

# Quality Assessment of Multi-population Genetic Algorithms Performance

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**Abstract**— The quality of performance of multi-population genetic algorithms (MpGA) has been assessed for the purposes of parameter identification of *S. cerevisiae* fed-batch cultivation. Intuitionistic fuzzy logic has been implemented aiming to derive intuitionistic fuzzy estimations of obtained model parameters. Three kinds of MpGA, differ from each other in the sequence of execution of main genetic operators, namely selection, crossover and mutation, have been assessed before and after the application of the recently developed procedure for purposeful model parameters genesis. Results obtained after the implementation of intuitionistic fuzzy logic for MpGA performances assessment have been compared and MpGA with a sequence selection and crossover after the procedure for purposeful model parameters genesis application has been distinguished as the fastest and quite reliable one.

**Index Terms**— Quality assessment, intuitionistic fuzzy logic, multi-population genetic algorithms, parameter identification, yeast fed-batch cultivation.

## 1 INTRODUCTION

Genetic algorithms (GA) [10] are one of the most representative examples of methods based on biological evolution. GA are inspired by Darwin's theory of "survival of the fittest" and they are based on the mechanics of natural selection and genetics. GA seek for the global optimal solution in complex multidimensional search space by simultaneously evaluating many points in the parameter space. Their properties such as hard problems solving, noise tolerance, easiness to interface and hybridize, make GA a suitable and quite workable tool especially for tasks which are not completely determined. Such a real challenge for researchers is the parameter identification of fermentation processes [1], [2], [12], [13], [14] which modeling is a specific task, rather difficult to be solved. The idea genetic algorithms to be tested as an alternative technique for parameters identification of fermentation process model has been provoked by the inability of conventional optimization methods to reach to a satisfactory solution [2], [13].

Goldberg [10] initially presents the standard single-population genetic algorithm (SGA) inspired by natural genetics, which searches for a global optimal solution using three main genetic operators in a sequence selection, crossover and mutation. More similar to nature is multi-population genetic algorithm (MpGA), since there many populations, called subpopulations, evolve independently from each other. After a certain number of generations (isolation time), a part of individuals are distributed between the subpopulations (migration).

According to [10], [11], working principle of standard MpGA is shown in the following nine-step procedure:

1. **[Start]**  
Generate  $k$  random subpopulations each of them with  $n$  chromosomes
2. **[Objective function]**  
Evaluate the objective function of each chromosome  $x$  in the subpopulation
3. **[Fitness function]**  
Find the fitness function of each chromosome  $x$  in the subpopulation
4. **[New population]**  
Create a new population by repeating following steps:
  - 4.1. **[Selection]**  
Select parent chromosomes from the subpopulation according to their fitness function
  - 4.2. **[Crossover]**  
Cross over the parents to form new offspring with a crossover probability
  - 4.3. **[Mutation]**  
Mutate new offspring at each locus with a mutation probability
5. **[Accepting]**  
Place new offspring in a new population
6. **[Replace]**  
Use new generated population for a further run of the algorithm
7. **[Migration]**  
Migration of individuals between the subpopulations after following isolation time
8. **[Test]**  
If the end condition is satisfied, stop and return the best solution in current population, else move to **Loop** step
9. **[Loop]**  
Go to **Fitness step**.

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Since the basic idea of GA is to imitate the mechanics of natural selection and genetics, one can make an analogy with the processes occurring in nature, saying that the probability one of the genetic operators to be executed before or after the other is comparable to the probability that processes to occur in a reverse order. Thus, following that idea, altogether six

modifications of MpGA have been developed and investigated towards model accuracy and algorithms convergence time. All considered MpGA have a similar structure and follow the nine-step procedure presented above, but differ from each other in the sequence of execution of the main genetic operators selection, crossover and mutation. The standard MpGA, originally presented in [10], is here denoted as MpGA\_SCM (coming from sequence selection, crossover, mutation). MpGA\_CMS (crossover, mutation, selection), MpGA\_SMC (selection, mutation, crossover) and MpGA\_MCS (mutation, crossover, selection) have been proposed in [6]. Another two kinds of MpGA, omitting mutation operator, namely MpGA-SC (selection, crossover) and MpGA\_CS (crossover, selection), are further developed [4] provoked by promising results obtained in SGA [3].

