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Abstract

History matching is an important step in reservoir simulation study. The objective is to validate a reservoir model before it is used for prediction. In conventional way, people do history matching by manually adjusting uncertain parameters until an acceptable match is achieved. As a consequence, history matching becomes a delicate problem and consumes a lot of time. Furthermore, in several cases it is hard to obtain a match by manual process.

In order to have a more efficient history matching process, many researchers conducted studies by involving a computer based program to obtain a match. The method is normally called *assisted history matching* (AHM). One of the AHM methods involves the use of experimental design, proxy model and optimization algorithm. The basic concept of this method is to use proxy model which is generated from set of experiments to replace reservoir simulation in the optimization process. This method has practical application in the industry. However, without a proper understanding, using this method to solve a history matching problem would be as difficult as conventional way.

In this master thesis, an extensive study of AHM methodology is performed in order to have a comprehensive understanding on how the methodology solves a history matching problem. The methodology limitations are also identified so that proper improvements can be carried out. The main improvements are the introduction of average proxy error in objective function and the proposal of selecting response variables to become matching variables based on the quality of proxy model.

This study also investigates different experimental design methods, proxy models and global optimization algorithms. In experimental design subject, *complete CCF design* and *fractional CCF design* are elaborated. Two types of proxy models e.g. *kriging* and second *polynomial equation* were investigated. Four optimization algorithms e.g. *simulated annealing, direct search, global search* and *genetic algorithm* are analyzed to select the best performance algorithm. In the final stage, the improved methodology was used to solve history matching problem of two artificial study cases.

Acknowledgments

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Stavanger, June 2013

Ibnu Hafidz Arief

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Chapter 1

Introduction

1.1 Study Background

Reservoir simulation plays an important role in the petroleum industry. Its common applications are calculation of petroleum reserves and prediction of petroleum production. Since reserves and production profiles are the two most important figures in the petroleum business, it is important that reservoir simulation gives output with an acceptable degree of accuracy. To achieve an accurate prediction of both reserves and production profiles, the reservoir model used in the simulation must be reliable.

The only way of obtaining a reliable reservoir model is by doing history matching. History matching is a tuning process of reservoir model by adjusting values of uncertain reservoir parameters in order to achieve a better match between simulated and observation data. In conventional history matching, the engineer adjusts the value of uncertain reservoir parameters manually by trial and error until a sufficient match is achieved. In most cases, history matching is a delicate, exhaustive and time consuming process and furthermore in some cases it is difficult to achieve an acceptable match with the conventional approach.

Assisted History Matching (AHM) consists of optimization techniques which automatically adjust uncertain reservoir parameters until stopping criteria are achieved. The aim is to make history matching less time consuming and more reliable. The AHM procedures studied in this work involve the use of experimental design, proxy model and optimization algorithm as the tools for finding the matching solutions. It is important that the engineer has a comprehensive understanding of the AHM methodology before they use it to solve history matching problem. Therefore, in this study a comprehensive investigation of the methodology is emphasized.

1.2 Study Objectives

This study is set to achieve the following objectives:

a) Basic understanding of the concepts involved in the methodology

b) Identify limitations of the existing workflow so that some improvements can be carried out
c) Investigate different types of experimental design methods, different proxy models and different global optimization algorithms

The result of this study will be a comprehensive explanation of the methodology, some improvements of the existing workflow enabling acceleration of the matching process, the selection of the best proxy model and the global optimization algorithm.

1.3 Thesis outlines

This thesis report consists of six chapters. Chapter 1 includes discussion of the general study background, the objectives to be achieved and the outline of the thesis report.

Underlying theory is covered in chapter 2. In this chapter, the discussion begins with the review of published studies in the AHM area. Then it is continued with the explanation of three main components in AHM methodology e.g. experimental design, proxy model and global optimization algorithm.

Chapter 3 comprises detail explanation of AHM methodology used in this study. In addition, an assisted history matching toolbox which was developed to conduct this study is also explained in this chapter.

Chapter 4 discuses about an artificial 3D reservoir model which was developed as history matching cases. These cases will be matched by using the proposed AHM methodology. This chapter also includes detail information about uncertain parameters used in history matching cases.

Discussions of the results are further elaborated in chapter 5. This chapter covers a deep investigation of the methodology, improvements of the existing workflow and comparison analysis of different experimental designs, proxy models and global optimization algorithms. In addition, the matching process of the two study cases is also shown in this chapter. Summary, conclusions and possible future works will be elaborated in the chapter 6.

Chapter 2

Underlying Theory

2.1 Assisted History Matching

Many papers have been published in the area of assisted history matching. Generally, there are two types of assisted history matching methodology. First method is called *"direct"* assisted history matching and second method is called *"indirect"* assisted history matching.

In *"direct"* assisted history matching, every step in the optimization process corresponds to one reservoir simulation. The objective function value of every solution given at each step is directly evaluated by reservoir simulation. The advantage of using this approach is that the solutions which give minimum objective function are close to the matching solution, but the main disadvantage is that it needs a lot of time. Figure 2.1 is an example of direct AHM workflow. From that figure, it is shown that this method needs to run reservoir simulations simultaneously until the minimum objective function value is achieved.

The main tool in direct AHM method is optimization algorithm e.g. evolutionary algorithm, direct search algorithm, simulated annealing, etc. Many authors have done researches using this approach with the main objective of developing an optimization algorithm which is able to minimize the objective function with minimum number of iterations [1, 2, 3, and 4].

In this study, we will investigate further indirect assisted history matching. This method consists of 3 main components: experimental design, proxy model and optimization algorithm. Figure 2.2 is an example of indirect AHM workflow. The basic concept of this method is that there is no direct involvement of reservoir simulation in the optimization process. The role of reservoir simulation in the optimization process is replaced by proxy model. Therefore, the optimization process will take significantly less time. The disadvantage of this method is that the optimum solution doesn't necessarily give an acceptable match; consequently the process has to be repeated until an acceptable match is achieved.

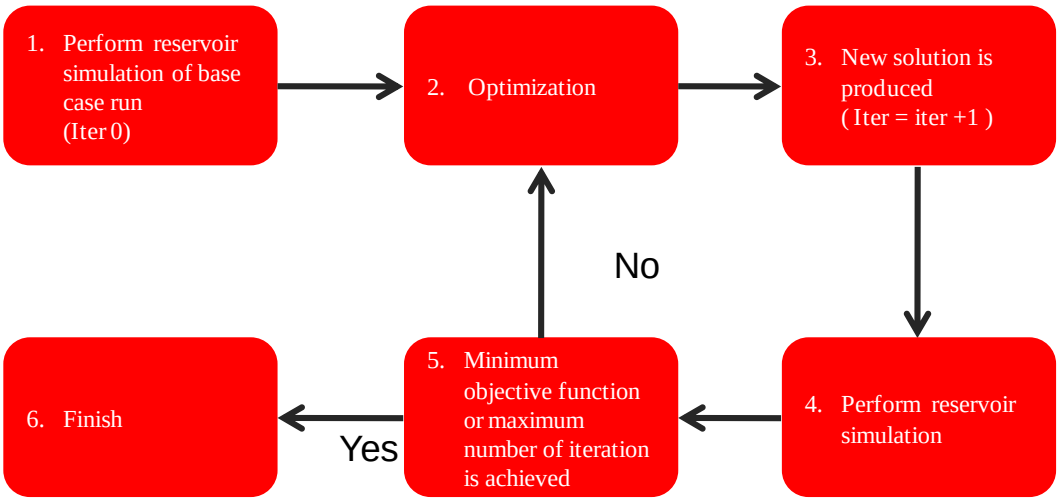


Figure 2.1 Workflow of "direct" assisted history matching

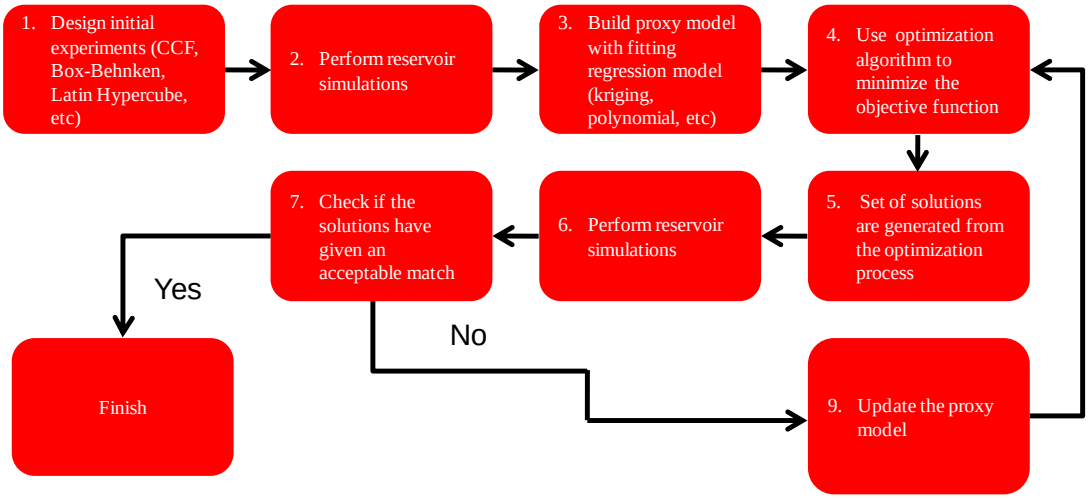


Figure 2.2 Workflow of "indirect" assisted history matching with proxy model

Experimental design is used to generate initial experiments. The initial experiments are the basis of creating a proxy model. The proxy model will replace reservoir simulation in the optimization process. The optimization algorithm searches optimum solutions which give minimum objective function. However, these optimum solutions do not necessarily give an acceptable match and the optimization has to be repeated with an improved proxy model. The proxy model is improved by adding the optimum solutions to the initial experiments. This recursive procedure is stopped when an acceptable match is achieved. Related works about indirect AHM have been published in SPE paper [5, 6, 7, 8, and 9] where each researcher focused on different subjects of this method. Baoyan Li and F. Friedmann studied proxy model [9] and L. den Boer et al used experimental design

method to generate probabilistic of static and dynamic uncertain parameters as to obtain a match [8].

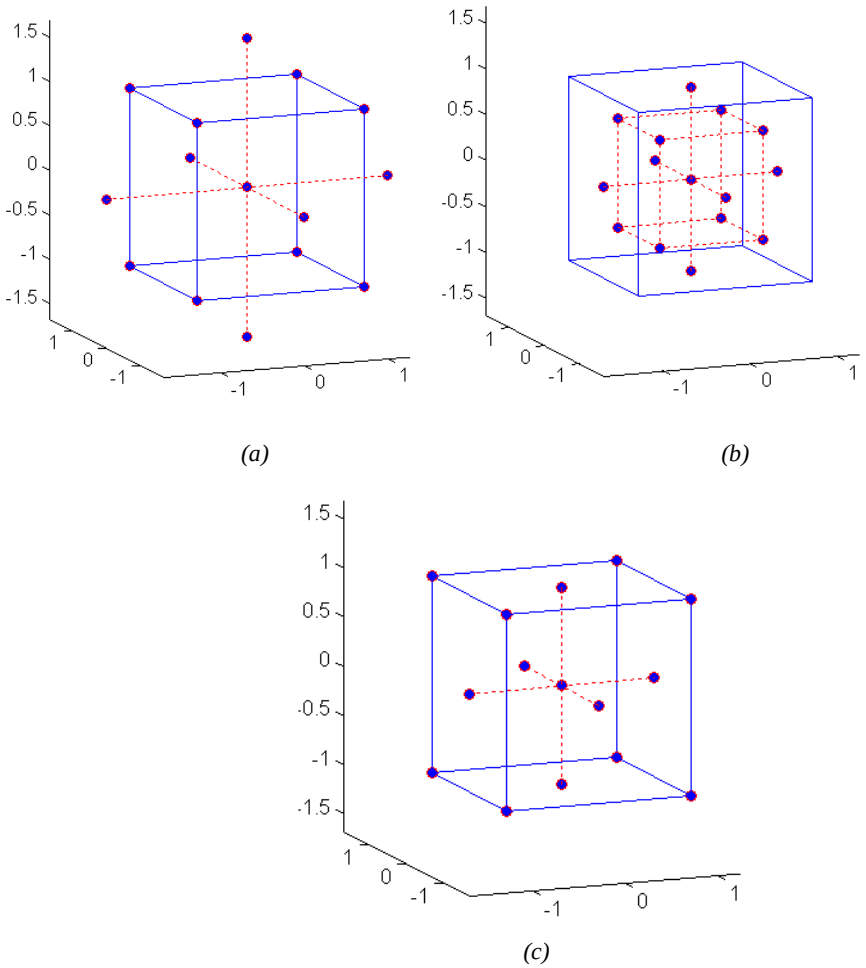


Figure 2.3 Central composite design (CCD) consists of 3 types of structure (a) circumscribed (CCC), (b) inscribed (CCI) and (c) face centered (CCF)

2.2 Experimental Design

Experimental design or *design of experiments* (DOE) is a method of collecting any information where variation is present. The objective is to understand the impact of each parameter to the observed model. DOE in its application for the history matching problem has been used for another purpose in addition to the previously mentioned. The application of DOE in history matching problem is explained as follow:

a) Uncertain parameters screening

   Reservoir model used in the simulation study is made up by many subsurface parameters which are uncertain. It is not practical to include all uncertain parameters in the history matching process, therefore only the most sensitive uncertain parameters are involved.

In order to select the most sensitive parameters, a screening process is required. DOE together with the proxy model of polynomial equation are normally used as a screening tool. Details of the application of DOE and proxy model in screening process will be discussed further in chapter 3.

b) Assisted history matching

In assisted history matching, DOE and proxy model are used to replace the role of reservoir simulation in the optimization process.

There are several published methods for designing experimental sampling. Table 1 and 2 show different design methods and its number of experiments. The design selection depends on the study purposes and also the available resources. The common rule is that higher number of experiments will result in more accurate proxy model.

