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Why Unified Statistics Theory by MCMC Towards Linear and Nonlinear Programming Problems?

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Abstract- *Unified statistics theory by MCMC is considered. A new proposed algorithm is presented to obtain surely empirical analysis conclusions in order to turn to surely theoretical analysis results about the behavior of* ***any general linear or nonlinear programming problem*** *in order to introduce a complete framework and to solve any too large dimensional deterministic and probabilistic (the grouping data, both continuous and discrete) linear or nonlinear programming problems by the proposed algorithm that has two obvious criteria towards the* ***second resounding success*** *of unified statistics theory by MCMC.*

Keywords- *Unified statistics theory by MCMC; General nonlinear programming problem; General linear programming problem; Grouping data .*

1. INTRODUCTION

Unified statistics theory by MCMC has been proposed by Abou El-Enien [1].

Unique chromosomes by simple random sampling without replacement theorem for any objective real valued function of n - variables of the form $f(x_1, x_2, \ldots, x_n)$, where $a_i \le x_i \le b_i$ for $i = 1, 2, \ldots, n$ within the framework of unified statistics theory by MCMC has been proposed by Abou El-Enien and Khalil [2].

There is **no known method** of determining the global maximum (or minimum) to the general nonlinear programming problem. Only if the objective function and the constraints satisfy certain properties, the global optimum can sometimes be found. Several algorithms were developed for unconstrained and constrained problems [4].

Despite the active research and progress in global optimization in recent years [3], it is probably fair to say that **no efficient solution** procedure is in sight for the general nonlinear problems [4].

The rest of the paper is organized as follows. In Section 2, we give the formulation of the problem. In Section 3, we state the main result. Then in Section 4, the proof of the main result is given in five steps. In Section 5, we propose the algorithm. In Section 6, we give numerical example. In Section 7, we give some concluding remarks.

2. FORMULATION OF THE PROBLEM

In this paper, we consider a problem, namely: Why unified statistics theory by MCMC towards linear and nonlinear programming problems ?.

Throughout this paper, we consider any objective real valued function (linear or nonlinear) of n - variables $f(x_1, x_2, \ldots, x_n)$, where $a_i \le x_i \le b_i$ for $i = 1, 2, \ldots, n$ are domains of each variable x_i and a_i and b_i are real numbers:

$u \ge 0$ equations:

$$q_i(x_1, x_2, \ldots, x_n) = 0 \text{ (linear or nonlinear)},$$
$$i = 0, \ldots\ldots, u, \rightarrow \quad \text{(I)}$$

and $m - u \ge 0$ inequalities:

$$q_i(x_1, x_2, \ldots, x_n) \le 0 \text{ (linear or nonlinear)},$$
$$i = u+1, \ldots\ldots, m . \rightarrow \quad \text{(II)}$$

Proposition 2.1. We restrict an arbitrary uncountable set $S = \{a_i \le x_i \le b_i$ for $i = 1, 2, \ldots, n\}$ to be a subset of n -space $\mathbf{R^n}$ as a sample space, restrict an arbitrary countable set T to be set of all $(x_1, x_2, \ldots, x_n)$ in $S = \{a_i \le x_i \le b_i\}$ for which $P(x_1, x_2, \ldots, x_n) > 0$ as a sample space (see [5]).

Proposition 2.2. We divide each interval $a_i \le x_i \le b_i$, $i = 1, 2, \ldots, n$ into **k** (**k** is a different optional integer number for each interval $a_i \le x_i \le b_i$) subintervals $a_i \le x_i \le c_i$, $c_i \le x_{i+1} \le d_i$, ……, $w_i \le x_{k-1} \le y_i$, $y_i \le x_k \le b_i$ and c_i, d_i, ……, w_i and y_i (the new population) are optional real numbers, list the possible simple random samples without replacement of n (n as n of S) subintervals from this new population.(see [2]).

