

University of Alberta

**Optimization of steam/solvent injection methods: Application of hybrid
techniques with improved algorithm configuration**

by

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A thesis submitted to the Faculty of Graduate Studies and Research
in partial fulfillment of the requirements for the degree of

**Master of Science
in
Petroleum Engineering**

Department of Civil and Environmental Engineering

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Fall 2012
Edmonton, Alberta

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I dedicate this work to Allah, and then to my parents, Mugren and Meznah, and my wife Manahel who always motivate and encourage me toward the success with their countless support

Abstract

Heavy oil and bitumen recovery processes need to be optimized in order to increase the recovery, reduce costs, and minimize the environment impact. Most of the optimization studies published in petroleum engineering literature focus on a few design parameters by combining the elements of numerical flow simulation with graphical or analytical techniques. Limited efforts, particularly in the areas of enhanced heavy oil recovery design, combine global optimization techniques with flow simulation to achieve better performance and design. The challenge remains because of high computational costs and slow convergence efficiency of the algorithms. In this research, genetic algorithm and simulated annealing are considered first as a single optimization technique. Then, the hybridization of these with the orthogonal arrays and response surface proxy techniques are tested. Savings up to 85% on the execution time are obtained for steam and solvent applications in oilsands and fractured carbonates.

Acknowledgements

Usually you do not realize the wisdom behind advice of the people who experienced life until you do them. I will never forget the encouragements and motivations of my parents, Mugren and Meznah, to excel in my study, and the words would not express my gratitude toward them. In addition, I do not forget Waleed Al-Awadh who supported and encouraged me to pursue my master in petroleum engineering. Special appreciations for my advisors Dr. Tayfun Babadagli and Dr. Juliana Leung for their support and advice that made this work see the lights. In addition, I would like to acknowledge Abo Sagr who simplified petroleum engineering learning for me. The wonderful time during my study would not be possible without my wife Manahel who always does the best. Finally, I would like to thank Saudi Aramco for providing the scholarship for my MSc study at the University of Alberta specially Claire Cardwell who coached me during my training assignment (Ch. 14).

A partial support for this research was obtained from Dr. Tayfun Babadagli's NSERC Industrial Research Chair in Unconventional Oil Recovery (industrial partners are Schlumberger, CNRL, SUNCOR, Petrobank, Sherritt Oil, and APEX Eng.). In addition, this research was partially supported by Dr. Juliana Leung's "NSERC Discovery Grant".

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Chapter 1: Introduction

Unconventional resources such as oil sands, heavy oil, coal-to-liquids, biofuels, gas-to-liquids, and shale oil rise on average by 4.6 percent per year over the coming 25 years. Canadian oil sands are the largest components of future unconventional production, which is about 4.8 million barrel per day (Conti and Holtberg 2011). Although there is an increase on unconventional resources production, still it faces production development difficulties such as high cost, complex processes, and environmental concerns. Canadian oil reserves, including oil sands, are about 175 billion barrels, (Conti and Holtberg 2011); however, the development difficulties limit the projects and investments. Higher recovery, lower cost, and less environmental impact can be achieved by better recovery processes design.

Global optimization techniques are useful tools for process optimization and design in various petroleum engineering disciplines. One of the drawbacks, however, is that these techniques, such as genetic algorithm and simulated annealing, have very slow computation time because they have to evaluate large numbers of models to reach the optimum.

This research focus on optimizing heavy oil and bitumen recovery processes, SAGD, ES-SAGD, heterogeneous ES-SAGD, and thermal recovery process in fractured reservoirs SOS-FR, using global optimization techniques as well as hybrid algorithms to enhance the process efficiency with minimal computation overburden. The solution methodology applied in this research is elaborated in Chapter 3.

Selecting an efficient algorithm is an important step toward achieving the best outcome in terms of accuracy and computation efficiency. Chapter 4 address this by comparing the performance of genetic algorithm and simulated annealing for SAGD and solvent additive SAGD optimization. The objective function was defined to obtain the lowest cumulative steam-oil ratio (cSOR) and highest recovery factor. It was used later as scoring function by changing operating pressure, solvent-to-steam ratio, and steam injection rates. The results in this chapter can be implemented directly in the efforts of minimization of cost and environmental impacts while accelerating the recovery in SAGD.

Having an efficient and robust optimization technique is critical in the design of SAGD or solvent-additive SAGD processes. Chapter 5 proposes a hybrid strategy that combines the elements of experimental design, response surface proxy, and genetic algorithm to investigate the effects of heterogeneity in the design process; optimization of solvent-assisted SAGD was performed on various synthetic heterogeneous reservoir models of varying porosity, permeability, and shale distributions. Computational time associated with flow simulations of heterogeneous reservoirs typically render most global optimization schemes rather challenging. It is shown that the proposed implementation of hybrid techniques can greatly enhance the proxy model predictability

and computational efficiency. Hexane was co-injected with steam. The objective function, defined based on cumulative steam-oil ratio (cSOR) and recovery factor, was optimized by changing injection pressures, production pressures, and injected solvent-to-steam ratio. The results from these hybrid approaches revealed that an optimized solution could be achieved with less CPU time (e.g. fewer number of full flow simulation) compared to the conventional GA method. Sensitivity analysis was also conducted on the choice of proxy model to study the robustness of the proposed methods. Our results highlight the potential application of the proposed techniques in other solvent-enhanced heavy oil recovery processes.

Chapter 6 focuses on optimizing Steam-Over-Solvent Injection for Fractured Reservoirs (SOS-FR) process using a hybrid technique applied in Chapter 5. The complexity of the process suggests that our objective function, defined by the money recovery factor, can be increased significantly by adjusting the steam and solvent usage and their injection profiles.

As this is a paper-based thesis, each chapter contains its own literature review, conclusion and references. The major contributions of this research are highlighted in Chapter 7.

Nomenclature

ES-SAGD: Expanded solvent steam assisted gravity drainage thermal recovery process also known as solvent additive SAGD.

GA: Genetic Algorithm.

NOA: Nearly-Orthogonal Array.

OA: Orthogonal Array.

SAGD: Steam assisted gravity drainage thermal recovery process.

SOS-FR: Steam-Over-Solvent for Fractured Reservoirs.

References

Conti J., and Holtberg P. 2011. International Energy Outlook 2011. A report published in U.S. Energy Information Administration. [http://www.eia.gov/forecasts/ieo/pdf/0484\(2011\).pdf](http://www.eia.gov/forecasts/ieo/pdf/0484(2011).pdf)

Chapter 2: Problem Statement & Research Objectives

In order to reach the ultimate heavy oil and bitumen recovery with minimal cost, efficient and optimized design for recovery processes operation strategies is necessary. Despite huge amount of heavy oil and bitumen reserves around the world, the production is limited due to the production development difficulties such as high cost, complex processes, and environmental concerns. Many design and performance evaluation studies published in the literature combine numerical simulation with graphical or analytical techniques; however, only few design elements are handled due to the difficulties of handling large number of factors. Because of high computation requirements, limited attention that integrated the simulation exercise with global optimization algorithms has been paid to handle more design elements. Without efficient and optimized recovery process design, the ultimate recovery from unconventional resources will not be achieved, or it could be achieved with great cost and large environmental impact. Thus, this research studies how global optimization techniques can be enhanced and upgraded to be a robust tool for the design and performance evaluation of unconventional recovery processes.

The objective of this research is to develop an approach that combines the techniques of experimental design, proxy models, and global optimization for the design of key process elements in the thermal/solvent methods. It is well known that computing costs associated with flow simulation of complex recovery processes (solvent and steam injection) in heterogeneous reservoirs can pose significant challenges on the optimization procedure. The use of hybrid techniques, as implemented in this thesis, aims to minimize the computational costs and to improve the solution accuracy.

Chapter 3: Solution Methodology

There are many techniques (either heuristic or mathematical) available to maximize an objective function for non-linear processes (Palke and Horne, 1997). **Figure 3-1** presents a classification of these techniques. This chapter aims to provide additional details about the methodologies used in the research.

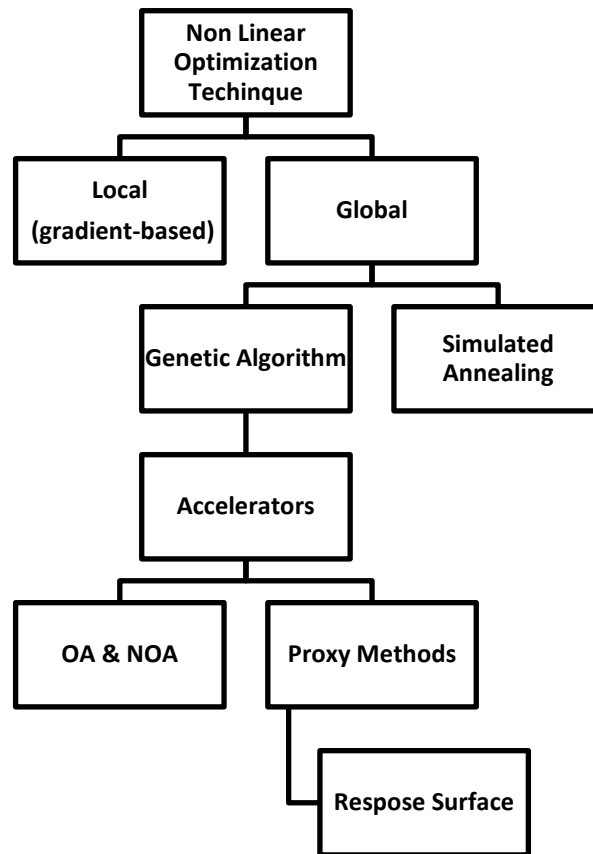


Figure 3-1: Optimization algorithms classification

Global Optimization Techniques

In optimization algorithms, one needs to start with specifying the effective parameters (and their respective ranges of values) to be evaluated. Next, the algorithm proposes various trial solutions, and the objective (or scoring) function would be evaluated for each trial solution. This process is repeated until specified number of iterations is reached or once certain stopping or convergence criteria are met. **Figure 3-2** shows the global optimization techniques process schematically.

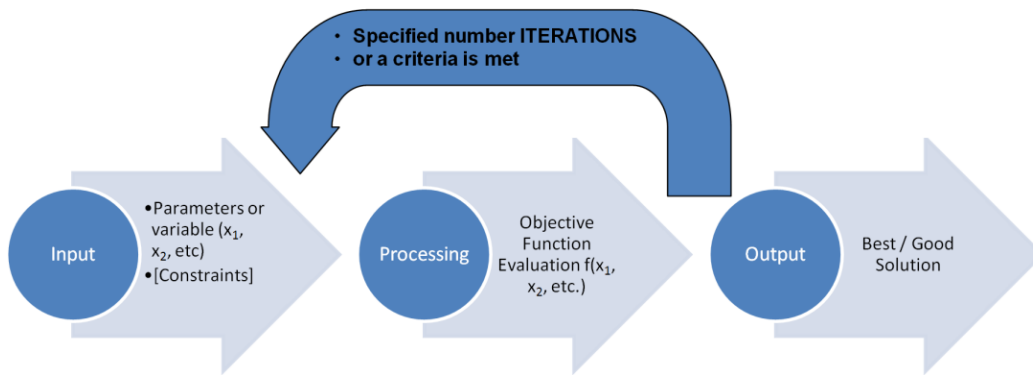


Figure 3-2: Schematic representation of optimization process.

Genetic Algorithm

GA is a stochastic search technique based on the principle of “survival of the fittest” (Guyaguler et al., 2002; Chen et al., 2010). **Figure 3-3** shows the overall optimization process (as similar to Figure 3-2) using genetic terminology. **Figure 3-4** summarizes the mechanisms of a typical GA algorithm. The population or genotype, a partial space solution, is picked initially and modified subsequently in each evolution, which is called iteration. In each evolution, the fitness of each chromosome, containing genes, is calculated; each gene represents a parameter and each chromosome represents a trial. Then, two parents are selected based on their fitness value to create an offspring or child by performing crossover, which is simply exchanging genes between parents (**Figure 3-5**). The newly generated offspring is mutated by changing some of its binary digits (**Figure 3-6**). The new offspring is inserted in the new population.

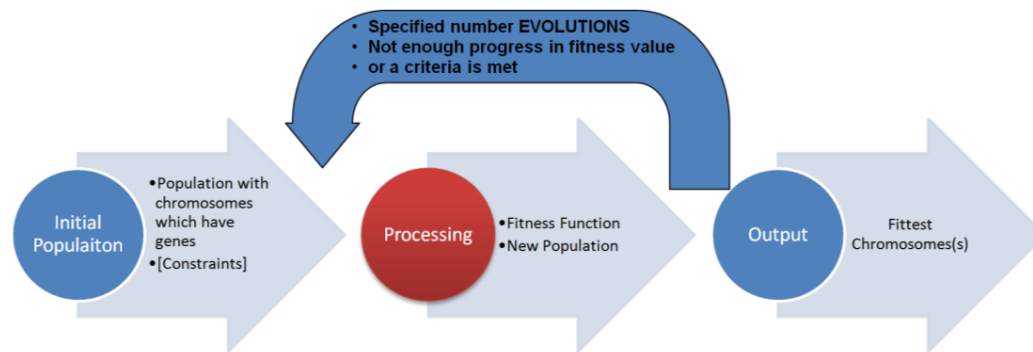


Figure 3-3: Optimization process in genetic algorithm terminology

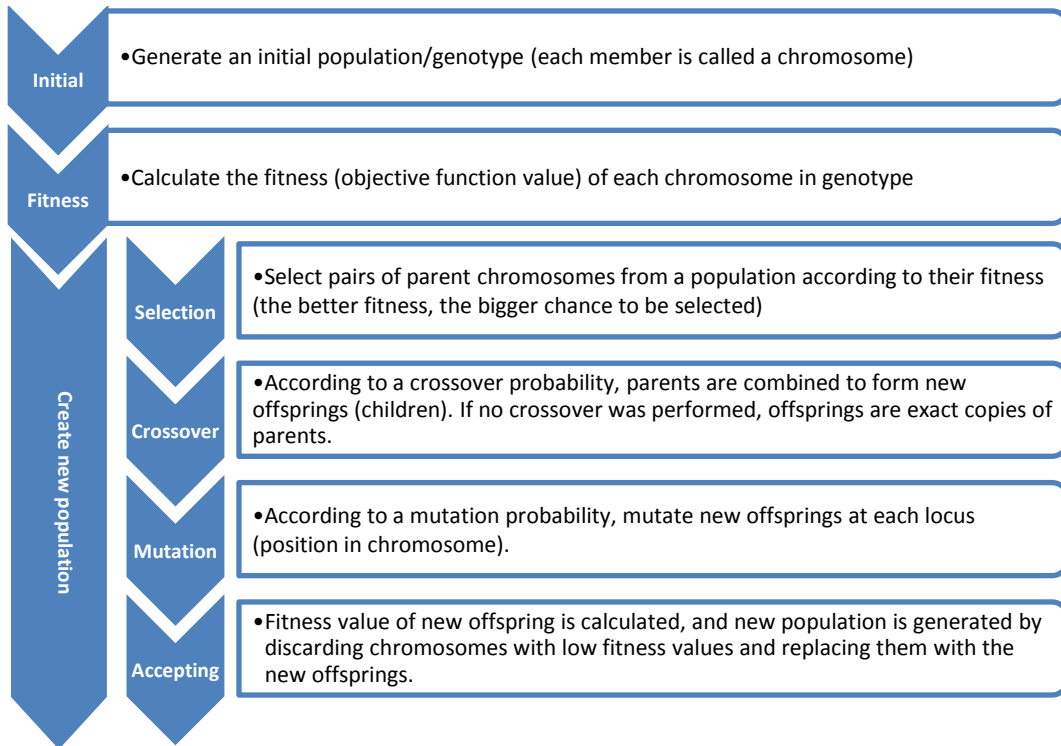


Figure 3-4: Genetic algorithm flow diagram

	Gene	Gene	Gene	Gene	Gene
Parent Chromosome 1	01110000011	1111101000	1000100110	101101110	11001100010
Parent Chromosome 2	11111001111	1001000010	1110011111	1000010010	11000100000
Child Chromosome 1	01110000011	1111101000	1110011111	1000010010	11000100000
Child Chromosome 2	11111001111	1001000010	1000100110	101101110	11001100010

Figure 3-5: Example of crossover of two parent chromosomes.

	Gene	Gene	Gene	Gene	Gene
Parent Chromosome	10101111	11110010111	11100101010	1001011111	10110100100
Child Chromosome	10101111	01110010111	11100101010	1001011111	10110100100

Figure 3-6: Example of mutation of a parent chromosome.

GA Advantages

1. GA initiates the search with a population of parameter realizations, instead of a single realization.
2. The used rules are probabilistic rather than deterministic.
3. It manipulates a chromosome (or string of individual parameters) rather than changing each individual parameter.
4. It uses function evaluations instead of derivatives or other secondary descriptors (Bittencourt and Horne, 1997)
5. It has the ability to be combined with other algorithm in order to avoid suboptimal solution. (Guyaguler et al., 2002)
6. It is easy to be parallelized which is a potential to accelerate the calculation (Guyaguler et al., 2002)

GA Disadvantages

1. Even though it is good that the initial population is randomly allocated, this may covers bad regions. This randomness continues on the generation process, which depends on the values of the initial members (Bittencourt and Horne, 1997).
2. It can be time-consuming to apply GA to complex optimization problem because it suffers from potentially low convergence speed (Chen et al., 2010).

GA Accelerators

To avoid GA drawbacks, several techniques have been studied and chosen in this research.

Orthogonal Array and Nearly-Orthogonal Array for Initial Population Generation

Techniques from the experimental design literature, namely Orthogonal Array (OA) and Nearly-Orthogonal Array (NOA), can be implemented with GA to improve the quality of initial population (Chen et al., 2010) by generating evenly distributed samples while reducing the redundancy between chromosomes. The objective is to design experiments or chromosomes by determining the levels at which the parameters should be varied. Instead of testing all combinations of parameters at all levels, only the ones containing principal information are included. This reduces the population size and the associated computational costs. In this research, we used Gendex DOE Toolkit (website: <http://designcomputing.net/gendex>) to generate nearly orthogonal arrays based on the Taguchi method average and minimax criterion described by Ma et. al. (2000) and Lu et. al. (2003). **Table 3-1** shows an example where there are 4 runs for 3 factors with 4, 3, 2 levels, respectively.

Table 3-1: Nearly orthogonal array example

Run	Factors		
	Factor 1	Factor 2	Factor 3
1	2	2	0
2	3	0	0
3	1	0	1
4	0	1	1

Proxy Method for Objective Function Evaluation

As can be seen in Figure 3-3, the fitness function must be evaluated for every chromosome at every evolution. In our particular application, evaluation of the fitness function involves calculation of the recovery factor, typically obtained from results of a numerical flow simulation. Depending on the level of complexity of the processes that are being modeled, each flow simulation could take up to days to complete. Hence, the costs of objective function evaluation are often the most important computational considerations in any optimization scheme. Proxy methods are viable “cheaper” alternatives that approximate the actual fitness function to enhance computing efficiency. The technique implemented in this study was the response surface method. Response surface is a relationship between the parameter sets and the corresponding fitness function. Once calibrated in the form of regression, it can be used as a proxy for flow simulation and allows the fitness function to be evaluated rapidly. In particular, we compared the first-order linear model and the second-order (quadratic) non-linear model, as discussed in Myers and Montgomery (2002). Equations for the linear and non-linear models are shown in Eqs. 1 and 2, respectively, where J is the response (fitness function value), u_i 's are the variables (optimization parameters), β_i 's are the regression coefficients, and ϵ is an error term.

$$J = \beta_0 + \beta_1 u_1 + \cdots + \beta_n u_n + \epsilon \quad (1)$$

$$J = \beta_0 + \beta_1 u_1 + \cdots + \beta_n u_n + \sum_{i=1}^n \beta_{ii} u_i^2 + \sum_{i < j} \sum_{j=2}^n \beta_{ij} u_i u_j + \epsilon \quad (2)$$

The regression equation for both models, if the problem is over-determined, is expressed in Eq. 3:

$$\beta = (U^T U)^{-1} U^T J \quad (3)$$

If there are many factors, a U matrix is constructed with fewer experiments than the number of unknown parameters, the problem becomes under-determined and Eq. 4 is used:

$$\beta = U^T (U U^T)^{-1} J \quad (4)$$

Proxy Method for Objective Function Evaluation with Periodic Updating

In order to achieve a better representation of the solution space and regression accuracy, the proxy is re-calibrated or updated periodically by performing detailed flow simulation using parameters of the chromosome with the highest fitness value and incorporating its simulation result after each evolution. This updating step is illustrated in the flow chart as shown in **Figure 3-7**.

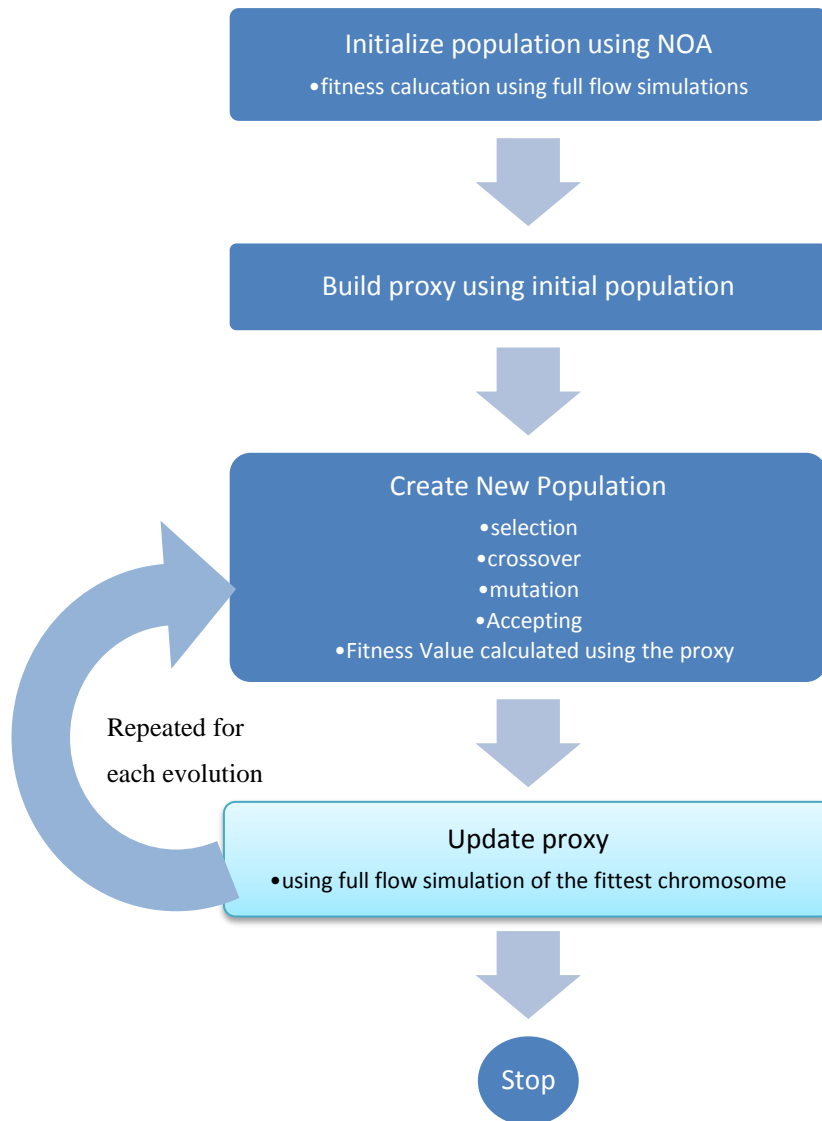


Figure 3-7: Flow diagram for the periodic updating approach where proxy is updated with the additional flow simulation results of the fittest chromosomes after each evolution

Simulated Annealing

Metropolis proposed a search algorithm called simulated annealing (SA), which, at a given temperature, finds the equilibrium configuration of a number of atoms. The key benefit of using the SA is avoiding local minimum (Gates and Chakrabarty, 2008). **Figure 3-8** shows simulated annealing flow chart.

