Multidimensional Crossover in Genetic Algorithms

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(Abstract)

1 Introduction

Most of the genetic algorithms (GA's) used in practice work on linear chromosomes (e.g. binary strings or sequences of some other types of symbols). However some results have been published revealing that for certain problems multidimensional encoding may give better results than the one dimensional (linear) ones []. While some theoretical results have been obtained, no clear criteria for deciding the suitable dimensionality of the encoding to be used for a given problem.

In this paper we consider a class of problems for which we define a multidimensional encoding and a corresponding genetic operator. We show that for a GA using this encoding and operator we can obtain theoretical results similar to (under certain conditions even better than) those known for linear encoding. Finally we demonstrate these theoretical results using a set of test examples.

2 Multidimensional Encoding and Crossover

In this section we first define what we mean by a multidimensional (search) problem. We then briefly present the classical (one dimensional) encoding used in solving such problems using GA's, followed by our proposal for a multidimensional encoding. Next we define a crossover operator on multidimensional codes and prove a Schema Theorem-like result for a

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GA using it. Finally we show that for certain types of problems multidimensional encoding and the defined crossover operator may give better results than the linear ones.

2.1 Multidimensional Problems

Our definition of multidimensional problems is based on the following definition of a-ary relations:

Definition 2.1.1. Let $A_1, A_2, ..., A_n$ be sets. An n-ary relation ρ over these sets is a set

$$\rho \subseteq A_1 \times A_2 \times ... \times A_n.$$

In the followings we shall only consider relations defined over finite sets. The set of all relations over the sets $A_1, A_2, ..., A_n$ will be denoted by $R(A_1, A_2, ..., A_n)$.

Let us note here that an n-ary relation ρ over $A_1, A_2, ..., A_n$ can be represented by an n-dimensional matrix $M(\rho) = (m_{i_1,i_2,...,i_n})$ over $\{0, 1\}$ as follows:

Let $A_i = \{a_i^1, a_i^2, ..., a_i^{k_i}\}$ for $i = \overline{1, n}$.

$$m_{i_1,i_2,...,i_n} = \begin{cases} 1 & \text{if } (a_1^{i_1}, a_2^{i_2}, ..., a_n^{i_n}) \epsilon \rho \\ 0 & \text{otherwise} \end{cases}$$

For the two-dimensional case this corresponds to the adjacency matrix associated with the graph corresponding to the relation.

Definition 2.1.2. Given the (finite) sets $A_1, A_2, ..., A_n$ by an *n-dimensional (search) problem* attached to a predicate P defined over $R = R(A_1, A_2, ..., A_n)$ we mean the problem of finding an n-ary relation $\rho^* \epsilon R(A_1, A_2, ..., A_n)$ such that $P(\rho^*)$ is true.

Our goal in the followings is to study some aspects of using genetic algorithms for solving n-dimensional problems. To be able to do this we assume that for every n-dimensional search problem considered there is a *fitness function* $f : R \to \Re^+$, which measures the "quality" of any given relation. For our purposes the nature of this function is irrelevant.

2.2 The Common Approach

In using GA's to solve problems of the above mentioned type the current practice is to choose a (binary) coding for each of the dimensions of a relation and concatenate them. One-point crossover of two relations then means choosing a crossover point, cutting both of the codes in that point and exchanging their "tails", producing two offsprings. Other, multi-point crossover operations, have been also defined [], however none of them is able to provide the type of improvement we are looking for.

Intuitively the drawback of these approaches is that they don't take into consideration the dimensionality of the problem, i.e. they don't try to preserve subrelations of the original relations [][].

2.3 n-dimensional Encoding and Crossover

In this section we propose another approach to using GA's for solving multidimensional search problems. Similar approaches have been proposed in [], [] and []. Our approach is based on the use of multidimensional matrices for encoding and a crossover operator specific to this encoding. This was first defined in [] and is similar to the encoding used by algorithm R1 in []. To make our discussion clear we first present our results for two dimensional problems, the generalization to n-dimensional ones being discussed in a separate subsection.

Two-dimensional Encoding and One-Point Crossover

Let $A = \{a_1, a_2, ..., a_m\}$ and $B = \{b_1, b_2, ..., b_n\}$ be finite sets, and let us consider the two dimensional search problem attached to a given predicate P over $R(A, B)$. To solve this problem using a genetic algorithm we have to choose a representation for the relations in P. We propose that the representation of a relation $\rho \epsilon R(A, B)$ be the corresponding $M(\rho)$ matrix as defined in Subsection 2.1. In this case a two dimensional matrix representing a relation will be a chromosome processed by the genetic algorithm. Let us now define a crossover operator for a GA using the above considered encoding.

