

DEVELOPMENT OF AUTOMATED HISTORY-MATCHING PROGRAM BASE ON GENETIC ALGORITHM FOR X-RAY CT CORE FLOODING EXPERIMENT

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Abstract

Recently it has become a common practice to construct 3D coreflooding simulation model to interpret water displacement experiments conducted under X-ray CT scanning. The unknown grid block parameters i.e. kro/krw and Pc curves are required to be optimized to get reasonable matching with experimental data such as changes of grid block water saturation. In order to evaluate the matching process efficiently a new automated history-matching program has been developed. This program applies Genetic Algorithm to optimize several coefficients for normalized kro/krw and Pc curves for each litho-facies.

Several blind tests were carried out on hypothetical coreflooding models by changing the conditions of velocity and wettability to investigate the degree of accuracy and limitation of the program. The result of the reproducibility of the relative permeabilities was excellent for both water-wet and oil-wet cases regardless the velocity of coreflooding. On the other hand, the degree of reproducibility was not necessarily satisfactory for capillary pressure curves especially in high velocity case.

Sensitivity of the controlling parameter in Genetic Algorithm such as crossover rate and mutation ratio was also investigated. The suitable values are estimated, though no simple trend was found.

The program was finally applied to the interpretation of actual water displacement tests on oil-wet carbonate cores. The program successfully gave a reasonable set of kro/krw and Pc curves for each litho-facies and demonstrated its capability of grid block parameter optimization.

Introduction

One of the most important parameters that are taken from core experiment would be relative permeability. As it is generally agreed by laboratory researchers, it is difficult to get correct relative permeability because of the effect of capillary and gravity forces. Recently, it has become a common practice to construct a 3D core flooding simulation model to reproduce an experiment data. Interpretation results are utilized to generate representative relative permeabilities on the core. This method can deal with all kinds of

effects such as capillary and gravity forces. However, no efficient procedure has been established. Especially in history-matching process, the result depends on individual engineer's skill and it takes long time to reach the best match. Furthermore, there is no guarantee to assure that it is the optimum solution. In order to solve those problems, a new automated history matching program was developed based on Genetic Algorithm and an interpretation procedure of core flood experiment under X-ray CT scanning was proposed.

Genetic Algorithm

There are many methods, how to find some suitable solution for certain problem. We are usually looking for the best solution in its search space. However, if the search space spread widely i.e. the problem is complicate, some methods show a local extreme (minimum, maximum) point as a solution. Genetic Algorithm is one of the most suitable methods for complicate problems.

In petroleum engineering, the Genetic Algorithm has been utilized several times. David E. Goldberg applied the algorithm to the solution of two phase pipeline flows optimization ⁽ⁱ⁾. J. H. Fang was used the algorithm for predicting porosity and permeability from compositional and textural parameters of sandstone, and comparing the results with those obtained from linear regression analysis and nonlinear least-squares method ⁽ⁱⁱ⁾. E.R. Jefferys suggested future potential of the algorithm in petroleum engineering ⁽ⁱⁱⁱ⁾. Xuefei Sun applied the algorithm to automatic history matching of core flooding experiment to estimate Kr/Pc curves ^(iv). Some fundamentals of the algorithm are introduced in an internet homepage ^{(v)(vi)}. The page can be used for learning about the algorithm without any previous knowledge from the area.

In natural world, one organism that fits to an environment can survive longer and its genetic information is transmitted to new offspring by recombining (crossover) and mutating those genes. The fitness of an organism is measured by success of the organism in its life. Genetic Algorithm is inspired those Darwin's theory about evolution.

Figure 1 shows workflow of Genetic Algorithm. The algorithm is started with a set of solutions (represented by chromosomes) called population. Solutions from one population are taken and used to form a new population. This is motivated by a hope, that the new population will be better than the old one. Solutions that are selected to form new solutions (offspring) are selected according to their fitness - the more suitable they are for certain condition the more chances they reproduce. This is repeated until some condition (for example number of populations or improvement of the best solution) is satisfied.

In Genetic Algorithm, the most import part is how to create new population i.e. how to look for new solutions. Repeating following 4 steps creates new populations.