2.2.1 Cubic Centered Face (CCF)

CCF is one of the design structures involved in the *central composite design* (CCD). There are three types of structure in central composite design e.g. *circumscribed* (CCC), *inscribed* (CCI) and *face centered* (CCF) as shown in figure 2.3 [11]. From that figure, it is clearly shown that only CCF fits with the purpose of this study. CCD requires larger space than the specified boundaries while CCI explores less space than the specified boundaries.

Nb of Parameters	Number of Experiments	
	Complete CCF	Fractional CCF
2	9	7
3	15	11
4	25	17
5	43	27
6	77	45
7	143	79
8	273	81
9	531	147
10	1045	149
11	2071	151
12	4121	249

Table 2.1 Two types of CCF design and its number of experiments

Nb of Parameters	Number of Experiments
	Plackett-Burman
11	12
19	20
23	24
35	36

Table 2.2 Plackett-Burman design

Generally, CCF design consists of a 2^k full factorial (or 2^{k-p} fractional factorial with $1/2^p$ fraction) with n_f runs, 2k axial or star runs and 1 center run with k is the number of parameters [10]. An example with k=5, for complete CCF design there are 2^5 runs plus 10 star runs and 1 center run, therefore by total there are 43 experiments. For the case of fractional CCF with ½ fractions the number of experiments is calculated as follow, 2^{5-1} = 16 runs plus 10 star runs and 1 center run, therefore by total there are 27 experiments.

2.2.2 Plackett-Burman

Plackett-Burman is another design method which is used in this study. This design is two level factorials design. For studying k= N-1 variables in N runs, where N is the multiple of 4 e.g. N = 12, 16, 20, 24. Figure 2.4 shows the example of the design sampling with 11 parameters. Plackett-Burman is a dedicated design for fitting first order model. It is aimed to find the influence of the main effect of each parameter. It requires less number of experiments for large number of parameters involved. For the other experimental design methods are provided in the appendix.

Experiments \ Parameters	1	2	3	4	5	6	7	8	9	10	11
1	+1	+1	+1	+1	+1	+1	+1	+1	+1	+1	+1
2	+1	+1	+1	+1	+1	+1	-1	-1	-1	-1	-1
3	-1	+1	+1	+1	+1	+1	+1	-1	-1	-1	-1
4	-1	-1	+1	+1	+1	+1	+1	+1	-1	-1	-1
5	-1	-1	-1	+1	+1	+1	+1	+1	+1	-1	-1
6	-1	-1	-1	-1	+1	+1	+1	+1	+1	+1	-1
7	-1	-1	-1	-1	-1	+1	+1	+1	+1	+1	+1
8	+1	-1	-1	-1	-1	-1	+1	+1	+1	+1	+1
9	+1	+1	-1	-1	-1	-1	-1	+1	+1	+1	+1
10	+1	+1	+1	-1	-1	-1	-1	-1	+1	+1	+1
11	+1	+1	+1	+1	-1	-1	-1	-1	-1	+1	+1
12	+1	+1	+1	+1	+1	-1	-1	-1	-1	-1	+1

Figure 2.4 sampling points of Plackett-Burman design with 11 parameters

2.3 Proxy Model

The results from the experiments are then modeled with an empirical equation. This equation can be used for at least two purposes. First, the equation generated can be used to determine the sensitivity of each parameter and it is normally applied in parameter

screening process. Second, the empirical equation can also be used to replace real experiment/simulation in order to predict the response of non sampling points.

In this study, there are two types of empirical equation that will be investigated e.g. polynomial equation and kriging equation. By the end of this study, one of the equations will be recommended as the proxy model in the AHM workflow.

2.3.1 Polynomial Equation

Equation 2.1 and 2.2 are two types of polynomial equation. Equation 2.1 is first order polynomial equation while equation 2.2 is second order polynomial equation.

$$Y = \beta_o + \sum_{i=1}^{n} \beta_i x_i \quad \text{..... (2.1)}$$

$$Y = \beta_o + \sum_{i=1}^{n} \beta_i x_i + \sum_{j=1}^{n} \beta_j x_j + \sum_{k=1}^{n} \sum_{l=1}^{n-1} \beta_{kl} x_k x_l \quad \text{..... (2.2)}$$

The values of coefficient βi, βj, β_{kl} are determined through least square method which minimizes the sum of the deviations between the predicted value and the real value [12]. Index "n" in equation 2.1 and 2.2 is the number of parameters.

2.3.2 Ordinary Kriging Equation

Kriging is a popular method to solve spatial prediction problem. It is commonly used for predicting the value of non sampling point. Equation 2.4 shows the kriging system where the property's value of non sampling points (s_0) is a weighted average of the property's value of sampling points (s_i) [13]. Distance is used as variogram model. Details equation can be seen in appendix.

$$\hat{Z}(s_0) = \sum_{i=1}^{n} w_i Z(s_i) \quad \text{..... (2.3)}$$

For the application in AHM, some adjustments have to be made especially at the parameters scale. The scale of the uncertain parameters has to be normalized with the same maximum and minimum values as it is the in real spatial problem.

2.4 Global Optimization Algorithm

Optimization algorithm has an important role in solving history matching problem. It helps the engineer to find the solutions which could give an acceptable match to the historical data. However, sometimes, several algorithms are trapped in the local minima before they could find the matching solutions. Therefore, in this study, different

algorithms are investigated to see which algorithm is able to find the matching solutions without being trapped in the local minima.

Four global optimization algorithms are selected in this study e.g. simulated annealing, genetic algorithm, direct search, and global search algorithm. These algorithms can be found in the *Global Optimization Toolbox* MatLab™.

2.4.1 Simulated Annealing Algorithm

Simulated annealing is an algorithm for solving constrained or unconstrained optimization problems. The basic concept of simulated annealing is a model of heating material and then slowly lowering the temperature to decrease defects, thus minimizing the system energy [14].

The main parameter in this algorithm is temperature. Temperature significantly influences the algorithm in a way such that not to get trapped in local minima. At the beginning of the program an initial temperature is set, then cooling rate is applied in order to reduce the temperature so that it can achieve a convergence.

$$Random\ value < e^{-\Delta FObj/T} \quad \text{..... (2.4)}$$

$$\Delta FObj = FObj(NewSol) - FObj(CurSol) \quad \text{..... (2.5)}$$

Figure 2.5 shows the workflow of simulated annealing algorithm. New solution which is random neighboring points of current solutions is generated in order to compare their objective function value. If the objective function of new solution is smaller than current solution then this new solution becomes best solution so far. Nevertheless, in order to avoid to get trapped in local minima, current solution could still become best solution if the evaluation criterion of the probability function is met (equation 2.9 and 2.10). For the next iteration temperature is reduced by specified cooling rate.

2.4.2 Genetic Algorithm

Genetic algorithm is a powerful, domain independent, search technique that was inspired by Darwinian Theory [15]. Genetic algorithm is population based algorithm which means that at each iteration more than one solution are created. The basic concept of this algorithm is natural selection that strong individuals are more survive and will also inherit their strong characteristics to their offspring.

There are two main genetic operators in this algorithm e.g. crossover and mutation. Crossover is a genetic operator which provides mechanism for the offspring to inherit characteristics of both parents. Mutation is a probabilistic

based operator, which happen to some individuals in population. By having mutation, new characteristics are introduced into the population which they don't inherit from their parents. Genetic algorithm scheme is shown in figure 2.8 [16].

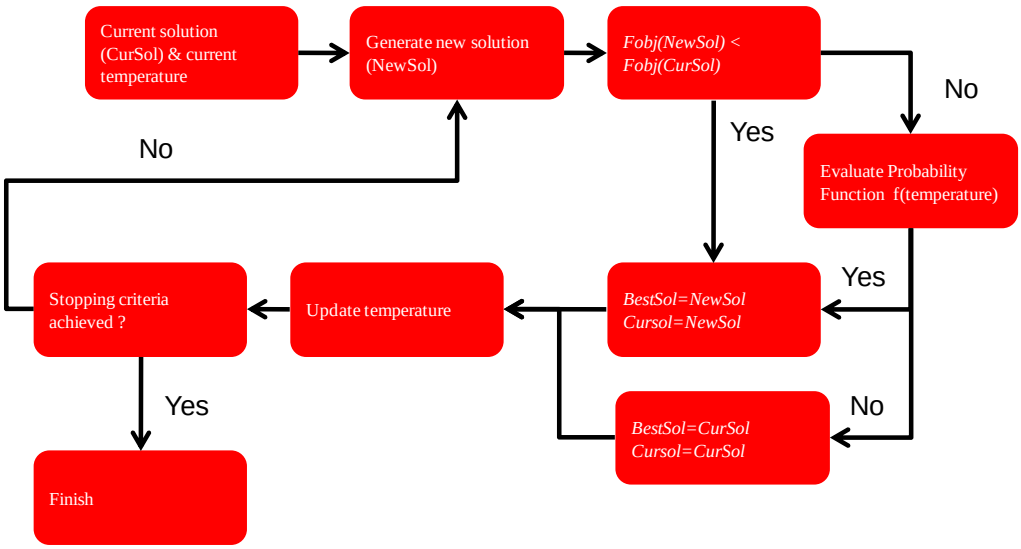


Figure 2.5 Simulated annealing algorithm workflow

2.4.3 Direct Search Algorithm

Another global optimization algorithm is direct search algorithm. Mechanism in direct search algorithm is that it searches a set of points around the current points which gives lower value of objective function than current point. At each step, the algorithm searches a set of points, called a *mesh*, around the current point. The mesh is formed by adding the current point to a scalar multiple of a set of vectors called a *pattern*. If the pattern search algorithm finds a point in the mesh that improves the objective function at the current point, the new point becomes the current point at the next step of the algorithm [16].

Figure 2.6 shows a current solution (red dot) and the rectangle which consists of four possible solutions (black dot) forms a mesh network. In each step, possible solutions in the current mesh are evaluated. The best solution will become current solution for the next iteration. Also at each iteration mesh size is always updated, basically if the current mesh could give a better solution than the current solution then the mesh size will be bigger in the next iteration, but if a better solution could not be found in the current mesh then the mesh size is reduced in the next iteration.

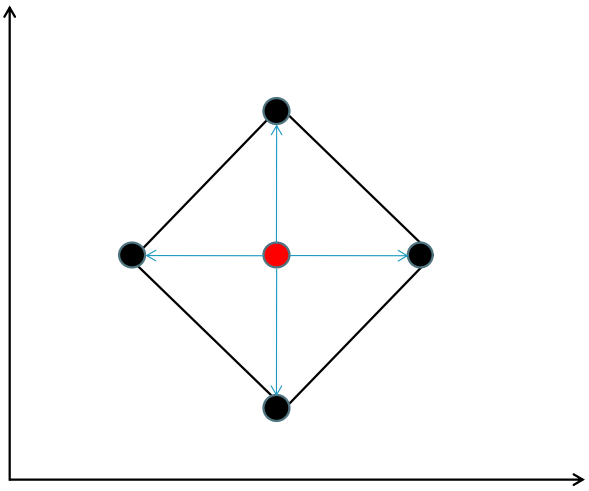


Figure 2.6 Illustration of pattern search with mesh

2.4.4 Global Search Algorithm

Global search algorithm has more complex algorithm than the three previous algorithms. Basic concept of global search is actually local solver, different trial points are generated using scatter search algorithm [17], these trial points later becomes candidate of starting point for local solver if they are likely to improve the best local minimum so far [14]. Figure 2.7 [14] is a diagram on how global search algorithm works. *Fmincon* is local solver which is used in global search collaborated with scatter search algorithm.

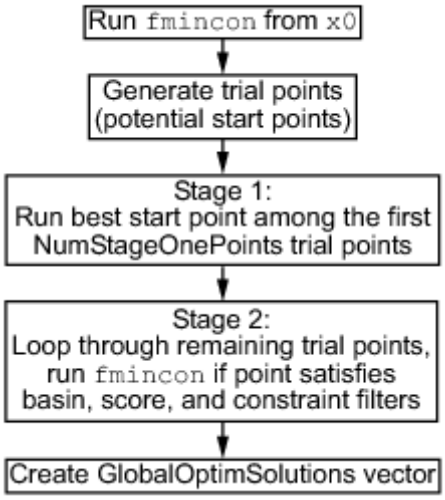


Figure 2.7 Global search algorithms workflow

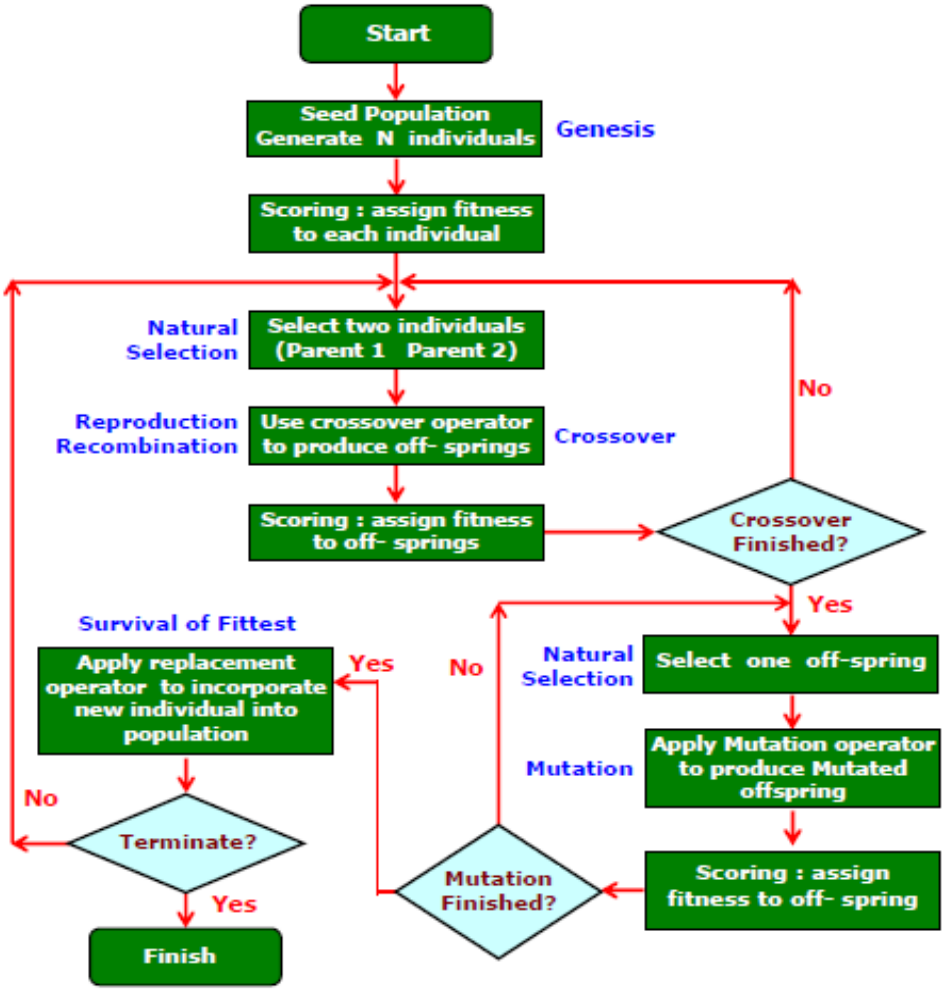


Figure 2.8 Genetic algorithm

Chapter 3

Methodology Description

3.1 Methodology Workflow

Figure 2.2 shows a general workflow of assisted history matching that is investigated in this study. There are at least 3 major components in the workflow. First is generation of experimental design, second is generation of proxy model and the last component is optimization process.

