Stopping Criteria for Genetic Algorithms with Application to Multiobjective Optimization

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Abstract. For a general Markov chain model of genetic algorithm, we establish an upper bound for the number of iterations which must be executed in order to generate, with a prescribed probability, a population consisting entirely of minimal solutions to a multiobjective optimization problem. However, since populations may contain multiple copies of the same element, we can only guarantee that at least one minimal solution is found. Using this upper bound, we then derive a stopping criterion which ensures that at least one minimal element is a member of the last population generated.

Keywords: Random Heuristic Search, genetic algorithm, stopping criterion, multiobjective optimization.

1 Introduction

Obtaining sensible stopping criteria is an important issue in the theory of genetic algorithms. One of the possible approaches to this problem is to obtain upper bounds for the number of iterations necessary to ensure finding an optimal solution with a prescribed probability (see [1] and references therein). In an earlier paper [6], we have presented some results of this type for a general model of genetic algorithm, based on the theory developed in [4] and [7]. The aim of this paper is to modify the results of [6] so as to obtain some stopping criteria for the case of multiobjective optimization.

2 The RHS Algorithm as a Markov Chain

The RHS (*Random Heuristic Search*) algorithm, described in [7], is defined by an *initial population* $P^{(0)}$ and a *transition rule* τ which, for a given population $P^{(i)}$, determines a new population $P^{(i+1)}$. Iterating τ, we obtain a sequence of populations:

$$P^{(0)} \xrightarrow{\tau} P^{(1)} \xrightarrow{\tau} P^{(2)} \xrightarrow{\tau} \dots \tag{1}$$

Each population consists of a finite number of *individuals* which are elements of a given finite set Ω called the *search space*. Populations are *multisets*, which means that the same individual may appear more than once in a given population.

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FINDING ALL MINIMAL ELEMENTS OF A FINITE PARTIALLY ORDERED SET BY GENETIC ALGORITHM WITH A PRESCRIBED PROBABILITY

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ABSTRACT. For a general Markov chain model of genetic algorithm, we establish an upper bound for the number of iterations which must be executed in order to find, with a prescribed probability, an optimal solution in a finite multiobjective optimization problem.

1. **Introduction.** In an earlier paper [6], the author has obtained some probabilistic stopping criteria for a general model of genetic algorithm described by Vose [8]. They are given in the form of an upper bound for the number of iterations necessary to ensure finding an optimal solution with a prescribed probability, similarly as it has been done before in [1] for the case of classical genetic algorithm with bitwise mutation. However, all these results are valid for single-objective optimization only. In a more recent paper [7], we consider the same general Markov chain model of genetic algorithm, but for a multiobjective optimization problem. We establish an upper bound for the number of iterations which must be executed in order to generate, with a prescribed probability, a population consisting entirely of minimal solutions. However, since populations may contain multiple copies of the same element, we can only guarantee that at least one minimal solution is found. The results of [7] have the obvious drawback that they do not ensure generating the whole Pareto front even if it is finite and of small cardinality. The aim of this paper is to improve the previous stopping criteria so that they enable us to find, with a prescribed probability, all minimal solutions in a finite multiobjective optimization problem.

2. **Random heuristic search.** The RHS (*Random Heuristic Search*) algorithm, described in [8], is defined by an *initial population* $P^{(0)}$ and a *transition rule* τ which, for a given population $P^{(i)}$, determines a new population $P^{(i+1)}$. Iterating τ, we obtain a sequence of populations:

$$P^{(0)} \xrightarrow{\tau} P^{(1)} \xrightarrow{\tau} P^{(2)} \xrightarrow{\tau} \dots \qquad (1)$$

Each population consists of a finite number of *individuals* which are elements of a given finite set Ω called the *search space*. Populations are *multisets*, which means that the same individual may appear more than once in a given population.

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Key words and phrases. Genetic algorithm, Markov chain, vector optimization, stopping criteria.

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NEW CHARACTERIZATIONS OF WEAK SHARP AND STRICT LOCAL MINIMIZERS IN NONLINEAR PROGRAMMING

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Abstract. We consider the problem of identifying weak sharp local minimizers of order m, an important class of possibly non-isolated local minimizers. A characterization of such minimizers is obtained for a nonlinear programming problem with an abstract set constraint. The results are formulated in terms of certain normal and tangent cones to given sets, and generalized directional derivatives of the objective function. A particular case where the constraint set is given by a system of inequalities is also considered. As a consequence, we obtain a useful characterization of strict local minimizers of order m.

Keywords: weak sharp minimizer; strict local minimizer; Mordukhovich normal cone; contingent cone, interior Ursescu tangent cone; directional derivative.

