The (μ, λ, α, β) Distribution: A Selection Scheme For Ranked Populations

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Abstract

A bilinear selection scheme for ranked populations is presented. The development of the selection scheme is motivated by the desire for a generationally dependant selection mechanism that can be adjusted in an intuitive manner. The selection mechanism is defined by a four parameter (μ, λ, α, β) bilinear cumulative probability distribution. Expressions for the mean and variance of the proposed bilinear distribution are developed along with expressions for takeover time. The mean and variance equations derived for the proposed bilinear distribution are equated with those for tournament selection for tournament sizes ranging from 2 to 10. It is shown that simple superposition of the proposed bilinear distribution allows one to approximate more complex cumulative probability distributions in an efficient manner. Expressions for the mean and variance for two superimposed bilinear distributions are provided. The resulting multi-linear selection mechanism (μ_i, λ_i, α_i, β_i, f_i), is shown to be efficient to program and allows for uncoupled control of the section pressure and selection variance in a dynamic and intuitive manner.

1 INTRODUCTION

Basic evolutionary algorithms are generally composed of two processes. The first is selection of participants for the production of the next generation and the second is manipulation of the selected individuals to form the next generation. This paper is limited in scope to the first process: selection. In particular, it focuses on development of a selection mechanism that can be used to generationally modify the selection pressure and variance in a way that is both intuitive and efficient to implement.

The motivation for a generationally dependent selection pressure is based on the argument that early generations may have individuals with small problems that are magnified by the fitness function. By lowering the selection pressure for early generations, these otherwise excluded individuals can exchange some of their genetic material with others who might find it beneficial. Later on in the genetic process, when it is necessary to focus on a particular solution (or solutions in the pareto optimal case), one can increase the selection pressure to orchestrate a soft landing in the area of the current best solution(s).

A rank based generationally dependant selection mechanism allows one to control population diversity (with the goal of preventing premature convergence) by modifying the selection pressure. It should be noted that similar effects can also be achieved with fitness proportionate selection, by strategically controlling the fitness landscape (DeJong 1999, DeJong 1975). Controlling the convergence trajectory through manipulation of the fitness landscape alone may become difficult for multi-criteria optimization problems, and it is in this respect that the authors feel that ranking combined with generationally dependant penalty exponents and generationally dependant selection pressure as proposed in (Voss and Foley 1999b, Voss and Foley 1999a) may be an effective alternative.

It should be noted that (Voss and Foley 1999b, Voss and Foley 1999a) emphasized the creation of redundant mechanisms for maintaining population diversity at the expense (somewhat) of algorithm efficiency with respect to convergence on a particular individual.

2 SELECTION MECHANISM

The selection mechanism is the heart of the genetic algorithm in that it brings individuals into the next generation. The question is: what selection mechanism is optimal for a particular evolutionary algorithm ? The optimal selection mechanism is largely a function of what combination of exploration and exploitation is appropriate for the fitness landscape being explored.

There has been considerable work to date performed on the subject of selection. The theoretical work of Holland pertaining to the optimal allocation of trials regarding the 2-armed bandit problem (Holland 1975) illustrates the tradeoffs between exploitation and generation of new information. (Goldberg and Deb 1991) introduced the concept of takeover time as a measure that can be used to compare selection schemes. Recently, the important concepts of selection intensity, selection variance, and loss of diversity have been introduced and used to compare the various selection schemes used in modern genetic algorithms (Bäck 1994a, Blickle and Thiele 1997, Gillespie 1998). The aforementioned works were primarily concerned with Generational GAs (GGAs), where all members of the previous population are deleted. Markov chain analysis has been recently used to quantify the effect of replacement strategies with respect to Steady State GAs (SSGAs). For SSGAs there are choices for the replacement strategy being implemented: Replace-Worst, Replace-Random, Replace-Oldest, and First-In First-Out (Smith and Vavak 1999).

