

Multi-population Genetic Algorithm Quality Assessment Implementing Intuitionistic Fuzzy Logic

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□

Abstract— Intuitionistic fuzzy logic has been implemented in this investigation aiming to derive intuitionistic fuzzy estimations of *S. cerevisiae* fed-batch cultivation model parameters obtained using multi-population genetic algorithm (MpGA). Performances of the examined algorithm have been tested before and after the application of the procedure for purposeful model parameters genesis for three different values of generation gap which is the most sensitive genetic algorithms parameter toward convergence time. Results obtained after the implementation of intuitionistic fuzzy logic for the algorithm performance assessment have been compared and MpGA with GGAP = 0.1 after the purposeful model parameters genesis procedure application has been distinguished as the fastest and the most reliable one.

INTRODUCTION

GENETIC algorithms (GA), based on biological evolution, are preferred and widely used technique for global optimization in various areas of science. Some 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 an intractable problem and a real challenge for researchers is parameter identification of fermentation models [1-5]. Modeling of fermentation processes (FP), known as complex, dynamic systems with interdependent and time-varying process variables, is a specific task, rather difficult to be solved. Inability of conventional optimization methods to reach to a satisfactory solution for model parameters identification of FP [1, 4] provokes idea genetic algorithms to be tested as an alternative technique.

A standard single-population genetic algorithm (SGA) initially presented in Goldberg [6] and inspired by natural genetics searches a global optimal solution using three main genetic operators in a sequence selection, crossover and mutation. Multi-population genetic algorithm (MpGA) is more similar to nature than SGA since in it many populations, called subpopulations, evolve independently from each other. After a certain number of generations a part of individuals are distributed between the subpopulations (migration).

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According to [6] structure of standard MpGA could be shortly presented below in eight steps:

- Step 1: **[Start]** Generate k random subpopulations each of them with n chromosomes
- Step 2: **[Object function]** Evaluate the object function of each chromosome n in the subpopulations
- Step 3: **[Fitness function]** Evaluate the fitness function of each chromosome n in the subpopulations
- Step 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
- Step 5: **[Replace]** Use new generated loop in a old subpopulation for a further run of the algorithm
- Step 6: **[Migration]** Migration of individuals between the subpopulations after following isolation time
- Step 7: **[Test]** If the end condition is satisfied, stop and return the best solution in current population
- Step 8: **[Loop]** go to Step 2.

There are many operators, functions, parameters and settings in GA that might be improved and implemented differently in various problems [6, 7]. In [7] generation gap (GGAP) (the portion of the population that is replaced each generation) has been investigated for four different values and has been distinguished as the most sensitive genetic algorithm parameter towards convergence time. Up to almost 40% of the algorithm calculation time can be saved in the case of MpGA application using GGAP = 0.5 instead of 0.9 without loss of model accuracy. Obtained promising results in [7] provoke the idea of subsequent reduction of the generation gap value. Thus the topic of the present work is to be investigated the MpGA quality of performance for three different values of generation gap – GGAP = 0.9, GGAP = 0.5 and GGAP = 0.1.

The quality of MpGA performance could be appraised by some representative criteria such as the objective function value and the algorithm convergence time. Intuitionistic fuzzy logic (IFL) is an alternative for assessing the quality of different algorithms for various purposes. The main goal is the degrees of uncertainty and discrepancy to be lower than

measurement error thus inducing to be obtained parameters values of a high degree of accuracy. However, for constructing the degree of uncertainty and discrepancy it is required the algorithms to be performed in two different intervals of model parameters variation. One interval could be determined as so-called "broad range" known from the literature [8]. The other interval could be defined based on some criterion for shrinking the range – e.g. based on the average values or when the procedure for purposeful model parameters genesis presented in [8] has been implemented.

The aim of the study is intuitionistic fuzzy estimations to be applied for assessing the multi-population genetic algorithm implemented in parameter identification of *S. cerevisiae* fed-batch cultivation with three different values of generation gap. 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.

INTUITIONISTIC FUZZY ESTIMATIONS

In intuitionistic fuzzy logic [9] 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 using different formula depending on the problem considered.

In this investigation the degrees of validity/non-validity can be obtained, e.g., by the following formula:

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

where m is the lower boundary advisable after the procedure application; u – the upper boundary of the "broad range"; n – the upper boundary advisable after the procedure application [8].

