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Genetic algorithms: bridging the convergence gap ☆

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Abstract

In this paper we consider the extension of genetic algorithms (GAs) with a probabilistic Boltzmann reduction operator and prove their convergence to the optimum. The algorithm can be seen as a hybridisation between GAs and simulated annealing (SA), i.e. a SA-like GA. The "temperature" parameter allows us to control the size of the entries of the probabilistic transition matrix of the corresponding Markov chain. In the limit case of temperature zero, the reduction operator becomes a kind of strong elitism. Convergence to the optimum is shown under very mild conditions for the sequence of temperatures $\{c_k\}$. This means that the proposed algorithm is quite robust, and can be expected to perform well on practical applications. © 1999 Elsevier Science B.V. All rights reserved.

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1. Introduction

We assume that the reader is familiar with the concepts involved in the application of GAs and SA to combinatorial optimisation problems. In this context, GAs act as global random search algorithms. To study them, the appropriate formal setting is their formulation as Markov processes. There has been, in the recent literature, a lot of work on the Markov modelling of GAs, from which a conclusion has become common knowledge: it can not be proven that simple (sometimes called canonical) genetic algorithms (selection + crossover + mutation) converge to the optimum of the fitness function. The Markov chain that models them converges towards a probability distribution that assigns non-zero probabilities to every population.

However there is a class of GAs that converges to the optimum: the Elitist GA [4, 15]. On the other hand elitist GA convergence can be trivially verified from the

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observation of the structure of the transition matrix of the Markov chain. This chain converges towards a probability distribution that assigns non-zero probabilities only to the populations that contain the optimum.

But the deterministic decision of preserving the best fitted individual seems to crack the idea of GAs as global *random* search algorithms. Elitism can be seen as an instance of a reduction operator.

Reduction operators were introduced by Eiben et al. [5], where rather general conditions for convergence were discussed. In this work, a strong condition on the reduction operator was set to guarantee convergence: the reduction operator must be conservative (it must preserve the best fitted individual). Our work in this paper shows that a probabilistic reduction operator based on a Boltzmann distribution built up from the fitness of the individuals, is enough to guarantee the convergence to the optimum under very general conditions on the sequence of "temperatures" $\{c_k\}_{k=0,1,\ldots}$ used.

The use of a Boltzmann distribution is clearly inspired by the well-known results obtained for the SA [17]. There have been in the literature other attempts to bring the desirable convergence properties of SA into the GA realm [2, 3, 11, 16]. All of them have failed to prove the convergence to the optimum of their respective instances of the GA, unless they introduce basic changes in the algorithm.

Davis and Príncipe [3] tried to use the mutation probability as a temperature parameter. They proved that as the mutation probability goes to zero, the Markov chain converges towards a stationary probability distribution in which only states (i.e. populations) with all the individuals identical (i.e. uniform populations) have non-zero probabilities. This result is far away from the desired convergence to the optimum. However, their work together with the work of Vose [18], Rudolph [13, 14] and Suzuki [15, 16] have set the analytical framework of the GA study, and we have made an extensive use of these ideas in this paper.

Suzuki [16] using the Davis and Príncipe approximation designed a SA-like GA. His algorithm is based not only in making the mutation probability go to zero, but also the crossover probability and a fitness ratio. He proved that his algorithm converges to the uniform population with the optimum individual as we do. This work has very similarities with our own. Instead of using a reduction operator he used a probabilistic selection operator that in the limit case acts as a elistist selection same as our reduction operator. The main difference with our approach is that for converge he has to maintain the same bound as Davis and Príncipe on the decreasing sequence of the mutation probability, while we have not any bound on the sequence of our "temperature" parameter.

Bilbro et al. [2], give an algorithm called genetic-annealing algorithm where they consider basically a SA but, instead of maintaining an individual in each step, they have a population. They showed that this algorithm can inherit the convergence properties of SA.