The bilinear distribution proposed in this paper is developed in accordance with the methods given in (Goldberg and Deb 1991). Given the amount of existing research with respect to takeover time this was deemed a logical framework for introduction of a new selection mechanism. Application of the simple model proposed to more advanced analysis is straight-forward should the selection scheme be implemented by a wider audience.

Figure 1 graphically illustrates the proposed bilinear distribution (μ, λ, α, β) The critical parameters used in the distribution are defined as follows: μ is the highest rank that can be selected, λ is the population size, and α, β are the parameters that control the location of the *knee* in the bilinear distribution. As illustrated in the figure, α and β range from 0 to 1. The fundamental difference in the definition of the bilinear distribution when compared to commonly used distributions, is that the bilinear distribution starts by defining a cumulative probability distribution from which the selection probability distribution is inferred, but may never need to be explicitly calculated.

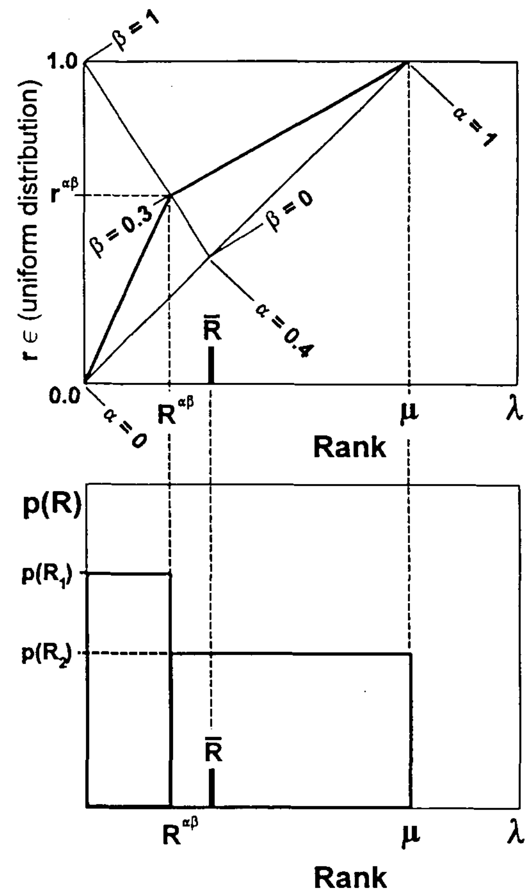

Figure 1: Bilinear Distribution (μ, λ, α, β).

Therefore, the linear cumulative distribution can be inverted so that the rank of a selected individual can be calculated directly from the following linear relationships,

$$R_1 = \frac{r\,\mu\,\alpha(1-\beta)}{\beta+\alpha(1-\beta)} \qquad \text{for } r \le r^{\alpha\beta}$$
$$R_2 = \frac{\mu\left[r\left(1-\alpha\,(1-\beta)\right)-\beta\right]}{(1-\alpha)(1-\beta)} \qquad \text{for } r > r^{\alpha\beta} \tag{1}$$

where: R is the rank of the individual and $r^{\alpha\beta}$ is the vertical location of the *knee* in the bilinear distribution given by,

$$r^{\alpha\beta} = 1 - (1-\alpha)(1-\beta) \tag{2}$$

The bilinear distribution can be contrasted with the familiar nonlinear selection probability (Bäck 1996, Michalewicz 1996),

$$p(R) = \frac{q(1-q)^{R-1}}{\left[1-(1-q)^{\lambda}\right]} \tag{3}$$

where: λ is the population size; and $q \in (0...1)$. Larger values of q imply stronger selective pressure.

If it is desired to modify the selection dynamically, a generationally dependent selection pressure parameter, q, can be defined as (Voss and Foley 1999a),

$$q = \gamma + \zeta \left[\min \left(1 , \frac{G_{curr} + 5}{G_{max}} \right) \right]^{rankExp} \tag{4}$$

where; γ and ζ are user defined constants; and *rankExp* controls how fast the pressure is modified.

