

## Swell Correction of Shallow Marine Seismic Reflection Data Using Genetic Algorithms

SUNG HOON PARK, YOUNG SAE KONG, HEE JOON KIM AND BYUNG-GUL LEE\*  
*School of Ocean Engineering, Pukyong National University, Pusan 608-737, Korea*  
*\*Department of Ocean Civil Engineering, Cheju National University, Cheju 690-756, Korea*

Some CMP gathers acquired from shallow marine seismic reflection survey in offshore Korea do not show the hyperbolic trend of moveout. It originated from so-called swell effect of source and streamer, which are towed under rough sea surface during the data acquisition. The observed time deviations of NMO-corrected traces can be entirely ascribed to the swell effect. To correct these time deviations, a residual statics is introduced using Genetic Algorithms (GA) into the swell correction. A new class of global optimization methods known as GA has recently been developed in the field of Artificial Intelligence and has a resemblance with the genetic evolution of biological systems. The basic idea in using GA as an optimization method is to represent a population of possible solutions or models in a chromosome-type encoding and manipulate these encoded models through simulated reproduction, crossover and mutation. GA parameters used in this paper are as follows: population size  $Q=40$ , probability of multiple-point crossover  $P_c=0.6$ , linear relationship of mutation probability  $P_m$  from 0.002 to 0.004, and gray code representation are adopted. The number of the model participating in tournament selection ( $nt$ ) is 3, and the number of expected copies desired for the best population member in the scaling of fitness is 1.5. With above parameters, an optimization run was iterated for 101 generations. The combination of above parameters are found to be optimal for the convergence of the algorithm. The resulting reflection events in every NMO-corrected CMP gather show good alignment and enhanced quality stack section.

### INTRODUCTION

When reflection seismic data are acquired on land, sources and receivers are generally placed on or near the surface. Eventual processing and interpretation of seismic data assume that they were collected on level terrain. If this is not the case, rough corrections for variations in elevation are made early in processing. These constant (static) time shifts are called field statics because the corrections are based on a surveyor's field measurement. However the field statics corrections are only an approximation; the unconsolidated, near-surface weathering layer can exhibit substantial variations in seismic velocity that also cause static timing differences. Thus the application of field statics never leaves the seismic data completely free of static anomalies. These static anomalies are due to unaccounted variations in the low velocity layer, and the secondary procedures to correct them are

called residual statics.

Because of homogeneous velocity distribution in the water layer, the residual statics corrections are rarely applied to marine seismic reflection data. However not all cases would be true. Fig. 1 shows some selected CMP gathers acquired from shallow marine seismic reflection survey in offshore south-eastern Korea at Feb. 22, 1993. Note that the trend of gradual increase in the traveltimes of reflected waves toward far channel is disturbed. It originated from so-called swell effect of source and streamer, which are towed under rough sea state during the data acquisition. It is impractical to measure exact depth variations of source and streamer in a shallow seismic cruise. Thus the method of field statics for land data can not be applied to marine data. As an alternative, however, the idea and method of residual statics for land data can be introduced into the swell correction.

The residual statics corrections use various statis-

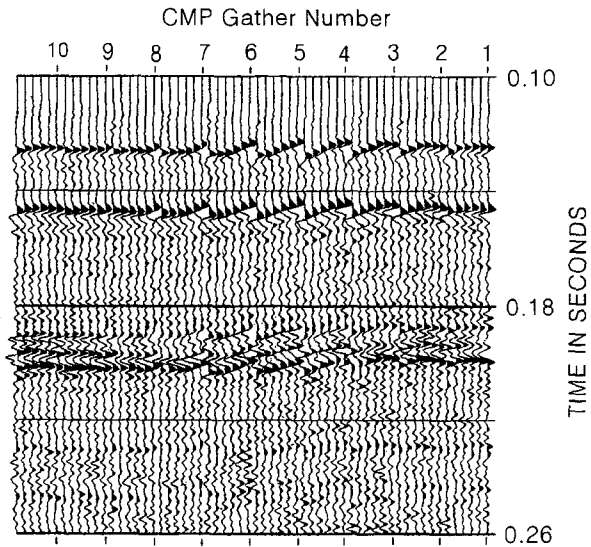


Fig. 1. Some selected CMP gathers acquired in offshore southeastern Korea.

tical techniques which enhance the quality of the stacked traces by correctly aligning the reflection events. In the present case, a trace with certain statics information is utilized only in a single CMP gather. The problem to be solved, therefore, belongs to the field of combinatorial minimization rather than multiparameter function optimization. To solve the problem of combinatorial minimization for the swell correction, we have adopted a new methodology, Genetic Algorithms (GA).