The sequence of algorithm steps in different kinds of MpGA, according to the presented above nine-step procedure, is as follows:

- **MpGA-SCM** 1, 2, 3, 4.1, 4.2, 4.3, 5, 6, 7, 8, 9
- **MpGA-CMS** 1, 2, 3, 4.2, 4.3, 4.1, 5, 6, 7, 8, 9
- **MpGA-SMC** 1, 2, 3, 4.1, 4.3, 4.2, 5, 6, 7, 8, 9
- **MpGA-MCS** 1, 2, 3, 4.3, 4.2, 4.1, 5, 6, 7, 8, 9
- **MpGA-SC** 1, 2, 3, 4.1, 4.2, 5, 6, 7, 8, 9
- **MpGA-CS** 1, 2, 3, 4.2, 4.1, 5, 6, 7, 8, 9

The subject of current investigation are three of MpGA modifications with the selection operator on first place, namely MpGA-SCM, MpGA-SMC and MpGA-SC.

The evaluation of the quality of any algorithm performance could be based on some representative criteria such as the objective function value and the algorithm convergence time. As an alternative for assessing the quality of different algorithms intuitionistic fuzzy logic (IFL) might be applied for various purposes. IFL is based on the construction of degrees of validity and non-validity which requires the algorithms to be performed in two different intervals of model parameters variation. One interval could be so-called "broad" range known from the literature [14]. The other one, called "narrow" range, is user-defined and might be obtained using different criteria - e.g. based on the minimum and maximum values, or on the average ones, or after the implementation of the recently developed procedure for purposeful model parameters genesis [5].

The aim of this study is intuitionistic fuzzy estimations to be applied for assessing the quality of performance of three different kinds of MpGA, namely MpGA-SCM, MpGA-SMC and MpGA-SC, for the purposes of parameter identification of *S. cerevisiae* fed-batch cultivation. Aiming to save decreased convergence time while keeping or even improving model accuracy, intuitionistic fuzzy estimations overbuild the results obtained after procedure of purposeful model parameters genesis.

## 2 BACKGROUND

### 2.1 Procedure for purposeful model parameter genesis

The procedure for purposeful model parameter genesis (PMPG) has been originally developed in [5] and firstly applied for parameter identification of *S. cerevisiae* using simple genetic algorithms. Due to the stochastic nature genetic algo-

gorithms, a great number of algorithm runs have to be executed if one would like to obtain reliable results no matter of the object considered. Firstly, the genetic algorithm searches for solutions of model parameters in wide but reasonably chosen boundaries according to the statements in [14] - so-called "broad" range. When results from many algorithms executions were accumulated and analyzed, they showed that the values of model parameters can be assembled and predefined boundaries of model parameters could be restricted. This is the main idea of PMPG, which results in the defining of more appropriate boundaries for variation of the model parameters values. The procedure application leads to decrease convergence time while at least saving or even improving the model accuracy.

### 2.2 Intuitionistic fuzzy estimations

In intuitionistic fuzzy logic (IFL) [7], [8] if  $p$  is a variable then its truth-value is represented by the ordered couple

$$V(p) = \langle M(p), N(p) \rangle, \quad (1)$$

so that  $M(p), N(p), M(p) + N(p) \in [0, 1]$ , where  $M(p)$  and  $N(p)$  are degrees of validity and of non-validity of  $p$ . These values can be obtained applying different formula depending on the problem considered.

For the purpose of this investigation the degrees of validity/non-validity can be obtained as follows:

$$M(p) = \frac{m}{u}, N(p) = 1 - \frac{n}{u}, \quad (2)$$

where  $m$  is the lower boundary of the "narrow" range;  $u$  - the upper boundary of the "broad" range;  $n$  - the upper boundary of the "narrow" range.