Selection

Two parent chromosomes are selected from a population according to their fitness. The better the chromosomes are, the more chances to be selected they have. There are lot of selection method such as ranking selection and steady-state selection. For our case, elite selection and roulette selection are mainly adopted. Elite selection is name of method,

which first copies the best chromosome to new population. On roulette selection, every chromosome in the population has its place (probability) big accordingly to its fitness function like roulette wheel shown in **Figure 2**. Then a marble is thrown there and selects the chromosome. Chromosome with bigger fitness will be selected more times.

Crossover

Crossover selects genes from parent chromosomes and creates a new offspring. For binary encoding, the simplest way to do this is to choose randomly some crossover point and copy everything from a first parent before this point and do some from the second parent after this point. By assigning a crossover probability, crossover is decided to perform or not. If no crossover was performed, the offspring is an exact copy of the parents.

Mutation

Mutation is to prevent all solutions in population from falling into a local optimum of solved problem. Mutation changes randomly the new offspring. For binary encoding we can switch a few randomly chosen bits from 1 to 0 or from 0 to 1. By assigning a mutation probability, mutation is decided to perform or not at each bits (position in chromosome).

Accepting

In accepting, new offspring is replaced in a new population.

Application to core flood simulation

In applying Genetic Algorithm to automated history-matching program for core flood experiments, it is necessary to consider how to describe the problem and evaluate solution in equations. The objective of the program is that the unknown grid block parameters i.e. kro/krw and Pc curves are required to be optimized by getting reasonable matching with experimental data such as changes of grid block water saturation and differential pressure. In this program, normalized relative permeability and capillary pressure curves are set to as following equations.

$$K_{rw}(S_w) = krw \max R_1^{nw} \quad (1)$$

$$K_{ro}(S_w) = kro \max R_2^{no} \quad (2)$$

For water wet

$$P_c = Pcmax[-cR_1^a + (1-c-d)R_2^b + dR_2 + c] \quad (3)$$

For oil wet

$$P_c = Pcmax[(1-c+d)R_1^a + cR_2^b - dR_1 + c] \quad (4)$$

For intermediate wet

$$P_c = Pcmax[(1-c+d)R_1^a + (1-c-d)R_2^b + 2dR_2 + c + d] \quad (5)$$

$$R_1 = \frac{S_w - S_{wi}}{1 - S_{wi} - S_{or}} \quad (6)$$

$$R_2 = \frac{1 - S_w - S_{or}}{1 - S_{wi} - S_{or}} \quad (7)$$

Eq. (1) and (2) are Corey-type formulations ^(vii) and include 4 unknown parameters (n_o , n_w , k_{romax} , k_{rwmax}). Eq. (3), (4), and (5) are newly defined equations which enable to express Pc curve of not only water-wet but also oil-wet and intermediate wet with 5 unknown parameters (a , b , c , d , $Pcmax$).

In this program, population consists of n pieces of chromosomes (solutions). Each chromosome contains information of 9 coefficients that are shown in equation (1)-(7) as unknown parameters. Each parameter is encoded to one binary string. All parameters are joined together and show one chromosome. **Figure 3** shows example of chromosome.

In order to evaluate matching degree of accuracy, a fitness function was defined as follows.

$$F_{obj} = W_{sw} \frac{\sum_{ijk=1}^{ijk \max} (W1_t W_{ijk} A_{ijk} |S_{w_{ijk}}^{sim} - S_{w_{ijk}}^{exp}|)}{\sum_{ijk=1}^{ijk(\max)} (W1_t W_{ijk} A_{ijk})} + W_{dp} \frac{\sum_{t=1}^{t \max} (W2_t |dP_t^{sim} - dP_t^{exp}|)}{\sum_{t=1}^{t \max} W2_t} \quad (8)$$

Fitness function is calculated by comparing difference between experiments results and simulation results for every time step. Water saturations are compared for every grid block in eq. (8), because water saturation data are taken for each grid block in experiments under X-ray CT scanning. On the other hand, only one differential pressure is taken from inlet and outlet in each time step. In order to meditate difference of dimension between water saturation and differential pressure, there are lot of weight and flag shown as W and A respectively.