Recently a new class of methods, to solve non-linear optimization problems, has generated considerable interest in the field of Artificial Intelligence. This method, known as GA, is able to solve highly non-linear and non-local optimization problems and belongs to the class of global optimization techniques, which includes Monte Carlo and Simulated Annealing (SA) (Holland, 1992; Sambridge and Drijkoningen, 1992; Gallagher and Sambridge, 1994). Unlike local techniques, GA avoids all use of curvature information on the objective function. This means that it does not require any derivative information and therefore one can use any type of misfit function equally well. Most iterative methods work with a single model and find an improvement by perturbing it in some fashion. GA, however, works with a group of models simultaneously and uses stochastic processes to guide the search for an optimal solution. Both GA and SA are modeled on natural optimization systems. GA has an analogy with biological evolution; SA uses an analogy with thermodynamics. This evolution leads to an effi-

cient exchange of information between all models met with, and allows the algorithm to rapidly assimilate and exploit the information gained to find better data fitting models.

We first describe the basic GA in the context of a general optimization problem and append some variations on the basic GA. Finally, the method is applied to field data in order to correct the swell effect as shown in Fig. 1.

## GENETIC ALGORITHMS

Many geophysical optimization problems are non-linear and result in irregular objective functions. Consequently, local methods can depend strongly on starting models, are prone to entrapment in local minima, and can often become unstable. In addition, the calculation of derivative information can become difficult and costly. Global methods avoid nearly all the limitations of local methods and are therefore more attractive for problems which are not too labor intensive in forward modeling. However, the nature of random searching such as the Monte Carlo method for near-optimal solutions involves a large degree of potentially wasteful computation through sampling unfavorable regions of model space. This usually means that a large number of models must be sampled and so the Monte Carlo method becomes prohibitively slow for large-scale problems and in such cases local methods are commonly considered the only viable approach (Sambridge and Drijkoningen, 1992).

The process of randomly exploring relatively large regions of model space is in stark contrast to local methods, which exploit the information gained through the sampling of only a few models and their partial derivatives to reduce the data misfit. A trade-off exists therefore between robust exploration of the model space and efficient exploitation of the information provided from this sampling. A general optimization method ideally should combine both of these desirable characteristics. This end is achieved by a new class of methods such as GA.

A global optimization method known as GA has recently been developed in the field of Artificial Intelligence. Like the Monte Carlo method, it is completely non-linear, uses random processes and requires no derivative information, yet it has potential for significant increases in efficiency over the random walk strategy. GA is related to Simulated Annealing (SA) (Kirkpatrick *et al.*, 1983) in that they

are both stochastic search techniques, employing probabilistic mechanisms to solve complex optimization problems with multiple minima. SA uses an analogy with physical annealing in thermodynamic systems, whereas GA has a resemblance with the genetic evolution of biological systems (Sambridge and Drijkoningen, 1992).

As related by Davis (1991), the features of evolution intrigued John Holland about 20 years ago. Holland believed that computer algorithm simulating evolution could be developed to evolve solutions to complex problems (Holland, 1992). It is generally accepted that evolution occurs by natural selection so that, within a given environment, more successful organisms survive and propagate, whereas the less well adapted decline. We could regard evolution as an effectively self-optimizing process in that the evolving system does not know a priority that constitutes a successful organism. Furthermore, the current population of organisms has no memory of what has gone before (Gallagher and Sambridge, 1994).

The complex mechanisms of evolution are not particularly well understood but some general characteristics emerge. First, evolutionary changes occur at a molecular (or chromosome) level and the combination of these changes leads to macroscale evolutionary characteristics with which most of us are familiar (Gallagher and Sambridge, 1994). The second relevant characteristic of evolution is that changes in chromosomes and genotypes occur during reproduction and these changes are facilitated through the relatively simple processes of crossover and mutation. Reproduction generates offspring and crossover allows the chromosome structure of parent organisms to be modified by the exchange and recombination of parts of each parent structure. The crossover allows offspring to have a combination of the parents' characteristics and the offspring also may develop some different features depending on how chromosome structures are recombined. Mutation is a random process that also provides the opportunity to introduce new characteristics unrelated to the parents. In the general scheme of evolution, mutation is generally regarded as secondary to crossover. In part, this is because mutation occurs relatively infrequently but, more importantly, it is a less efficient optimizing process because it fails to exploit the information contained in the parent structures which contribute to successful organisms (Gallagher and Sambridge, 1994).

