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A COMPARATIVE STUDY OF MULTI OBJECTIVE OPTIMIZATION ALGORITHMS FOR A CELLULAR AUTOMATA MODEL

ESTUDIO COMPARATIVO DE ALGORITMOS DE OPTIMIZACIÓN CON OBJETIVOS MÚLTIPLES PARA UN MODELO DE AUTÓMATA CELULAR

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Abstract

Cellular Automata (CA) models can represent dynamic systems which are discrete in space and time that reflects the effect of intrinsic parameters where individual events are considered to occur from randomness. A CA model of two agents' chemical kinetics has been optimized earlier using NSGA-II based on Evolutionary Algorithm (EA). But the stochastic nature of the CA model along with its high sensitivity on the model parameters requires extensive investigation using different optimization algorithms. For this purpose, in the current study, four more recently developed and popular optimization algorithms based on EA, called NSGA-IIr, NSGA-IIa, AbYSS and MOEA/D, have been considered for investigation based on various performance measuring parameters. The study also compares the performances of the algorithms for different computational efforts with an objective to minimize the required number of objective function evaluations. Simulation results and Friedman rank statistical test show NSGA-IIa and NSGA-IIr as the best choices to optimize the CA stochastic model across any number of objective function evaluations. Though the choice of optimization algorithm does not change with function evaluations, higher function evaluations improve the pseudo-pareto front for the CA optimization problem. Such results will facilitate the use of stochastic CA models to represent complex (bio)-chemical networks.

Keywords: cellular automata, evolutionary algorithm, NSGA-IIr, biochemical kinetics, stochastic modeling.

Resumen

Los modelos de autómatas celulares (CA) pueden representar sistemas dinámicos que son discretos en el espacio y el tiempo, que reflejan el efecto de parámetros intrínsecos en los que se considera que los eventos individuales ocurren de forma aleatoria. Un modelo de CA de la cinética química de dos agentes se ha optimizado anteriormente utilizando NSGA-II basado en el algoritmo evolutivo (AE). Sin embargo, la naturaleza estocástica del modelo CA junto con su alta sensibilidad en los parámetros del modelo, requiere una investigación exhaustiva utilizando diferentes algoritmos de optimización. Para el propósito mencionado en este estudio, se han considerado cuatro populares algoritmos de optimización desarrollados recientemente, llamados NSGA-IIr, NSGA-IIa, AbYSS y MOEA/D; dichos algoritmos están basados en AE así como en varios parámetros de medición del rendimiento. El estudio también compara el rendimiento de los algoritmos para diferentes esfuerzos computacionales, con el objetivo de minimizar el número requerido de evaluaciones de funciones objetivas. Los resultados de la simulación y la prueba estadística de Friedman muestran a NSGA-IIa y a NSGA-IIr como las mejores opciones para optimizar el modelo de CA para cualquier número de evaluaciones de funciones objetivas. Aunque la elección del algoritmo de optimización no cambia con las evaluaciones de funciones, las evaluaciones de funciones más altas mejoran el frente de pseudo-pareto para el problema de optimización de CA. Dichos resultados facilitan el uso de modelos estocásticos de CA para representar redes (bio)-químicas complejas.

Palabras clave: autómata celular, algoritmo evolutivo, NSGA-IIr, cinética bioquímica, modelado estocástico.

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1 Introduction

In a complex system model, it is difficult to choose the properties of the system that influence the model more to ignore other properties that influence the model less (Chu, 2011). If a lower scale detail is considered, it can complicate the model interpretation process, while in a higher scale detail simplification may ignore important properties. Note that by following a bottom-up approach of representation, engineering the lower scale interactions can be sufficient to obtain higher scale properties (Bruggeman *et al*., 2007). For example, modeling the biological cells as a unit and then considering many of them together can describe properties for a certain tissue. Cellular automata (CA) is a candidate class of systems that can be modeled at a mesoscale level with neighborhood-based rules influencing target agents, but when the interacting agents are observed together it can produce properties at a global scale for the system (Wolfram^a, 1994; Wolfram^b, 1994).

In recent decades, there is an extensive use of CA encompassing various fields of research ranging from pattern recognition in geological science (Kier *et al*., 2005; Seybold *et al*., 1997; Li and Gar-On, 2002; Gong *et al*., 2015) to crystallization in material science (Raabe, 2004; Popova, *et al*., 2015) and from cell population dynamics in biochemical engineering (Galbusera *et al*., 2007; Anitha and Peter, 2015) to image representation in bioinformatics (Xiao *et al*., 2005; Tsai *et al*., 2015). In Kar *et al*. (2010), a stochastic CA model represents two agent chemical interactions such as enzyme-inhibitor based reactions where the target agent interacts with another agent from its neighborhood based on some pre-defined probabilistic rules. It shows that the application of probabilistic rules in random order mimic the model best as a natural system. A sensitivity analysis was performed studying the various probabilistic parameters of the model identifying the model parameters that may cause larger perturbations in Kar *et al*. (2014). Results from the sensitivity analysis indicated the transition probabilities, specifically the probabilistic rules governing the transformation of the agents to different forms to be influential to the final model characteristics. The random movement of agents, hence representing diffusion as in natural systems, are also observed to play a crucial role in the effectiveness of the interactions.

