Misfit Proxy Models To Guide Genetic Method To Generate An Improved Set Of Final Reservoir Models

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Abstract:

A detailed geological understanding of the reservoir along with a reservoir simulation is required to gain a detailed reservoir description and determine the optimal recovery method for oil reservoirs. Moreover, time-lapse seismic data may provide the changes in dynamic parameters (saturation and pressure) with time. Fluids within the reservoir could change dramatically when an enhanced oil recovery (EOR) process is used. Therefore, maximising production of oil and gas reservoirs requires predictive tools that can be used to plan wells by anticipating unswept regions, optimise facilities for fluid handling, and generally forecasting

reservoir behaviour. Such tools are created using pre-production data that includes 3D seismic, well logs, cores and geological analysis via a model. In mature fields, production and other monitoring data such as 4D seismic can also be used to condition reservoir models by history matching.

In this paper, we present new modifications to genetic algorithm, to search the parameter space automatically to find optimal models and compare its results to neighbourhood algorithm. The proxy based method improves the convergence rate by a factor of three generally. With improved convergence, we have the ability run fewer models or search the parameter space more widely to obtain an improved set of final reservoir models. Several reliable simulation scenarios can be used to provide insight about the injected fluid, injection scheme, well pattern, injector well completion, and well spacing.

KEYWORD: Stochastic algorithms; Proxy Models; Convergence rate; Time-lapse (4D) seismic.

Introduction:

Time-lapse (4D) seismic data provide information on the dynamics of fluids in reservoirs, relating variations of seismic signal to saturation and pressure changes. This information can be integrated with history matching to improve convergence towards a simulation model that predicts available data. It is now becoming common in some fields to use time-lapse (4D) seismic as additional history data to detect pressure and/or saturation changes spatially.

Traditionally, history matching has been applied manually but this can be labour intensive. Automatic or computer assisted history matching, where mathematical optimization routines are used to guide changes to

model properties, enables models to be generated more efficiently. This technology is becoming more common in the industry but it is still not yet mature and a subject of research. Numerous options exist depending on whether the sub-surface team wish to update the model quickly or whether a wider uncertainty analysis is required and they are often characterized by their exploitative or exploratitive nature (Sambridge and Mosegaard, 2002). The exploitation uses more of the information linking the misfit, the measure of accuracy of the model prediction, to the parameters of the model that are changed. Automatic methods are rarely used in the industry when history matching using 4D seismic.

Gradient based methods are most exploitative and several flavours have been used with 4D seismic including Steepest Descent method (Roggero *et al*., 2007), Gauss-Newton method (Gosselin *et al*., 2001), and Levenberg-Marquardt algorithm (Arenas *et al*. 2001). Gradient methods explore the parameter space locally but have been combined with geographically global parameterization schemes including gradual deformation (Roggero *et al*., 2007) and probability perturbation (Castro, 2006). There are also probabilistic methods such as the Ensemble Kalman Filter (Skjervheim *et al*., 2007, Chen and Oliver, 2009). The latter has become very popular in history matching production data but when using time-lapse seismic the shear volume of data can cause problems (Aanonsen *et al*., 2009). Stochastic inversion routines tend to be more explorative and include Genetic Algorithm (GA) (Walker, *et al.*, 2006), Simulated Annealing (Lygren *et al.*, 2003) and the Neighbourhood Algorithm (NA) (Stephen *et al*., 2006).

Such an approach is used here where multiple flow simulations are generated simultaneously using a suitable parameterisation of the reservoir description. The output is used to predict a 4D seismic response, which is

quantitatively compared to observed seismic data via a petro-elastic model and then updated in an objective manner as seen in Figure (1). Stochastic inversion approaches are used including a Genetic Algorithm (GA) and the Neighbourhood Algorithm (NA). The major problem with such approaches is that they can be inefficient at finding local and global minimum misfits. The aim of this work is to explore methods to improve their exploitative nature without compromising the exploration. We derive a proxy model of the misfit response surface and use that to derive sensitivities of the misfit with respect to the parameters that we modify. These sensitivities are then used to guide the stochastic search element to improve convergence rates. We apply this approach to a synthetic misfit equation and then to a synthetic model of the Schiehallion field.