3.1.1 Initial Experiments

Initial experiments are required to build a proxy model. In AHM, common methods used are CCF, Box Behnken and Latin Hypercube design. Initial experiments play an important role in determining the quality of proxy model. Basically, more initial experiments would result in a better proxy model. In this study, two types of CCF design; fractional CCF and complete CCF are investigated.

3.1.2 Proxy Model

Proxy model replaces the role of reservoir simulation in the optimization process. Therefore, an accurate proxy model is required to have a good result from the optimization. Several methods that can be used to generate a proxy model are polynomial, kriging, EnKf and etc. In this study, only kriging and polynomial proxy model are further researched.

Proxy model is basically built from set of empirical equations, either is kriging, polynomial or other types of equation. The number of empirical equations required to build proxy model is depends on the number of response variables and time steps used. As an illustration, in this study there are 12 response variables used in history matching process with 72 number of time steps, so there are 864 empirical equations required.

3.1.3 Objective Function

In order to find a matching solution, we need to define an objective function. Equation 3.1 shows the objective function used in this study. The value of objective function shows an average percentage of error of all matching variables

and time steps. The consequence of using this objective function is not to involve zero observation data.

$$FObj = \frac{1}{p}\sum_{t=1}^{p}\left[\sum_{i=1}^{k} W_i \left| Ycalc_{i,t} - YObs_{i,t} \right| / YObs_{i,t}\right] x100\% \quad \text{..... (3.1)}$$

$FObj$ = objective function

p = number of time steps

k = number of response variables

W = weighting factor

Y_{calc} = value of observe response from proxy model

Y_{obs} = observation data

3.1.4 Global Optimization Algorithm

There are many available optimization algorithm but not all of them are powerful enough to find the most optimum solution. Some algorithms are often getting trapped in local minima before it could find the optimum solution. In this study, four algorithms that are classified as global optimization algorithm in MatLab Toolbox are researched further. Those algorithms are simulated annealing, direct search, global search and genetic algorithm.

3.2 Assisted History Matching Toolbox

In order to conduct this study, a computer program is used to run the whole workflow. Below are the main steps that need to be developed in the program:

a. Generation of experimental sampling
b. Generation of simulation input files
c. Importing simulation results and observation data
d. Generation of proxy model
e. Generation of objective function
f. Optimization

In order to do steps from point a to e, an Excel VBA based toolbox was developed. This toolbox is able to generate sampling points from some design methods e.g. complete CCF, fractional CCF, Latin hypercube, Box Behnken and Plackett-Burman. After sampling points have been generated, the next step is to write simulation input file for all those experiments. It would be time-consuming if the simulation input file is written manually for every experiment. Therefore, this step is done automatically in the toolbox. This toolbox also contains a program to import and format simulation results and

observation data before they are being processed. The main part of this toolbox is to generate proxy model from previously entered simulation results and to create an objective function. This toolbox is able to build both kriging and polynomial proxy model. The optimization of the objective function is done in MatLab by using Global Optimization Toolbox.

Chapter 4

Reservoir Model Description

4.1 Reservoir Model

In order to test methodology performance, an artificial reservoir model was developed as study case. Figure 4.1 shows a snapshot of the reservoir model. This model has grid dimension of 25 x 25 x 10 with total number of cells are 6250. There are 4 production wells and 3 injection wells in this model. All of the wells were operated since 1st January 2007. History matching should be done in this model with the observation data from 1st January of 2007 until 1st December 2012 or 72 time steps.

The model consists of 3 phases; oil, gas and water and no capillary pressure is introduced. This model is simulated in black oil simulator. The observation data are oil rate, water cut, gas oil ratio and well bottom-hole pressure of all wells. In matching process, well oil rate is a constrained variable. Set of parameters values are used to generate observation data. These values are then called as true solution which will be explained later in this chapter.

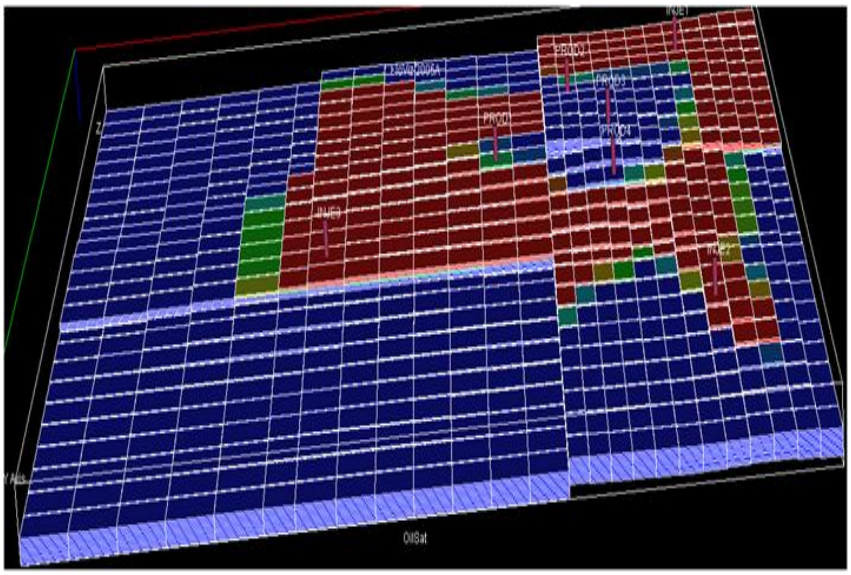


Figure 4.1 Reservoir model snapshot

4.2 Uncertain Parameters

There are 19 uncertain parameters defined in this model as shown in table 4.1. The uncertain parameters consist of 5 faults multiplier, multiplication factor of permeability in

X direction in 5 regions, porosity multiplication factor in 4 regions and 5 groups of multiplication factor of permeability in Z direction. Figure 4.2 shows the location of all 5 faults. Figure 4.3 and 4.4 shows region definitions of permeability in X direction and porosity respectively. Table 4.2 shows how groups of permeability in Z direction are classified. All of the region definition, grouping of layer and fault definition were made without any specific reason in geological point of view. The definition of uncertain parameter was purely to only generate set of parameters for history matching purpose.

Nb	Parameters Name	Range	
		Min	Max
1	MULTFLT_1	0.0001	1
2	MULTFLT_2	0.0001	1
3	MULTFLT_3	0.0001	1
4	MULTFLT_4	0.0001	1
5	MULTFLT_5	0.0001	1
6	K_MULTX_1	0.1	2
7	K_MULTX_2	0.1	2
8	K_MULTX_3	0.1	2
9	K_MULTX_4	0.1	2
10	K_MULTX_5	0.1	2
11	K_MULTZ_1	0.05	0.5
12	K_MULTZ_2	0.05	0.5
13	K_MULTZ_3	0.05	0.5
14	K_MULTZ_4	0.05	0.5
15	K_MULTZ_5	0.05	0.5
16	POR_MULT_1	1	1.5
17	POR_MULT_2	1	1.5
18	POR_MULT_3	1	1.5
19	POR_MULT_4	1	1.5

Table 4.1 Uncertain parameters with their boundary values

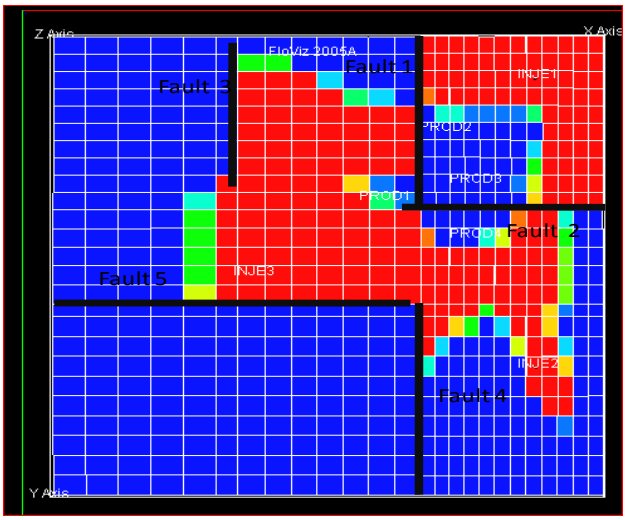


Figure 4.2 Fault definitions

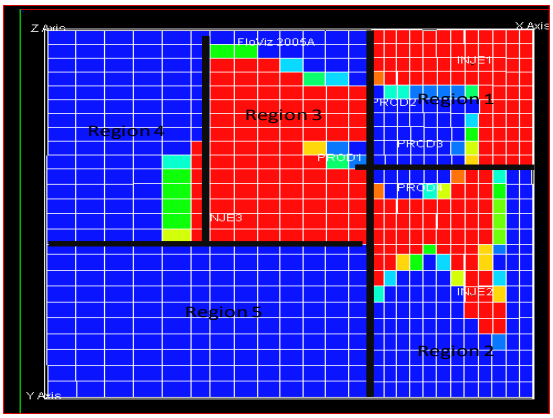


Figure 4.3 Region definitions of multiplication factor of permeability in X direction

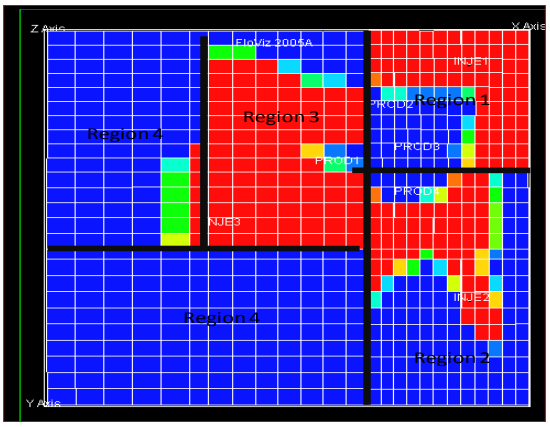


Figure 4.4 Region definitions of porosity multiplication factor

Layer	PERM_Z Group
1	1
2	2
3	3
4	4
5	5
6	
7	
8	
9	
10	

Table 4.2 Group of multiplication factor of Permeability in Z direction

4.3 Selection of Uncertain Parameters

From 19 uncertain parameters which are defined in the previous part, only at maximum 10 uncertain parameters are involved in history matching case study. This is aimed to avoid a complex history matching case when all of the uncertain parameters are involved. However, in order to have robust case study, only the most sensitive parameters are selected. Therefore sensitivity study was done to select 10 parameters out of 19 uncertain parameters.

The method used in sensitivity study is response surface method. Placket-Burman design was used to generate sample of experiments and first degree polynomial equation was

used to model the response as shown in equation 4.1. It has to be noted that the scale of all uncertain parameters have to be normalized so that the coefficient value of one parameter can be compared with the others. The response variables are cumulative production of oil, gas and water in both well and field level.

