Self-Potential Inversion Using Genetic Algorithm

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Abstract. A new technique is presented for automatic inversion of SP anomalies due to a polarized infinitely conductive simple geometrical source model structures, based on an artificial intelligence search strategy entitled genetic algorithm (GA) and the evolution theory. The genetic algorithm is used to find the minimum of fitness or cost function of the unknown depth, polarization angle, and shape factor. The study of synthetic examples shows fast and stable recovery of the true parameters even if the input data contain different percentages of noise. The GA leads to very realistic values for the inverted parameters in all tested examples and the root-mean squared error (rms) between the true and inverted field is accepted. The technique is further applied to real examples from Germany and Turkey.

Introduction

Self-potential (SP) prospecting is one of the oldest geoelectrical methods, and is still used in many fields of applied geophysics. The SP measurements refer to that part of the natural electrical field which is stationary in time, or nearly so, and whose current source system is generated and sustained by phenomena occurring underground within geologic structures. Many source mechanisms have been proposed to explain the genesis and time and space pattern of the SP field. The common aspect of the many source models is that an electric charge polarization is set up, which is responsible for electric current circulation in conductive rocks. For more details about this aspect, the reader is referred to

Di Maio & Patella (1991), Patella *et al.* (1997), Sailhac & Marquis (2001) and Patella (2003). Hence the detected SP anomalies are simply the surface evidence of a more or less steady state of electric polarization. It follows that, in a final analysis, the SP inverse problem merely consists of finding the location and delineating geometry of any electric charge accumulation underground (Patella, 2003).

Self-potential data have been quantitatively interpreted using visual correlation between observed profiles, logarithmic curve matching, and characteristic points. In the last two decades, with the availability of fast computers, several numerical-based techniques have been developed to interpret SP anomalies. The use of available geometric source models, including charged points, lines, spheres, cylinders, and sheets provided very useful estimates of source parameters. These source parameters can simply be described by a self-potential (SP) anomaly expression produced by simple geologic forms that are represented as a continuous function of the parameter space.

The above mentioned techniques can be classified into three main categories as follows:

1. Graphical-based techniques. The different interpretation techniques available are using selected points on the anomaly curve. These were developed by Yüngül (1950); Paul (1965); Paul *et al.* (1965); Rao *et al* .(1970); Bhattacharya and Roy (1981) and Atchuta Rao & Ram Babu (1983). The logarithmic curve matching were developed by Meiser (1962); and Murty and Haricharan, (1985). The drawback of the above methods is the complexity in case of numerous variable (El-Arabi, 2004).

2. Numerical-based techniques. These include analysis of SP fields using Fourier analysis in wavenumber domain (Asfahani *et al.*, 2001), nomograms (Murty and Haricharan, 1985) and least-squares methods (Abdelrahman and Sharafeldin, 1997, and Abdelrahman *et al.*, 1997b). Furthermore, derivative analysis and gradients have been also used (Abdelrahman *et al.*, 1997a, 1998a, b, 2003, and Sundararajan *et al.*, 1998). Although, the above techniques provide the best fit parameters using proper initial guess and characteristic points, they are greatly influenced by noise in the measured data and may lead to serious errors (El-Arabi, 2004).

3. Complex analytical modeling-based techniques. More complex and advanced techniques based on physical tomography (Patella, 2003). Where imaging of a properly defined probability function of electric charge distribution in the surveyed volume was found to be consistent with the observed SP anomaly pattern.

In the first two categories, traditional algorithms have been successfully used. However, two main problems may limit the effectiveness of these techniques:

first, by increasing the number of inverted parameters, the dimensionality of the energy surface increases, thereby greatly increasing the probability of the optimization stalling in a local minimum (Abdelrahman *et al.*, 1998b). This is due to the fact that the SP inversion problem is an ill-conditioned and non-linear problem. Such ill-posed conditions were greatly damped where the depth and shape factor were estimated simultaneously by minimizing an objective function of depth and shape factor using the nonlinear simplex polytope algorithm (Gobashy, 2000). Secondly, discretization of the data and parameterization of model space, make the topology of the objective or fitness function exhibit several local minima (Ramillien and Mazzega,1999), as opposed to a continuous inverse where the number of solutions is infinite. Such conditions make the estimated models differ from the true and the appraisal problem arises. Moreover, ambiguity is inherited in the inversion of potential field data. Traditionally this problem has been tackled using detailed a priori information on the problem constraints. Such information is not commonly available in real geophysical problems. To detect the location of the global minima in the parameter space, classical techniques and even gradient-based methods that follow the steepest-descent direction are not a perfect choice. Unfortunately, even these search methods are local in scope and stop at the first local minimum they find (Ramillien, 2001).

This paper outlines the development of a scheme for the constraint inversion of SP anomalies through the use of evolutionary-based technique, the genetic algorithm (GA), which appears to be effective to overcome the above limitations. In the present approach, the shape factor, depth and polarization angle for the source models are estimated. Due to the evolutionarily structure of the GA, the appraisal problem is minimized and a good solution can be estimated. Synthetic and real examples are presented to test the validity of the proposed procedure.