However, due to the inherently stochastic nature of the model, it is unrealistic to be able to mathematically predict the model output for a set of specific input parameter values. Also, the representational automata model is expected to attain multiple goals, predefined by the representing chemical kinetic equations. For the same, search techniques are required that can optimize the input parameters while satisfying multiple targeted goals. For this reason, optimization using a metaheuristic approach like Genetic Algorithm (GA) to fine tune the model parameters are considered, which can attain a predefined state representing specific two-agent chemical reactions (Kar *et al*., 2014). A commonly used Multi-objective Evolutionary Algorithm (MOEA) namely NSGA-II (Deb *et al*., 2002) was used for this study. NSGA-II is a non-dominated sorting based elitist MOEA used for multi-objective optimization problems with the flexibility of defining constraints. Two conflicting objective functions, one being minimizing the initial speed of reaction and the other being minimizing the distance between the final state and the desired state of the model, were successfully optimized NSGA-II. As mentioned in Kar *et al*. (2014), MOEAs are used to solve optimization problems having multiple conflicting objective functions based on certain ranges of variable values and constraints. Studies have indicated that different MOEAs provides different quality of results even for the same optimization problem (Zitzler *et al*., 2003; Radziukynienė and Žilinskas, 2008). Such comparative studies for different MOEAs rarely exist for stochastic problems and is the focus of the present study. Hence, a comparative analysis is performed between five different popular MOEAs namely, non-dominated sorting genetic algorithm II (NSGA-II), two modified versions of NSGA-II: NSGA-II random (NSGA-IIr) and NSGA-II adaptive (NSGA-IIa), multi-objective evolutionary algorithm based on decomposition (MOEA/D) and archive-based hybrid scatter search (AbYSS) algorithms as an attempt to find the most effective algorithm for the stochastic CA-based optimization problem.

2 Model description

The Cellular Automata (CA) model used in this study has been developed and validated in earlier works (Kar *et al*., 2010; Kar *et al*., 2014; Dutta *et al*., 2015). The model representation is made in a two-dimensional grid with periodic boundary conditions and the consideration of a von-Neumann neighborhood. Rule application is considered as continuous, because how small the time difference be, each event occurs in a unique instance of time. The parameters namely, size of CA grid, the percentage composition of the interacting agents, probabilistic interaction rules and their threshold values, number of update iterations are considered as the input parameters of the model. The concentration of different interacting agents after completion of target update iterations is considered to define the resultant state of the model.

2.1 Multi Objective Evolutionary Algorithm (MOEA)

Evolutionary Algorithm (EA) is a population-based probabilistic optimization search technique. It is evolutionary in nature and follows the mechanism of Darwin's principle of natural selection and evolution (Fonseca and Fleming, 1993). EA uses three biologically inspired genetic operators namely, selection, crossover and mutation. EA starts with an initial population generated at random. Each member of the population is a chromosome which essentially represents a possible solution to the search space. In MOEA, each solution is assigned a fitness vector of m objective functions (OFs). An OF corresponding to an objective evaluates the fitness of a solution which can be used to compare with the same objective of another solution. The fitness vector of the chromosome indicates how to fit a chromosome is compared to others. The OFs map a chromosome from decision variable space (genotype) to objective space (phenotype). In the selection process, a solution having better fitness value is selected more compared to the solution having less fitness value. Crossover and mutation operations are performed on the selected chromosomes to create a new set of solutions, i.e., the population for the next generation. A Multi-objective Optimization Problem (MOP) can be formulated as follows.

$$Minimize\ F(x) = (f_1(x), f_2(x), \ldots, f_m(x)) \in \Re^m$$

such that

$$\begin{aligned} g_i(x) &\le 0; i = 1, 2, \ldots, p \\ h_j(x) &= 0; j = p+1, p+2, \ldots, q \\ x = (x_1, x_2, \ldots, x_n)^T &\in \Re^n \quad \forall x_l \in [x_l^L, x_l^U], \end{aligned}$$

where x is a solution in decision space and $f_i \Re^n \rightarrow \Re^m$ consists of m real valued objective functions. f_k is the objective function for k^{th} objective, q_i is the i^{th} inequality constraint and h_j is the j^{th} equality constraint.

In a multi-objective optimization problem, there exists a tradeoff between the objectives due to their conflicting nature. An improvement in one objective causes degradation of at least one of the remaining objectives. Hence, for a given MOP, MOEA generates a set of optimal solutions, not a single solution. These optimal solutions are not comparable with each other, i.e., no one is better than the other. They are also called non-dominated solutions, defined as follows.

Let p, $q \in \Re^m$ are two solutions of in objective space, then p is said to dominate q (or $p < q$) if and only if

a) for any objective f_k, $p_k \le q_k \quad \forall k \in \{1, 2, \ldots, m\}$

b) $\exists$ at least one objective f_r such that $p_r < q_r$, where $r \in \{1, 2, \ldots, m\}$.

p and q are said to be non-dominated to each other if neither $p < q$ nor $q < p$.

A solution $x^* \in \Re^n$ is called pareto optimal (global), if there is no $x \in \Re^n$ such that $F(x)$ dominates $F(x^*)$. The set of all pareto optimal solutions denoted by PS is called the pareto Set. The corresponding set of solutions in the objective space is called pareto Front (PF), i.e., $PF = \{F(x) \in R^m | x \in PS\}$. Different PFs corresponding to a different type of optimization (minimization/maximization) problems is shown in Figure 1 by considering two objectives, f1 and f2.

Literature shows significant progress in the development of Multi-objective Evolutionary Algorithm (MOEA) for solving complex multi-objective optimization problems. Objectives in MOPs are conflicting with each other. Therefore, a single solution that simultaneously optimizes each of the objectives is not possible. MOEA finds multiple equally optimal solutions that minimize two or more objective functions (OFs) at the same time. The performance of MOEA is evaluated as per the convergence and the diversity of the obtained solution set. Convergence shows how close the obtained solution set is to the true optimal solution set of the problem and the diversity shows how well the solution set is evenly spread in reference to the true optimal solution set.