If there is a database collected having elements with the form  $\langle p, M(p), N(p) \rangle$ , different new values for the variables can be obtained. In case of considered here three records in the database, the following new values can be obtained:

$$V_{strong\_opt} = \langle M_1(p) + M_2(p) + M_3(p) - M_1(p)M_2(p) - M_1(p)M_3(p) - M_2(p)M_3(p) + M_1(p)M_2(p)M_3(p), N_1(p)N_2(p)N_3(p) \rangle \quad (3)$$

$$V_{opt} = \langle \max(M_1(p), M_2(p), M_3(p)), \min(N_1(p), N_2(p), N_3(p)) \rangle, \quad (4)$$

$$V_{aver} = \langle (M_1(p) + M_2(p) + M_3(p))/3, (N_1(p) + N_2(p) + N_3(p))/3 \rangle, \quad (5)$$

$$V_{pes} = \langle \min(M_1(p), M_2(p), M_3(p)), \max(N_1(p), N_2(p), N_3(p)) \rangle, \quad (6)$$

$$V_{strong\_pes} = \langle M_1(p)M_2(p)M_3(p), N_1(p) + N_2(p) + N_3(p) - N_1(p)N_2(p) - N_1(p)N_3(p) - N_2(p)N_3(p) + N_1(p)N_2(p)N_3(p) \rangle \quad (7)$$

Therefore, for each  $p$

$$V_{strong\_pes}(p) \leq V_{pes}(p) \leq V_{aver}(p) \leq V_{opt}(p) \leq V_{strong\_opt}(p).$$

### 2.3 Procedure for genetic algorithms quality assessment applying IFL

As mentioned above, the implementation of IFL for assessment of genetic algorithms performance quality requires construction of degrees of validity and non-validity in two different intervals of model parameters variation: so-called "broad" range as known from the literature and so-called "narrow" range which is user-defined. Here the authors applied a procedure for assessment of algorithm quality performance (AAQP) implementing IFL. The procedure starts with performance of a number of runs of each of the algorithms, object of the investigation in both "broad" and "narrow" ranges of model parameters. Then the average values of the objective function, algorithms convergence time and each of the model parameters for each one of the ranges and each one of the investigated algorithms are obtained. According to (2), degrees of validity/non-validity for each of the algorithms, object of the investigation, are determined. Then, in case of three objects, strong optimistic, optimistic, average, pessimistic and strong pessimistic values are calculated for each one of the model parameters according to (3)-(7). Next determined in such way values are assigned to each of the model parameters for each of the ranges for each of the algorithms. Finally, based on these assigns, the quality of each one of considered algorithm is assessed.

### 2.4 Mathematical model of *S. cerevisiae* fed-batch cultivation

Experimental data of *S. cerevisiae* fed-batch cultivation is obtained in the *Institute of Technical Chemistry - University of Hannover, Germany* [13]. The cultivation of the yeast *S. cerevisiae* is performed in a 2 l reactor, using a Schatzmann medium. Glucose in feeding solution is 35 g/l. The temperature was controlled at 30°C, the pH at 5.5. The stirrer speed was set to 1200 rpm. Biomass and ethanol were measured off-line, while substrate (glucose) and dissolved oxygen were measured on-line.

Mathematical model of *S. cerevisiae* fed-batch cultivation is commonly described as follows, according to the mass balance [13]:

$$\frac{dX}{dt} = \mu X - \frac{F}{V} X \quad (8)$$

$$\frac{dS}{dt} = -q_s X + \frac{F}{V} (S_{in} - S) \quad (9)$$

$$\frac{dE}{dt} = q_E X - \frac{F}{V} E \quad (10)$$

$$\frac{dO_2}{dt} = -q_{O_2} X + k_L^{O_2} a (O_2^* - O_2) \quad (11)$$

$$\frac{dV}{dt} = F, \quad (12)$$

where  $X$  is the concentration of biomass, [g/l];  $S$  - concentration of substrate (glucose), [g/l];  $E$  - concentration of ethanol, [g/l];  $O_2$  - concentration of oxygen, [%];  $O_2^*$  - dissolved oxygen saturation concentration, [%];  $F$  - feeding rate, [l/h];  $V$  - volume of bioreactor, [l];  $k_L^{O_2} a$  - volumetric oxygen transfer coefficient, [1/h];  $S_{in}$  - initial glucose concentration in the

feeding solution, [g/l];  $\mu$ ,  $q_s$ ,  $q_E$ ,  $q_{O_2}$  - specific growth/utilization rates of biomass, substrate, ethanol and dissolved oxygen, [1/h]. All functions are continuous and differentiable.