Problem Formulation

The self-potential anomaly $V(x,h,\alpha,q)$ caused by a polarized infinitely conductive sphere or a cylinder in a homogeneous half-space (Fig. 1) at any point, $P(x_j)$ along the principal *x*-axis can be expressed (Yüngül, 1950; Bhattacharya and Roy, 1981; Murty and Haricharan, 1985; Abdelrahman *et al.*, 1998a; El-Arabi, 2004) as follows:

$$V\left(x_j, h, \alpha, q\right) \;=\; M \; \frac{x_j \; \cos \; \alpha + h \; \sin \; \alpha}{\left(x_j^2 = h^2\right)^q} \tag{1}$$

where *M* is the electric dipole moment, *h* is the depth to the center of the sphere or cylinder, x_j is a discrete point along *x*-axis where the observed anomaly is located, *q* is the shape factor, and α is the polarization angle. The axis of the in-
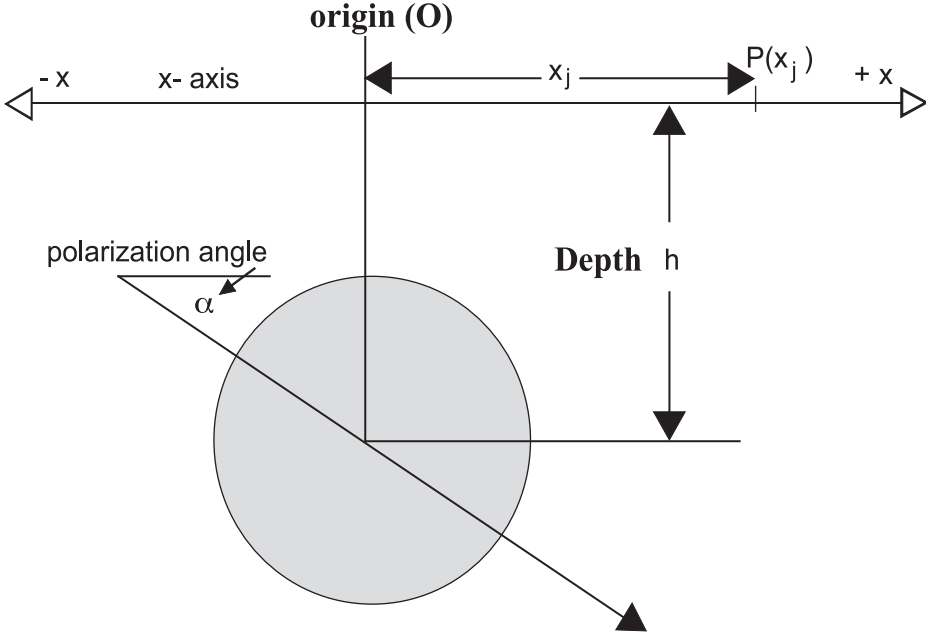
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Fig. 1. Geometry of a 2-D cylinder or a sphere.

finite cylinder is perpendicular to the page and parallel to the Y-axis. In Eq. (1) $q = 1$ for the horizontal cylinder, zero for a horizontal sheet and 1.5 for a sphere. α is measured from the surface to the polarization axis from the center of the sphere or cylinder to the surface (Fig. 1). The point O is on the surface at a point vertically above the center of the anomaly source. The main target is to find, through a convenient numerical approach, the unknown parameters h, α, and q that best represent an observed anomaly V_{obs}. The problem would be transformed into the problem of minimization of an objective or fitness function ψ of the same unknowns. The form of this function, commonly used in geophysics, is simply:

$$\psi\left(x_j, h, \alpha, q\right) = \sum_{i=1}^{m} \left|V_{obs}(x_j, h, \alpha, q) - V_{calc}(x_j, h, \alpha, q)\right| \qquad (2)$$

Where m is the number of data points and V_{calc} is the calculated response. The target now is to minimize $\psi(x_j, h, \alpha, q)$ to estimate the unknowns under bound constraints on the unknown variables. In a mathematical form, this may be expressed as;

$$\min_{\psi \subseteq R^m} \psi\left(x_j, h, \alpha, q\right) \qquad (3)$$

Such an optimization problem can be solved using an evolutionary scheme based on the genetic algorithm (GA) global optimizer. The next section gives a brief overview of the genetic approach and how to implement the SP problem.

Principles of Genetic Algorithms

Many optimization problems are very complex and quite hard to be solved by conventional optimization techniques. Over the last decade, genetic algorithms (GAs) have been extensively used as search and optimization tools in various problem domains (Wilson *et al.*, 1994). The primary reasons for their success are their broad applicability, ease of use and global perspective (Goldberg, 1989; Billings *et al.*, 1994; Boschetti *et al.*, 1996; Stoffa and Sen, 1991 and Boschetti *et al.*,1997). Genetic algorithms mimic natural selection and biological evolution to achieve their power, and their operational characteristics are typically analogous to the evolution theory. Generally speaking, GAs initially works with a *population* of individuals, each representing a possible solution to a given problem. Each candidate solution, or individual, is generally represented as a string of bits (a set of binary character strings) analogous to *chromosomes* and *genes* in evolution theory. GAs assigns a fitness score to each individual based on the quality of the solution it represents, and highly fit individuals are reproduced by breeding with other individuals.