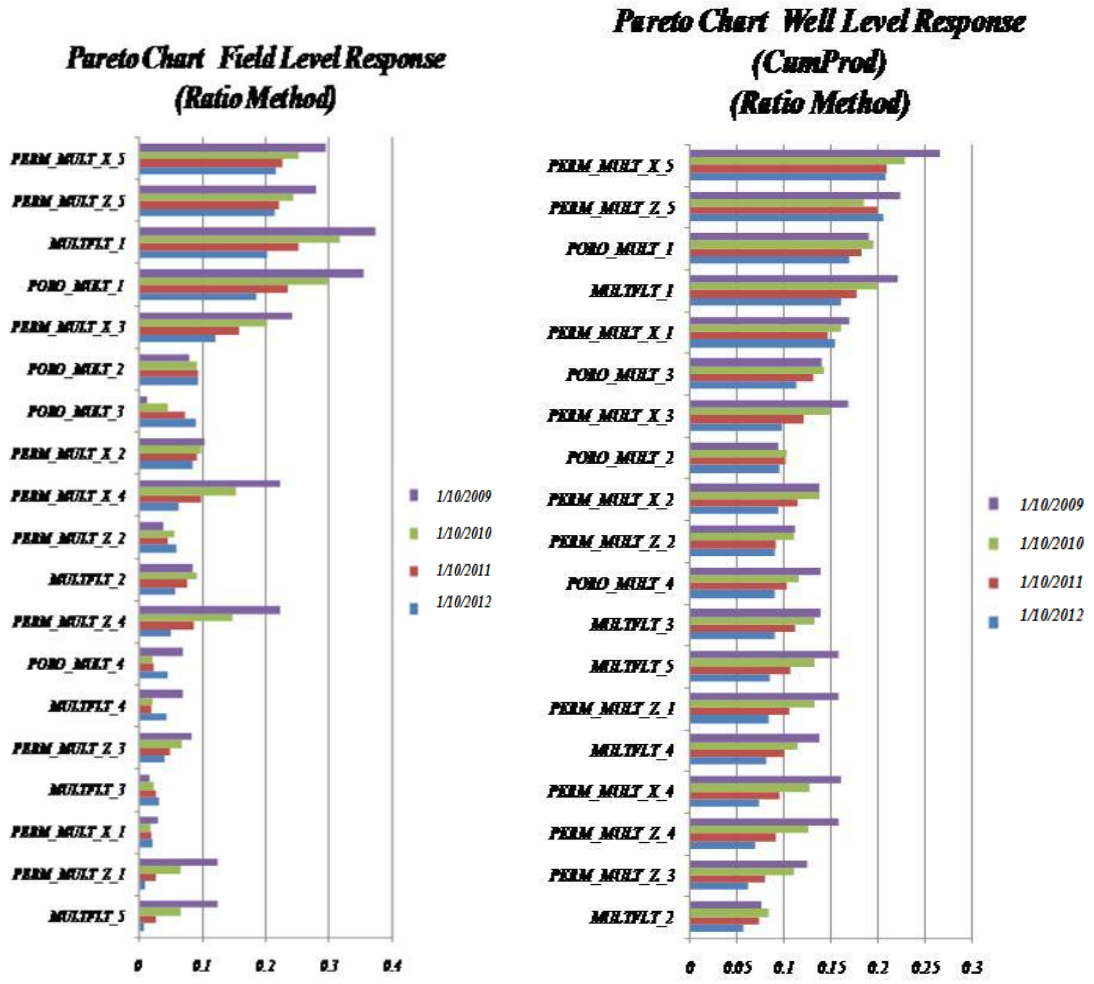
$$Y = \beta_o + \sum_{i=1}^{n} \beta_i x_i \quad \text{..........} \quad (4.1)$$

The basic concept of determining the most sensitive parameter in the response surface is by looking at the value of its coefficient in the equation. It is possible that one parameter has the biggest coefficient value in a particular time step but not in the other time steps at a particular response variable. It is also possible to find one parameter which has the biggest coefficient in one response variable but not in the other response variables at a particular time step. Therefore, to account for those variations, we need to involve all 12 response variables (WOPT, WWPT and WGPT of all 4 production wells) in well level and all 3 response variables (FWPT, FOPT and FGPT) in field level. The coefficients value of each uncertain parameter need to be normalized by dividing it with the highest coefficient value within the equation. The normalized coefficients from one response variable now can be compared with the other response variables. The sum of those normalized coefficient are shown in figure 4.5. In that figure, the sum of normalized coefficient for different time steps is also provided.

Selection of 10 most sensitive uncertain parameters is based on the sum of normalized coefficient as shown in figure 4.5. There is a consistent profile between well level and field level so that we can conveniently select 10 most sensitive uncertain parameters. The selected 10 most sensitive uncertain parameters are tabulated in table 4.3. These uncertain parameters will be used in history matching study case.

Rank	Parameter Name	Symbol
1	K_MULT_X_5	x(1)
2	K_MULT_Z_5	x(2)
3	POR_MULT_1	x(3)
4	MULTFLT_1	x(4)
5	K_MULT_X_3	x(5)
6	K_MULT_Z_4	x(6)
7	POR_MULT_2	x(7)
8	K_MULT_X_1	x(8)
9	K_MULT_X_2	x(9)
10	MULTFLT_2	x(10)

Table 4.3 10 most sensitive uncertain parameters



(a) *(b)*

Figure 4.5 Sum of normalized coefficient at different time step, well level (a) and field level (b)

4.4 Study Case Definition

In this part we will formulate two history matching study cases. First case is a simple history matching problem. It involves only 5 uncertain parameters and the other 14 parameters are assumed to be correctly predicted. Table 4.4 shows those 5 uncertain parameters and the true solution in the table is uncertain parameters value to generate observation data.

Second case is a more complex history matching problem. It involves 10 uncertain parameters and the other 9 parameters are assumed to be correctly predicted. Table 4.5 shows those 10 uncertain parameters and the true solution in the table is uncertain parameters value to generate observation data.

Nb	Parameter Name	Symbol	Range		True Solution
			Min	Max	
1	MULTFLT_1	x(1)	0.0001	1	0.00065
2	K_MULT_X_3	x(2)	0.1	2	0.87
3	K_MULT_X_5	x(3)	0.1	2	1.56
4	POR_MULT_1	x(4)	1	1.5	1.325
5	K_MULT_Z_5	x(5)	0.05	0.5	0.353

Table 4.4 Uncertain parameters of Case 1

Nb	Parameter Name	Symbol	Range		True Solution
			Min	Max	
1	MULTFLT_1	x(1)	0.0001	1	0.00065
2	K_MULT_X_3	x(2)	0.1	2	0.87
3	K_MULT_X_5	x(3)	0.1	2	1.56
4	POR_MULT_1	x(4)	1	1.5	1.325
5	K_MULT_Z_5	x(5)	0.05	0.5	0.353
6	MULTFLT_2	x(6)	0.0001	1	0.00256
7	K_MULT_X_1	x(7)	0.1	2	0.345
8	K_MULT_X_2	x(8)	0.1	2	0.856
9	POR_MULT_2	x(9)	1	1.5	1.234
10	K_MULT_Z_4	x(10)	0.05	0.5	0.125

Table 4.5 Uncertain parameters of Case 2

Chapter 5

Results Discussions

This chapter consists of three main discussion topics. The first discussion is methodology validation which comprises comparison of several methods in experimental design, proxy model and global optimization algorithm. Second discussion is about the workflow improvements which are aimed to accelerate the matching process. The matching results of the two study cases are explained in the last discussion topic.

5.1 Methodology Validation

The three main concepts which are introduced in the previous chapter e.g. experimental design, proxy model and global optimization algorithm will be studied further in this section.

5.1.2 Selection of Experimental Design Method

Initial experiments are the basis for creating a proxy model. A proxy model is represented as a second degree polynomial equation. For the purpose of this study, it is necessary to have a good proxy model. Therefore, two methods of experimental design are studied in order to investigate the accuracy of proxy model generated from each method.

R-squared and residual errors are used as the main criteria to assess the quality of proxy model. The criteria can be explained as follow:

a. R-squared

   The R squared value is a measure of how well observed outcomes are reproduced by the model, as the proportion of total variation of outcomes explained by the model. The closer the magnitude of r squared to unity then the more the correlation between proxy model and real simulation results.

b. Residual error

   In addition to r squared criteria, an accurate proxy model would also have residual error close to zero. The equation of r squared and residual error are presented in equation 5.1 and 5.2.

$$R^2 \equiv 1 - \frac{\sum_{i=1}^{n} (y_{calc,i} - y_{sim,i})^2}{\sum_{i=1}^{n} (y_{sim,i} - \bar{y}_{calc,i})^2} \quad \text{..... (5.1)}$$

$$RS(\%) = \frac{|y_{calc} - y_{sim}|}{y_{sim}} x100\% \quad \text{..... (5.2)}$$

RS = residual error

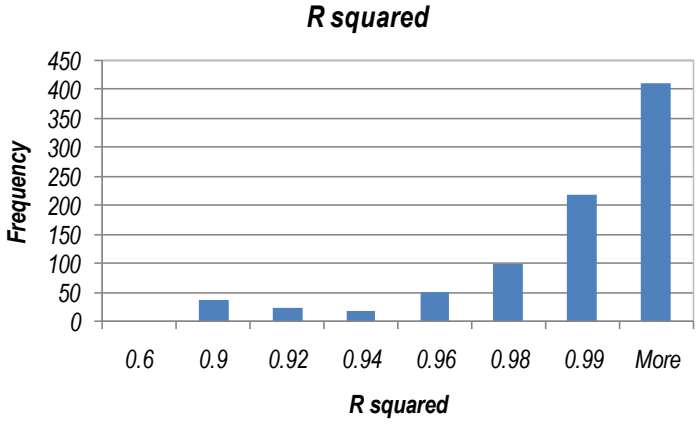
n = number of experiments

Y_{calc} = value of observe response of proxy model

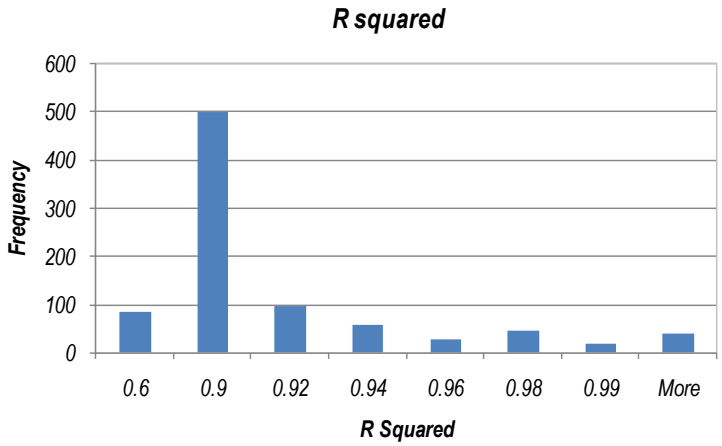
Y_{obs} = observation data

Complete CCF design is used in Case 1 which results in 43 initial experiments. For Case 2, because it involves 10 uncertain parameters, fractional CCF design is employed in order to have a practical number of initial experiments (149 initial experiments). The proxy models were generated for 12 response variables and 72 time steps.

Figure 5.1 and 5.2 show the distribution of r squared and residual error of both cases. It is shown that r squared distribution of complete CCF design is closer to unity than fractional CCF design. In addition, complete CCF design would also generate a proxy model which has smaller residual error than fractional CCF design. Therefore, complete CCF design would result in a better proxy model than fractional CCF design.

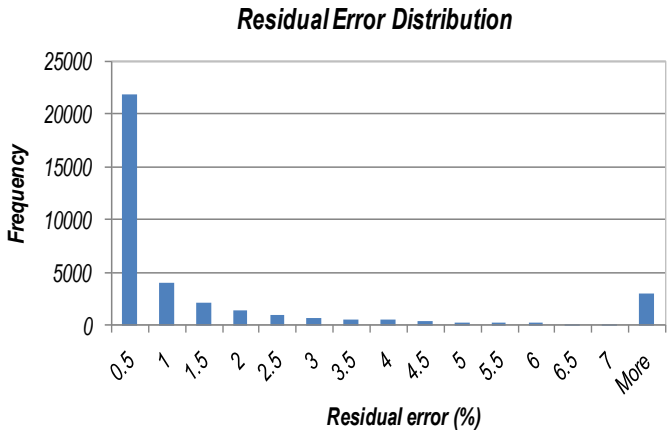


(a)

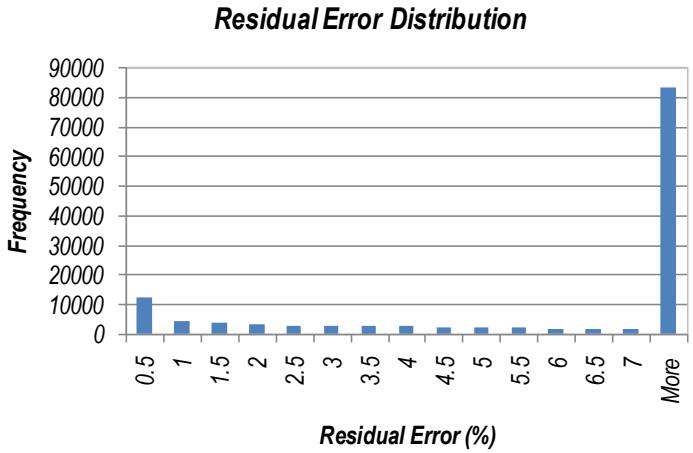


(b)

Figure 5.1 R-squared distributions of complete CCF (a) and fractional CCF (b)



(a)



(b)

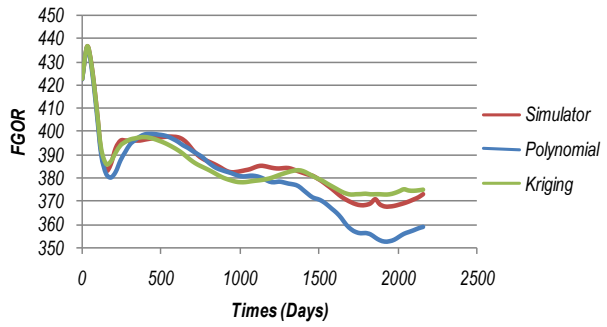
Figure 5.2 Residual error distributions of complete CCF (a) and fractional CCF (b)

5.1.3 *Selection of Proxy Model*

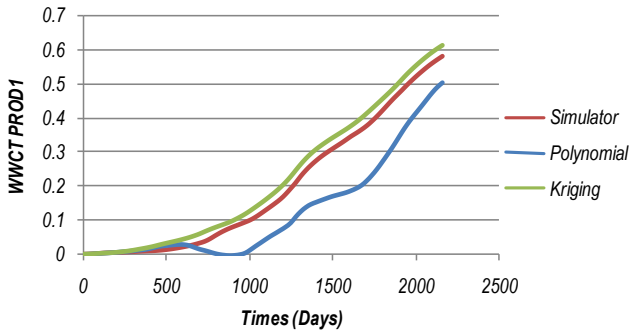
The quality of proxy model also depends on the fitting regression model. In this study there are two proxy models that are investigated e.g. second degree polynomial equation and ordinary kriging equation. The model which results in a better proxy model will be used further for matching process.

In order to select the best proxy from the two models, a comparison to the simulator is conducted. The true solution of the uncertain parameters in Case 1 and Case 2 are entered into second degree polynomial equation and kriging equation. The profiles generated from the two equations are then compared with the result from simulation.

Figure 5.3 and 5.4 shows plot of the two equations in comparison to simulation result. A good proxy model is indicated if it approaches the simulation result. From all the figures, plots of kriging show a better proxy model than second degree polynomial equation, even though in figure of Case 2 both kriging and polynomial equation have more deviation from the simulation. This deviation is due to the selection of the initial experiments design which is described in the previous part.