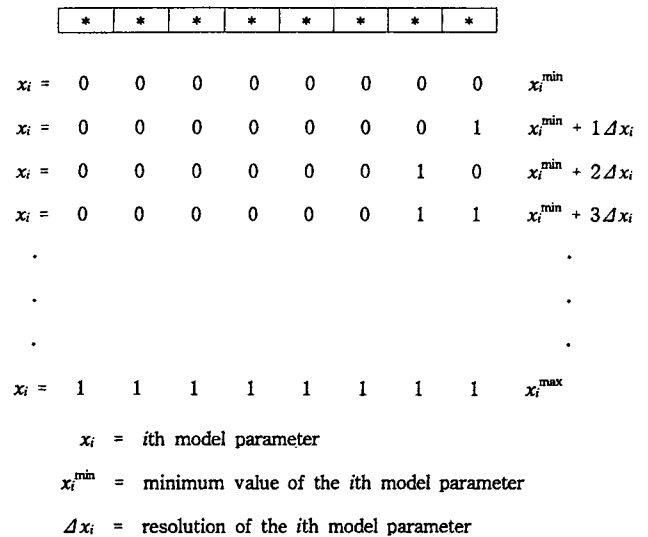
## BASICS OF GA

### Binary-code representation

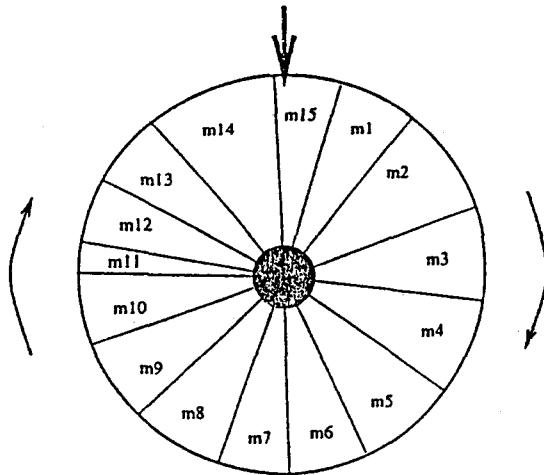
A key aspect of GA is the representation of complex model by simple encoding. The encoding, initially considered by Holland (1975), is the representation of a model by binary code (Fig. 2). When we consider a binary coding for a series of models, the patterns of 1s and 0s in the individual binary strings represent parameters of the corresponding model. Thus the first step in GA is to represent a model using a binary code. Once coded, a finite population of models is generated at random and the next three operators act on them in sequence.

### Reproduction

This stage selects an interim population with  $Q$  models by way of some stochastic selection process. Because the aim is to propagate the better or fitter models, those with higher values of the fitness function should have a higher probability of proceeding to the next generation. The intuitive measure of this probability then is the value of the fitness function itself or, if necessary, a scaled fitness value, that will be discussed later. One of the simplest procedures to select models to pass into the interim population is known as roulette wheel selection (Fig. 3). The probability of a particular model being selected is determined by its relative contribution to the total or



**Fig. 2.** A binary model parameter coding scheme. It is illustrated for the  $i$ th model parameter,  $x_i$ , with range  $x_i^{\min}$  to  $x_i^{\max}$  and resolution  $\Delta x_i$  (after Stoffa and Sen, 1991).



**Fig. 3.** Roulette wheel selection. Each model in the current population gets a portion of a roulette wheel according to the model's relative fitness. We select parents by spinning the wheel once for each parents (after Smith *et al.*, 1992).

summed fitness of the population.

**Crossover**

The next step is the creation of a "child" model from the selected parents. This step is in some sense the inner magic of GA because it is mainly here that searching extends into new regions of model space. Crossover, often called recombination, between two models paired or mated via the selection process is carried out with a specified probability,  $P_c$ . The simplest type of crossover, called one-point crossover (Fig. 4), selects a single crossover site between strings (Sen and Stoffa, 1992). After a crossover point is chosen randomly from the string of coded model parameters, each child is constructed by taking the first portion of its string from one parent and the second portion from the other.

**Mutation**

Finally mutation is possible based on a mutation probability  $P_m$ , which involves a random change of a bit within the string. Mutation acts to randomly

Parent					Offspring				
1	0	0	0	0	1	1	1	0	0
1	1	1	1	1	1	0	0	1	1

**Fig. 4.** One-point crossover. Each model is coded as a five-bit binary string. The two left models are the parents (and are already present in the population) and the two right models are the offspring produced by the crossover.

perturb a randomly chosen element in an occasional (randomly selected) child for the purpose of adding diversity to the population. In the absence of mutation, no child could ever acquire a chromosome gene value which was not already present in the population. After the three steps are completed, a new population of models is produced which may be used as input to the next generation.