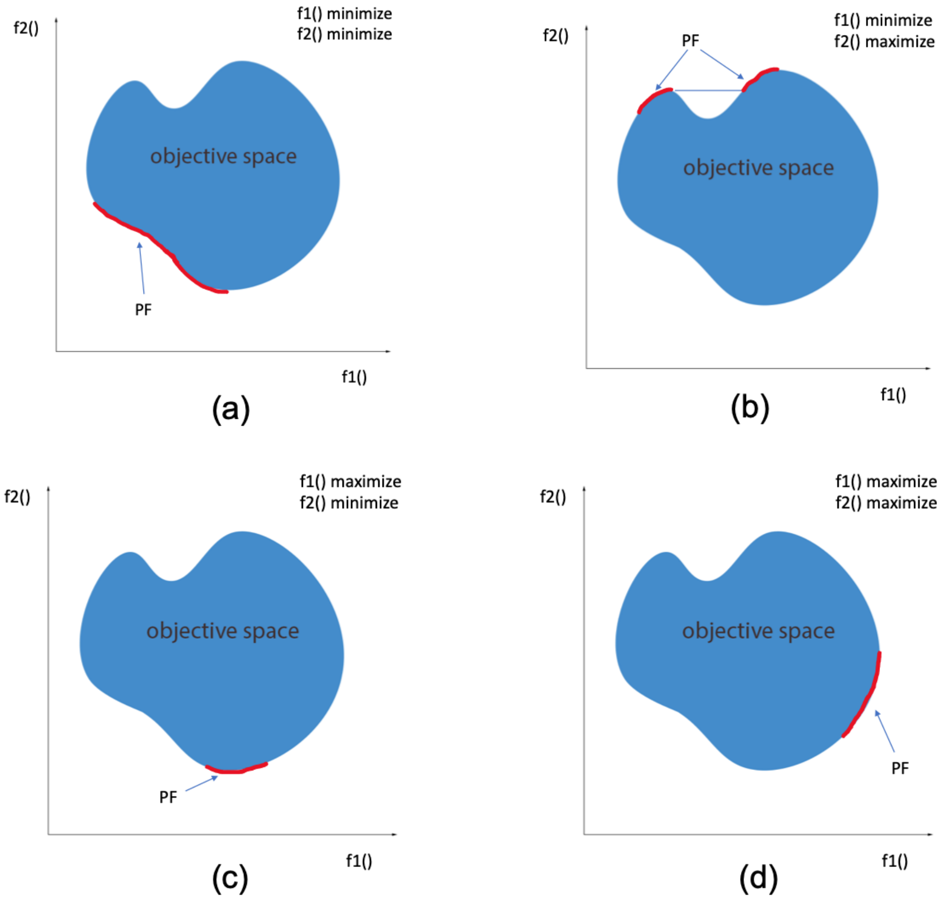


Fig. 1. Different pareto fronts (PFs) generated for different types of optimizations of a bi-objective problem: (a) minimization of both f1 and f2 (b) minimization of f1 and maximization of f2 (c) maximization of f1 and minimization of f2 and (d) maximization of both f1 and f2.

Several MOEAs exist in the literature, such as Horn *et al*. (1994), Srinivas and Deb (1995), Zitzler *et al*. (2001), Deb *et al*. (2002), Zang and Li (2007), Nebro *et al*. (2008), Nebro *et al*. (2013), Coello *et al*. (1999), Coello *et al*. (2006), Konak *et al*. (2006) and Nag *et al*. (2015). Performances of MOEAs can be domain specific of problems, hence extensive case study for a variety of problem types and MOEAs is required. In the present study, five MOEAs have been considered: i) NSGA-II (Deb *et al*., 2002), ii) NSGA-IIr (Nebro *et al*., 2013), iii) NSGA-IIa (Nebro *et al*., 2013), iv) MOEA/D Zang and Li (2007) and v) AbYSS Nebro *et al*. (2008). The following section discusses briefly the basics of these algorithms.

The Non-dominated Sorting Genetic Algorithm (NSGA-II) is one of the most popular MOEAs. NSGA-II is proposed by Deb *et al*. (2002). It is an elitist model which ensures retaining a small portion of the fittest candidates, into the next population to enhance the convergence. In a generation, the parent of size N produces the same number of offspring using the genetic operators: selection, crossover and mutation. These offspring are then combined with the parent population to form a total of $2N$ solutions. They are sorted according to their ranking based on dominance rule. For this purpose, a fast-non-dominated sorting procedure is applied. A lower rank (assuming the problem as a minimization problem) corresponds to a better solution. It results in a series of non-dominated fronts, all solutions having the same rank belonging to the same front. The best N solutions are used as the population for the next generation. In the case of having more than one solution with the same rank, they are sorted according to a density estimation metric, called crowding distance (CD). CD of a solution is computed with regards to its neighbours as shown in Figure 2.5 for a bi-objective problem. A solution with less crowding distance (i.e., a low populated region in the search space) is preferred to maintain the diversity among the solutions.

NSGA-IIr (random NSGA-II) and NSGA-IIa (adaptive NSGA-II) (Nebro *et al*., 2013) are the two variants of NSGA-II. The variation operators, like crossover probability and mutation probability, used in MOEAs are usually fixed and applied in the same way during the execution of the algorithms. The authors have allowed a more dynamic approach on NSGA-II and developed NSGA-IIr and NSGA-IIa combining different operators with variable application rate along the search process to improve the static classical behavior of NSGA-II. They have explored the combined use of three different operators: simulated binary crossover (SBX), differential evolution and polynomial mutation to create new solutions in NSGA-II. Two strategies are considered for selecting the operators: random and adaptive, resulting in the variants NSGA-IIr and NSGA-IIa respectively. The resulting variants have been tested on a set of 19 complex problems, and results have shown best overall results in the bi- and three-objective problems.