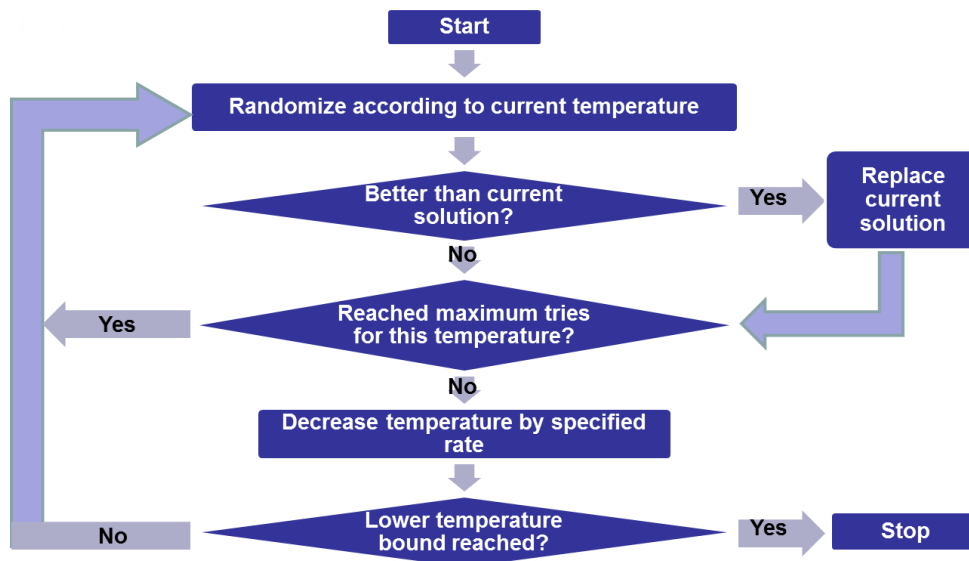


Figure 3-8: Simulated annealing one iteration flow chart

Research optimization framework

In this research, we have developed a framework that integrates the previously mentioned techniques with CMG STARS, a numerical flow simulation package for thermal recovery process, to optimize steam and solvent injection processes. A JGAP runner package is implemented to generate an initial population either randomly or using the NOA reader package and customize the genetic algorithm configuration, e.g. crossover and mutation rate. After that, JGAP runner calls JGAP package to start evolving the evolutions where each chromosome is evaluated using the objective function evaluation package. This package calls either the CMG agent package to fully execute a scenario or the response surface package to get an estimated value. **Figure 3-9** shows the framework packages and the interaction within the framework (blue packages) and with external software.

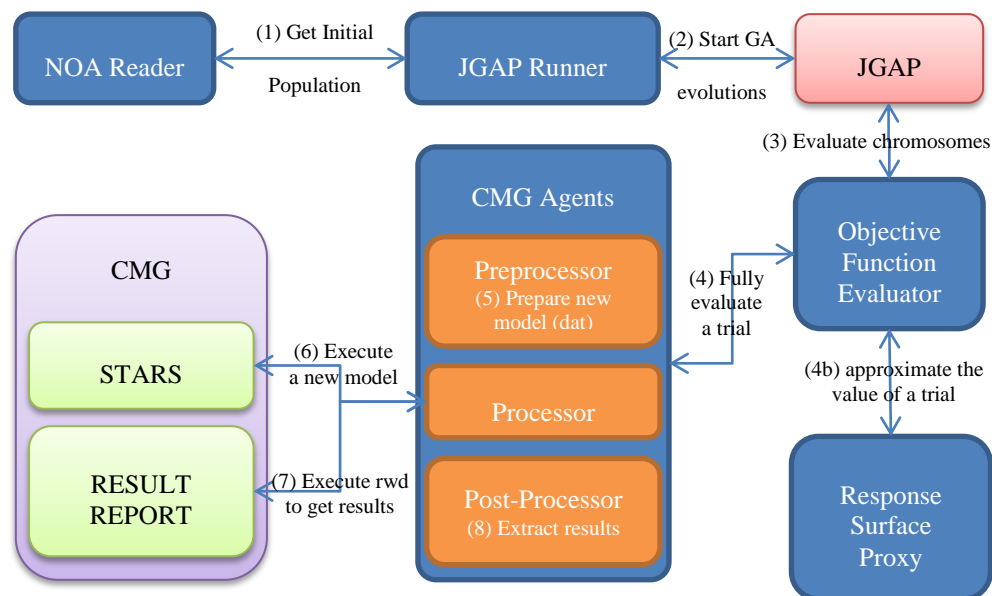


Figure 3-9: Optimization framework packages interaction.

JGAP Runner for initialization and executing

In this research, we used the JGAP package (Java Genetic Algorithm Package (JGAP) website: <http://jgap.sourceforge.net/>) for the GA modeling. This package needs to be initialized by specifying GA configuration such as crossover and mutation rates, initial population, and objective function. Example code is shown in Appendix 1.

Objective function evaluation package

Global optimization techniques rely mainly on objective function evaluation for the generated trials. In our framework, this package is responsible about calling the CMG Agent package to get the results that are needed in the objective function calculation. Example code from SOS-FR experiments is shown in Appendix 2.

CMG Agents package

This package handles the interaction between our software and CMG products. It has three stages pre-processing, processing, and post post-processing. Pre-processing is needed to build a new simulation model file (.dat) using old model file by changing the parts that need to be changed using the values provided by the optimization algorithm. In the processing stage, the simulation is executed. Post-processing stage extracts the relevant results from a *.rwo file, which is built by executing the *.rwd file generated using CMG “Result Report” tool. Example code from SOS-FR experiments is shown in Appendix 3.

Response surface proxy package

This package is used to build and calibrate the linear and non-linear proxy described before to approximate the objective function. This package code is shown in Appendix 4.

Nearly Orthogonal Arrays (NOA) reader package

In this research, we used Gendex DOE Toolkit (website: <http://designcomputing.net/gendex>) to generate the NOA arrays. This tool generates numbers that represent the level at which each factor (parameter) should be used in a particular trial. These numbers must be converted to values appropriate for the parameter ranges. For example, for injection rate ranging from 100 to 300 units, five levels, indicated by 0, 1, 2, 3, and 4, would correspond to actual parameter values of 100, 150, 200, 250, and 300 units, providing a 50-unit resolution for the parameter. This step can be done manually using excel spreadsheet. After that, the newly generated OA is copied into a text file to be read using this reader package. Example code from SOS-FR experiments is shown in Appendix 5.

Nomenclature

β_i : represent a regression coefficients for one trial.

$\boldsymbol{\beta}$: a vector which contains all regression coefficients.

$F(\mathbf{u})$ or FX : objective function value.

F : objective function.

GA : Genetic Algorithm.

J : the actual response or actual objective function value calculated based simulation output for one trial.

J : the repose obtained from the regression model.

J_0 : the best trial actual response in the initial population.

\mathbf{J} : a vector that contains all the trials response.

NOA : Nearly-Orthogonal Array.

OA : Orthogonal Array.

$SOS-FR$: Steam-Over-Solvent for Fractured Reservoirs.

\mathbf{u} : a ($1*n$) vector which contains the optimization variables for a trial.

u_i : represent an optimization variable for one trial.

\mathbf{U} : a matrix with all \mathbf{u} 's.

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Chapter 4: Optimization of SAGD and Solvent Additive SAGD Applications: Comparative Analysis of Optimization Techniques with Improved Algorithm Configuration

Abstract

Heavy oil and bitumen recovery cost is excessive mainly due to high energy requirement to generate heat and its environmental impacts. Steam Assisted Gravity Drainage (SAGD) is an example of this case. The determination of optimal operating conditions, such as injection rates and well locations, based on reservoir and fluid characteristics is essential in the design of field applications.

Many Steam Assisted Gravity Drainage (SAGD) optimization studies published in the literature combined numerical simulation with graphical or analytical techniques for design and performance evaluation. There have been limited efforts that integrated the simulation exercise with global optimization algorithms. Some studies focused on optimization of cumulative steam-to-oil ratio (cSOR) in SAGD by altering steam injection rates, while others focused on optimization of cumulative net energy-to-oil ratio (cEOR) in solvent-additive SAGD by altering injection pressures and fraction of solvent in the injection stream. Typical scoring functions were the net present value per hectare of land (NPV/ha) by controlling steam and solvent rates. Several studies also considered total project net present value calculation by changing total project area, capital cost intensities, solvent prices, discount rate, and risk factors to determine the well spacing and drilling schedule. Optimization techniques commonly used in those studies were scattered search, simulated annealing, and genetic algorithm (GA). In continuation of these efforts, we focused on optimizing the SAGD process and its extension to solvent-additive SAGD and several optimization techniques including simulated annealing and genetic algorithm were tested and compared. Additional procedures were incorporated to improve the implementation configuration and initial population or seed. The objective function was defined to obtain the lowest cumulative steam-oil ratio (cSOR) and highest recovery factor. It was used later as scoring function by changing solvent-to-steam ratio and steam injection rates. The results in this chapter can be implemented directly in the efforts of minimization of cost and environmental impacts while accelerating the recovery in SAGD.

Introduction

A great portion of Alberta's oil sand reserves can be produced only by in-situ recovery techniques (Al-Bahlani and Babadagli, 2009). Steam Assisted Gravity Drainage (SAGD) is the most widely applied in situ recovery method but the cost of this process is excessive because of the need to generate heat and its environmental effects. Maximizing the recovery with minimum impacts by determining the optimal process variables such as injection rate is essential in the design of field application.

Most of the earlier studies focused on optimizing the SAGD process. Limited amount of work has been performed in the area of solvent-additive SAGD optimization. In particular, two groups of researchers performed studies that are interesting examples of this kind of optimization exercise. In the first group, Gates and Chakrabarty (2006) focused on SAGD optimization to reduce cumulative steam-to-oil ratio (cSOR) by altering steam injection rates. Later, they expanded their work to include solvent injection to reduce cumulative net energy-to-oil ratio (cEOR) by adjusting the injection pressures and fraction of solvent in the injection stream (Gates and Chakrabarty, 2008).

In the second group, Peterson et al. (2009) used net present value per hectare of land (NPV/ha) as scoring function by controlling steam and solvent rates. Later, they used total project net present value calculation as an objective function (Peterson et al., 2010). The user would specify total project area, capital cost intensities, solvent prices, discount rate and risk factors. The optimization process determines the well spacing, drilling schedule and facility size (Edmunds et al., 2010).

One of the critical questions in the optimization of complex applications is to select an efficient algorithm. As seen, limited number of works in the area of SAGD optimization adopted and tested different techniques (Bittencourt et al., 1997). Yet, the selection of efficient algorithm is a critical issue to reduce the optimization time. This work focuses on testing and comparing different algorithms to demonstrate their efficiency for the optimization of SAGD and solvent additive SAGD applications and how they can help in selecting the optimal case for maximum recovery and minimum cSOR. In addition, improvements in the implementation configuration and initial population (or seed) of the algorithms tested are also made.

Global Optimization Techniques

In optimization algorithms, one needs to start with specifying the effective parameters (and their respective ranges of values) to be evaluated. Next, the algorithm proposes various trial solutions, and the objective (or scoring) function would be evaluated for each trial solution. This process is repeated until specified number of iterations is reached or once certain stopping or convergence criteria are met. **Figure 4-1** shows the global optimization techniques process schematically. In this chapter, we adopted two algorithms as described below.

Genetic Algorithm

The Genetic Algorithm (GA) is a stochastic and structured search technique that uses the principle of “survival of the fittest” and natural selection (Guyaguler et al., 2002; Chen et al., 2010). **Figure 4-2** shows the overall optimization process (as similar to **Figure 4-1**) using genetic terminology. **Figure 4-3** summarizes how the algorithm works. The population or genotype is partial space solution picked initially and modified in each evolution which is called iteration. In each evolution, the fitness of each chromosome, which consists of numerous genes, is calculated; each gene represents a parameter while each chromosome represents a trial. Subsequently, two parents are selected based on their fitness value to create an offspring or child by performing crossover which is simply exchanging genes between parents (**Figure 4-4**). The newly generated offspring is mutated by changing some of its binary digits (**Figure 4-5**). The new offspring is inserted in the new population.

The GA is a popular optimization technique in the petroleum industry as one of the most powerful and robust optimization technique. Chen et al. (2010) used GA with nearly orthogonal arrays (NOA) to design a Water-Alternating-Gas (WAG) process in a CO₂-Miscible Flooding project. Edmunds et al. (2010) applied GA for optimization of solvent-additive SAGD process. This technique was also used for non-thermal applications, mainly for the purpose of reservoir development (Palke and Horne, 1997; Bittencourt and Horne, 1997). On the basis of all these efforts, the advantages and disadvantages of this method can be summarized as follows:

Advantages

1. GA initiates the search with a population of parameter realizations, instead of a single realization.
2. The rules used are probabilistic rather than deterministic.
3. It manipulates a chromosome (or string of individual parameters) rather than changing each individual parameter.
4. It uses function evaluations instead of derivatives or other secondary descriptors (Bittencourt and Horne, 1997)
5. It has the ability to be combined with other algorithm to avoid suboptimal solution. (Guyaguler et al., 2002)
6. It is easy to be parallelized which is a potential to accelerate the calculation (Guyaguler et al., 2002)

Disadvantages

3. Even though it is good that the initial population is randomly allocated, this may covers bad regions. This randomness continues on the generation process, which depends on the values of the initial members (Bittencourt and Horne, 1997).
4. It can be time-consuming to apply GA to complex optimization problem because it suffers from potentially low convergence speed (Chen et al., 2010).

GA Accelerators

To avoid GA drawbacks, several techniques have been proposed, yet many of them are at the initial development stage with room for improvements.

Orthogonal Array and Nearly-Orthogonal Array

Orthogonal Array (OA) and Nearly-Orthogonal Array (NOA) can be integrated with the GA to improve the quality of initial members. They are commonly used in the efficient experimental design process (Chen et al., 2010). Chen et al. (2010) used GA with nearly orthogonal arrays (NOA) to design a Water-Alternating-Gas (WAG) process.

Proxy Method

Proxy method is used to approximate the actual evaluation function and to increase the computing efficiency. Some of the techniques used as proxies are kriging, neural networks (Guyaguler et al., 2002) and response surface methodology which is a relationship between the parameter sets and the corresponding fitness function. It can be used as a proxy for flow simulation for faster evaluation of the fitness function after calibration (Algosayir et. al. 2011). Myers and Montgomery (2002) showed that the first-order linear model and the second-order non-linear model are examples of such proxy.

Simulated Annealing

Metropolis et al. (1953) proposed a search algorithm called simulated annealing (SA), which, at a given temperature, finds the equilibrium configuration of a number of atoms. The key benefit of using the SA is avoiding local minimum (Gates and Chakrabarty, 2008). This technique was first used by Gates and Chakrabarty (2008) to optimize solvent additive SAGD.

In this chapter, we implemented three different schemes including (1) the conventional GA, (2) GA with nearly orthogonal arrays, and (3) simulated annealing to optimize steam injection rate over four periods in SAGD and additive mole fraction in solvent-additive SAGD cases over 10 period.

Objective function

In many enhanced oil recovery applications, maximizing recovery is essential as it directly affects profit. Reduction of cost is also critical in profit maximization. Thus, the process optimization focused on the maximization of recovery factor and reduction of cumulative steam-oil-ratio which help to reduce costs and minimize environments impacts due to steam generation process. After several attempts, we proposed an equally weighted objective function ($F(X)$) for recovery factor (RF) and cumulative steam oil ratio (cSOR) as different from earlier works mentioned above. Ideally, objective function should be dimensionless. Therefore, RF is assigned a unit weight because its value ranges between 0 and 1, while cSOR has to be normalized to be between 0 and 1. This is achieved by dividing its value by the maximum observable cumulative steam oil ratio [$\max(cSOR)$]. In order to minimize the cSOR, its weighted value should be subtracted from the recovery factor. The adopted GA implementation assesses the objective (fitness) function (equation 1) and aims to maximize its value:

$$F(x_1, x_2, x_3, x_4) = RF - \frac{cSOR}{\max(cSOR)} + 1 \quad (1)$$

An adjusting factor of “1” was added to the objective function to shift its range from [-1, 1] to [0, 2], such that a positive objective function value would always be obtained.

On the other hand, our implementation of simulated annealing aims to minimize the objective function, which is defined in equation (2):

$$F(x_1, x_2, x_3, x_4) = \frac{cSOR}{\max(cSOR)} - RF + 1 \quad (2)$$

where x_1, x_2, x_3, x_4 are the parameters explained in reservoir model section.

Reservoir model

A two-dimensional simulation model of laboratory-scale experiments provided by Ayodele et al. (2010) was constructed and used in the case studies. Then, this model was scaled-up to the field dimensions by changing the grid sizes. The simulation input properties are described in **Table 4-1**. The cases GA-1, SA and OGA-1 are SAGD optimization, while HA-GA case is an ES-SAGD application using the OGA-1 approach. The SAGD optimization process evaluates Eqs. 1 and 2 by adjusting the 2-year steam injection schedule (injection rates over four 6-month periods). On the other hand, ES-SAGD optimization process evaluates Eq. 1 by adjusting 2-year injection strategy by changing fluids injection rates and hexane mole fraction over four months period. These optimized parameters injection rate and hexane model fraction have been studied over reasonable range of values that are suitable for the reservoir model and research objective as shown in **Table 4-2**.

Results

In all cases, $[\max(cSOR)]$ is fixed to $3 \text{ m}^3/\text{m}^3$. Results obtained with the various optimization algorithms are presented below.

Genetic Algorithm Case 1 (GA 1)

The purpose of this Genetic Algorithm case (GA-1) is to investigate the different ways of generating initial population. Three different options were used for this purpose. The first conventional way was to generate the initial population randomly using stock random generator providing by the JGAP package (Java Genetic Algorithm Package (JGAP) website: <http://jgap.sourceforge.net/>). The second and third ways use nearly orthogonal array (NOA) hybrid technique with GA. The array used is $L_{40}(17^4)$ which have 4 factors, 17 levels, and 40 runs (**Table 4-3**). The factors are basically the parameters desired to be adjusted, hence, X values in our case are injection rates. The levels are how many cases each factor should have. The number of runs refers to the desired number of combined cases (i.e. number of chromosomes in GA terminology). The difference between the two NOAs is that the second way uses the average criterion (Ma et. al 2000, Lu et. al. 2003) while the third applies the minimax criterion (Lu et. al. 2003). Among these, we observed that NOA minimax returned good fitness value after executing 434 reservoir models which is the least number of trials among these cases. It also converged faster from the lowest fitness value to a good fitness value as seen in **Figure 4-6**.

Simulated Annealing case (SA)

The simulated annealing (SA) algorithm initial seed was selected based on the best value in NOA minimax run used in GA-1 minimax case. A better solution than GA-1 NOA Minimax was found after performing only 78% total number of trials. However, this does not necessarily mean that GA is less efficient, as GA can be improved with better configuration selection. The SA algorithm was initialized using the values given in **Table 4-4**.

Optimized Genetic Algorithm Cases (OGA 1)

In order to have a good configuration for genetic algorithm implementation, we ran full optimization experiments to optimize the mutation and crossover rates in addition to the population size and evolution count to have a higher objective function value. This experiment and the other experiments using GA and SA were performed through exhaustive number of simulations to reach the optimum. As a result, the best experiment optimum case objective function value was found to be 0.9548 with the least number of trials about 133 trials while SA reached the same solution after executing 169 trials. As seen in **Table 4-6** all SAGD results using different algorithms and different configurations are very similar in terms of the objective function, recovery factor, and cSOR. The objective function value differs only after the third

decimal number. However, the major difference is in the number of cases needed to reach an acceptable optimum value, which implies reducing the number of flow simulation runs needed and the execution time needed to reach the optimum. Fluid flow simulations in porous media under non-isothermal conditions usually require remarkable amount of time to execute comparing with other optimization operations. For example, in our applications, the average execution time of flow simulation is about 2 minutes and this saved about 80 minutes on running optimization using OGA compared to SA. **Table 4-5** summarizes the configuration parameters for all the GA cases. All of these experiments were initialized with the same $L_{40}(17^4)$ NOAs in order to make the results comparable. The convergence behaviour of SA and these optimized GA case are shown in **Figure 4-7**. **Table 4-6** shows the final optimal solution for each case and at which trial the optimal solution was reached. Also tabulated are the corresponding injection periods, the final objective function value, recovery factor, and cumulative steam oil ratio.

Figure 4-8 and **Figure 4-9** show the steam injection rates with function value for all the periods for the SA and OGA case. It is interesting to note that SA reaches its optimal solution by gradually adjusting its parameter values; while GA attempts to identify the optimal solution by running different scenarios (because of the crossover feature) of adjusting the parameter values (hence the abrupt jumps in objective function values). Furthermore, the results suggest that the optimal injection rate for period one and three around $8 \text{ m}^3/\text{day}$ and increasing the injection in the second period to be around $8.5 \text{ m}^3/\text{day}$ while the last period should be decreased to around $7 \text{ m}^3/\text{day}$. As a result, it appears that the optimal injection strategy would be to alternate between high and low values over several injection periods.