Definition 2.3.1. Let $\rho_1, \rho_2 \epsilon R(A, B)$ be two relations and $M(\rho_1)$ and $M(\rho_2)$ the corresponding chromosomes. Let us further consider two positive integers k_1 and k_2 such that $1 \leq k_1 \leq m$ and $1 \leq k_2 \leq n$. The *two-dimensional crossover* of the two chromosomes using crossover point (k_1, k_2) produces two new chromosomes $M_1 = (m^1_{i,j})$ and $M_2 = (m^2_{i,j})$ defined by

$$m^1_{i,j} = \begin{cases} r_{i,j} & \text{for } i < k_1 \wedge j < k_2 \text{ or } i \geq k_1 \wedge j \geq k_2 \\ q_{i,j} & \text{for } i < k_1 \wedge j \geq k_2 \text{ or } i \geq k_1 \wedge j < k_2 \end{cases}$$

$$m^2_{i,j} = \begin{cases} q_{i,j} & \text{for } i < k_1 \wedge j < k_2 \text{ or } i \geq k_1 \wedge j \geq k_2 \\ r_{i,j} & \text{for } i < k_1 \wedge j \geq k_2 \text{ or } i \geq k_1 \wedge j < k_2 \end{cases}$$

respectively.

Example. Let us consider the following two-dimensional chromosomes:

$$\begin{array}{|cc|ccc|} \hline 1 & 0 & 1 & 1 & 0 \\ 0 & 1 & 1 & 0 & 1 \\ 0 & 0 & 0 & 1 & 1 \\ \hline 1 & 1 & 0 & 1 & 0 \\ 0 & 1 & 0 & 1 & 1 \\ \hline \end{array} \qquad \begin{array}{|cc|ccc|} \hline 0 & 1 & 1 & 1 & 0 \\ 1 & 1 & 0 & 0 & 0 \\ 1 & 0 & 0 & 0 & 0 \\ \hline 1 & 1 & 1 & 0 & 0 \\ 0 & 0 & 0 & 1 & 1 \\ \hline \end{array}$$

and crossover point $(4,3)$. Applying the two dimensional crossover to the above chromosomes the newly created chromosomes will be

$$\begin{array}{|cc|ccc|}\hline 1 & 0 & 1 & 1 & 0 \\ 0 & 1 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 \\ \hline 1 & 1 & 0 & 1 & 0 \\ 0 & 0 & 0 & 1 & 1 \\ \hline \end{array} \qquad \begin{array}{|cc|ccc|}\hline 0 & 1 & 1 & 1 & 0 \\ 1 & 1 & 1 & 0 & 1 \\ 1 & 0 & 0 & 1 & 1 \\ \hline 1 & 1 & 1 & 0 & 0 \\ 0 & 1 & 0 & 1 & 1 \\ \hline \end{array}$$

The Two-Dimensional Schema Theorem

In order to give our first result we need some more definitions similar to those given for the classical Schema Theorem [][].

Definition 2.3.2. A *two-dimensional schema* of size $m \times n$ is a matrix of dimension $m \times n$ over $\{0, 1, *\}$.

As in the Schema Theorem "*" means "either 0 or 1". We call the positions having values 0 or 1 *specific positions*.

A two-dimensional scheme represents a set of matrices. More precisely: a two-dimensinal schema with specific positions $S(\sigma) = \{(i_1, j_1), (i_2, j_2, ..., (i_k, j_k)\}$ defines the following matrix set:

$$\sigma = \{(a_{i,j})_{i=\overline{1,m}, j=\overline{1,n}} \mid a_{i,j} = \sigma_{i,j}, \forall (i,j) \epsilon S(\sigma)\}$$

By analogy with the one-dimensional Schema Theorem we also need the following definition:

Definition 2.3.3. The *defining matrix* of a schema σ is the smallest submatrix of σ that contains all its specific positions $(\Delta(\sigma))$

Definition 2.3.4. if the dimensions of $\Delta(\sigma)$ are d_1 and d_2 respectively, then (δ_i, δ_j) is the *defining size* of σ, where $\delta_i = d_1 - 1$ and $\delta_j = d_2 - 1$.

