Pyramid-Z: Evolving Hierarchical Specialists in Genetic Algorithms

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Keywords: Hierarchical GAs, Incremental Evolution, Layered Learning, Individuals Processed, Pyramid, Z-test.

Abstract: *Pyramid* is a hierarchical approach to Evolutionary Computation that decomposes problems by first tackling simpler versions of them before scaling up to increasingly more difficult versions with **smaller** populations. Previous work showed that Pyramid was mostly as good or better than a standard GA approach, but that it did so with a fraction of individuals processed. Pyramid requires two key parameters to manage the problem complexity; (i) a threshold α as the performance bar, and (ii) β as the container with the maximum number of individuals to survive to the next level down. *Pyramid-Z* addressed the shortcomings of Pyramid by automating the choice of α (to assure that the top individuals are highly significantly better from the original population at the current level) and makes β less aggressive (to maintain a moderately sized population at the final level). In cases where evolution starts to stagnate at the final level, the population enters into a different form of evolution, driven by a form of hyper-mutation that runs until either a satisfactory fitness has been found or the total evaluation budget has been exhausted. The experimental results show that Pyramid-Z consistently outperforms the previous version and the baseline too.

1 INTRODUCTION

There is a growing body of literature that recognize the importance of hierarchies in evolutionary algorithms. Pyramid (Ryan et al., 2020) is a hierarchical genetic algorithm that first tackles a simpler version of a problem, before being exposed to more complex version, while also reducing the population size. A key aspect of Pyramid is that it achieves the same fitness score as traditional algorithm but with a significantly smaller computational cost.

Pyramid was constructed in such a way that the smallest genome, largest population and simplest fitness function are at the top, and the largest genome, smallest population and most complex fitness function are at the bottom. Each step in the Pyramid adjusts the population size down and the genome size up, as shown in Fig. 1.

It evolves population at each level, until the promotional criteria has been met and some part of the population is promoted to the next level. The promotional criterion is denoted by α and size of the promoted population by β. Several variants of Pyramid were examined, with levels varying from 2 to 5, referred to as HL-2 and HL-5 respectively. However, in the case of 4 and 5 level Pyramid, the population size (β) becomes very small at the final levels.

This paper attempts to automate the α and make β less aggressive in reducing the population size for the Pyramid, and to add a form of hyper-mutation at the final level if there is still some budget left and the fitness has not arrived at a satisfactory level (this takes the form of increasing the mutation rate from 0.05 to 0.2). By satisfactory level, we mean that our approach should outperform baseline.

The performance of proposed algorithm is measured using two unimodal and two multimodal functions (the same as in (Ryan et al., 2020)) and we show that our proposed new approach outperformed than the traditional algorithm as well as the previous Pyramid. We call our approach as Pyramid-Z.

In the next section, we highlight the existing hierarchical techniques in EC and describe Pyramid and its limitations. The proposed method is explained in Section 3. We then present the experimental setup in Section 4. Experimental results are discussed in Section 5. Finally, Section 6 draws conclusions and future work.

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Rafiq, A., Naredo, E., Kshirsagar, M. and Ryan, C.
Pyramid-Z: Evolving Hierarchical Specialists in Genetic Algorithms.
DOI: 10.5220/0010657400003063
In *Proceedings of the 13th International Joint Conference on Computational Intelligence (IJCCI 2021)*, pages 49-58
ISBN: 978-989-758-534-0; ISSN: 2184-3236

2 BACKGROUND AND RELATED WORK

2.1 Other Approaches

Based on the concept of Hierarchy, researchers have experimented with different approaches to overcome the scaling problems. These can be divided into three broad categories:

Hierarchical Genetic Algorithms (HGAs). consist of hierarchies of GAs that generally employ different fitness functions. Individuals can migrate up (and occasionally down) through the various levels. Several Studies (Sefrioui and Périaux, 2000), (Hong et al., 2016), (Hong et al., 2017) (de Jong et al., 2004) have employed hierarchy in GA and have achieved promising results.

Incremental Evolution (IE). starts with a population that is already trained on a simpler but related task, rather than starting from initial random population. Using this approach, many researchers (Barlow et al., 2004), (Winkeler and Manjunath, 1998), (Duarte et al., 2012), (Assunção et al., 2020) have been able to tackle difficult problems.

Layered Learning (LL). is an approach where learning achieved at the lower layers helps facilitate learning required at upper layers. Various studies (Stone and Veloso, 1997),
(Astarabadi and Ebadzadeh, 2018),
(Jackson and Gibbons, 2007) have assessed the efficacy of LL in order to overcome the bootstrapping problems.