**VARIATIONS ON THE BASIC GA**

There are a large number of possible encodings and these can be developed for the most appropriate representation of the problem or in response to desirable behavior of the operators on the encoded models. For example, the mutation operator is generally desired to provide a local perturbation, yet in the simple binary encoding it is equally likely that a high-order bit (i.e., a large power of 2) and a low-order bit are flipped in parity. Obviously, flipping a low-order bit to the encoded model is a local perturbation to the decoded model, but the same is not applied to high-order bit. Gray coding provides one solution to this problem and in this mutation (i.e., flipping 1 bit) changes the decoded model by 1 (Forrest, 1993). Gray codes have the property that incrementing or decrementing any number by 1 is always a one-bit change (Fig. 5).

In the roulette wheel selection, the probability of a particular model being selected is proportional to its relative contribution to the total fitness of the population. However, random selection may cause to pick out the worst model and may fail to select the best model. Tournament selection provides one solution to this problem. This method is based on relative rank rather than the absolute value of fitness. Some models are selected at random from the current population of  $Q$  models and the highest fitness model proceeds into the interim population. This process is repeated until the interim population also

Decimal	Binary	Gray	Decimal	Binary	Gray
0	0000	0000	8	1000	1100
1	0001	0001	9	1001	1101
2	0010	0011	10	1010	1111
3	0011	0010	11	1011	1110
4	0100	0110	12	1100	1010
5	0101	0111	13	1101	1011
6	0110	0101	14	1110	1001
7	0111	0100	15	1111	1000

**Fig. 5.** Comparison of Binary-coded and Gray-coded Integers.

has  $Q$  models. The selection force depends on the number of the model competing in selection ( $nt$ ) and generally 2 or 3 of  $nt$  are favorable.

Goldberg (1989) describes a stretching of the objective function to either deemphasize major differences, as the run matures, or accentuate minor differences, at the start or interim of the run, among the objective functions in the current population. In both cases, linear scaling of the fitness function can help to solve these problems (Fig. 6). Let us define the raw fitness  $f$  and the scaled fitness  $f'$ . Linear scaling requires a linear relationship between  $f'$  and  $f$  as follows:

$$f' = af + b.$$

The coefficients  $a$  and  $b$  may be chosen in a number of ways; however, in all cases we want the average scaled fitness  $f'_{avg}$  to be equal to the average raw fitness  $f_{avg}$  because subsequent use of the selection procedure will insure that each average population member contributes one expected offspring to the next generation. To control the number of offspring given to the population member with the maximum raw fitness, we choose the other scaling relationship to obtain a scaled maximum fitness,  $f'_{max} = C_{mult} \cdot f_{avg}$ , where  $C_{mult}$  is the number of expected copies desired for the best population member. For typical small populations ( $Q=50$  to  $100$ ),  $C_{mult}=1.2$  to  $2$  has been used successfully.

Binary codes for each model parameter result in a long string of binary numbers. A crossover site is then selected somewhere within the long string. Stoffa and Sen (1991) used "multiple-point crossover" and found that the performance of their algorithm was slightly improved by choosing a crossover site for each model parameter within the string. This is intuitively appealing for refining each

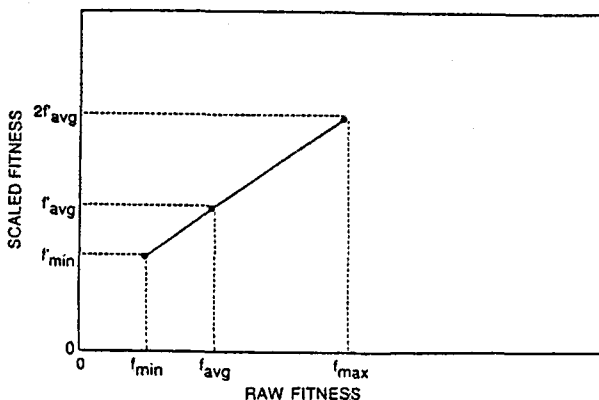


Fig. 6. Linear scaling of fitness (after Goldberg, 1989).

parameter to generate a new model. In the present case it was used instead of the single crossover.