The *fitness* is a computation that evaluates the quality of the chromosome as a solution to a particular problem. By analogy with biology, the chromosome is referred to as the *genotype*, whereas the solution it represents is known as the *phenotype.* The translation process can be quite complicated. In timetabling and manufacturing scheduling GAs, for example, a chromosome is translated into a timetable or set of scheduled activities involving large numbers of interacting resources. The fitness computation will then go on to measure the success of this schedule in terms of various criteria and objectives such as completion time, resource utilization, cost minimization and so on. This complexity is reminiscent of biological evolution, where the chromosomes in a DNA molecule are a set of instructions for constructing the phenotypical organism. A complex series of chemical processes transforms a small collection of embryonic cells containing the DNA into a full-grown organism, which is then "evaluated" in terms of its success in responding to a range of environmental factors and influences.

New populations are continuously evolved over *generations*. The total number of solutions in one generation is called the population size denoted by N_{pop}. As different individuals compete for resources in the environment, those individuals that are fittest are more likely to survive and propagate their genetic material. Thus, during the evolution process, the quality of the population increases, leading to an optimal solution. Finally, the population is expected to

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converge towards an optimal solution to the encoded problem after a certain number of generations (N_{gen}) are completed (Hashem and Alex, 1999). A simple flowchart for GA is given in Fig. 2.
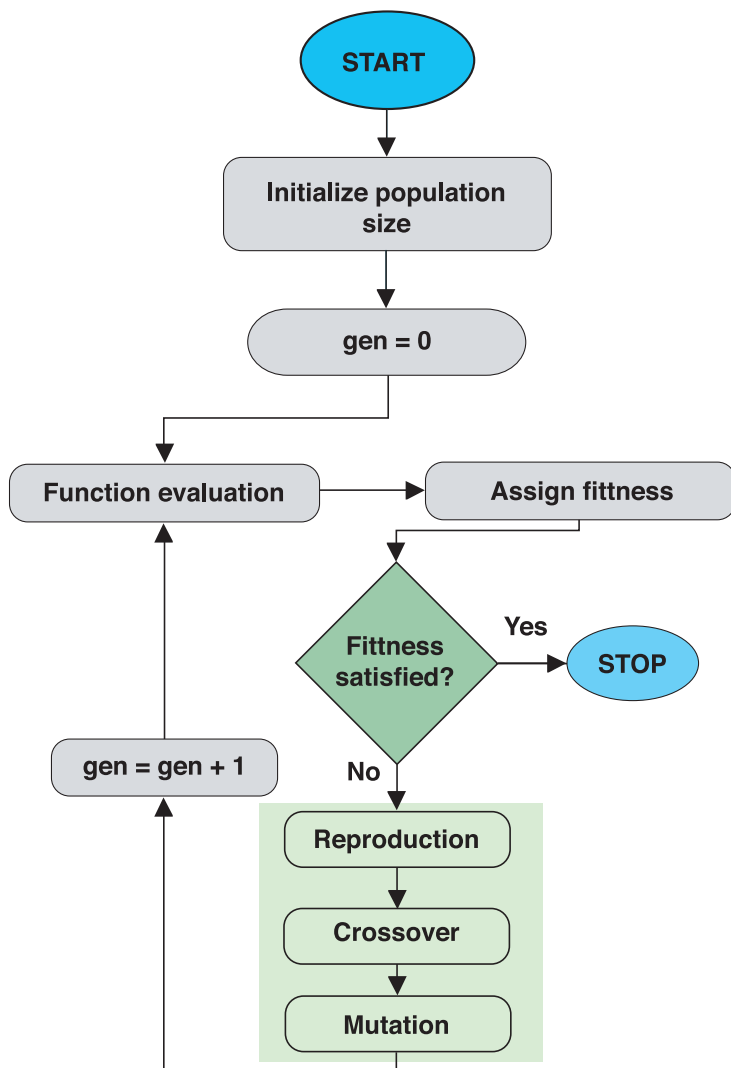

Fig. 2. A flow chart of the working principle of GA.

Selection of Initial Population

As we previously mentioned, GA starts by a group of individuals or population, in order to avoid any bias at the beginning of the evolutionary operation, each of the parameters defining each individual in the initial population is initialized with uniformly distributed random number $R \in [0.0, 1.0]$. The fitness is then calculated for each individual phenotype and stored in 1D array. The fitter the chromosome, the more times it is likely to be selected to reproduce.

In its simplest form, a genetic algorithm involves three types of reproduction operators: *Selection*, *crossover* and *mutation*, in the following sections, we discuss the reproduction operators used in this study.

Reproduction Operators

Reproduction operators of genetic algorithms provide a means to weed out bad solutions and to generate a new and better set of solutions during every iteration. Desirable characteristics of the parents are inherited by offspring during the reproduction phase by combining the best characteristics of both parents.