Hexane Additive SAGD Case (HA-GA)

After studying the optimization techniques using SAGD models, the good optimization methodology learned have been applied into Solvent-Additive SAGD case in order to show how the optimized Solvent-Additive SAGD have better recovery and cSOR. Hexane additive SAGD case was executed using GA with initial NOA minimax array $L_{40}(17^8)$. The optimum solution has better fitness function value than all SAGD cases, which implies higher recovery (about 3.7% increase) and lower cSOR (about $1 \text{ m}^3/\text{m}^3$ decrease) as shown in **Table 4-6**, which also include the optimized fluid injection rate compared to the SAGD cases. Since Hexane additive is costly, it was optimized over the same periods and the optimized hexane mole fraction is shown in **Table 4-7**.

Conclusions

The GA and SA techniques are powerful in finding an optimized solution; however, both require evaluating number of trials in order to reach the optimum solution which is in our case running simulation model. Execution of several models requires more computation time.

In this chapter, several optimization techniques were tested to reduce the computational time such as choosing the right configuration and the initial population or seed. As a result, the SA converged faster than most of the GA cases. After optimizing the GA configuration, we obtained a case that converges in reasonable time. Even though the SA converged faster, the GA has some advantages such as having initial population, which can guide the algorithm to better solution, and the final population gives more than one scenario that can be used.

On the other hand, the SA may end up being slower than GA if it is initialized with a very bad seed. In order to improve its performance, several other options can be implemented such as running the algorithm in parallel computing environment for one flow simulation or running multiple flow simulations simultaneously, which can be implemented in Genetic Algorithm.

As seen, several options can be used to improve the performance. However, one has to answer the critical question eventually: what is the most time consuming part? Clearly, the answer is running time of the flow simulation. Reducing the number of runs by up to 40% is an optimal solution but it is difficult to obtain such percentage often times as it is hard to know in advance what the best configuration is. Hence, to reduce the time required for running a flow simulation, implementation of a proxy, which approximates the flow simulation result in fraction of second instead of two minutes in our cases, could be a solution. This implies that more than 95% of simulation run time is saved and all we need is to run a couple of cases to build the proxy.

Nomenclature

ANN: Artificial Neural Networks.

cEOR: cumulative net energy-to-oil ratio.

CMG: Computer Modeling Group.

cSOR: steam-to-oil ratio.

F(X): objective function.

GA-1: Genetic Algorithm SAGD cases.

GA: Genetic Algorithm

HA-GA: Hexane Additive SAGD Case executed using GA.

JGAP: Java Genetic Algorithm Package.

NOA: Nearly-Orthogonal Array.

NPV: Net Present Value.

OA: Orthogonal Array.

OGA-1: Optimized Genetic Algorithm configuration SAGD case.

P1, 2, 3, 4: four 6 months injection periods.

RF: Recovery Factor.

SA: Simulated Annealing Algorithm

SAGD: Steam Assisted Gravity Drainage thermal recovery process.

STARS: CMG thermal reservoir simulator.

WAG: Water-Alternating-Gas recovery process.

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A version of this chapter was submitted and accepted by Journal of Petroleum Science and Engineering and it is a revision of the conference paper: Al-Gosayir, M., Babadagli, T., and Leung, J. 2011. Optimization of Solvent Additive SAGD Applications using Hybrid Optimization Techniques. Paper 144963 presented at the SPE Enhanced Oil Recovery Conference, Kuala Lumpur, Malaysia, 19–21 July.

Tables

Table 4-1: Reservoir simulation input parameters.

Item	Value
Grid	Cartesian 40*1*15
Grid Dimensions (I)	2 m
Grid Dimensions (J)	50 m
Grid Dimensions (K)	2 m
Initial Reservoir Temperature	20 oC
Initial Reservoir Pressure	2090 kPa
Minimum Producer BHP	1500 kPa
Injected steam temperature	200 oC
Injected steam quality	1
Porosity	20%
Permeability	1 Darcy
Rock heat capacity	2.35 J/cm ³ -C
Rock thermal conductivity	2.5833 J/cm-min-C
Water thermal conductivity	0.3715 J/cm-min-C
Oil thermal conductivity	0.07986 J/cm-min-C
Hexane k-value coefficients	KV1 = 1.01x10 ⁶ kPa KV4 = -2697.55 C KV5 = -224.37 C
Mechanical Dispersivity (All components in all phases)	0.024 cm
Molecular Diffusion of Hexane in oleic phase (All components)	0.000250596 cm ² /min
Molecular Diffusion of Hexane in vapour phase (All components)	0.0250596 cm ² /min

Table 4-2: Optimized parameters ranges.

Item	Range
Injection Rate	0 – 10 m ³ /day
Hexane injection mole fraction	0 – 0.3

Table 4-3: NOA Tables.

Average Criterion Array					Minimax Criterion Array				
	Factors					Factors			
Run	1	2	3	4	Run	1	2	3	4
1	3	7	7	9	1	9	9	0	0
2	3	8	5	8	2	8	2	3	3
3	9	9	1	0	3	6	5	6	4
4	4	2	5	4	4	8	4	6	9
5	1	4	1	1	5	1	8	0	10
6	2	0	4	6	6	0	2	5	8
7	6	0	1	2	7	4	3	8	4
8	3	5	3	8	8	6	3	9	2
9	9	1	3	8	9	9	3	3	7
10	1	10	3	7	10	1	3	1	3
11	4	3	6	9	11	4	5	8	3
12	0	9	9	10	12	5	1	8	7
13	10	5	8	3	13	1	9	1	9
14	5	1	4	1	14	0	6	1	1
15	0	6	3	2	15	1	7	8	2
16	7	6	1	4	16	6	9	3	0
17	1	1	9	5	17	3	0	9	4
18	9	3	8	0	18	7	2	9	3
19	8	1	6	8	19	3	0	4	8
20	8	4	3	4	20	2	9	6	1
21	4	10	9	3	21	0	4	7	6
22	7	2	1	1	22	4	10	2	5
23	2	6	6	1	23	4	1	10	9
24	3	1	9	0	24	3	4	1	6
25	3	3	10	6	25	5	6	3	3
26	2	4	4	3	26	8	1	10	10
27	1	8	2	3	27	1	3	6	1
28	10	3	2	4	28	3	4	0	8
29	5	4	2	1	29	3	6	4	3
30	4	3	3	9	30	9	1	2	9
31	6	6	10	6	31	10	0	5	0
32	6	9	0	9	32	3	8	3	1
33	1	0	6	7	33	2	8	9	5
34	9	8	7	3	34	10	6	3	6
35	0	3	8	1	35	6	10	4	1
36	6	7	0	3	36	2	3	1	2
37	3	2	0	2	37	9	8	4	8
38	1	8	8	6	38	8	1	2	6
39	8	1	1	10	39	7	7	1	1
40	8	9	4	5	40	1	1	7	4

Table 4-4: Simulated annealing configuration.

Initial temperature	1
Acceptance rule temperature	1
Maximum temperature iterations	600
Random moves	10

Table 4-5: GA cases configuration.

	GA-1	OGA-1	HA-GA
Crossover	0.35	0.85	0.85
Mutation	12%	17%	17%
Population	40	20	20
Evolutions	30	7	30

Table 4-6: Comparison of the selected solution.

Case	Trial#	Evolution	F(X)	Steam/Fluids injection rates (m ³ /day)				RF	cSOR
				P1	P2	P3	P4		
GA-1 (Random)	445	27	0.9564	7.7	8.4	7.7	7.0	61.2%	1.967
GA-1 (Average)	442	25	0.9535	7.8	8.4	7.7	6.7	60.9%	1.966
GA-1 (Minimax)	434	22	0.9557	8.1	8.8	7.9	6.8	61.9%	1.991
SA	341	-	0.9577	7.8	8.6	7.8	7.0	61.6%	1.976
SA reached 0.9548	169	-	0.9548	8.5	8.7	7.7	6.9	62.1%	1.997
OGA-1	133	5	0.9548	8.1	8.8	8.0	7.0	62.2%	2.003
HA-GA	265	23	1.3448	8.8	9.0	8.1	6.7	65.3%	0.925

Table 4-7: Optimized Hexane Mole Fraction.

P1	P2	P3	P4
0.30	0.24	0.29	0.26

Figures

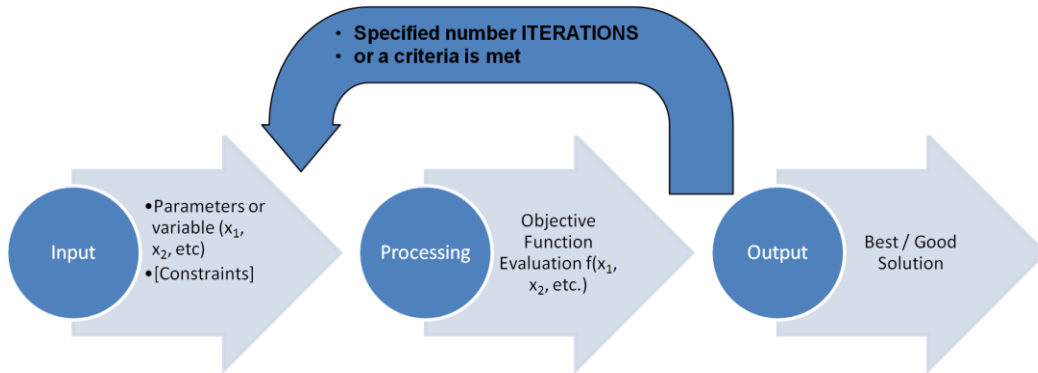


Figure 4-1: Schematic representation of optimization process.

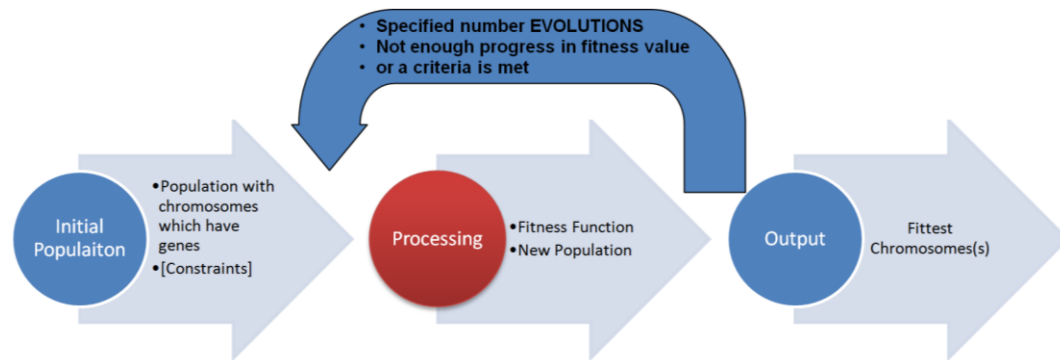


Figure 4-2: Optimization process in Genetic Algorithm terminology.

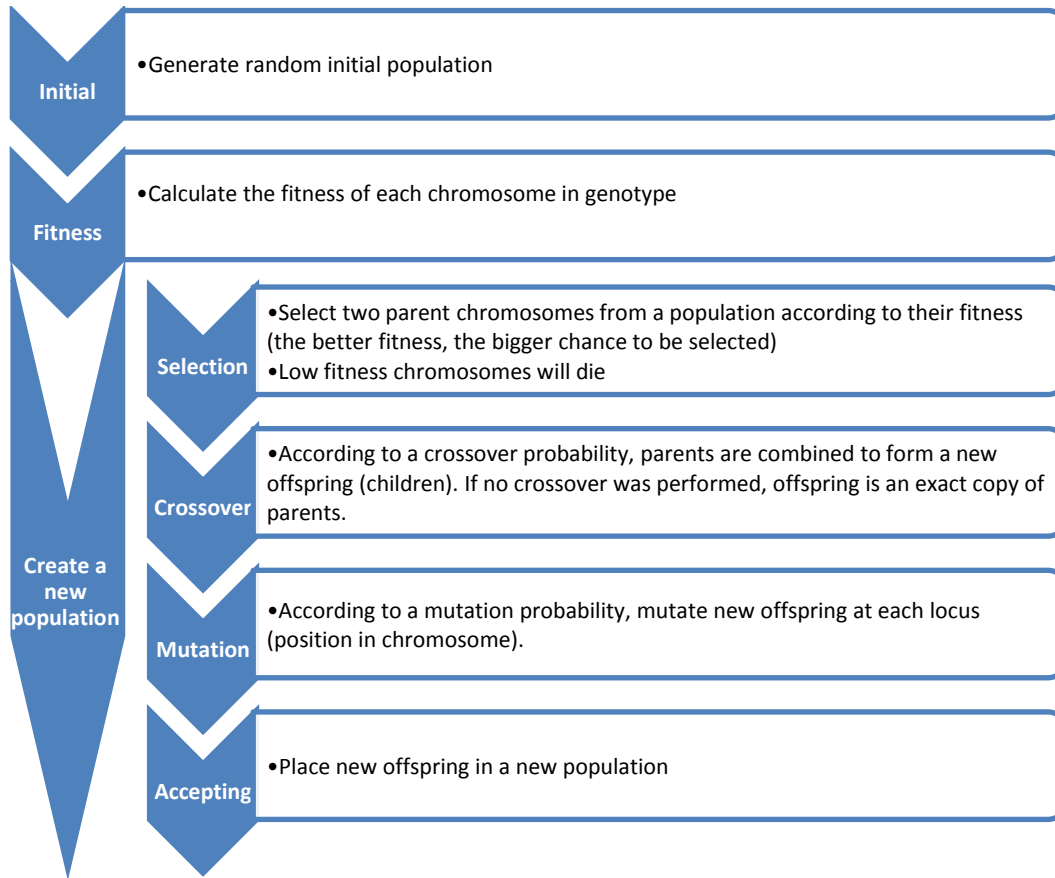


Figure 4-3: Genetic Algorithm flow diagram.

	Gene	Gene	Gene	Gene	Gene
Parent Chromosome 1	0111000011	1111101000	1000100110	101101110	11001100010
Parent Chromosome 2	11111001111	1001000010	1110011111	1000010010	11000100000
Child Chromosome 1	0111000011	1111101000	1110011111	1000010010	11000100000
Child Chromosome 2	11111001111	1001000010	1000100110	101101110	11001100010

Figure 4-4: Example of crossover of two parent chromosomes.

	Gene	Gene	Gene	Gene	Gene
Parent Chromosome	10101111	11110010111	11100101010	1001011111	10110100100
Child Chromosome	10101111	01110010111	11100101010	1001011111	10110100100

Figure 4-5: Example of mutation of a parent chromosome.

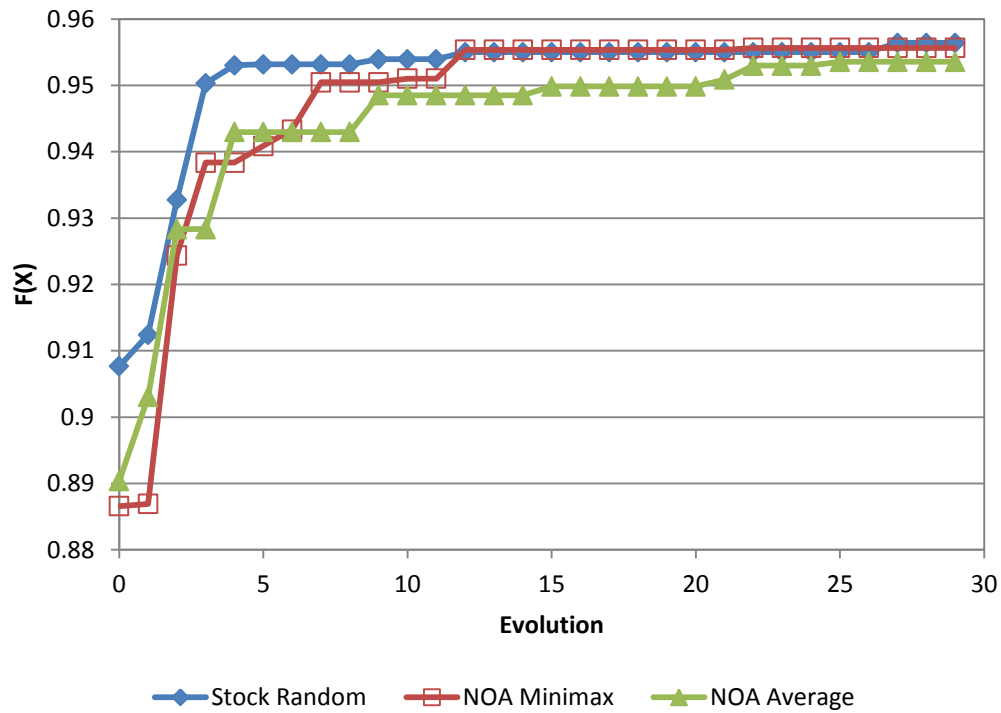


Figure 4-6: Function value for the GA with different ways of generating initial population.

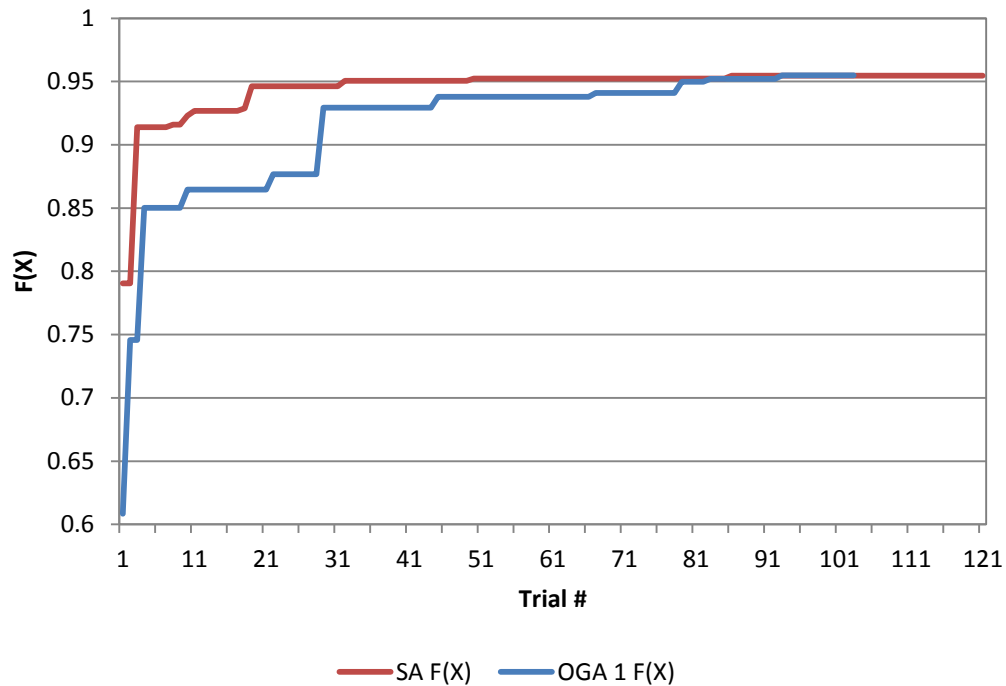


Figure 4-7: Convergence speed comparison between SA and Optimized GA case.

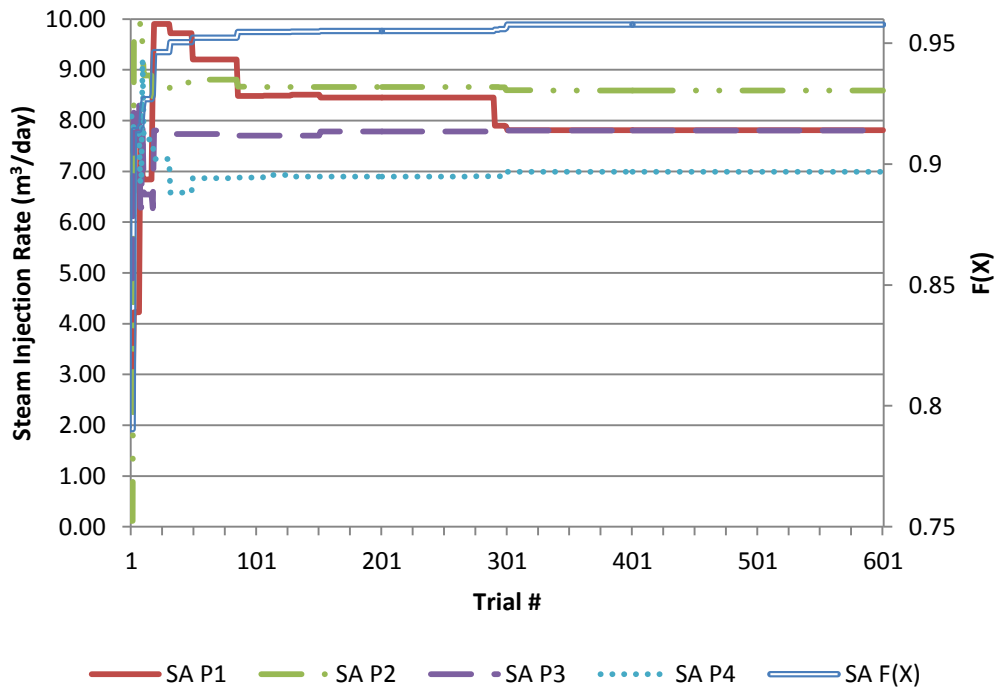


Figure 4-8: Simulated Annealing (SA) function value ($F(X)$) and injection rates (X values).

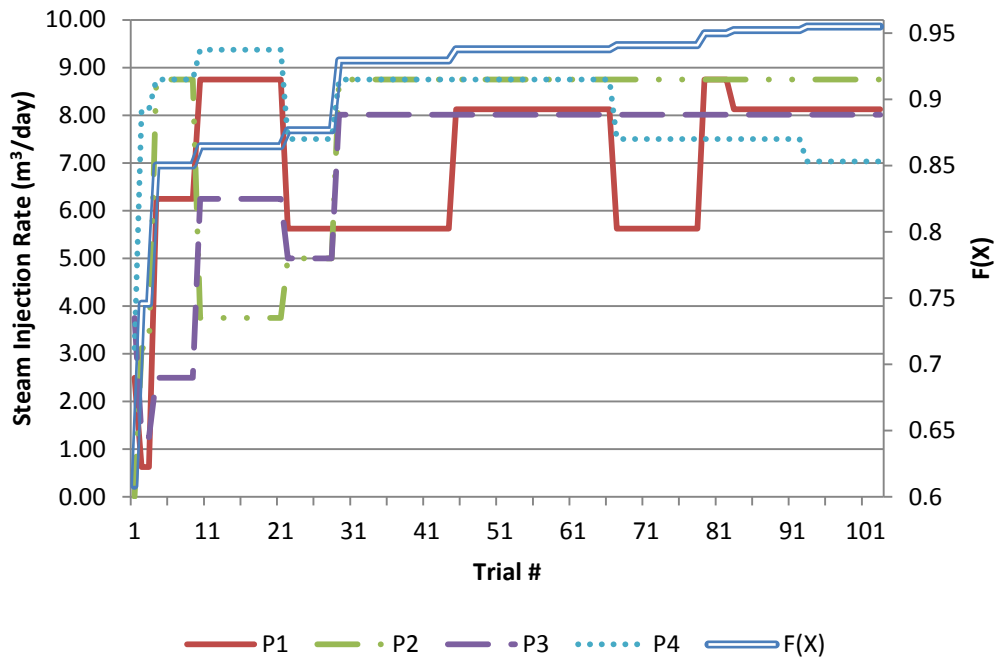


Figure 4-9: Optimized Genetic Algorithm Case 1 (OGA-1) function value ($F(X)$) and injection rates (X values).

