# An Investigation of Exploration and Exploitation Within Cluster Oriented Genetic Algorithms (COGAs)

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## Abstract

When conducting a preliminary search across an engineering design space using an evolutionary search method such as the Genetic Algorithm (GA) it is important to achieve the correct balance between exploration and exploitation. If search is too explorative, progress may rapidly degenerate into a random walk where the benefits of evolutionary search are quickly lost. Conversely, if the degree of exploitation is too high, premature convergence may result, with significant areas of the search space remaining largely under explored. This paper introduces a number of COGA strategies developed to better explore and exploit the search space thereby promoting its subsequent decomposition into regions of high performance. Each technique is compared with Variable Mutation COGA (vmCOGA) upon a multi-dimensional high modality test function.

## 1 INTRODUCTION

COGAs support the rapid exploration of complex design spaces and their subsequent decomposition into succinct regions of high performance, thereby offering an alternative to multi-modal optimisation. The research described here relates to the conceptual design environment where design models tend to be coarse representations of the engineering system, single peak identification must therefore be treated with caution, since such peaks may at best be indicative of local high performance or at worst erroneous (Parmee, 1997). Furthermore, design information such as variable sensitivity may be extracted directly from the high performance regions, eliminating the need for further localised search. The designer is therefore presented with a series of high performance regions and a selection of quantitative and qualitative performance characteristics relating to each decomposed region. Optimal design configurations may then be found by selecting one or more regions for further local exploitation. A number of GA based multi-modal optimisation (MMO) algorithms have been developed which locate multiple optima. In many cases significant apriori knowledge relating to the search space is required in order to tune the algorithm parameters. This makes the generic application to higher dimensionality models problematic and severely limits the practical application of such algorithms. A further problem is an inability to maintain stable niches within the population, increasing the chances of eliminating useful design information during search.

Research at the Plymouth Engineering Design Centre (PEDC) (Parmee, 1996 and Parmee *et. al.*, 1997) has addressed these problems through the development of COGAs. COGAs consist of two parts: a diverse search algorithm, which generates the solutions and an adaptive filter, which dynamically extracts high performance solutions during search. With vmCOGA, search is split into five sequential search stages, in this instance each of 25 generations in length. During the initial stage a high probability of mutation (0.08) promotes a diverse search of the design space, at each subsequent stage the mutation probability is reduced by 0.02, promoting the convergence upon high performance regions. After each generational stage the fittest solutions within the population are extracted by an adaptive filter and stored in the Final Clustering Set (FCS). When the population is filtered, individual population fitnesses are normalised in terms of the mean and standard deviation of the overall population fitness. Each chromosome within the population is then checked against a predefined filtering threshold (Rf). If the scaled fitness of the chromosome is greater than Rf, the solution is copied, with replacement to the FCS. To maximise the amount of extracted information; during every search stage (excluding the first) a solution also enters the FCS if its fitness exceeds that associated with the previous filtering threshold.

It has been shown (Bonham *et. al.*, 1998a), that that the filtering threshold: controls the number and average fitness of solutions in the FCS and eliminates both the need to maintain stable niches within the population and the need for apriori search space knowledge relating to the fitness landscape of the design model. Variable mutation represented an initial approach to achieving the correct exploration / exploitation balance. Further research has also investigated replacing variable mutation with a collection of diverse search MMO algorithms (Bonham *et. al.*, 1998b). This paper re-visits this theme by presenting two novel approaches, Halton Injection and Spatial Selection.

### 1.1 HALTON INJECTION COGA (HICOGA)

Replacing mutation by injecting randomly generated strings has been addressed by Eshelman in his CHC algorithm (Eshelman, 1991), where random chromosomes are injected when search has stagnated to some degree. The best chromosome is used as a template and a new population is generated by randomly flipping a fixed percentage of the template bits. Grefenstette (Grefenstette, 1992) supplements mutation by replacing a percentage of the population at each generation by randomly generated chromosomes, called random immigrants. However, to have any effect upon the evolving population the immigrants must be selected for crossover, this possibility is reduced further if the relative fitness of the immigrants is poor. This drawback is called the non-effect problem (Lin *et. al.*, 1994).