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

- strong optimistic

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

- optimistic

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

- average

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

- pessimistic

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

- strong pessimistic

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

PROCEDURE FOR PURPOSEFUL MODEL PARAMETER GENESIS

Due to the stochastic nature of GA, a great number of algorithm runs have to be executed in order to obtain reliable results in parameter identification of a fermentation process model. When results were analyzed, they showed that the values of model parameters can be assembled and predefined boundaries could be restricted. Thus the idea for purposeful model parameter genesis (PMPG) has been created.

The procedure for purposeful model parameter genesis has been originally developed for single-population genetic algorithms [8] consisting of six steps, which are shortly outlined below for completeness:

Step 1: Performance of N runs of genetic algorithms.

Step 2: Determination of the minimum and maximum values of the objective function.

Step 3: Determination of the top level (TL), middle level (ML) and low level (LL) of performance with corresponding low boundary (LB) and up boundary (UB) following the scheme:

3.1 Determination of discrimination number Δ by

$$\Delta = \frac{\max J - \min J}{3}$$

3.2 Determination of level boundaries

Top level low boundary (TL_LB)	min J
Top level up boundary (TL_UB)	min J + $\Delta - \epsilon$
Middle level low boundary (ML_LB)	min J + Δ
Middle level up boundary (ML_UB)	min J + 2 $\Delta - \epsilon$
Low level low boundary (LL_LB)	min J + 2 Δ
Low level up boundary (LL_UB)	max J

where ϵ is a small number, ensuring the difference between levels.

Step 4: Determination of minimum, maximum and average value for each parameter at each level.

Step 5: Determination of new intervals of model parameters variations, basing on averaged values.

Step 6: Run of the genetic algorithm with intervals, determined in Step 5.

This is a stepwise procedure that passes through all the six steps described above, not omitting any of them and without cycles.

MPGA QUALITY ASSESSMENT FOR PARAMETER IDENTIFICATION 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 [1]. 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 [1]:

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

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

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

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

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

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]; μ , 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 [1]. 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 μ_{2S} , μ_{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:

$$J = \sum_{i=1}^4 (Y_i - Y_i^*)^2 \rightarrow \min, \quad (14)$$

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

The procedure for purposeful model genesis has been applied to parameter identification of *S. cerevisiae* fed-batch cultivation using MpGA. Following model (8)-(13) of *S. cerevisiae* fed-batch cultivation, nine model parameters have been estimated altogether, applying MpGA with three different GGAP values. GGAP is the most sensitive genetic algorithms parameter towards the algorithms convergence time [7]. The values of other GA parameters and type of genetic operators in MpGA considered here are tuned according to [7]. 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 [10] 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 procedure for purposeful model parameter genesis. For each value of GGAP, thirty runs of MpGA have been executed. Table I presents obtained results before applying procedure for purposeful model parameter genesis.

TABLE I.
LEVELS OF PERFORMANCE OF MPGA BEFORE PMPG APPLICATION

MpGA	Objective function		Levels of performance		Average convergence time
	min J	max J	TL_LB	TL_UB	
GGAP = 0.9	min J	0.0220	TL_LB	0.0220	159.67
			TL_UB	0.0221	
	max J	0.0222	LL_LB	0.0221	
			LL_UB	0.0222	
GGAP = 0.5	min J	0.0221	TL_LB	0.0221	98.96
			TL_UB	0.0221	
	max J	0.0222	LL_LB	0.0222	
			LL_UB	0.0222	
GGAP = 0.1	min J	0.0221	TL_LB	0.0221	34.15
			TL_UB	0.0222	
	max J	0.0223	LL_LB	0.0223	
			LL_UB	0.0223	

The obtained results are analyzed according to achieved objective function values. For each GGAP value the minimum and the maximum of the objective function are determined, and the levels of performance according to the procedure [8] have been constructed. According to the values of obtained objective function there are only two levels of performance in MpGA. The best results hit the interval $[\min J; \min J + \Delta - \varepsilon]$ and they the top level of

MpGA performance has been formed. The worst solutions for the objective function fall in the interval $[\min J + \Delta; \max J]$ and thus the low level of performance has been created.

For each of the levels, constructed in such a way, the minimum, maximum and average values of each model parameter have been determined. Table II presents these values only for the top levels, according to Table I.