The Multi-objective Evolutionary Algorithm based on Decomposition (MOEA/D) (Zhang and Li, 2007) decomposes a MOP into scalar sub-problems and optimizes them simultaneously by exploiting the neighborhood relationships among those sub-problems. The sub-problems correspond to the objectives of the given MOP. Each sub-problem is transformed into a scalar aggregation function and optimized using the information only from its neighboring subproblems. This neighborhood information is defined based on the distances between their aggregation coefficient vectors. As each objective is handled separately in MOEA/D, diversity is maintained in it from this natural behavior.

Archieve-Based hYbrid Scatter Search, (AbYSS) is introduced in 2008 by Nebro *et al*. It is a multi-objective version of a scatter search which uses evolutionary operators such as polynomial mutation, binary crossover, and solution combination to enhance its search capability while exploring the search space of the MOPs. It incorporates the concepts of pareto dominance, density estimation and an external archive. The external archive is used to store the non-dominated solutions.

MOEA modifies the values of the input parameters for generating optimal solutions based on the predefined objective functions. The goal of a MOEA is to converge the solution set to the pareto front by improving the proximity between the pareto front and optimized front (non-dominated solutions) generated by the MOEA and simultaneously maintain the diversity among the optimized solutions to cover the spectrum of the front as much as possible. Figure 2 shows different fronts generated by a MOEA during the execution of a bi-objective optimization problem. In this figure, the shaded region represents the feasible objective space and the pareto front (PF) is represented by P_f. The front close to the PF is the first front. There are two other fronts, second and third. It has been mentioned earlier that all the solutions in the front are non-dominated to each other. Moreover, no solution in the first front is dominated by any solution of the other fronts. Similarly, no solution in the second front is dominated by any solution of the third front, but a solution in the second front is dominated by at least one solution of the first front. The fronts, thus generated, try to maintain the convergence and diversity among the solutions. The third front in Figure 2 covers the spectrum of the PF much less compared to that of the second front, *i.e*., the solutions of the third front are less diverse in nature compared to the second front. During the optimization of MOP, the fronts approach towards PF with generation by improving the quality of the solutions.

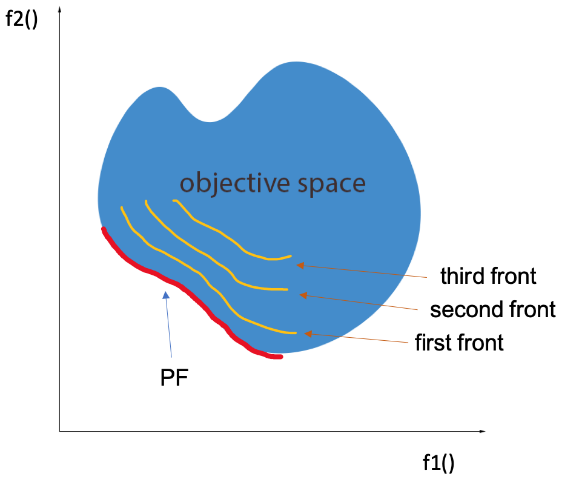


Fig. 2. Different fronts, generated by a MOEA for a bi-objective optimization problem.

2.2 *Performance metrics*

Convergence (i.e., closeness to PF) and diversity (i.e., coverage of a diverse set of solutions)) are at conflict in the execution of MOEAs. Developing a single metric is difficult to exactly measure these two qualities by a solution set. For assessing the performance of different MOEAs on the CA model, two different issues are normally considered: minimize the distance of the pareto front generated by the proposed algorithm to the exact pareto front, and to maximize the spread of solutions found, so that a distribution of vectors as smooth and uniform as possible can be obtained. Typically, four metrics are considered: Inverted Generational Distance (IGD), Spread (S), Hypervolume (HV) and additive Epsilon (ε). They are defined below.

2.2.1 *Inverted Generational Distance (IGD)*

It measures the distance from the pareto optimal solutions to a set of non-dominated solutions (Van and Lamont, 1998) and is expressed as:

$$IGD = \frac{\sum_{i=1}^{|P^*|} d(\rho_i, N_D)}{|P^*|} \quad \forall \rho_i \in P^*, \tag{1}$$

with P^* as the pareto front, N_D is a non-dominated solution vector and $d(\rho_i, N_D)$ is the Euclidian distance between ρ_i and its closest neighbor in $N_D \rho_i$ represents a solution in P^*. A smaller value of IGD is always preferred.

2.2.2 *Spread (S)*

It determines the diversity in a non-dominated front that measures the extent of spread achieved among the solutions obtained from the simulation. This metric was first proposed by Deb *et al.* (2002) for bi-objective problems and then extended to multi-objective problems by Zhou *et al.* (2007). It is expressed as:

$$S = \frac{\sum_{i=1}^{m} d(e_i, Q) + \sum_{X \in Q} |d(X,Q), -\overline{d}|}{\sum_{i=1}^{m} d(e_i, Q) + |Q| \times \overline{d}} \quad \forall e_i \in P \tag{2}$$

such that, $d(Y,Q) = \underset{Y \in S, Y \neq X}{\min} \|F(X) - F(Y)\|^2$ and $\overline{d} = 1/|P| \sum_{X \in P} d(X,Q)$, where, Q is the set of solutions, F is the set of m objectives and P is the pareto front of the problem. So less the value of S, more is the diversity among the solutions.