So far, we have treated both crossover and mutation as a single bundle. However, we do not have to not only run both operators together but also keep their probabilities constant during an optimization run. Instead, a linear relationship between the value in the first generation and that in the last generation may be favorable. Each favorable part consisting of optimal solution is scattered over the initialized population and then assembles progressively to form optimal solution by crossover. When the population converges small model space, the effect of crossover becomes diminished accordingly. To search better model space than the current space, higher mutation probability is needed. Therefore it is favorable to increase mutation probability as progression of an optimization run (Kim, 1995).

## OPTIMIZATION PROBLEM

Residual statics corrections are not usually applied to marine seismic reflection data, because source and streamer are forced to locate at constant depth and the velocities of the water layer surrounding them change little with depth. The CMP gathers acquired under the above general condition show that normal moveout (NMO), the difference between the two-way time  $t(x)$  at a given offset  $x$  and the two-way zero-offset time  $t(0)$ , increases with offset according to the relationship

$$\Delta t_{NMO} = t(0) \left\{ \left[ 1 + \left( \frac{x}{v_{NMO} t(0)} \right)^2 \right]^{1/2} - 1 \right\},$$

so moveout is hyperbolic and is given by

$$t^2(x) = t^2(0) + \frac{x^2}{v_{NMO}^2}$$

where  $v_{NMO}$  is normal moveout velocity (Yilmaz, 1987). Thus the reflection events in each NMO-corrected CMP gather show a good alignment to result in the best quality stack of signal.

In certain cases, however, residual statics corrections have produced dramatic improvements in marine seismic data. Areas with irregular water-bottom topography in shallow water (less than 25 m), and areas with rapidly varying velocity in the sediments beneath the water bottom are places where statics corrections have been successful (Yil-

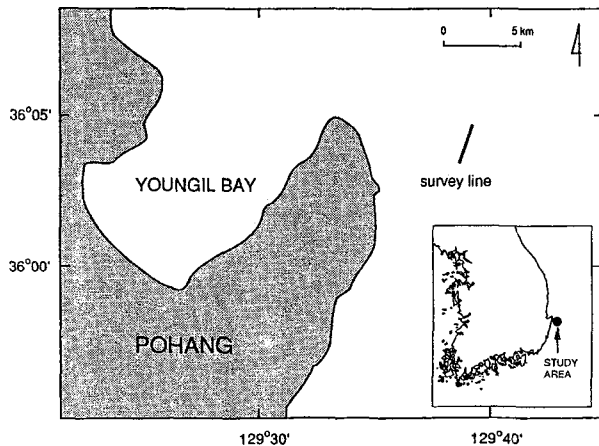


Fig. 7. Map showing seismic profile line.

maz, 1987). Furthermore, when source and streamer fluctuate during the entire survey, residual statics corrections are needed.

Fig. 1 shows some selected CMP gathers acquired from shallow marine seismic reflection survey in offshore southeastern Korea in Feb. 22, 1993 (see Fig. 7 for the location). Seismic source is an airgun of  $10 \text{ in}^3$ , and the receiver is an analog streamer of 6 channels with channel spacing of 5 m. The distance between source and the nearest channel is 14.7 m. One shot per one second and 2.5 m riding per one shot makes 600% CMP stacking. The recording system is capable of recording 2,500 samples divided among a recording length ranging from 0 s to 0.5 s, thus the sampling rate is 0.2 ms. In data processing, 1,000 samples picked out every other sample from 0.1 s to 0.5 s are utilized, and thus the sampling rate is 0.4 ms. From Fig. 1, notice the deviation of the moveout from hyperbolic trends on some CMP gathers. This is because source and streamer are located at shallow depth, and are towed under rough sea surface, and move up and down during the entire survey (swell effect). Measuring exact variation in depth of source and streamer is nearly impossible. Thus the method as field statics corrections for land data can not be applied to this marine data. As an alternative, residual statics corrections for land data are introduced into the swell correction.

The conventional model for obtaining residual statics solutions (Wiggins *et al.*, 1976; Taner *et al.*, 1974) expresses the observed static time deviations of NMO-corrected traces as a sum of the unknown surface-consistent time shifts and the component due to residual NMO. The surface-consistent time shifts in land data are due to near-surface velocity

anomalies. In marine survey, to the contrary, source and streamer are surrounded by the water layer and seismic waves travel through it with the same velocity. Thus the time distortions of NMO-corrected traces are not caused by velocity anomalies. Instead, the variation in depth of source and streamer makes traveltimes deviated. Even though major cause for time deviation in both land and offshore data is different, we do in the end correct the time deviation rather than elevation or depth. Therefore the introduction of the residual statics corrections into our marine data is not absurd, and the static time deviations of NMO-corrected traces can be expressed only as surface-consistent parts. That is, the observed time deviations of NMO-corrected traces can be entirely ascribed to the swell effect.