2.2 Pyramid

Pyramid (Ryan et al., 2020) is a Hierarchical Genetic Algorithm that decomposes problems by first tackling simpler versions of them, before automatically scaling up to more difficult versions while also **reducing** the population size (shown in Fig. 1). It takes inspiration from several systems, as it uses increasingly more complex individuals as in (Astarabadi and Ebadzadeh, 2018) and increasingly more precise fitness functions as in (Sefrioui and Périaux, 2000).

Pyramid was constructed in such a way that the smallest genome, largest population and simplest fitness function are at the top, and the largest genome, smallest population and most complex fitness function are at the bottom. With each step in the Pyramid, the authors (Ryan et al., 2020) adjusted the population size down and the genome size up, because the longer the individuals are, the more precise the fitness function is. Two important research questions in Pyramid were (i) when should individuals be promoted to next level; indicated by α and (ii) how many individuals should be promoted; indicated by β.

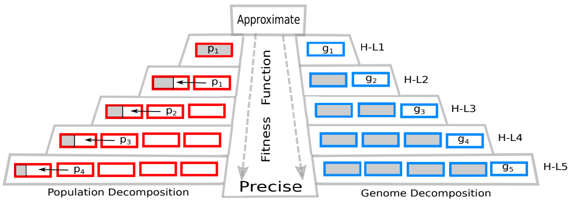


Figure 1: Graphical representation of the Pyramid approach with 5 levels. On the left side we see the population size decreasing, while on the right, the genome length increases. The fitness function gets increasingly more precise as we descend (image taken from (Ryan et al., 2020)).

The trigger point for promotion was that the top 20% of the population was **five times better** than the average fitness of the population and these 20% were the promoted individuals. In all but one problem, Pyramid performed either the same or statistically significantly better with substantially fewer evaluations.

2.3 Pyramid Drawbacks

In Pyramid, the choice of parameters (α and β) were arbitrary. According to experimental results in the original, in some problems, the population evolved for hundreds of generations before meeting α but in some problems, it took just a few generations.

Moreover, the choice of β led to a too-small population at the final levels. Although the evolution started with 5000 individuals, the population size reduced to 40 and 8 in the final level of HL-4 (four level Pyramid) and HL-5 (five level Pyramid) respectively. This tiny population size sometimes does not contain enough genetic material and population can easily become stuck into local optima.

3 Pyramid-Z

Pyramid-Z addresses the limitations of Pyramid. The right time about when to promote the individuals to next level is determined using a new promotional criteria $\alpha2$ (explained in next Section 3.1). This parameter confirms that population has highly significantly improved and now the individuals can be promoted to next level to deal with another level of complexity.

In this parameter, the population in each generation is compared with the initial generation at that level. If the population at that generation is significantly better than the initial generation, then it is time to promote individuals to next level.

Secondly, Pyramid-Z also ensures that there is a sufficiently large population at final levels. This is achieved using new parameter β2 (explained in Section 3.2). Lastly, a new insight of increased mutation, explained in Section 3.3, is incorporated for the cases where Pyramid-Z has not attained a satisfactory fitness. Note that (α2, β2) **replace** (α, β); we use different names in this paper to facilitate comparison. Fig. 2 depicts the logic of the Pyramid-Z.

3.1 α2

We replace the arbitrary α parameter with a statistical test that tests if two distributions are equal or different from one another, specifically, the Z-test:

$$Z = \frac{(\bar{X_1} - \bar{X_2})}{\sqrt{\left(\frac{\sigma_{X_1}}{\sqrt{n_1}}\right)^2 + \left(\frac{\sigma_{X_2}}{\sqrt{n_2}}\right)^2}} \tag{1}$$

where X_1 is the initial distribution (initial generation, at each level, in our case) and $\bar{X_1}$ is its mean value. X_2 is the second distribution (each next generation in our case) and $\bar{X_2}$ is its mean value. σ_{X_1} is the standard deviation of distribution X_1 and then it is divided by the square root of the number of data points (n is the population size of each distribution in our case).

σ_{X_2} is the standard deviation of distribution X_2 and then it is divided by the square root of the number of data points. Based on the value of Z-test, as shown in Table 1, one can see how much the distributions differ from each other. The Z-test is applied at each generation against the initial generation at that level. If the value of Z at a certain generation is greater than 3, then it means that the two generations are highly significantly different from each other. Here, by different we assume the improvements. Now, at that specific generation, we stop the current level and promote the individuals to next level.

Table 1: Meaning of Z-test. In our experiments, we choose the >**3** to make sure that two populations are highly significantly different from each other.