Verification of the program

Model description

Before applying the program to real experiments, several blind tests were carried out on hypothetical coreflooding model by changing the conditions of wettability to investigate the degree of accuracy and limitation of the program. A 1D core model that imitated real core was constructed. Parameters of this model are shown in **Table 1**.

Wettability conditions

The model was simulated on 0.05 [cc/min] injection rate, which assumed same velocity of fluid movement in real reservoir (1ft/day), and the water saturation and the differential pressure data are taken from the simulation result as experiment data. Then, Genetic Algorithm program was applied. Genetic Algorithm parameters that were used in those run are shown **Table 2**. The results are shown in **Figure 4**. Genetic Algorithm uses random number such as crossover rate and mutation rate. Results are different even

though the runs use same model and parameter range. Hence the runs are repeated 20 times for each wettability condition. Black line is best results.

Gray line is the average of all cases. In all wettability conditions, the degree of the matching in the best case is excellent. On the other hand, it is slightly bad in the average of all cases. It means that 20 times runs are enough to get reasonable k_r/P_c curves, but only one run is not enough.

Velocity conditions

Injection rate are changed to 0.5 [cc/min] (high velocity case) that is 10 times of low velocity case. The results are shown **Figure 5**. The result of the reproducibility of the relative permeabilities was excellent for the best case regardless the velocity of injection. On the other hand, the degree of reproducibility was not necessarily satisfactory for capillary pressure curves in high velocity case. It could be explained that the effect of capillary force relatively decreased in high velocity case, which resulted in worse matching compared with in low velocity case.

3D model

Finally, the verification of the program on more complex model that was expanded to the actual 3D with 2 rock types was carried out. The dimension of model is change to $(i, j, k) = (13, 5, 5)$. The model composed of 5mm length cubes ($DX = DY = DZ = 0.5[\text{cm}]$). Each grid block porosity and saturation end points were defined by results of X-ray CT experiments. Permeability distribution is generated based on air-permeability obtained by mini-permeameter and modified to match with experimental results in single-phase tracer test. Front advancement in single-phase tracer test could reflect the heterogeneity of permeability distribution of the core. Two lithofacies (Rock Type) distribution was determined by detailed core examination by geologist on the plug core that was cut into several slices after water flood experiments. Hypothetical k_{ro}/k_{rw} and P_c curves are defined as triangle point in **Figure 6**. The automated history-matching program was applied to the model. The matching results are shown in **Figure 6**. As the results of matching with 3D model, the reproducibility of the relative permeabilities was excellent especially for the high velocity case and also for capillary pressure curves especially in low velocity case. For relative permeability curves, band of 20% confidence interval for 20 runs in high velocity narrower than that in low velocity case. On the other hand, for capillary pressure curves, band of 20% confidence interval in high velocity wider than that in low velocity case. It could be also explained that the effect of capillary force relatively decreased in high velocity case, which resulted in worse matching compared with in low velocity case as sensitivity of velocity conditions with 1D homogeneous model.

The interpretation combining the low and the high velocity cases drastically increase the quality of matching for both of relative permeabilities and capillary pressures.

Sensitivity of Genetic Algorithm parameter

Sensitivity of the controlling parameters in Genetic Algorithm was investigated. The 1D model shown in **Table 1** was used. Oil wet and low velocity conditions are assumed.

Sensitivity of population size

It may be surprising, that very big population size usually does not improve performance of Genetic Algorithm (in meaning of speed of finding solution). In general, it is reported that good population size is about 20-30, however, sometimes sizes 50-100 are reported as best. It depends on the problem to solve. Sensitivity of population size was investigated. Three population sizes (25, 50, 100) were tested. Generation size was adjusted to same total run (population times generation). Genetic Algorithm performance much depends on crossover rate and mutation rate. So for each population size, 4 crossover rates (0.4, 0.6, 0.8, 1.0) and 4 mutations rates (0.000 0.005 0.0010 0.0020) were tested. **Figure 7** and **Figure 8** shows the results of sensitivity of population. **Figure 7** show fitness function of best case in 20 runs. **Figure 8** show fitness function of average of 20 runs. From both figures, we can recognize that population size 50 is reasonable, because the black area which show low fitness function is dominant. The results showed also that more population size goes to monotone color. That means the dependence on crossover rate and mutation rate decrease.