In Mahfoud and Goldberg [11] a summary of other attempts made in the same way can be found. In addition they propose a new algorithm called Parallel Recombinative Simulated Annealing (PRSA). PRSA can be interpreted as a GA where to choose the individuals that go to the next population a competition is carried out between the

parents and the children using a Boltzmann-like function. They give a convergence proof for a variant of their algorithm. It differs from our own in several points: their selection is uniform, their algorithm can be seen as a steady state algorithm, their reduction operator is local, and our convergence results are more general than those discussed in their paper.

Boltzmann-like functions have been used in GAs in the selection operator. Goldberg [7] and Mahfoud [10] have explored the use of a Boltzmann distribution as the selection function: the Boltzmann tournament selection (BTS). As it is clearly impossible to prove the convergence to the optimum by the mere application of BTS, their aim was to demonstrate the BTS preservation of diversity, which implies that the GA will fall less frequently into "bad" absorbing states given by uniform populations of suboptimal individuals. The key parameter to ensure the preservation of diversity is, of course, the temperature.

Finally it is convenient to mention the quantity of work that has been dedicated to create hybrid algorithms between the SA and the GA, as an example can be seen [9].

In this paper, we construct a SA-like GA giving a concrete form to the probabilistic reduction operator: a Boltzmann reduction operator. We believe that the proposed algorithm is the most natural and elegant mixture between GAs and SA, preserving the fundamental concepts behind each of them. The proposed algorithm maintains the use of evolving populations to perform the search in the solution space as it is done by the GA, and allows the control of the convergence via a parameter as SA.

In addition, we show the convergence of the algorithm to the optimum as $c_k \to 0$ for any descending scheduling of c_k. We will show that the algorithm can be modelled by an inhomogeneous Markov chain and this chain converges towards a probability distribution that assigns non-zero probabilities only to the uniform population whose individuals are the optimum.

Moreover, the temperature parameter gives us the possibility to control the diversity in the population as with the BTS, and in some sense the *degree* of elitism. The Boltzmann reduction operator can be interpreted in two different ways. It can be seen as a relaxed strong elitism or as a probabilistic model for strong elitism.

The remaining of the paper is arranged as follows. Section 2 describes the GA with reduction operator and gives the one used in this paper. Section 3 gives the Markov model for the algorithm and section 4 shows the weak and strong ergodicity of the Markov chain. The paper finishes with a conclusion section.

2. GA with reduction operator

We propose an algorithm in which an iteration is composed by the application of selection, crossover, mutation and the reduction operator. The concrete form of the reduction operator is the main difference between our approach and simple GAs, or the GA exposed in [5]. This operator depends on the temperature parameter which can change in each iteration of the algorithm.

```
Initialize_Population(P_0)
Initialize_Temperature(c_0)
k = 0
while not stop do
  begin
  do n/2 times
    begin
      Select two parents from P_k
      Generate two children using a recombination operator
      Mutate the two children
      Introduce the children in the children population CH
    end
  Make the extended population P' = P_k ∪ CH
  Using the reduction operator reduce the extended population P' to
    the original size to obtain P_{k+1}
  Modified_Temperature (c_{k+1})
  k := k + 1
  end
```

Fig. 1. A pseudo-code for the GA with reduction operator.

If we suppose that the size of the population for the algorithm is n, then a pseudo-code for the algorithm can be seen in Fig. 1.

In this algorithm we suppose that the selection is carried out as in the simple GA, i.e. an individual is selected with certain probability proportional to its fitness function. If other selection schemas are applied the convergence results are still valid. The recombination operator may be one-point, two-point or uniform crossover, for all of them the convergence results are maintained. We suppose that this operator is carried out with probability $p_c = 1$. The mutation operator is as in the simple GA, i.e., a bit is flipped with a small probability p_m.