An implementation difficulty with the nonlinear distribution is that at each generation the rank probabilities need to be calculated and a cumulative distribution formed. The rate at which the selection pressure is increased using equation (4) is not intuitive and it is not straight-forward to alter the selection variance. The cumulative distribution also takes the form of an array with makes the inversion of the distribution awkward. Comparison of the proposed bilinear distribution with the nonlinear distribution of (Michalewicz 1996) is shown in Figure 2.

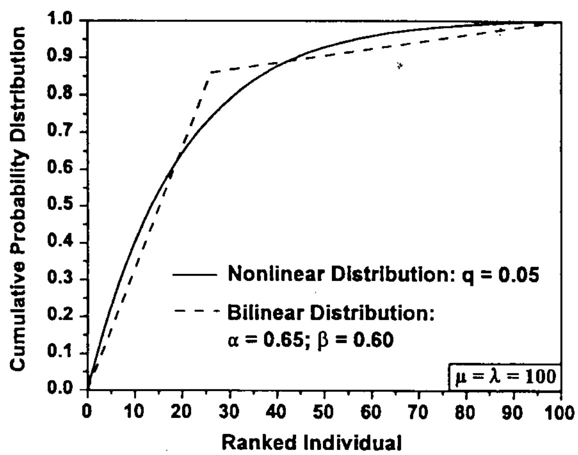

Figure 2: Comparison of Bilinear with Nonlinear Distribution.

Figure 2 illustrates that the bilinear distribution is a good approximation to the more complicated nonlinear probability model. The approximation should be adequate for most rank based evolutionary algorithms, but as it will be shown, the approximation can be improved to any degree of accuracy desired by the superposition of more than one bilinear distribution to form a multi-linear cumulative probability distribution.

The mean and the variance for the bilinear distribution where derived, and are defined as follows,

$$\bar{R} = \frac{\mu}{2}(1-\beta) \tag{5}$$

$$\sigma^2(R) = \frac{\mu^2}{12}(1-\beta)(1+3\beta-4\alpha\beta) \tag{6}$$

It should be noted that the mean not a function of α, while the variance is a function of both α and β, and that increasing α corresponds to decreasing the variance. Later the takeover time is shown to be largely a function of β.

3 TAKEOVER TIME

The takeover time for the bilinear distribution was derived using the cumulative assignment function (Goldberg and Deb 1991). This required breaking the integration into two parts:

$$\left(0 \rightarrow \frac{R^{\alpha\beta}}{\lambda} \right) \quad and \quad \left(\frac{R^{\alpha\beta}}{\lambda} \rightarrow \frac{\mu - 1}{\lambda} \right) \tag{7}$$

This results in a rather cumbersome power series with non-straightforward boundary conditions that can be solved by standard methods.

The solution of the power series resulted in the following expression for the takeover time,

$$t^{*} = \frac{\ln[\mu\alpha(1-\beta)]}{\ln\left[\frac{\beta+\alpha(1-\beta)}{\alpha(1-\beta)}\left(\frac{\lambda}{\mu}\right)\right]} + \left[1 + \frac{\ln\left[\frac{\lambda((1-\beta)+(\mu-1)\alpha(1-\beta)-\mu)+\mu(\mu-1)(1-\alpha(1-\beta))}{\lambda(1-\alpha)(1-\beta)(\alpha(1-\beta)(\mu-\lambda)-\beta\lambda)}\right]}{\ln\left[\frac{(1-\alpha)(1-\beta)}{1-\alpha(1-\beta)}\left(\frac{\lambda}{\mu}\right)\right]}\right] \tag{8}$$

which simplifies to the following when $\mu = \lambda$,

$$t^{*} = \frac{\ln[\lambda\alpha(1-\beta)]}{\ln\left[\frac{\beta+\alpha(1-\beta)}{\alpha(1-\beta)}\right]} + \left[1 + \frac{\ln\left[\frac{1}{\lambda(1-\alpha)(1-\beta)}\right]}{\ln\left[\frac{(1-\alpha)(1-\beta)}{1-\alpha(1-\beta)}\right]}\right] \tag{9}$$

The following investigation of the characteristics of the takeover time derived for the bilinear distribution was done for the case when ($\mu = \lambda = 100$) . The conclusions reached can be extended to other cases without loss of generality.

