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Inverse Problem for a Parabolic System

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Abstract

In this paper a numerical approach combining the least squares method and a genetic algorithm is proposed for the determination of the source term in an inverse parabolic system (IPS). A numerical experiment confirm the utility of this algorithm as the results are in good agreement with the exact data. Results show that a reasonable estimation can be obtained by the genetic algorithm within a CPU with clock speed 2.7 GHz.

Keywords: Inverse parabolic system; Least squares method; Genetic algorithm

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1. Introduction

Inverse problems are encountered in many branches of engineering and science. In one particular branch, heat transfer, the inverse problem can be used to such conditions as temperature or surface heat flux, or can be used to determine important thermal properties such as the thermal conductivity or heat capacity of solids.

Several functions and parameters can be estimated from the inverse parabolic problem: static and moving heating sources, material properties, initial conditions, boundary conditions, optimal shape etc. Fortunately, many methods have been reported to solve inverse parabolic problems (Alifanov, 1994; Beck et al., 1985; Beck et al., 1996; Beck, et al., 1986; Dowding and Beck, 1999; Cabeza et al., 2005; Liu, 2008; Molhem and Pourgholi, 2008; Murio, 1993; Murio and

Paloschi, 1988; Pourgholi et al., 2009; Pourgholi and Rostamian, 2010; Shidfar et al., 2006; Zhou et al., 2010).

In this paper, for $0 < x < 1, 0 < t < t_M$, we consider the following IPS in the dimensionless form

$$\begin{cases} Ut (x,t) - Uxx(x,t) + a(x,t)U(x,t) + b(x,t)V(x,t) = f(x,t), \\ Vt (x,t) - Vxx(x,t) + a(x,t)V(x,t) + b(x,t)U(x,t) = g(x,t) \end{cases}$$
(1)

$$\begin{cases} U(x,0) = w_1(x), \quad V(x,0) = w_2(x), \quad 0 \le x \le 1, \\ U(0,t) = p_1(t), \quad V(0,t) = p_2(t), \quad 0 \le t \le t_M, \end{cases}$$
(2)

$$(U(1,t) = q_1(t), V(1,t) = q_2(t), 0 \le t \le t_M,$$

and the over specified condition

$$s(t) = U(a,t), \quad 0 \le t \le t_M,$$
 (3)

where g(x,t), a(x,t) and b(x,t) are continuous known real-valued functions, $w_1(x), w_2(x), p_1(t), p_2(t), q_1(t)$ and $q_2(t)$ are infinitely differentiable known real-valued functions and t_M represents the final existence time for the time evolution of the problem, while the function f(x,t) is unknown which remains to be determined from some interior temperature measurements.

System (1) - (3) arises, for example, in the study of chemical reactions (see e.g. (Bothe, 2003; Chipot et al. 2009; E'rdi and To'th, 1989)), and in a wide variety of mathematical biology and physical situations (see e.g. (Hillen, and Painter, 2009; Lauffenburger et al. 1982; Shigesada et al. 1979)). The controllability properties of system (1)-(3) has been studied, for example, in [Ammar-Khodja et al. 2006; Ammar-Khodja et al. 2011; L. de Teresa, 2000; Gonza'lez-Burgos and P'erez-Garc'1a, 2006; Le'autaud, 2010; Russell, 1973]. See also [Ammar-Khodja et al. 2011] for a nice survey on this issue. The recent work [Ferna'ndez-Cara et al. 2010] studies system (1)-(3) in one space dimension and with constant coupling coefficients. The cases of higher space dimensions and varying coupling coefficients (and in particular when the coefficients vanish in a neighborhood of the boundary) are, to our knowledge, completely open.