Z-test Value	Statistical Interpretation
<2.0	Same
2.0 - 2.5	Marginally Different
2.5 - 3.0	Significantly Different
>3.0	Highly Significantly Different

3.2 β2

Recall that the issue with β was that it could be too aggressive in reducing the population size. We replace this with a more gradual decrease in which we specify the total number of levels (L), the initial population size ($P_{initial}$) and the final population size (P_{final}). Then, we propose a way of reducing the population (D) at each level by using the algorithm 1.

Algorithm 1: How population size varies at each level.

```
$D = \left\lfloor \frac{P_{initial} - P_{final}}{L-1} \right\rfloor$
$i = 1$;
while $i¡L$ do
    $P_{new} = P_c - D$;
    $P_c = P_{new}$;
    $i++$;
end
```

Where P_{new} is the new population at the next level.

3.3 Hyper-mutation

After applying the parameters (α and β) and getting the initial results, we identify the cases where Pyramid-Z has not reached its desired goal. By desired goal, we mean that our approach should outperform baseline. In these cases, we increase the mutation rate from 0.05 to 0.2 for the population at the final level and let the population evolve again. This increased mutation ratio is chosen to fit with our other parameters (crossover rate, population size etc.) in accordance with (Hassanat et al., 2019) where authors have reviewed several methods for choosing the mutation and crossover rations in GAs. From Fig. 2, the highlighted area in red color is where the population gets another chance to evolve, when under-performed than baseline.

4 EXPERIMENTAL SETUP

As discussed in Section 2.2, two important research questions in Pyramid are indicated by (α, β) (shown in Table 2). Here, (α1, β1) were the original approaches, used in (Ryan et al., 2020), while (α2, β2) are those explored in this paper. By using the combination of both (α, β), four experiments were run such as (α1, β1) (Experiment 1), (α2, β1) (Experiment 2), (α1, β2) (Experiment 3) and (α2, β2) (Experiment 4).

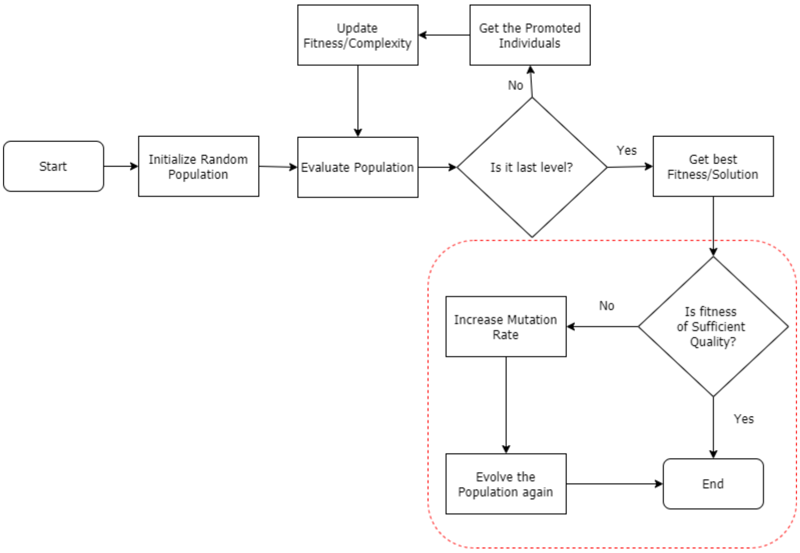


Figure 2: Pyramid-Z Flow Chart, the highlighted red dot area is where Pyramid-Z enters a period of hyper-mutation.

Table 2: A comparison of the approaches. The upper two rows show the alternative ways to promote individuals while, the number of individuals to promote are in the lower two. In the previous Pyramid, (α1, β1) were used.

Promotional Criteria (α)	α1	Top 20% of the population is five times better than the average fitness of the population.
	α2	When the value of z is greater than 3, explained in Section 3.1.
Population Threshold (β)	β1	20% of the top population.
	β2	Size of promoted individuals varies according to number of levels and initial/final population size, explained in Section 3.2.

4.1 Problems

Four mathematical functions, two uni-modal (Sphere and Rosenbrock) and two multi-modal (Rastrigin and Griewank), as shown in Table 3, were chosen to test the performance of our algorithm. These functions are well-known optimization problems (Jamil and Yang, 2013) and have been frequently used in other hierarchical studies (Hong et al., 2016) (Hong et al., 2017). The optimal value for all these functions is 0.

The experimental setup is graphically summarized in the Fig. 3 showing the four versions tested for Pyramid-Z applied on four problems (two unimodal and two multimodal) and each problem is tested with four variants of Pyramid-Z (from HL-2 to HL-5). All those cases, where Pyramid-Z out-performed than the baseline is highlighted in green and those cases are shown in the section of the experimental results.

Table 3: Benchmark Functions.