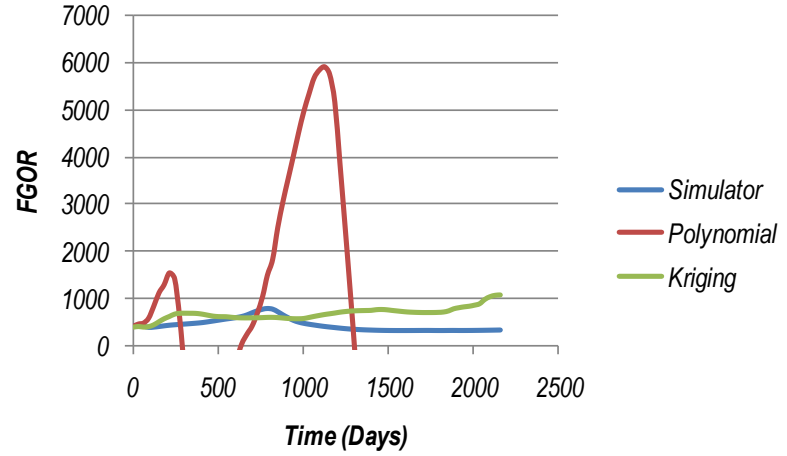


(a)

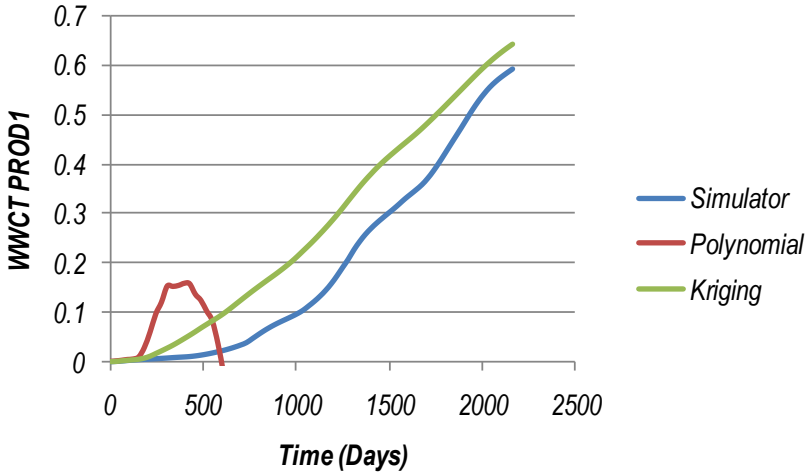


(b)

Figure 5.3 Comparison of simulation, polynomial and kriging proxy model of Case 1, FGOR (a) and WWCT PROD1 (b)



(a)



(b)

Figure 5.4 Comparison of simulation, polynomial and kriging proxy model of Case 2, FGOR (a) and WWCT PROD1 (b)

5.1.4 Selection of Global Optimization Algorithm

Another important aspect in the assisted history matching is selection of optimization algorithm. Four global optimization algorithms e.g. simulated annealing, direct search, genetic and global search algorithm are studied in order to select the best algorithm.

As explained in the previous part, none of the proxy model would result in identical profiles with simulation (zero residual error). Therefore before the optimization is performed, the proxy model should be firstly corrected. In order to correct the proxy model, simulation of the true solution is entered in the initial experiments which build the proxy model. By doing this correction, we could

expect that the solution generated from the optimization has to be close to the true solution.

Algorithm properties

In general, most properties of all algorithms are set as their default value in MatLab Global Optimization Toolbox. Below are some changes that were made in this study:

a. Maximum iteration (or generations for genetic algorithm) is 1000
b. Number of population for genetic algorithm is 50
c. Minimum changes of objective function value is 1e-6

Each of algorithms is given five attempts to find the true solution. In order to have a robust optimization process, the initial solution is set to be random. The summary of the optimization process are shown in Table 5.1 and 5.2. The main comparison parameters are the value of objective function and the optimization time. The best algorithm is the one which could generate smallest objective function in a short processing time.

The optimization process of Case 1 can be seen in table 5.1. Global search algorithm gives the least value of objective function around 0.0001 but it needs 200 second for one attempt of optimization. Direct search algorithm also generates a small objective function less than 0.01 but with shorter processing time (27 seconds) than global search algorithm. The optimization process of direct search algorithm stopped because the changes in objective function have reached the minimum value. From five optimization attempts done by genetic algorithm, only one generates a solution which is close to the true solution. Genetic algorithm needs 46 seconds of optimization process before it stopped because of reaching the minimum change of objective function. Simulated annealing algorithm appears to be the worst since none of the generated solutions are close to the true solution. It stopped the optimization process because maximum number of iteration is reached. This is an indication that the convergence rate is slow.

Nb	Algorithm	x(1)	x(2)	x(3)	x(4)	x(5)	Fobj	Times(s)	Stop Crit
1	Global search	0.000649999	0.8700017	1.56	1.325	0.353	1.72E-05	200	Alltrials
2	Global search	0.00065	0.87000007	1.559998	1.325	0.353	1.05E-05	200	Alltrials
3	Global search	0.00065	0.87000073	1.56	1.325	0.353	1.19E-05	200	Alltrials
4	Global search	0.000649998	0.87000028	1.56	1.325	0.353	1.38E-05	200	Alltrials
5	Global search	0.000649999	0.87000055	1.559999	1.325	0.353	8.14E-06	200	Alltrials
1	Genetic algorithm	0.004132939	1.23484883	1.146626	1.36869	0.39014	3.726098	46	TolfFun
2	Genetic algorithm	0.000674073	0.9038489	1.543903	1.329277	0.357998	0.284454	46	TolFun
3	Genetic algorithm	0.000913767	0.94395333	1.501239	1.334652	0.362604	0.902614	46	TolfFun
4	Genetic algorithm	0.006228798	1.32076376	1.10649	1.381137	0.393608	4.30994	46	TolFun
5	Genetic algorithm	0.011179801	1.32675024	0.948703	1.386102	0.392564	4.95339	46	TolfFun
1	Direct search	0.000650248	0.87005806	1.559943	1.325008	0.353006	0.00105	27	TolFun
2	Direct search	0.000650408	0.87009517	1.559903	1.325012	0.353012	0.001724	27	TolfFun
3	Direct search	0.000650533	0.87012468	1.559876	1.325016	0.353017	0.002249	27	TolFun
4	Direct search	0.000649599	0.87010993	1.559875	1.325016	0.353008	0.002223	27	TolfFun
5	Direct search	0.000650363	0.87008247	1.559912	1.32501	0.353011	0.001534	27	TolFun
1	Simulated annealing	0.000775543	1.5581136	1.219487	1.391552	0.400931	3.28763	23	MaxIter
2	Simulated annealing	0.000918517	1.20624706	0.811455	1.36506	0.404037	3.285074	23	MaxIter
3	Simulated annealing	0.000727552	1.59748472	1.188983	1.384063	0.408414	3.342493	23	MaxIter
4	Simulated annealing	0.000702122	1.24751112	1.290606	1.353095	0.395194	2.178067	23	MaxIter
5	Simulated annealing	0.072340417	1.81757954	1.443165	1.435495	0.407474	6.497023	23	MaxIter
	True Solution	0.00065	0.87000	1.56000	1.32500	0.35300			

Table 5.1 Optimization process summary of Case 1

The optimization process of Case 2 with 10 uncertain parameters appears is more complex than Case 1 where only 5 uncertain parameters are involved. Table 5.2 shows the optimization process summary of Case 2. Only direct search algorithm which is able to find small objective function and provide solutions which are close to the true solution. The optimization time required for direct search algorithm to find the solution is 62.2 seconds. It is longer than Case 1 due to the complexity of Case 2.

From the above facts, it is recommended to use direct search algorithm for the history matching. It appears to be the most effective algorithm able to find the true solution. Global search algorithm could only find the true solution in a less complex case even with longer optimization time. Genetic algorithm for the above case is often trapped in local minima since it always reaches the minimum change of objective function before it could find the true solution. Simulated annealing algorithm shows a slow convergence rate with the fact that it always reaches maximum number of iterations before it could find the true solution.

Nb	Algorithm	x(1)	x(2)	x(3)	x(4)	x(5)	x(6)	x(7)	x(8)	x(9)	x(10)	Fobj	Times(s)	Stop Crit
1	Global search	0.00010	0.10001	0.49999	1.49999	0.10000	0.99989	1.99983	1.99983	1.49998	0.05000	3572.95050	1380	Alltrials
2	Global search	0.00010	0.10000	0.49995	1.49999	0.10000	0.99988	1.99989	1.99981	1.49998	0.05000	3572.95782	1380	Alltrials
3	Global search	0.00010	0.10001	0.49998	1.49999	0.10000	0.99959	1.99991	1.99995	1.49999	0.05000	3572.99220	1380	Alltrials
4	Global search	0.00010	0.10001	0.49998	1.49998	0.10000	0.99977	1.99995	1.99982	1.49998	0.05000	3572.96397	1380	Alltrials
5	Global search	0.00010	0.10000	0.49994	1.49999	0.10000	0.99993	1.99993	1.99985	1.49998	0.05000	3572.96283	1380	Alltrials
6	Genetic algorithm	0.01864	0.76731	1.27083	1.36046	0.28833	0.03539	0.44276	1.11372	1.28449	0.12044	93071.25	36.2	TolFun
7	Genetic algorithm	0.05427	0.78495	1.31523	1.38377	0.29193	0.01007	0.37476	1.33330	1.23284	0.12147	96603.61	36.2	TolFun
8	Genetic algorithm	0.00108	0.12309	0.48171	1.49673	0.10351	0.73999	1.84794	1.96916	1.49750	0.05627	64016.27	36.2	TolFun
9	Genetic algorithm	0.02998	0.78346	1.25725	1.33457	0.28234	0.02716	0.46541	1.13670	1.25692	0.10015	95543.44	36.2	TolFun
10	Genetic algorithm	0.00533	0.86097	1.46500	1.33910	0.33009	0.00720	0.34953	0.92934	1.23640	0.12272	64074.36	36.2	TolFun
11	Direct search	0.00065	0.86999	1.55999	1.32500	0.35300	0.00256	0.34500	0.85602	1.23400	0.12500	33.00446	62.2	TolFun
12	Direct search	0.00065	0.87000	1.56000	1.32500	0.35300	0.00256	0.34500	0.85601	1.23400	0.12500	9.77914	62.2	TolFun
13	Direct search	0.00065	0.87000	1.56000	1.32500	0.35300	0.00256	0.34500	0.85600	1.23400	0.12500	4.43425	62.2	TolFun
14	Direct search	0.00065	0.87000	1.56000	1.32500	0.35300	0.00256	0.34500	0.85600	1.23400	0.12500	10.52318	62.2	TolFun
15	Direct search	0.00065	0.86999	1.55998	1.32500	0.35299	0.00256	0.34500	0.85602	1.23400	0.12500	39.23555	62.2	TolFun
16	Simulated annealing	0.00010	0.15104	0.55180	1.39247	0.10841	0.00010	1.18221	1.23690	1.40065	0.42392	70999.33	28.2	MaxIter
17	Simulated annealing	0.00010	0.10709	0.67161	1.49111	0.09909	0.54938	1.48366	1.85853	1.49706	0.05018	42681.82	28.2	MaxIter
18	Simulated annealing	0.00018	0.48854	0.67556	1.34391	0.20432	0.00170	0.32917	1.80570	1.20756	0.11723	76021.41	28.2	MaxIter
19	Simulated annealing	0.00010	0.10451	0.74482	1.49327	0.10021	0.46375	1.50302	1.92220	1.48060	0.05351	48467.08	28.2	MaxIter
20	Simulated annealing	0.00044	0.54265	1.23617	1.36031	0.36563	0.00236	0.67041	1.62686	1.26684	0.12294	69634.66	28.2	MaxIter
	True Solution	0.00065	0.87000	1.56000	1.32500	0.35300	0.00256	0.34500	0.85600	1.23400	0.12500			

Table 5.2 Optimization process summary of Case 2

5.2 Improvement of the Existing Workflow

Previous discussion shows that the most important point in this methodology is to have an accurate proxy model. Once accurate proxy model has been created, direct search algorithm would be able to find the true solution.

The use of kriging equation has been introduced in the previous section in order to have a better proxy model. In addition, complete CCF is always a recommended design if there is no practical issue of simulating many experiments.

5.2.1 Selection of Response Variables

The selection of response variable is based on the performance of the proxy model. Response variables which have an accurate proxy model will be selected as the matching variables.

Since the quality of kriging proxy model can't be measured from the initial experiments, the selection is based on second degree polynomial equation. Having known from the previous explanation that kriging proxy model has a better quality than second degree polynomial equation, the selection based on polynomial equation is valid. The average residual error distribution of initial experiments is used as the assessment criteria of proxy model. Equation 5.1 shows the formula to calculate average residual error.

$$\bar{\varepsilon}_j = \frac{1}{p}\sum_{t=1}^{p}\left[\sum_{i=1}^{k} W_i \left| Ycalc_{i,t} - Ysim_{i,t} \right| / Ysim_{i,t}\right] x100\% \quad \text{..... (5.3)}$$

$\bar{\varepsilon}_j$ = average residual error of experiment j

p = number of time steps

k = number of response variables

W = weighting factor

Y_{calc} = value of observe response of proxy model

Y_{sim} = value of observe response of simulation

Below are examples of the selection process of Case 1 and Case 2:

a. Case 1

   At the beginning there are 12 response variables which will be used as matching variables. Those variables are WWCT, WGOR and WBHP of all four production wells with the same weighting factor. Average residual error is calculated for 72 time steps. Figure 5.5 shows the distribution of average residual error of 43 initial experiments. Most of the experiments have small average residual error. Therefore, all the 12 response variables could be used as the matching variables.

b. Case 2

   The same 12 response variables are used in Case 2 as candidates of matching variables. The weighting factor of all of response variables is set to be equal and average residual error is calculated for 72 time steps. As shown in figure 5.6, the average residual error is big. Therefore in Case 2, selection process is conducted in order to choose only those response variables which have a better proxy model. After analyzing average residual error of individual response variable, only WBHP of production well 1 and production well 4 are selected as matching variables since their average residual error is small, as shown in figure 5.7.