We should note that, for a given function f(x, t), we can prove the existence of a unique solution (U(x, t), V(x, t)) of (1)-(3). More precisely, one can easily observe that system (1) with the conditions (2) can be reduced to

$$\begin{cases} u_t(x,t) - u_{xx}(x,t) + a(x,t)u(x,t) + b(x,t)u(x,t) = F(x,t), \\ v_t(x,t) - v_{xx}(x,t) + a(x,t)v(x,t) + b(x,t)u(x,t) = G(x,t), \\ u(x,0) = \varphi(x), \quad v(x,0) = \psi(x), \\ u(0,t) = u(1,t) = v(0,t) = v(1,t) = 0, \end{cases}$$
(4)

where

$$\begin{aligned} \varphi(x) &= w_1(x) - xq_1(0) - (1 - x)p_1(0), \\ \psi(x) &= w_2(x) - xq_2(0) - (1 - x)p_2(0), \end{aligned}$$

$$F = f - p'_{1} - ap_{1} - bp_{2} - x(q'_{1} - p'_{1} + aq_{1} - ap_{1} - bq_{2} - bp_{2}),$$

and

$$G = g - p'_{2} - bp_{2} - ap_{1} - x(q'_{2} - p'_{2} + aq_{2} - bp_{2} - bq_{1} - bp_{1}).$$

We notice for $\Omega = (0, 1)$ that, on the space $(L^2(\Omega))^2$ endowed with the natural inner product

$$\langle \vec{u}, \vec{v} \rangle L^2(\Omega) \times L^2(\Omega) = \langle u_1, u_2 \rangle L^2(\Omega) \times L^2(\Omega) + \langle v^1, v^2 \rangle L^2(\Omega) \times L^2(\Omega),$$

with $\vec{u} = (u_1, u_2)$ and $\vec{v} = (v_1, v_2)$, the operator

$$\begin{pmatrix} -\Delta + a & b \\ b & -\Delta + a \end{pmatrix}$$

with domain $(H^2(\Omega) \cap H_0^1(\Omega))^2$, is self-adjoint, where $H^2(\Omega)$ and H_0^1 are the usual Sobolev spaces. As a consequence, for $F, G \in L^2(\Omega \times (0,T))$, a = a(x) and b = b(x) with $a, b \in L^{\infty}(\Omega)$ the Cauchy problem (4) is well-posed in $(L^2(\Omega))^2$, in the sense of semigroup theory [Lions, 1988]. Moreover, for the general case $a(x,t), b(x,t) \in L^{\infty}(\Omega \times (0,T))$, if we suppose that $F, G \in L^2((0,T); H_0^{-1}(\Omega))$ and $(\varphi, \psi) \in (L^2(\Omega))^2$, then there exists a unique solution (u, v) of (4) satisfying

$$u, v \in L^2((0,T); H^1_0(\Omega)) \cap C([0,T]; L^2(\Omega))$$

and

$$u_t$$
, $v_t \in L^2((0,T); H_0^{-1}(\Omega))$.

More precisely, this result can be obtained by defining the bilinear form

$$A: \left(H_0^1(\Omega)\right)^2 \times \left(H_0^{-1}(\Omega)\right)^2 \to R$$

by

$$A(t; \vec{u}, \vec{v}) = \int_0^1 (\vec{u}_x(x, t) \cdot \vec{v}_x(x, t) + au_1 v_1 + bu_2 v_2) dx,$$

verifying that A satisfies

- (i) for every \vec{u} , $\vec{v} \in (H_0^1(\Omega))^2$ the function $t \ 7 \to A(t; \vec{u}, \vec{v})$ is measurable,
- (ii) $|A(t; \vec{u}, \vec{v})| \leq C0 \| \vec{v} \|_{(H^{\frac{1}{0}}(\Omega))^2}^2 C2 \| \vec{v} \|_{(L^2(\Omega))^2}^2$,
- (iii) $A(t; \vec{u}, \vec{v}) \ge C_2 \| \vec{v} \|_{\left(H^{\frac{1}{0}}(\Omega)\right)^2}^2 C_2 \| \vec{v} \|_{\left(L^2(\Omega)\right)^2}^2$, for almost every $t \in [0, T]$ and for all $\vec{v} \in (H^1_0(\Omega))^2$,

where $C_1 > 0$, C_0 and C_2 are constants, and applying a similar argument to (Lions and Magenes, 1961 Theorem 7.1), see also (Lions and Magenes, 1961; Baiocchi, 1964; Lions and Magenes, 1960; Lions and Magenes, 1968).