The reduction operator consists of sampling a Boltzmann probability distribution in the extended population (the union as multisets of the parents and children populations). The value of this probability distribution depends on the fitness function of the individuals of the extended population. In this sense we assign to each individual i (parent or child) a probability:

$$\frac{1}{R(c_k)} \exp\left(\frac{F(i) - \overline{F}}{c_k} \right) \tag{1}$$

to be chosen for the next population, where $R(c_k)$ is the normalisation constant and $\overline{F}$ is the mean value of the fitness function F in the *parents* population. Therefore, for sampling the Boltzmann probability distribution the reduction operator, in the case of maximisation, works as follows (this is a development of the previous algorithm line: "Using the reduction operator reduce the extended population P' to the original size

to obtain P_{k+1}"):

while not n individuals have been selected **do**
begin
choose an individual i at random from the extended population
if $F(i) > \overline{F}$ **then**
select individual i for the next population
else
select individual i with probability equal to $\exp\left(\frac{F(i)-\overline{F}}{c_k}\right)$
end

i.e., an individual of the extended population is chosen at random, and if $F(i) > \overline{F}$ the individual is selected for the next population while in the opposite situation the individual is accepted with probability given by

$$\exp\left(\frac{F(i)-\overline{F}}{c_k}\right).$$

This cycle is repeated until n individuals have been selected.

Some other expressions for the reduction probability can be thought of, such as the exponential of the difference $F(i) - F_{\max}$ (where $F_{\max}$ is the maximum value of the fitness function in the parents population) and the convergence properties do not change. However, in Eq. (1), $\overline{F}$ is the smallest value that ensures convergence to the optimum (in a probabilistic sense).

Moreover, it can be seen that our probabilistic reduction operator becomes a kind of strong elitist reduction operator in the limit case $c_k \to 0$, in the sense that, this operator chooses only individuals whose fitness function is better than the mean fitness function value of the parents population.

3. Formalisation

This notation and the model that follows are borrowed mainly from [3, 12, 17].

We want to find the maximum F^* (the minimisation problem is similar) of a function $F : \Omega \to \mathbb{R}^+$, where the search space is $\Omega = \{0,1\}^l$, i.e. Ω is the set of the 0–1 vectors of length l. We denote the cardinality of this set $|\Omega| = N = 2^l$. A population in the algorithm is a subset (as multiset) of size n of elements of Ω. Each population can be represented as a vector $Z_s = (z_{0s}, z_{1s}, \ldots, z_{N-1s})$ where z_{is} is representing the number of i individuals in the population Z_s. Of course, $\sum_{i=0}^{N-1} z_{is} = n$. The number of different populations, r, is equal to the number of different ways to introduce $N-1$ balls in $n+N-1$ boxes, i.e.

$$r = \binom{n+N-1}{N-1}.$$

As the population in the $k+1$th step of the algorithm only depends on the population in the kth step, the algorithm can be modelled by means of a Markov chain. Given that this chain depends on the time (depends on the temperature parameter c_k used in the reduction operator), the chain will be a *time-inhomogeneous Markov chain*.

For simplicity, in the following we assume that F is an injective function, but the same results can be obtained for the most common case of non-injective fitness function.

For the Markov model formulation, it is essential to define an order among the populations. To do that we can make a permutation of the elements of the vectors representing the populations. This permutation is carried out following the order imposed by the injective function F on the individuals of the search space Ω. The number of the best individual is put in the first position, the number of second best in the second, and so on. Once this permutation has been made the vectors Z_s can be considered N-ary numbers and the order among the populations is given by the order of these numbers.

Under this order the first population will be the uniform population composed of the optimum individual, and the last population will be the uniform population composed by the worst individual of Ω.