Continuity between the reflectors obtained by the swell correction in a single CMP gather and those obtained by the swell correction in adjoining CMP gathers is not clear, and thus the reduction of the reflectors obtained by the swell correction to the reflectors with genuine traveltimes is difficult. To overcome this, the data in the nearest channel are filtered by a moving average method to get the trend of topography, and then are fixed in all CMP gathers. Thus the time shift value producing the best stack quality can be considered as the deviation by swell.

## OPTIMIZATION RUN

The shot gathers were rearranged into CMP gathers. There were 1195 CMP gathers, and each of them consisted of 6 traces. Then NMO corrections were applied to these gathers. Because of short offset, short spread length and small number of fold, we failed to get the velocity spectrum. As an alternative, the velocity information of subsurface reported from nearby refraction survey (Lee *et al.*, 1991) was used for NMO corrections. Some selected NMO-corrected CMP gathers without any application of statics for 0.1 s to 0.26 s are shown in Fig. 8. Two data windows for GA experiments were used. In the first experiment, a 0.116 s-0.134 s time window of data corresponding to 46 samples was used (large window). In the second, a time window of 11 samples wide was used, which covers the maximum amplitude point of the near channel (water bottom window) at its center. The entire data set is scaled to an RMS amplitude of 1000. The optimization function was set to be the crosscorrelation sum between the data in the nearest channel and the data in the

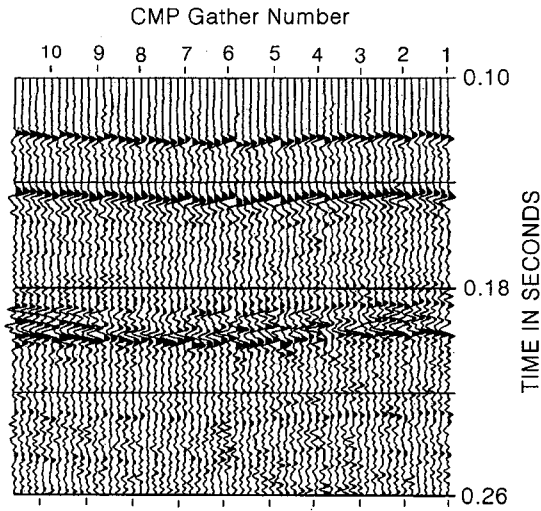


Fig. 8. NMO-corrected CMP gathers.

other channels of water bottom window. The stack section without the swell correction is shown in Fig. 9.

In the GA run, each population is initialized with a completely randomized population, except for one individual set to the input image. This individual has shift values of zero for each trace. The trace shifts of the other individuals are allowed to vary in the range of +7 and -7 ( $\pm 2.8$  ms) samples. Thus the search the GA performs is initially biased toward a region of model space containing the input stack. The conceptual reason for this biased start is to take advantage of the information contained within the uncorrected stack. In essence, why does it start with nothing when some information is already available? The GA parameters for optimizing statics are as follows: population size  $Q=40$ , probability of multiple-point crossover  $P_c=0.6$ , linear relationship of mutation probability  $P_m$  from 0.002 to 0.004, and gray

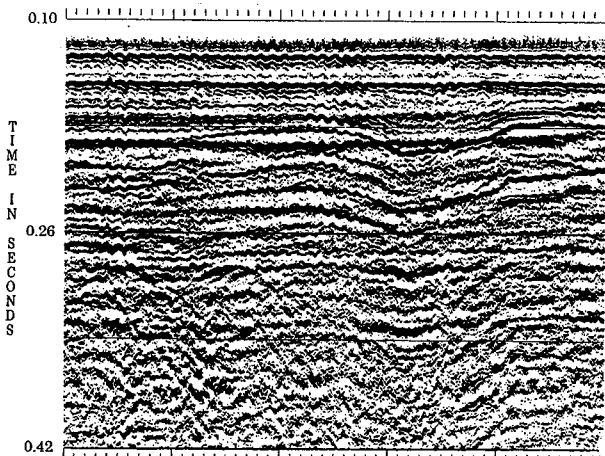


Fig. 9. Stack section before swell correction.

code representation are adopted. The number of the model participating in tournament selection ( $nt$ ) is 3, and  $C_{mult}$  in the scaling of fitness is 1.5. With above parameters, an optimization run was iterated for 101 generations.