The fed-batch cultivation of *S. cerevisiae* considered here is characterized by keeping glucose concentration equal to or below its critical level ( $S_{crit} = 0.05$  g/l), sufficient dissolved oxygen  $O_2 \geq O_{2crit}$  ( $O_{2crit} = 18\%$ ) and availability of ethanol in the broth. This state corresponds to the so called mixed oxidative state (FS II) according to functional state modeling approach [13]. Hence, specific rates in Eqs. (8)-(12) are:

$$\mu = \mu_{2S} \frac{S}{S + k_s} + \mu_{2E} \frac{E}{E + k_E}, \quad q_s = \frac{\mu_{2S}}{Y_{SX}} \frac{S}{S + k_s},$$

$$q_E = -\frac{\mu_{2E}}{Y_{EX}} \frac{E}{E + k_E}, \quad q_{O_2} = q_E Y_{OE} + q_s Y_{OS}, \quad (13)$$

where  $\mu_{2S}$ ,  $\mu_{2E}$  are the maximum growth rates of substrate and ethanol, [1/h];  $k_s$ ,  $k_E$  - saturation constants of substrate and ethanol, [g/l];  $Y_{ij}$  - yield coefficients, [g/g]; and all model parameters fulfill the non-zero division requirement.

As an optimization criterion, mean square deviation between the model output and the experimental data obtained during cultivation has been used:

$$J = \sum (Y - Y^*)^2 \rightarrow \min, \quad (14)$$

where  $Y$  is the experimental data,  $Y^*$  - model predicted data,  $Y = [X, S, E, O_2]$ .

### 3 MPGA QUALITY ASSESSMENT

The procedure for purposeful model genesis has been applied to parameter identification of *S. cerevisiae* fed-batch cultivation using three kinds of MpGA. Following model (8)-(13) of *S. cerevisiae* fed-batch cultivation, nine model parameters have been estimated altogether, applying consequently MpGA\_SCM, MpGA\_SMC and MpGA\_SC. The values of GA parameters and type of genetic operators in MpGA considered here are tuned according to [6]. GA is terminated when a certain number of generations is fulfilled, in this case 100. Scalar relative error tolerance *RelTol* is set to  $1e^{-4}$ , while the vector of absolute error tolerances (all components) *AbsTol* - to  $1e^{-5}$ . Parameter identification of the model (8)-(12) has been performed using *Genetic Algorithm Toolbox* [9] in *Matlab 7* environment. All the computations are performed using a PC Intel Pentium 4 (2.4 GHz) platform running Windows XP.

The quality of MpGA performance is assessed before and after application of PMPG, that means that the "narrow" range is obtained applying PMPG. The obtained results are firstly analyzed according to achieved objective function values and convergence time. For each of MpGA investigated here the minimum and the maximum of the objective function are determined, and the levels of performance are constructed according to PMPG [5]. For each of the levels, obtained in such a way, the minimum, maximum and average values of each model parameter have been determined. The new boundaries of the model parameters are constructed in a way that the new minimum is lower but close to the minimum of the top level, and the new maximum is higher but close to the maximum of the top level. Table 1 presents previously used "broad"

boundaries for each model parameter according to [14] as well as new boundaries proposed based on PMPG when applying MpGA. Additionally, Table 1 consists of intuitionistic fuzzy estimations, obtained based on (2).