Figure 3 illustrates the variation in takeover time (equation 9) with the parameters α and β. It is observed that the takeover time in the bilinear expression is virtually independent of α. This implies a solid correlation between the takeover time and mean which is a function of β only. Therefore, the takeover time expression given by equation (9) can be simplified considerably by setting $\alpha = 0.5$ and expanding the resulting expression in a 2[nd] order power series about $\beta = 0$.

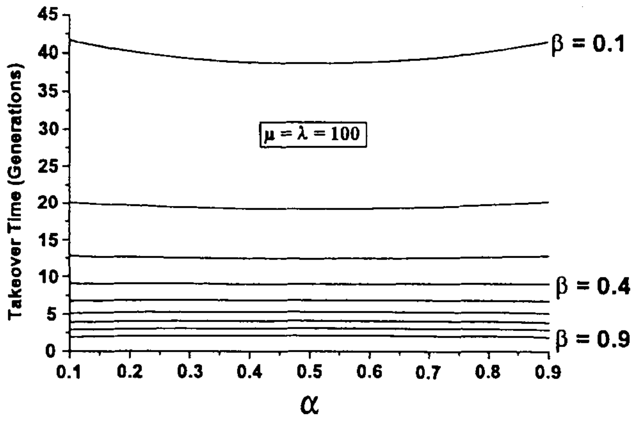

Figure 3: Variation of Takeover Times for the Bilinear Distribution

This simplification results in (valid for $\mu = \lambda$),

$$t^{*} = \frac{(3-\beta^2)\ln\lambda - (2+\beta^2)}{3\beta} \tag{10}$$

The maximum percentage error between the simplified expression given in equation (10) and the power series expression given in equation (9) is shown in Figure 4.

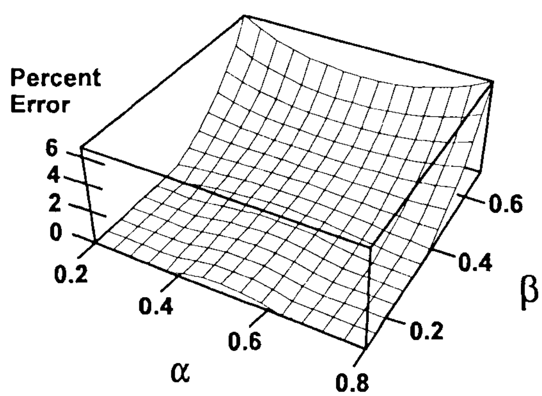

Figure 4: Percentage Error as a Function of α and β; $\mu = \lambda = (100, 1000, 10000)$.

Since the surface was generated by taking the maximum error for population sizes (λ = 100, 1000, 10000) for given values of α and β, it is demonstrated that the simplified formula is valid for large ranges of λ. As indicated in the figure, the percentage error between equation (9) and (10) is less than 7% for values of β between 0.1 and 0.7 and values of α between 0.2 and 0.8.

4 UNCOUPLED VARIANCE

Figure 5 illustrates the effect of the variance on the shape of the generational takeover distribution.

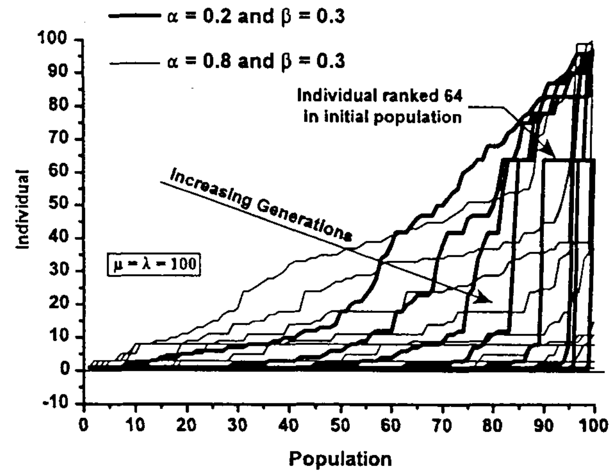

Figure 5: Generational Progression of Population Ranks Using Various Bilinear Distributions with Equal Takeover Times and Unequal Variances