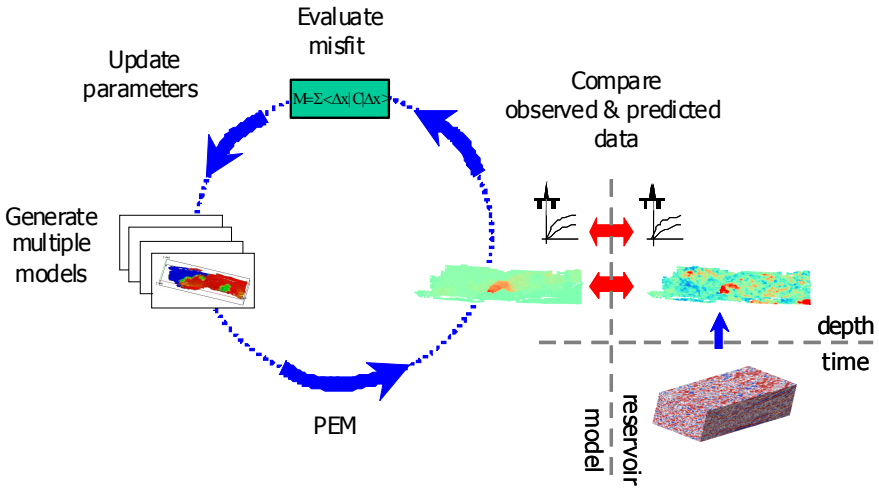

Figure 1. Assisted seismic history matching workflow. For full details see Stephen *et al.*, 2006.

Method:

We perform seismic history matching starting with a reservoir simulation model created by conventional methods where 3D seismic, well

logs and cores, well test data and other pre-production data are used to condition a geological model. This has been upscaled for flow simulation and then used as a base case. Figure (1) illustrates the iterative loop that is applied to obtain a good match to production and 4D seismic data. In stochastic methods of inversion, multiple models are generated simultaneously exploiting cluster technology and we use a parameterisation scheme suitable for the problem we are working on to perturb the base case model. These are passed to a standard simulator and then a petro-elastic model is used to predict changes in accoustic impedance. For details of this approach see Stephen *et al*. (2006). For each cell in the model a pressure dependent dry bulk modulus, κ^{dry}, is obtained as well as shear modulus, μ. The saturated bulk modulus, κsat, is obtained via Gassmann (1951) and the p-wave modulus ($\kappa^{sat}+ 4\mu/3$) is upscaled vertically using Backus (1962) and combined with the bulk density to obtained the acoustic impedance. This provides a map over a reservoir interval. The observed time traces (often a cube of coloured inversion, phase rotated amplitudes or inverted elastic impedance) are analysed to generate suitable attributes that are pseudo impedance properties. With suitable cross scaling (the observed data may be averaged areally or the model data interpollated), the predicted and observed data may then be compared via a misfit *M* where:

$$\mathrm{M}(\underline{\lambda}) = \sum_{all\ data} \frac{(y^{obs} - y^{mod})}{\sigma_d^2} \qquad (2)$$

where λ is the vector of parameters that are updated during history matching, yobs and ymod are the observed and modeled data respectively while σd is the uncertainty of the measurements (assuming that errors are Gaussian and uncorrelated). A similar equation is used for the production data so that we obtain a single misfit for each model.

The new model parameters are then chosen by one of two possible choices. We use either a Genetic Algorithm or the Neighbourhood Algorithm. Both approaches are initialized with a random selection of parameters to generate ni initial models.

Genetic Algorithm (GA):

Genetic algorithms (GAs) were invented by John Holland in the 1960s and were developed by Holland and his students and colleagues at the University of Michigan in the 1960s and the 1970s. Later, several computer scientists independently studied evolutionary systems with the idea that evolution could be used as an optimization tool for engineering problems. The idea in all these systems was to evolve a population of candidate solutions to a given problem, using operators inspired by natural genetic variation and natural selection. 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 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 (2) 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 (Tokuda *et al*., 2004).