Proposition 2.3. We get unique chromosomes $(=2^k)$, k bits {0,1}, for all simple random samples without replacement of n subintervals from the new population, substitute in (I) and (II), get **subset of unique chromosomes**, get globally optimum value(s), compare all globally optimum value(s) of all simple random samples without replacement of n subintervals and have the globally optimum value(s) of the real valued function.

3. MAIN RESULT

In this section, we shall state the main theorem.

Theorem 3.1. For any objective real valued function (linear or nonlinear) of n - variables $f(x_1, x_2, \ldots, x_n)$, where $a_i \le x_i \le b_i$ for $i = 1, 2, \ldots, n$ are domains of each variable x_i and a_i and b_i are real numbers:

$u \ge 0$ equations:

$q_i(x_1, x_2, \ldots, x_n) = 0$ (linear or nonlinear), $i = 0, \ldots\ldots, u$, and $m - u \ge 0$ inequalities:

$q_i(x_1, x_2, \ldots, x_n) \le 0$ (linear or nonlinear), $i = u+1, \ldots\ldots, m$, the following holds:

(1) A real valued function is one that contains all possible simple random samples without replacement of n (n as n of S) subintervals from the new population.

(2) Every simple random sample without replacement of n subintervals has unique chromosomes and **subset of unique chromosomes**, and has globally optimum value(s).

(3) By comparing all globally optimum value(s) of all simple random samples without replacement of n subintervals. We have the globally optimum value(s) of the real valued function.

4. PROOF OF THE MAIN RESULT

In this section, we prove the main result in Theorem 3.1.

We shall prove Theorem 3.1 in five steps.

Proof of Theorem 3.1. Steps 1, 2 and 3 (see [2]).

Step 4. We get unique chromosomes $(=2^k)$, k bits {0,1}, for all simple random samples without replacement of n subintervals from the new population, get **subset of unique chromosomes**, and get globally optimum value(s).

Step 5. We compare all globally optimum value(s) of all simple random samples without replacement of n subintervals and have the globally optimum value(s) of the real valued function.

On the basis of Steps 1-5, we complete the proof of Theorem 3.1.

5. PROPOSED ALGORITHM

We prepared programs by using MATLAB 7.5. We named the proposed algorithm subset of unique chromosomes by simple random sampling without replacement (**SUCSRSR**), the basic steps of the **SUCSRSR** algorithm are as follows:

1. Divide each interval $a_i \le x_i \le b_i$, $i = 1, 2, \ldots, n$ into **k** subintervals, define the new population.
2. List the possible simple random samples without replacement of n subintervals from this new population. For each random sample without replacement of n subintervals, do the following:
   a. Input number of bits k.
   b. Get unique chromosomes = 2^k.
   c. Get **subset of unique chromosomes**, and Get the globally optimum value(s).
3. Compare all globally optimum value(s) of all simple random samples without replacement of n subintervals and have the globally optimum value(s) of the real valued function.

6. NUMERICAL RESULTS AND DISCUSSION

6.1. A numerical example

Minimize

$$f(x, y) = -10.5x_1 - 7.5x_2 - 3.5x_3 - 2.5x_4 - 1.5x_5 - 10y - 0.5\sum_{i=1}^{5} x_i^2$$

Subject to :

$$6x_1 + 3x_2 + 3x_3 + 2x_4 + x_5 \le 6.5,$$
$$10x_1 + 10x_3 + y \le 20,$$
$$0 \le x_i \le 1,$$
$$0 \le y.$$

Since $y \le 20 - 10x_1 - 10x_3$ and $0 \le x_i \le 1$, we restrict $0 \le y \le 20$.

By the **SUCSRSR** method, the globally optimum value = (0.000000, 1.000000, 0.000000, 0.999999, 1.000000, 20.000000) for which the objective function is equal to -213.

7. DISCUSSION

In this paper, the main result is the subset of unique chromosomes by simple random sampling without replacement theorem for any objective real valued function of n - variables. Using this, we propose subset of unique chromosomes by simple random sampling without replacement method to solve any too large dimensional deterministic and probabilistic linear or nonlinear programming problems toward two obvious criteria (speed and accuracy).

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