Based on this order for the populations it is possible to give an expression for the entries of the transition matrix $Q(c_k) = (q_{s,t}(c_k))_{s,t=1,\ldots,r}$ of the inhomogeneous Markov chain that models the algorithm with reduction operator. Here $q_{s,t}(c_k) = P(Z(k+1) = Z_t \mid Z(k) = Z_s)$ is representing the probability to go from population Z_s in the kth generation to population Z_t in the $k+1$th generation. The entries of the matrix can be written as

$$q_{s,t}(c_k) = \sum_{v \in C_s^t} p_{s,v} PR_{s \cup v,t}(c_k)$$

where

- $p_{s,v}$ is the probability to go from the population Z_s to the population Z_v by the application of selection, crossover and mutation. Note that it is a time-independent expression.
- C_s^t is the set $\{Z_v \mid \forall i \in Z_t \Rightarrow i \in Z_s \cup Z_v\}$ where the $\cup$ is considered the union in multisets. This is the set of all possible populations that can be generated from Z_s so that the application of the reduction operator could obtain Z_t from $Z_s \cup Z_v$.
- $PR_{s \cup v,t}(c_k)$ is the probability to obtain, through the application of the reduction operator, the population Z_t from the union (as multisets) of the populations Z_s and Z_v.

The probabilities $p_{s,v}$ can be found explicitly in [3, 12].

The new term in the latter expression, that is, the reduction probability PR, is given by the next formula:

$$PR_{s \cup v,t}(c_k) = \frac{n!}{z_{0t}! z_{1t}! \ldots z_{N-1t}!} \prod_{i=0}^{N-1} \left(\frac{z_{is \cup v}}{R_s^v(c_k)} \exp\left(\frac{F(i) - \overline{F}^s}{c_k} \right) \right)^{z_{it}}$$

$$= \frac{n!}{z_{0t}!z_{1t}!\ldots z_{N-1t}!} \frac{(z_{0s\cup v})^{z_{0t}}(z_{1s\cup v})^{z_{1t}}\ldots(z_{N-1s\cup v})^{z_{N-1t}}}{(R_s^v(c_k))^n}$$
$$\times \exp\left(\frac{(\sum_{i=0}^{N-1} z_{it}F(i)) - n\overline{F}^s}{c_k}\right)$$

where the expression $\overline{F}^s$ is the mean value that takes the fitness function F in the population Z_s, and $R_s^v(c_k)$ is the normalisation constant that can be written as

$$R_s^v(c_k) = \sum_{i=0}^{N-1} z_{is\cup v} \exp\left(\frac{F(i) - \overline{F}^s}{c_k}\right)$$

$z_{is\cup v}$ representing the number of i individuals in the population union $Z_s \cup Z_v$. This is a multinomial distribution in which each individual is selected according to Eq. (1).

The structure of the matrix is controlled by the "annealing" parameter c_k. In the limit case $c_k \to 0$, the matrix $Q(c_k)$ becomes lower triangular by boxes, that is, the best population (the population Z_1) becomes the only absorbing state of the Markov process. This limit case is quite similar to the deterministic elitism, where we take the best n individuals from the union of the parents and children populations to form the population in the next generation. It supports the claim made in the introduction about the Boltzmann reduction operator as a probability model for strong elitism.

4. Convergence

In this section we examine the convergence of the algorithm.

If we denote by $q(c_k)$ the probability distribution of the different populations after k steps of the algorithm, i.e.:

$$q(c_k) = q(c_0)Q(c_0)Q(c_1)\ldots Q(c_{k-1})$$

and if we denote by $Q(c_{m,k})$, for $m < k$, the next stochastic matrix:

$$Q(c_{m,k}) = Q(c_m)Q(c_{m+1})\ldots Q(c_{k-1})$$

then it will be shown that there exists a probability distribution q that assigns probability 1 to the uniform population that has all its individuals equal to the optimum (we call this the optimum population), and such that for all m:

$$\lim_{k\to\infty} \sup_{q(c_0)} ||q(c_0)Q(c_{m,k}) - q|| = 0$$

i.e., the sequence converges in norm towards the distribution q. That means in terms of the algorithm that it converges to the optimum population. The results will be given for the L_1 norm.