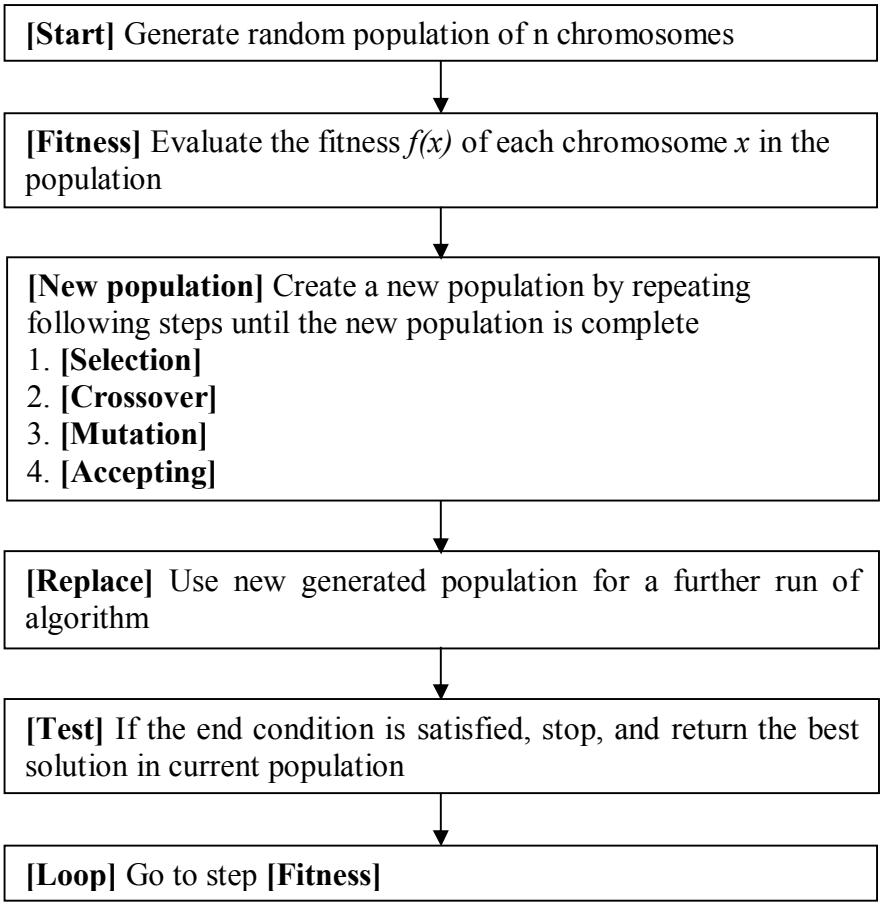

Figure 2. Simple workflow of the Genetic Algorithm (Tokuda *et al.* 2004).

We use a GA particularly suited to real number problems (Eshelman and Schafer 1993). The whole ensemble is ranked in a non-generational manner and the best models are chosen as parents and they are randomly and uniquely paired for "mating" via "cross-over". In this process two child models are generated and the models are mixed such that for each child model the parameters are obtained from:

$$\lambda_i^{child} = \frac{(\lambda_i^p + \lambda_i^q)}{2} + \alpha_i^{child}(\lambda_i^p - \lambda_i^q) \qquad (2)$$

Where λ_i^p is the i^{th} element of the pth model in the ensemble and α_i child is a random number generated typically between -1 and 1 with a uniform distribution. After cross-over we consider jump mutation where one element of the parameter vector may be randomly changed across the whole range possible while creep mutation changes it within, 5 per cent of its current value. New models are then added to the ensemble.

Neighbourhood Algorithm :

The Neighbourhood Algorithm (NA) was developed originally by Malcolm Sambridge to solve a seismic waveform inversion problem (Sambridge, 1999a). The main principle which the NA algorithm is based on is that at every stage of the search process the model space is represented by the Voronoi diagram of all previously sampled models and that this representation helps the algorithm to concentrate sampling on the most promising regions. The neighbourhood algorithm arose with the intention of responding to the next question:" How can a search for new models be best guided by all previous models for which the forward problem has been solved?". The neighbourhood algorithm begins the

optimization with an initial random generation and after estimating the fitness of those models by using the objective function, NA finds out the nearest neighbour region of each model in the parameters space by constructing the Voronoi diagram. Figure (3) shows a set of Voronoi cells which was calculated by NA for 10, 100 and 1000 irregularly distributed points in a 2D example.