We should remark that if the assumptions given above hold and f is known, one can obtain a unique solution (u, v) of (1)-(2). But in the case when f(x, t) depends only on x or t, by using the overspecified condition (16), one can find a unique solution [(u, v), f] of the inverse problem (1) - (3).

2. Numerical Technique

In this section we will numerically investigate our IPS. Problem (1) - (3) can be solved in leastsquare sense and a cost function can be defined as a sum of squared differences between measured temperatures and calculated values of U(x,t) by considering guesses estimated values of f(x,t).

$$f(G) = \sum_{j=1}^{m} (U_j - s_j)^2, \qquad (5)$$

where U_j , j = 1, 2, 3, ..., m, are calculated by solving the direct heat problem. To do this, we consider prior guess for f(x, t). Also, $s_j = s(t_j)$, j = 1, 2, 3, ..., m, are measured temperatures. To find optimal solution f(x, t), Equation (5) must be minimum.

Remark 1.

In this study we use implicit finite difference approximation (Crank-Nicolson method) for discretizing problem (1) - (3). Therefore,

$$- rU_{i-1,j+1} + (2 + 2r)U_{i,j+1} - rU_{i+1,j+1} = 2kf_{i,j} + rU_{i-1,j} + (2 - 2r)U_{i,j} + rU_{i+1,j} - 2ka_{i,j}U_{i,j} - 2kb_{i,j}V_{i,j}, i = 1, ..., N - 1, j = 0, ..., N - 1$$

$$(6)$$

$$- rV_{i-1,j+1} + (2 + 2r)V_{i,j+1} - rV_{i+1,j+1} = 2kg_{i,j} + rV_{i-1,j} + (2 - 2r)V_{i,j} + rV_{i+1,j} - 2ka_{i,j}V_{i,j} - 2kb_{i,j}U_{i,j}, i = 1, ..., N - 1, j = 0, ..., N - 1$$

$$(7)$$

$$U_{i,0} = w_1(ih), \ V_{i,0} = w_2(ih), \ j = 0, i = 1, ..., N - 1,$$
 (8)

$$U_{0,i} = p_1(jk), V_{0,i} = p_2(jk), \quad i = 0, \quad j = 0, 1, \dots, N-1,$$
 (9)

$$U_{N,j} = q_1(jk), \quad V_{0,j} = p_2(jk), \quad l = 0, \ j = 0, 1, \dots, N-1, \quad (10)$$

where x = ih and t = jk.

By using Equations (6) - (10), we obtain the following linear algebraic system of equations