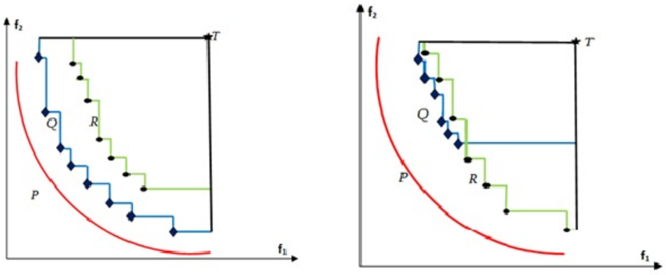
2.2.3 *Hypervolume (HV)*

It is the volume covered by the set of all non-dominated solutions, N_D. The volume is generally the region enclosed by all the elements of N_D with respect to a reference point T which is a vector that constitutes the worst fitness values of OFs. For each solution e, a hypercube is constructed with respect to T and the cumulative contribution of all the solutions in a front form of the hypervolume (Azevedo and Araújo, 2011). It is expressed as:

$$HV = volume(U_{e \in N_D} h_e), \tag{3}$$

with h_e being the hypercube for each $e \in N_D$. Larger values of HV is always desirable. More is the value of HV, the closer will be the final front, generated by a MOEA to the PF and at the same time the solutions are well diverse. The hypervolume of an optimized front is a measure with respect to a reference solution of worst quality in the entire objective space of MOP.

In Figure 3(a) two fronts Q and R are generated for say two different MOEAs for the same problem, whose PF is represented by P. Q is closer to P as well as more diverse compared to R.



(a) (b)

Fig. 3. HV for different optimized fronts (Q, R) with respect to the pareto front (P). (a) The front Q is closer to P than R hence shall have higher HV value, (b) both Q and R are similar in distance from P but R is more diversely spread than Q, hence shall have higher HV value.

As a result, the value of HV for Q is more than that for R. If solutions of Q are not well diverse compared to R as depicted in Figure 3(b), a better HV for R than that of Q with respect to the reference solution T can be obtained.

2.2.4 Additive Epsilon (ε)

It is used to determine how much worse a non-dominated set of solutions compared to the pareto optimal solution set with respect to all the objectives to be minimized (Zitzler *et al.*, 2003). Precisely, the additive epsilon $I_{\varepsilon+}(N_D, P^*)$ metric indicates a small positive quantity ε such that for any solution in P^* there is at least one solution in N_D which is not worse by ε with respect to all the objectives. It is evaluated by the following expression.

$$I_{\varepsilon+}(N_D, P^*) = inf\{\forall z^2 \in P^* \exists z^1 \in N_D : z^1 \geq_{\varepsilon+} z^2\}, \quad (4)$$

where $\varepsilon \in \Re$, $z^1 = \{z_1^1, z_2^1, \ldots, z_n^1\}$, $z^2 = \{z_1^2, z_2^2, \ldots, z_n^2\}$, n is the number of objectives and $z^1 \geq_{\varepsilon+} z^2$, if and only if, $z_i^1 \leq z_i^2 + \varepsilon, \forall i \in [1, n]$. Smaller value of additive epsilon is desirable. Further, in the manuscript, we represent additive Epsilon as Epsilon.

3 Model setup

The grid size of the CA model is fixed at 50×50. Its number of update iterations has been fixed to 1000 based on the observation of attainment of steady state when running with the standard values for the probability rules (Dutta *et al.*, 2015). The reaction agents used in the model are Substrate (S), Product (P), Enzyme (E), Inhibitor (I) and Water (W). The chemical reaction structure represented in the CA is shown in Figure 4. The initial percentage occupancy for the reacting agents are 40% of S, 5% of E, 5% of I, 16% of water, zero P and rest 34% as void space.

For optimization by MOEAs, ten stochastic parameter rules for CA model: four rules for probabilities of Join between E and S, between E and P, between E and I and between S and W; four rules for probabilities of Break between E and S, between E and P, between E and I and between S and W; two rules for transition probabilities from ES complex to EP and from EP complex to ES have been considered. Two objective functions (OFs) have been used for the optimization: (a) to minimize the rate of reaction for the initial 100 update iterations and (b) to minimize the difference between the target concentration of agent P and mean concentration of agent P, averaged for the last 100 update iterations. The principle behind selecting first OF is to induce the tendency of slowing down the interactions, hence increasing the details of the reactions. The final concentration of the agent P as a mean value over the last 100 iterations to minimize the stochastic fluctuation is obtained. An 80% of S conversion to P has been considered as the target P concentration.

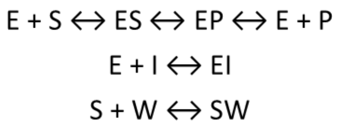


Fig. 4. Empirical reaction structure for the CA model.

For simulation purpose of five MOEAs, Java based jMetal 4.5 framework version (Durillo and Nebro, 2011) has been used. Seven different values of the maximum number of function evaluations have been considered: 27000, 51000, 75000, 80000, 85000, 90000 and 95000 for each of five different MOEAs: NSGA-II, NSGA-IIr, NSGA-IIa, AbYSS and MOEA/D, resulting 35 different simulation configurations each of which has been executed ten times independently. As the MOEAa are probabilistic in nature, each simulation configuration has been executing independently 50 times. Due to high computational requirement, a high-performance computing cloud available on credit basis from Amazon Web Service (AWS) has been used. The multi-thread ability of jMetal 4.5 allows parallel execution of 35 individual simulations hence reducing the execution time.

For a given multi-objective application problem, if the pareto front (PF) is known, evaluating the performance (in terms of the convergence and diversity) of the MOEA used for its optimization becomes easy. But for a real-world problem, the pareto front is generally unknown. In that case, a pseudo pareto optimal front, i.e., reference front is created by collecting and aggregating the best possible non-dominated solutions obtained from different MOEAs. It is important to note that for the CA model, studied here, no PF is available in the literature. The reference front for the CA model is created by collecting all the best quality solutions from five MOEAs. To compare the performance of these algorithms used to optimize the CA problem, performance metrics (Spread, Inverted Generational Distance, Hypervolume and Epsilon) have been computed based on the reference front.