Sensitivity of crossover rate and mutation rate

Crossover and mutation are two basic operators of Genetic Algorithm. Performance of Genetic Algorithm much depends on them. Crossover rate generally should be high, about 80%-95%, however, some results show that for certain problems crossover rate about 60% is the best. On the other hand, mutation rate should be very low. Best rates are reported to be about 0.5%-1%. In order to search best crossover rate and mutation rate, sensitivity runs were carried out. Population size is fixed to 50 because of results of sensitivity run in previous section. Results of sensitivity of crossover rate shown in **Figure 9**. It might be difficult to find out suitable crossover rate because of scattering values. But a second look confirms that the fitness functions of the best case locate around 0.8 though the average fitness functions are almost constant.

Results of sensitivity of mutation rate are shown in **Figure 10**. Both fitness functions of the best case and the average locate around 0.01-0.03.

Application to actual water displacement tests

The program was applied to the interpretation of actual water displacement tests on oil-wet carbonate plug cores. A total of 3 water displacement tests were carried out on the 1 inch-diameter plug samples. The tests were subjected to the detail interpretation by 3D coreflood simulation model. Each model was composed of 5mm length cubes and constructed based on the data such as X-ray CT porosity/ Swi/ Sor, mini-permeameter permeability and distribution on 3 lithofacies. The contents of lithofacies and the average end points for the cores were shown **Table 3**.

Results of sensitivity runs with the program show that reproducibility of the relative permeabilities become worse for the low velocity case and also for capillary pressure curves in high velocity case. However, the excellent result can be taken by repeating run in homogeneous (1D) model.

Figure 11 shows kro/krw and Pc curves of 3 lithofacies derived by history-matching. In order to improve the accuracy and efficiency of the interpretation, the program was

started from plug-1 that has almost homogeneous lithofacies as shown in **Table 3**. We assumed that the reproducibility for plug-1 should be high because of its homogeneity. The runs for plug-1 were repeated 20 times and the kro/krw and Pc curves of litho-1 were optimized first. The results proved that the assumption was right by narrow band of confidence interval for litho-1 as shown in **Figure 11**. Then plug-2 and plug-3 were interpreted using curves of litho-1 to get kro/krw and Pc curves of litho-2 and litho-3 respectively. Except relative permeability for litho-3, the degrees of confidence for derived curves were high as shown in **Figure 11** which have narrow ranges of confidence interval.

Figure 12, **Figure 13** and **Figure 14** are examples of the results of matching on the plug-2.

These figures show excellent match of front advancement during water flood test on the plug cores. Pressure difference between each end of the core was also matched. The program successfully gave a reasonable set of kro/krw and Pc curves for each litho-facies and demonstrated its capability of grid block parameter optimization.

Conclusions

It has been demonstrated that the developed program is a powerful tool in history-matching of model for core flood experiment under X-ray CT scanning. The technique enabled to optimize kro/krw and Pc curves of lithofacies. The method can be used to determine the representative core-scale kro/krw and Pc curves.

1. The automated history-matching program for water flood experiments was developed based on Genetic Algorithm
2. The program is suitable to all wettability conditions.
3. In simple (1D) model, the result of the reproducibility of the relative permeabilities was excellent regardless the velocity of injection. On the other hand, the degree of reproducibility was not necessarily satisfactory for capillary pressure curves in high velocity case. It needs to repeat run and select the best case.
4. In complex (3D-2lithofacies) model, the result of the reproducibility of the relative permeabilities was excellent especially for the high velocity case and also for capillary pressure curves especially in low velocity case. The interpretation combining the low and the high velocity cases drastically the quality of matching.
5. It was suggested that 0.8 and 0.01 are suitable values for crossover rate and mutation rate respectively, though no simple trend was found.
6. The program was successfully applied to the interpretation of the actual water displacement tests on several oil-wet carbonate plug cores to derived kro/krw and Pc curves of lithofacies.