HICOGA overcomes the non-effect problem by injecting low discrepancy chromosomes directly into the crossover phase. Low discrepancy sequences (LDS) generate points that uniformly fill an n-dimensional hypercube. The LDS used here is the Halton Sequence Leaped (HSL), which is an improved version the Halton sequence (Kocis *et. al.*, 1997). The HSL is a quasi-random sequence, this means that every generated sequence of $m$ numbers in $n$ dimensional space will be exactly the same. A degree of randomness must therefore be induced into each subsequent $n \times m$ HSL sequence without disrupting the low discrepancy of the points. This is achieved by using a +wrap technique. Firstly $m$ points are generated in an $n$ dimension unit hypercube (each hypercube being wrapped around to form a torous). A single random number of the interval [0,1] is generated and then added to every $n$ component of the $m$ points. This results in differing HSL sequences being produced for each generation, whilst maintaining the low discrepancy nature of the sequence overall. Let $n_{cross}$ be the total number of chromosomes mated at each generation and $n_{HI}$ be the required number of HSL injected chromosomes. Then at every injection phase, $n_{HI}$ HSL chromosomes are paired with $n_{HI}$ chromosomes selected on a fitness basis. The remaining ($n_{cross}$ - $2n_{HI}$) chromosomes are all selected using objective function fitness.

### 1.2 SPATIAL SELECTION COGA (SSCOGA)

At later stages of genetic search the evolving population rapidly converges to a single optima. The ability of a niche to sustain solutions within the population is dependent upon both the maximum fitness and the local fitness landscape of the niche. If an optima is highly sensitive (large changes in fitness for small input perturbations), it may only be able to sustain a handful of solutions which constitute only a fraction of the overall population. As search continues, solutions from other, more robust regions quickly dominate the evolutionary process. The subsequent elimination of the sensitive peak from the gene pool is likely. SSCOGA overcomes this problem by utilising a dual selection scheme; where $n_{SS}$ parents are selected using a local solution density metric and paired with $n_{SS}$ parents selected in terms of objective function fitness. The remaining ($n_{cross}$ - 2 $n_{SS}$) chromosomes are all selected using objective function fitness. Two local solutions density metrics are presented;

1. Euclidean density - For a given chromosome ($X_1$) its local density fitness is the Euclidean distance between itself and its nearest neighbour.
2. Hypersphere density - For a given chromosome ($X_1$), a hypersphere of radius r with centre at $X_1$ is constructed. The local density count of $X_1$ is the total number of chromosomes (including $X_1$) that lie within the hypersphere. The fitness of $X_1$ is the inverse of the local density count.

Unlike the first measure, the disadvantage of the second metric is the need to select a value for r. For a unit search space, appropriate values of r are given by,

$$r = \sqrt{n \times r_{h1}^2} \qquad r_{h1} \in [0,1]$$

$r_{h1}$ is the hypersphere radius in a single unit plane.

## 2 THE TEST FUNCTION

Developing a multi-modal, high dimensionality test function and specifying the regions of high performance with the search space is not a simple matter. In one or two dimensions, the search space may be easily

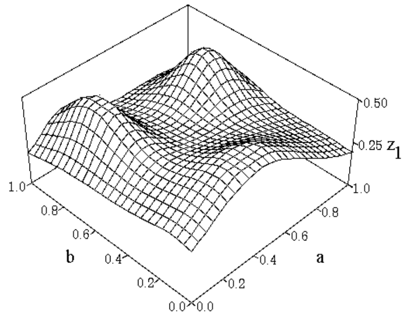


Figure 1: Plane 1 (no added noise)

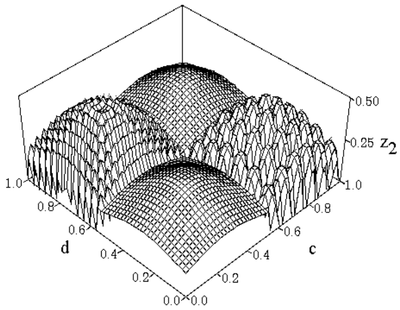


Figure 2: Plane 2 (no added noise)

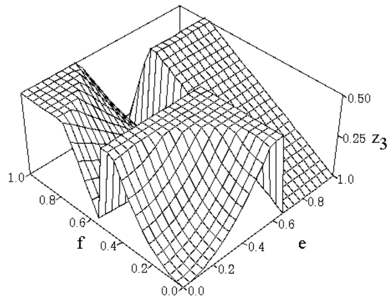


Figure 3: Plane 3 (no added noise)