Chapter 5: Design of Solvent-Assisted SAGD Processes in Heterogeneous Reservoirs Using Hybrid Optimization Techniques

Abstract

Many Steam Assisted Gravity Drainage (SAGD) optimization studies published in the literature combined numerical simulation with graphical or analytical techniques for design and performance evaluation. There have been numerous efforts that integrated the simulation exercise with global optimization algorithms. Some studies focused on optimization of cumulative steam-to-oil ratio (cSOR) in SAGD by altering steam injection rates, while others focused on optimization of cumulative net energy-to-oil ratio (cEOR) in solvent-additive SAGD by altering injection pressures and fraction of solvent in the injection stream. Several studies also considered total project net present value calculation by changing total project area, capital cost intensities, solvent prices, and risk factors to determine the well spacing and drilling schedule. Optimization techniques commonly used in those studies were scattered search, simulated annealing, and genetic algorithm (GA). However, the applications of hybrid genetic algorithm were rarely found.

In this chapter, we focused on optimization of solvent-assisted SAGD using various GA implementations. In our models, hexane was selected to be co-injected with steam. The objective function, defined based on cumulative steam-oil ratio (cSOR) and recovery factor, was optimized by changing injection pressures, production pressures, and injected solvent-to-steam ratio. Techniques including orthogonal arrays (OA) for experimental design (e.g. Taguchi's arrays) and proxy models for objective function evaluations were incorporated with the GA method to improve computational and convergence efficiency. Results from these hybrid approaches revealed that an optimized solution could be achieved with less CPU time (e.g. fewer number of iterations) compared to the conventional GA method. Sensitivity analysis was also conducted on the choice of proxy model to study the robustness of the proposed methods.

To investigate the effects of heterogeneity in the design process, optimization of solvent-assisted SAGD was performed on various synthetic heterogeneous reservoir models of porosity, permeability, and shale distributions. Our results highlight the potential application of the proposed techniques in other solvent-enhanced heavy oil recovery processes.

Introduction

Different versions of steam injection are used to extract most of Alberta's oil sand reserves (Al-Bahlani and Babadagli, 2009). The most common application is Steam Assisted Gravity Drainage (SAGD) recovery. It, however, requires generation of excessive amount of steam, which is very costly and has adverse environmental impacts, and it is often considered as a limiting factor in the efficiency of the entire process. One of the suggested ways to reduce steam consumption is addition of solvent to steam to maximize the recovery.

Several studies focused on optimization of SAGD processes that are with or without solvent addition. A number of efforts focused on utilizing global optimization techniques. Gates and Chakrabarty (2006) used genetic algorithm in order to optimize SAGD operating conditions such as steam injection rates to reduce cumulative steam-to-oil ratio (cSOR). The same authors have also implemented simulated annealing to optimize expanded solvent SAGD (ES-SAGD) by altering the fraction of solvent in the injected steam and the injection pressures in order to reduce cumulative net energy-to-oil ratio (cEOR) (Gates and Chakrabarty, 2008). Yang et al. (2009) applied the Designed Exploration and Controlled Evolution (DECE) algorithm to optimize the net present value (NPV) of a three-dimensional model. Peterson et al. (2010) utilized genetic algorithm to optimize steam and solvent rates on solvent-additive SAGD to maximize NPV per hectare of land (NPV/ha).

Having an efficient and robust optimization technique is critical in the design of SAGD or solvent-additive SAGD processes. Hence, this work focuses on hybrid techniques to enhance the computational efficiency of the Genetic Algorithm to design solvent-additive SAGD processes in heterogeneous reservoirs.

Methodology

Global Optimization Techniques

In this chapter, we adopted the Genetic Algorithm (GA) and integrated it with two other techniques in a hybrid formulation. GA is a stochastic search technique based on the principle of "survival of the fittest" (Guyaguler et al., 2002; Chen et al., 2010). An initial population or genotype is constructed by sampling the solution space randomly. Individual members of the population are called "chromosomes", and they define the parameter sets for the optimization problem. In each evolution, the fitness of each chromosome is calculated. Then, multiple pairs are selected based on their fitness value to create an offspring via crossover and mutation. The new offspring is inserted in the population, while the chromosomes with lowest fitness values are discarded. **Figure 5-1** summarizes the mechanisms of a typical GA algorithm.

To improve the convergence behaviour and computational efficiency of GA, we proposed a hybrid formulation by integrating the following two techniques into the conventional framework of GA:

Orthogonal Array and Nearly-Orthogonal Array for Initial Population Generation

Techniques from the experimental design literature, namely Orthogonal Array (OA) and Nearly-Orthogonal Array (NOA), can be implemented with GA to improve the quality of initial population (Chen et al., 2010) by generating evenly distributed samples while reducing the redundancy between chromosomes. The objective is to design experiments or chromosomes by determining the levels at which the parameters should be varied. Instead of testing all combinations of parameters at all levels, only the ones containing principal information are included. This reduces the population size and the associated computational costs. In this study, we used Gendex DOE Toolkit (website: <http://designcomputing.net/gendex>) to generate nearly-orthogonal arrays based on the Taguchi method average criterion described by Ma et. al. (2000) and Lu et. al. (2003).

Proxy Method for Objective Function Evaluation

As can be seen in **Figure 5-1**, the fitness function must be evaluated for every chromosome at every evolution. In our particular application, evaluation of the fitness function involves calculation of the recovery factor, typically obtained from results of a numerical flow simulation. Depending on the level of complexity of the processes that are being modeled, each flow simulation could take up to days to complete. Hence, costs of objective function evaluation are often the most important computational considerations in any optimization scheme. Proxy methods are viable “cheaper” alternatives that approximate the actual fitness function to enhance computing efficiency. The technique implemented in this study was the response surface method. Response surface is a relationship between the parameter sets and the corresponding fitness function. Once calibrated in the form of regression, it can be used as a proxy for flow simulation and allows the fitness function to be evaluated rapidly. In particular, we compared the first-order linear model and the second-order non-linear model, as discussed in Myers and Montgomery (2002). Equations for the linear and non-linear models are shown in Eqs. 1 and 2, respectively, where J is the response (fitness function value), u_i 's are the variables (optimization parameters), β_i 's are the regression coefficients, and ϵ is an error term.

$$J = \beta_0 + \beta_1 u_1 + \cdots + \beta_n u_n + \epsilon \quad (1)$$

$$J = \beta_0 + \beta_1 u_1 + \cdots + \beta_n u_n + \sum_{i=1}^n \beta_{ii} u_i^2 + \sum_{i < j} \sum_{j=2}^n \beta_{ij} u_i u_j + \epsilon \quad (2)$$

The regression equation for both models is expressed in Eq. 3:

$$\boldsymbol{\beta} = (\mathbf{U}^T \mathbf{U})^{-1} \mathbf{U}^T \mathbf{J} \quad (3)$$

where \mathbf{J} is a vector that contains all the response, $\boldsymbol{\beta}$ is a vector which contains all regression coefficients and \mathbf{U} is a matrix with all the \mathbf{u} vectors evaluated.

In this research, we used the JGAP package (Java Genetic Algorithm Package (JGAP) website: <http://jgap.sourceforge.net/>) for the GA modeling.

Objective Function

Profit maximization and cost reduction are important aspects in many engineering projects, especially in enhanced oil recovery applications. In this chapter, our focus is to maximize the recovery and minimize cumulative steam-oil-ratio during SAGD application with solvent addition. After several trials (Algosayir et al., 2011), we proposed an equally-weighted objective function (F) for recovery factor (RF) and cumulative steam oil ratio (cSOR), which is different from earlier works mentioned previously. Ideally, the objective function should be dimensionless. Therefore, the RF is assigned a unit weight because its value ranges between 0 and 1, while cSOR has to be normalized to be between 0 and 1. This is achieved by dividing its value by a user-defined maximum observable cumulative steam oil ratio [$\max(\text{cSOR})$]. Assembling the various terms together, our proposed GA implementation assesses and aims to maximize the following objective (fitness) function:

$$F(x_1, x_2, x_3, x_4, x_5, x_6) = RF - \frac{\text{cSOR}}{\max(\text{cSOR})} + 1 \quad (4)$$

where $x_1, x_2, x_3, x_4, x_5, x_6$ are the optimized parameters. In our study, the optimization process evaluates Eq. 1 by adjusting the 10-year injection pressure, production pressure, and hexane mole fraction over two 5 years periods (a total of 6 model parameters). Ranges of these model parameters are shown in **Table 5-1**. The normalizing parameter [$\max(\text{cSOR})$] is set to a value of three (in m^3/m^3) for the homogenous Expanded Solvent SAGD (ES-SAGD) case, and a value of five (m^3/m^3) was used for the heterogeneous cases. It should be noted that an adjusting factor of “1” is added to the fitness function in Eq. 6 to shift its range from [-1, 1] to [0, 2], such that a positive objective function value would always be obtained.

All optimization cases follow the same Genetic Algorithm configuration as presented in **Table 5-2**. In each evolution, 35% of the population chromosomes are crossovered to generate new chromosomes, and 3% of them are mutated by changing parts of the bit in binary encoding. This crossover and mutation process is repeated 30 times per evolution and, in each evolution, a constant population size of 30 is maintained.

Case Study

Model Description

In our case studies, three two-dimensional simulation models were constructed originally based on the laboratory-scale simulation model with homogeneous and isotropic reservoir properties provided by Ayodele et al. (2010). These models were subsequently scaled-up to the field dimensions by adjusting the grid definition as described in **Table 5-3**. The homogenous model has a constant porosity of 20% and permeability of 1 Darcy for all cells. The homogeneous model was used to (1) investigate the sensitivity of the optimization results to the choice of response surface proxy models and (2) assess the computational savings with the use of proxy techniques as compared to the conventional method (no proxy). Success with the homogeneous case allows us to subsequently apply the proposed implementation to cases with heterogeneous reservoir properties. In particular, two heterogeneous models exhibiting different shale distributions (30% and 10% shale content) were used in our study, and they are shown in **Figure 5-2** and **Figure 5-3**, respectively.

Response Surface Proxy Models

To reduce the computation time required, a linear first-order (Eq. 1) and non-linear second-order (Eq. 2) response surface models were constructed for the three reservoir models. These proxies (or response surfaces) were calibrated using flow simulation results of an initial population, constructed using the nearly-orthogonal array (NOA) $L_{30}(17^6)$ consists of 6 factors, 17 levels, and 30 runs (**Table 5-4**) and applying Eqs. 1-3.

Results and Discussion

The primary objective of this chapter is to study the impacts of reservoir heterogeneities on the optimization of solvent-assisted SAGD recovery process. Given that objective function evaluations using detailed flow simulation results are extremely time consuming, particularly for heterogeneous reservoirs, our first step is to evaluate various response surface proxy techniques that can be easily integrated for GA optimization.

First, we established a base case by performing conventional GA optimization (no proxy) for a homogenous reservoir with an initial population constructed using the NOA in **Table 5-4**. The entire experiment required a total of 52 hours to execute about 900 simulation cases to obtain the optimum, which has 1.31 fitness value, 68% recovery and 1.13 (m^3/m^3) cSOR. **Figure 5-4** shows the oil production profile for the optimum field scale case. In order to evaluate the reproducibility of our optimization results, we repeated the optimization experiment and similar results were obtained: 1.32 fitness value, 69% recovery and 1.14 (m^3/m^3) cSOR. Results of the two trials are labelled as “Conventional (1)” and “Conventional (2)”, respectively in **Table 5-5**. Next, linear and

non-linear response surface proxies were tested. The proxies were constructed based on flow simulation results of the initial population generated using the NOA. In other words, the computation requirement was reduced significantly to only that was required to execute the cases of the initial population. It was observed that the non-linear proxy approximated the initial data actual responses closely while the match with the linear proxy was not satisfactory as shown in **Figure 5-5**. The trials are sorted based on the fitness values obtained from actual flow simulations.

Similarly, we built linear and non-linear proxies for the 30% and 10% shale content (heterogeneous) cases as shown in **Figure 5-6** and **Figure 5-7**, respectively. In the 30% case, the non-linear shows excellent match, while in the 10% case, it did not yield a satisfactory match.

In the homogenous case, optimization performed with the linear proxy was completely unsuccessful as it was not able to improve the fitness during the evolutions. On the other hand, the non-linear proxy showed very good improvement in the fitness function value during the evolutions as shown in **Figure 5-8**. In order to compare the optimal solution obtained using the proxy to that of the conventional approach, we performed flow simulation on the final optimized solution to obtain the actual response J , instead of the proxy estimated value J' . In the case of linear proxy, the actual response J was lower than the best case in the initial population J_0 , indicating that the fitness function was not maximized. In contrast, for the case of non-linear proxy, the actual response J matched closely with the conventional optimization result even though the proxy was amplifying the response values. This is due to the extrapolation of the response surface corresponding to parts of parameter space. The actual response value for the optimum case J_{opt} was 1.3 with 68% recovery and 1.15 (m^3/m^3) cSOR as shown in Table 5-5. It is important to note that this result was obtained in 105 minutes where we saved about 97% of the computational efforts from the conventional optimization as indicated in **Table 5-6**.

This improvement in computational efficiency becomes particularly important in applications for heterogeneous reservoirs because of the increase in flow simulation execution time with reservoir heterogeneity. On average, a single flow simulation in this study takes about five minutes for the 30% shale case and about 6 minutes for the 10% shale case to execute. If optimization of these heterogeneous models was performed with the conventional GA implementation, the computational time would have been over three days, thus rendering the method unfeasible due to computational constraints. This consideration motivates the use of proxy for objective function evaluation and allows optimization to be performed efficiently in the case of heterogeneous reservoirs. Our proposed hybrid approach took 138 minutes for the 30% shale case and 187 minutes for 10% shale case to complete (Table 5-6). This is equivalent to a savings of 152 hours (or approximately 97%) of the total computational time.

Our results suggest that the performance of the linear proxy in the heterogeneous cases was better than the homogenous case; the fitness function increased with evolution shown in **Figure 5-9** and **Figure 5-10** as opposed to staying constant in **Figure 5-8**. However, the non-linear proxy was still providing better results. For the 30% shale case, the linear proxy actual response value for the optimum case J_{opt} was 0.65 with 5% recovery and 1.98 (m^3/m^3) cSOR while the non-linear proxy actual response value for the optimum case J_{opt} was 0.71 with 7% recovery and 1.77 (m^3/m^3) cSOR. Similarly, in the 10% shale case, the linear proxy actual response value for the optimum case J_{opt} was 1.13 with 40% recovery and 1.28 (m^3/m^3) cSOR while the non-linear proxy actual response value for the optimum case J_{opt} was 1.14 with 42% recovery and 1.38 (m^3/m^3) cSOR. Optimization results of all cases are shown in **Table 5-5**. It is worthwhile to point out that the calculated response value J' of the linear proxy is similar in range to the actual value J , while higher degree of extrapolation in the non-linear proxy model leads to a larger deviation from this range.

Several ways were investigated to reduce the degree of extrapolation and to obtain more accurate approximation of the fitness function using the non-linear proxy. The approach that gave the most promising results was the one where flow simulation was performed for the fittest chromosome after every evolution, and the corresponding simulation result would be incorporated to fit a new proxy. It was observed that updating the proxy after evolution with an additional flow simulation output using the fittest chromosome could significantly improve the predictability of the non-linear proxy. The flow diagram of the modified approach is shown in **Figure 5-11**. It is noted from **Figure 5-12** that each time the proxy was updated using the fittest chromosome's simulation results, more accurate proxy values (as compared to the actual flow simulation outputs) were achieved. **Figure 5-12** also shows that towards the end of the optimization exercise, there was no noticeable differences between the proxy values and actual flow simulation outputs, indicating that the predictability of the non-linear was significantly improved. Finally, as shown in **Table 5-5**, applying this modified approach to the homogeneous case achieved a better (more optimized) scenario than the conventional method with a higher fitness value of 1.4, a higher recovery of 76% and a lower cSOR of 1.07 (m^3/m^3).

The modified approach was also applied to the 10% and 30% shale cases to update the non-linear proxy after every evolution. Similar improvement as in the homogeneous case was achieved: updating the proxy using the fittest chromosome after every evolution gave the best optimized parameters among all scenarios, while the proxy predictability was excellent (as evidenced by the identical values for J and J' in **Table 5-5**). The optimization results (fitness value as a function of evolution) are shown in **Figure 5-13** and **Figure 5-14**. It should be noted that the total number of flow simulation runs performed in this modified approach was 90 (30 for the initial population

plus an additional one per every evolution). The increased computational expenses could easily be justified given the considerable improvements in the predictability of the response surface models and the final optimized scenario. Furthermore, the computational savings as compared to the conventional approach is still important (Table 5-6).

Conclusions

Proxy methods are convenient ways to improve efficiency of an optimization algorithm. In our application, we observed that the execution time for objective function evaluation is the largest. Other factors like the algorithm convergence speed and the input/output (I/O) processing that serves as an interface between the flow simulator and the rest of the algorithm implementation are negligible in comparison to the time needed to execute the simulation. This computational consideration becomes particularly important for heterogeneous reservoirs. To alleviate the computational burden, we constructed the initial population by the process of experimental design using nearly-orthogonal arrays. Flow simulations were performed on this initial population to calibrate a response surface, which was subsequently used as a proxy for fitness function evaluation. Our initial results verified the applicability of the proxy for the homogeneous case. It is important to note that a proxy should be chosen with care such that it gives an accurate representation of the relationship between the objective function and its control variables; we found in our cases that the non-linear proxy is better for this purpose. Although it yields better optimal solution, it does not necessarily reflect the true fitness function value precisely due to non-linear extrapolation corresponding to parts of the parameter space. Therefore, a proxy-updating step was introduced after evolution in which flow simulation results of the fittest chromosome were added to fit a new proxy. Our results indicated that this updating step not only improves the predictability of the response surface model, it also enhances the capability of the GA algorithm to identify a more optimized set of model parameters than the conventional approach in a computationally-efficient manner. This improvement (as compared to the case where the proxy was calibrated using only simulation runs of the initial population) should justify the incremental costs incurred because of additional flow simulation runs being performed in the updating step.

Nomenclature

cEOR: cumulative net energy-to-oil ratio.

cSOR: steam-to-oil ratio.

F(X): objective function value.

GA: Genetic Algorithm.

HMF: Hexane injection mole fraction.

IBHP: Injector maximum Bottom-hole Pressure.

J: the actual response or actual objective function value calculated based simulation output for one trial.

J': the repose obtained from the regression model.

J₀: the best trial actual response in the initial population.

NL: Nonlinear Proxy

NOA: Nearly-Orthogonal Array.

NPV: Net Present Value.

OA: Orthogonal Array.

PBHP: Producer minimum Bottom-hole Pressure.

RF: Recovery Factor.

SAGD: Steam Assisted Gravity Drainage thermal recovery process.

u: a (1*n) vector which contains the optimization variables for a trial.

u_i : represent an optimization variable for one trial.

β_i : represent a regression coefficients for one trial.

J: a vector that contains all the trials response.

U: a matrix with all **u**'s.

β: a vector which contains all regression coefficients.

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Tables

Table 5-1: Optimized parameters' ranges

Optimization Parameters	Range
Injector maximum Bottom-hole Pressure (IBHP)	2100-2800 kPa
Producer minimum Bottom-hole Pressure (PBHP)	1500-2000 kPa
Hexane injection mole fraction (HMF)	0-0.2

Table 5-2: GA configuration

Item	Value
Crossover	0.35
Mutation	3%
Population	30
Evolutions	30

Table 5-3: Reservoir simulation input parameters

Item	Value
Grid	Cartesian 40*1*15
Grid Dimensions (I)	2 m
Grid Dimensions (J)	50 m
Grid Dimensions (K)	2 m
Initial Reservoir Temperature	20 oC
Initial Reservoir Pressure	2090 kPa

Table 5-4: Nearly-Orthogonal Array (6 factors, 17 levels, and 30 runs) used for generating initial population

Run	Factors					
	1	2	3	4	5	6
1	0.06	2275	1563	0.13	2581	2000
2	0.14	2319	1750	0.06	2144	1906
3	0.01	2538	1781	0.06	2406	1531
4	0.18	2144	1625	0.01	2319	1938
5	0.01	2756	1656	0.04	2713	1844
6	0.14	2669	1719	0.00	2800	1688
7	0.00	2713	2000	0.15	2494	1781
8	0.16	2100	1750	0.14	2625	1781
9	0.08	2144	1563	0.18	2231	1750
10	0.04	2450	1906	0.03	2231	1625
11	0.09	2231	1531	0.11	2450	1688
12	0.20	2363	1625	0.13	2363	1500
13	0.08	2581	1500	0.08	2100	1563
14	0.03	2406	1531	0.00	2319	1719
15	0.05	2319	1813	0.11	2756	1500
16	0.10	2188	1688	0.01	2188	1656
17	0.05	2450	1719	0.16	2450	1594
18	0.15	2625	1875	0.15	2669	1625
19	0.11	2494	1781	0.08	2494	1719
20	0.19	2494	1813	0.04	2100	1875
21	0.10	2581	1594	0.14	2144	1875
22	0.15	2538	1688	0.09	2538	1969
23	0.13	2100	1875	0.10	2406	1594
24	0.13	2800	1594	0.03	2275	1750
25	0.11	2188	1844	0.05	2625	1813
26	0.04	2231	1844	0.19	2581	1531
27	0.00	2275	1656	0.05	2275	1656
28	0.03	2625	1969	0.10	2363	1813
29	0.09	2363	1938	0.09	2188	1563
30	0.06	2406	1500	0.20	2538	1844

Table 5-5: Comparison of the selected solution values

Case	J ₀	J	J'	Period 1			Period 2			RF	cSOR (m ³ /m ³)	
				HMF	IBH P	PBH P	HMF	IBH P	PBH P			
Homogeneous	Conventional (1)	1.04	1.31	-	0.20	2616	1651	0.16	2669	1669	68%	1.13
	Conventional (2)	1.04	1.32	-	0.19	2756	1624	0.18	2650	1842	69%	1.14
	Linear Proxy	1.04	0.93	1.04	0.15	2625	1875	0.05	2756	1635	39%	1.38
	Non-Linear (NL) Proxy	1.04	1.30	3.66	0.20	2800	1512	0.19	2800	1506	68%	1.15
	Updated NL Proxy	1.04	1.4	1.4	0.20	2795	1515	0.16	2800	1576	76%	1.07
30% shale sand	Linear Proxy	0.58	0.65	0.75	0.20	2115	1986	0.20	2109	2000	5%	1.98
	Non-Linear Proxy	0.58	0.71	1.33	0.00	2124	2000	0.19	2286	1927	7%	1.77
	Updated NL Proxy	0.58	0.73	0.73	0	2104	1970	0.20	2116	1814	7%	1.69
10% shale sand	Linear Proxy	1.04	1.13	1.15	0.20	2793	1504	0.20	2756	1500	40%	1.23
	Non-Linear Proxy	1.04	1.14	5.15	0.20	2777	1536	0.19	2756	1523	42%	1.38
	Updated NL Proxy	1.04	1.2	1.2	0.05	2450	1718	0.16	2450	1593	39%	0.96

Table 5-6: Cases execution time

	Case	# Actual Simulation runs	Average time per simulation run	Total Execution Time
Homogenous	Conventional	900	3.5 minutes	2 Days, 4 hours and 23 minutes
	Linear Proxy	30	3.5 minutes	1 hours and 45 minutes
	Non-Linear (NL) Proxy	30	3.5 minutes	1 hours and 45 minutes
	Updated NL Proxy	90	3.5 minutes	5 hours and 15 minutes
30% shale sand	Linear Proxy	30	4.6 minutes	2 hours and 18 minutes
	Non-Linear Proxy	30	4.6 minutes	2 hours and 18 minutes
	Updated NL Proxy	90	4.6 minutes	6 hours and 54 minutes
10% shale sand	Linear Proxy	30	6.3 minutes	3 hours and 07 minutes
	Non-Linear Proxy	30	6.3 minutes	3 hours and 07 minutes
	Updated NL Proxy	90	6.3 minutes	9 hours and 27 minutes

* The homogenous cases executed by utilizing all the two 6 cores and 2.66 GHz processors of total 12 cores, where the heterogeneous cases was executed in 6 cores 2.66 GHz processor.