5.2.2 Modified objective function

The selection process in the previous part is aimed to select only responses variables which are accurately predicted by the proxy model. However, the proxy model still has some errors. This error has to be reduced in order to have a better proxy model.

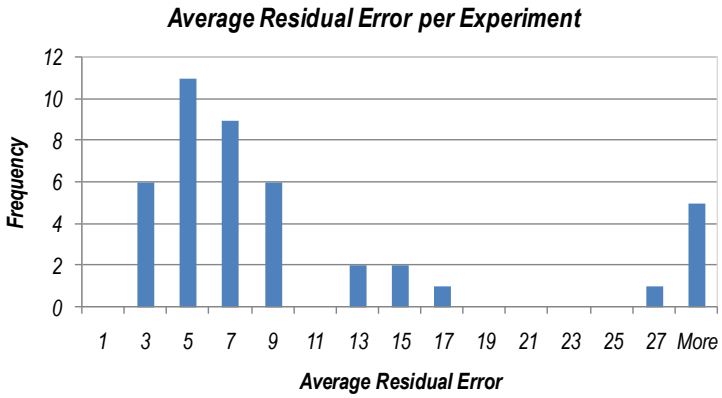


Figure 5.5 Average residual errors of 12 response variables of Case 1

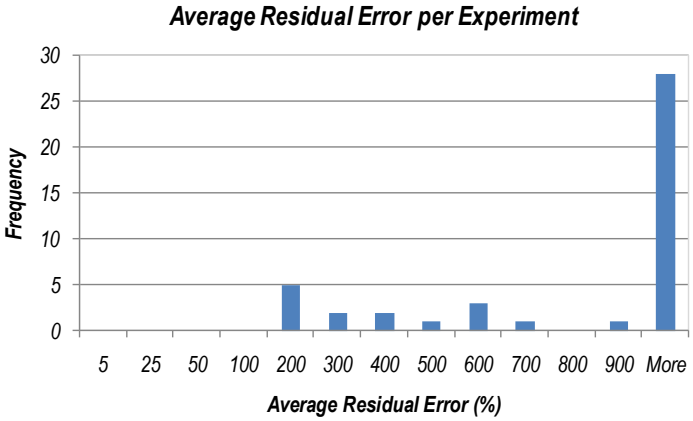


Figure 5.6 Average residual errors of 12 response variables of Case 2

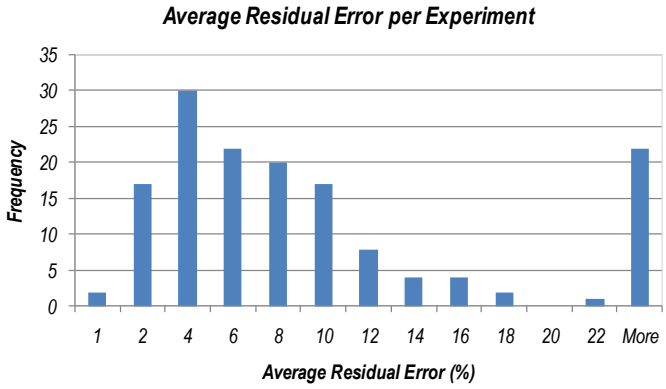


Figure 5.7 Residual error distributions of WBHP PROD1 and WBHP PROD4 of Case 2

To improve the quality of kriging proxy model, additional experiments are required. These additional experiments are supposed to be close to the matching solution so that the proxy model could predict accurately the response variables of matching solution.

These additional experiments are obtained from the optimization process. There are two options which can be used to generate additional experiments that are explained as follow:

a. Optimization process without proxy error

   In this option, optimization is aimed to minimize the previously defined objective function. By setting different initial solution in the optimization process, different optimum solutions could be obtained even though there is always a possibility of getting identical solutions. This option has been introduced in the existing methodology.

b. Optimization process with proxy error

   Knowing the proxy model still has some errors; minimizing the objective function might not generate solutions which are close to the matching solution. Therefore, a modification is required in the objective function by introducing average proxy error term. The modified objective function is shown in equation 5.2. The optimization process now can generate different solutions by minimizing new objective function with different inputs of average proxy error.

$$FObj = \left| \frac{1}{p} \sum_{t=1}^{p} \left[\sum_{i=1}^{k} W_i \left| Ycalc_{i,t} - Yobs_{i,t} \right| / Yobs_{i,t} \right] x100\% - \bar{\varepsilon}_p \right| \quad \ldots\ldots\ldots\ldots \quad (5.4)$$

$FObj$ = objective function

$\bar{\varepsilon}_p$ = average proxy error

p = number of time steps

k = number of response variables

W = weighting factor

Y_{calc} = value of observe response of proxy model

Y_{obs} = observation data

In real case, since the true solution is unknown, the true value of average proxy error is also unknown. The true average proxy error is the error of proxy model with respect to the true solution. Figure of average residual error distribution of initial experiments can be used as the basis for estimating the true average proxy error. From figure 5.5, the true average proxy error of Case 1 is expected to be in the range between 0 to 15%. From figure 5.7, the true average proxy error of Case 2 is expected to be in the range between 0 to 16%.

A study is performed to determine which option reduces the true average proxy error most. Case 2 is selected as case study. The true average proxy error of WBHP PROD 1 and WBHP PROD4 from the initial experiments is 6.2%.Optimization process is performed with and without introducing average proxy error in objective function. The optimization is aimed to generate 6 solutions in each option. Table 5.3 shows values of average proxy error which form the input set of the objective function.

Solution	$\bar{\varepsilon}_p$ (%)
1	15
2	14
3	13
4	12
5	11
6	0

Table 5.3 Average proxy errors used in the objective function

Option	True average proxy error (%)
Without average proxy error	6.05
With average proxy error	5.83

Table 5.4 True average proxy error after additional experiments

Table 5.4 shows how the true average proxy error is reduced after the additional experiments. It is clearly concluded that by introducing residual error in the objective function, the solutions generated from the optimization are able to improve proxy model more than if no residual error is introduced in the objective function.

After all of the above analysis, the existing workflow of assisted history matching is modified as shown in figure 5.8. The main modifications are selection of matching variables, introduction of average proxy error in objective function and preference of using kriging proxy model and direct search algorithm in the optimization process. These changes are highlighted in blue boxes.

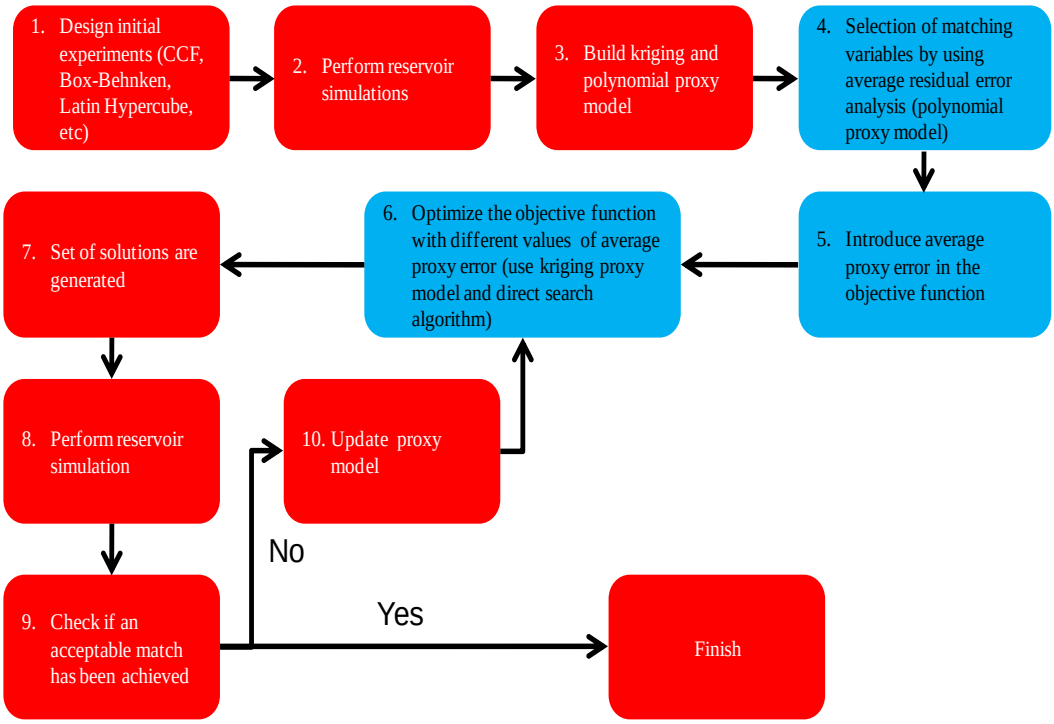


Figure 5.8 New indirect assisted history matching workflow

5.3 History Matching Results

The new workflow is used to solve two history matching cases. The first case is a simple history matching problem with only 5 uncertain parameters involved. If the methodology successfully solves the first case then it will be tested with Case 2 with 10 uncertain parameters. Detail of both cases can be seen in chapter 4.

5.3.1 Matching of Case 1

To solve Case 1 complete CCF design is used to produce initial experiments. This design generates 43 initial experiments with 5 uncertain parameters. Both kriging and second polynomial proxy model are constructed from the initial experiments. Residual analysis of second degree polynomial proxy model is then used as the basis of selection of matching variables. From the previous, all of the 12 response variables can be used as matching variables. Those 12 matching variables are WBHP, WGOR and WWCT of all four production wells. The selected range of residual error to be applied in objective function is from 0 % to 15%. For the optimization process, kriging proxy model and direct search algorithm are used.

An acceptable match is obtained after seven matching steps with 34 additional simulation runs. Plots of history matching are shown in figure 5.9 to figure 5.12. As shown in that figure, the best matching solution almost has an identical profile

as the observation data. The best matching solution and the true solution are shown in table 5.5. It is seen in that table that the best matching solution is close to the true solution.

Another interesting point is shown in table 5.6. This table shows the evolution of the true residual error in every matching step. Initially kriging proxy model has 14.5% true average proxy model and with the inclusion of average proxy error in the objective function, the true average proxy error is reduced to 2.8% in 7th matching step. The best matching solution is found at 7th matching step. This proves the initial hypothesis that the matching solution can only be found if the proxy model contains small average proxy error.

Run	x(1)	x(2)	x(3)	x(4)	x(5)
Matching Solution	0.001976	0.87252117	1.476626	1.325684	0.350288
True Solution	0.00065	0.87	1.56	1.325	0.353

Table 5.5 Best matching solution and true solution of Case 1

Matching Step	Residual error (%)
1	14.5366
2	13.1175
3	10.0618
4	6.9583
5	5.7774
6	3.5042
7	2.887