Selection

The process of selection of both parents in the study is carried out using a stochastic sampling mechanism that is mainly based on the Roulette wheel algorithm (Goldberg, 1989). The selection procedure is such that the probability of an individual being selected is proportional to that individual's fitness. However, directly using fitness as a measure of breeding probability suffers from a number of shortcomings (Goldberg, 1989 and Davis, 1991). In the present GA, the selection pressure or ranking procedure is implemented. In ranking theory, each individual is assigned a rank r_j based on its fitness S_j. By convention, let r = 1 correspond to the fittest individual, and r = np (np : number of populations) to the least fit. Then the relative fitness S' in terms of the rank is:

$$S'_j = \frac{np - r_j + 1}{np} \ , \ \ S'_j \in [0,1]$$

This relative fitness is then used as a measure of selection probability in the roulette wheel algorithm in place of the true fitness S_j. In this way, a constant fitness differential is imposed across the population.

Crossover

Crossover is the second reproduction process by which a portion of two fit parent individuals combine to produce two child individuals. There are three types of crossover operations typically used: single-point, two-point and uni-

form crossover. Single-point crossover is usually performed by swapping the fragments between two parents at a random point along the bit-string. Crossover is generally applied to randomly paired strings with a moderate to high probability denoted Pc (usually the value of Pc falls between 60 and 100%). The two-point crossover is used in this study (Fig. 3). It has the advantage of overcoming the end-point bias by selecting two randomly chosen splicing points along the string, and exchanging the string segments located in between these splicing points in a manner otherwise identical to one point crossover.
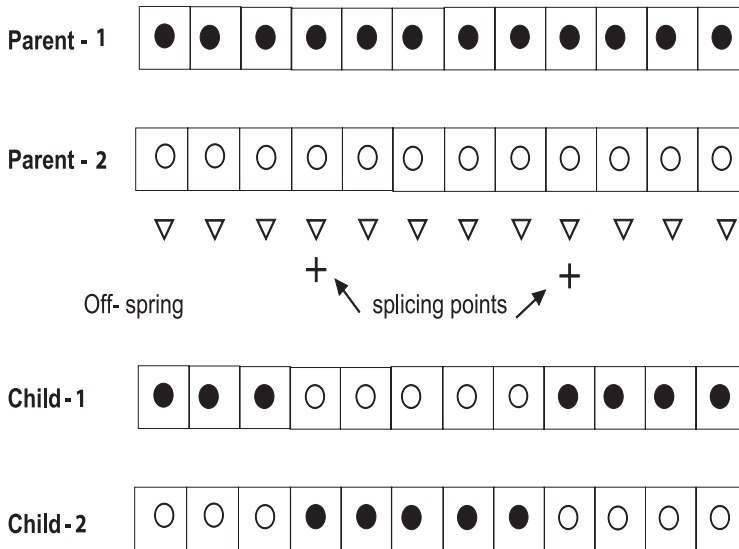
Parent - 1

Parent - 2

Off- spring   splicing points

Child - 1

Child - 2

Fig. 3. Two-point crossover mechanism.

Mutation

Mutation is the third reproductive operator that provides a theoretical guarantee that no bit value is ever permanently fixed in all strings. Mutation introduces random modifications, thereby inducing a random walk through the search space. During mutation, with a low probability, a portion of the new individuals will be flipped to generate a new bit. In conjunction with the decimal/ decoding scheme, the uniform-one point mutation included in many GA routines is liable in getting stuck at Hamming Walls problem (Charbonneau, 2002). These problems arise, when a population of relatively good trial solution is being refined primarily by the action of mutation. The process of creep mutation used in these work overcome such a problem in a simple way. Once the digit has been targeted for mutation, the corresponding digit is either incremented or decremented with equal probabilities.

Adjustment of Mutation Rate

In the present work, creep-mutation probability p_m is self-adapted at the end of each generational iteration. The degree of clustering of the population is computed using as a measure, the normalized fitness difference between the best and median individuals (according to the fitness-based rank): $\Delta f = \left(f^{max} - f^{med} \right) / \left(f^{max} - f^{med} \right)$, where $f^{max} \equiv f\left(x^{max} \right)$, and $f^{med} \equiv f\left(x^{med} \right)$, and x_{max}, x_{med} are the parameter sets defining the best and median individuals, respectively. When $\Delta f \to 0$, the population is strongly clustered, while if $\Delta f \to 1$ the population is scattered across parameter space. The idea is to increase the probability p_m in the former case, and decrease it in the later. The population clustering in this study is measured using the metric distance between the best and median as follows.

$$\Delta_d \;=\; \frac{1}{n} \left(\sum_{j=1}^{n} \left(x^{max} - x^{med} \right)^2 \right)^{1/2} \tag{4}$$

where, n is the number of parameters in a solution vector x (the three parameters; shape factor, depth and polarization angle). The mutation rate is varied according to:

$$p_m \to \begin{cases} p_m \times \delta & if\ \Delta \le \Delta^{low} \\ p_m & if\ \Delta^{low} < \Delta < \Delta^{high} \\ p_m \times \delta & if\ \Delta >= \Delta_{low} \end{cases}$$

Where $\delta = 1.5$, $\Delta^{low} = 0.05$, $\Delta^{high} = 0.25$, and Δ stands for either Δf or Δ_d.