The only condition that we have to impose is that the sequence of $\{c_k\}$ complies with the next properties:

- $\exists\ k^*$ such $\forall k > k^* \quad c_{k+1} \leqslant c_k$
- $\lim_{k\to\infty} c_k = 0$

To prove the previous convergence to the optimum we have to show that the inhomogeneous Markov chain is *weakly* (Section 4.1) and *strongly* (Section 4.2) ergodic. Once we have shown the strong and weak ergodicity it is sure that the inhomogeneous Markov chain converges towards a probability distribution. Even more, this probability distribution is the same as the limit of the sequence of the different stationary distributions $\{\pi(c_k)\}_{k=0}^{\infty}$ of the homogeneous Markov chains $Q(c_k)$ (with c_k fixed). So finally, we have to show that this sequence converges towards a distribution that assigns probability 1 to the optimum population (Section 4.3).

Weak and strong ergodicity will be shown making use of the classical characterisation theorems which we reproduce as stated in [8], p. 151 and p. 160, but adapted to our problem and notation:

Theorem 1. *An inhomogeneous Markov chain is weakly ergodic if there exists an increasing sequence of integers* $k_1, k_2, \ldots, k_l, \ldots$ *such that*

$$\sum_{l=1}^{\infty} \alpha(Q(c_{k_l,k_{l+1}})) = \infty$$

where $\alpha(Q)$ *is representing the ergodicity coefficient of an* $r \times r$*-matrix* Q*, and is defined as*:

$$\alpha(Q) = \min_{s,v} \sum_{t=1}^{r} \min(q_{s,t}, q_{v,t}).$$

Theorem 2. *An inhomogeneous Markov chain is strongly ergodic if it is weakly ergodic and if for all* k *there exists a vector* $\pi(c_k)$ *such that* $\pi(c_k)$ *is an eigenvector with eigenvalue* 1 *of* $Q(c_k)$*, and complies*:

- $\sum_{s=1}^{r} \pi_s(c_k) = 1$,
- $\sum_{k=0}^{\infty} \sum_{s=1}^{r} |\pi_s(c_k) - \pi_s(c_{k+1})| < \infty$.

Moreover, if $\pi = \lim_{k\to\infty} \pi(c_k)$ *then* π *satisfies*

$$\lim_{k\to\infty} q_{s,t}(c_{m,k}) = \pi_t$$

where $q_{s,t}(c_{m,k})$ *is the* (s,t) *entry of the matrix* $Q(c_{m,k})$.

That a Markov chain is weakly ergodic means that the effect of the initial distribution is lost with the time. A strongly ergodic Markov chain is a chain where the sequence of the probability distributions $\{q(c_k)\}_{k=0,1,\ldots}$ converges in norm towards a probability distribution q.

4.1. Weak ergodicity

To prove the weak ergodicity of the Markov chain we are going to examine the entries of the first column of the matrices, i.e., the probabilities to obtain the optimum population (denoted by **1**) from any other population. We show that all these numbers

are greater than 0 for any value of c_k and they are bounded by a number greater than zero. This will suffice for implying that the sum $\sum_{k=0}^{\infty}\alpha(Q(c_k))$ is ∞ (we take as sequence k_l of the theorem as the numbers $0,1,2,\ldots$).

The entries of the first column of the matrix are

$$q_{s,\mathbf{1}}(c_k)=\sum_{t\in C_s^{\mathbf{1}}} p_{s,t}PR_{s\cup t,\mathbf{1}}(c_k) \tag{2}$$

$$=\sum_{t\in C_s^{\mathbf{1}}} p_{s,t}\frac{n!(z_{0s\cup v})^{z_{01}}(z_{1s\cup v})^{z_{11}}\ldots(z_{N-1s\cup v})^{z_{N-11}}}{z_{01}!z_{11}!\ldots z_{N-11}!}\frac{\exp\left(\frac{n(F^*-\overline{F}^s)}{c_k}\right)}{R_s^t(c_k)^n} \tag{3}$$

where

$$R_s^t(c_k)=\sum_{i=0}^{N-1} z_{is\cup t}\exp\left(\frac{F(i)-\overline{F}^s}{c_k}\right).$$