Performance versus generation is shown in Fig. 10 for the CMP 145. The other CMP gathers also display performance curves similar to Fig. 10. Well-performing schemata become established more easily, and then passed into subsequent generation, leading to a rapid increase in the overall performance. Fig. 11 shows swell-corrected CMP gathers using the best performing individual from the above run. NMO-corrected CMP gathers are shown in Fig. 12. Stack section in Fig. 13 shows a significant improvement over the Fig. 9.

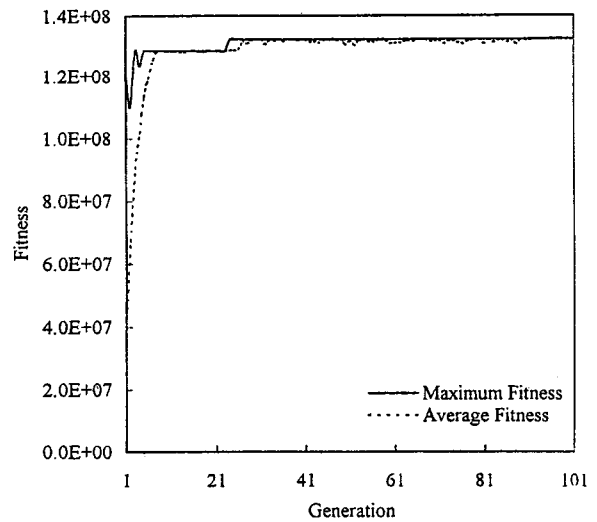


Fig. 10. Performance curve for the CMP No. 145.

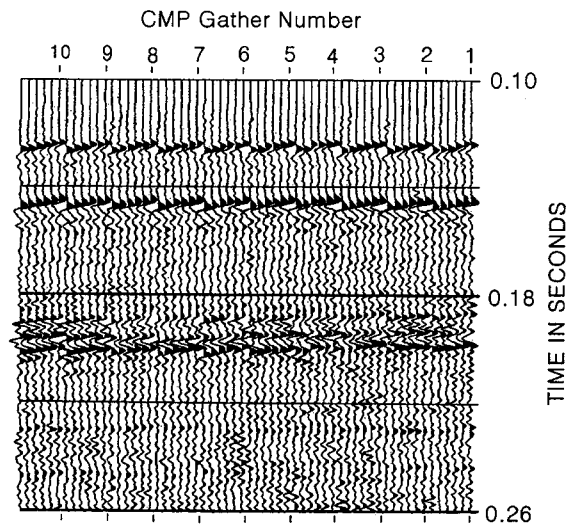


Fig. 11. Swell-corrected CMP gathers.

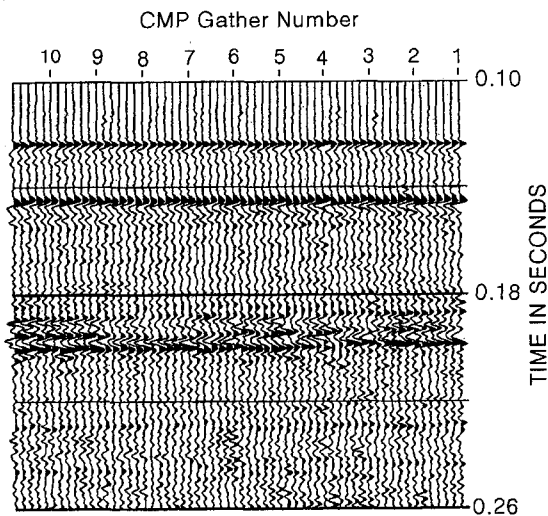


Fig. 12. NMO-corrected CMP gathers of Fig. 11.

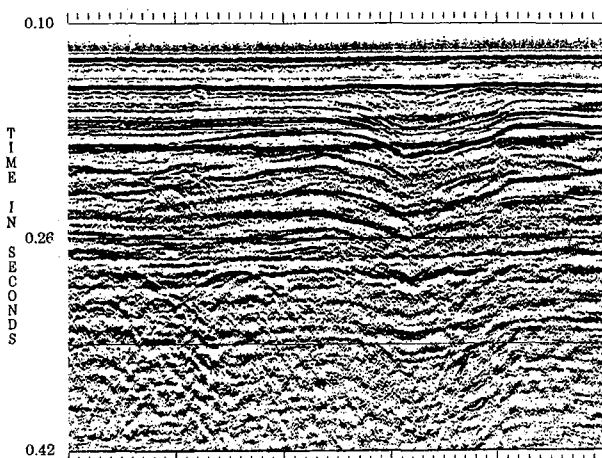


Fig. 13. Stack section after swell correction.