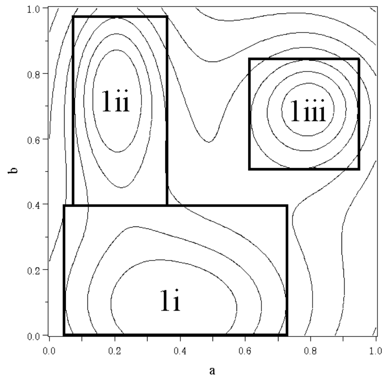


Figure 4: Plane 1 high performance regions (no added noise)

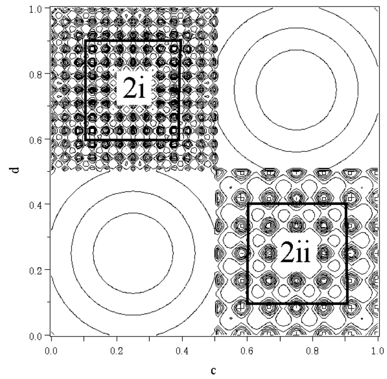


Figure 5: Plane 2 high performance regions (no added noise)

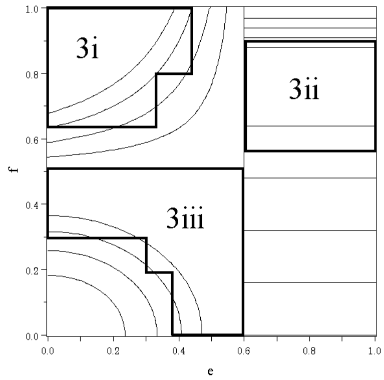


Figure 6: Plane 3 high performance regions (no added noise)

| Global HP Region | Planar HP Regions | | |
|---|---|---|---|
| 1 | 1i | 2i | 3i |
| 2 | 1i | 2i | 3ii |
| 3 | 1i | 2i | 3iii |
| 4 | 1i | 2ii | 3i |
| 5 | 1i | 2ii | 3ii |
| 6 | 1i | 2ii | 3iii |

| Global HP Region | Planar HP Regions | | |
|---|---|---|---|
| 7 | 1ii | 2i | 3i |
| 8 | 1ii | 2i | 3ii |
| 9 | 1ii | 2i | 3iii |
| 10 | 1ii | 2ii | 3i |
| 11 | 1ii | 2ii | 3ii |
| 12 | 1ii | 2ii | 3iii |

| Global HP Region | Planar HP Regions | | |
|---|---|---|---|
| 13 | 1iii | 2i | 3i |
| 14 | 1iii | 2i | 3ii |
| 15 | 1iii | 2i | 3iii |
| 16 | 1iii | 2ii | 3i |
| 17 | 1iii | 2ii | 3ii |
| 18 | 1iii | 2ii | 3iii |

Table 1: The global high performance regions (HP = High performance)

visualised using techniques such as surface or contour plotting. However, as dimensionality is increased, the visualisation and subsequent interpretation of the test function becomes increasingly problematic. Exhaustive search offers a solution, but exponential runtimes and the need to store each solution offline, quickly renders this technique impractical as dimensionality increases.

The DeJong test suite (DeJong, 1975) consists of five functions all possessing different characteristics. DeJong developed the suite to assess the performance of single optima optimisation algorithms, they are therefore impractical when assessing the performance of the design space decomposition algorithms such as those presented in this paper. More specific multi-modal test functions have been developed. Goldberg discusses a massively multi-modal deceptive function (Goldberg *et. al.*, 1992) where the fitness of a solution is dependent upon the unitation of the bit string. The MDO test suite (Padula, *et, al.*, 1996) consists of a number of "real world" test functions, unfortunately only the position of the global optima are stated, the local fitness landscape of the optima are not discussed, this again renders the use of techniques such as exhaustive search necessary. We overcome this problem by using a six dimensional test function, consisting of three local, 2-dimensional planes (figures 1-3) where,

$$z_1 = fn(a,b) \qquad a,b \in [0,1]$$
$$z_2 = fn(c,d) \qquad c,d \in [0,1]$$
$$z_3 = fn(e,f) \qquad e,f \in [0,1]$$

$$z_{1\min} = z_{2_{\min}} = z_{3_{\min}} = 0$$
$$z_{1\max} = z_{2_{\max}} = z_{3_{\max}} = 0.5$$