Since the distributions have identical means they also have nearly identical theoretical takeover times. It is seen that large values of α (which correspond to lower selection variance) select individuals equally from a large partition consisting of the better individuals with a small selection pressure with respect to an upper partition consisting of the unfit individuals. Lower values of α (which correspond to a higher selection variance) tend to select individuals with a high selection pressure from a small partition consisting of the better individuals and a moderate selection pressure with respect to a larger partition consisting of the unfit individuals. This tends to suggest a generationally dependant selection scheme that starts out with low values of β and high values of α and transitions into high values of β and low values of α. The authors feel that this might allow maximum exploration during early generations around large areas of promising individuals while in later generations employing an elitist strategy, combining any beneficial remaining genetic material from nearly identical individuals.

5 CONVERGENCE TO (μ, λ) DISTRIBUTION

The takeover time for the (μ, λ) distribution is given by,

$$t^{*} = \frac{\ln\lambda}{\ln\left(\frac{\lambda}{\mu}\right)} \tag{11}$$

Theoretically, the bilinear distribution is an extension of the well studied (μ, λ) distribution (Bäck 1996, Bäck 1994b, Bäck 1994a). Figure 6 demonstrates the convergence of the derived takeover time (equation 9) with respect to the

(μ, λ) takeover time. The takeover time of the bilinear distribution should converge to the takeover time of the (μ, λ) distribution when $\mu = \lambda$ and α tends towards one. The graph was truncated at alpha equal to 0.9 since the derived expression for the takeover time for the bilinear distribution is based on a power series solution that is only valid for at least one generation past the knee point in the bilinear distribution.

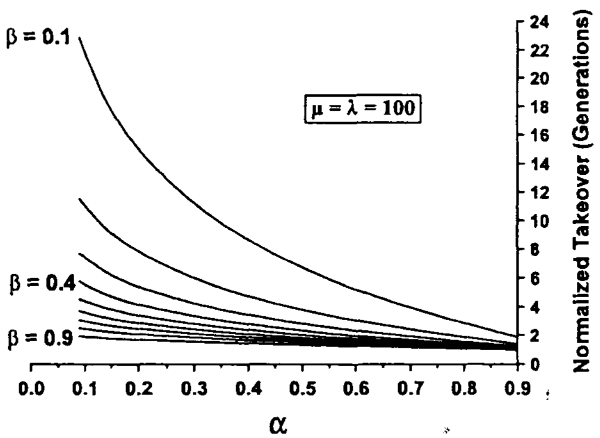

Figure 6: Bilinear Takeover Times Normalized With Respect to the (μ, λ) Distribution

Although the limiting values are not orders of magnitude off the expected value of one, they are none the less inaccurate. This is not considered a problem for practical values of α and β.

6 TOURNAMENT SELECTION

It has been shown that under certain conditions, linear ranking is equivalent to binary tournament selection (Goldberg and Deb 1991). With the admission of nonlinear ranking, the two methods can be configured to be identical from a probabilistic standpoint. Tournament selection has one major advantage over other selection methods. Namely, tournament selection has the shortest time complexity; *O(n)*. Also, since tournament selection does not require that the entire population is processed, it has advantages in distributed evolutionary environments (Harvey 1992).