Figures

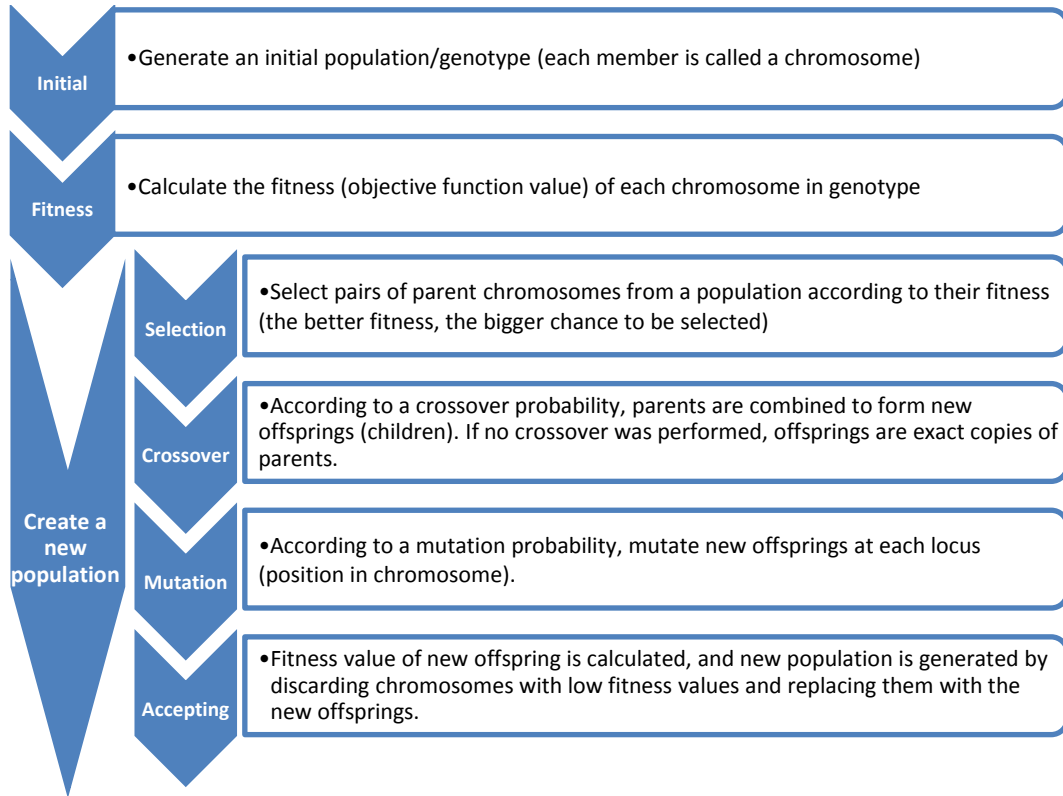


Figure 5-1: Conventional Genetic Algorithm flow diagram (modified from Algosayir et al. 2011).

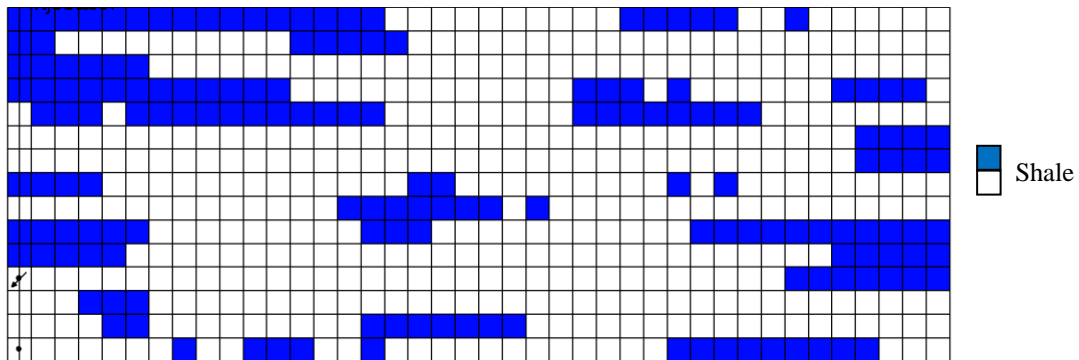


Figure 5-2: 30% shale sand distribution.

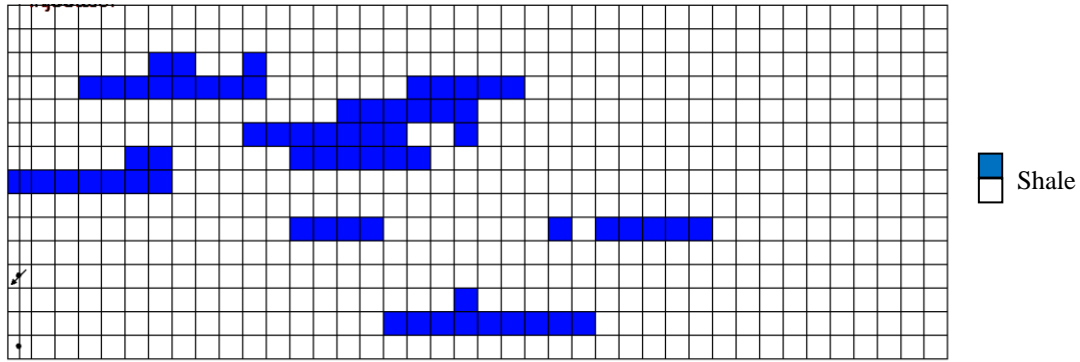


Figure 5-3: 10% shale sand distribution.

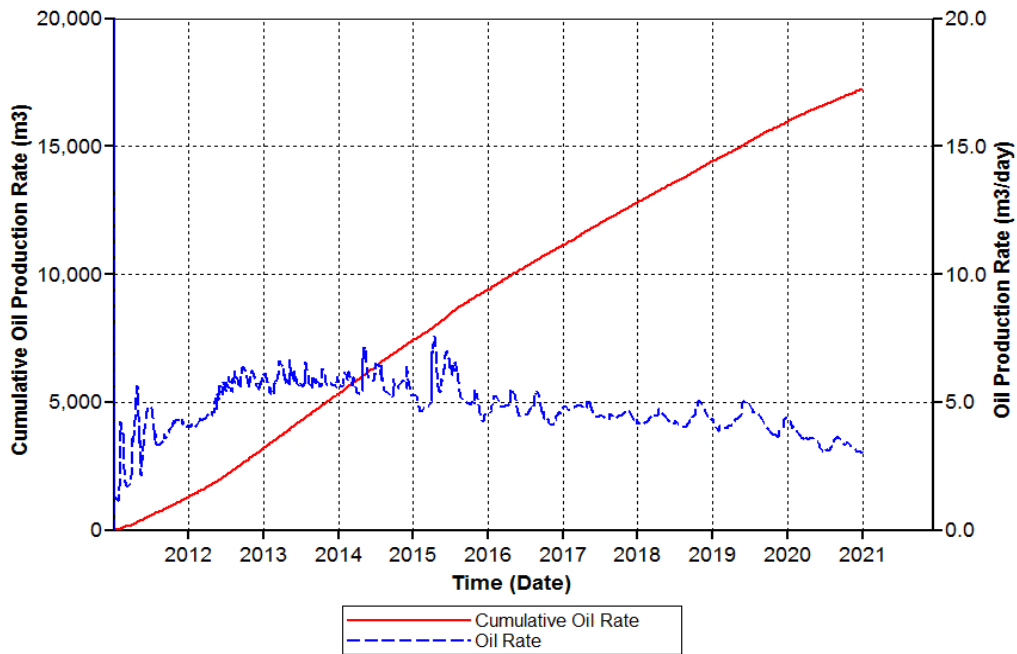


Figure 5-4: Optimized ES-SAGD homogeneous case oil production profile.

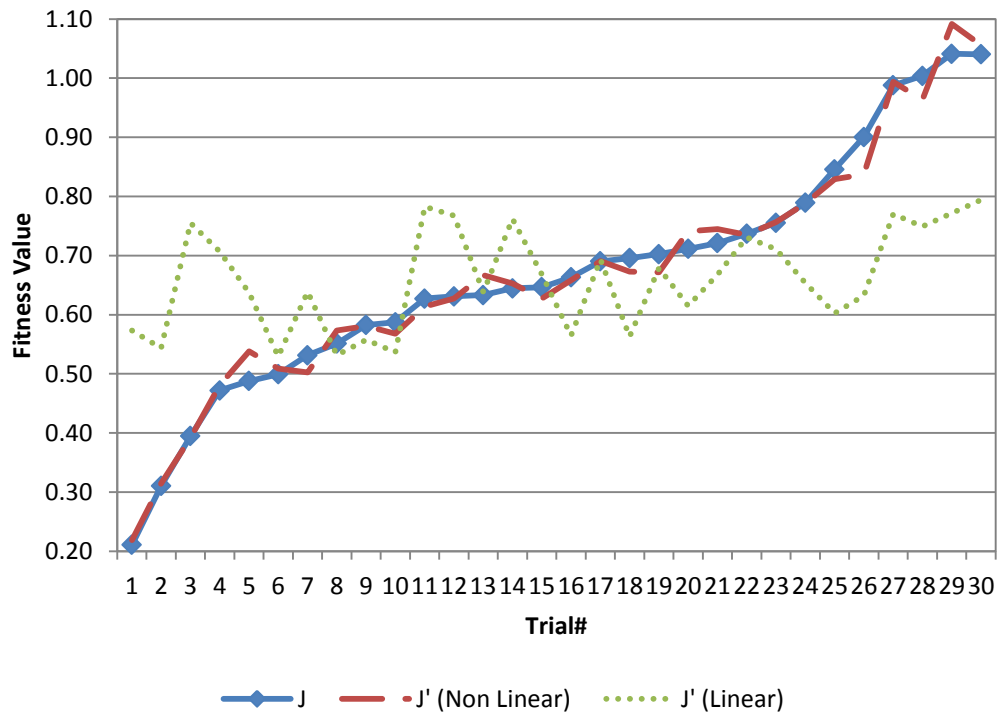


Figure 5-5: Proxies approximation for the homogeneous case: trials are sorted based on actual flow simulation fitness value J.

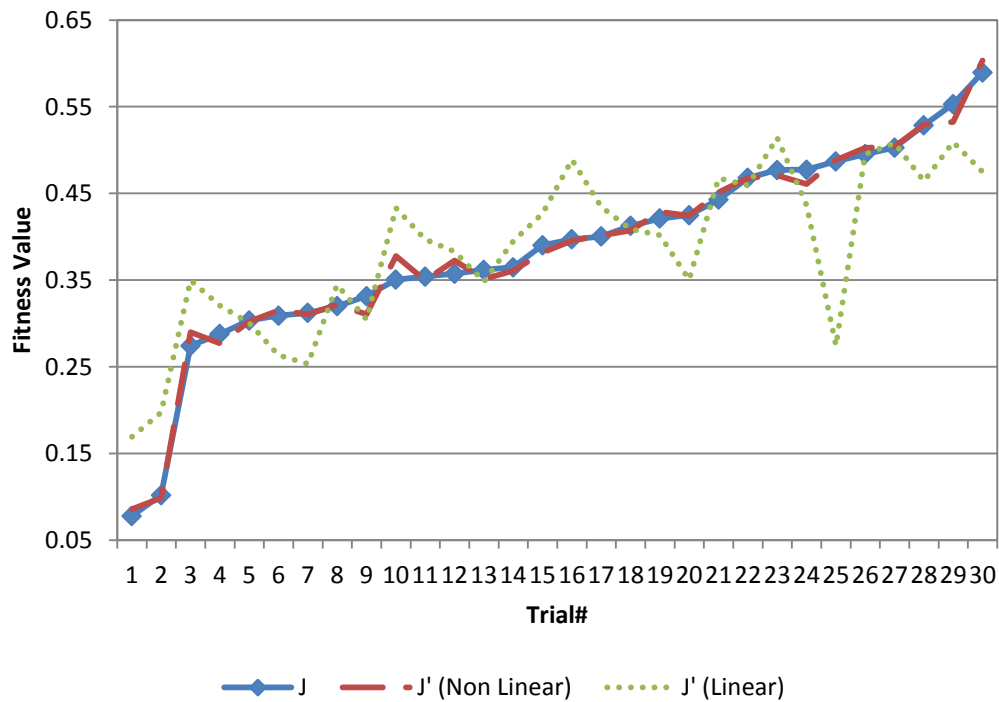


Figure 5-6: Proxy approximation for the 30% shale case.

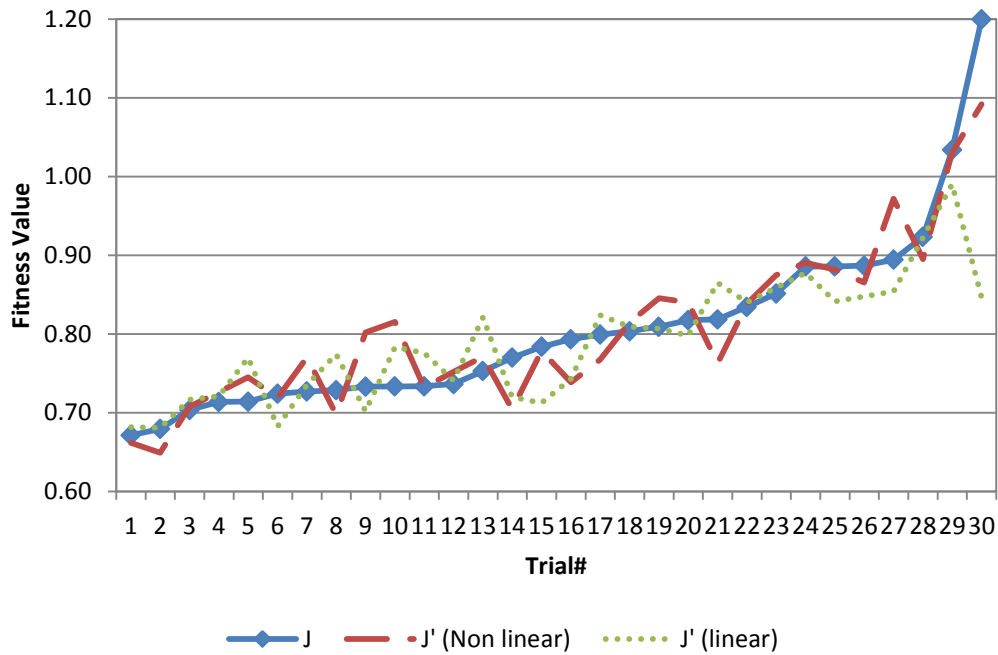


Figure 5-7: Proxy approximation for the 10% shale case.

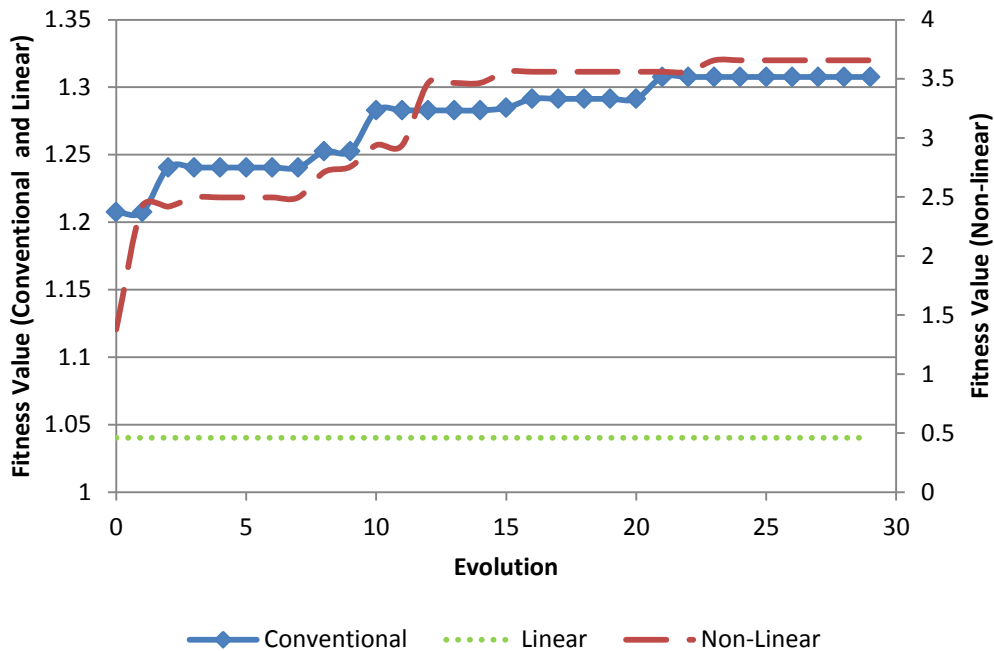


Figure 5-8: Fitness value as a function of evolution for the homogeneous case.

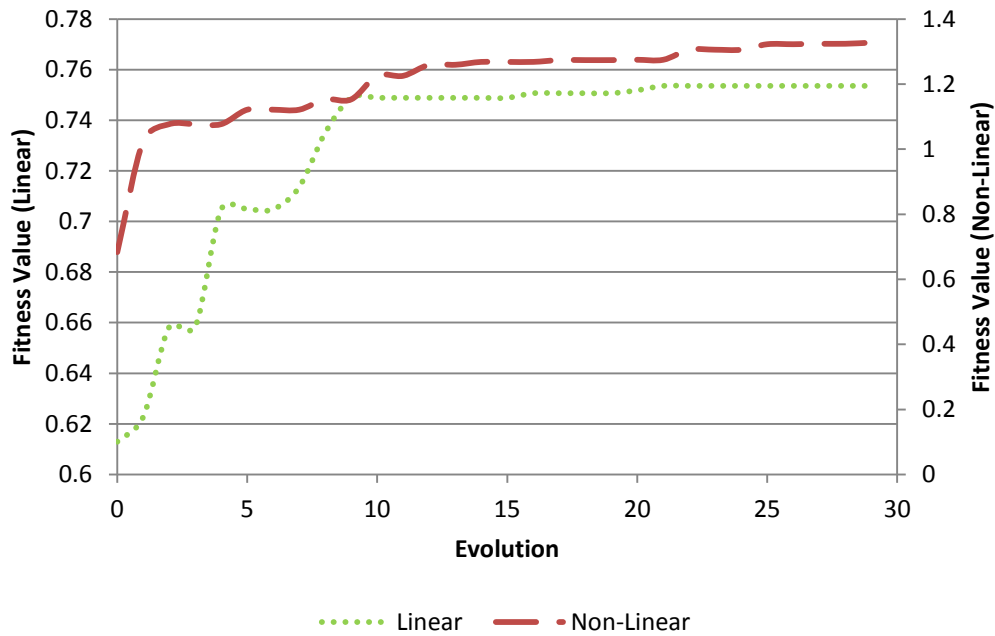


Figure 5-9: Fitness value as a function of evolution for the 30% shale case.

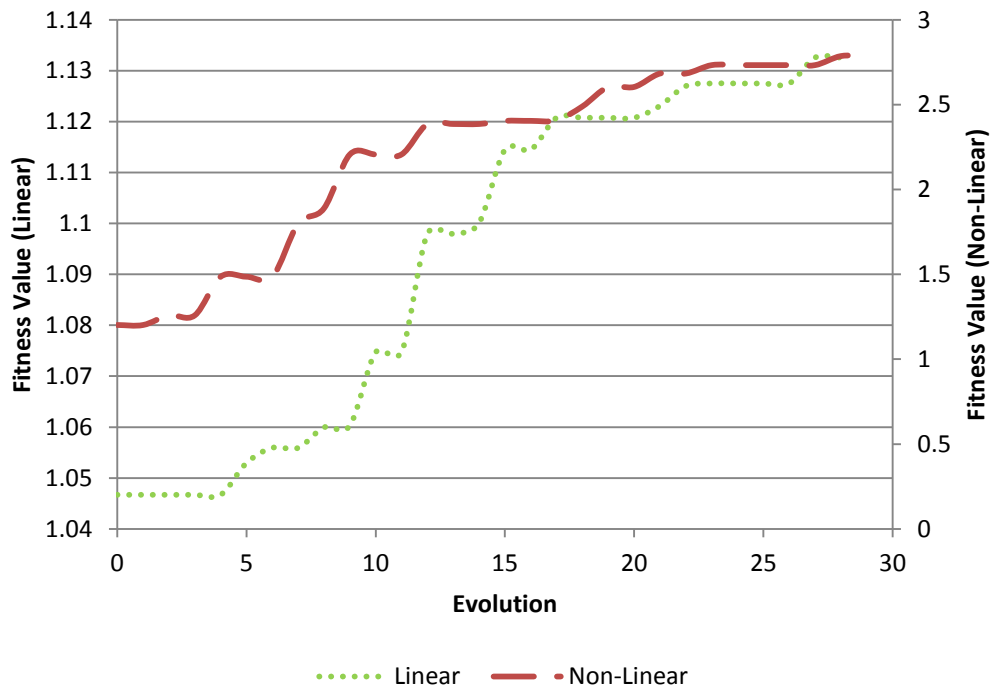


Figure 5-10: Fitness value as a function of evolution for the 10% shale case.

