Viability principles for constrained optimization using a (1+1)-CMA-ES

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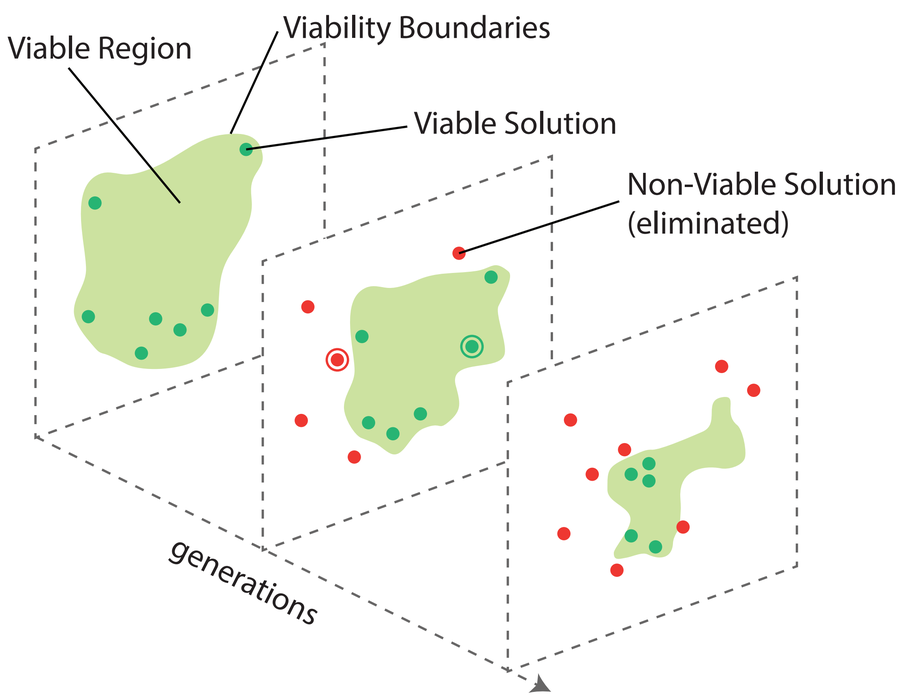
Abstract

Viability Evolution is an abstraction of artificial evolution that operates by eliminating candidate solutions that do not satisfy viability criteria.

Viability criteria are defined as boundaries on the values of objectives and constraints of the problem being solved. By adapting these boundaries it is possible to drive the search towards desired regions of solution space, discovering optimal solutions or those satisfying a set of constraints.

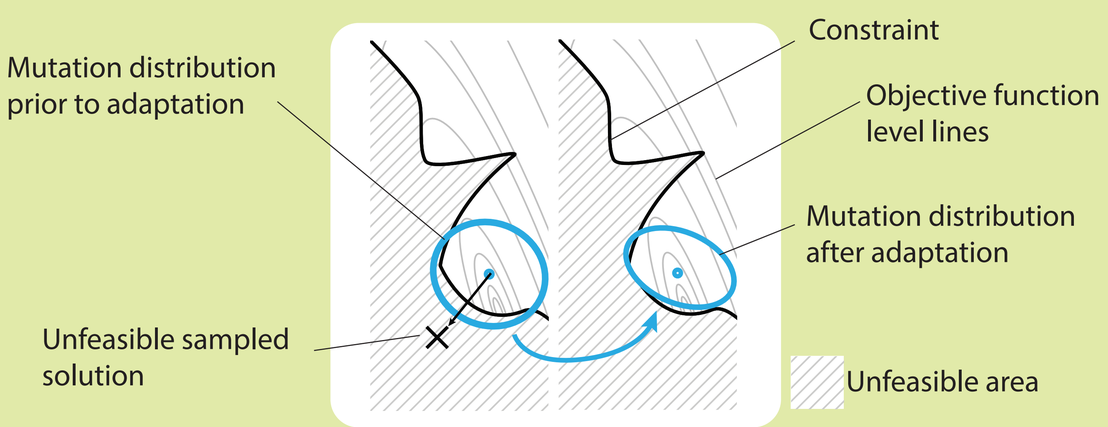
In this work, we test Viability Evolution principles on a modified (1+1)-CMA-ES for constrained optimization. The resulting method shows competitive performance when tested on eight unimodal problems.

The Viability Evolution paradigm [1], [2]



- Viability Evolution [1], [2] is an alternative paradigm for Evolutionary Computation.
- Survival criteria (viability boundaries) for the solutions are defined on objectives and constraints. These criteria determine which solutions survive (viable) or not (non-viable solutions).
- Viability boundaries are modified during the evolutionary process. This reflects in a change of the traits of evolving individuals.
- Dyanmic (adaptive) viability boundaries can be used to drive the population towards desired regions of search space.

Arnold and Hansen [3] method for constrained optimization with CMA-ES

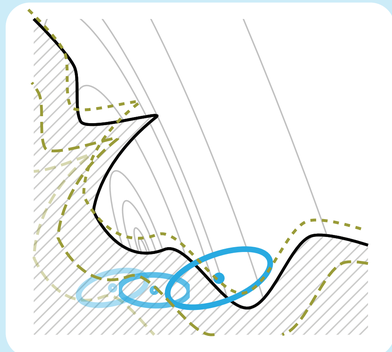


1) Maintains a low-pass filtered direction, that represents the vector normal to the constraint

2) When a solution that violates a constraint is sampled (left panel), the method uses this information to adapt the covariance matrix for decreasing the variance in the direction normal to the boundary (right panel)

Proposed Method

A) Use viability boundaries to drive the search towards feasible areas



1) Models constraints as "viability boundaries"

2) Relaxes thse boundaries at the beginning of the search to encompass the starting solution

3) Tightens boundaries to move towards feasible areas, exploiting active covariance matrix updates, as presented in [3]

B) Adapts the step size according to information from boundary violations

1) The different boundaries may have different probabilities of being violated at each iteration

2) Tracks the observed frequency of constraint violations and updates these probabilities

3) When a non-feasible (non-viable) solution is sampled, and any of these probabilities is smaller than 0.5, decreases the global probability of success used in the (1+1)-CMA-ES to adapt the step size

Results

	Constraint Evaluations							
	g06		g07		g09		g10	
	VIE-CMA	acCMA	VIE-CMA	acCMA	VIE-CMA	acCMA	VIE-CMA	acCMA
10th	797	**827**	**7184**	10435	**3474**	3626	**7360**	15621
50th	**900**	1060	**7545**	11283	**3660**	4106	**8295**	18781
90th	**986**	1223	**8032**	12704	**3913**	5075	**11322**	23088
	TR2		2.40		2.41		HB	
10th	751	**616**	**3166**	4551	**3183**	5235	**2659**	2338
50th	812	**708**	**3570**	6994	**3449**	8108	**2893**	2912
90th	884	**839**	**3899**	11114	**3801**	12056	**3185**	3970

- The method is competitive on seven out of eight tested problems.
- Our method has median number of constraint evaluations lower than those reported in [3] by a factor of 0.15, 0.33, 0.11, 0.56, 0.49, 0.57 on g06, g07, g09, g10, 2.40, 2.41 respectively and almost identical performance on HB.
- In the linear constrained sphere function problem TR2, our method exceeds values reported by Arnold and Hansen [3] by a factor 0.15.

Extensions

- Recently tested on a framework for protein assembly prediction.
- Extended into a memetic computing approach that uses a population of local units, based on this method, and recombines local information by means of global search operators [4].

References

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