Rank based selection requires sorting the entire population, which has a time complexity; $O(n \cdot ln(n))$. If the time complexity of sorting is small relative to the time complexity an individual fitness value, then the computational savings obtained using tournament selection may be negligible. In this case, ranking has the advantage of being able to *engineer* the selection distribution. As will be shown, ranking can be used to dynamically change the selection mechanism in an intuitive manner. Many researchers are already familiar with using static tournament selection. Therefore, values of α and β needed get similar convergence results to those found in tournament selection are provided. This will allow easy migration for researchers that are interested in studying dynamic selection mechanisms via the framework provided by the bilinear distribution.

The mean and variance (not given here) for tournaments sizes from 2 to 10 were set equal to equations (5) and (6) which define the mean and variance for the bilinear distribution and solved for α and β. The results are tabulated in Table 1. Equations (12) through (14) give formulas for the equivalent α and β parameters for tournament sizes 2, 3, and 4,

<u>*2-at-a-time Selection*</u>:

$$\alpha = \frac{3\lambda(-3-\lambda+\lambda^2)}{2(-1-5\lambda-5\lambda^2+2\lambda^3)}$$
$$\beta = \frac{1+3\lambda-\lambda^2}{3\lambda^2} \tag{12}$$

<u>*3-at-a-time Selection*</u>:

$$\alpha = \frac{-4-11\lambda+\lambda^2+4\lambda^3}{5(1+\lambda)(-1-2\lambda+\lambda^2)},$$
$$\beta = \frac{1+2\lambda-\lambda^2}{2\lambda^2} \tag{13}$$

<u>*4-at-a-time Selection*</u>:

$$\alpha = \frac{15\lambda^3(3-14\lambda-16\lambda^2+6\lambda^3+6\lambda^4)}{2(-1+\lambda+9\lambda^2+6\lambda^3)(1-10\lambda^2-15\lambda^3+9\lambda^4)}$$
$$\beta = \frac{-1+10\lambda^2+15\lambda^3-9\lambda^4}{15\lambda^4} \tag{14}$$

Figure 8 experimentally verifies equation (9) for the bilinear distribution takeover time. The means and variances for the bilinear probability distributions are determined using the equivalent α and β values given in Table 1.

It can be seen from the experimental data that the theoretical formula for tournament time taken from (Goldberg and Deb 1991) somewhat underestimates the experimental takeover time. This is expected since the formula given in (Goldberg and Deb 1991) is approximate and becomes more accurate as the population becomes larger. The correlated bilinear distribution was developed by matching the mean and variance of a continuous model (bilinear) with a discrete model (tournament). Therefore, the small difference in takeover time curves may be due to this approximation.

Table 1: Bilinear Distribution Parameters Corresponding to Tournament Selection (Equal Mean and Variance) for Various Population Sizes.

Tournament Selection	Population Size					
	25	50	75	100	200	400
2	$\alpha = 0.7996$	0.7736	0.76546	0.7615	0.7557	0.7528
	$\beta = 0.2628$	0.3132	0.3199	0.3233	0.3283	0.3308
	$E = 8.84$	17.17	25.50	33.835	67.168	133.83
	$\sigma^2 = 34.6994$	138.861	312.47	555.528	2222.2	8888.9
3	0.8422	0.8205	0.8136	0.8101	0.8050	0.8025
	0.4592	0.4798	0.4866	0.4899	0.4950	0.4975
	6.760	13.005	19.253	25.502	50.501	100.50
	23.40	93.71	210.90	375.00	1500.0	6000.0
4	0.8737	0.8531	0.8464	0.8431	0.8382	0.8358
	0.5589	0.5797	0.5865	0.5899	0.5950	0.5975
	5.513	10.507	15.504	20.503	40.502	80.501
	16.617	66.617	149.95	266.62	1066.6	4266.6
6	0.9144	0.8944	0.8880	0.8847	0.8798	0.8774
	0.6727	0.6939	0.7008	0.7042	0.7093	0.7118
	4.091	7.653	11.221	14.791	29.074	57.644
	9.507	38.206	86.037	153.00	612.18	2448.9
8	0.9391	0.9194	0.9129	0.9097	0.9048	0.9024
	0.7356	0.7572	0.7642	0.7676	0.7727	0.7753
	3.304	6.069	8.842	11.618	22.726	44.946
	6.108	24.627	55.491	98.701	395.00	1580.2
10	0.9556	0.9360	0.9295	0.9263	0.9215	0.9191
	0.7755	0.7975	0.8046	0.8080	0.8131	0.8157
	2.806	5.062	7.329	9.599	18.686	36.866
	4.237	17.150	38.672	68.802	275.41	1101.9