There exists an $i^*\in\{0,1,\ldots,N-1\}$ such that $F(i^*)=F^*$. Hence, if we only have into account the terms that depend on c_k we have that the limit when $c_k\to 0$ is

$$\lim_{c_k\to 0}\frac{\exp(\frac{n(F^*-\overline{F}^s)}{c_k})}{R_s^t(c_k)^n}=\frac{1}{(z_{i^*}s\cup v)^n}.$$

so finally we obtain:

$$\lim_{c_k\to 0} q_{s,\mathbf{1}}(c_k)=\sum_{t\in C_s^{\mathbf{1}}} p_{st}.$$

Therefore as for all k the numbers $q_{s,\mathbf{1}}(c_k)$ are for all s different from zero (it is clear from the definition of these numbers) and the limit is different from zero, now it can be stated that

$$\sum_{k=1}^{\infty}(\alpha(Q(c_k))=\sum_{k=1}^{\infty}\min_{s,v}\sum_{t=1}^{r}\min(q_{s,t}(c_k),q_{v,t}(c_k))\geqslant\sum_{k=1}^{\infty}\delta=\infty$$

where $\delta=\min_{k,s}(q_{s,\mathbf{1}}(c_k))$ which completes the proof.

Observe that to prove the weak ergodicity, we have not needed to impose any condition on the sequence c_k of values of the control parameter. So, that implies that the algorithm will be extremely robust in the sense that almost any $\{c_k\}$ sequence will give good approximations. Compare with the slow $\{c_k\}$ sequence needed for the SA, where $c_k\geqslant\Gamma/\log k$ for a given constant Γ [17].

This lack of bound in the sequence $\{c_k\}$ allows us to tune it as we want. If there exists a k' such that for all $k>k'$ the sequence of $\{c_k\}$ is non-increasing then the convergence is guaranteed.

4.2. Strong ergodicity

To show the strong ergodicity using Theorem 2, first we have to give an explicit expression for the stationary distribution of the different Markov chains for all k (or

the left eigenvectors with eigenvalue 1). These distributions exist because if we fix c_k, the Markov chain is homogeneous, so following Feller [6] if the chain is irreducible (it is possible to go from one state to another in a finite number of steps) and aperiodic (given that it is irreducible it is enough that $q_{ss} > 0$) there exists a stationary distribution, and both conditions are complied trivially.

It has been showed by Anily and Ferdergruen [1] that this stationary distribution can be expressed as follows:

$$\pi_s(c_k) = \frac{|Q_s(c_k) - I|}{\sum_{t=1}^{r} |Q_t(c_k) - I|} \tag{4}$$

where the matrix $Q_s(c_k)$ is the matrix $Q(c_k)$ but with the s line changed by zeros.

Using the Perron–Frobenious theorem (e) (Appendix), it can be seen that because $Q_s(c_k) \leqslant Q(c_k)$ we have that 1 is not an eigenvalue for $Q_s(c_k)$ so all of these determinants are different from 0, and all have the same sign.

On the other hand because the entries of the stochastic matrices $q_{s,t}(c_k)$ are rational functions with exponential functions in the numerator and in the denominator it can be deduced that these expressions are continuous and their first derivates are again continuous functions of c_k (for all $c_k \neq 0$) if we consider it as a continuous parameter. Then it is possible to apply the mean value theorem to obtain:

$$|\pi_s(c_{k+1}) - \pi_s(c_k)| = \left| \frac{\mathrm{d}\pi_s(c)}{\mathrm{d}c}\bigg|_{c=c_*} (c_k - c_{k+1}) \right|$$

with c_* a real number in the interval (c_{k+1}, c_k).