The 4-performance metrics are calculated individually for each of the simulation design - including 7 generation size options and 5 MOEA optimization algorithms. These computed performance metrics help to identify the best fitting optimization algorithm for the CA problem. To identify if there is any significant difference across the MOEAs for each generation size setting, we perform Friedman test testing against the null hypothesis being there is no difference between the performance metrics sets (each set has 50 independently computed metrics values from the 50 independent simulations). If the null hypothesis is rejected based on a 5% confidence interval, we perform pairwise comparisons finding the exact p-values based on the method published in Eisinga *et al.*, 2017. These statistical tests are performed using PMCMRplus R package (Thorsten, 2018). Finally, we count the number of significant 'wins' (better performing algorithm) to identify the best fitting MOEA for the CA problem.

4 Results

It has been mentioned that the CA model implemented in this study has been optimized using five different MOEAs: NSGA-II, NSGA-IIr, NSGA-IIa, MOEA/D and AbYSS. Their results are compared and analyzed in terms of different performance metrics, discussed above. Comparison studies between MOEAs on the CA model with various characteristics will help to understand the strengths and weaknesses of these different methodologies and to choose and/or modify an algorithm for solving the CA model.

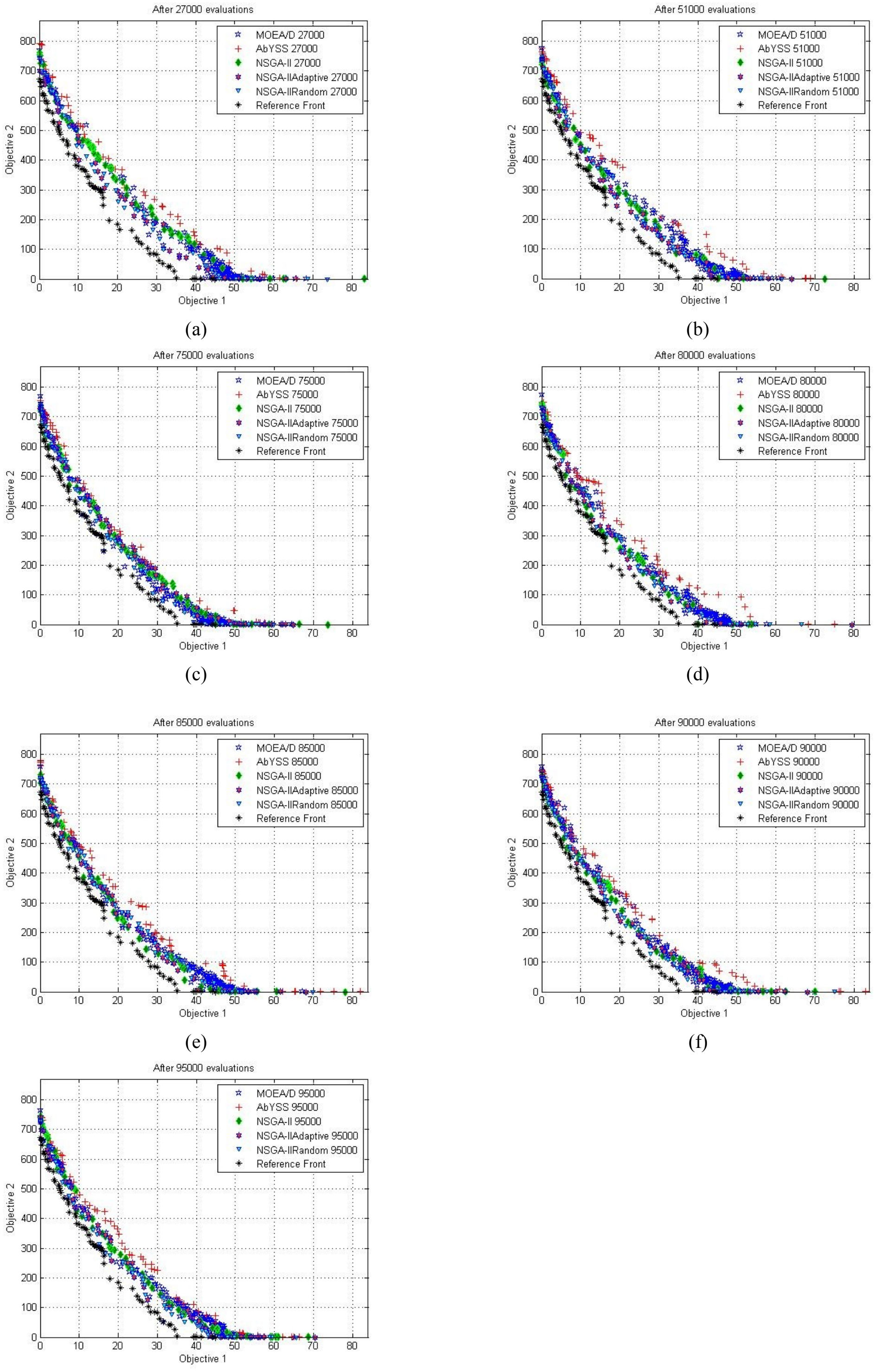
It is important to note that for the CA model studied, no PF is available in the literature. So, an approximate PF is created by generating a reference front by collecting all the best quality solutions from every independent execution of these five MOEAs. A different set of non-dominated solutions, generated while executing five MOEAs for the CA model at different function evaluations, create different non-dominated fronts which are shown along with the reference fronts in Fig. 5(a) - 5(g). It indicates that more the number of function evaluations, closer a non-dominated solution is to the reference front. Table 1 summarizes the different parameters and their values as used for simulating the different MOEAs. Except for the population size, the other parameter values were selected based on a few ad-hoc runs of the simulation setting.

For each of the seven function evaluation (generation size) values (27000, 51000, 75000, 80000, 85000, 90000 and 95000), all the MOEAs are executed 50 times, and in each execution of a MOEA, the four performance metrics, HV, S, IGD and ε, are evaluated for the obtained set of non-dominated solutions with respect to the reference front. Due to the probabilistic nature of the MOEAs, statistical dispersion among the values of each of the performance metrics is studied for each MOEA, which are enlisted in supplementary information Table SI-1 and Table SI-2. Based on Friedman non-parametric test, it is confirmed that the presence of significant difference across the 5 MOEAs' performance metric values for each combination of generation size and performance metric set.