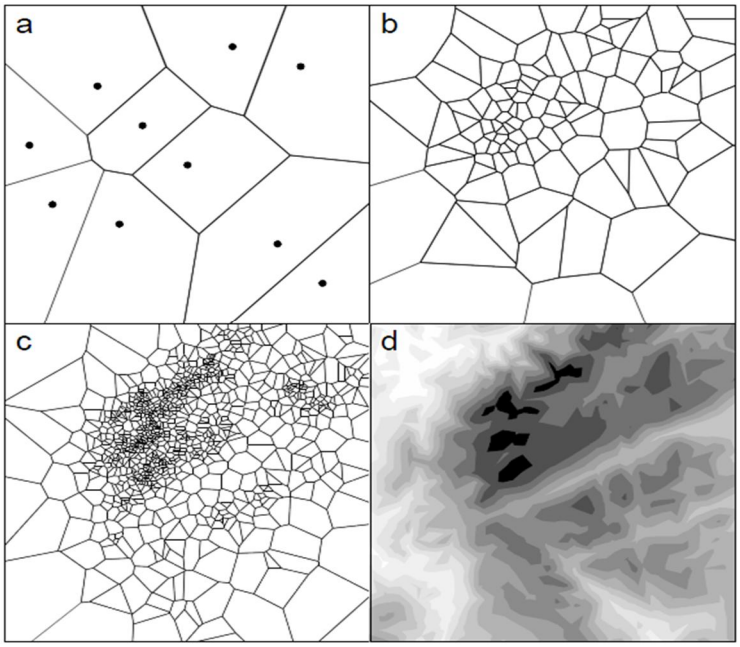

Figure 3. Quasi-uniform random points and Voronoi cells for a) 10 points, b) the Voronoi cells of 100 points generated by the neighbourhood approximation, c) as b but for 1000 points and d) contours of the test objective function. The black dots in Figure belong to the misfit value of different models (Sambridge, 1999a).

In both processes the best models are selected to identify a new sub-volume of the parameter space to search as illustrated in Figure (4). The NA searches around single models and their neighbourhoods identified using Voronoi cells. The GA takes pairs of the best models and seeks to

combine them to identify which parameters provide the best chance of reducing the misfit further. The new search space is set as the region surrounding the selected pair of models. Conventionally both methods then sample the sub-volume of the search space with a uniform probability distribution to generate new models. The aim in this work is to find an appropriate sampling strategy that improves the efficiency as high dimensional problems require a search of a very large hyper-volume.

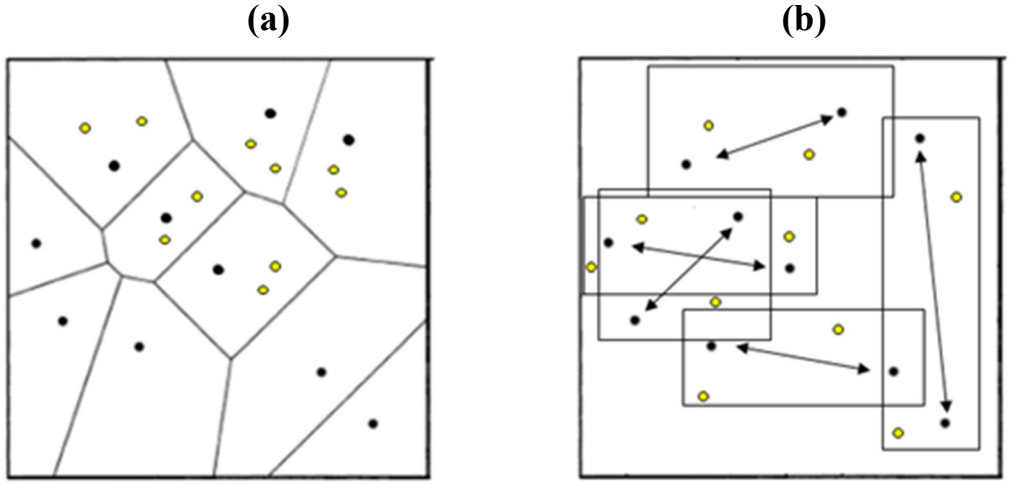

Figure 4. Comparison of how the parameter space is subdivided on the first iteration of (a) the NA and (b) the GA routines. 10 models are generated on in a two-dimensional parameter space randomly. The best 5 are used in the NA routine with 2 models per Voronoi cell being randomly distributed. In the GA all models are initially used as parents and this defines rectangular sub-volumes.