Then the expression that we have to bound is written as follows:

$$\sum_{k=0}^{\infty} \sum_{s=1}^{r} |\pi_s(c_{k+1}) - \pi_s(c_k)| = \sum_{k=0}^{\infty} \sum_{s=1}^{r} \left| \frac{\mathrm{d}\pi_s(c)}{\mathrm{d}c}\bigg|_{c=c_*^{s^k}} (c_{k+1} - c_k) \right|$$

and it is possible to define a new continuous function Θ extending π by continuity in 0,

$$\Theta(c) = \begin{cases} \frac{\mathrm{d}\pi}{\mathrm{d}c} & \text{if } c \neq 0 \\ \lim_{c \to 0} \frac{\mathrm{d}\pi}{\mathrm{d}c} & \text{if } c = 0 \end{cases}$$

which we will use to bound the latter series. The function Θ can be bounded in $[0, 1]$ because it is continuous. If we call Δ its maximum we have

$$|\pi_s(c_{k+1}) - \pi_s(c_k)| \leqslant \Delta(c_{k+1} - c_k)$$

and therefore

$$\sum_{k=0}^{\infty} \sum_{s=1}^{r} |\pi_s(c_{k+1}) - \pi_s(c_k)| \leqslant \sum_{s=1}^{r} \Delta c_0 \leqslant r\Delta c_0 < \infty$$

Hence the strong ergodicity has been shown.

It is important to note at this point, that the sequence $\{\pi(c_k)\}_{k=0,1\ldots}$ of stationary distributions of the homogeneous Markov chains $Q(c_k)$ with c_k fixed are only tools to demonstrate that the inhomogeneous Markov chain converges. The algorithm does not need to realize all this homogeneous stationary Markov chains, in fact note that the temperature parameter can change in each step of the algorithm.

4.3. Convergence of the stationary distributions sequence

To finish we must show that the sequence $\{\pi(c_k)\}_{k=0,1,\ldots}$ converges to a probability distribution that assigns non-zero probabilities only to those populations that contain the optimum. We can even prove something stronger: the limit of this stationary distribution is going to assign non-zero probabilities only to the state **1**, i.e. the state that has all the individuals the same: the optimum. In the case of a non-injective function, the limit probability distribution would assign non-zero probability to the states that only contain optimal individuals. This is evident if we take into account the next limit property:

$$\lim_{k\to\infty} q_{\mathbf{11}}(c_k) = 1$$

The latter limit can be deduced easily using Eq. (3). This implies that:

$$\lim_{k\to\infty} \pi_s(c_k) = \lim_{c_k\to 0} \frac{|Q_s(c_k) - I|}{\sum_{t=1}^{r} |Q_t(c_k) - I|} = \begin{cases} 0 & \text{if } s \neq \mathbf{1} \\ 1 & \text{if } s = \mathbf{1} \end{cases}$$

Therefore the convergence to the optimum has been shown.

5. Conclusions

This paper has introduced an explicit random reduction operator which endows GA with convergence to the optimum without having to use deterministic elitism. At the same time the algorithm proposed seems to be the logical and more natural mixture between Genetic Algorithm and Simulated Annealing. The freedom in the scheduling sequence of the c_k allows us to control the evolution of the algorithm. Further work must be addressed to study the convergence speed and its dependence on the scheduling of the c_k. Other desirable properties of GAs like diversity preservation must be studied in detail for this algorithm too. Experimental work to demonstrate the practical usefulness of the proposed algorithm is on the way.

Appendix

Definition 3. *If there exists a positive integer k such that the stochastic matrix P satisfies $P^k > 0$ then P is primitive.*

An irreducible, aperiodic stochastic matrix is primitive.

The Perron–Frobenius follows:

Theorem 4. *Let P be a primitive, stochastic matrix. Then, there exists an eigenvalue ρ of P such that*

(a) $\rho = 1$.
(b) *With $\rho = 1$ can be associated strictly positive left and right eigenvectors.*
(c) $\rho = 1 > |\lambda|$ *for any eigenvalue* $\lambda \neq \rho$.
(d) *The eigenvectors associated with $\rho = 1$ are unique to constant multiples.*
(e) *If $0 \leqslant B \leqslant P$ and β is an eigenvalue of B, then $|\beta| \leqslant r$. Moreover, $|\beta| = \rho = 1$ implies $B = P$.*

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