Name	**Function**
Sphere	$\sum_{i=1}^{n} x_i^2$
Rosenbrock	$\sum_{i=1}^{n-1}[100(x_{i+1}-x_i^2)^2+(x_i-1)^2]$
Rastrigin	$10n+\sum_{i=1}^{n}(x_i^2-10cos(2\pi x_i))$
Griewank	$1+\sum_{i=1}^{n}\frac{x_i^2}{4000}-\prod_{i=1}^{n}cos(\frac{x_i}{\sqrt{i}})$

We used OpenGA (Mohammadi et al., 2017), an open source C++ library for GAs to implement this version of Pyramid.

5 EXPERIMENTAL RESULTS AND ANALYSIS

5.1 Experiments

Initially, a baseline experiment was run using a traditional GA, followed by four variants of our experiment and each experiments has four variants of our Pyramid-Z, each with varying levels (2 to 5), as shown in Table 4. These are referred to as **H-LX** where **X** is the number of levels in the hierarchy.

5.2 Results

The correlation between the best fitness and the number of individuals processed were tested. All these results are the average of 50 runs. We describe the results for each problem separately below.

Table 4: Parameters for Pyramid-Z: The target genome length for each H-LX is 30, which is divided into different values according to specific experiment. The values for Chromosome length that show a calculation refer to the previous length plus the additional length, e.g. 20+10=30 means the previous length was 20 and we are adding 10 more to give a length of 30. β1 and β2 are the ways in which the population size varies at each level. β1 promotes 20% population size to next level, while β2 assures that the minumum population size at the final level is 200.

Level		**Chrom. length**	β1	β2	**Max-Gener**
Baseline		30	5,000	5,000	3,000
H-L2	**L1**	15	5,000	5,000	1,500
	L2	15+15=30	1,000	200	1,500
H-L3	**L1**	10	5,000	5,000	1,000
	L2	10+10=20	1,000	2600	1,000
	L3	20+10=30	200	200	1,000
H-L4	**L1**	7	5,000	5,000	700
	L2	7+8=15	1,000	3400	800
	L3	15+7=22	200	1800	700
	L4	22+8=30	40	200	800
H-L5	**L1**	6	5,000	5,000	600
	L2	6+6=12	1,000	3800	600
	L3	12+6=18	200	2600	600
	L4	18+6=24	40	1400	600
	L5	24+6=30	8	200	600

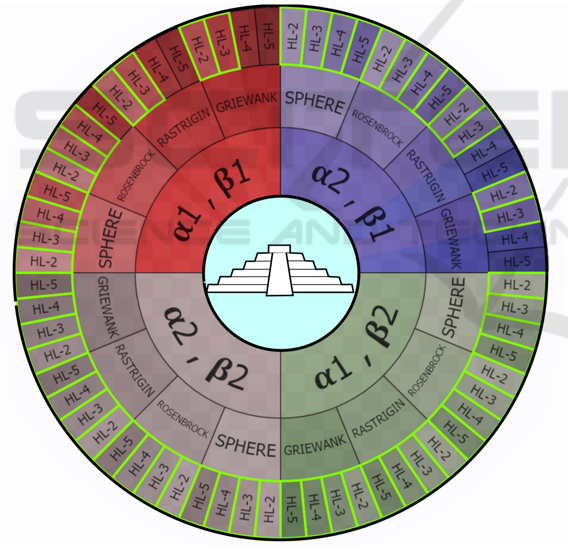


Figure 3: Mayan-like calendar showing all experiments with Pyramid-Z. Each quadrant with different color shows a combination of (α, β) parameters. There are four sections in the quadrants corresponding to the optimization problem addressed and each sub-section shows the four levels of complexity decomposition for each of them. All levels where Pyramid-Z outperform the baseline are outlined in green.