Table 1. Model parameters boundaries for MpGA

			$\mu_{2S}$	$\mu_{2E}$	$k_s$	$k_E$	$Y_{SX}$	$Y_{EX}$	$k_L^{O_2}a$	$Y_{OS}$	$Y_{OE}$
MpGA_SCM	previously used	LB	0.90	0.05	0.08	0.50	0.30	1.00	0.001	0.001	0.001
		UB	1.00	0.15	0.15	0.80	10	10	300	1000	1000
	advisable after procedure application	LB	0.9	0.11	0.13	0.7	0.39	1.5	60	470	220
		UB	0.94	0.15	0.15	0.8	0.42	2	120	930	810
	degrees of validity of p	$M_1(p)$	0.90	0.73	0.87	0.88	0.04	0.15	0.20	0.47	0.22
	degree of non-validity of p	$N_1(p)$	0.06	0.00	0.00	0.00	0.96	0.80	0.60	0.07	0.19
MpGA_SMC	previously used	LB	0.90	0.05	0.08	0.50	0.30	1.00	0.001	0.001	0.001
		UB	1.00	0.15	0.15	0.80	10	10	300	1000	1000
	advisable after procedure application	LB	0.9	0.11	0.14	0.7	0.4	1.5	60	480	20
		UB	0.94	0.14	0.15	0.8	0.42	2	120	950	710
	degrees of validity of p	$M_2(p)$	0.90	0.73	0.93	0.88	0.04	0.15	0.20	0.48	0.02
	degree of non-validity of p	$N_2(p)$	0.06	0.07	0.00	0.00	0.96	0.80	0.60	0.05	0.29
MpGA_SC	previously used	LB	0.90	0.05	0.08	0.50	0.30	1.00	0.001	0.001	0.001
		UB	1.00	0.15	0.15	0.80	10	10	300	1000	1000
	advisable after procedure application	LB	0.90	0.11	0.13	0.70	0.40	1.40	50	420	480
		UB	0.92	0.14	0.15	0.80	0.42	2.00	120	900	710
	degrees of validity of p	$M_3(p)$	0.90	0.73	0.87	0.88	0.04	0.14	0.17	0.42	0.48
	degree of non-validity of p	$N_3(p)$	0.08	0.07	0.00	0.00	0.96	0.80	0.60	0.10	0.29

Table 2. Prognoses for MpGA performance

	$\mu_{2S}$		$\mu_{2E}$		$k_s$		$k_E$		$Y_{SX}$		$Y_{EX}$		$k_L^{O_2}a$		$Y_{OS}$		$Y_{OE}$	
	LB	UB	LB	UB	LB	UB	LB	UB	LB	UB	LB	UB	LB	UB	LB	UB	LB	UB
$V_{strong\_opt}$	1.00	1.00	0.15	0.15	0.15	0.15	0.80	0.80	1.14	1.21	3.79	4.88	140	235.20	840.15	999.65	602.51	984.02
$V_{opt}$	0.90	0.94	0.11	0.15	0.14	0.15	0.70	0.80	0.40	0.42	1.50	2.00	60	120	480	950	480	810
$V_{ave}$	0.90	0.93	0.11	0.14	0.13	0.15	0.70	0.80	0.40	0.42	1.47	2.00	56.67	120	456.67	926.67	240	743.33
$V_{pes}$	0.90	0.92	0.11	0.14	0.13	0.15	0.70	0.80	0.39	0.42	1.40	2.00	50	120	420	900	20	710
$V_{strong\_pes}$	0.73	0.81	0.06	0.13	0.11	0.15	0.54	0.80	0.00	0.00	0.03	0.08	2.00	19.20	94.75	795.15	2.11	408.32

Table 2 presents the boundaries (low LB and up UB) for the strong optimistic, optimistic, average, pessimistic and strong pessimistic prognoses for the performances of MpGA algorithm, obtained based on intuitionistic fuzzy estimations (2) and formula (3)-(7).

Investigated here three kinds of MpGA have been again applied for parameter identification of *S. cerevisiae* fed-batch cultivation involving newly proposed according to Table 1 boundaries. Several runs have been performed in order reliable results to be obtained. Table 3 presents the average values of the objective function, convergence time and model parameters when MpGA\_SCM, MpGA\_SMC and MpGA\_SC have been executed in "broad" and "narrow" ranges.