If the total (global) fitness of a solution, $f_{tot}$ is the summation of the three planar fitnesses from each individual plane $z_1$, $z_2$, $z_3$. It follows,

$$f_{tot} = fn(a,b,c,d,e,f)$$
$$f_{tot_{\min}} = 0 \qquad f_{tot_{\max}} = 1.5$$

In this sense each local plane acts as an individual level of the overall global test function; in a similar manner to Goldberg's 30-bit function constructed by summating five six-bit sub functions. This technique not only provides a more demanding optimisation task but also allows the easy declaration of all local and global high performance regions within the search space.

The three local planes can be seen in figures 1-3. The first contains three peaks of varying sensitivity (1i, 1ii and 1iii) and each of magnitude 0.5, ± 10% random noise is added to the function. Plane two contains two diagonally opposed, highly multi-modal regions. Region 2i has twice as many optima, which are twice as sensitive as those contained within region 2ii. Plane two also contains two sub-optimal robust regions that distract search away form regions 2i and 2ii. The third plane contains three discontinuous regions of high performance (3i, 3ii and 3iii), ± 10% noise was also added to this plane.

A solution is defined as being of global high performance if its fitness lies within 90% of the optimal fitness, in this case 1.35. For a particular solution, it follows that if its local planar fitnesses are all greater than 0.45 the solution must lie within a high performance region. However there are instances where a solution may lie outside these planar boundaries, but may have a global fitness of 1.35 or greater (a hypothetical example being $z_1 = 0.5$, $z_2 = 0.5$, $z_3 = 0.35$). Local high performance regions are therefore defined as areas where the local planar fitness is greater than 0.35 (figure 4-6). However, a further fitness check must be made since a proportion of solutions lying within the local planar regions may not be of global high performance, consider the example $z_1 = 0.35$, $z_2 = 0.35$, $z_3 = 0.35$. Consequently, for a solution to be a member of a global high performance region, it must first belong to a planar high performance region within all three planes and posses a global fitness greater than 1.35. This defines 18 global high performance regions, which are shown in table 1.

# 3 PERFORMANCE MEASURES

When assessing the performance of a regional decomposition algorithm a number of factors must be taken into account. Firstly global set cover (FCS size) should be as large as possible coupled with a high percentage of the FCS being in the defined global high performance regions (Decomposition efficiency). However, these measures by themselves do not detect if premature convergence is present. To overcome this we also measure how many solutions lie in each of the individual 18 global (HP) regions. Furthermore, the Average fitness of the FCS and the best fitness contained within it are used to measure the degree of convergence of each algorithm. To increase accuracy, measurements are averaged over 100 independent trials. The standard deviation is taken over these trials and is used to give a measure of the sensitivity of each algorithm to the effects of genetic drift.

# 4 DISCUSSION

## 4.1 $\text{SSCOGA}_1$, $\text{SSCOGA}_2$, $\text{HICOGA}_1$ and $\text{HICOGA}_2$

It has been shown that the degree of convergence of a COGA population may be ascertained to some degree by the statistical nature of the FCS (Bonham *et. al.*, 1998a), whereby larger decomposition efficiencies and higher average FCS fitnesses indicate higher levels of convergence and a more exploitative search. When comparing the FCS characteristics (table 3) for $\text{SSCOGA}_{1\text{-}2}$ and $\text{HICOGA}_{1\text{-}2}$, it can be seen that both HICOGA algorithms produce results that suggest lower states of convergence when compared with their SSCOGA counterparts, suggesting that Halton injection is a more disruptive operator than spatial selection. As expected, when the number of Halton injections or Spatial selections is reduced (from $\text{HICOGA}_1$ to $\text{HICOGA}_2$ and from $\text{SSCOGA}_1$ to $\text{SSCOGA}_2$ respectively) the degree of convergence increases. In all four cases the FCS sizes are smaller than that obtained with vmCOGA, however in each case, excluding $\text{HICOGA}_1$, the decomposition efficiency is higher. As a consequence of this, in all but two of the HP regions (8 and 18) vmCOGA is outperformed by at least one of the HICOGA, SSCOGA algorithms (figure 7). In general $\text{SSCOGA}_2$ gave the best performance outperforming all other algorithms in 10 of the 18 HP regions (1, 2, 3, 4, 7, 9, 10, 12, 15 and 16). $\text{HICOGA}_1$ and $\text{HICOGA}_2$ performed poorly over the majority of regions, however in two of the most sensitive HP regions (14 and 17) the more exploratitive $\text{HICOGA}_1$ gave the best performance.