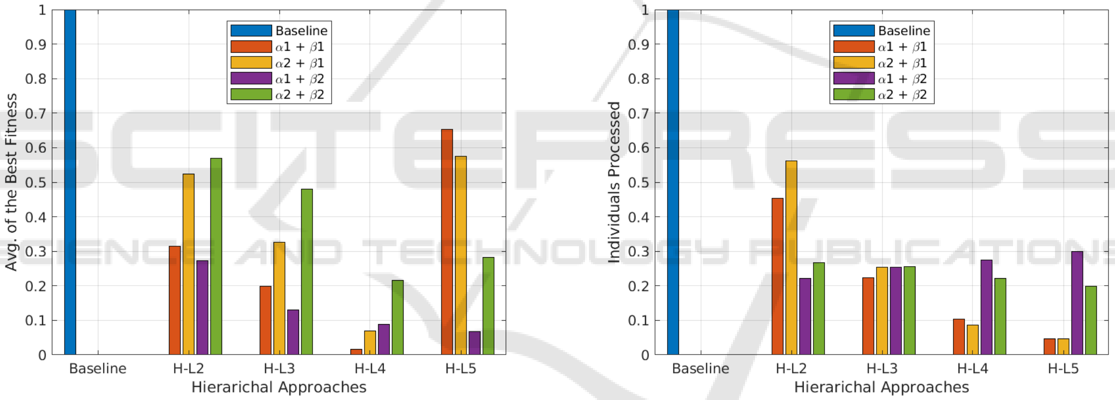
5.2.1 Sphere

Table 5 shows the statistical comparison. The table divides the results into two groups. In the first group, we have Individuals Processed and the average and standard deviation of the fitness. In the second group, hyper-mutation kicked in, in all those cases where Pyramid-Z required extra evaluations. In baseline, the number of individuals processed is shown in bold **651,749**. This is actually the budget limit for this problem. As can be seen from the table that HL-4 and HL-5 Pyramid-Z under-performed than the baseline in (α1, β1) and (α2, β1) setup respectively. In those cases, we show updated values of fitness and standard deviation after hyper-mutation kicked in. Although the budget has increases (more individuals have been processed), these cases now out-perform the baseline. All the bold values in the table shows where the various Pyramids out-performed than the baseline. For the statistical analysis, t-test was used, which returns the p-value < 0.01 in all the cases.

Fig. 4 compares the values of fitness and individuals processed. The resulting values from Table 5 are normalized from 0 to 1 in order to visualize better. The figure has two parts, part (a) compares the fitness values of each of our experiment with Baseline and the part (b) compares the number of individuals processed. From part (b) of each figure, we can clearly see that the number of individuals processed in our experiments are much smaller than the baseline and from part (a) it is also clear that the fitness in all our experiments is better than the baseline. All our cases, out-performed in Sphere function.

Table 5: Results from the **Sphere** function. **+** indicates Pyramid-Z performed statistically significantly better, **-** that Pyramid-Z performed statistically significantly worse. In all **-** cases, the budget has been increased and results improve.

	H-LX	Individuals Processed	Best Fitness		Updated Budget	Updated Fitness	
			Avg	std		Avg	std
Baseline		**651,749**	1.0012	0.0784			
α1 β1	H-L2	37,049	**0.5644 +**	0.0523			
	H-L3	36,680	**0.3547 +**	0.0867			
	H-L4	34,892	5.8534 -	2.7289	60,252	**0.0292 +**	0.0310
	H-L5	30,375	15.9313 -	5.6826	62,583	**1.1700 +**	0.6292
α2 β1	H-L2	410,000	**0.9403 +**	0.1805			
	H-L3	185,200	**0.5847 +**	0.1832			
	H-L4	43,680	2.7202 -	1.5829	84,840	**0.1241 +**	0.2899
	H-L5	20,392	4.5929 -	4.5929	52,792	**1.0315 +**	0.5181
α1 β2	H-L2	194,600	**1.0213 +**	0.3534			
	H-L3	186,600	**0.8599 +**	0.2860			
	H-L4	161,400	**0.3873 +**	0.0743			
	H-L5	144,600	**0.5058 +**	0.1408			
α2 β2	H-L2	162,200	**0.4896 +**	0.1306			
	H-L3	184,800	**0.2327 +**	0.0423			
	H-L4	20,800	**0.1601 +**	0.0315			
	H-L5	218,400	**0.1195 +**	0.0215			



(a) Fitness (b) Individuals Processed

Figure 4: **Sphere Results:** The fitness value and number of individuals processed of baseline is compared against our experiments, on left and right hand side respectively. It can be clearly seen that that fitness value in our experiment is always better than baseline (a) and always with less individuals processed (b).