The results confirm that as the number of function evaluations increases from 27000 to 95000, the standard deviation and IQR of all the performance metrics of each of the five MOEAs tends to reduce. The increase in the number of function evaluations increases in the number of generations and with improvement in each generation the resulting non-dominated front becomes closer to reference front as depicted in Figure 5, which eventually improves the value of the performance metrics.

Table 1: The parameter settings of different MOEAs as used while optimizing the CA model.

	population size	*crossover probability (pc)*	*mutation probability (pm)*	*crossover rate (CR)*	*mutation rate (F)*	*Others*
NSGA-II [14]	300	0.9	0.03	NA	NA	NA
NSGA-IIr [25]				0.95	0.4	NA
NSGA-IIa [25]						NA
AbYSS [24]				NA	NA	ref. set size = 150, improvement round = 4
MOEA/D [23]		NA	NA	0.95	0.4	NA



(a)

(b)

(c)

(d)

(e)

(f)

(g)

Fig. 5. Non-dominated fronts obtained by NSGA-II, NSGA-IIr, NSGA-IIa, MOEA/D and AbYSS after (a) 27,000 function evaluations, (b) 51,000 function evaluations, (c) 75,000 function evaluations, (d) 80,000 function evaluations, (e) 85,000 function evaluations, (f) 90,000 function evaluations and (g) 95,000 function evaluations.

Statistical interpretation is that for all the metrics the variation around the mean becomes smooth as well as the dispersion between the lower and upper quartiles is reduced and progressively approached towards the median as the number of function evaluations increases for all the five MOEAs.

In Figure 5, it can be observed that the optimized fronts generated by different MOEAs gradually approach towards the reference front by generating a more optimized set of solutions of the CA problem with an increase in the maximum number of function evaluations. The optimized fronts of the CA problem generated by NSGA-IIr and NSGA-IIa are closer to the reference front for all values of the maximum number of function evaluations have been observed. It implies that these two algorithms, NSGA-IIr and NSGAIa, can produce superior results compared to other MOEAs. The same is also inferred from the values of performance metrics, given in Tables 2 and Table 3. It is observed in Fig. 5 that the optimized front generated by MOEA/D has the majority of the solutions crowded at lower part of the front, whereas the fronts generated by NSGA-II, NSGA-IIr, NSGA-IIa and AbYSS contain solutions from less crowded regions and thus they cover more spectrum of the reference front (i.e., more diverse solutions) than MOEA/D. For selecting the most suitable one among these five MOEAs and appropriate value for the maximum number of function evaluations for its execution, it is noted that HV of NSGA-IIr improves from 27000 to 95000. But for S there is a marginal improvement on performance for the cases above 75000 function evaluations. For IGD and ε the improvement above 80000 function evaluations are also marginal. Hence it can be concluded that increasing the number of function evaluations above 75000 function evaluations is not cost effective for the CA model. So, the two agent CA model of chemical kinetics can, therefore, be better optimized using NSGA-IIr when executed for 75000 evaluations.