Nomenclature

A_{ijkt} = Flag for active cell @(i, j, k, t)

a = Unknown parameter for capillary pressure

b = Unknown parameter for capillary pressure

c = Unknown parameter for capillary pressure

d = Unknown parameter for capillary pressure

dp_t^{exp} = Differential pressure of experiment @(t)

dp_t^{sim} = Differential pressure of simulation @(t)

k_{ro} = Oil phase relative permeability

$kromax$ = Oil phase relative permeability @ S_{wi} (unknown parameter)

k_{rw} = Water phase relative permeability

$krwmax$ = Water phase relative permeability @ S_{or} (unknown parameter)

no = Unknown parameter for oil phase relative permeability

nw = Unknown parameter for water phase relative permeability

P_c = Capillary pressure

PV = Pore volume

S_w = Water saturation

S_{wi} = Initial water saturation

S_{or} = Critical oil saturation

S_{ijkt}^{exp} = Grid block water saturation of experiment @(i, j, k, t)

S_{ijkt}^{sim} = Grid block water saturation of simulation @(i, j, k, t)

$W1$ = Weight of time for dp

$W2$ = Weight of time for S_w

W_{dp} = Weight of dp

W_{sw} = Weight of S_w

W_{ijkt} = Weight of cell @(i, j, k, t)

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Table 1: Hypothetical model parameters

| | I=1,13 (well) | I=2,12 | I=3-11 |
|----------------------|------------------------|---|--------|
| Dimension | (i, j, k) = (13, 1, 1) | | |
| Total length [cm] | 6.05 | | |
| DX [cm] | 0.5 | 0.25, 0.305 | 0.5 |
| DY = DZ [cm] | 2.22 | 2.22 | |
| Porosity | 0.0001 | 0.33 | |
| Permeability [mD] | 1000000 | 13.6 | |
| Saturation end point | Swi = 0, Sor =0 | Cross section average on X-ray CT experiments | |
| kr/krw and Pc curves | kr: straight, Pc: 0 | Hypothetical curves | |

Table 2: Genetic Algorithm parameters

| | |
|-----------------|-------|
| Population Size | 50 |
| Max Generation | 50 |
| Crossover Rate | 0.800 |
| Mutation Rate | 0.010 |

Table 3: Contents ratio of typical lithofacies and average end point

| | Plug 1 | | | Plug 2 | | | Plug 3 | | |
|---------|----------------|-------------|---------------|----------------|-------------|---------------|----------------|-------------|---------------|
| | Contents Ratio | Average Swi | Average 1-Sor | Contents Ratio | Average Swi | Average 1-Sor | Contents Ratio | Average Swi | Average 1-Sor |
| Litho-1 | 98.0% | 0.122 | 0.657 | 53.1% | 0.120 | 0.715 | 78.9% | 0.220 | 0.799 |
| Litho-2 | 1.2% | 0.105 | 0.278 | 46.5% | 0.106 | 0.725 | 0.6% | 0.021 | 0.488 |
| Litho-3 | 0.8% | 0.078 | 0.649 | 0.4% | 0.09 | 0.641 | 20.6% | 0.206 | 0.777 |