$$\begin{pmatrix} 2+2r & -r & 0 & 0 & 0 & 0 & 0 \\ -r & -2+2r & -r & 0 & 0 & 0 & 0 & 0 \\ \vdots & \vdots & \ddots & \vdots & \ddots & \vdots & \vdots & \vdots \\ 0 & 0 & 0 & 0 & -r & 2+2r & -r & 0 \\ 0 & 0 & 0 & 0 & 0 & -r & 2+2r \end{pmatrix} \begin{pmatrix} U_{1,j+1} \\ U_{2,j+1} \\ \vdots \\ U_{N-2,j+1} \\ U_{N-1,j+1} \end{pmatrix} = 2k \begin{pmatrix} f_{1,j} \\ f_{2,j} \\ \vdots \\ U_{N-2,j} \\ f_{N-1,j} \end{pmatrix} \\ + \begin{pmatrix} 2-2r & r & 0 & 0 & 0 & 0 & 0 & 0 \\ \vdots & \vdots & \ddots & \vdots & \ddots & \vdots \\ 0 & 0 & 0 & 0 & 0 & r & 2-2r & r \\ 0 & 0 & 0 & 0 & 0 & r & 2-2r & r \\ 0 & 0 & 0 & 0 & 0 & r & 2-2r & r \\ 0 & 0 & 0 & 0 & 0 & r & 2-2r & r \\ 0 & 0 & 0 & 0 & 0 & r & 2-2r & r \\ \end{pmatrix} \begin{pmatrix} U_{1,j} \\ U_{2,j} \\ \vdots \\ U_{N-2,j} \\ U_{N-1,j} \end{pmatrix} \\ + r \begin{pmatrix} U_{0,j} + U_{0,j+1} \\ \vdots \\ U_{N,j} + U_{N,j+1} \end{pmatrix} - 2k \begin{pmatrix} a_{1,j}U_{1,j} \\ a_{2,j}U_{2,j} \\ \vdots \\ a_{N-2,j}U_{N-2,j} \\ a_{N-1,j}U_{N-1,j} \end{pmatrix} - 2k \begin{pmatrix} b_{1,j}V_{1,j} \\ b_{2,j}V_{2,j} \\ \vdots \\ \vdots \\ b_{N-2,j}V_{N-2,j} \\ b_{N-1,j}V_{N-1,j} \end{pmatrix} \\ \begin{pmatrix} 2+2r & -r & 0 & 0 & 0 & 0 & 0 \\ \vdots & \vdots & \ddots & \vdots & \vdots \\ 0 & 0 & 0 & 0 & -r & 2+2r & -r \\ 0 & 0 & 0 & 0 & 0 & -r & 2+2r \end{pmatrix} \begin{pmatrix} V_{1,j+1} \\ V_{2,j+1} \\ \vdots \\ V_{N-2,j+1} \\ V_{N-1,j+1} \end{pmatrix} = 2k \begin{pmatrix} g_{1,j} \\ g_{2,j} \\ \vdots \\ g_{N-2,j} \\ g_{N-1,j} \end{pmatrix} \\ + \begin{pmatrix} 2-2r & r & 0 & 0 & 0 & 0 & 0 \\ r & -2-2r & r & 0 & 0 & 0 & 0 \\ \vdots & \vdots & \vdots & \vdots & \vdots \\ 0 & 0 & 0 & 0 & 0 & -r & 2+2r & r \\ \vdots & \vdots & \vdots & \vdots & \vdots \\ 0 & 0 & 0 & 0 & 0 & 0 & r & 2-2r & r \\ \vdots & \vdots & \vdots & \vdots & \vdots \\ 0 & 0 & 0 & 0 & 0 & 0 & r & 2-2r & r \end{pmatrix} \begin{pmatrix} V_{1,j+1} \\ V_{2,j+1} \\ \vdots \\ V_{N-2,j+1} \\ V_{2,j} \\ \vdots \\ \vdots \\ V_{N-2,j} \\ V_{N-1,j} \end{pmatrix}$$

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$$+ r \begin{pmatrix} V_{0,j} + V_{0,j+1} \\ \cdot \\ \cdot \\ \cdot \\ \cdot \\ V_{N,j} + V_{N,j+1} \end{pmatrix} - 2k \begin{pmatrix} a_{1,j}V_{1,j} \\ a_{2,j}V_{2,j} \\ \cdot \\ \cdot \\ a_{N-2,j}V_{N-2,j} \\ a_{N-1,j}V_{N-1,j} \end{pmatrix} - 2k \begin{pmatrix} b_{1,j}U_{1,j} \\ b_{2,j}U_{2,j} \\ \cdot \\ \cdot \\ b_{N-2,j}U_{N-2,j} \\ b_{N-1,j}U_{N-1,j} \end{pmatrix}.$$

3. Genetic algorithm

Genetic algorithms, primarily developed by Holland (Holland, 1975), have been successfully applied to various optimization problems. It is essentially a searching method based on the Darwinian principles of biological evolution. Genetic algorithm is a stochastic optimization algorithm which employs a population of chromosomes, each of which represents a possible solution. By applying genetic operators, each successive incremental improvement in a chromosome becomes the basis for the next generation. The process continues until the desired number of generations has been completed or the predefined fitness value has been reached. Typically binary coding is used in classic genetic algorithm, where each solution is encoded as a chromosome of binary digits. Each member of the population represents an encoded solution in the classic genetic algorithm. For many problems, this kind of coding is not natural. The genetic algorithm used in this work is not a classic genetic algorithm. Instead, the application of genetic algorithm (RVGA). The continuous function is discrete for numerical computation and simulated by a chromosome. The value of each gene is a real number and indicates the heat generation at each time step (Liu, 2008).