Table 5.6 Evolution of true average proxy error of Case 1

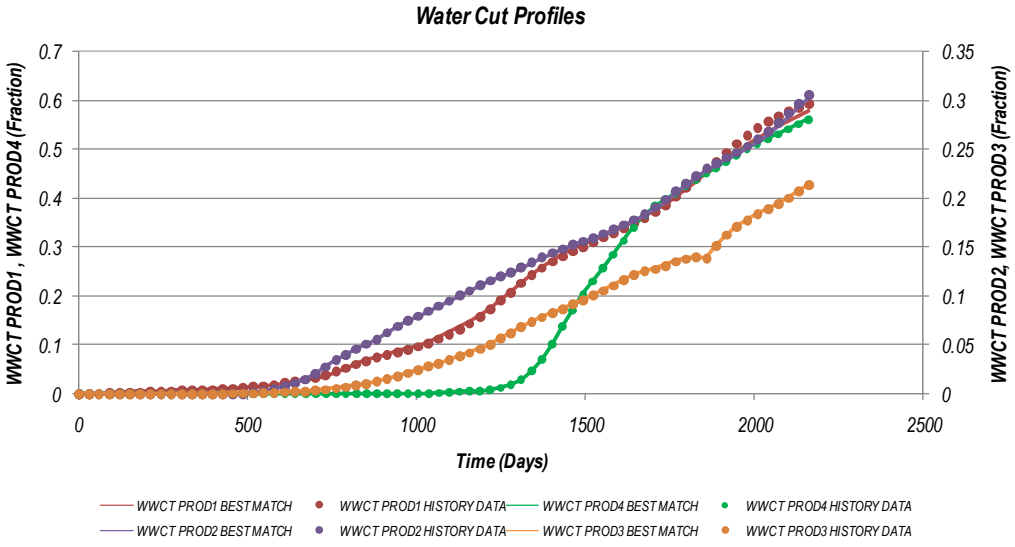


Figure 5.9 Well water cut profile of Case 1

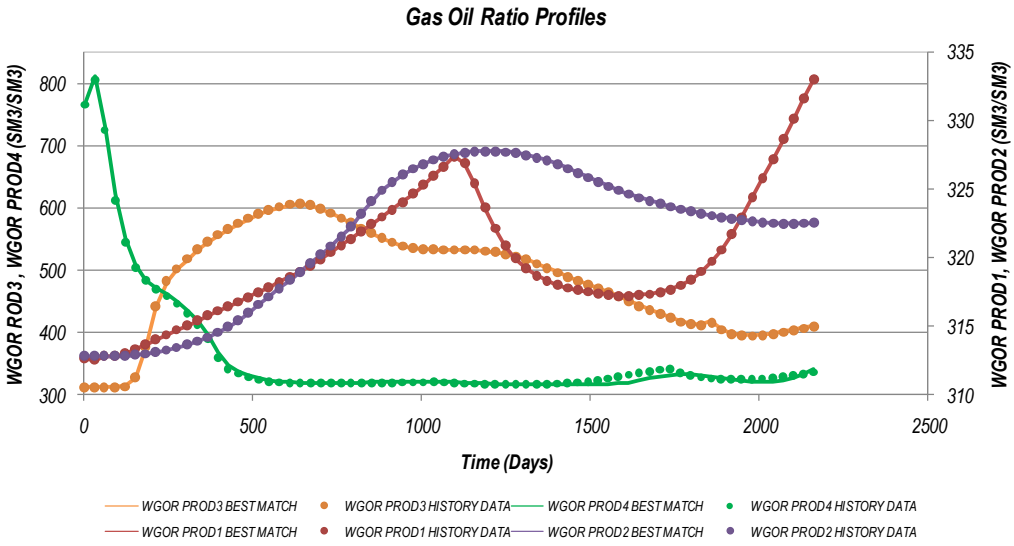


Figure 5.10 Well gas oil ratio profile of Case 1

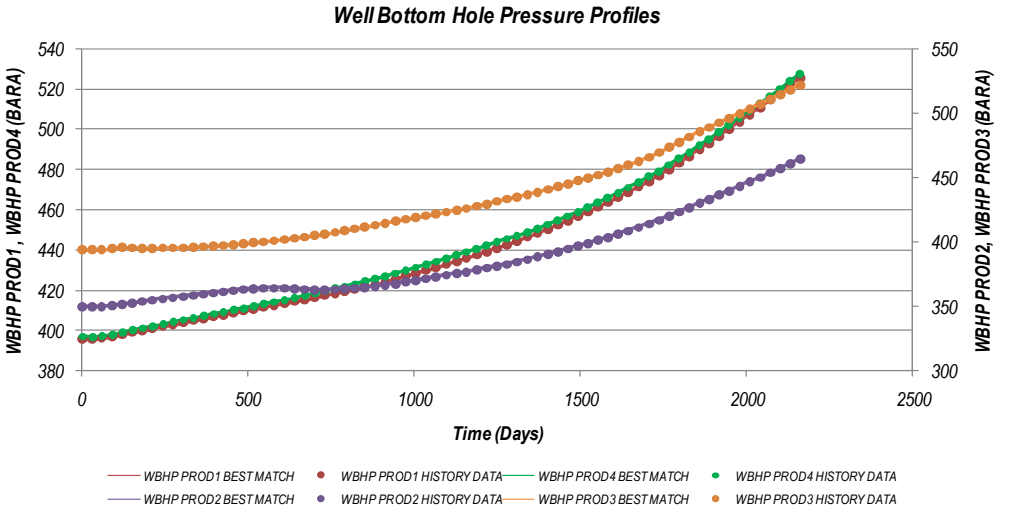


Figure 5.11 Well bottom hole pressure profile of Case 1

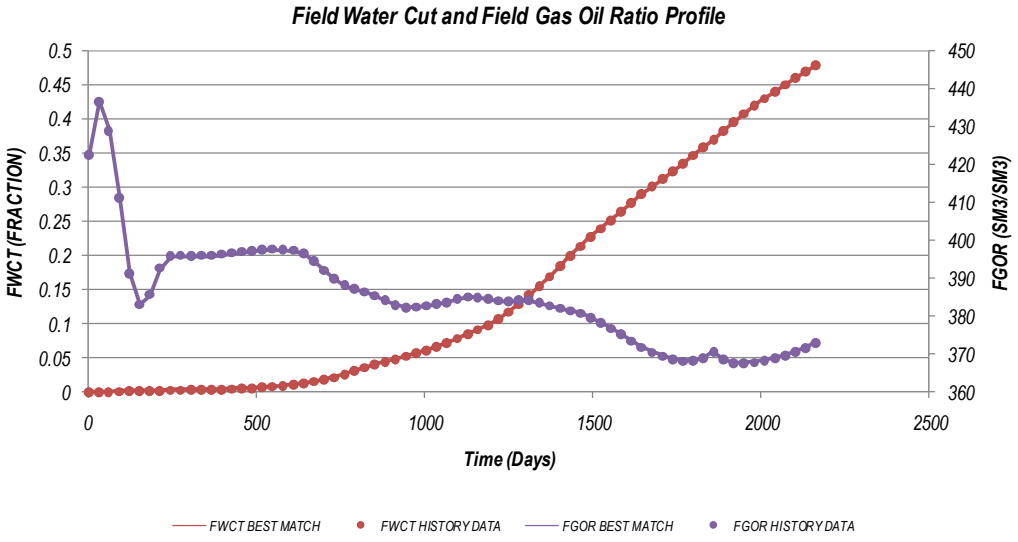


Figure 5.12 Field water cut and field gas oil ratio profile of Case 1

5.3.2 Matching of Case 2

Following the successful of matching process in Case 1, the methodology is challenged to solve a more complex case which involves 10 uncertain parameters. Due to the practical issue, complete CCF design can't be used in this case. As a result, fractional CCF design is used with 149 initial experiments.

From the selection of matching variables analysis, the usage of 12 matching variables would result a huge residual error. There are only proxy model of WBHP PROD1 and WBHPR PROD2 which have small residual error. Therefore those two variables become matching variables and oil production rate is constrained. From the analysis of residual error as shown in figure 5.7 the range of residual error is considered from 0 % to 16 %.

Since Case 2 is more complex than Case 1, the matching process also requires more matching steps and more additional simulation runs. In addition, the matching process in this case is slightly different from Case 1. The optimization process initially used parameters boundary as being defined in chapter 4. But looking at the fact that the matching solution still has not yet been found until 15 matching steps therefore sampling distribution analysis is conducted.

In sampling distribution analysis is we analyze the distribution of uncertain parameters value of all solutions given by the optimization. The objective is to identify the non explored value's range of each uncertain parameter by the optimization algorithm. The analysis in this study involves 100 solutions generated from first matching step until 15^{th} matching step. The result of the analysis is that there are three parameters which are not fully explored due to the limitation of optimization algorithm. Figure 5.13 shows the distribution of the value of the three parameters which are not fully explored. Figure 5.13(a) and (b) shows the distribution of value of x (1) and x (6), it is clearly identified that value less than 0.01 are not explored yet. Figure 5.13 (c) shows that values between 1.129 and 1.5 are not fully explored. Table 5.9 shows the modification of parameters boundary after sampling distribution analysis.

The revision of parameters boundary give a positive impact on the reduction of true average proxy error. The initial true average proxy error is 6.2%. Before the boundary revision the error reduction rate is only 0.09% per matching step but after boundary revision reduction rate is 3.86% per matching step. In conclusion,

sampling distribution analysis is a useful tool to evaluate the results of the optimization process. The true average proxy error evolution is shown in table 5.7. An acceptable match finally is achieved at 27th matching step. There are 183 additional simulation runs in addition to 149 initial simulation runs to obtain this match. Figure 5.14 to 5.17 show the history matching plots of Case 2. Table 5.8 shows the best matching solution. It is clearly noticed that in general the matching quality is less than matching quality in Case 1, only WBHP PROD1 and WBHP PROD4 perfectly match the observation data. The involvement of only those two matching variables could explain this phenomenon. This selective process of response variables has an advantage of avoiding long matching step to reduce a huge initial proxy error but in the other hand it can also produce a matching solution which only matches with those matching variables.

Matching Step	Residual Error (%)
1	6.20
2	5.89
3	5.63
4	5.31
5	5.27
6	4.76
7	4.69
8	4.63
9	4.61
10	4.45
11	4.42
12	4.35
13	4.22
14	4.16
15	4.75

Matching Process	Residual Error (%)
16	4.72
17	4.69
18	3.92
19	3.41
20	3.32
21	1.81
22	1.36
23	0.93
24	0.87
25	0.77
26	0.70
27	0.86

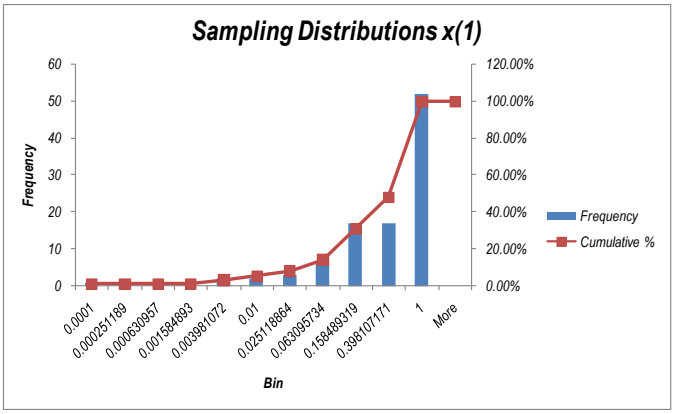
Table 5.7 Evolution of true average proxy error of Case 2, before boundaries revision (left) and after boundaries revision (right)

Run	x(1)	x(2)	x(3)	x(4)	x(5)	x(6)	x(7)	x(8)	x(9)	x(10)
Matching Solution	0.00100	0.91574	0.24151	1.41528	0.50000	0.00207	0.43098	0.84344	1.29000	0.16309
True Solution	0.00065	0.87000	1.56000	1.32500	0.35300	0.00256	0.34500	0.85600	1.23400	0.12500

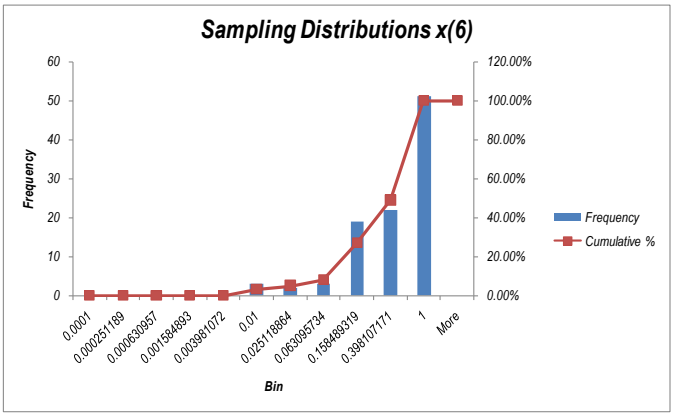
Table 5.8 Best matching solution and true solution of Case 2

Nb	Parameter Name	Parameter symbol	Old Boundary		New Boundary	
			Min	Max	Min	Max
1	MULTFLT_1	x(1)	0.0001	1	0.0001	0.01
2	MULTX_3	x(2)	0.1	2	0.1	2
3	MULTX_5	x(3)	0.1	2	0.1	2
4	MULTPV_1	x(4)	1	1.5	1	1.5
5	MULTZ_5	x(5)	0.05	0.5	0.05	0.5
6	MULTFLT_2	x(6)	0.0001	1	0.0001	0.01
7	MULTX_1	x(7)	0.1	2	0.1	2
8	MULTX_2	x(8)	0.1	2	0.1	2
9	MULTPV_2	x(9)	1	1.5	1.129	1.5
10	MULTZ_4	x(10)	0.05	0.5	0.05	0.5

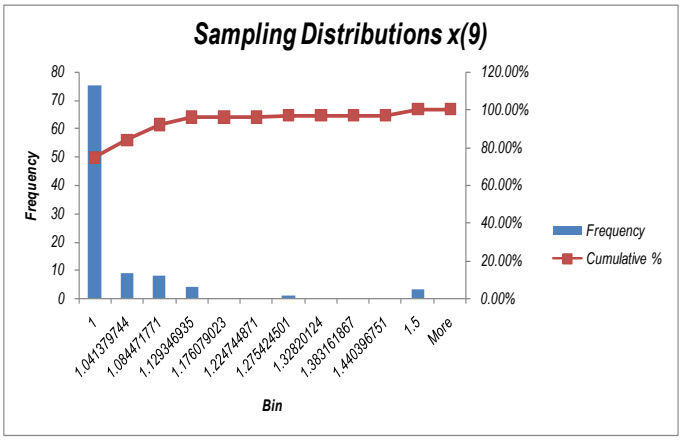
Table 5.9 New parameter boundaries, modified boundaries are highlighted in green color



(a)



(b)



(c)

Figure 5.13 Sampling distribution of parameter x1 (a), x6 (b) and x9 (c)