The above section gave a brief description to the GA used in this study, for more detail the reader can referee Charbonneau and Knapp, 1995, and Charbonneau, 2002.

Application to Synthetic Examples

Synthetic Case 1

We proposed a 2-D polarized infinitely conductive horizontal cylinder model with the shape factor $q = 1.0$, the electric dipole moment $M = -300$, the depth to the center of the model $h = 13$ units, and the polarization angle $\alpha = 48$ degrees. We propose to measure the data along a profile extended along the surface from $x = -25$ to $x = +25$ units. The GA optimizer used has the following parameters (strategy parameters): number of individuals = 100, number of generations (N_{gen}) is 3500, number of genes, *i.e.* number of significant digits retained in

chromosomal encoding = 6 (machine dependent), the crossover probability = 0.85 which is the probability in which any one gene locus will mutate in any one generation, the mutation mode is taken variable, the initial mutation rate (probability P_m) is 0.005. The bounds on the mutation rate are = 0.0005 and 0.25, respectively and the relative fitness differential S_j is chosen as 1.

Table 1. Results of inversion of synthetic example 1.

	Noise added	True parameters	Inverted parameters	Error %	Optimum fitness	rms error
Shape factor (q)		1.0	1.000	0		
Depth (h)	0%	13	13.1546	1.18	1.0059	0.0026
Polarization (α)		48	48.0001	0		
Shape factor (q)		1.0	1.0002	0		
Depth (h)	5%	13	13.202	1.55	0.0706	0.0299
Polarization (α)		48	47.862	0.28		
Shape factor (q)		1.0	1.0009	0		
Depth (h)	13%	13	13.225	1.73	0.0277	0.067
Polarization (α)		48	47.432	1.18		

The results of the inversion using the GA approach are shown in Fig. (4a) and Table (1), which represents noise-free data. The root-mean square error (rms) is calculated and found to be 0.0026 mV. This is a measure of how close the calculated model response is to the measured data. The optimum fitness, 1.005 mV, and both the shape factor and the polarization angle are obtained with a high resolution (0% error). The depth is obtained with 1.18% relative error. The same example is inverted after adding 5% and 13% noise to the synthetic data (Fig. 4b,c). Results are shown in Table (1). The table specifies the parameters, both true and inverted ones. It also shows the percentage of noise added to the synthetic data and the percentage of error in the parameters estimated. Similarly, relative errors in all parameters are calculated. The most resolved parameter is the shape factor q. The magnitude of the overall (rms) error is always less than 0.02mV. The value of the minimum objective function is also given for each inversion process.

Synthetic Case 2

This is similar to synthetic case 1. We proposed a polarized infinitely conductive spherical model with depth to center $h = 10.5$ units, shape factor $q = 1.5$,
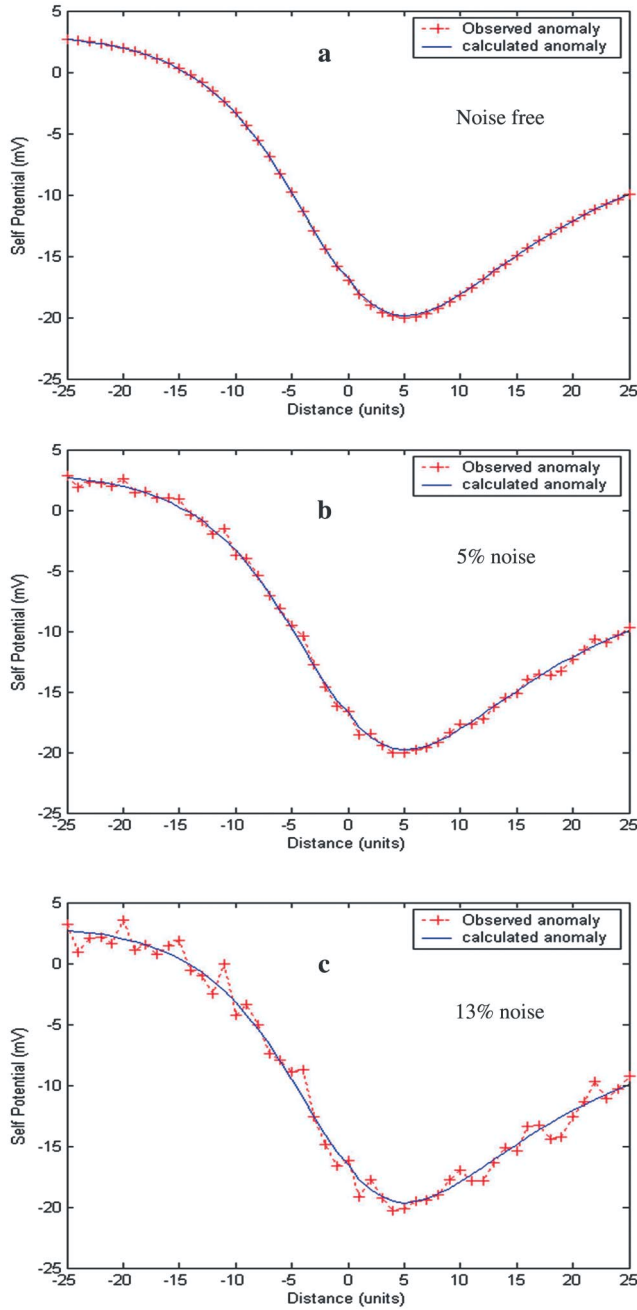
Fig. 4. The results of the inversion of a synthetic SP anomaly due to a 2-D horizontal cylinder model (h = 13, q = 1.0, and α = 48) with 0% noise (a). Same data with 5% noise (b), and 13% noise (c).