## 4.2 $\text{SSCOGA}_3$, $\text{SSCOGA}_4$ AND $\text{SSCOGA}_5$

The replacement of the Euclidean density measure by the hypersphere measure, appears to further slow down the rate of convergence. In all three cases ($\text{SSCOGA}_{3,4}$ and $_5$) the decomposition efficiency and average FCS fitness are smaller than the equivalent Euclidean SSCOGA algorithm ($\text{SSCOGA}_2$). Of the three hypersphere density

| Algorithm | Description |
|---|---|
| vmCOGA | (Parmee, 1996) |
| $SSCOGA_1$ | (Euclidean density) {25, 20, 15, 10, 5} |
| $SSCOGA_2$ | (Euclidean density) {20, 15, 10, 5, 0} |
| $HICOGA_1$ | {25, 20, 15, 10, 5} (no mutation) |
| $HICOGA_2$ | {20, 15, 10, 5, 0} (no mutation) |
| $SSCOGA_3$ | (Hypersphere density) {20, 15, 10, 5, 0} $r_{h1} = 0.35$ |
| $SSCOGA_4$ | (Hypersphere density) {20, 15, 10, 5, 0} $r_{h1} = 0.25$ |
| $SSCOGA_5$ | (Hypersphere density) {20, 15, 10, 5, 0} $r_{h1} = 0.15$ |
| $HICOGA_3$ | 30 Halton injections every 5 generations (no mutation) |
| $HICOGA_4$ | 30 Halton injections every 15 generations (no mutation) |
| $HICOGA_5$ | 30 Halton injections every 25 generations (no mutation) |
| $SSCOGA_6$ | (Euclidean density) 30 spatial selections every 5 generations |
| $SSCOGA_7$ | (Euclidean density) 30 spatial selections every 15 generations |
| $SSCOGA_8$ | (Euclidean density) 30 spatial selections every 25 generations |

Table 2: The test algorithms, (unless otherwise stated, the five values in parenthesis relate to the number of spatial selections or Halton injections made during every generation for each of the five generational stages. An example being $SSCOGA_1$ where {25, 20, 15, 10, 5} indicates 25 spatial selections made for each generation during stage one, 20 spatial selections made for each generation during stage two and so on.

| Algorithm | FCS size | Decomposition efficiency | Average fitness of FCS | Best fitness within FCS |
|---|---|---|---|---|
| vmCOGA | 285.72 (28.00%) | 42.11% (30.16%) | 1.344 | 1.471 |
| $SSCOGA_1$ | 236.61 (34.03%) | 44.59% (34.93%) | 1.358 | 1.470 |
| $SSCOGA_2$ | 231.05 (29.77%) | 66.30% (29.80%) | 1.371 | 1.473 |
| $HICOGA_1$ | 202.29 (30.80%) | 33.28% (37.32%) | 1.331 | 1.465 |
| $HICOGA_2$ | 218.12 (30.15%) | 46.67% (34.90%) | 1.350 | 1.470 |
| $SSCOGA_3$ | 232.24 (33.45%) | 59.02% (30.40%) | 1.363 | 1.473 |
| $SSCOGA_4$ | 251.97 (32.46%) | 56.22% (30.61%) | 1.360 | 1.472 |
| $SSCOGA_5$ | 235.75 (29.32%) | 59.84% (29.03%) | 1.365 | 1.473 |
| $HICOGA_3$ | 128.16 (31.51%) | 72.71% (27.22%) | 1.378 | 1.470 |
| $HICOGA_4$ | 151.25 (42.13%) | 89.04% (17.45%) | 1.405 | 1.476 |
| $HICOGA_5$ | 161.11 (43.14%) | 95.67% (9.86%) | 1.420 | 1.477 |
| $SSCOGA_6$ | 194.94 (32.32%) | 78.08% (23.49%) | 1.383 | 1.474 |
| $SSCOGA_7$ | 200.02 (34.19%) | 85.91% (18.58%) | 1.395 | 1.476 |
| $SSCOGA_8$ | 177.02 (39.80%) | 89.01% (15.96%) | 1.400 | 1.475 |