5.2.2 Rosenbrock

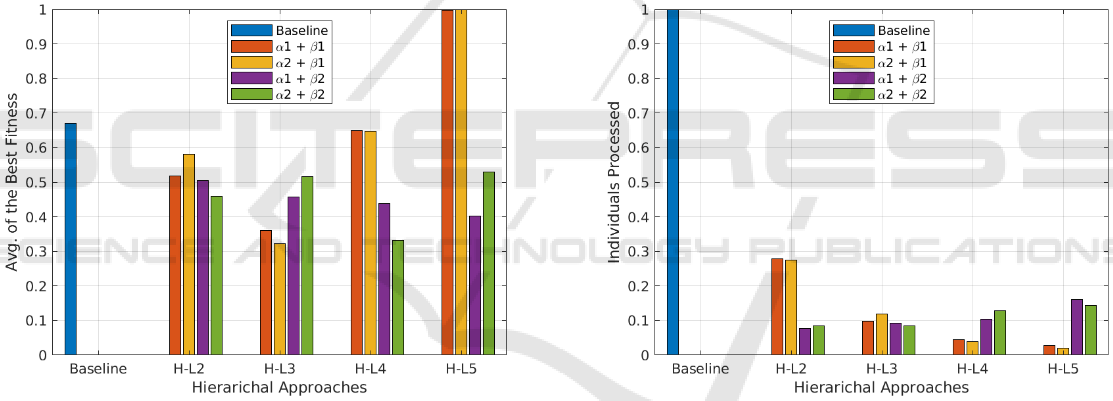
Table 6 shows the various results. In the first group, we can see the Pyramid-Z did not perform well in most cases. With hyper-mutation, all the cases now out-performed except HL-5 in both (α1, β1) and (α2, β1) setup. This is due to the way β1 behaves as it reduces the population size to very small (can also be seen from Table 4) at the final level of HL-5. All cases where Pyramid-Z out-performed are shown in bold. Similarly, Fig. 5 compares the fitness and number of individuals processed from part (a) and part (b) respectively. In rosenbrock, all the cases out-performed except HL-5 in both (α1, β1) and (α2, β1).

5.2.3 Rastrigin

Table 7 shows the results. We can see that in first part of the table Pyramid-Z did not perform as well as the baseline, albeit with far fewer evaluations. This is where again the hyper-mutation plays its part. We increased the budget and can see that our Pyramids now start out-performing. Fig. 6 compares the fitness and number of individuals processed from part (a) and part (b) respectively. Rastrigin function out-performed in all the cases except HL-4 and HL-5 in both (α1, β1) and (α2, β1) setup.

Table 6: Results from the **Rosenbrock** function. **+** indicates Pyramid-Z performed statistically significantly better, **-** that Pyramid-Z performed statistically significantly worse. In all **-** cases, the budget has been increased and results improve.

	H-LX	Individuals Processed	Best Fitness		Updated Budget	Updated Fitness	
			Avg	std		Avg	std
Baseline		**920,000**	70.658	5.622			
α1 β1	H-L2	254,000	**54.522 +**	4.248			
	H-L3	71,800	84.457 -	14.639	109,600	**37.807 +**	7.869
	H-L4	21,560	248.277 -	68.201	59,280	**68.2384 +**	25.593
	H-L5	19,320	394.118 -	167.147	45,040	104.822 -	28.200
α2 β1	H-L2	252,000	**60.950 +**	6.347			
	H-L3	66,000	100.524 -	22.146	119,000	**33.894 +**	5.112
	H-L4	16,640	253.094 -	50.998	47,640	**68.006 +**	23.231
	H-L5	13,184	381.126 -	125.725	31,920	105.071 -	46.524
α1 β2	H-L2	69,000	102.970 -	20.940	88,400	**53.129 +**	16.017
	H-L3	63,000	98.484 -	20.763	105,200	**48.022 +**	14.021
	H-L4	72,400	92.833 -	21.109	137,600	**46.025 +**	9.537
	H-L5	80,600	111.512 -	33.328	204,800	**42.342 +**	9.739
α2 β2	H-L2	71,200	97.347 -	22.984	85,600	**48.302 +**	12.590
	H-L3	85,800	74.855 -	14.187	105,400	**54.2198 +**	19.872
	H-L4	93,600	**67.200 +**	12.111			
	H-L5	109,600	**61.633 +**	9.371			



(a) Fitness (b) Individuals Processed

Figure 5: **Rosenbrock Results:** The fitness value and number of individuals processed of baseline is compared against our experiments, on left and right hand side respectively. It can be clearly seen that that fitness value for Pyramid-Z is always better, except in two cases (a), and our experiments always processed less individuals (b).

5.2.4 Griewank

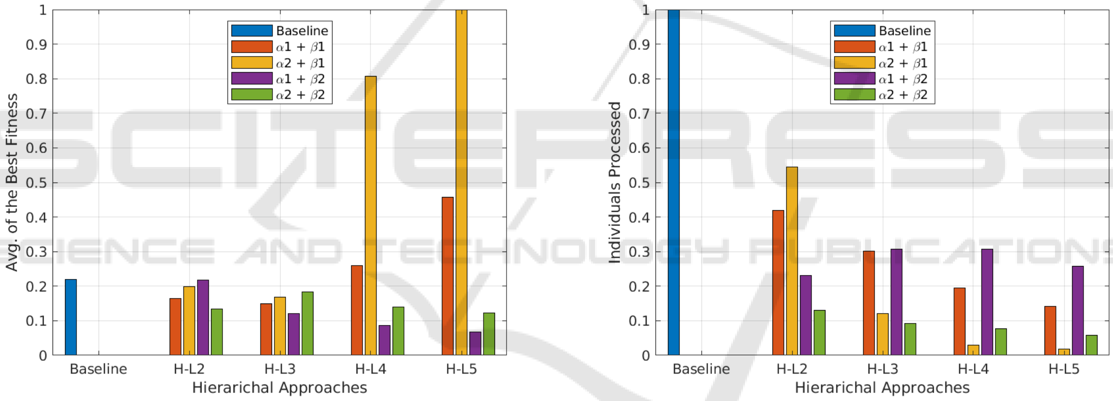
Table 8 is the comparison of statistical values. We can see that our experiment did not perform well in all cases. Now, when we increased the budget and let the population evolve again, we can see the almost all cases are out-performing. These results are similar to Rastrigin, as Pyramid-Z out-performed in all cases except HL-4 and HL-5 in both (α1, β1) and (α2, β1) setup.