The procedure of an RVGA is as follows:

- Step 1. Generate at random an initial population of chromosomes.
- Step 2. Evaluate the fitness of each chromosome in the population.
- Step 3. Select chromosomes, based on the fitness function, for recombination.
- Step 4. Recombine pairs of parents to generate new chromosomes.
- Step 5. Mutate the resulting new chromosomes.
- Step 6. Evaluate the fitness of new chromosomes.
- Step 7. Update population.
- Step 8. Repeat Step 3 to Step 7, until the fitness function is convergent or less than a predefined value.

4. A modified real-valued genetic algorithm (RVGA) to determine f(x, t)

In this paper we use a modified RVGA for determining f(x, t). In this algorithm, chromosomes are encoded as real-valued matrices. The J^{th} column of each chromosome illustrates $f_{i,i}$, i =

1, 2, 3, ..., N - 1. We consider each column of chromosomes as a gene. That $g_{p,j}$ illustrates J^{th} gene of chromosome of p. For finding optimal solution of f(x,t), Equation (5) must be minimum. For this purpose, we consider Equation (5) as fitness function and calculate simulated s by solving direct system for each chromosome. At the end of algorithm, the chromosome by lowest fitness is the best solution of f(x,t). To determine the f(x,t) we interpolate the best solution. To improve performance of RVGA, we added new step to algorithm after "mutation" operation, for modifying new chromosomes at each iteration. Figure 15 shows the flowchart of modified RVGA.

The procedure of a modified RVGA is as follows:

- Step 1. Generate at random an initial population of chromosomes.
- Step 2. Evaluate the fitness of each chromosome in the population.
- Step 3. Select some chromosomes as parents by tournament selection.
- Step 4. For generating pair of new chromosomes, pair of parents crossover together as follow:

$$g_{ch1,j} = \alpha \times g_{p1,j} + (1 - \alpha) \times g_{p2,j}, j = 1, 2, 3, ..., M, g_{ch2,j} = \beta \times g_{p1,j} + (1 - \beta) \times g_{p2,j}, j = 1, 2, 3, ..., M,$$

where p_1 illustrates first parent, p_2 illustrates second parent, ch_1 illustrates first new chromosome, ch_2 illustrates second new chromosome, α and β are random numbers in [-0.25, 1.25].

- Step 5. For applying "Mutation" operation on new chromosomes, selecting a gene of each new chromosome randomly and each element of genes adding by random number.
- Step 6. Finding the first best gene between new chromosomes and copy that gene to first gene of all chromosomes. Then finding the second best gene between new chromosomes and copy that gene to second gene of all chromosomes. Continue this procedure for all genes. Now all new chromosomes are the same. For generating new hopeful chromosomes, genes of second to end chromosomes replace by genes of first chromosome adding by random small values.
- Step 7. Evaluate the fitness of new chromosomes.
- Step 8. Update the population.
- Step 9. Repeat Step 3 to Step 8, until the fitness function is convergent or less than a predefined value.

The flowchart of the proposed algorithm for determining q(t) has been presented in Figure 15.

5. Numerical Results and Discussion

The aim of this section is to see the applicability of the present numerical method described in Section 4 for solving our IPS. As expected IPS (1) is ill-posed and therefore it is necessary to investigate the stability of the present method by giving a test problem. Now, we give the following examples in 0 < x < 1, 0 < t < 1.