Example. Let us consider the 5 by 5 quadratic chromosome:

$$\begin{array}{ccccc} * & * & * & * & * \\ * & * & * & * & * \\ * & * & 0 & * & 1 \\ * & * & 1 & 0 & * \\ * & * & * & * & * \end{array}$$

The defining matrix of this chromosome is the sub-matrix defined by the positions $(3,3)$ and $(4,5)$, while its defining size is $(1,2)$.

Similar to the Schema Theorem presented in Goldberg's book and using the same notations we have the following result:

Theorem 2.3.1.(ST for two dimensional crossover) if σ is a two-dimensional schema of size $n_1 \times n_2$, then

$$n(\sigma, t+1) \geq n(\sigma, t) \cdot \frac{f(\sigma, t)}{\overline{f(t)}} \cdot$$

$$\cdot [1 - p_c \frac{\delta_i \cdot n_2 + \delta_j \cdot n_1 - \delta_i \cdot \delta_j}{(n_1 \cdot n_2 - 1)} - \omega(\sigma) p_m],$$

Proof. In most of its parts the proof of this theorem is identical to that of the one-dimensional Schema Theorem. Thus we will only insist on the only significant difference which is the estimation of the survival probability of a schema from one generation to the next one.

It is easy to observe that there are $\delta_I \cdot_2 + \delta_j \cdot_1 - \delta_I \cdot \delta_j$ crossover points in an $n \times m$ chromosome that disrupt a schema of dimension $\delta(\sigma) = (\delta_I, \delta_j)$.

This allows us to state that the survival probability of a schema σ of defining size $\delta(\sigma) = (\delta_I, \delta_j)$ is given by

$$p_s(\sigma) = \frac{n(\delta_i + \delta_j) - \delta_i \cdot \delta_j}{n^2 - 1}.$$

The remaining part of the proof is identical to the proof of the one-dimensional Schema Theorem. □

This theorem only shows that a GA using the chosen coding and the above defined crossover operator behaves in a similar way to the one using linear coding and crossover.

Crossover: Two dimensional vs. One dimensional

In the previous subsection we showed that a genetic algorithm using the two-dimensional encoding and crossover operator defined earlier behaves the same way as one using a linear encoding and single-point crossover.

In the following we shall study in what situations the use of this encoding and crossover can be advantageous. To do this let us consider a schema of dimensions (n_1, n_2) with the defining matrix given by (i_1, j_1) and (i_2, j_2), where $j_1 < j_2$). We shall estimate the probability with which this schema will be disrupted on one hand if the schema is rearranged by rows and a one-point linear crossover is applied, on the other hand if the two-dimensional crossover is used.

We illustrate our reasoning on the following example. Let us consider again the schema used earlier:

$$\begin{array}{ccccc} * & * & * & * & * \\ * & * & * & * & * \\ * & * & 0 & * & 1 \\ * & * & 1 & 0 & * \\ * & * & * & * & * \end{array}$$

If we rearrange this schema by rows we obtain the following linear schema:

centerline* * * * * * * * * * * * $\boxed{0 * 1}$* * $\boxed{1 0 *}$* * * * *

We can note that the defining length of the linear schema is $\delta(\sigma) = \delta_i n_2 + \delta_j$.

Generally we can state that the probability $p_d(\sigma)$ that a two-dimensional schema σ of dimension (n_1, n_2) and defining size (δ_I, δ_j) is disrupted by a single point crossover applied to its linear encoding satisfies the following double inequality:

$$\frac{\delta_i n_2 - \delta_j}{n_1 \cdot n_2 - 1} \le p_d(\sigma) \le \frac{\delta_i n_2 + \delta_j}{n_1 \cdot n_2 - 1}.$$

On the other hand we have already seen that the probability that the same schema is disrupted by a two-dimensional crossover is given by

$$\frac{\delta_i \cdot n_2 + \delta_j \cdot n_1 - \delta_i \cdot \delta_j}{n_1 \cdot n_2 - 1}$$

$$d_p^1 \le d_p^2 \le D_p^1,$$

where d_p^1 and D_p^1 denote the least and greatest disruption probability respectively for the one dimensional crossover, while d_p^2 denotes the disruption probability for the two dimensional crossover.