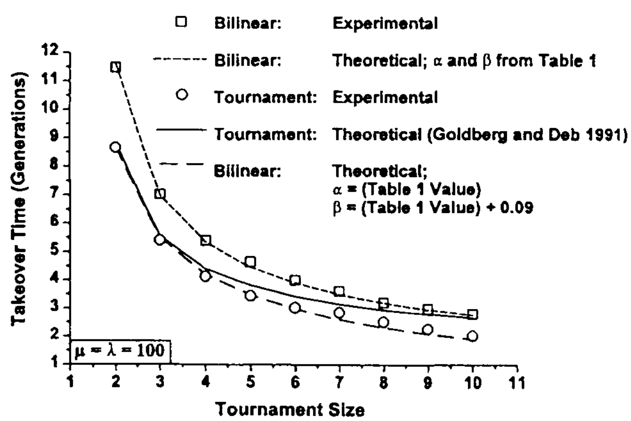

Figure 8: Comparison of Bilinear Selection with Tournament Selection.

The shifted bilinear distribution matches experimental tournament data almost exactly for selection sizes that are a significant proportion of the overall population. This would suggest that the derived formulas for takeover time for the bilinear distribution could be used to approximate takeover times for tournament selection when the tournament size is a significant proportion of the population size.

7 SUPERPOSITION OF MULTIPLE BILINEAR DISTRIBUTIONS

In Figure 9, it is shown that superposition of the proposed bilinear distribution allows one to approximate more complex cumulative distributions in an efficient manner.

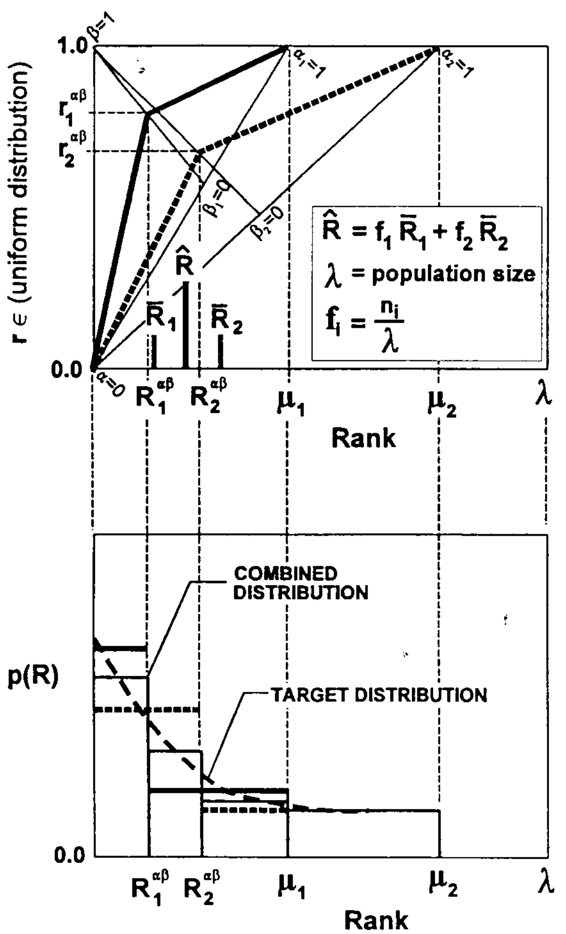

Figure 9: Superposition of Two Bilinear Distributions to Form a Multi-linear Distribution (μ_i, λ_i, α_i, β_i, f_i)

