Modified Multi-Population Genetic Algorithms for Parameter Identification of Yeast Fed-batch Cultivation

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In this investigation two new modifications of standard multi-population genetic algorithm have been developed. Modifications differ from each other in the sequence of execution of main genetic operators selection, crossover and mutation. The main idea of both modifications is the operator selection to be executed between the operators crossover and mutation, or between mutation and crossover, respectively. Newly elaborated modifications of multi-population genetic algorithms together with the standard one have been investigated for a parameter identification of yeast fed-batch cultivation. Obtained results have been compared and newly proposed modifications have been shown as accurate as the standard one multi-population genetic algorithms even proved to be faster.