TABLE II.
MODEL PARAMETERS VALUES FOR THE TOP LEVELS

MpGA		μ_{2S}	μ_{2E}	k_S	k_E	Y_{SX}	Y_{EX}	$k_L^{O_2-a}$	Y_{OS}	Y_{OE}
GGAP = 0.9	min	0.9000	0.1104	0.1465	0.7999	0.4002	1.4678	62.727	498.511	11.1317
	max	0.9235	0.1461	0.1500	0.8000	0.4177	1.9747	116.435	919.304	903.614
	avrg	0.9060	0.1262	0.1492	0.7999	0.4088	1.6867	83.021	659.883	308.790
GGAP = 0.5	min	0.9002	0.1161	0.1313	0.7979	0.3987	1.5408	61.129	473.491	228.867
	max	0.9378	0.1438	0.1500	0.8000	0.4182	1.9290	118.423	921.284	809.902
	avrg	0.9155	0.1283	0.1453	0.7998	0.4097	1.7212	92.780	656.597	508.501
GGAP = 0.1	min	0.9131	0.1068	0.1257	0.7540	0.3988	1.4308	64.118	514.4939	229.0956
	max	0.9667	0.1348	0.1496	0.8000	0.4236	1.8399	117.223	900.8675	630.1261
	avrg	0.9382	0.1191	0.1388	0.7927	0.4093	1.5843	97.800	757.586	493.1139

TABLE III.
MODEL PARAMETERS BOUNDARIES FOR MPGA

MpGA			μ_{2S}	μ_{2E}	k_S	k_E	Y_{SX}	Y_{EX}	$k_L^{O_2-a}$	Y_{OS}	Y_{OE}
GGAP = 0.9	previously used	LB	0.9	0.05	0.08	0.5	0.3	1	0.001	0.001	0.001
		UB	1	0.15	0.15	0.8	10	10	300	1000	1000
	advisable after procedure application	LB	0.90	0.11	0.14	0.79	0.40	1.4	60	490	10
		UB	0.93	0.15	0.15	0.80	0.42	2	120	920	910
	degrees of validity of p	$M_1(p)$	0.90	0.73	0.93	0.99	0.13	0.14	0.20	0.49	0.01
degree of non-validity of p	$N_1(p)$	0.07	0.00	0.00	0.00	0.86	0.80	0.60	0.08	0.09	
GGAP = 0.5	previously used	LB	0.9	0.05	0.08	0.5	0.3	1	0.001	0.001	0.001
		UB	1	0.15	0.15	0.8	10	10	300	1000	1000
	advisable after procedure application	LB	0.90	0.11	0.13	0.79	0.39	1.5	60	470	220
		UB	0.94	0.15	0.15	0.80	0.42	2	120	930	810
	degrees of validity of p	$M_2(p)$	0.90	0.73	0.87	0.99	0.13	0.15	0.20	0.47	0.22
degree of non-validity of p	$N_2(p)$	0.06	0.13	0.00	0.00	0.86	0.80	0.60	0.07	0.19	
GGAP = 0.1	previously used	LB	0.9	0.05	0.08	0.5	0.3	1	0.001	0.001	0.001
		UB	1	0.15	0.15	0.8	10	10	300	1000	1000
	advisable after procedure application	LB	0.91	0.10	0.12	0.75	0.39	1.4	60	510	220
		UB	0.97	0.14	0.15	0.80	0.43	1.9	120	910	640
	degrees of validity of p	$M_3(p)$	0.91	0.67	0.80	0.94	0.13	0.13	0.20	0.50	0.21
degree of non-validity of p	$N_3(p)$	0.03	0.00	0.00	0.00	0.86	0.80	0.60	0.09	0.36	

TABLE IV.
PROGNOSSES FOR MPGA PERFORMANCE

	μ_{2S}		μ_{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	1.03	1.10	3.64	4.88	146.40	235.20	864.85	999.50	397.68	993.84
V_{opt}	0.91	0.97	0.11	0.15	0.14	0.15	0.79	0.80	0.40	0.43	1.50	2.00	60.00	120.00	500.00	930.00	220	910.00
V_{aver}	0.90	0.95	0.11	0.14	0.13	0.15	0.78	0.80	0.39	0.42	1.40	2.00	60.00	120.00	486.67	920.00	150	786.67
V_{pes}	0.90	0.93	0.10	0.13	0.12	0.15	0.75	0.80	0.39	0.42	1.30	2.00	60.00	120.00	470.00	910.00	10	640.00
V_{strong_pes}	0.74	0.85	0.05	0.13	0.10	0.15	0.73	0.80	0.01	0.01	0.03	0.08	2.40	19.20	115.15	778.60	0.48	471.74

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 III presents previously used “wide” boundaries for each model parameter according to [8] as well as new boundaries proposed based on the procedure for purposeful model parameter genesis when applying MpGA. Additionally Table III consists of intuitionistic fuzzy estimations, obtained based on (2) as described in Section II.

