Population sizing of cellular evolutionary algorithms

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Abstract

Cellular evolutionary algorithms (cEAs) are a particular type of EAs in which a communication structure is imposed to the population and mating restricted to topographically nearby individuals. In general, these algorithms have longer takeover times than panmictic EAs and previous investigations argue that they are more efficient in escaping local optima of multimodal and deceptive functions. However, most of those studies are not primarily concerned with population size, despite being one of the design decisions with a greater impact in the accuracy and convergence speed of population-based metaheuristics. In this paper, optimal population size for cEAs structured by regular and random graphs with different degree is estimated. Selecto-recombinative cEAs and standard cEAs with mutation
and different types of crossover were tested on a class of functions with tunable degrees of difficulty. Results and statistical tests demonstrate the importance of setting an appropriate population size. Event Takeover Values (ETV) were also studied and previous assumptions on their distribution were not confirmed: although ETV distributions of panmictic EAs are heavy-tailed, log-log plots of complementary cumulative distribution functions display no linearity. Furthermore, statistical tests on ETVs generated by several instances of the problems conclude that power law models cannot be favored over log-normal. On the other hand, results confirm that cEAs impose deviations to distribution tails and that large ETVs are less probable when the population is structured by graphs with low connectivity degree. Finally, results suggest that for panmictic EAs the ETVs’ upper bounds are approximately equal to the optimal population size.

Keywords
Spatially structured evolutionary algorithms; Cellular evolutionary algorithms; Optimal population size; Event takeover values

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