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Grant Title: Bell-Curve Based Evolutionary Strategies for Structural Optimization
Report Type: Summary of Research
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Introduction.

Evolutionary methods are exceedingly popular with practitioners of many fields; more so than perhaps any optimization tool in existence. Historically Genetic Algorithms (GAs) led the way in practitioner popularity (Reeves 1997). However, in the last ten years Evolutionary Strategies (ESs) and Evolutionary Programs (EPS) have gained a significant foothold (Glover 1998). One partial explanation for this shift is the interest in using GAs to solve continuous optimization problems. The typical GA relies upon a cumbersome binary representation of the design variables. An ES or EP, however, works directly with the real-valued design variables. For detailed references on evolutionary methods in general and ES or EP in specific see Back (1996) and Dasgupta and Michalesicz (1997). We call our evolutionary algorithm BCB (bell curve based) since it is based upon two normal distributions.

BCB for continuous optimization, first presented in Sobieszczanski-Sobieski et al. (1998), is similar in spirit to ESs and EPs but has fewer parameters to adjust. A new generation in BCB is selected exactly the same as a $(\mu+\lambda)$-ES with $\lambda = \mu$. That is, the best μ individuals out of μ parents plus λ children are selected for the next generation. Thus fit individuals may continue from one generation to the next. The recombination and mutation mechanisms are illustrated in Figure 1. Consider the line through two n-dimensional parent vectors $\vec{P}_1$ and $\vec{P}_2$ selected for mating. First, determine the weighted mean $\vec{M}$ of these two vectors where the weights are given by the fitness (KS value) of each parent. Next, sample from a normal distribution N(0,σ_m). The resulting point $\vec{B} = \vec{M} + |\vec{P}_2 - \vec{P}_1| * N(0, \sigma_m)$ is the child, prior to mutation. Note that $\vec{B}$ is *not* restricted to lie on the line segment $\overline{P_1 P_2}$. Mutation ensues by first generating a radius r for an $n-1$ dimensional hypersphere. The radius is a realization from a $N(0, \sigma_r)$. Typically ($\sigma_r >> \sigma_m$). Finally the mutated child $\vec{C}$ is selected by sampling uniformly on the surface of the

$n - 1$ dimensional hypersphere. Hence, there are two parameters σ_r and σ_m in addition to the traditional parameters of population size and number of generations.

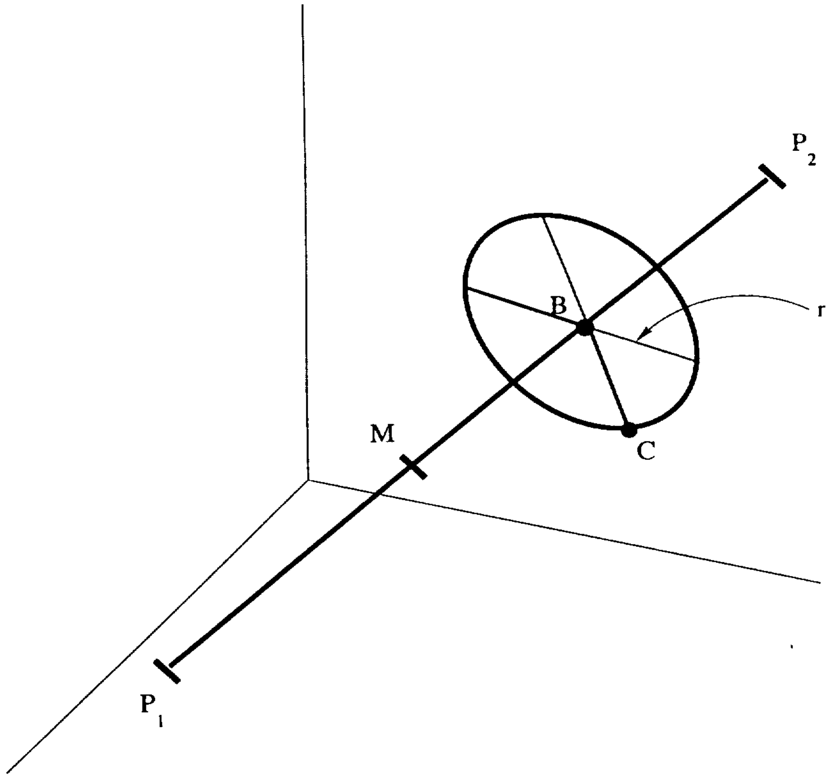

Figure 1. BCB Geometrical Construct in 3D Space

Summary of Research.

The research effort over the grant period has resulted in two manuscripts—Kincaid et al. (2001a) and Kincaid et al. (2001b). In Kincaid et al. (2001a) a new version of BCB to solve purely discrete optimization problems is described and its performance is tested against a tabu search code for an actuator placement problem. Next, the performance of a combined version of discrete and continuous BCB is tested on 2-dimensional shape problems and on a minimum weight hub design problem. In the latter case the discrete portion is the choice of the underlying beam shape (I, triangular, circular, rectangular, or U).

In Kincaid et al. (2001b) we presented an extension of BCB to applications that encompass a mix of continuous and quasi-discrete, as well as truly-discrete decision variables. The extension combines a definition of the distance between the parent designs in the space that comprises discrete and continuous variables with application to optimization of statically indeterminate structures in which the order of design variables, e.g. the type of the cross-section, does matter. As expected, the algorithm that accommodates the order information produces better results. In addition, we provide a comparison allowing sampling from the tails of a discrete normal distribution versus a standard mutation scheme. Adding sampling from the tails brings the continuous and discrete versions of BCB into agreement. Moreover, given the same computing resources, we show that sampling from the tails of the discrete normal leads to higher quality solutions than the standard genetic algorithm mutation approach.

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