Table IV 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 MpGA has been again applied for parameter identification of *S. cerevisiae* fed-batch cultivation involving newly proposed according to Table III boundaries at GGAP = 0.9, GGAP = 0.5 and GGAP = 0.1. Several runs have been performed in order reliable results to be obtained. Table V presents the average values of the objective function and computation time of MpGA after application of purposeful model parameter genesis. The applied procedure for model parameter genesis reduces the computation time of MpGA with 6 to almost 10% but saving the model accuracy. In addition the results hit the top level of presentation and have one and same reduced objective function, thus showing good effectiveness of proposed procedure for purposeful model parameter genesis when MpGA is applied.

TABLE V.
LEVELS OF PERFORMANCE OF MPGA AFTER APPLICATION OF PURPOSEFUL MODEL PARAMETER GENESIS

MpGA	Objective function		Levels of performance		Average convergence time
			TL_LB	0.0221	
GGAP = 0.9	min J = max J	0.0221	TL_LB	0.0221	148.91
GGAP = 0.5	min J = max J	0.0221	TL_LB	0.0221	90.51
GGAP = 0.1	min J = max J	0.0221	TL_LB	0.0221	32.13

Table VI presents the average values of the objective function, computation time and model parameters when MpGA has been executed at three investigated here values of GGAP before and after the application of the purposeful model parameter genesis. Table VII lists the estimations assigned to the each of the parameters concerning Table IV for the three values of GGAP and before and after the PMPG application.

As seen form Table VII, there are no any strong pessimistic and pessimistic prognoses. In four of the cases there are 4 strong optimistic prognoses, and in three of them the next 5 prognoses are optimistic – these are the cases of GGAP = 0.5 before and after PMPG and GGAP = 0.1 after PMPG. In these three distinguished the most reliable cases, the value of the objective function is equal to the lowest one

that means they are with the highest achieved degree of accuracy. But if one compares the time, the MpGA with GGAP = 0.1 after PMPG is about three times faster than MpGA with GGAP = 0.5 before and after PMPG and about 5 times faster than the slowest case of GGAP = 0.9 before PMPG.

TABLE VI.
RESULTS FROM MODEL PARAMETER IDENTIFICATION BEFORE AND AFTER PMPG

Parameter	GGAP = 0.9		GGAP = 0.5		GGAP = 0.1	
	Before PMP G	After PMPG	Before PMP G	After PMP G	Before PMP G	After PMP G
J	0.0221	0.221	0.0221	0.0221	0.0222	0.0221
CPU time, s	159.67	148.91	98.96	90.51	34.16	32.13
μ_{2S} , 1/h	0.91	0.90	0.91	0.91	0.94	0.91
μ_{2E} , 1/h	0.12	0.13	0.13	0.13	0.11	0.13
k_S , g/l	0.15	0.15	0.15	0.15	0.14	0.15
k_E , g/l	0.80	0.80	0.80	0.80	0.79	0.80
Y_{SX} , g/g	0.41	0.41	0.41	0.41	0.42	0.41
Y_{EX} , g/g	1.64	1.77	1.69	1.76	1.45	1.70
$k_L^{O_2 a}$, 1/h	84.24	93.74	94.40	89.37	95.57	88.86
Y_{OS} , g/g	669.65	742.89	742.47	708.43	743.15	708.15
Y_{OE} , g/g	334.89	404.11	516.92	468.28	458.77	475.75

TABLE VII.
MODEL PARAMETER ESTIMATION BEFORE AND AFTER PMPG

	GGAP = 0.9		GGAP = 0.5		GGAP = 0.1	
	Before PMP G	After PMPG	Before PMPG	After PMPG	Before PMPG	After PMP G
str_opt	3	4	4	4	2	4
opt	6	4	5	5	6	5
aver	0	1	0	0	1	0
pes	0	0	0	0	0	0
str_pes	0	0	0	0	0	0

Thus, based on the intuitionistic fuzzy estimations of the model parameters and further constructed prognoses, MpGA with GGAP = 0.1 and after the procedure for the purposeful model parameter genesis has been distinguished as more reliable algorithm 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 the procedure for the purposeful model parameter genesis has been applied for MpGA with GGAP = 0.1.