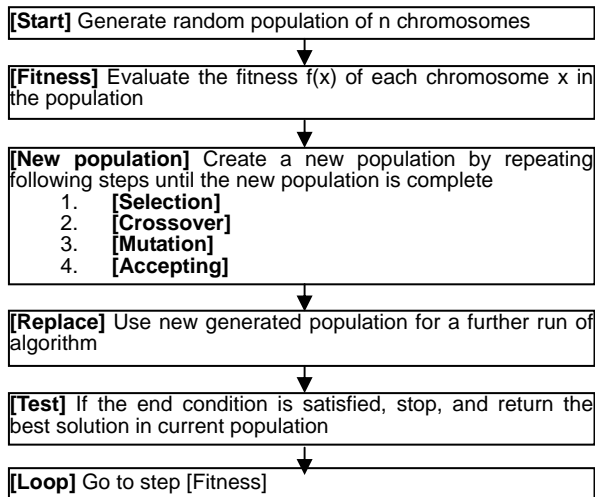


Figure 1: Outline of the Genetic Algorithm

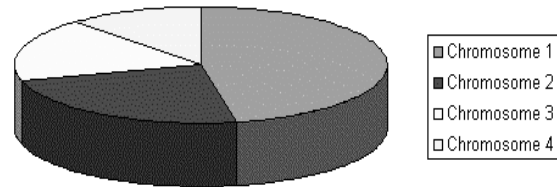


Figure 2: Roulette Wheel of Fitness

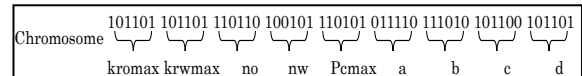


Figure 3: Example of chromosome coded by 6 bits of 9 parameters

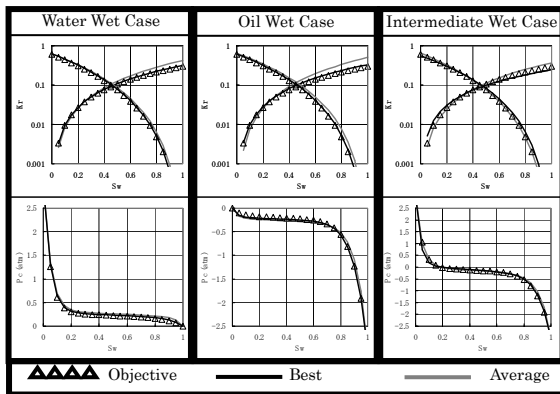


Figure 4: Matching results on some wettability conditions

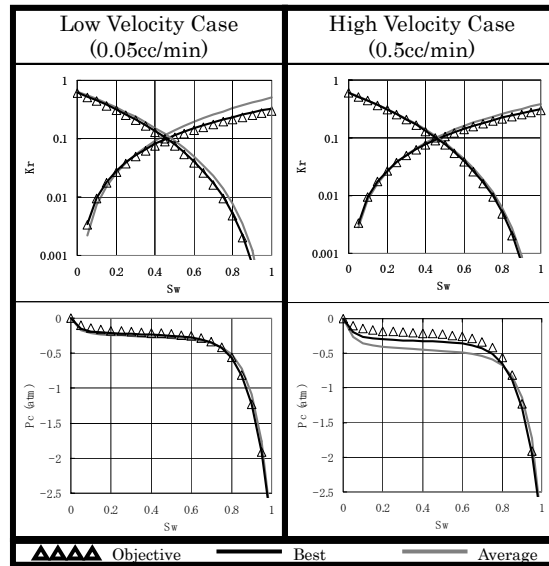


Figure 5: Difference of matching results by velocity

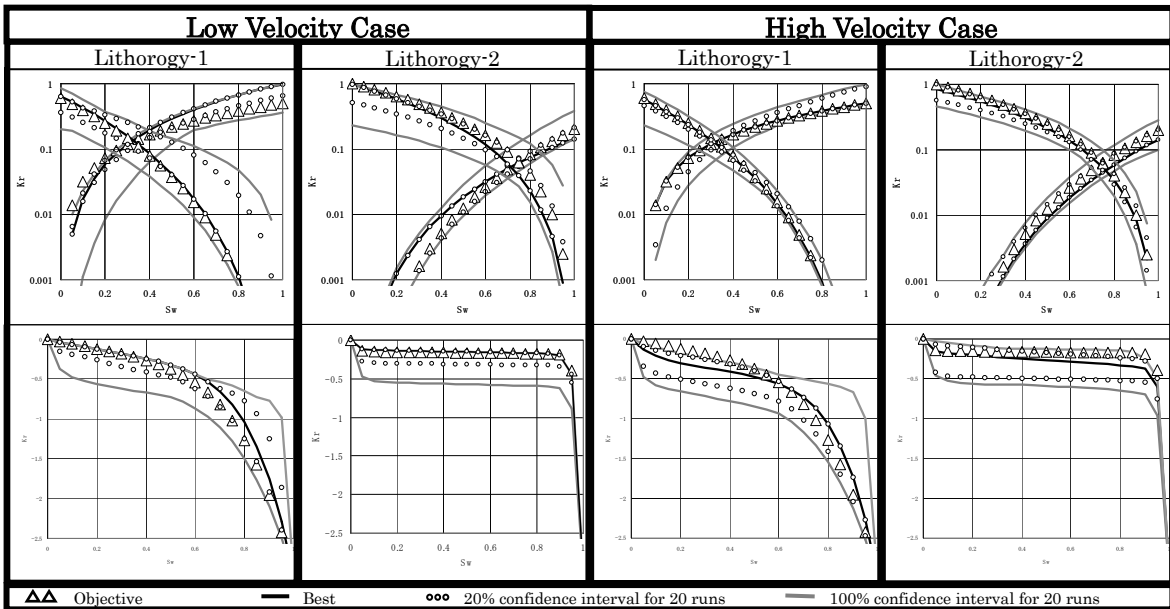