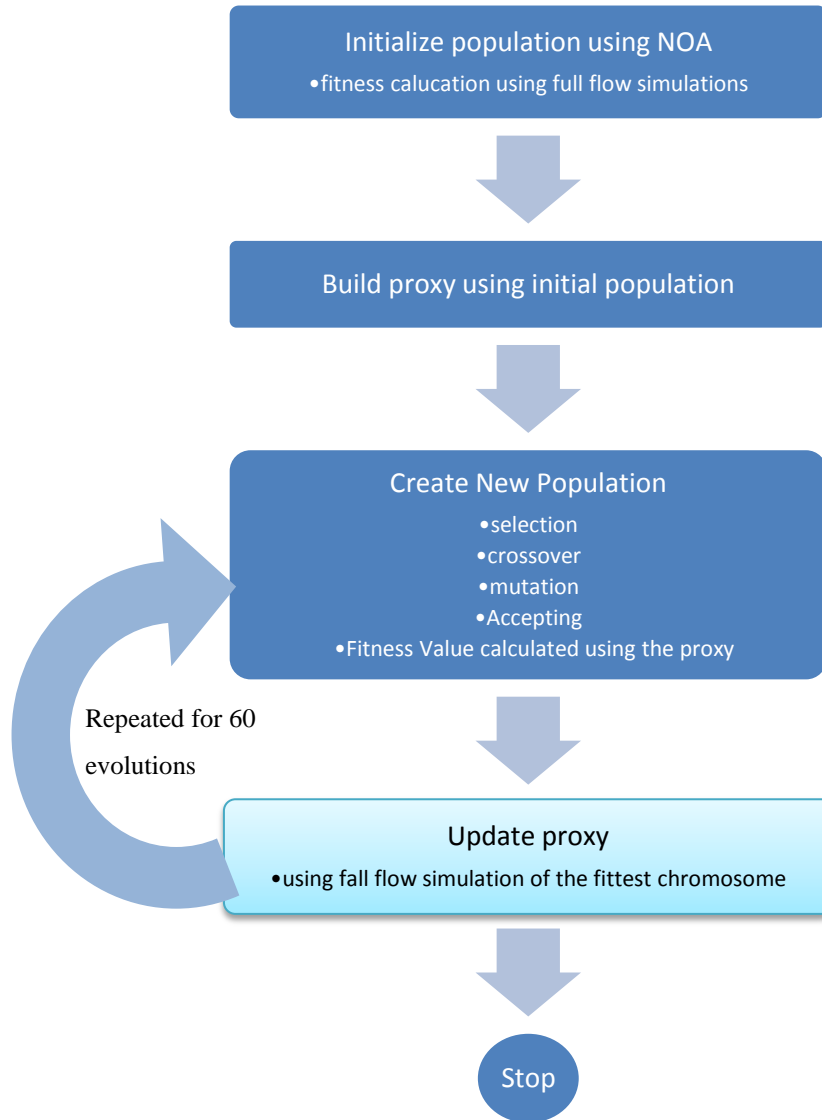


Figure 5-11: Flow diagram for the modified approach where proxy is updated with the additional flow simulation results of the fittest chromosomes after each evolution.

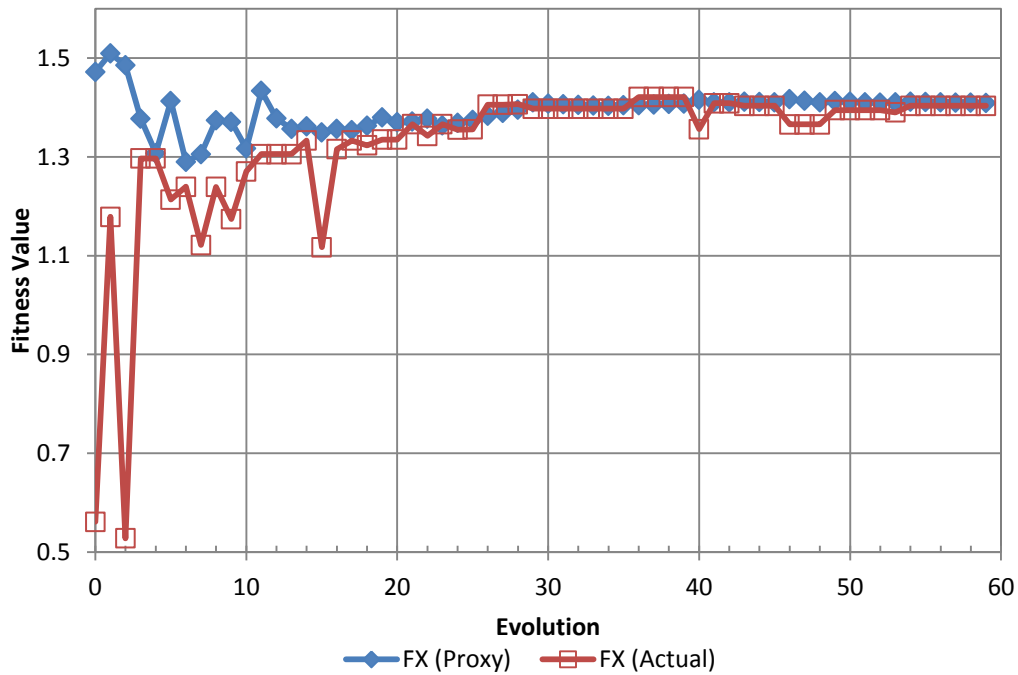


Figure 5-12: Fitness value as a function of evolution for the homogeneous case using the modified approach with non-linear proxy updating.

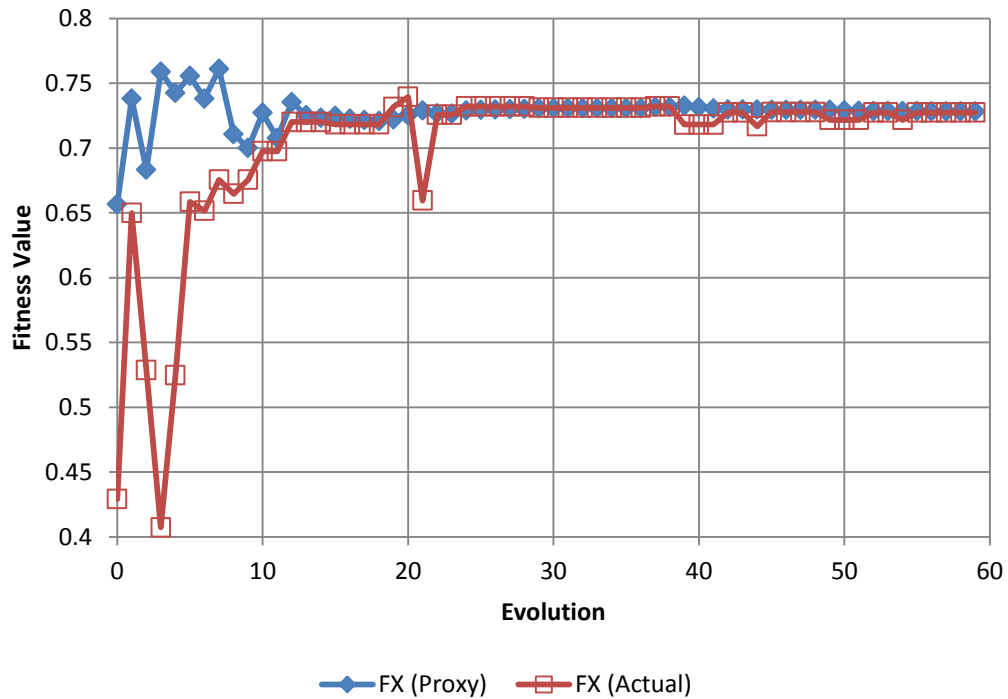


Figure 5-13: Fitness value as a function of evolution for the 30% shale case using the modified approach with non-linear proxy updating.

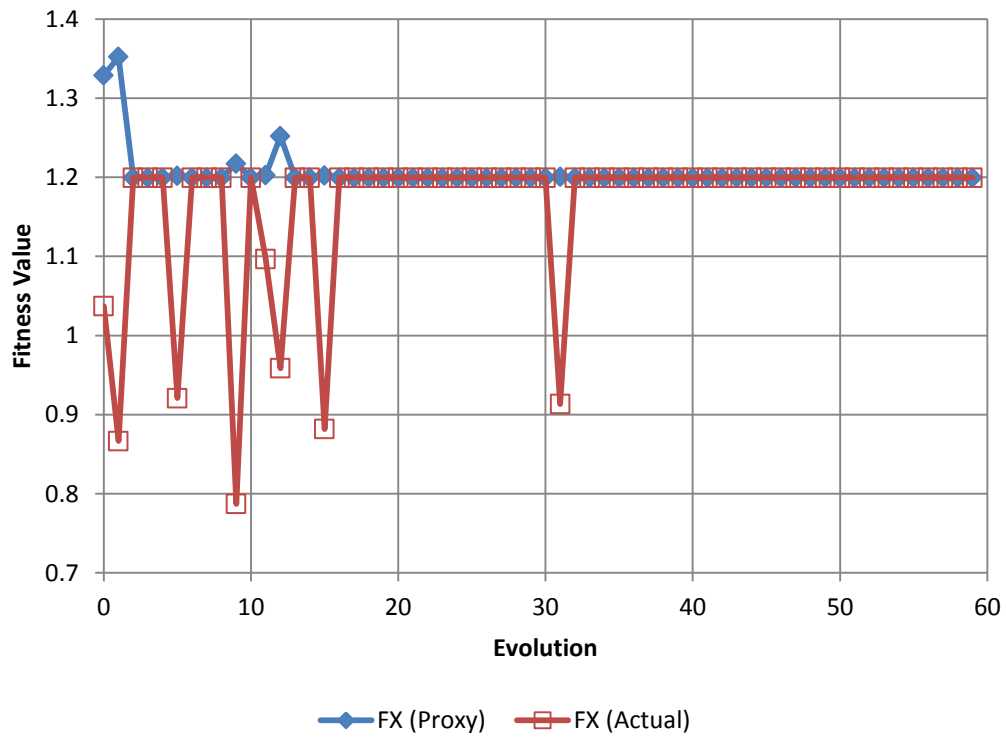


Figure 5-14: Fitness value as a function of evolution for the 10% shale case using the modified approach with non-linear proxy updating.

Chapter 6: Optimization of SOS-FR (Steam-Over-Solvent Injection in Fractured Reservoirs) Method Using Hybrid Techniques: Testing Cyclic Injection Case

Abstract

Many processes and techniques have been proposed to improve the heavy oil recovery from fractured reservoirs. Such complex processes require careful operation planning and management to achieve optimal efficiency with minimal costs and environmental impacts. Steam injection is one of the options for heavy-oil recovery from fractured reservoirs but significant steam requirement for effective matrix heating due to heterogeneous structure poses important challenges in terms of cost, water availability, and environment impacts due to water processing and steam generation. Al-Bahlani and Babadagli (2008, 2009a) proposed a new process called Steam-Over-Solvent in Fractured Reservoirs (SOS-FR) by adding solvent component to minimize the heat needed. The SOS-FR technique consists of a heating phase using steam injection, subsequent solvent injection, and low temperature steam injection for solvent retrieval and additional oil recovery. Optimization of this process is a critical step to determine optimal injection (and soaking) schedules as the heterogeneous structure of this kind of reservoirs may easily yield an inefficient process due to high cost and excessive use of steam and solvent. In this study, we adopted a global optimization scheme, where genetic algorithm is integrated with orthogonal arrays and response surface proxies for better convergence behavior and higher computational efficiency, to optimize the SOS-FR process for cyclic injection option. The results show that one may be able to double the profit obtained with the benchmark model using the optimal injection scheme suggested by our optimization procedure.

Introduction

Unconventional solutions are needed to overcome the challenge of heavy oil production. In high permeability non-fractured sand reservoirs, steam injection processes showed acceptable production, however, they require the availability of a large amount of water that is a major challenge in remote areas with limited water accessibility, and this water consumption has to be managed and processed in an environment friendly manner (Al-Bahlani and Babadagli, 2011).

Alternative to steam injection, Butler and Mokrys (1991) introduced the VAPEX (vapor extraction) process, which is pure solvent injection from a horizontal well to displace the oil by gravity drainage to another horizontal producer. Later, different schemes of steam/solvent injection were tested at laboratory or simulation conditions as well as field pilots. Nasr et al.

(2003) developed Expanding Solvent-SAGD (ES-SAGD) method to minimize the use of steam in heavy-oil production. This method relies on addition of small percentage of gas or liquid solvent into steam during steam assisted gravity drainage process (SAGD). Subsequently, steam-alternating-solvent (SAS) technique was introduced as an application of alternative injection of steam and solvent (Zhao et al., 2005; Zhao, 2007). Leaute and Carey (2007) demonstrated that addition of small amount solvent into steam during cyclic steam injection improves the recovery. Their technique called Liquid Addition to Steam for Enhancing Recovery (LASER) showed a success in a pilot scale field application.

A major consideration for these advanced recovery processes is that the recovery performance is highly influenced by factors such as steam and solvent injection rate, solvent concentration, injection pressure, and injection schedule. This matter of optimal design was addressed in the literature for several processes. For example, several studies employed global optimization techniques and detailed flow simulations. Gates and Chakrabarty (2006, 2008) used genetic algorithm and simulated annealing for SAGD and ES-SAGD (expanding solvent SAGD) optimization. Peterson et al. (2010) utilized genetic algorithm for solvent-additive SAGD optimization. Al-Gosayir et al. (2011b) studied the design of solvent-assisted SAGD processes in heterogeneous reservoirs using hybrid genetic algorithm. A more common approach has been the design and performance evaluation of these processes using a combination of numerical simulations, sensitivity analysis, and graphical or analytical techniques.

Optimization of steam/solvent methods in fractured carbonate reservoirs is more challenging as the efficiency becomes critically important due to excessive steam/solvent requirement for matrix oil recovery. Although ample amount of lab studies exist, steam injection in fractured carbonates is limited to a few field scale applications due to inefficiency of the process (Al-Bahlani and Babadagli, 2008). Al-Bahlani and Babadagli (2009a-b) suggested the use of solvent to reduce the cost of steam and improve the recovery for fractured carbonates with oil-wet matrix containing heavy-oil. Accordingly, they proposed Steam-Over-Solvent Injection for Fractured Reservoirs (SOS-FR) process to enhance the recovery efficiency by injection of both steam and solvent. The SOS-FR process consists of three main phases (Al-Bahlani and Babadagli, 2008, 2009a-b):

Phase 1: It consist of pre-heating by steam (or hot water) injection. In this phase, thermal expansion of oil (expected recovery is ~10% as reported by Al-Bahlani and Babadagli, 2008) is the main recovery mechanism and no water capillary imbibition is expected if matrix is not strongly water-wet, which is a common situation in carbonates. The matrix oil is also conditioned for the subsequent solvent injection.

Phase 2: Solvent injection phase: Solvent (heptane was used by Al-Bahlani and Babadagli [2008, 2009a]) is injected to be diffused into matrix and further reduce the viscosity of oil. Then, the matrix oil is produced by gravity drainage caused by the density difference between original oil and oil diluted by the solvent. Al-Bahlani and Babadagli (2011) numerically tested two scenarios: (1) Continuous solvent injection and (2) cyclic solvent simulation (CSoS) which consist of three stages: (a) solvent injection, (b) solvent soaking, and (c) production.

Phase 3: Solvent retrieval period: To retrieve the solvent (and recover additional oil); steam is injected at a temperature near to the boiling point of the solvent, which causes rapid thermal expansion of solvent.

Al-Bahlani and Babadagli (2011) compared, by building each case manually, the injection of exclusively steam or solvent for the whole period with the two scenarios of SOS-FR process at the field scale; continuous solvent injection and cyclic solvent injection (Huff-and-Puff) in a single fracture and multiple fractures system. Their results showed that cyclic application of the SOS-FR technique gives promising result for multiple fracture models in terms of the economics of the process. The cyclic solvent SOS-FR process has numerous operating parameters that could affect the recovery including duration of heating period during Phase 1, steam injection rate and duration, solvent cycles schedule – duration of injection and soaking cycles as well as the number of cycles for Phase 2, and the steam injection rate for Phase 3. Such a large number of factors require testing remarkably large number of scenarios to reach an optimal solution, which would be very exhaustive to achieve manually.

In this paper, we focus on optimizing the (SOS-FR) process and apply a hybrid technique introduced in our previous publication for ES-SAGD optimization (Al-Gosayir et al., 2011b) to propose optimal application conditions that maximized the recovery and profit.

Optimization methodology

Global Optimization Techniques

Similar to our work on ES-SAGD optimization (Al-Gosayir et. al., 2011b), we integrated the Genetic Algorithm (GA) with two other techniques in a hybrid formulation. The GA is a probabilistic search technique based on the principle of “survival of the fittest” (Guyaguler et al., 2002; Chen et al., 2010). An initial population or genotype can be constructed by sampling the solution space randomly or by utilizing an experimental design strategy such nearly orthogonal arrays. Additional scenarios constructed manually can be incorporated to accommodate the engineer’s judgement and to accelerate the convergence. Each population contains members called “chromosomes” which define the parameters for the optimization problem. In each evolution, each chromosome’s fitness is calculated. Then, pairs of parent chromosomes are selected based on their

fitness values to create new offsprings (children) via crossover and mutation as illustrated in **Figure 6-1**. Examples for crossover and mutation genetic operations that are used to generate new offsprings are shown **Figure 6-2** in and **Figure 6-3**. The new chromosomes are added to the population, while the chromosomes with low fitness values are discarded.

Computational behavior of genetic algorithm is highly sensitive to the choice of initial population. Thus, we proposed a hybrid formulation to improve the computational and convergence efficiency by integrating the following experimental design and response surface techniques into the conventional framework of GA.

Orthogonal Arrays for Experimental Design

Orthogonal Array (OA) and Nearly-Orthogonal Array (NOA) experimental design techniques can be integrated with GA to improve the quality of initial population (Chen et al., 2010) by generating evenly distributed samples and reducing the redundancy between chromosomes. Instead of trying all combinations of parameters at all levels, just the ones that contain principal information are included by determining the levels at which parameters should be varied. In this paper, we utilized Gendex DOE Toolkit (website: <http://designcomputing.net/gendex>) for NOAs generation based on the Taguchi method minimax criterion described by Ma et. al. (2000) and Lu et. al. (2003).

Proxy Method for Objective Function Evaluation with Periodic Updating

For each chromosome in each evolution, its fitness function must be evaluated. In our application, the money recovery factor as defined in the next section is calculated from the results of a numerical flow simulation. Depending on the reservoir size and process complexity, each flow simulation could take up to days to complete. Proxy methods are feasible and computationally efficient alternatives for fitness value estimation. The response surface technique, a method in which a relationship between the parameter sets and the corresponding fitness function is approximated via regression, has been implemented in this study. Once calibrated using the results obtained from detailed flow simulations, this response surface can be used as a proxy for flow simulation. Results presented in our previous work demonstrated that a second-order non-linear proxy model typically provides satisfactory performance for our optimization applications (Al-Gosayir et. al., 2011b, Myers and Montgomery, 2002). The equations for non-linear (quadratic) models are shown in Eq. 1, where J is the response (fitness function value), u_i 's are the variables (optimization parameters), β_i 's are the regression coefficients, and ϵ is an error term.

$$J = \beta_0 + \beta_1 u_1 + \dots + \beta_n u_n + \sum_{i=1}^n \beta_{ii} u_i^2 + \sum_{i < j} \sum_{j=2}^n \beta_{ij} u_i u_j + \epsilon \quad (1)$$

Eq. 2 is the regression equation for over-determined problem:

$$\beta = (U^T U)^{-1} U^T J \quad (2)$$

When the number of optimization parameters is larger than the number of experiments, the problem becomes under-determined and Eq. 3 should be used:

$$\beta = U^T(U U^T)^{-1}J \quad (3)$$

where J is a vector that contains all the response, β is a vector which contains all regression coefficients and U is a matrix with all the u vectors evaluated.

In order to achieve a better representation of the solution space and regression accuracy, the proxy is re-calibrated or updated periodically by performing detailed flow simulation using parameters of the chromosome with the highest fitness value and incorporating its simulation result after each evolution (Al-Gosayir et al., 2011b). This updating step is illustrated in the flow chart given in **Figure 6-4**.

In this research, we used the JGAP package (Java Genetic Algorithm Package (JGAP) website: <http://jgap.sourceforge.net/>) for the GA modeling.

Objective Function

Efficiency of recovery processes can be assessed by their profit by calculating the Money Recovery Factor, MRF, (Al-Bahlani and Babadagli, 2011) which incorporate the major elements (mainly steam, solvent, and oil), which influence the profit. The MRF focuses on the key elements and omits the other factors, which may vary from one field to another. The MRF is defined as follows:

$$MRF = \frac{Revenue - Cost}{STOIIP \times Oil Price}$$

where the cost is:

$$Cost = Cumulative\ Steam\ Injected * Steam\ Cost + Cumulative\ Solvent\ Injected * Solvent\ Price$$

and the revenue is:

$$Revenue = Cumulative\ Oil\ Produced * Oil\ Price + Cumulative\ Solvent\ Produced * Solvent\ Price$$

The steam cost and solvent and oil prices are shown in **Table 6-1**.

This objective function eliminates the revenue of the steam since it is not a common practice to treat the produced water and re-inject it again as steam. On the other hand, solvent is considered to have the same price for revenue and cost even if it is not extracted from the oil because it upgrades the oil and reduces the need to add solvent for pipeline transportation and it is recovered

in the distillation tower. The capital expenditures (CAPEX) are considered the same for all scenarios (Al-Bahlani and Babadagli, 2011).