The obtained results show that the highest achieved model accuracy can be reached using MpGA with GGAP = 0.1 for much less computational time additionally reduced after the application of purposeful model parameter genesis procedure.

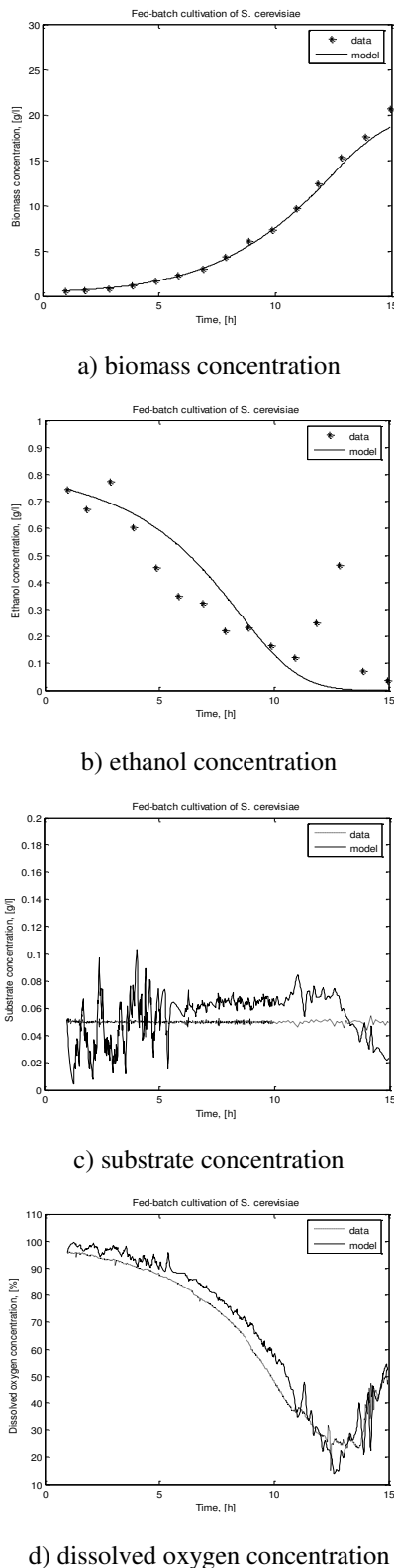


Fig. 1 Model prediction compared to experimental data

CONCLUSION

In this investigation intuitionistic fuzzy logic has been implemented in order to obtain intuitionistic fuzzy estimations of model parameters of fed-batch cultivation.

Aiming to save obtained promising results, namely less convergence time at kept model accuracy, intuitionistic fuzzy logic overbuilds the results obtained after the application of recently developed procedure for purposeful model parameter genesis. This procedure has been applied to MpGA at three different values of GGAP as the most sensitive genetic algorithm parameter, for the purposes of parameter identification of *S. cerevisiae* fed-batch cultivation. After the implementation of intuitionistic fuzzy logic for obtaining of intuitionistic fuzzy estimations of model parameters and further for construction of strong optimistic, optimistic, average, pessimistic and strong pessimistic prognoses for the algorithm performances, results have been compared and MpGA with GGAP = 0.1 after the procedure for purposeful model parameter genesis application has been distinguished as more reliable. Among the distinguished three “leaders”, MpGA with GGAP = 0.1 after PMPG is more than three times faster than MpGA with GGAP = 0.5 before and after PMPG saving the highest achieved values of model accuracy.

Presented here “cross-evaluation” of three different values of GGAP demonstrates the workability of intuitionistic fuzzy estimations to assist in assessment of quality of MpGA performance. Thus, the estimations based on intuitionistic fuzzy logic might be considered as an appropriate tool for reliable assessment for other genetic algorithm parameters, for different optimization algorithms as well as to be applied to various objects of parameter identification.

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