Proof.

$$d_p^1 = \frac{\delta_i n_2 - \delta_j}{n_1 \cdot n_2 - 1}$$

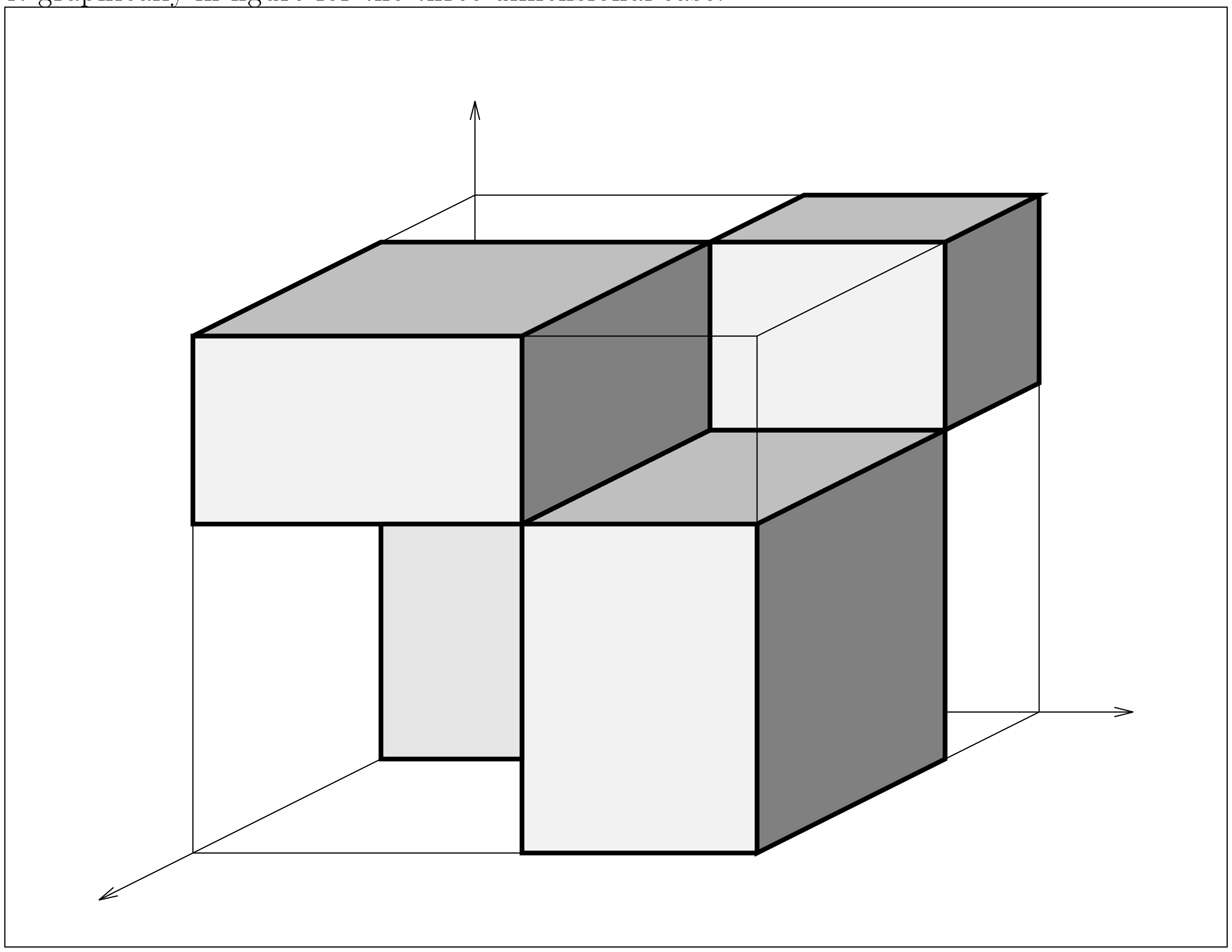
$$d_p^2 = \frac{\delta_i \cdot n_2 + \delta_j \cdot n_1 - \delta_i \cdot \delta_j}{n_1 \cdot n_2 - 1}$$

$$D_p^1 = \frac{\delta_i n_2 + \delta_j}{n_1 \cdot n_2 - 1}.$$

2.4 Multidimensional Encoding and Crossover

In this section we only present the results obtained for the n-dimensional case. The reasoning behind these results is similar to the two-dimensional case, the difference consisting only in the complexity of the computations needed.

To give an intuitive idea of how crossover is defined in the n-dimensional case we illustrate it graphically in figure for the three-dimensional case.



