Behavior Analysis of Real–Valued Evolutionary Algorithms for Independent Loci in an Infinite Population

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Although most of theoretical researches on behavior of Evolutionary Algorithms (EAs) through generations are ones using discrete variables as chromosomes, some researchers have focused their attention on EAs that use real–valued chromosomes. Here, we also provide results on behavior of EAs with real–valued chromosomes for cases that stochastic variables on some loci of chromosomes and them on the others are independent each other, by combining our previous results (Nomura and Shimohara, 2001) with them of Qi and Palmieri (1994).

We formalize EA as follows; a chromosome is a stochastic variable in the m–dimensional Euclidean space, and alternation of one generation consists of roulette selection, recombination, and mutation by addition of independent noise with zero mean, in that order. Furthermore, we assume that the fitness function f has only finitely many global maxima and finitely many discontinuous points, and satisfies $0 < f(x) < \infty$ for $\forall x \in R^m$. Moreover, we describe the probability density function (pdf) of chromosomes in the k–th generation as $p^{(k)}(x)$. Under these assumptions, Qi and Palmieri (1994) proved that (i) the pdf after selection is $\frac{f(x)p^{(k)}(x)}{\int_{R^m} f(x)p^{(k)}(x)dx}$, (ii) the pdf after mutation is the convolution of the pdf before mutation and the pdf of additive noise in mutation, and (iii) selection and mutation maintain Gaussian property in the population.

First, we assume that f is separable for some groups of variables in the sense of $f(x_1, \ldots, x_m) = \prod_{j=1}^{L} f_j(x_{i_{j1}}, \ldots, x_{i_{jd_j}})$ $(\sum_{j=1}^{L} d_j = m)$, and the corresponding groups of loci are independent each other in the k–th generation (that is, $p^{(k)}(x_1, \ldots, x_m) = \prod_{j=1}^{L} p_j^{(k)}(x_{i_{j1}}, \ldots, x_{i_{jd_j}})$ and $p_j^{(k)}$ is the pdf of i_{j1}, …, i_{jd_j}–th loci in the k–th generation). Then, it is easily shown that the same groups of loci in the $(k+1)$–th generation are independent each other if recombination maintains this independence.

Second, we consider a special case of the above assumptions on the fitness function and loci. If f is completely separable and all the loci in the k–th generation are independent each other (that is, $L = m$), it can be shown that all the loci in the $(k+1)$–th generation are independent each other if recombination is any of one–point, multi–point, and uniform crossovers. This is shown by the fact that the pdf after these recombinations is described as the sum of the products of the pdf of some loci and that of the other loci before the recombinations (Nomura and Shimohara, 2001).

Finally, as a more special case, we assume that f is completely separate and Gaussian (that is, $f(x) = \prod_{i=1}^{m} \exp(-Q_i(x_i - x_i^*)^2/2)$), and the pdf in the 0–th generation is independent Gaussian with mean values $(\mu_1^{(0)}, \ldots, \mu_m^{(0)})$ and variances $(\Sigma_1^{(0)}, \ldots, \Sigma_m^{(0)})$. Moreover, we assume that mutation is also independent Gaussian with variances $(\sigma_{w1}, \ldots, \sigma_{wm})$ in any k-th generation. If recombination is any of one–point, multi–point, and uniform crossovers, then it is shown that the pdf in any k–th generation is also independent Gaussian with mean values $(\mu_1^{(k)}, \ldots, \mu_m^{(k)})$ and variances $(\Sigma_1^{(k)}, \ldots, \Sigma_m^{(k)})$. Furthermore, we can obtain recursive equations of $\mu_i^{(k)}$ and $\Sigma_i^{(k)}$, and it is shown that $\lim_{k\to\infty} \mu_i^{(k)} = x_i^*$ and $\lim_{k\to\infty} \Sigma_i^{(k)} = \frac{1}{2}\left\{\sigma_{wi} + \sqrt{\sigma_{wi}^2 + \frac{4\sigma_{wi}}{Q_i}}\right\} > \sigma_{wi}$.

References

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