## CONCLUSIONS

The above results point out several interesting aspects of the GA when applied to the shallow marine reflection data, the quality of the obtained section has been degenerated by swell. Even though the data set used in this study needed only very small statics shifts inside the range  $\pm 6$  samples ( $\pm 2.4$  ms) and the problem is considered to be combinatorial minimization rather than multiparameter function optimization, GA run using a biased start with crosscorrelation sum function leads the GA to locate reasonably high-performing regions of the model space.

By using the uncorrected CMP gather as a member of the initial population, GA can be carried out with some success. Biased start makes the best

use of the information contained in the input CMP gather. As this information is enhanced, the volume of model space searched is expanded to include a wider range of statics value.

## REFERENCES

- Davis, L., 1991. Handbook of Genetic Algorithms. Van Nostrand Reinhold, New York, 385pp.
- Forrest, S., 1993. Genetic algorithms: Principles of natural selection applied to computation. *Science*, **261**: 872-878.
- Gallagher, K. and M. Sambridge, 1994. Genetic algorithms: A powerful tool for large-scale nonlinear optimization problems. *Comp. and Geosci.*, **20**: 1229-1236.
- Goldberg, D.E., 1989. Genetic Algorithms in Search, Optimization, and Machine Learning. Addison-Wesley Publ. Co. 412pp.
- Holland, J.H., 1975. Adaptation in Natural and Artificial Systems. Univ. of Michigan Press.
- Holland, J.H., 1992. Genetic algorithms. *Scientific American*, **267P**: 44-50.
- Kim, H.J., 1995. Inversion of geophysical data using genetic algorithms. *Econ. Environ. Geol.*, **28**: 425-431 (in Korean).
- Kirkpatrick, S., C.D. Gelatt and M.P. Vecchi, 1983. Optimization by simulated annealing. *Science*, **220**: 671-680.
- Lee, H.Y., C.M. Kim, W.S. Kim, C.H. Cho, J.K. Kim, and S.W. Kim, 1991. Shallow Marine Seismic Refraction Data Collection and Analysis Using Digital Technique (Part II). Korea Institute of Energy and Resources Report KR-91(T)-18, 102pp (in Korean).
- Ronen, S. and J. Claerbout, 1985. Surface-consistent residual statics estimation by stack-power maximization. *Geophysics*, **50**: 2755-2767.
- Rothman, D.H., 1985. Nonlinear inversion, statistical mechanics, and residual statics estimation. *Geophysics*, **50**: 2784-2796.
- Sambridge, M.S. and G. Drijkoningen, 1992. Genetic algorithms in seismic waveform inversion. *Geophys. J. Int.*, **109**: 323-342.
- Sambridge, M.S. and B.L.N. Kennett, 1986. A novel method hypocentre location. *Geophys. J. R. Astr. Soc.*, **87**: 679-697.
- Sen, M.K. and P.L. Stoffa, 1992. Rapid sampling of model space using genetic algorithms: Examples from seismic waveform inversion. *Geophys. J. Int.*, **108**: 281-292.
- Smith, M.L., J.A. Scales and T.L. Fischer, 1992. Global search and genetic algorithms. *The Leading Edge*, **11**: 22-26.
- Stoffa, P.L. and M.K. Sen, 1991. Nonlinear multiparameter optimization using genetic algorithms: Inversion of plane wave seismogram. *Geophysics*, **56**: 1794-1810.
- Taner, M.T., F. Koehler and K.A. Alhilali, 1974. Estimation and correction of near-surface time anomalies. *Geophysics*, **39**: 441-463.
- Vasudevan, K., W.G. Wilson and W.G. Laidlaw, 1991. Simulated annealing statics computation using an order-based energy function. *Geophysics*, **56**: 1831-1839.
- Wiggins, R., K. Larner and D. Wisecup, 1976. Residual statics analysis as a general linear problems. *Geophysics*, **41**: 922-938.
- Wilson, W.G., W.G. Laidlaw and K. Vasudevan, 1994. Residual statics estimation using the genetic algorithm. *Geophysics*, **59**: 766-774.
- Yilmaz, O., 1987. Seismic Data Processing. Soc. Expl. Geophys., 526pp.