Table 3. Results from model parameter identification before and after PMPG

Parameter	MpGA_SCM		MpGA_SMC		MpGA_SC	
	before PMPG	after PMPG	before PMPG	after PMPG	before PMPG	after PMPG
$J$	0.0210	0.0221	0.0220	0.0221	0.0221	0.0221
CPU time, s	98.76	92.61	111.78	91.36	99.12	90.11
$\mu_{2S}$ 1/h	0.92	0.90	0.90	0.90	0.92	0.91
$\mu_{2E}$ 1/h	0.13	0.14	0.14	0.14	0.14	0.14
$k_{sp}$ g/l	0.15	0.15	0.15	0.15	0.14	0.15
$k_{ps}$ g/l	0.80	0.80	0.80	0.80	0.78	0.80
$Y_{SX}$ g/g	0.41	0.40	0.40	0.40	0.40	0.40
$Y_{EX}$ g/g	1.72	1.89	1.87	1.83	1.90	1.89
$k_L^{O_2}a$ , 1/h	92.78	88.87	118.45	94.67	96.78	88.69
$Y_{OS}$ g/g	729.79	702.24	939.52	755.45	762.18	704.36
$Y_{OE}$ g/g	508.50	411.53	664.08	452.11	558.26	451.65

It is worth to note that in three considered here kinds of MpGA, running of algorithms in “narrow” range leads to expecting decrease of the convergence time while saving the high model accuracy, as it was shown in the case of SGA and also expected here. Running MpGA in “narrow” range reduces the computation time 1.07, 1.22 and 1.10 times when MpGA\_SCM, MpGA\_SMC and MpGA\_SC have been respectively applied. In addition the results obtained in the “narrow” range hit the top level of performance, thus showing good effectiveness of all considered here kinds of MpGA.

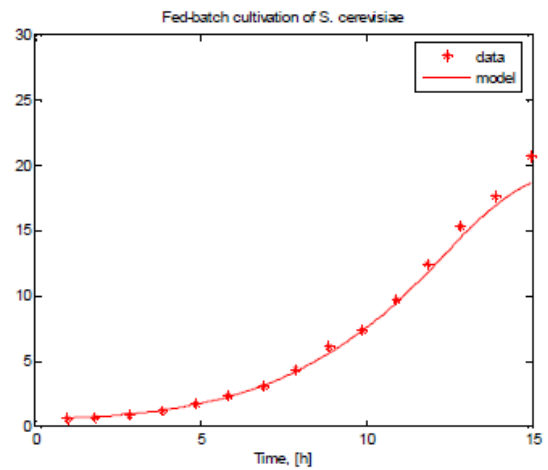
Table 4 lists the number and type of the estimations assigned to each of the parameters for three considered here kinds of MpGA, applied and before and after the PMPG.

Table 4. Model parameter estimations before and after PMPG

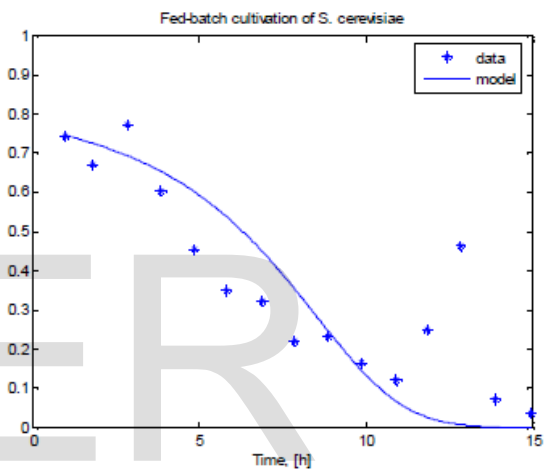
	MpGA_SCM		MpGA_SMC		MpGA_SC	
	before PMPG	after PMPG	before PMPG	after PMPG	before PMPG	after PMPG
<i>strong_opt</i>	2	2	4	2	0	2
<i>opt</i>	7	6	5	6	9	6
<i>aver</i>	0	1	0	1	0	1
<i>pes</i>	0	0	0	0	0	0
<i>strong_pes</i>	0	0	0	0	0	0

As seen from Table 4, there are no any strong pessimistic and pessimistic prognoses. One of the cases significantly stands out of the others with 4 strong optimistic and 5 optimistic prognoses - this is the case of MpGA\_SMC in “broad” range. Moreover, this is the case with the highest model accuracy achieved, but in the same time this is the slowest one case among all considered here. It is quite interesting that all MpGA in “narrow” range have been assessed absolutely equally - with 2 strong optimistic, followed by 6 optimistic and 1 average prognoses. In these three distinguished as more reliable cases, the value of the objective function is almost equal to the lowest one that means they are with the highest achieved degree of accuracy. Among them the fastest one is the case of MpGA\_SC. Thus, based on the intuitionistic fuzzy estimations of the model parameters and further constructed prognoses, MpGA\_SC in “narrow” range is distinguished as an acceptable compromise - not the highly assessed, but the fastest one, if one would like to obtained results with a high level of relevance and for less computational time.