Our first example is

$$\begin{cases} U_t(x,t) - U_{xx}(x,t) + 2U(x,t) + 3V(x,t) = f(x,t), \\ V_t(x,t) - V_{xx}(x,t) + 2V(x,t) + 3U(x,t) = 0, \end{cases}$$
(11)
$$U(x,0) = e^{-2x} + e^{2x} - \cos(\sqrt{2}x) - \sin(\sqrt{2}x), \qquad 0 \le x \le 1, \\ V(x,y) = \frac{1}{3}e^{-x} + e^{-2x} + e^{2x} - \cos(\sqrt{2}x) - \sin(\sqrt{2}x), \qquad 0 \le x \le 1, \\ U(0,t) = e^{-t}, \qquad 0 \le t \le 1, \\ V(0,t) = (\frac{10}{3})e^{-t}, \qquad 0 \le t \le 1, \end{cases}$$
(12)

$$U(1,t) = (\frac{1123}{176})e^{-t}, \qquad 0 \le t \le 1,$$

$$V(1,t) = (\frac{3807}{449})e^{-t}, \qquad 0 \le t \le 1,$$

by the over specified condition

$$s(t_j) = U(0.1, t_j) + \sigma R, \quad t_j = 0.01 \times j, \quad j = 0, 1, 2, ..., 99,$$
 (13)

Here, the exact values of f(x, t), U(x, t) and V(x, t) are $e^{-t} e^{-x}$, $e^{-t}(e^{-2x} + e^{2x} - \cos(\sqrt{2x}) - \sin(\sqrt{2x}))$ and $e^{-t} (1/3e^{-x} + e^{-2x} + e^{2x} - \cos(\sqrt{2x}) + \sin(\sqrt{2x}))$, respectively.

The second example is

$$\begin{cases} U_t(x,t) - U_{xx}(x,t) + 2 + (-xsin(x))U(x,t) + (xcos(x))V(x,t) = f(x,t), & (14) \\ V_t(x,t) - V_{xx}(x,t) + (-xsin(x))V(x,t) + (xcos(x))U(x,t) = 0 \end{cases}$$

$$\begin{cases}
U(x,0) = \sin(x) & 0 \le x \le 1, \\
V(x,y) = \cos(x) & 0 \le x \le 1, \\
U(0,t) = 0, & 0 \le t \le 1, \\
V(0,t) = e^{-t}, & 0 \le t \le 1, \\
U(1,t) = (\frac{1327}{_{1577}} & 0 \le t \le 1, \\
V(1,t) = (\frac{429}{_{794}})e^{-t}, & 0 \le t \le 1,
\end{cases}$$
(15)

by the over specified condition

$$s(t_j) = U(0.1, t_j) + \sigma R, \quad t_j = 0.01 \times j, \quad j = 0, 1, 2, ..., 99,$$
 (16)

where the exact values of f(x,t), U(x,t) and V(x,t) are $e^{-tx}\cos(2x)$, $e^{-t}\sin(x)$ and $e^{-t}\cos(x)$, respectively.

The experimental data $s(t_j)$ (measured temperatures at 0 < t < 1) are obtained from the exact solution of the direct problem by adding a random perturbation error to the exact solution of the direct problem in order to generate noisy data, where $\sigma = 0.01$ and *R* is random value in (0, 1).

Remark 2.

In an IS there are two sources of error in the estimation. The first source is the unavoidable bias deviation (or deterministic error). The second source of error is the variance due to the amplification of measurement errors (stochastic error). The global effect of deterministic and stochastic errors is considered in the mean squared error or total error, (Dowding and Beck, 1999).

$$S = \left[\frac{1}{(N-1)(M-1)}\sum_{i=1}^{N}\sum_{j=1}^{M}(\widehat{f_{i,j}} - f_{i,j})^2\right]^{\frac{1}{2}},$$
(17)

where (N - 1)(M - 1) is the total number of estimated values, $\widehat{f_{i,j}}$ is calculated values from interpolated equation and $f_{i,j}$ is exact values of f(x, t).

In our examples here, a population of 20 chromosomes of 100 genes ($t = 0.01, 0.02, 0.03, \cdots$., 0.99) is used as the initial guess to obtain for numerical results of modified RVGA. Also each gene has 9 elements ($x = 0.1, 0.2, 0.3, \cdots, 0.9$). Table 1 presents the results for 1 to 1000 generations for the first example and also Table 2 presents the results for 1 to 10000 generations for the second example. Note that *S* calculated by 900 total number of points.