Figure 6: Matching results on 3D model with 2 rock types

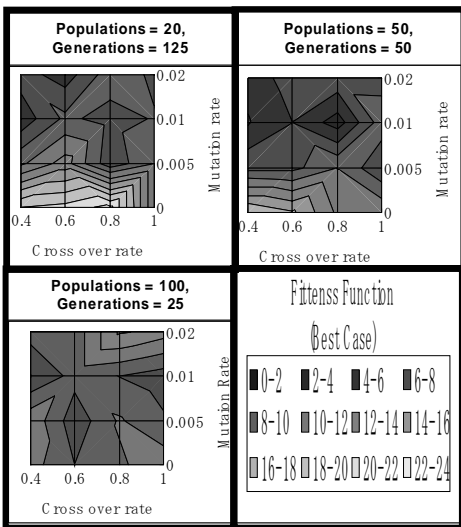


Figure 7: Sensitivity of population size (fitness function of best in 20 runs)

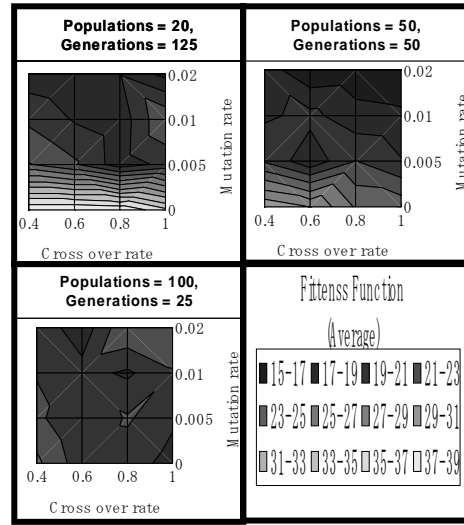


Figure 8: Sensitivity of population size (fitness function of average of 20 runs)

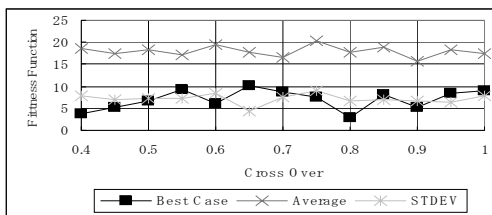


Figure 9: Sensitivity of crossover rate (Mutation rate = 0.01)

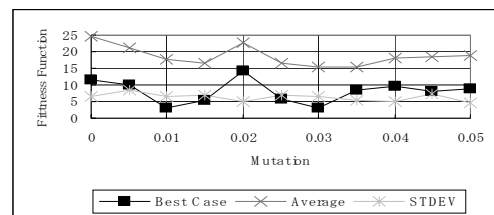


Figure 10: Sensitivity of mutation rate (Cross over rate = 0.80)