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1. Introduction

The notion of a weak sharp minimum was introduced by Burke and Ferris in [1]. It is an extension of a strict (or strongly unique [4]) minimum to include the possibility of a non-unique solution set. Weak sharp minima play an important role in the convergence analysis of iterative numerical methods (see Section 4 of [1]). Some results concerning characterizations of such minimizers for constrained optimization problems were derived in [14], with special attention given to weak sharp local minimizers of order two. In [11],

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This paper is dedicated to the memory of my wife Monika.

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Higher-order conditions for strict local Pareto minima in terms of generalized lower and upper directional derivatives

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ABSTRACT

We introduce lower and upper limits of vector-valued functions with respect to the usual positive cone in a finite-dimensional space. Using these concepts, we extend the definitions of m-th order lower and upper directional derivatives introduced in Studniarski (1986) [1] to vector-valued functions, and prove some necessary and sufficient conditions for strict local Pareto minimizers of order m.

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1. Introduction

In [1] Studniarski introduced new generalized lower and upper directional derivatives of order m for an arbitrary extended-real-valued function $f : \mathbb{R}^n \to \bar{\mathbb{R}}$ (see formulas (22)–(23)). More recently, these derivatives were applied to obtain higher-order optimality conditions for some classes of scalar and vector optimization problems (see [2–5]), but this was done without extending the definitions themselves to vector-valued functions. However, Sun and Li [6] defined and used similar objects for set-valued maps.

In this paper we define the generalized lower and upper directional derivatives of order m, which extend the notions from [1] to functions with values in finite-dimensional vector spaces. We also show that these derivatives can be used to formulate higher-order optimality conditions for strict local Pareto minima in a multiobjective optimization problem. In this way, we improve some results from [5] by relaxing the assumptions concerning the minimized function.

2. Infima and suprema of sets in extended Euclidean spaces

Let $\bar{\mathbb{R}} = \mathbb{R} \cup \{-\infty, \infty\}$ be the set of extended real numbers. The arithmetic operations in $\mathbb{R}$ are extended to $\bar{\mathbb{R}}$ in an obvious manner, except for the combinations $0 \cdot (-\infty)$, $0 \cdot \infty$, $-\infty + \infty$ and $\infty - \infty$ which we regard as undefined rather than defining them in any special way (such as, for example, in [7, p. 15]). The weak inequality $\leqq$ in $\mathbb{R}$ is extended to $\bar{\mathbb{R}}$ by assuming that the following (and only the following) inequalities hold for infinite elements:

$$\begin{aligned} &-\infty \leqq \alpha \leqq \infty \quad \text{for all } \alpha \in \mathbb{R}, \\ &-\infty \leqq -\infty, \quad -\infty \leqq \infty, \ \infty \leqq \infty. \end{aligned} \tag{1}$$

Definition 1. For any positive integer p, the *extended Euclidean space* $\bar{\mathbb{R}}^p$ is defined as the Cartesian product of p copies of $\bar{\mathbb{R}}$. The operations of addition and scalar multiplication in $\bar{\mathbb{R}}^p$ are performed componentwise whenever the respective

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Stopping criteria for a general model of genetic algorithm

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Abstract. We consider a general Markov chain model of genetic algorithm described in [3], Chapters 5 and 6. For this model, we establish an upper bound for the number of iterations which must be executed in order to find an optimal (or approximately optimal) solution with a prescribed probability. For the classical genetic algorithm with bitwise mutation, our result reduces to the main theorem of [1] in the case of one optimal solution, and gives some improvement over it in the case of many optimal solutions.

1 Introduction

Obtaining sensible stopping criteria is an important issue in the theory of genetic algorithms. One of the possible approaches to this problem is to obtain upper bounds for the number of iterations necessary to ensure finding an optimal solution with a prescribed probability (see [1] and references therein). In this paper we present some results of this type for a more general model of genetic algorithm, based on the theory developed in [3] and [5].

2 Random Heuristic Search

The RHS (*Random Heuristic Search*) algorithm, described in [5], is defined by an *initial population* $P^{(0)}$ and a *transition rule* τ which, for a given population $P^{(i)}$, determines a new population $P^{(i+1)}$. Iterating τ, we obtain a sequence of populations:

$$P^{(0)} \xrightarrow{\tau} P^{(1)} \xrightarrow{\tau} P^{(2)} \xrightarrow{\tau} \ldots \tag{1}$$

Each population consists of a finite number of *individuals* which are elements of a given finite set Ω called the *search space*. Populations are *multisets*, which means that the same individual may appear more than once in a given population.

To simplify the notation, it is convenient to identify Ω with a subset of integers: $\Omega = \{0, 1, ..., n-1\}$. The number n is called the *size of search space*. Then a population can be represented as an *incidence vector* (see [3, p. 141]):

$$v = (v_0, v_1, ..., v_{n-1})^T, \tag{2}$$