Overall, these results show that Pyramid-Z out-performed in most cases. One possible reason where Pyramid-Z did not perform well is the choice of β1. According to this parameter, the population size is very small in the last level (40 and 8 for HL-4 and HL-5 respectively), so there is not enough genetic material. Interestingly, most of the cases now outperforms baseline.

In summary, all the results are shown in the form of a hierarchical pie chart from Fig. 3. The hierarchical pie chart briefly summarizes the experimentation results for the system Pyramid-Z. Two Unimodal and two multimodal sample problems were tested for each of the four budget scenarios for (α, β). For example, for the case with (α1, β1) the Pyramid-Z achieved optimal solution at all 2-5 levels Pyramids for sphere, for Rosenbrock at 2-4 levels Pyramid, for both Rastrigin and Griewank at 2 and 3 levels. The best performing

Table 7: Results from the **Rastrigin** function. **+** indicates Pyramid-Z performed statistically significantly better, **-** that Pyramid-Z performed statistically significantly worse. In all **-** cases, the budget has been increased and results are better.

	H-LX	Individuals Processed	Best Fitness		Updated Budget	Updated Fitness	
			Avg	std		Avg	std
Baseline		**2,110,000**	15.0649	3.0383			
α1 β1	H-L2	886,000	**11.3094 +**	5.6589			
	H-L3	590,400	16.0864 -	9.0095	1,053,600	**10.5174 +**	4.7767
	H-L4	383,720	41.3362 -	13.8260	791,520	20.8209 -	6.9686
	H-L5	279,968	57.4871 -	15.2764	576,304	30.9646 -	12.1054
α2 β1	H-L2	1,085,000	20.4950 -	5.0858	1,134,000	**13.6199 +**	13.9235
	H-L3	205,800	47.9625 -	12.2669	283,000	**11.5174 +**	5.7167
	H-L4	18,560	204.9727 -	35.6858	74,040	60.6924 -	31.8871
	H-L5	13,312	234.1956 -	26.4372	51,520	68.4385 -	23.6885
α1 β2	H-L2	253,200	48.4930 -	29.6217	506,200	**14.9440 +**	5.7609
	H-L3	195,200	47.7511 -	23.1457	674,600	**8.2364 +**	3.7970
	H-L4	164,200	58.3643 -	30.8686	686,200	**5.8924 +**	3.3659
	H-L5	120,800	90.2085 -	45.4135	597,400	**4.6677 +**	2.2798
α2 β2	H-L2	458,400	21.3997 -	9.4226	488,400	**9.2264 +**	3.7090
	H-L3	584,400	**12.5549 +**	6.3339			
	H-L4	622,600	**9.5348 +**	5.6753			
	H-L5	530,600	**8.4187 +**	4.5301			



(a) Fitness

(b) Individuals Processed

Figure 6: **Rastrigin Results:** The fitness value and number of individuals processed of baseline is compared against our experiments, on left and right hand side respectively. It is clearly seen that fitness value in our experiment is always better, except in 4 cases, than baseline (a) but our experiments always processed less individuals (b).

levels for each set of problems are highlighted.