Improving Convergence:

To improve the efficiency of sampling, we seek to replace the uniform distribution with one that reflects the information learned about the misfits as we proceed through the iterative process. We begin with Bayes Theorem to obtain the likelihood of the data, *d*, given a model from the misfit, *M*, via:

$$P(d \mid \theta) \propto exp(-M(\underline{\lambda})/2) \qquad (3)$$

where $\underline{\lambda}$ is the parameter vector. We calculate $M(\underline{\lambda})$ for each model in an ensemble from Equation (1). For any one of these models, we can apply a Taylor expansion:

$$P(d \mid \lambda) \propto exp(-M(\underline{\lambda}^*)/2)(1-\frac{1}{2}\sum\frac{\partial M}{\partial \lambda_i}(\lambda_i - \lambda_i^*) + ...) \qquad (4)$$

The probability of λ_i is approximated by:

$$P(d \mid \lambda_i) = P^*(1+k(\lambda_\iota - \lambda_\iota^*)) \qquad (5)$$

Where $k = -\frac{1}{2}\frac{\partial M}{\partial \lambda_i}$

We can then use Equation (4) to obtain the cumulative distribution function, *cdf,* for a given parameter, λ_{Ii} by integrating over the range of the parameter, λ_i and λ_2, obtained from the boundaries of the Voronoi cell. We normalise this integral so that it is unity over the whole range:

$$cdf = \int_{\lambda 1}^{\lambda} P d\lambda \Big/ \int_{\lambda 1}^{\lambda 2} P d\lambda \qquad (6)$$

The solution for λ is:

$$\lambda = \frac{-(1-k\lambda^*) \pm \sqrt{(1-k\lambda^*)^2 + k(\tau_1 + cdf(\tau_2 - \tau_1))}}{k} \qquad (7)$$

Where $\tau_i = k\lambda_i^2 + 2(1-k\lambda^*)\lambda_i$

Thus if we randomly generate the *cdf* value between 0 and 1, and we can solve this equation to get λ_i. As a result, instead of randomly sampling between λ_i and λ_2, with a linear cumulative distribution around λ^*, we use a square root function.

Response Surface Method :

To complete the process above, we need to obtain *k* for which we use a proxy response surface as a representation of the real misfit. Response surfaces are often constructed with polynomial regression techniques. A proxy model becomes very useful, because full SHM is too expensive and time consuming. In this study, the Singular Value Decomposition technique with least square regression (Sedighi and Stephen *in press*) is used to fit the data and coefficients, C_0, C_i and C_{ij} are derived to construct 2^{nd} order polynomial misfit function:

$$M(\underline{\lambda})=C_0+\sum_{i=1}^{nd} C_i\lambda_i+\sum_{i=1}^{nd} C_{i+nd}\lambda_i^2+\sum_{i=1}^{nd-1}\sum_{j=1+1}^{nd} C_{ij}\lambda_i\lambda_j \qquad (9)$$

The derivative of this polynomial is then:

$$\frac{\partial(\underline{\lambda})}{\partial\theta_i} = C_i + 2C_{i+nd}\lambda_i + \sum_{\substack{j=1 \\ j\neq i}}^{nd} C_{ij}\lambda_j \qquad (10)$$

Thus for a given model, we can calculate an updated parameter value using Equation (7). We previously defined the Neighbourhood Algorithm with Proxy Derived gradients the NAPG method (Arwini and Stephen 2010). Here we similarly define the Genetic Algorithm with Proxy Derived Gradients the GAPG approach.

GA approximation:

When using the GA, we consider pairs of models for breeding (Feeney *et al*. 2006) and sample in a box surrounding them. These may be used to estimate the gradient such that:

$$\frac{\partial M(\underline{\lambda})}{\partial \theta_i} \approx \frac{M(\lambda^p)-M(\lambda^q)}{\lambda^p-\lambda^q} \qquad (11)$$

We call this the *GAPG from differences*.