Expressions for the mean and variance for two superimposed bilinear distributions are given by,

$$\hat{R} = f_1 \bar{R}_1 + f_2 \bar{R}_2 \tag{16}$$

$$\begin{aligned}\hat{\sigma}^2(R) = & f_1 \frac{\mu_1^2}{3}(\beta_1 - 1)(\alpha_1 \beta_1 - 1) \\ & - f_1 \left[f_1 \frac{\mu_1}{2}(\beta_1 - 1) + f_2 \frac{\mu_2}{2}(\beta_2 - 1) \right]^2 \\ & + f_2 \frac{\mu_2^2}{3}(\beta_2 - 1)(\alpha_2 \beta_2 - 1) \\ & - f_2 \left[f_1 \frac{\mu_1}{2}(\beta_1 - 1) + f_2 \frac{\mu_2}{2}(\beta_2 - 1) \right]^2 \end{aligned} \tag{17}$$

$$f_i = \frac{n_i}{\lambda} \tag{18}$$

where: λ is the total number of individuals; and n_i corresponds to the number of individuals taken from the ith bilinear distribution.

The simple pseudo-code shown below was the primary motivation for the development of the bilinear distribution

```
do   i = 1, n1
     α1 = 0.8  - 0.6 * ( current_gen / max_gen)^rateExp
     β1 = 0.3  + 0.5 * ( current_gen / max_gen)^rateExp
     individual(i) = CalcRank( μ1, α1, β1 )
end  do

do   i = n1+1,  n1 + n2
     α2  =  0.4   - 0.2 * ( current_gen / max_gen)^rateExp
     β2  =  0.3  + 0.5 * ( current_gen / max_gen)^rateExp
     individual(i) = CalcRank( μ2, α2, β2 )
end  do
```

where: *CalcRank* is a function that returns a rank value from the bilinear distribution; n_1, n_2 are the number of individuals that are to be chosen from the first and second distributions, respectively; *current_gen* is the current generation; *max_gen* is the number of generations in the evolutionary simulation; and *rateExp* is an exponent that controls how fast the selection parameters are modified.

The pseudo-code illustrates that selection during early generations is *engineered* so that exploration is around large areas of promising individuals and transitions to an elitist selection strategy that has a large selection variance. This would allow the algorithm to converge while combining any beneficial remaining genetic material from nearly identical individuals.

The implementation of a fairly sophisticated selection mechanism that alters both the takeover time and the distribution variance generationally in an intuitive manner is implemented in just a few lines of code. The code also implies the ease in which more than two bilinear distributions could be superimposed to *engineer* selection distributions to any degree of accuracy advocated by a particular evolutionary algorithm.

8 CONCLUSIONS

Once it has been decided that a rank based selection scheme is appropriate for the type of evolutionary algorithm being implemented, the current choices are linear(Whitley 1989), non-linear (Michalewicz 1996) and tournament selection (Harvey 1992) (which is philosophically a rank based selection scheme). It has been shown that the proposed bilinear (μ, λ, α, β) distribution has some useful theoretical features that should make it a good candidate for addition to the rank based selection scheme tool box.

As was previously stated, the bilinear (μ, λ, α, β) distribution can be understood as an extension of the (μ, λ) distribution. The takeover time for the (μ, λ, α, β) distribution was demonstrated to be largely a function of β for static values of μ and λ. It was also demonstrated that for set values of μ, λ and β, the selection pressure (takeover time) is relatively constant, allowing selection variance to be controlled independently via the parameter α.

Superposition of bilinear distributions allows one build up multi-linear distributions that can approximate a desired cumulative probability distribution to any accuracy required. The variance of a built-up distribution is still largely a function of α_i for set values of the μ_i, λ_i, β_i and f_i parameters. This approximate uncoupling of the takeover time and variance should allow for the design of evolutionary experiments which clarify the interaction of selection pressure and variance in both static and dynamic selection environments. These evolutionary experiments should be facilitated by the efficient manner in which the multi-linear distribution can be programmed and implemented.

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