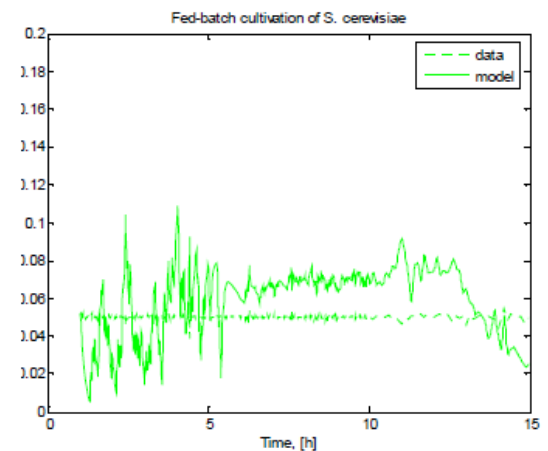
Fig. 1 shows results from experimental data and model prediction, respectively, for biomass, ethanol, substrate and dissolved oxygen when MpGA\_SC after the procedure for the purposeful model parameter genesis has been applied.



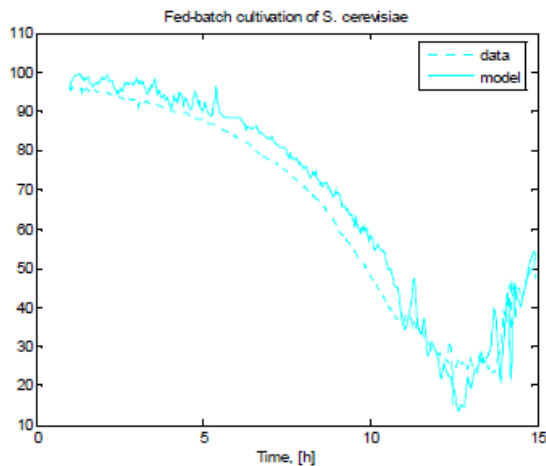
a) biomass concentration



b) ethanol concentration



c) substrate concentration



d) dissolved oxygen concentration

Fig. 1 Model prediction compared to experimental data when MpGA\_SC in "narrow" range has been applied

Overall, obtained results show the workability and the effectiveness of the procedure for purposeful model parameter genesis.

#### 4 CONCLUSION

Intuitionistic fuzzy logic has been implemented in this investigation in order to assess the genetic algorithms quality performance for the purposes of parameter identification of *S. cerevisiae* fed-batch cultivation. Aiming at keeping obtained promising results, namely less convergence time at saved and even improved model accuracy, intuitionistic fuzzy logic overbuilds the results from the application of recently developed procedure for purposeful model parameter genesis. This procedure has been here applied to three kinds of MpGA differ from each other in the sequence of execution of main genetic operators. Intuitionistic fuzzy logic has been implemented to obtain intuitionistic fuzzy estimations of model parameters and further to construct strong optimistic, optimistic, average, pessimistic and strong pessimistic prognoses for the algorithms performances. Thus, based on the intuitionistic fuzzy estimations of the model parameters and further constructed prognoses, the following summaries can be outlined: 1) the highly assessed MpGA\_SMC in "broad" range is the slowest one, thus getting the user to make a decision between reliability and speed; 2) among the three equal performances of MpGA in "narrow" range, MpGA with a sequence selection and crossover and omitting the mutation is the fastest one. As an acceptable compromise, MpGA\_SC in "narrow" range is distinguished as not the highly assessed, but the fastest one, if one would like to obtained results with a high level of relevance and for less computational time.

Presented here IFL based "cross-evaluation" of three kinds of MpGA demonstrates the workability of intuitionistic fuzzy estimations to assist in assessment of quality of algorithms performance. The estimations based on intuitionistic fuzzy logic might be considered as an appropriate tool for reliable assessment for genetic algorithm parameters, for different op-

timization algorithms as well as to be applied to various objects of parameter identification.

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