It is easy to show that the disruption probability for the n-dimensional case is given by

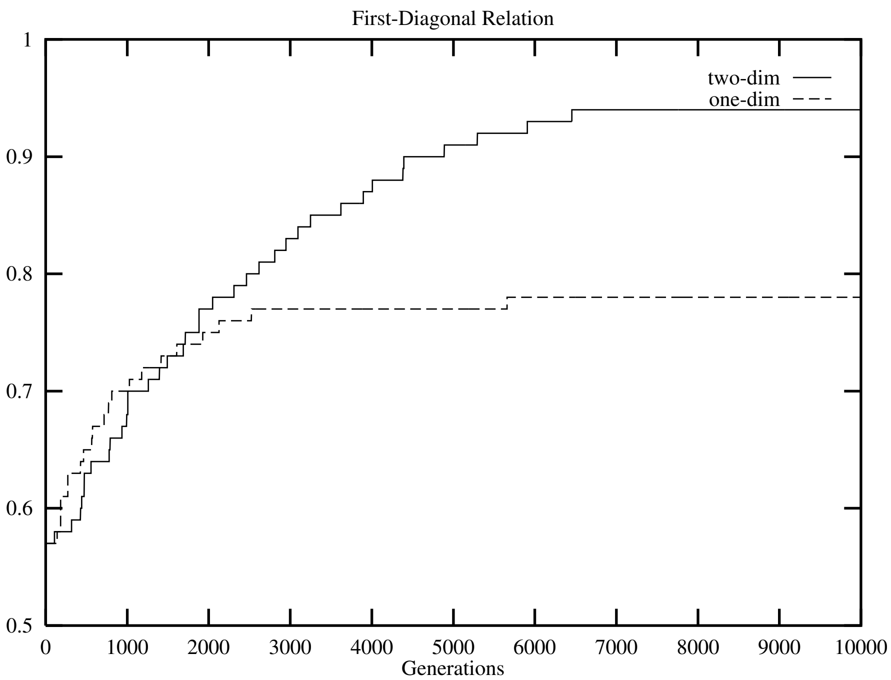
$$p_d = \frac{\sum_{i=1}^{n} \delta_1 ... \delta_{i-1} d_i \delta_{i+1} ... \delta_n - (n-1) \prod_{i=1}^{n} \delta_i}{\prod_{i=1}^{n} d_i}$$

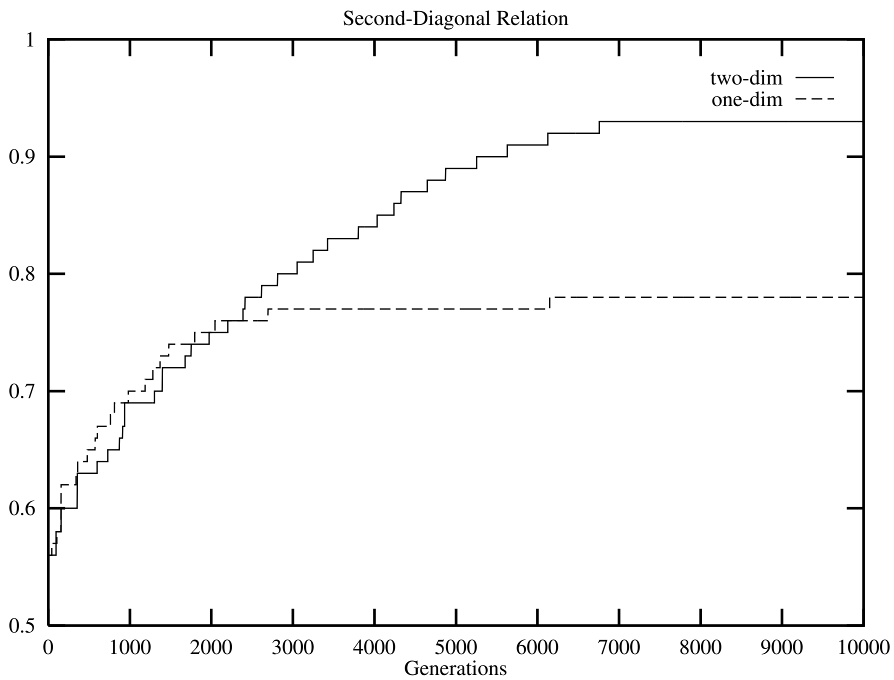
Based on tthis the n-dimensional Schema Theorem (using similar definitions and notations as above) can be formulated as follows:

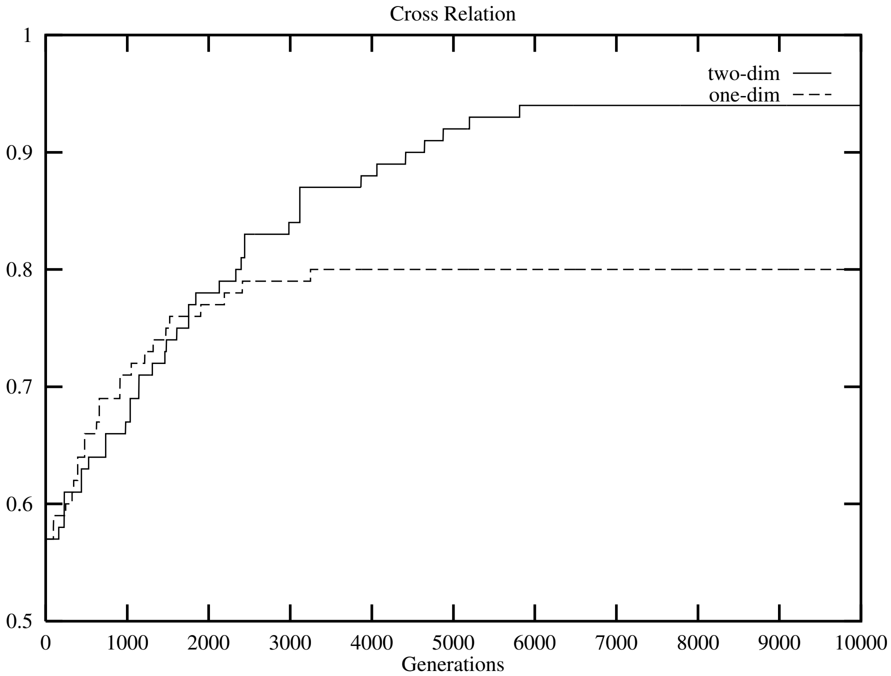
Theorem 2.4.1. if σ is an n-dimensional schema of size $d_1 \times d_2 ... \times d_n$, then

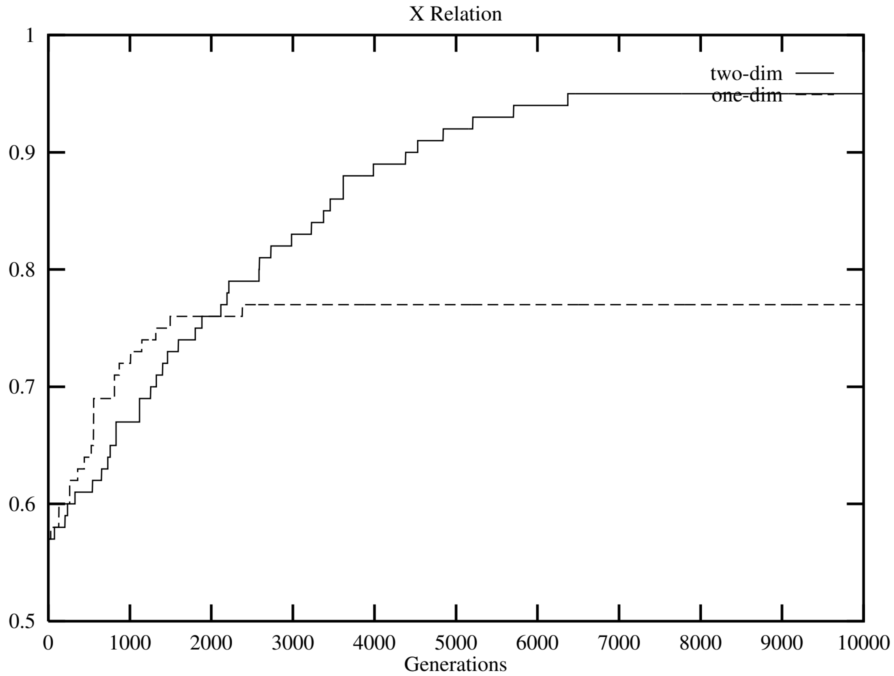
$$n(\sigma, t+1) \geq n(\sigma, t) \cdot \frac{f(\sigma, t)}{\overline{f(t)}}[1 - p_c \cdot p_d - \omega(\sigma) p_m],$$

3 Experimental Results









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