and polarization angle α = 35 degrees. For the sake of comparison, the GA strategy parameters are the same as those used in case 1 (number of individuals = 100, N_{gen} is 3500, number of genes is 6, the crossover probability = 0.85, mutation probability P_m is 0.005. The bounds on the mutation rate are = 0.0005 and 0.25, and the relative fitness differential S_j is chosen also as 1). Noise-free anomaly was firstly used and inverted using GA procedure. Results are shown in Fig. 5a and Table (2). The most resolved parameters after the inversion process is the shape factor q. The over all (rms) error is approximately zero. The optimum fitness is 0.0696 mV. The same inversion process is repeated with noise levels 6% and 14% (Fig. 5b,c). The resolution of the different inverted parameters varies. The optimum fitness in the low noise is 0.56 mV, while in the high noise 0.26 mV. The (rms) error is less than 0.0044 mV in both cases.

Field Examples

Field Example 1

The present approach is further applied to a field example from Germany, the graphite deposits in Bavarian Woods (Meiser, 1962). These deposits are situated in a hercynic gneissic complex. Conformably intercalated between paragneiss and crystalline limestone of the same age, they form seams that are to be designated as bituminous sediments of presumably Precambrian age. The target deposit lying between limestone and gneisses forming a parallel-running sequence of lenses, which are very variable in their thickness, this deposit can be approximated in some localities by simple geometrical models. The GA optimizer has been applied with a number of individuals = 100 and number of genes equals to 3500. All other GA strategy parameters are kept fixed as stated in the synthetic examples. The results of the inversion are shown in Fig. 6 and Table 3. The parameters obtained are: depth h = 35.50 meters, polarization angle α = –62.99 degrees, and shape factor q = 0.792. The (rms) error calculated between the observed and calculated SP anomalies from the obtained parameters is =1.7043 mV, which is much better than that of the earlier studies (Abdelrahman *et al*. 2003, (rms = 25.3 mV). The obtained shape factor also suggests that a 2D horizontal cylinder model buried at a depth of 35.5 meters can represent the shape of the source body. These results (shape factor and polarization) are relatively close to those proposed by Meiser (1962) using double logarithmic net method and master curves, and Abdelrahman *et al.* (2003) using higher derivatives and least-squares method. Table (3) summarizes the above results. The calculated depth shows diversity from the results of Meiser and Abdelrahman (about 14 m). We believe that our solution is close to reality because our data fitting is much better (rms = 1.704). Moreover, synthetic study on the
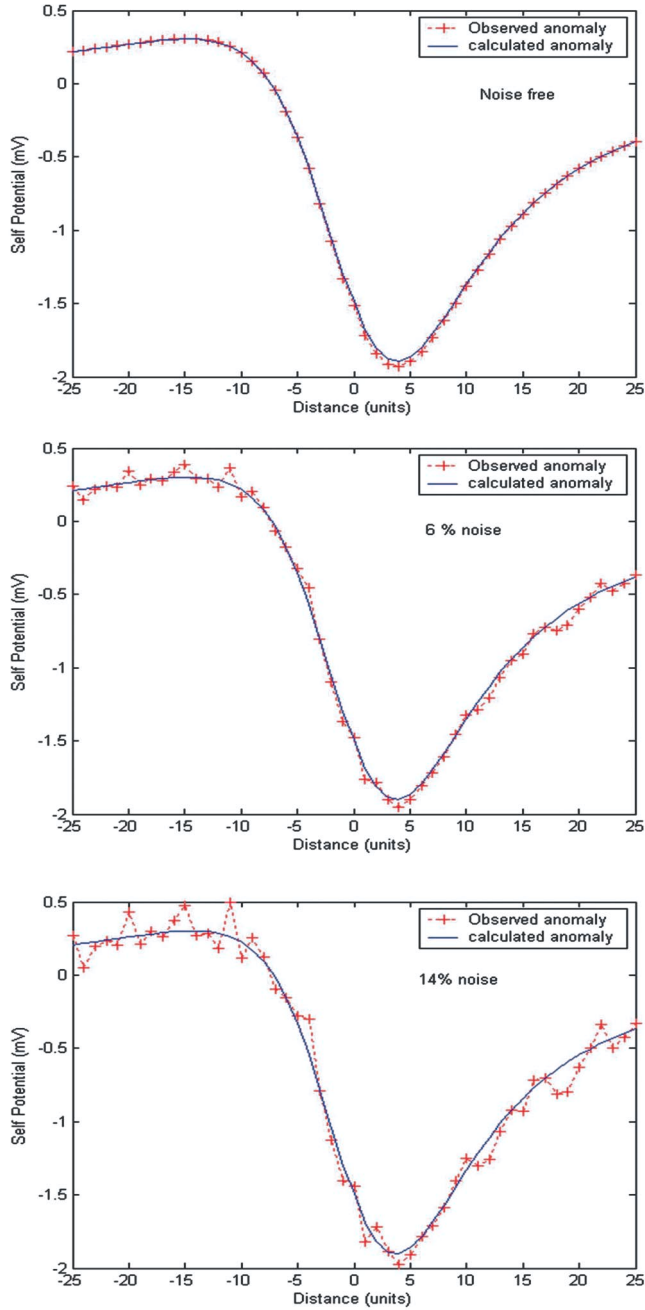
Fig. 5. The results of the inversion of a synthetic SP anomaly due to a spherical model (h = 10.5, q = 1.5, and α = 35). The noise levels added to the data are 0% (a), 6% (b), and 14% (c).