Case Study I: Synthetic Misfit functions

The new method is tested on a simple quadratic response function:

$$M = \sum_{i=1}^{nd} \lambda_i^2 \qquad (12)$$

The gradient is obtained analytically and used rather than the approximation at this stage. We chose nd = 12. Figure (5a) shows the reduction of misfits as we iterate using the NA, GA, NAPG and equivalent GAPG. We also used the GA with gradients derived from the pair of parents selected. In each case 128 models were generated initially and then 64 models were generated for each iteration. For the NA the best 32 models selected and for each of those, 2 models were generated in their neighbourhood. For the GA, the best 64 models were selected creating 32 pairs of parents, each with 2 offspring. The NA was slowest overall to converge. The NAPG offered considerable speedup by a factor of 3. The GA was faster still, however by a factor of 5 compared to the NA. Using the parents to approximate the gradients, rather than using the analytical form, showed negligible improvement. The GAPG approach worked best of all. Figure (5b) confirms this for one of the parameters. In the slowest case, the parameter showed lots of scatter while for the GAPG case, there was virtually no change in the parameter after 1000 models.

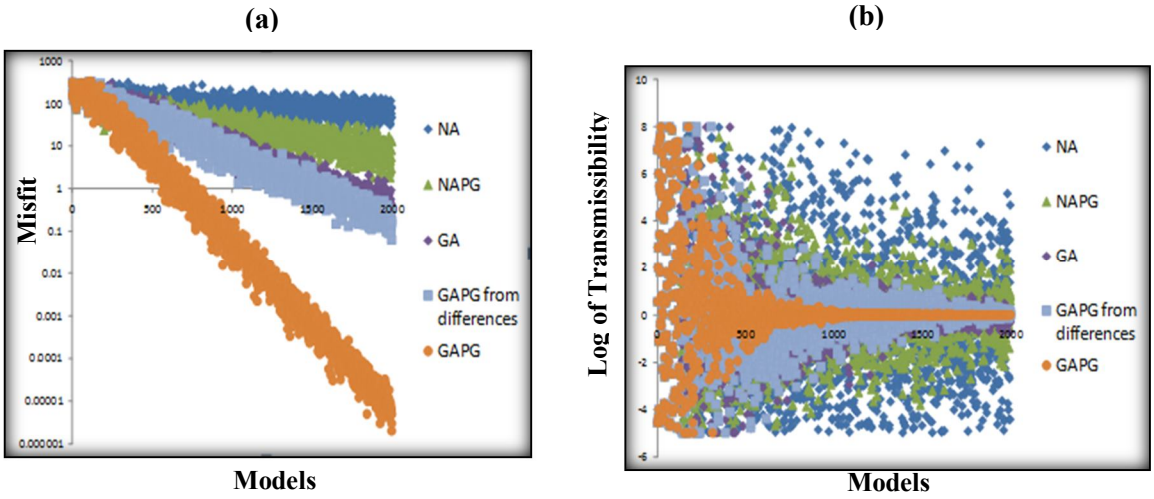

Figure 5. (a) Convergence of various methods where the 12 dimensional quadratic equation is used as the misfit function. (b) Convergence of one of the parameters.

Case Study II: Synthetic SHM -Schiehallion Field Case

The Schiehallion field is situated to the west of Shetland on the UK Continental Shelf (UKCS). The original model of this heavily faulted turbidite reservoir was constructed by the field operator using conventional approaches to map reservoir properties to the simulation model. The model used for this study on Segment 4 of the reservoir where the focus was on capturing the 4D signatures around a particular injector well, by updating the transmissibility of 10 barriers and faults nearby as shown in Figure (6) and Table 1. The model was upscaled vertically to 4 layers and the porosity lies between 23-30% while permeability varies from 250 to 2000 mD. This sector measured 146 × 44 × 7 (26616 active cells typically measuring 100 × 100 × 6 m).

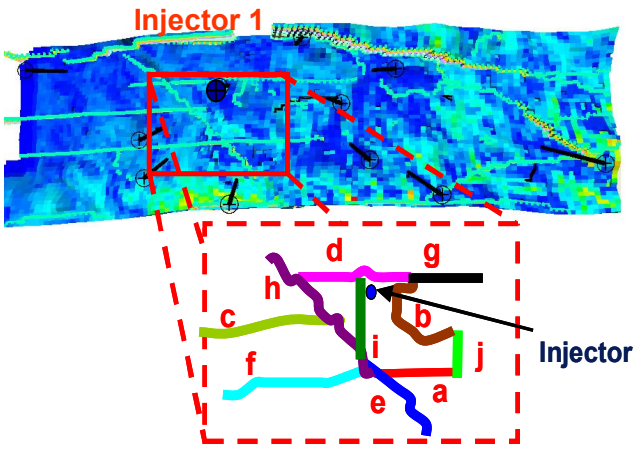

Figure 6. Faults and barriers in simulation model of Segment 4.