Gen.	Best fitness	Time(s)	S
1	3.3079e - 003	1.4602	0.3800
100	3.1073e - 004	99.7811	0.0756
200	1.8876e - 004	199.5500	0.0727
300	9.6134e - 005	298.7181	0.0420
400	7.7658e - 005	397.6857	0.0479
500	1.1534e - 005	491.71616	0.0343
600	1.7591e - 005	601.0169	0.0415
700	5.1188e - 006	701.3476	0.0286
800	3.2938e - 006	791.4607	0.0168
900	8.5618e - 007	0.0068	0.0112
1000	4.7571e - 007	996.1871	0.0072

Table 1. The results of modified RVGA for a population of 20 chromosomes of 100 genes for1 to 1000 generations

Gen.	Best fitness	Time(s)	S
1	3.1719e - 001	2.9304	1.7655
100	3.2618e - 002	3068.7060	0.5948
200	7.1283e - 002	6091.6555	0.1425
300	7.4315e - 002	9049.7577	0.0973
400	8.4910e - 003	11930.9340	0.0867
500	4.9218e - 003	15032.7922	0.0965
600	9.5096e - 004	18152.1576	0.0733
700	9.7175e - 004	21188.5469	0.0764
800	6.3248e - 005	24124.0975	0.0178
900	9.0588e - 006	26981.9134	0.0134
1000	4.1515e - 006	29998.4709	0.0068

Table 2. The results of modified RVGA for a population of 20 chromosomes of 100 genes for1 to 10000 generations.

Figures 1 and 2 show the exact and numeric f(x, t) for the first example by implementing the modified RVGA for 1000 generations.



Figure 1. Exact f(x, t) of the first example



Figure 2. Numeric f(x, t) by implementing modified RVGA for 1000 generation in the first example

Figures 3 to 7 show exact and numeric $f(\alpha, t)$ for the first example by implementing modified RVGA for 1000 generations, where $\alpha = 0.1, 0.3, 0.5, 0.7$ and 0.9 respectively.



Figure 3. Exact and numeric f(0.1, t) by implementing the modified RVGA for 1000 generations in the first example



Figure 4. Exact and numeric f(0.3, t) by implementing the modified RVGA for 1000 generations in the first example



Figure 5. Exact and numeric f(0.5, t) by implementing the modified RVGA for 1000 generations in the first example



Figure 6. Exact and numeric f(0.7, t) by implementing the modified RVGA for 1000 generations in the first example



Figure 7. Exact and numeric f(0.9, t) by implementing the modified RVGA for 1000 generations in the first example

Figures 8 and 9 show the exact and numeric f(x, t) for the second example by implementing the modified RVGA for 10000 g.



Figure 8. Exact f(x, t) of the second example



Figure 9. Numeric f(x, t) by implementing the modified RVGA for 10000 generations in the second example

Figures 10 to 14 show exact and numeric $f(\alpha, t)$ for the second example by implementing the modified RVGA for 10000 generations, where $\alpha = 0.1, 0.3, 0.5, 0.7$ and 0.9, respectively.



Figure 10. Exact and numeric f(0.1, t) by implementing the modified RVGA for 10000 generations in the second example



Figure 11. Exact and numeric f(0.3, t) by implementing the modified RVGA for 10000 generations in the second example



Figure 12. Exact and numeric f(0.5, t) by implementing the modified RVGA for 10000 generations in the second example



Figure 13. Exact and numeric f(0.7, t) by implementing the modified RVGA for 10000 generations in the second example



Figure 14. Exact and numeric f(0.9, t) by implementing the modified RVGA for 10000 generations in the second example



Figure 15. Flowchart of the modified RVGA

6. Conclusion

- i. The present study successfully applied a numerical method to IPS (1) (3).
- ii. To solve the IPS by using our genetic algorithm, the unknown function will be guessed and we do not need the regularization. This will improve the execution time.
- iii. Results show that a reasonable estimation can be obtained by a genetic algorithm within a CPU with clock speed 2.7 GHz.
- iv. The present method has been found stable with respect to small perturbation in the input data.

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