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# Sufficiency and duality for $E$ -differentiable multiobjective programming problems involving generalized $V$ - $E$ -invex functions

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In our considerations, a class of  $E$ -differentiable multiobjective programming problems with both inequality and equality constraints is considered. We introduce the concepts of  $V$ - $E$ -pseudo-invex, strictly  $V$ - $E$ -pseudo-invex and  $V$ - $E$ -quasi-invex functions, in which the involved functions are not necessarily differentiable, but they are  $E$  differentiable. Based upon these generalized  $V$ - $E$ -invex functions, the sufficiency of the so-called  $E$ -Karush-Kuhn-Tucker optimality conditions are established for the considered  $E$  differentiable vector optimization problems with both inequality and equality constraints. Furthermore, the so-called vector  $E$ -dual problem in the sense of Mond-Weir and Wolfe are defined for the considered  $E$ -differentiable multiobjective programming problem and several  $E$ -duality theorems are derived also under appropriate (generalized)  $V$ - $E$ -invexity assumptions.

Keywords:  $V$ - $E$ -invex function;  $E$ -differentiable function;  $E$ -optimality conditions;  $E$ -Mond-Weir duality;  $E$ -Wolfe duality

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## A parallel island-based genetic algorithm for inferring metabolic network

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The problem of biological network inference has become an essential problem in computational system biology. Inferring the presence or absence of links among objects involved in such networks provides a more comprehensive picture and essential information about molecular behavior for further analysis, understanding the functionality and control of complex biological networks. In our recent work, we formulated the problem of metabolic network and protein-protein interaction network inference as a multi-objective optimization method that utilizes two sources of prior knowledge: omics data and the structural properties of a scale-free network. The proposed multiobjective genetic algorithm-based method showed promising results in inferring two different types of biological networks: metabolic network and protein interaction network. However, the proposed method to reconstruct the network is time-consuming because several evaluations must be performed. GPU computing is recently revealed as a powerful high-performance way to solve large size and time-intensive problems. In this paper, we introduce a parallel island genetic algorithm, executed on Nvidia GPU, to infer metabolic network aiming at achieving faster execution time and better performance. The preliminary results showed that the parallel island model has accelerated the execution time of the multi-objective GA-based reconstruction method; the overall performance over NVIDIA Tesla K10.G2.8GB GPU card reaches a 600-fold speedup.

Keywords: biological Network Inference; genetic algorithm; optimization; island model; GPU