Table 1. Barrier multiplier range on log scale.

Fault	Barrier Transmissibility multiplier	Range	
		Min	Max
a	0.001	-2.0	1.0
b	0.0009	-2.0	1.0
c	0.0009	-2.0	1.0
d	0.0009	-2.0	1.0
e	0.0009	-1.0	2.0
f	0.001	0.0	3.0
g	0.0009	-1.0	2.0
h	0.0009	0.0	3.0
i	0.0009	-2.0	1.0
j	0.0009	-1.0	2.0

A synthetic truth case was generated using the multipliers in Table 1 for the identified faults. The truth case maps of acoustic impedance are shown in Figure (7). We ignore noise in the seismic data as we found previously that this was largely uncorrelated (Stephen *et al.* 2006) at the scale of the simulator cell and if Gaussian, the noise is simply an additive term if date and model errors are uncorrelated (Arwini and Stephen 2010). Wells are indicated in Figure (7a) but there was little impact of the barrier transmissibilities on the predicted behavior so we focused on the seismic misfit in this work. The major 4D signature shows a pressure up anomaly around injector I2 in the first year. In the second year, the well is switched off and pressure relaxation is seen. Over the two years, a net pressure increase is observed. These maps are qualitatively similar to the maps observed and reported in Stephen *et al.* 2006. The base case model is shown in Figure (8) where the barriers "i" and "j" were open.

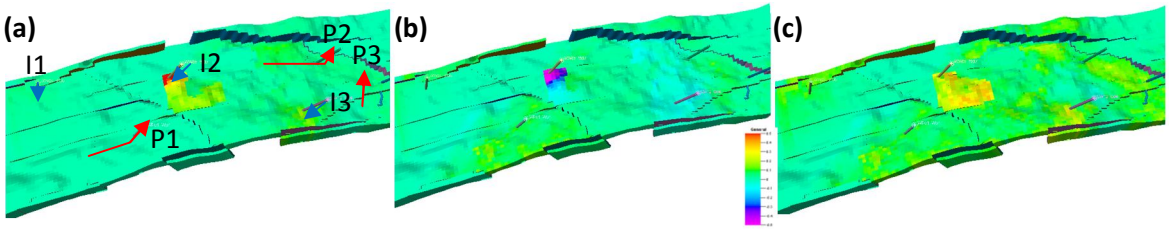

Figure 7. Maps of change of impedance for (a) 1999-1993, (b) 2000-1999 and (c) 2000-1993 for the truth case model. The colour bar indicates a scale relative to the mean plus or minus half the standard deviation of the 1993 map of impedance. Red indicates pressure up or gas coming out of solution while blue indicates water invasion or pressure decline. The wells I1-I3 indicate injectors and I2 is only active in the 1st year. P1-P3 indicate producers and P1 was only active in the second year.

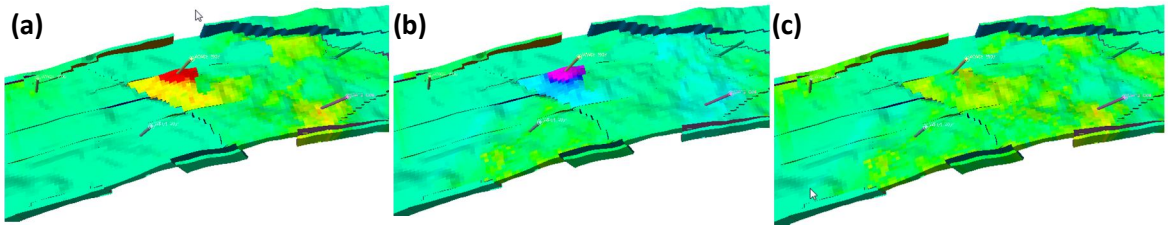

Figure 8. Maps of change of impedance for (a) 1999-1993, (b) 2000-1999 and (c) 2000-1993 for the operator's base case model. The colour bar in Figure 8 indicates a scale relative to the mean plus or minus half the standard deviation of the 1993 map of impedance. Red indicates pressure up or gas coming out of solution while blue indicates water invasion or pressure decline.