Table 2. Results of inversion of synthetic example 2.

|	Noise added	True parameters	Inverted parameters	Error %	Optimum fitness	rms error
Shape factor (q)		1.5	1.4999	0.006		
Depth (h)	0%	10.5	10.6861	1.77	0.0698	0.0000433
Polarization (a)		35	34.8000	0.571		
Shape factor (q)		1.5	1.50588	0.392		
Depth (h)	6%	10.5	10.5289	0.275	0.5613	0.0044
Polarization (a)		35	34.84921	0.430		
Shape factor (q)		1.5	1.5120	0.8		
Depth (h)	14%	10.5	10.36351	1.299	0.2651	0.0092
Polarization (a)		35	34.7874	0.607		
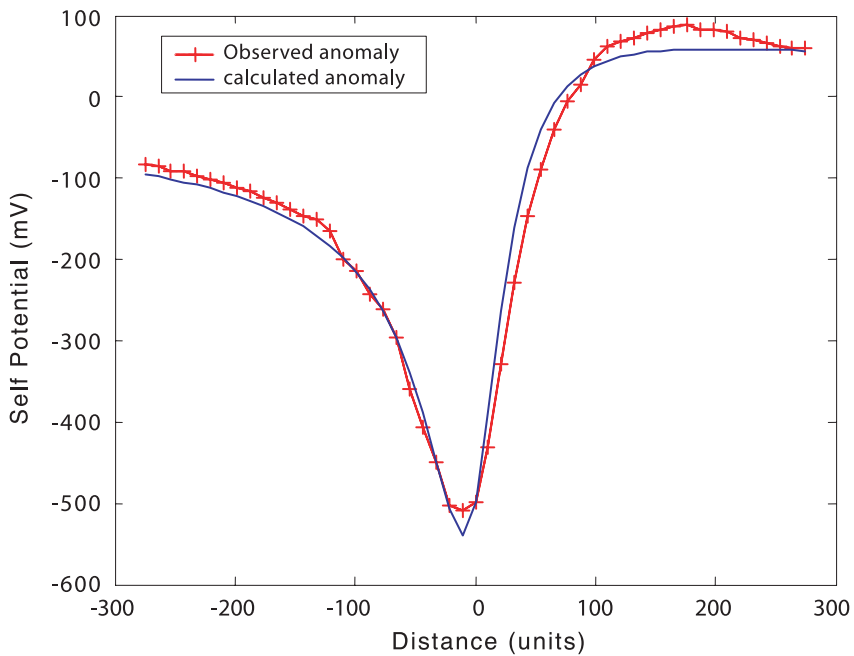
Fig. 6. Measured and calculated SP anomaly over a graphite ore body, southern Bavarian woods, Germany (after Meiser, 1962). With calculated rms = 1.704mV at one unit = 1 meter.

**Table 3. Results of the present technique using genetic algorithm applied to the field ex-
ample and a comparison with the previous techniques.**

Parameter	Meiser (1962)	Abdelrahman *et al.,* (2003) (higher derivatives)	Abdelrahman *et al.,* (2003) (least squares)	Present approach
Depth (*h*)	53	53	49.3	35
Polarization angle (α)	–	–	– 55.7	– 62.9
Shape factor (*q*)	–	0.9	0.91	0.792
Root mean square error (rms)	–	–	25.3	1.704

same model with much higher noise level (13%), assume confidence level of
± 1.73 mV for the depth parameter.