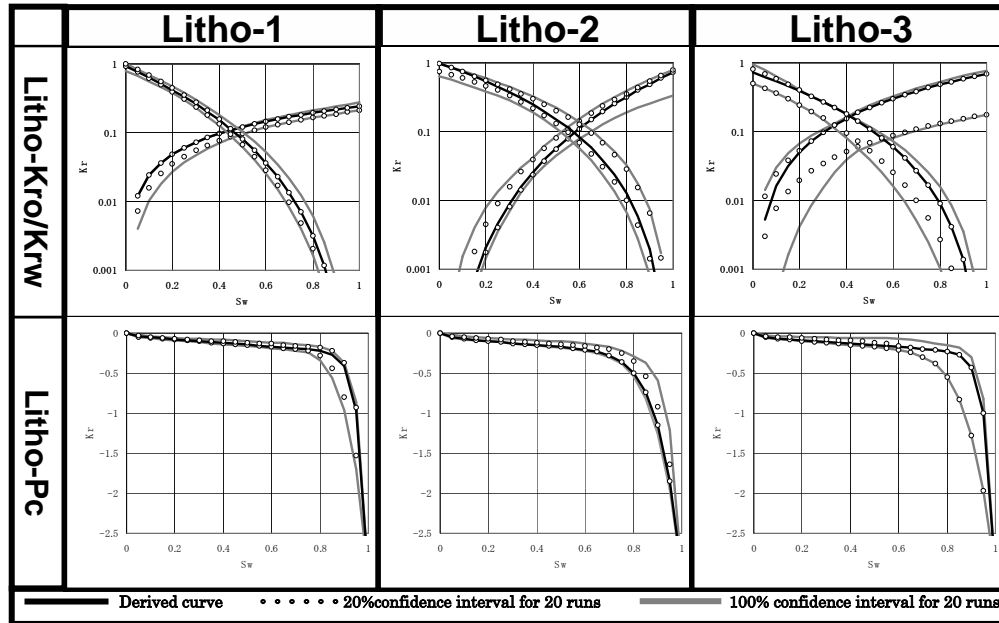


Figure 11: kro/krw and Pc curves of 3 lithofacies derived by matching

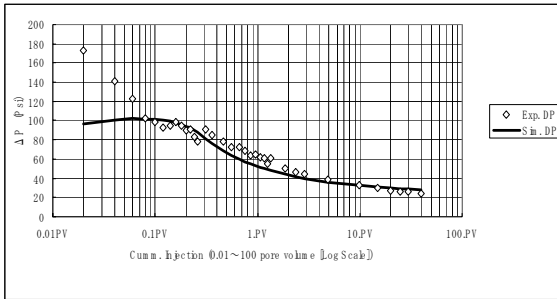


Figure 12: Matching results of differential pressure (Plug-2)

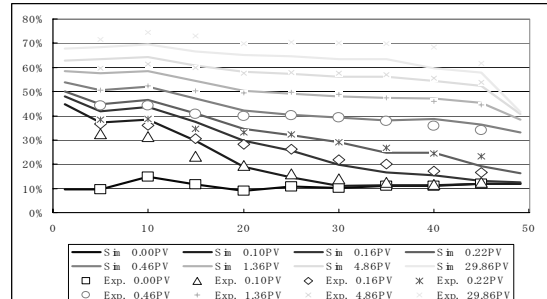


Figure 13: Matching results of slice water saturation (Plug-2)

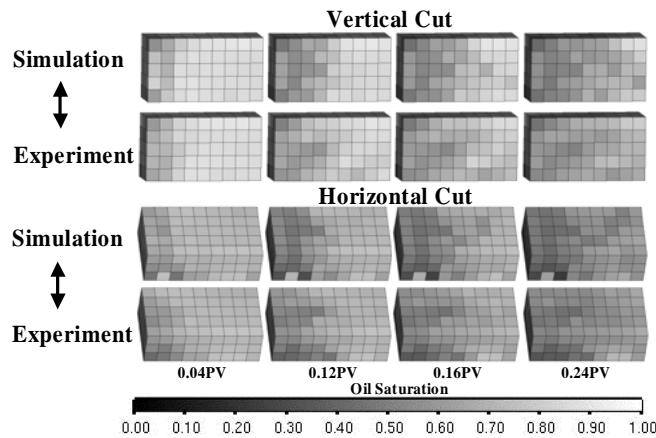


Figure 14: Matching results of grid block water saturation