500 models were generated using random sampling of the model parameter space. These were then used to generate the proxy model in Equation (9). Figure (9) shows the comparison of actual versus proxy derived misfits. The correlation was excellent with a coefficient (R^2) of 0.98.

The GA method was considerably faster and required that the gradients were calculated from the proxy (NAPG) rather than using the parents selected at each crossover step (GAPG from differences). The GAPG case was almost an order of magnitude faster compared to the NA.

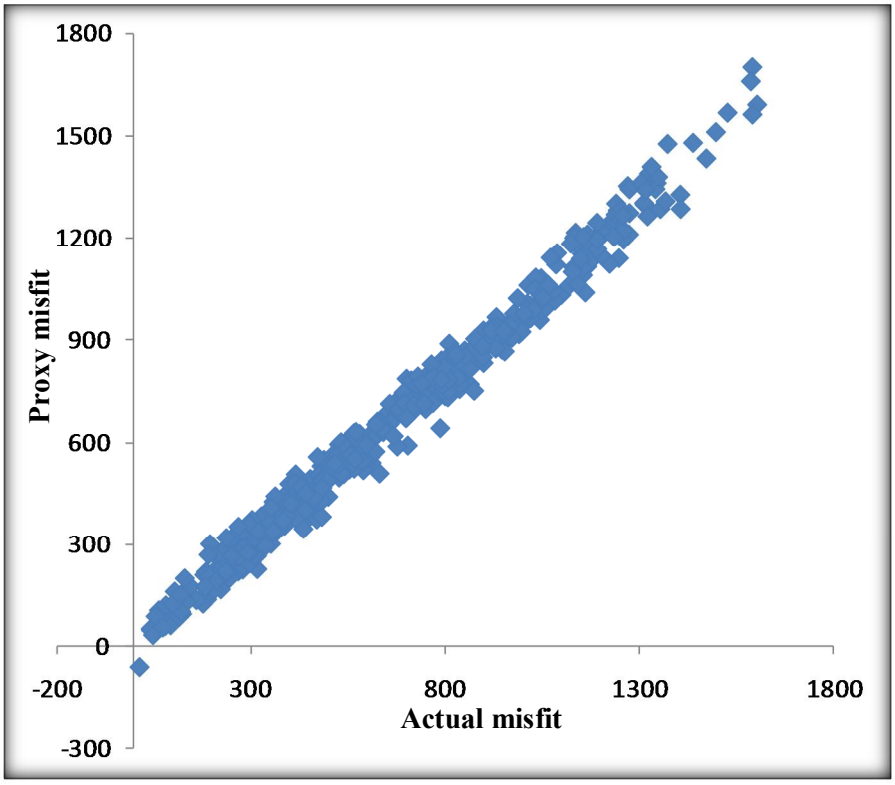

Figure 9. Comparison of actual versus proxy model derived

Discussion of Results :

Stochastic methods of optimization are favoured in cases where the nature of the misfit response surface is unknown and it may be hypothesized that multiple models may exist that produce minima. By sampling on a broad basis the chance of finding multiple minima is greater. This comes at an expense however such that additional models are required for sampling. The GA and NA methods are two such approaches which are recognized for both these positive and negative aspects. The GA that we use here is more sensitive to the misfit function as displayed in the quadratic case leading to a much faster convergence. It is only when there are multiple mnima that mixing betweem models approaching separate

solutions leads to inappropriate estimates. However, once the GA settles on one solution, the speed up is seen again.

The linear approximation to the probability density distribution seems to offer a reasonable speed up. For the NA this necessitates calculation of sensitivities from the proxy model. For the GA, we tried to estimate sensitivities from the parent models. It seems that the parent models underestimate the degree of correction required to the uniform distribution 'guess' at the new model compared to the senstitivities derived from the proxy model.

The cost of the proxy model estimation is relatively cheap. Both NA and GA methods require a large initial sample of models anyway and so the estimation of the proxy model costs very little.

Conclusions:

The following conclusions can be drawn from this study:

- This work has shown that genetic algorithms are promising in history matching
- The GA method uses more models as parents and is significanly faster than NA for simpler response surfaces but slower in more complex cases.
- Sampling may be made more efficient if a simplified representation of the likelihood is used to define the sample distribution
- NAPG and GAPG speed up convergence by a factor of two to three.

- Estimation of gradients in the GA using "parent" models shows some speed up but not significantly improved.

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