Field Example 2

The second real example is from eastern Turkey. The anomaly named
Süleymanköy lies in the Ergani copper district, 65 km, south east of Elazig
(Bhattacharya and Roy, 1981). The field measurements were performed and
described in Yüngül (1950). They represent a polarized copper ore body. The
anomaly has been digitized to 32 data points of 4.8 meters spacing. The in-
verted parameters are given in Table (4) to be compared with previous work re-
sults. The measured and inverted fields are shown in Fig. 7.

Table 4. Results of the Süleymanköy SP anomaly inversion as compared to previous work.

Parameter	Yüngül 1950	Bhattacharya & Roy, 1981	Asfahani *et al.*, 2001	Gobashy (2000)	Present GA technique
Depth (*h*) in meters	38.8	40	27	33.6	29.999
Polarization (α)	21	15	17.25	15	11.549
Shape factor (*q*)	h. cylinder	h. cylinder	h. cylinder	0.99	0.961

Summary and Conclusion

A new optimization strategy based on the genetic algorithm "global optimiz-
er" is used to determine the parameters of a buried simple geometrical source
model structures from their SP anomalies is used. The method uses the evolu-
tionary characteristics that mimic nature's evolutionary principles to derive its
search towards an optimal solution. The present approach uses a population of
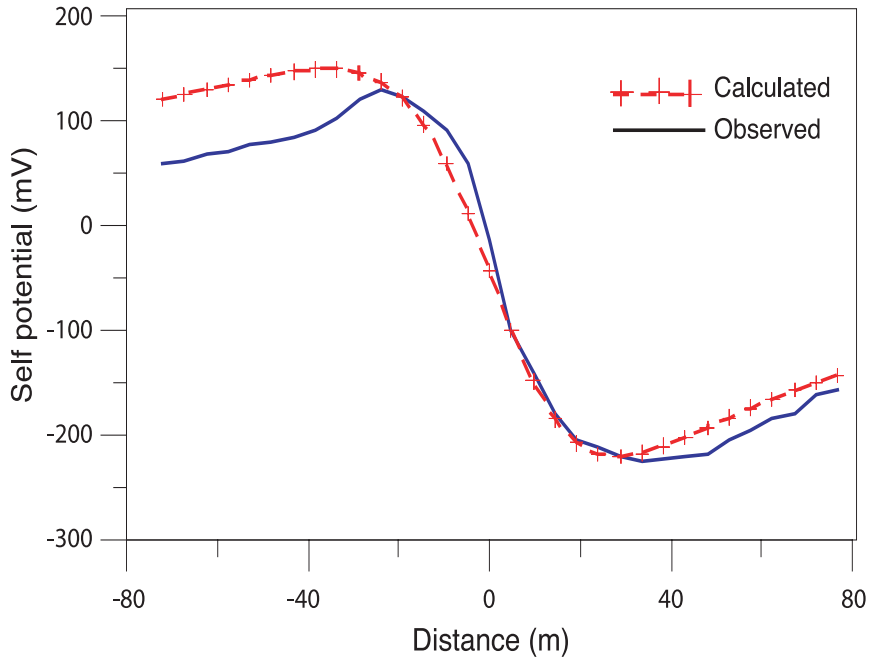solutions in each iteration instead of a single solution used in classical tech-

Fig. 7. **Measured and calculated SP anomaly over the Süleymanköy SP anomaly, Turkey (after Yüngül, 1950) at one unit = 4.8 meter.**

niques. The outcome populations of solutions all converge to the optimum or minimum assuming a single global minimum exists. Moreover the present technique overcomes the ill-poseness and non-linearity of the SP problem. No further graphical processing or derivative analysis is used. The solution is obtained automatically for a residual SP field. Genetic algorithm is proven to providing reasonable results and proven to be effective in the interpretation of Sp data.

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حل المشكلة العكسية للجهد الذاتي باستخدام الخوارزم الجيني

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المستخلص. يهدف هذا البحث إلى تقديم طريقة أوتوماتيكية جديدة لحل المشكلة العكسية لشاذات الجهد الذاتي، الناتجة عن مصادر تحت سطحية ذات بنية هندسية بسيطة، وذلك باستخدام خواص التطور للخوارزم الجيني، والذي يحاكي المبدأ العام للتطور في البيولوجيا، بهدف استنباط أحسن الحلول. وقد استخدم الخوارزم الجيني لإيجاد القيمة الصغرى المطلقة لدالة هدف محتوية على العمق، وزاوية الاستقطاب، ومعامل الشكل كمجاهيل مطلوب إيجادها. ودلت الدراسات التحليلية على أمثلة رياضية متعددة مدى سرعة وثبات الخوارزم الجيني في تعيين المعاملات المجهولة، حتى في حالة وجود شوشرة فى الشاذات الملاحظة. وقد أدى استخدام الطريقة المقترحة إلى نتائج جيدة فى جميع الأمثلة المطبقة عليها. وقد أيد ذلك قيم الاختلاف بين الشاذات المحسوبة وتلك الملاحظة. وفى النهاية طبقت الطريقة على مثالين حقيقيين من ألمانيا وتركيا، وكانت النتائج متوافقة مع مثيلاتها المستنبطة بالطرق التقليدية.