the influence of convergence time T over the model parameters in both case studies, two coincidences are observed – higher μ in pairs between specific growth rates and T, and lower μ between $Y_{S/X}$ and T. The only one difference between both case studies is the relation between saturation constants and T – with zero value in Case study 1 against higher degrees of agreement in Case study 2.

The last group of examined correlations is between model parameters themselves in both considered case studies. Different model structure in both fermentation models complicates the extraction of some common correlations. Although that fact, there is a coincidence between $Y_{S/X}$ and specific growth rates with lower μ. Other relations are contradictory – higher μ between specific growth rates and saturation constants in Case study 2 against lower μ in Case study 1. And in opposite - higher μ between saturation constant and $Y_{S/X}$ in Case study 1 against lower μ in Case study 2. Only for a completeness it should be noted that higher μ has been observed between two specific growth rates and two saturation constants in Case study 2, while the lower μ is noticed between $Y_{S/X}$ and saturation constants.

It is interesting to note that during the investigation of $nind$ and $maxgen$ influence, there have been some pairs of considered criteria with reported degree of uncertainty. All these facts have an obvious explanation – as it can be seen from IM $A_{1(nind)}$ and $A_{1(maxgen)}$ for Case study 1, there are equal evaluations of saturation constant. In analogy, as seen from IM $A_{2(nind)}$ and $A_{2(maxgen)}$ there are equal values for optimization criterion in Case study 2. These facts logically causing the

Table 3: Results from the ICA in case of *S. cerevisiae* fed-batch fermentation process

Correlation	$nind$		$maxgen$	
	$\langle \mu, \nu \rangle$	π	$\langle \mu, \nu \rangle$	π
$T \leftrightarrow nind \,/\, maxgen$	$\langle 1, 0 \rangle$	0	$\langle 1, 0 \rangle$	0
$J \leftrightarrow nind \,/\, maxgen$	$\langle 0, 0.6 \rangle$	0.4	$\langle 0, 0.8 \rangle$	0.2
$\mu_{2S} \leftrightarrow nind \,/\, maxgen$	$\langle 0.8, 0.2 \rangle$	0	$\langle 0.7, 0.3 \rangle$	0
$\mu_{2E} \leftrightarrow nind \,/\, maxgen$	$\langle 0.9, 0.1 \rangle$	0	$\langle 0.7, 0.3 \rangle$	0
$Y_{S/X} \leftrightarrow nind \,/\, maxgen$	$\langle 0.1, 0.9 \rangle$	0	$\langle 0.3, 0.7 \rangle$	0
$k_S \leftrightarrow nind \,/\, maxgen$	$\langle 0.8, 0.2 \rangle$	0	$\langle 0.7, 0.3 \rangle$	0
$k_E \leftrightarrow nind \,/\, maxgen$	$\langle 0.9, 0.1 \rangle$	0	$\langle 0.8, 0.2 \rangle$	0
$T \leftrightarrow J$	$\langle 0, 0.6 \rangle$	0.4	$\langle 0, 0.8 \rangle$	0.2
$\mu_{2S} \leftrightarrow J$	$\langle 0.1, 0.5 \rangle$	0.4	$\langle 0.2, 0.7 \rangle$	0.1
$\mu_{2E} \leftrightarrow J$	$\langle 0, 0.6 \rangle$	0.4	$\langle 0.2, 0.7 \rangle$	0.1
$Y_{S/X} \leftrightarrow J$	$\langle 0.6, 0 \rangle$	0.4	$\langle 0.7, 0.2 \rangle$	0.1
$k_S \leftrightarrow J$	$\langle 0, 0.6 \rangle$	0.4	$\langle 0.2, 0.7 \rangle$	0.1
$k_E \leftrightarrow J$	$\langle 0.1, 0.5 \rangle$	0.4	$\langle 0.2, 0.7 \rangle$	0.1
$\mu_{2S} \leftrightarrow T$	$\langle 0.8, 0.2 \rangle$	0	$\langle 0.7, 0.3 \rangle$	0
$\mu_{2E} \leftrightarrow T$	$\langle 0.9, 0.1 \rangle$	0	$\langle 0.7, 0.3 \rangle$	0
$Y_{S/X} \leftrightarrow T$	$\langle 0.1, 0.9 \rangle$	0	$\langle 0.3, 0.7 \rangle$	0
$k_S \leftrightarrow T$	$\langle 0.8, 0.2 \rangle$	0	$\langle 0.7, 0.3 \rangle$	0
$k_E \leftrightarrow T$	$\langle 0.9, 0.1 \rangle$	0	$\langle 0.8, 0.2 \rangle$	0
$\mu_{2S} \leftrightarrow \mu_{2E}$	$\langle 0.9, 0.1 \rangle$	0	$\langle 1, 0 \rangle$	0
$\mu_{2S} \leftrightarrow k_S$	$\langle 0.8, 0.2 \rangle$	0	$\langle 1, 0 \rangle$	0
$\mu_{2E} \leftrightarrow k_S$	$\langle 0.9, 0.1 \rangle$	0	$\langle 1, 0 \rangle$	0
$\mu_{2S} \leftrightarrow k_E$	$\langle 0.7, 0.3 \rangle$	0	$\langle 0.5, 0.5 \rangle$	0
$\mu_{2E} \leftrightarrow k_E$	$\langle 0.8, 0.2 \rangle$	0	$\langle 0.5, 0.5 \rangle$	0
$k_S \leftrightarrow k_E$	$\langle 0.7, 0.3 \rangle$	0	$\langle 0.5, 0.5 \rangle$	0
$Y_{S/X} \leftrightarrow \mu_{2S}$	$\langle 0.1, 0.9 \rangle$	0	$\langle 0, 1 \rangle$	0
$Y_{S/X} \leftrightarrow \mu_{2E}$	$\langle 0, 1 \rangle$	0	$\langle 0, 1 \rangle$	0
$Y_{S/X} \leftrightarrow k_S$	$\langle 0.1, 0.9 \rangle$	0	$\langle 0, 1 \rangle$	0
$Y_{S/X} \leftrightarrow k_E$	$\langle 0.2, 0.8 \rangle$	0	$\langle 0.5, 0.5 \rangle$	0

uncertainty and makes difficult the process of decision making.

5 Conclusion

In this paper a new approach – InterCriteria Analysis – is applied, for establishing relations and dependencies between two of the main GAs parameters $nind$ and $maxgen$, convergence time, model accuracy and model parameters. Parameter identification of two fermentation processes – of bacteria *E. coli* and yeast *S. cerevisiae* is performed applying standard GA with different values for $nind$ and $maxgen$.

The results from ICA show some relations and dependencies that result from the physical

meaning of the model parameters on the one hand, and from stochastic nature of the considered metaheuristics on the other hand. Moreover, some additional knowledge is achieved for existing correlations, that will be useful for more accurately GA application.

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