Benchmark (Base) Simulation Model

Since Al-Bahlani and Babadagli (2011), results indicated that cyclic solvent SOS-FR in reservoirs with multiple fractures yielded the highest money recovery factor (see Figure 16 of this reference), we considered this as a base case for our optimization study. This model is an IK Cartesian 2D single porosity-single permeability model with the dimensions of 20×30×15 m that contains multiple fractures of 1 cm aperture. Geological features of the model are provided in **Table 6-2**. Representation of the fracture-matrix model in a flow simulation is shown in **Figure 6-5**. This base case gives a money recovery factor (MRF) value of approximately 28. This base case gives a money recovery factor (MRF) value of approximately 28. This model was an implementation of cyclic option of the SOS-FR Process. This model has total process duration of three years and six months, and it is designed as follows (Al-Bahlani and Babadagli, 2011):

1. Phase 1: Heating period (HP) has 395 days length.
2. Phase 1: Heating period where steam is injected with rate of 20 m³/day.
3. Phase 1: Cooling period (CP) has 175 days length with cold-water injection with rate of 5 m³/day. This was included by Al-Bahlani and Babadagli (2001) in their simulation to simulate their laboratory experiments (Al-Bahlani and Babadagli, 2008, 2009a), which had a cooling period between Phase 1 (heating) and Phase 2 (solvent injection). In practice, this corresponds to the period switching to Phase 2 and a short period of soaking the reservoir with injected steam to condition the matrix oil for solvent diffusion.
4. Wells shut-in after the cooling period for 6 days.
5. Phase 2: 14 Cycles each cycle contains three periods: One week solvent injection, two weeks soaking, and two weeks production.
6. Phase 3: Recovery phase where the steam is injected with rate of 20 m³/day.
7. Phase 3: Recovery phase length is 198 days.

Semi-compositional commercial simulator (CMG STARS) was used for full flow simulations evaluation.

Results and Discussion

In order to identify the parameters that have the greatest impacts on the objective (fitness) function, a sensitivity analysis was carried out first. In particular, we varied the steam injection rate in the heating period (Phase 1), solvent injection rate, durations of soaking phase during the huff-and-puff stage (Phase 2), and the steam injection rate in the final recovery phase (Phase 3). As shown in **Figure 6-6**, for each of these parameters, except the solvent injection rate, an optimum value can be easily identified. However, MRF continues to increase as the solvent injection rate increase.

Experiment 1:

Based on the result of the sensitivity analysis we have developed an updated proxy and genetic algorithm experiment to increase the MRF by varying:

1. Phase 1: Heating period (HP) length between 60 to 790 days with 30 days resolution.
2. Phase 1: Heating period (HP) steam injection rate from 10 to 40 m³/day.
3. Phase 2: Cycle length indicators each cycle contains three periods:
 - a. 4 mandatory cycles [1-5].
 - b. 9 optional cycles [0-5].
4. Phase 2: 3 Cycles periods length indicators (Solvent Injection, Soaking, and Production) [1-3].
5. Phase 3: Recovery phase steam injection rate from 10 to 40 m³/day.

While the other properties fixed such as:

1. Phase 1: Cooling period (CP) length is 175 days
2. Phase 1: Cooling period (CP) injection rate is 5 m³/day.
3. Phase 3: Recovery phase length 198 days.

A comprehensive list of optimization parameters for all experiments carried out in this chapter is shown in **Table 6-3**.

This experiment gave better results than the base case; a value of 48 for the money recovery factor instead of 28 is obtained, with an increase of about two hundred thousand dollars in the profit. The result of this experiment suggests, as shown in **Table 6-4**, that the optimal solution can be achieved by reducing the length of the heating period (phase 1), with a minimum value of 60 days as the total length for heating period. Similarly, as in **Table 6-5**, the optimal length indicators for the soaking and production periods in each cycle (phase 2) were the minimum value of 1, while the optimized solvent injection period is the maximum value.

Analyzing the result of this experiment and noting that numerous optimized parameters coincide with either the lower or upper limits of the optimization range raise a few interesting questions: (1) Can we optimize the MRF by further reducing the duration of the phase 1 by adjusting the length of cooling period? Is it necessary to soak or produce in each cycle? To address such questions, two additional experiments were executed simultaneously (experiments 2 and 3).

Experiment 2:

Based on experiment 1 results, cooling period was eliminated and only optional heating period (with a minimum value of zero) was kept, cycles phase's length indicators were also made optional, allowing them to be eliminated for better flexibility. Ranges for other parameters are shown in Table 6-3.

Comparing with previous experiment, the MRF was increased by 4.2 with profit increase of about fifty thousand dollars. This experiment suggests that the optimal the heating period (phase 1) should be around three months.

Experiment 3:

Similarly, based on experiment 1 results, both phase 1 periods were optimized and the cycles' periods' length indicator range increased to 5. Cycles length indicators from the best case of experiment 1 were used in this experiment to minimize number of optimized parameters. Ranges for other parameters are listed in Table 6-3.

A MRF value of 58.4 and three hundred thousand dollars increase in the profit from base case were observed. This is better than the results obtained from the previous experiments as presented in **Table 6-6**. The result indicates that keeping two phase 1 periods are worthy, and similar to the previous experiments, the solvent injection phase is the dominant on all cycles. Based on the results from experiments 2 and 3, one might wonder if the process can be further optimized by varying the periods' duration in each cycle individually. This idea is explored in experiment 4.

Experiment 4:

A length indicator for each period in each cycle was introduced which result in 30 length parameters to represent 10 cycles, instead of 13 parameters in all the previous setups. Increasing the number of parameters increases the size of the solution space, which in turn reduces the convergence speed and accuracy of the proxy regression. In order to facilitate the convergence efficiency, we repeated the optimization scheme multiple times sequentially such that optimized models from the previous step are placed in the initial population for the next step. In other words, instead of taking a big step along the descent direction, a few smaller steps are taken.

First, two experiments (4-a and 4-b) with different initial populations, constructed based on nearly orthogonal arrays (minimax criterion) and randomly generated population (Al-Gosayir et. al., 2011b), were executed concurrently. Next, these two initial populations and the fully evaluated flow simulation models of their respective optimized solution in each evolution were combined into one initial population for experiment 4-c. Finally, even though satisfactory results were achieved, we repeated the optimization again using the initial population and flow simulation results from experiment 4-c as an initial population for a conventional genetic algorithm experiment (4-d) which takes longer time to ensure sampling more scenarios in the solution space to achieve the best result.

These experiments provided only slight improvement compared to experiments 2 and 3, as expressed in Table 6-6. The last experiment result was the best with a 65.5 money recovery factor, 82.2% oil recovery factor, and \$675,512 profit, which is more than double of the base case scenario as shown in **Figure 6-7** and **Figure 6-8**; and the cumulative solvent injected volume was lower than the optimized case from experiment 3 as in **Figure 6-9**. Based on the result of this experiment, we noticed that some periods could be eliminated from certain cycles, while the phase 1 cannot be eliminated though it can be shorter than the base case. **Figure 6-10** and **Figure 6-11** compare the injection and production schedules of the base case and best-case (experiment 4-d) scenarios, respectively, while **Table 6-7** shows all cases schedule. **Figure 6-11** shows that we need to start and finish with longer cycles of solvent injection. The solvent injection rate is low (5 m³/day), and it has already started to diffuse through the system during the injection period. In the middle cycles, one should adjust the lengths of the soaking or production periods alternatively between cycles. It is also noted that the solvent injection duration in the middle cycles is about 40 weeks, which is approximately equal to the other two periods' total.

Solvent injection in the optimum cases is much higher than the amount of steam injection. An important assumption in our simulation model is that the reservoir is confined such that we are able to recover most of the solvent, as shown in **Figure 6-9**. However, Experiment 4-b shows an interesting result, which has the least solvent injection and consequently the least cost as shown in **Figure 6-9**, **Figure 6-8**, and **Table 6-6**. At the same time, this experiment gives a good money recovery factor of about 51 and a profit of 526 thousand dollars. This experiment illustrates the benefit of soaking period in each cycle, which gives more time for the solvent to diffuse into the reservoir with less amount of solvent as shown in **Figure 6-12**. Since this experiment was initialized using random initial population that is different from the other experiments where minimax criterion nearly orthogonal array is used, the solution space was investigated from different angle. Minimax criterion tends to combine the parameters by maximizing some while minimizing the others.

Conclusions and remarks

Despite the challenge of optimizing the injection time and cycles of the SOS-FR process using hybrid genetic algorithm, the outcome was very promising and better results than the benchmark case were achieved. The money recovery factor and the profit were doubled and about 30% oil recovery increase was obtained. The results suggest that steam heating period should be decreased, while the solvent injection time to be increased without eliminating the necessity of having solvent soaking or production periods. Handling such complex process optimization is a challenge, which could be overcome by implementing a hybrid optimization scheme that incorporates a detailed sensitivity analysis with experimental design methods for initial population construction, followed by a global optimization scheme of genetic algorithm, whose convergence efficiency was improved with the use of response surfaces. In addition, the accuracy of the proxy model was further enhanced with a periodic updating step in which additional flow simulation results using the most optimal case were used to re-calibrate the response surface at each evolution. Furthermore, we noticed that hybrid genetic algorithm is a useful tool designing the operating strategy of a complex recovery process by optimizing the time required for each phase of the SOS-FR method.

Nomenclature

BC: Base/Benchmark case.

β_i : represent a regression coefficients for one trial.

$\boldsymbol{\beta}$: a vector which contains all regression coefficients.

CP: Cooling period in phase 1.

cSOR: cumulative steam-to-oil ratio (m^3/m^3).

CSoS: Cyclic Solvent Stimulation.

cS_VOR: cumulative net solvent injected (difference between cumulative solvent injected and produced) to oil ratio (m^3/m^3).

EIF: Economic Impact Factor.

F(u) or *FX*: objective function value.

F: objective function.

GA: Genetic Algorithm.

HMF: Hexane injection mole fraction.

HnP: Huff and Puff.

HP: Heating Period in phase 1.

IAV: Initial Asset Value.

IBHP: Injector maximum Bottom-hole Pressure (kPa).

J: the actual response or actual objective function value calculated based simulation output for one trial.

J: the repose obtained from the regression model.

J₀: the best trial actual response in the initial population.

J: a vector that contains all the trials response.

MRF: Money Recovery Factor.

NA: Not applicable.

NL: Nonlinear Proxy

NOA: Nearly-Orthogonal Array.

NPV: Net Present Value.

OA: Orthogonal Array.

PBHP: Producer minimum Bottom-hole Pressure.

PP: Production period in each cycle.

RF: Recovery Factor.

RP: Recovery phase 3.

SAGD: Steam Assisted Gravity Drainage thermal recovery process.

SIP: Solvent Injection period in each cycle.

SOP: Solvent Soaking period in each cycle.

SOS-FR: Steam-Over-Solvent for Fractured Reservoirs.

STOIP: Stock Tank Oil Initially In Place.

u: a $(1*n)$ vector which contains the optimization variables for a trial.

u_i : represent an optimization variable for one trial.

U: a matrix with all **u**'s.

USD United States Dollar.

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Tables

Table 6-1: Elements prices

Element	Price
Steam	18 \$/m ³
Solvent	1000 \$/m ³
Oil	80 \$/bbl

Table 6-2: Reservoir properties used in the simulations. (Al-Bahlani and Babadagli, 2011)

Item	Value
Reservoir depth	500 m
Matrix porosity	0.30
Fracture porosity	0.99
Matrix permeability	10 mD
Fracture permeability	550 D
Initial reservoir pressure	8 MPa
Initial reservoir temperature	50 °C
Oil density SC	965
Solvent type	Heptane
Initial water saturation	0.00
Solvent diffusion coefficient	2.88e–5m ² /day
Wettability	Oil wet

Table 6-3: Optimized parameters' ranges

Experiment	HP Length (days)	HP Injection Rate (m ³ /day)	CP Length (days)	CP Injection Rate (m ³ /day)	Recovery phase Injection Rate (m ³ /day)	3 Cycles periods LIs (Same for all Cycles)	Cycles Lengths Indicators (LIs)	Each Cycle period LIs (Different in each cycle)
Exp. 1	[60-790]	[1-40]	175	5	[10-40]	[1-3]	4*[1-5] and 9*[0-5]	NA
Exp. 2	[0-346]	[0-30]	NA	NA	[10-40]	[0-3]	13*[0-5]	NA
Exp. 3	[1-120]	[1-30]	[1-180]	[1-6]	40	[1-5]	Exp. 1 Best case setup	NA
Exp. 4-a	[1-120]	[1-30]	[1-180]	[1-6]	40	NA	NA	30*[0-5]
Exp. 4-b	[1-120]	[1-30]	[1-180]	[1-6]	40	NA	NA	30*[0-5]
Exp. 4-c	[1-120]	[1-30]	[1-180]	[1-6]	40	NA	NA	30*[0-5]
Exp. 4-d	[1-120]	[1-30]	[1-180]	[1-6]	40	NA	NA	30*[0-5]

Table 6-4: Optimal parameters values for all experiments.

Experiment	Number of Evolutions	FX (MRF)	HP Length (days)	HP Injection Rate (m ³ /day)	CP Length (days)	CP Injection Rate (m ³ /day)	Recovery phase Injection Rate (m ³ /day)
Base Case	-	28.0	395	20	175	5	20
Exp. 1	80	48.0	60	25	175	5	40
Exp. 2	85	52.8	90	26	-	-	36
Exp. 3	26	58.4	45	30	15	1	40
Exp. 4-a	72	56.9	120	29	1	2	40
Exp. 4-b	89	51.0	15	28	180	5	40
Exp. 4-c	10	58.7	120	29	1	2	40
Exp. 4-d	87	65.5	120	29	1	2	40

Table 6-5: Optimal lengths indicators of the base case, experiment 1, 2, and 3.

Experiment	Period Length Indicator of			Length indicator of Cycle:													
	Solvent Inj.	Soaking	Production	1	2	3	4	5	6	7	8	9	10	11	... 14		
Base Case	1	2	2	1	1	1	1	1	1	1	1	1	1	1	1		
Exp. 1	3	1	1	3	1	1	1	3	5	5	1	1	1	5	0		
Exp. 2	3	1	1	5	3	4	1	1	5	1	5	0	0	0	0		
Exp. 3	5	1	1	3	1	1	1	3	5	5	1	1	1	5	0		

Table 6-6: Comparison of the selected solution values

Exp.	MRF	Cum. Steam Inj.	Cum. Solvent Inj.	Cum. Solvent Prod.	Cum. Oil Prod.	RF	cSOR	IAV (mln \$)	Cost (mln \$)	Revenue (mln \$)	Profit (\$)
Base Case	28.5	12355	990	952	1099	53.7	6.3	1.03	1.21	1.51	\$290,000
Exp. 1	48.0	10277	2475	2468	1363	66.3	2.7	1.03	2.7	3.2	\$494,830
Exp. 2	52.8	9546	2910	2910	1422	69.5	2.2	1.03	3.1	3.6	\$545,005
Exp. 3	58.4	9286	3571	3584	1501	74.0	1.8	1.03	3.7	4.3	\$602,544
Exp. 4-a	56.9	11397	3201	3225	1525	75.7	2.4	1.03	3.4	4.0	\$586,785
Exp. 4-b	51.0	9261	2042	2067	1325	66.0	2.7	1.03	2.2	2.7	\$526,110
Exp. 4-c	58.7	11397	3245	3269	1560	77.4	2.4	1.03	3.5	4.1	\$605,337
Exp. 4-d	65.5	11397	3183	3250	1614	82.2	2.3	1.03	3.4	4.1	\$675,512

Table 6-7: Experiments huff-and-puff phases lengths in days

Exp.	Cycle 1			Cycle 2			Cycle 3			Cycle 4			Cycle 5			Cycle 6		
	SIP	SOP	PP	SIP	SOP	PP	SIP	SOP	PP	SIP	SOP	PP	SIP	SOP	PP	SIP	SOP	PP
BC	7	14	14	7	14	14	7	14	14	7	14	14	7	14	14	7	14	14
1	55	18	18	18	6	6	18	6	6	18	6	6	55	18	18	92	31	31
2	116	39	39	70	23	23	93	31	31	23	8	8	23	8	8	116	39	39
3	79	16	16	26	5	5	26	5	5	26	5	5	79	16	16	132	26	26
4-a	142	14	0	43	43	14	57	0	28	71	14	0	28	43	0	71	57	28
4-b	48	36	0	48	60	24	48	60	0	60	36	36	36	12	48	24	24	0
4-c	138	14	0	41	41	14	55	0	28	69	14	0	69	41	0	69	55	28
4-d	159	16	0	32	64	16	64	0	16	80	16	0	80	48	0	16	64	32

Exp.	Cycle 7			Cycle 8			Cycle 9			Cycle 10			Cycle 11			... Cycle 14		
	SIP	SOP	PP	SIP	SOP	PP	SIP	SOP	PP	SIP	SOP	PP	SIP	SOP	PP	SIP	SOP	PP
BC	7	14	14	7	14	14	7	14	14	7	14	14	7	14	14	7	14	14
1	92	31	31	18	6	6	18	6	6	18	6	6	92	31	31			
2	23	8	8	116	39	39												
3	132	26	26	26	5	5	26	5	5	26	5	5	132	26	26			
4-a	57	0	14	57	28	0	71	43	14									
4-b	60	24	0	60	48	0	24	48	0									
4-c	55	14	14	124	41	14												
4-d	16	0	16	159	48	0												

Figures

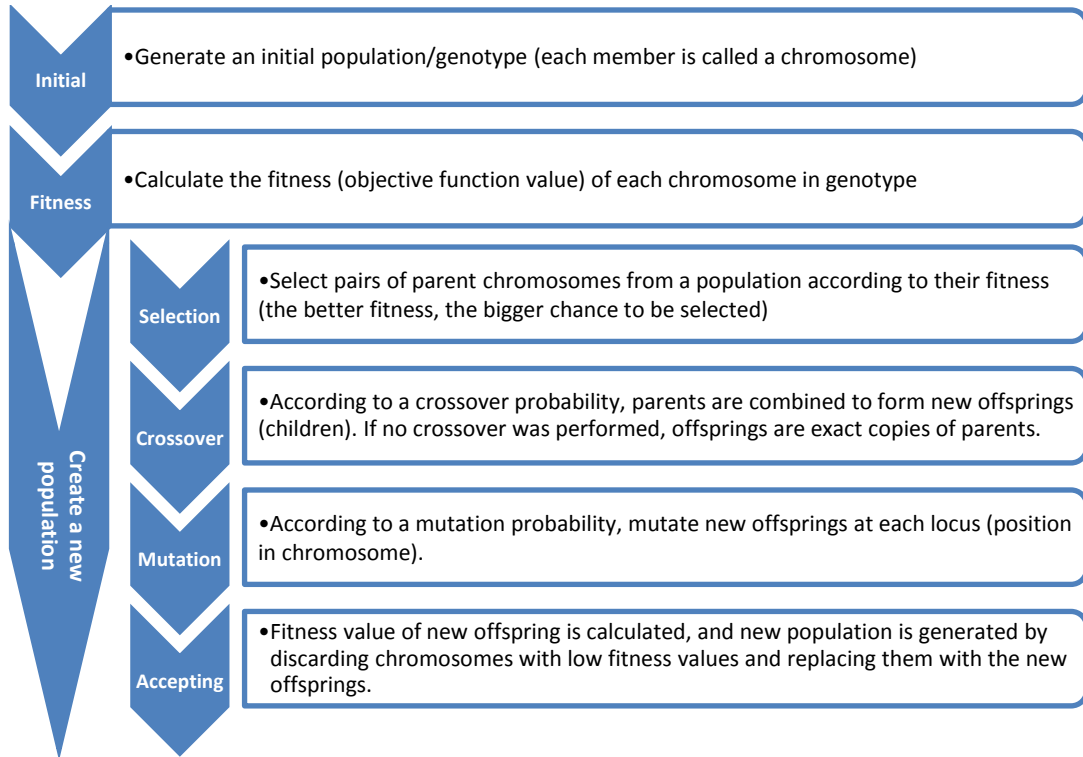


Figure 6-1: Conventional genetic algorithm flow diagram (Al-Gosayir et al. 2011b).

	Gene	Gene	Gene	Gene	Gene
Parent Chromosome 1	0111000011	1111101000	1000100110	101101110	11001100010
Parent Chromosome 2	11111001111	1001000010	1110011111	1000010010	11000100000
Child Chromosome 1	0111000011	1111101000	1110011111	1000010010	11000100000
Child Chromosome 2	11111001111	1001000010	1000100110	101101110	11001100010

Figure 6-2: Example of crossover of two parent chromosomes (Al-Gosayir et al. 2011a).

	Gene	Gene	Gene	Gene	Gene
Parent Chromosome	10101111	11110010111	11100101010	1001011111	10110100100
Child Chromosome	10101111	01110010111	11100101010	1001011111	10110100100

Figure 6-3: Example of mutation of a parent chromosome (Al-Gosayir et al. 2011a).