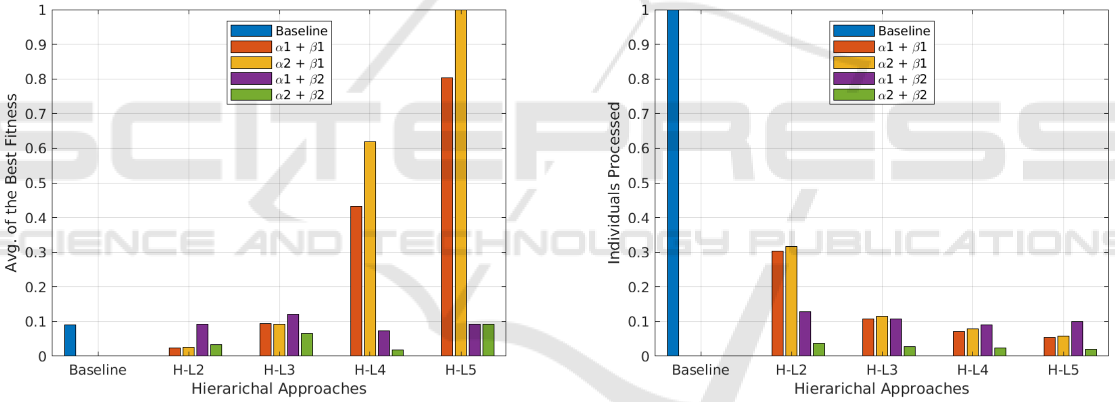
Similarly, we can observe that for scenario (α2, β2) and (α1, β2) the Pyramid-Z started outperforming the baseline from 2 level itself and consistently maintained the trend of reaching optimal solutions at subsequent higher levels. Finally, Table 9 summarizes about a comparison between the Traditional approach, Pyramid and Pyramid-Z.

6 CONCLUSIONS AND FUTURE WORK

In this paper, we present the new version of previously proposed Pyramid, called Pyramid-Z. Two key parameters of Pyramid, i.e. when to promote and how many individuals to promote, are tackled here. The first parameter from the original version was replaced by Z-test to identify when the current population is highly significant different from the original one on each hierarchical level and thus automate the promotional time, and second one made less ag-

Table 8: Results from the **Griewank** function. **+** indicates Pyramid-Z performed statistically significantly better, **-** that Pyramid-Z performed statistically significantly worse. In all **-** cases, the budget has been increased and results improve.

	H-LX	Individuals Processed	Best Fitness		Updated Budget	Updated Fitness	
			Avg	std		Avg	std
Baseline		**6,517,491**	1.0533	0.0802			
α1 β1	H-L2	1,369,560	1.8770 -	0.5976	1,943,560	**0.0287 +**	0.2520
	H-L3	176,310	6.3616 -	1.9758	693,110	**1.0931 +**	0.4826
	H-L4	30,946	23.0932 -	0.0784	478,826	5.0645 -	2.2795
	H-L5	91,126	37.9472 -	12.6262	439,638	9.4037 -	5.5654
α2 β1	H-L2	1,433,000	2.0789 -	0.6747	2,025,000	**0.2976 +**	0.2193
	H-L3	187,400	7.8081 -	2.1759	749,400	**1.0755 +**	0.0927
	H-L4	24,880	31.3044 -	8.8449	524,560	7.2382 -	3.1412
	H-L5	19,376	50.0469 -	15.2384	392,080	11.6984 -	6.8497
α1 β2	H-L2	235,400	11.3947 -	3.2584	842,400	**1.0880+**	0.4682
	H-L3	187,000	9.7794 -	2.6214	704,400	**1.4201 +**	0.5574
	H-L4	159,400	9.5497 -	3.0016	593,200	**0.6665 +**	0.2807
	H-L5	130,200	17.6775 -	4.9375	183,900	**1.0750 +**	0.3659
α2 β2	H-L2	234,800	10.6573 -	3.7879	918,600	**0.3916 +**	0.2993
	H-L3	202,800	5.7381 -	1.8355	823,600	**0.7615 +**	0.3601
	H-L4	215,800	3.2703 -	1.1426	835,400	**0.2171 +**	0.2913
	H-L5	205,600	4.2385 -	1.3597	1012,600	**1.0701 +**	0.4574



(a) Fitness

(b) Individuals Processed

Figure 7: **Griewank Results:** The fitness value and number of individuals processed of baseline is compared against our experiments, on left and right hand side respectively. It is clearly seen that that fitness value in our experiment is always better, except 4 cases, than baseline (a) but our experiments always processed less individuals (b).

Table 9: Comparative Analysis of Traditional Approach with Pyramid and Pyramid-Z.

Methods	**Results/Findings**
Traditional GA	Processes a large number of individuals to obtain optimal solutions.
Pyramid	Approximately 98% reduction in individuals being processed but does not guarantee optimal solutions always.
Pyramid-Z	90% reduction in individuals processed and also guarantees to always obtain optimal solution

gressive to maintain a moderate population size. The proposed new changes make the Pyramid-Z more efficient based on the results. As previous Pyramid, we always processed fewer individuals than the traditional algorithm processed.

We exploit the fact that we have so few individuals processed in the case where Pyramid-Z gets stuck to enter a new phase of evolution driven by hypermutation. Our results show that this almost always improves performance relative to standard approaches while still using significantly fewer evaluations.

Currently Pyramid-Z is only defined for real coded GAs. Future work will explore programming problems where the complexity of the problem will need to be moderated solely by the fitness function.

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