Table 3: FCS characteristics (values in brackets are standard deviations as a percentage of measured value)

SSCOGA algorithms, $SSCOGA_4$ ($r_{h1}$ = 0.25) appears to promote the most diverse search. Referring to figure 8, it may be seen that in every one of the 18 HP regions at least one of the hypersphere density SSCOGA algorithms outperforms vmCOGA. Furthermore, in the majority of HP regions {2, 5, 7, 8, 10, 11, 12, 13, 14, 16, 17 and 18} $SSCOGA_4$ produces the better results.

### 4.3 $HICOGA_3$, $HICOGA_4$ AND $HICOGA_5$

When higher numbers of Halton individuals (30) are injected less frequently (every 5, 15 and 25 generations for $HICOGA_{3\text{-}5}$ respectively). The decomposition efficiency and average FCS fitness increases dramatically. This result is an anticipated one since the absence of mutation results in higher convergence rates between the injection of Halton chromosomes. However, caution must be exercised when comparing with vmCOGA since the relatively high decomposition efficiencies must be balanced by considerably smaller FCS sizes. Figure 9 gives a clearer indication of the performance of these algorithms. In the more robust regions {1-6} $HICOGA_4$ and $HICOGA_5$ perform well, since search is allowed to converge to a greater extent due to the higher numbers of generations between Halton chromosome injection. In the more sensitive regions {13-18} an increase in performance of $HICOGA_3$ and to a greater extent vmCOGA is noted, since the chances of rapid convergence upon the more robust regions is reduced by the application of mutation (vmCOGA) and the more frequent injection of Halton chromosomes ($HICOGA_3$).

### 4.4 $SSCOGA_6$, $SSCOGA_7$ AND $SSCOGA_8$

In a similar manner to the $HICOGA_{3\text{-}5}$ cases (but to a lesser magnitude, due in part to the use of mutation), the degree of convergence increases as the number of generations between spatial selections increases. However, unlike the HICOGA cases, the general increase in FCS size is less evident. When looking at the regional decomposition of each algorithm (figure 10), it can be seen that vmCOGA outperforms all three SSCOGA algorithms in only three HP regions {8,14 and 17}.

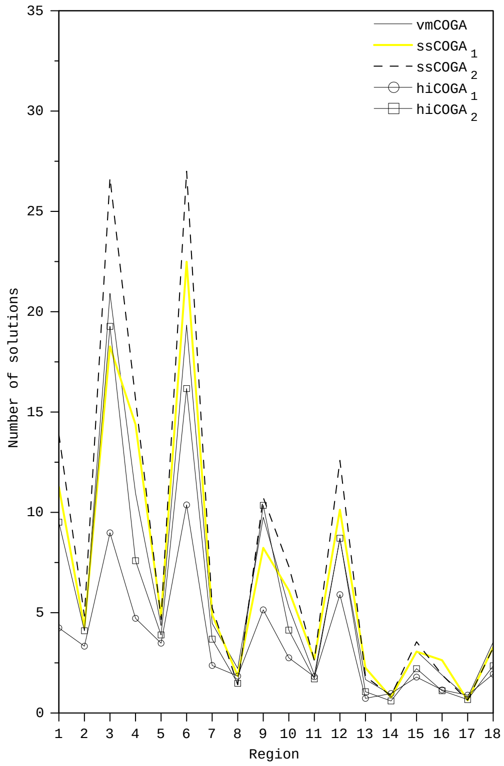


Figure 7: Regional decomposition results for vmCOGA, $SSCOGA_1$, $SSCOGA_2$, $HICOGA_1$ and $HICOGA_2$