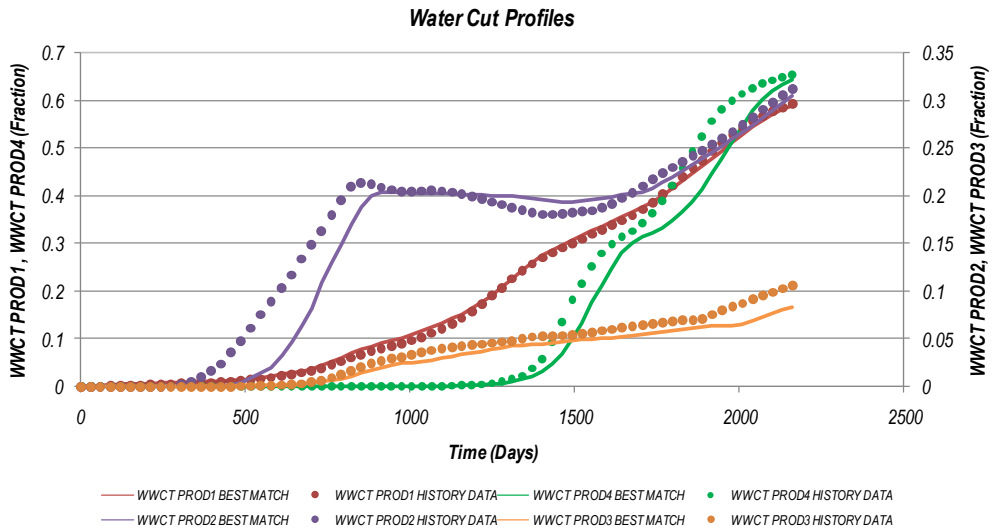


Figure 5.14 Well water cut profile of Case 2

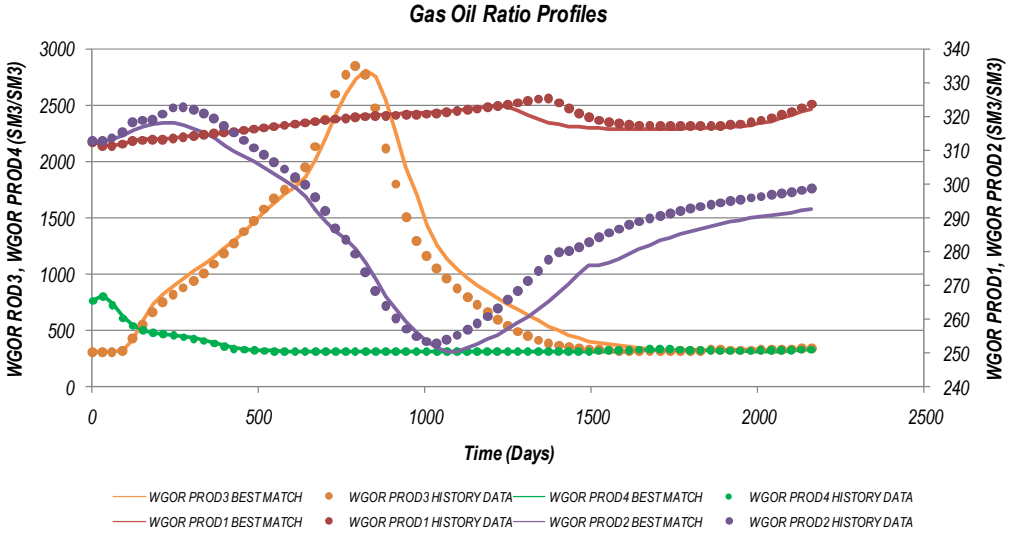


Figure 5.15 Well gas oil ratio profile of Case 2

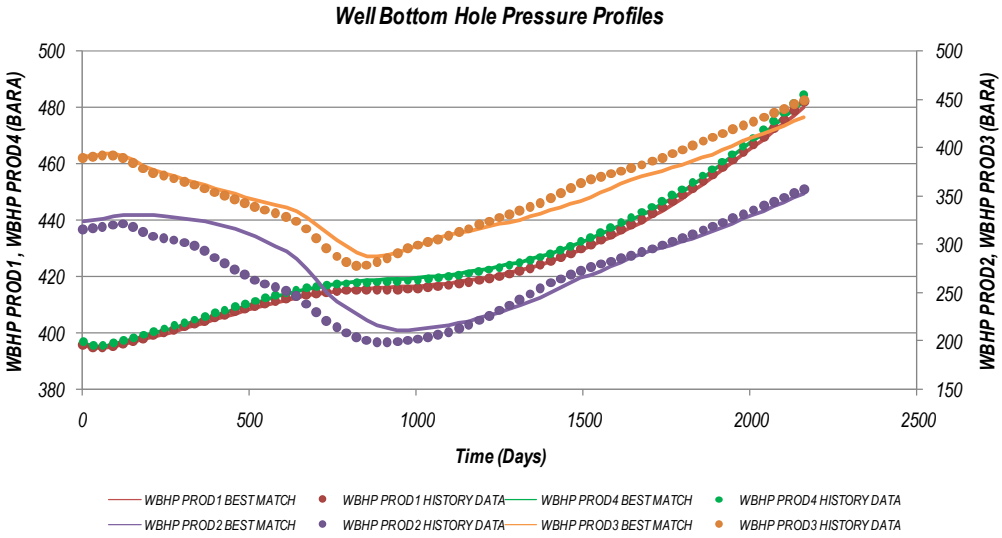


Figure 5.16 Well bottom hole pressure profile of Case 2

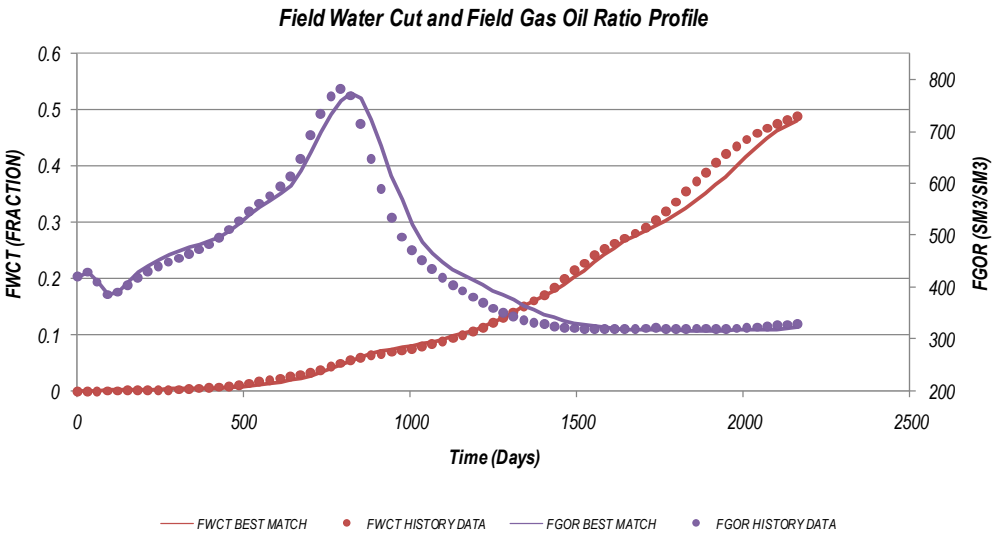


Figure 5.17 Field water cut and field gas oil ratio profile of Case 2

Chapter 6

Summary and Future Work

In this thesis, an investigation of computer assisted history matching is performed. A comprehensive understanding of the subject is required to identify methodology limitations so that improvements can be introduced in order to accelerate matching process. This study also compares two types of proxy models e.g. kriging equation and second degree polynomial equation which are used in the optimization process. Different global optimization algorithms were also investigated in order to determine the best performance algorithm in solving history matching problem.

6.1 Summary and Conclusions

a) The quality of proxy model plays an important role in assisted history matching. Optimization algorithm is able to find the matching solution only if the proxy model accurately predicts reservoir simulation responses.

b) Proxy model is initially built from a set of initial sample of experiments. The quality of this initial proxy model depends on the sampling method. This study shows that complete CCF design could generate a better proxy model than fractional CCF design.

c) Different types of proxy model have different degree of accuracy in predicting reservoir simulation. Kriging proxy model is able to predict reservoir simulation more accurately than second degree polynomial equation.

d) The initial proxy model always has some error. This error must be minimized so that the optimization algorithm is able to find a good match. This error can be reduced by adding more experiments in the population which build the proxy model. The additional experiments have to be located close to the matching or true solution so that kriging proxy model can predict the response in that location more accurate. These additional experiments are generated from the preceding optimization process. This study proves that the inclusion of average proxy error in the objective function is able to generate solutions which more improve the quality of proxy model.

e) Different values of average proxy error are inputted in the objective function in order to have different solutions from the optimization. These values can be obtained from

average residual error analysis of secondary polynomial proxy model of initial experiments.

f) From the investigation of different global optimization algorithms for the two cases, it is concluded that direct search algorithm give the best performance in finding a matching solution. Simulated annealing algorithm has slow convergence rate therefore the maximum iteration is reached before it could find the matching solution. Genetic algorithm is often trapped in the local minima. While global search algorithm needs a longer time to find the matching solution.

g) Case 1 can be easily matched with only 7 matching steps and 34 additional reservoir simulations in addition to the 43 initial experiments. The matching quality is almost perfect. This is because of several reasons: first, the initial residual error is quite small since complete CCF design is used to generate the initial experiments. Second, all of the 12 response variables are included as matching variables.

h) Case 2 is more difficult to solve. There were 27 matching steps with 183 additional simulations required to find an acceptable match. The matching quality is less than in Case1. This is first because fractional CCF was used instead of complete CCF so that the initial proxy model is not so accurate. Second, because the average quality of the initial proxy model is bad, therefore we could only select response variables which are accurately predicted by the proxy model.

i) Direct search algorithm in Case 2 could not explore all values of uncertain parameters so that the reduction rate of residual error is slow. To overcome this problem, sampling distribution analysis was conducted to redefine parameter boundaries to force direct search algorithm to explore unexplored zones. Reduction rate of residual error is significantly increased after the revision of boundary.

6.2 Future Work

a) Only two types of CCF design methods were investigated in this study. It will be useful to investigate other design methods such as Box Behnken and Latin Hypercube design.

b) Proxy model used in this study are second degree polynomial and ordinary kriging equation. It will be of interest to study other types of proxy model such as universal kriging, neural networks and Ensemble Kalman Filter.

c) A further improvement of direct search algorithm is also required so that it can explore all values of the uncertain parameters.

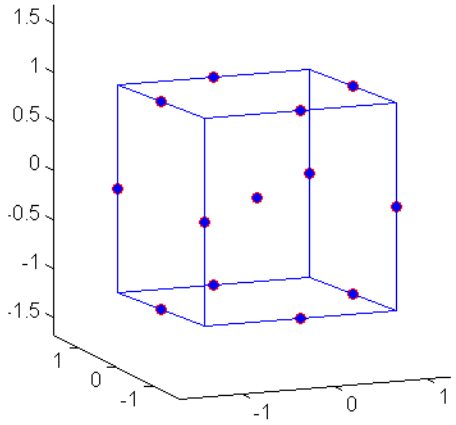
d) In this study, the methodology was used to solve an artificial history matching model. It will be of interest to use the same methodology to solve real history matching problem.

Appendix

A.1 Experimental design

a) Box-Behnken

The design is formed by combining 2^k factorials with incomplete block designs is shown in figure 2.1 point (d). Box-Behnken is a spherical design with all points lying on a sphere with radius $2^{0.5}$. In addition, Box-Behnken design doesn't contain any points at vertices of the cubic region created by the upper and lower limits for each variable [11]. Figure a.1 shows sample of Box-Behnken design with three parameters.



(c)

Figure a.1 Box Behnken Design

b) Latin Hypercube

Latin hypercube is a sampling method which produces the samples which are evenly distributed over the range of input parameters. Unlike the previous design methods where the number of experiments is fixed for specific number of parameters, in Latin hypercube the number of experiments can be determined by the users. The main concept behind Latin hypercube sampling is that there has to be only one sample in each row and column in case of two parameters and for n dimensions problems, there is only one sample in each axis hyper-plane containing it

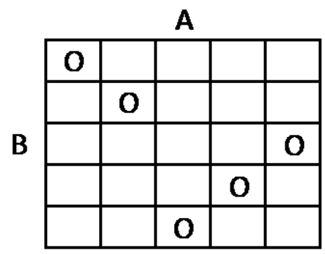


Figure a.2 example of Latin hypercube design for two parameters with 5 sample points

The main advantageous of this design is that the number of experiments doesn't depend on the number of variables, so that this design is suitable for a problem which involves many variables. Figure a.2 shows one example of Latin hypercube design of two parameters with 5 sample points.

A.2 Kriging Proxy Model

The values of weighting factor of all the sampling points are determined with the following equations:

$$\mathbf{W} = \mathbf{\Gamma}^{-1}\gamma \quad \ldots\ldots\ldots\ldots\ldots\ldots\ldots\ldots\ldots\ldots\ldots\ldots\ldots\ldots\ldots\ldots\ldots\ldots\ldots\ldots\ldots\ldots\ldots\ldots\ldots\ldots\ldots\ldots \text{(2)}$$

$$\mathbf{W} = (w_1, w_2, \ldots\ldots\ldots\ldots, w_{n,} \lambda) \quad \ldots\ldots\ldots\ldots\ldots\ldots\ldots\ldots\ldots\ldots\ldots\ldots\ldots\ldots\ldots\ldots\ldots\ldots\ldots\ldots \text{(3)}$$

$$\gamma = (\gamma(s_0 - s_1), \gamma(s_0 - s_2), \ldots\ldots\ldots\ldots, \gamma(s_0 - s_n), 1)^T \quad \ldots\ldots\ldots\ldots\ldots\ldots\ldots\ldots \text{(4)}$$

$$\mathbf{\Gamma} = \begin{cases} \gamma(s_i - s_j), \text{ for i} = 1,2,\ldots, \text{n}, \text{ j} = 1,2,\ldots, \text{n} \\ 1 \quad , \text{for i} = \text{n}+1, \text{ j} = 1,2,\ldots, n \\ 1 \quad , \text{for j} = \text{n}+1, \text{ i} = 1,2,\ldots, n \\ 0 \quad , \text{for i} = \text{n}+1, \text{ j} = \text{n}+1 \end{cases} \quad \ldots\ldots\ldots\ldots\ldots\ldots\ldots\ldots\ldots \text{(5)}$$

Based on the equations above, weighting factor is a function of two semi variogram functions: first is semi variogram of non-sampling point and sampling points and second, semi variogram between the sampling points.

Nomenclatures

AHM = Assisted History Matching

DOE = Design of Experiment

CCD = Central Composite Design

CCF = Cubic Centered Face

CCI = Cubic Centered Inscribed

CCC = Cubic Centered Circumscribed

Y = Response variables of polynomial equation

β = Parameters coefficient in polynomial equation

n = Number of parameters

Z = Response variables of kriging equation

s_0 = Point of interest / un-sampled point

s_i = Sampled point i

w_i = Weighting factor of sampled point s_i

Fobj = Objective function

T = Temperature

NewSol = New solution

CurSol = Current solution

p = Number of time steps

k = number of matching variables

VBA = Visual Basic Application

WWPT = Well water production total

WOPT = Well oil production total

WGPT = Well gas production total

FOPT = Field oil production total

FWPT = Field water production total

FGPT = Field gas production total

R^2 = R squared

RS = Residual error

y_{calc} = Value of observe variables calculated from proxy model

y_{sim} = Value of response variables obtained from simulation

y_{obs} = Observation data

$\bar{\varepsilon}_j$ = Average residual error of experiment j (%)

$\bar{\varepsilon}_p$ = Average proxy error

W_i = Weighting factor of matching variable i

TolFun = Minimum changes of objective function

MaxIter = Maximum number of iterations

$\mathbf{w}$ = Matrix vector of weighting factor (kriging formula)

γ = Semi variogram

s_i-s_j = Distance between sampled point i and point j

s_0-s_j = Distance between unsampled point and sampled point j

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