5 Discussions

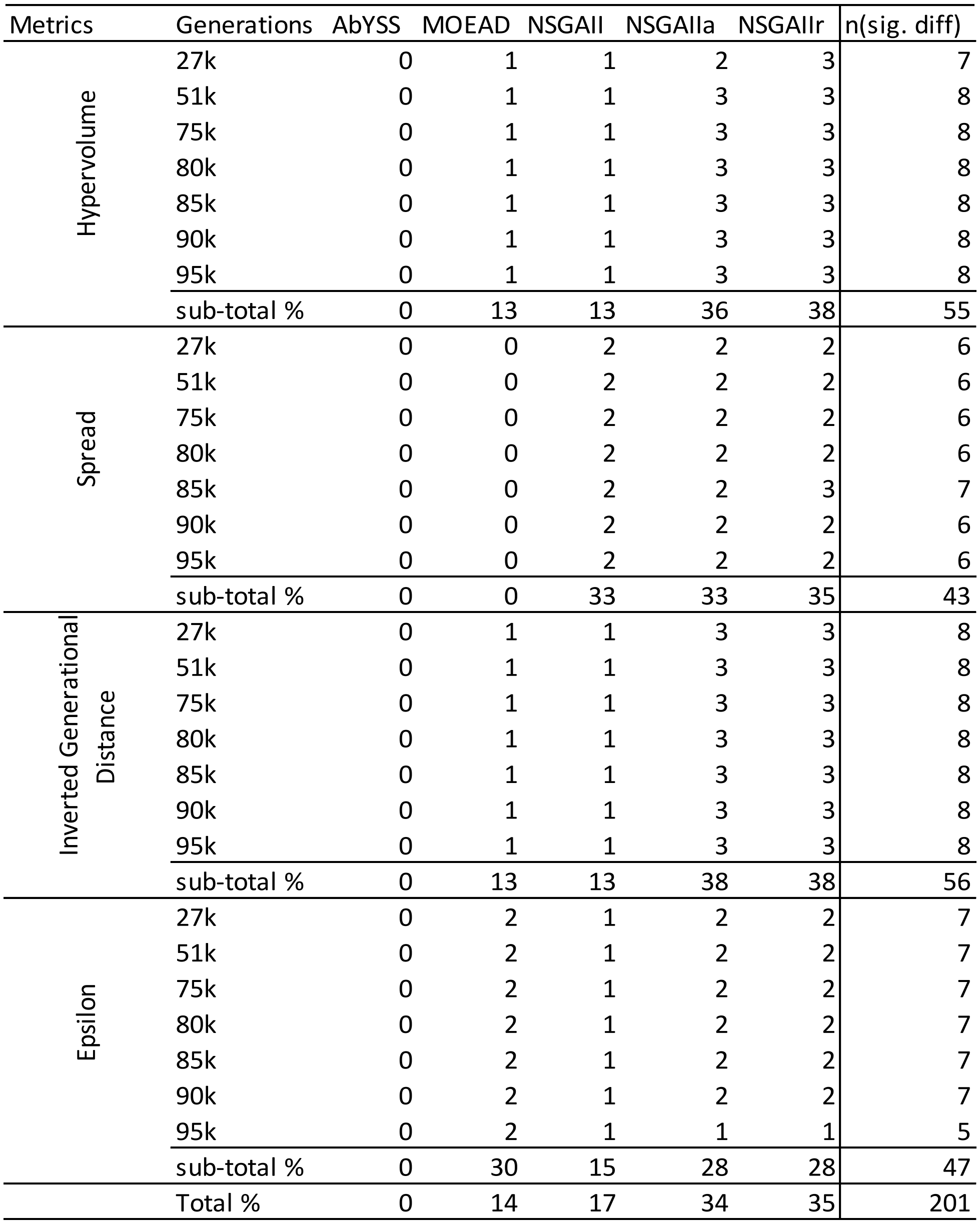
The stochastic generalized CA model based on two agent interactions can be optimized for its parameters to represent specific two chemical species in intermediate steps based chemical kinetic reactions. The objectives of the optimization are to make the representative model detailed showing a greater number of intermediate interaction steps and to attain the target reaction state of the model. MOEA is used to optimize the two objectives. A comparative study is performed to find the best fitted MOEA for the present problem. In this study, the CA model has been optimized with five MOEAs: NSGA-II, NSGA-IIr, NSGA-IIa, MOEA/D and AbYSS for 27000, 51000, 75000, 80000, 85000, 90000 and 95000 maximum number of function evaluations. During each execution, four performance metrics, HV, S, IGD and ε are evaluated. Due to the stochastic nature of the problem, the statistical dispersion of the performance metrics has been considered. Since the mean and median values share small differences between the different performance metrics, the Friedman rank test statistic is calculated to identify the presence of significant (5% level) difference among the studied algorithms for each generation size and performance metric sets. The significant difference is found to exist for all the groups ($p \leq 0.05$). Further, the pair-wise posthoc test is performed to find the exact p-values (Eisinga *et al*., 2017) for each of the pair. For each performance metric and generation combination, algorithms are counted for the number of times they are significantly better ($p < 0.05$). This is summarized in Table 2.

A total of 201 out of 280 comparison cases were found significant across all the performance metric and generation size combinations. Across all generation size and performance metrics, the MOEA NSGA-IIa (34%) and NSGA-IIr (35%) are found to perform close by and better than other algorithms, with MOEA/D 14% and NSGA-II 17% wins. For none of the cases, AbYSS is found to perform significantly better.

For the performance metric Hypervolume and Inverted Generational Distance, NSGA-IIa (36%, 38%) and NSGA-IIr (38%, 38%) are seen performing better, but also, NSGA-II is identified performing similarly better for the performance metric Spread. When Epsilon metric is studied, MOEA/D is seen to perform slightly better (30%) than NSGA-IIa and NSGA-IIr both with 38% wins. Wins for all the algorithms remain somewhat steady across the 7 generation sizes.

Hence, the NSGA-IIa and NSGA-IIr MOEAs are seen performing significantly better than AbYSS, MOEA/D and NSGA-II algorithms for optimizing the parameters of the CA problem. Even though the wins as seen in table 2 remains somewhat similar across the different tested generation size, a higher number of generations help improve the pseudo-pareto front for the unknown CA problem.

Table 2: A summary of count for the tested MOEA algorithms performing significantly (p < 0.05) better based on posthoc Friedman rank test (Eisinga *et al*., 2017)) for each performance metric and generation setting. A percentage for each performance metric summarizes an algorithm win. Also, the total % at the bottom row of the table summarizes algorithms performances across all the generation settings.



Metrics	Generations	AbYSS	MOEAD	NSGAII	NSGAIIa	NSGAIIr	n(sig. diff)
Hypervolume	27k	0	1	1	2	3	7
	51k	0	1	1	3	3	8
	75k	0	1	1	3	3	8
	80k	0	1	1	3	3	8
	85k	0	1	1	3	3	8
	90k	0	1	1	3	3	8
	95k	0	1	1	3	3	8
	sub-total %	0	13	13	36	38	55
Spread	27k	0	0	2	2	2	6
	51k	0	0	2	2	2	6
	75k	0	0	2	2	2	6
	80k	0	0	2	2	2	6
	85k	0	0	2	2	3	7
	90k	0	0	2	2	2	6
	95k	0	0	2	2	2	6
	sub-total %	0	0	33	33	35	43
Inverted Generational Distance	27k	0	1	1	3	3	8
	51k	0	1	1	3	3	8
	75k	0	1	1	3	3	8
	80k	0	1	1	3	3	8
	85k	0	1	1	3	3	8
	90k	0	1	1	3	3	8
	95k	0	1	1	3	3	8
	sub-total %	0	13	13	38	38	56
Epsilon	27k	0	2	1	2	2	7
	51k	0	2	1	2	2	7
	75k	0	2	1	2	2	7
	80k	0	2	1	2	2	7
	85k	0	2	1	2	2	7
	90k	0	2	1	2	2	7
	95k	0	2	1	1	1	5
	sub-total %	0	30	15	28	28	47
	Total %	0	14	17	34	35	201

This gives a good understanding of pairing of the different MOEAs for the stochastic CA problem and can support further development of stochastic CA model to represent complex biological chemical networks, giving an insight of their fundamental understanding.

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