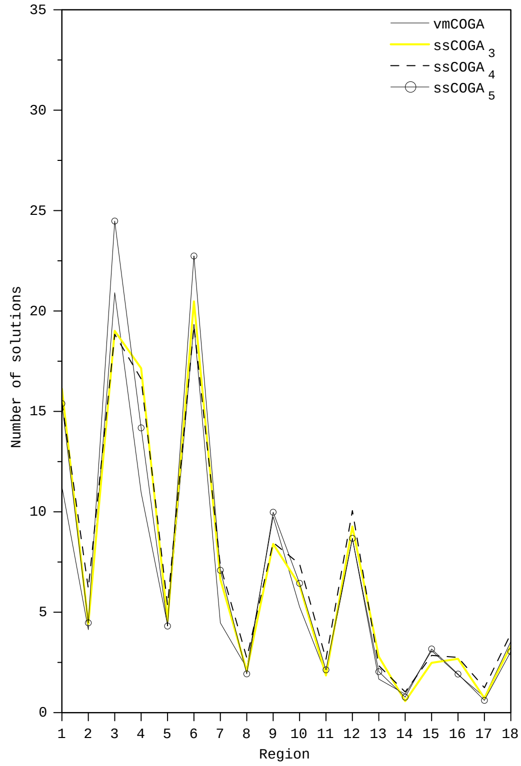


Figure 8: Regional decomposition results for vmCOGA, $SSCOGA_3$, $SSCOGA_4$ and $SSCOGA_5$

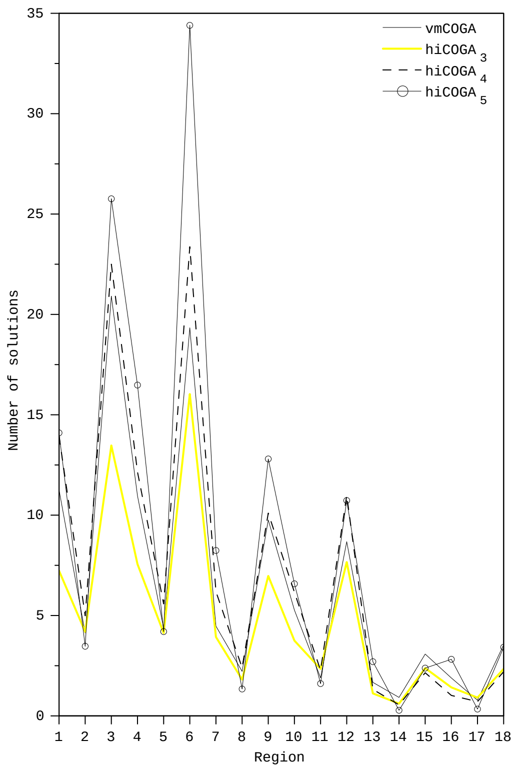


Figure 9: Regional decomposition results for vmCOGA, $HICOGA_3$, $HICOGA_4$ and $HICOGA_5$

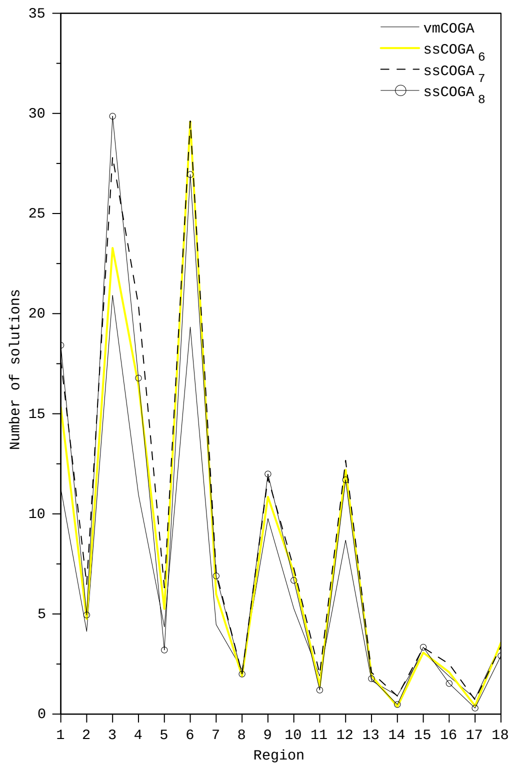


Figure 10: Regional decomposition results for vmCOGA, $SSCOGA_6$, $SSCOGA_7$ and $SSCOGA_8$

In all remaining regions vmCOGA is outperformed by at least one of the SSCOGA algorithms, furthermore in 12 regions {1-7, 9, 10, 12, 13 and 16} the performance of vmCOGA is surpassed all three SSCOGA algorithms simultaneously. $SSCOGA_7$ generally gave the best results, outperforming the remaining two algorithms in 10 regions, $SSCOGA_6$ and $SSCOGA_8$ gave the best results within only one and four regions respectively. These findings and the high and low average fitness of the FCS for $SSCOGA_6$ and $SSCOGA_8$ respectively, suggest that the number of generations between spatial selections is either too short, $SSCOGA_6$ (search too exploratitive) or too long $SSCOGA_8$ (search too exploitative). $SSCOGA_7$ appears to be a compromise between the two.

## 5 CONCLUSIONS

This paper has presented two novel COGA techniques, SSCOGA and HICOGA, both designed to more efficiently explore and exploit the search space. In each case it has been shown that the degree of exploratitive or exploitative search may be modified by altering either the number of Halton chromosomes injected or the number of spatial selections made. A number of SSCOGA and HICOGA algorithms are compared with vmCOGA on a multi-dimensional, multi-modal test function. In the overwhelming majority of cases vmCOGA was outperformed by both of the presented COGA algorithms.

To date, COGAs have only been used in the open loop sense where parameters are set before execution and remain unmodified during the COGA run. This makes the correct calibration of such parameters critical and places emphasis on the designer who may not be familiar with the either the search space under investigation or the COGA tool being used. Future work should therefore address the possibility of using COGA in a closed loop sense where convergence measures and the current nature of the FCS are used to "feed back" information which is used to modify the Halton injection or spatial selection rates. Furthermore, the designer may select "investigation profiles" where the nature of search is defined and controlled accordingly. For example preliminary runs may use a more exploratory COGA algorithm allowing maximum information relating to the whole search space to be extracted. At later stages of the design process where global domain knowledge is high more detailed runs may be controlled during search to give a more exploitative search thereby maximising the amount of local information generated.

**References**


Bonham, C. R. & Parmee, I. C., 1998. "Cluster Oriented Genetic Algorithms (COGAs) for the Decomposition of Multi-Dimensional Engineering Design Spaces". Advances in Computational Structures Technology, Civil-Comp Press, pp 87-95, 1998a

Bonham, C. R. & Parmee, I. C. "Using Variable Mutation Cluster Oriented Genetic Algorithms (vmCOGAs) to Support Conceptual Engineering Design", Procs. 6th European Congress on Intelligent Techniques & Soft Computing, Aachen, pp 402-406, 1998b

DeJong, K. A. "An Analysis of the Behaviour of a Class of Genetic Adaptive Systems", doctoral dissertation, University of Michigan, 1975

Eshelman, L. J. "The CHC Adaptive Search Algorithm: How to Have Safe Search when Engaging in Non-traditional Genetic Recombination", in Rawlings (ed.) Foundations of Genetic Algorithms, pp 265-283, 1991

Goldberg, D. E., Deb, K. & Horn, J. "Massive Multimodality, Deception and Genetic Algorithms", Parallel Problem Solving from Nature, 2, pp 37-46, 1992

Grefenstette, J. J. "Genetic Algorithms for Changing Environments", Parallel Problem Solving from Nature, 2, pp 137-144, 1992

Kocis, L. & Whiten, W. J. "Computational investigations of Low discrepancy sequences", ACM Transactions on Mathematical Software, 23, 2, pp 266-294, 1997

Lin, S-C, Punch, W. F. III & Goodman, E. D. "Coarse-Grain Genetic Algorithms: Categorisation and New Approach", Proc. 6th IEEE Parallel and Distributed Processing, pp 28-37, 1994

Padula, S. L., Alexandrov, N. & Green, L. L. "MDO Test Suite at NASA Langley Research Center", 6th AIAA / NASA / ISSMO Symposium on Multidisciplinary Analysis and Optimisation, AIAA paper No. 96-4028, 1996

Parmee, I. C. "Cluster Oriented Genetic Algorithms (COGAs) for the identification of High Performance Regions of Design Spaces", EvCA 96, pp 66-75, 1996

Parmee, I. C & Beck, M A "An Evolutionary Agent Assisted Strategy for Conceptual Design Space Decomposition", In Corn et al (ed.) Evolutionary Computing, Springer Verlag, pp 275-286, 1997

Parmee, I. C. "Evolutionary Computing for Conceptual and Detailed Design", In Quagliarella et al (ed.) Genetic Algorithms and Computer Science, John Wiley and Sons, pp 133-152, 1997