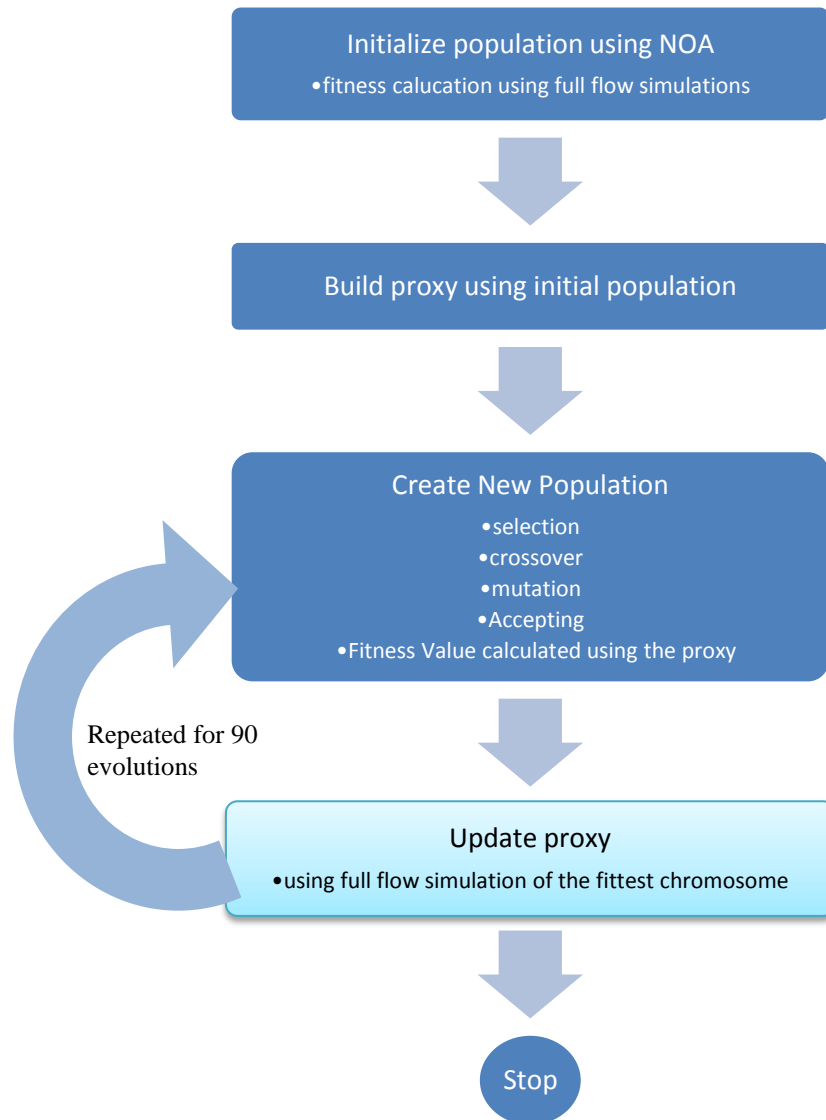


Figure 6-4: Flow diagram for the modified approach where proxy is updated with the additional flow simulation results of the fittest chromosomes after each evolution. (Al-Gosayir et al. 2011b)

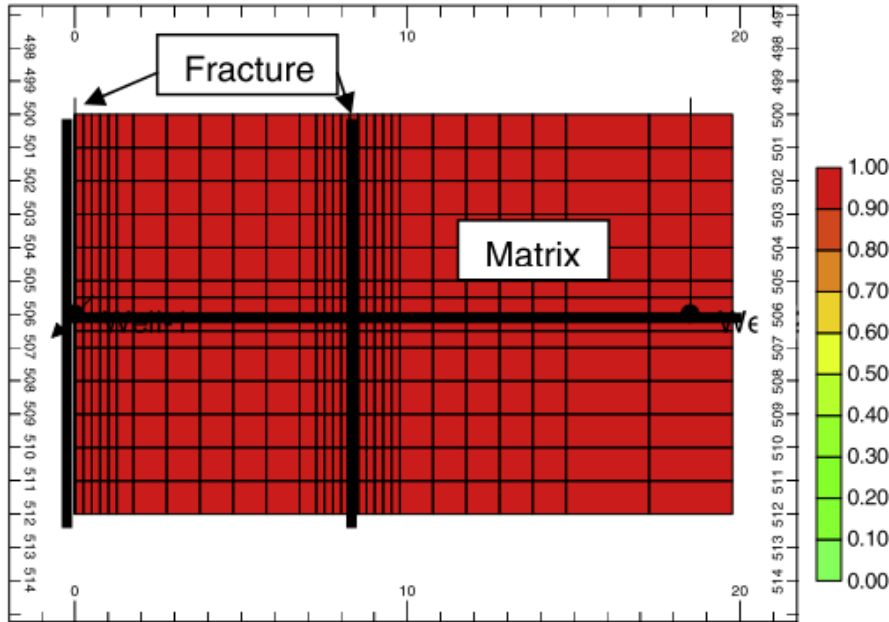


Figure 6-5: Representation of multiple-matrix block with unity oil saturation in flow simulation. (Al-Bahlani and Babadagli, 2011)

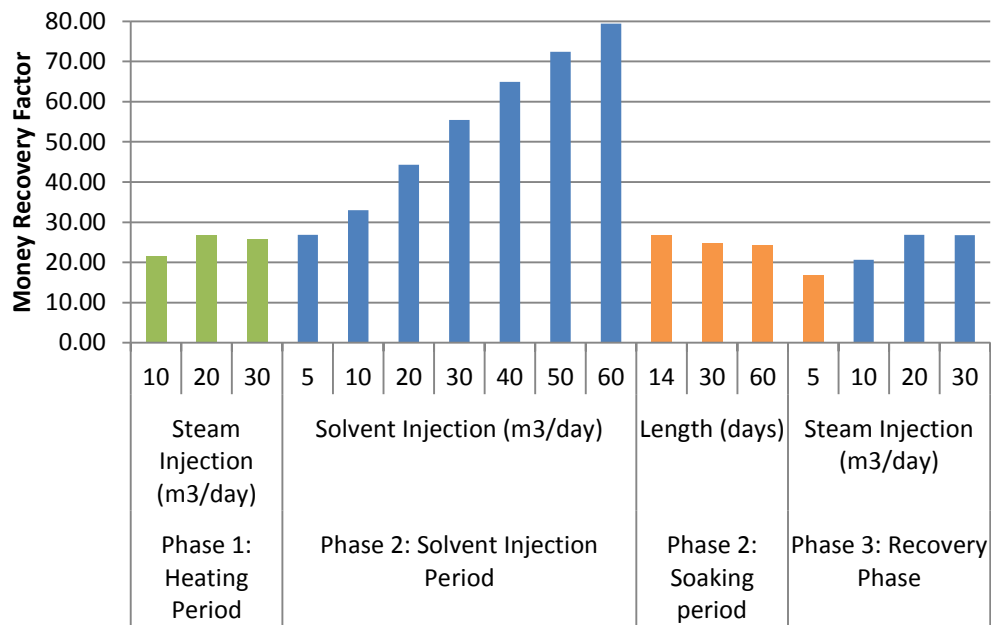


Figure 6-6: Sensitivity analysis for some key parameters before starting the optimization.

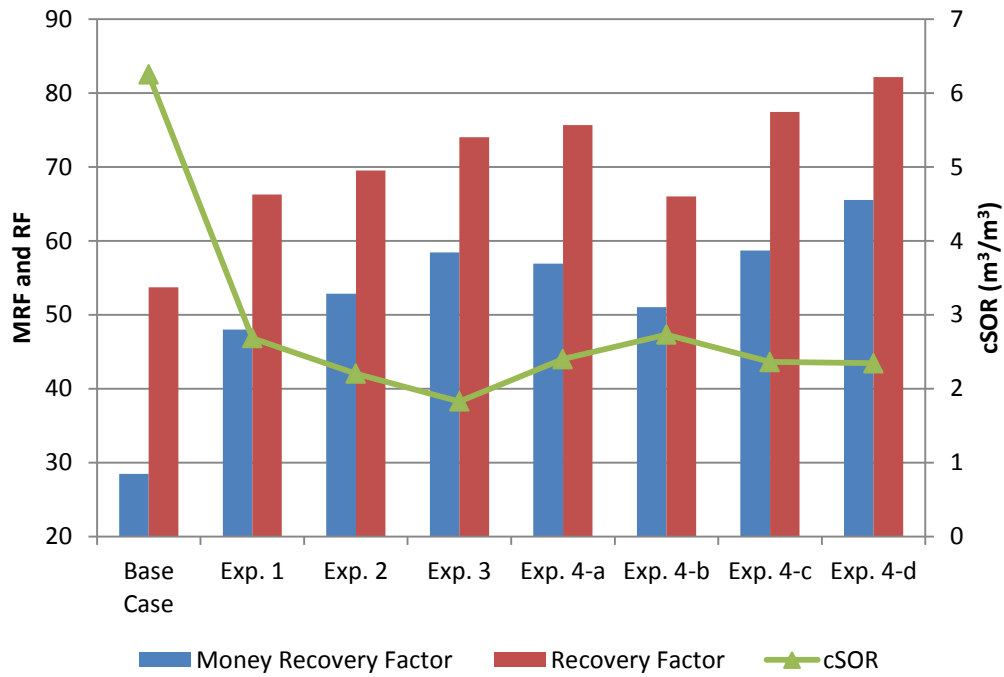


Figure 6-7: Optimized money recovery factor, oil recovery factor, and cumulative steam oil ratio of all experiment.

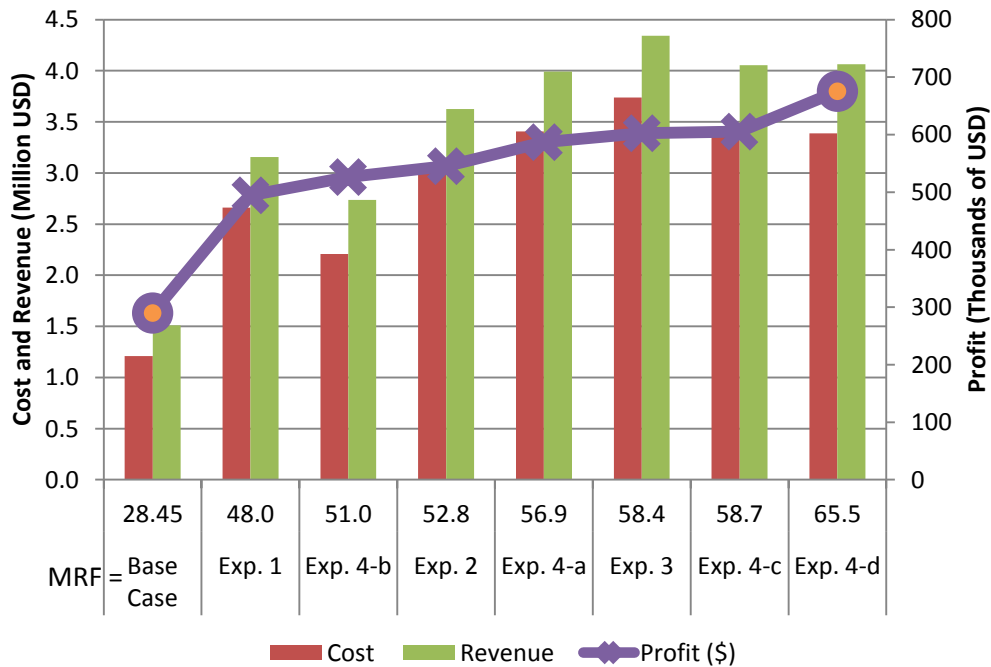


Figure 6-8: Optimized cost, revenue and profit of all experiments.

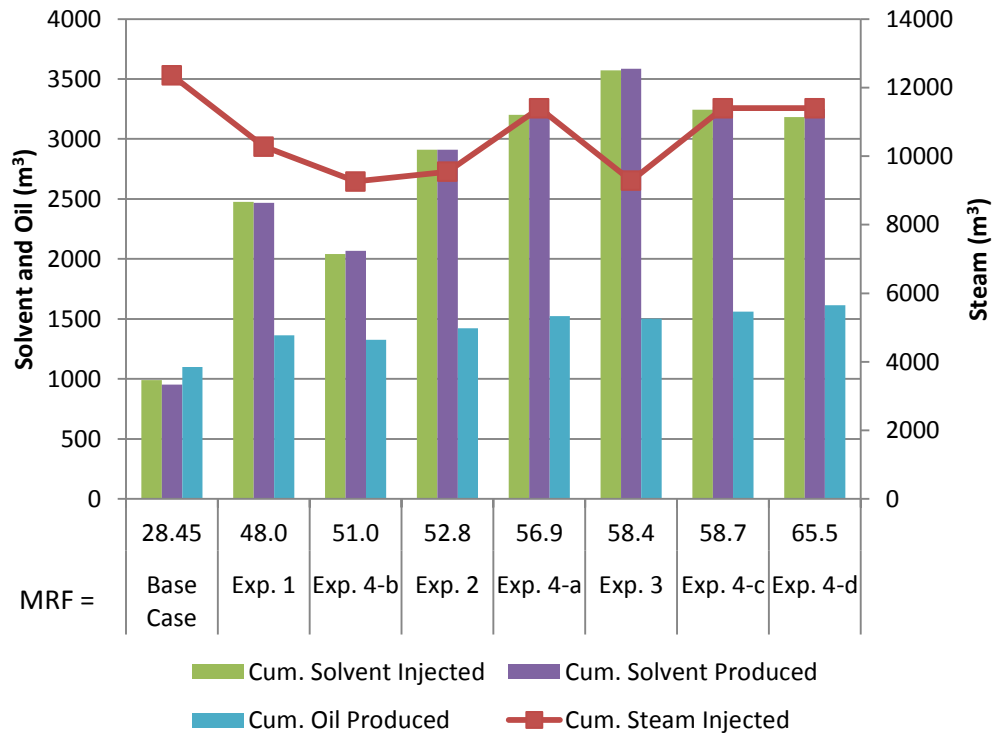


Figure 6-9: All experiments hydrocarbons and steam injected and produced.

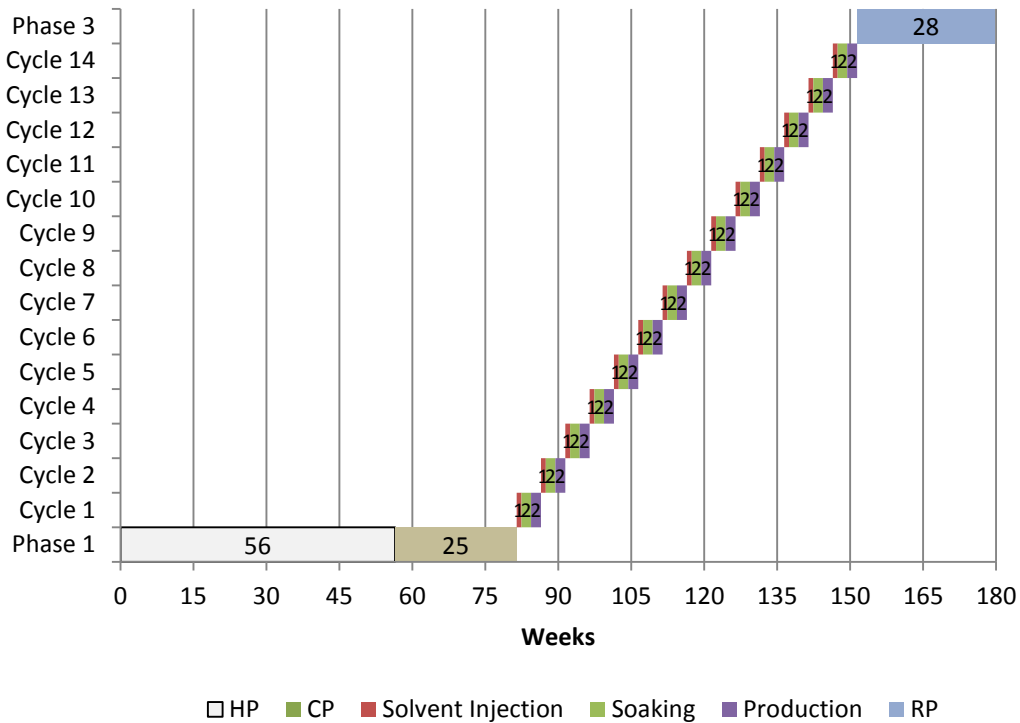


Figure 6-10: Base case Gantt-chart

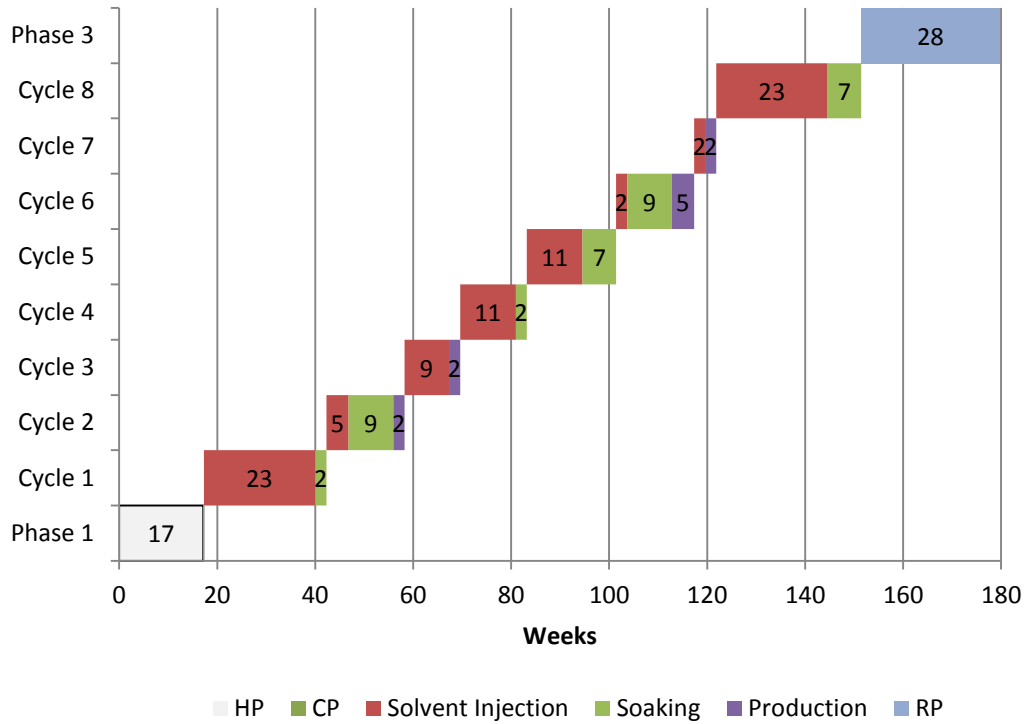


Figure 6-11: Experiment 4-d (best MRF) Gantt-chart.

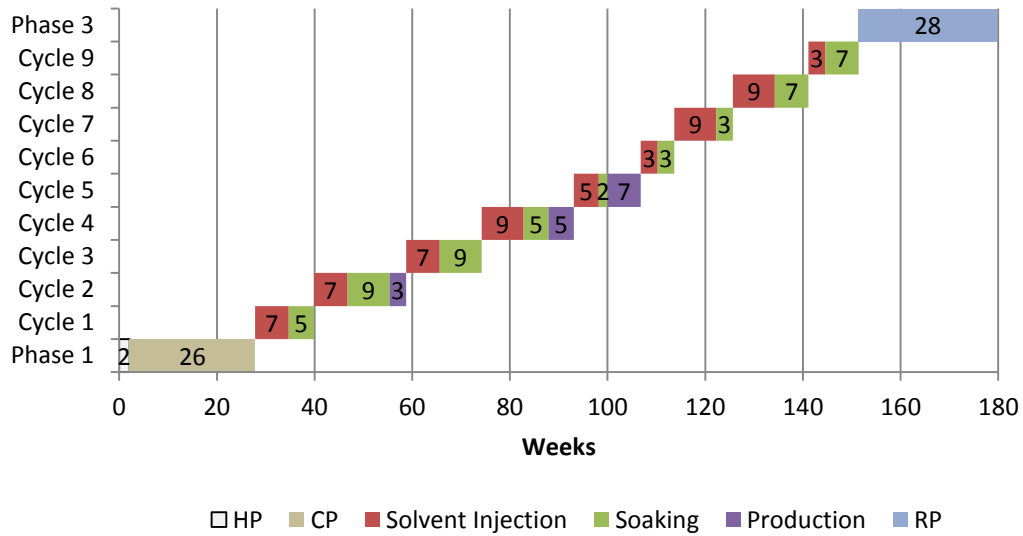


Figure 6-12: Experiment 4-b (random initial population) Gantt-chart.

Chapter 7: Contributions

There are several major contributions gained out of this thesis as listed below:

1. A hybrid optimization strategy, integrating elements of experimental design (orthogonal arrays) and response surface proxy into a global genetic algorithm optimization workflow, was developed. The adopted proxy provided a saving of 95% computational time, while the use of orthogonal arrays (with minimax criterion) was shown to improve the algorithm's convergence behavior in seeking the optimal solution.
2. It was observed that non-linear response surface proxy can potentially give a more accurate representation of the true objective function value, but it also tends to over-shoot during extrapolations. Therefore, a periodic updating scheme was proposed and implemented. The success of this step was illustrated by the improved predictability of the objective function and minimal increase in computational time.
3. The proposed technique was applied to construct optimal designs for three different heavy oil recovery processes using steam and solvent. In particular, the computational efficiency of the technique allows optimization to be carried out successfully for heterogeneous reservoirs. These case studies illustrated that the hybrid optimization framework is a useful tool for designing complex recovery processes and increasing the profit.

Appendix 1: JGAP initializer code

```

package mmm.ga.tests;

import java.io.BufferedReader;
import java.io.FileReader;
import java.io.IOException;
import java.util.List;
import java.util.Vector;

import mmm.ga.MyGenericChromosome;

import org.jgap.*;
import org.jgap.audit.ChainedMonitors;
import org.jgap.audit.EvolutionMonitor;
import org.jgap.audit.FitnessImprovementMonitor;
import org.jgap.audit.IEvolutionMonitor;
import org.jgap.audit.TimedMonitor;
import org.jgap.impl.*;

import Jama.Matrix;

public abstract class GenericRunner {
    int evolutions;
    Genotype population;
    IEvolutionMonitor monitor;
    FitnessFunction objectiveFunction;

    public GenericRunner(String runTitle, int evolutions, int
a_sizeOfPopulation, FitnessFunction objectiveFunction) throws Exception {
        System.out.println(runTitle);
        this.evolutions = evolutions;
        this.objectiveFunction = objectiveFunction;

        // Start with a DefaultConfiguration, which comes setup with the
        // most common settings.
        // -----
        Configuration gaConf = new DefaultConfiguration();

        // Care that the fittest individual of the current population is
        // always taken to the next generation.
        // -----
        boolean preservFittestIndividual = false;
        gaConf.setPreservFittestIndividual(preservFittestIndividual);
        System.out.println("setPreservFittestIndividual\t"
            + preservFittestIndividual);

        // Set the fitness function we want to use, which is our
        // -----
        gaConf.setFitnessFunction(this.objectiveFunction);

        boolean alwaysCaculateFitness = true;
        System.out.println("alwaysCaculateFitness\t" +
alwaysCaculateFitness);

        gaConf.setAlwaysCaculateFitness(alwaysCaculateFitness);

        double crossoverRatePercentage = 0.35d;
        int mutationRate = 3;
        gaConf.getGeneticOperators().clear();
        gaConf.addGeneticOperator(new CrossoverOperator(gaConf,
            crossoverRatePercentage));
        gaConf.addGeneticOperator(new MutationOperator(gaConf,
mutationRate));

        System.out.println("Crossover rate\t" + crossoverRatePercentage);

```

```

System.out.println("Mutation rate\t" + mutationRate);

boolean allowDoublette = false;
double originalRate = 0.9;
BestChromosomesSelector s = (BestChromosomesSelector) gaConf
    .getNaturalSelector();
s.setDoubletteChromosomesAllowed(allowDoublette);
s.setOriginalRate(originalRate);
System.out.println("allowDoublette\t" + allowDoublette);
System.out.println("originalRate\t" + originalRate);

List monitors = new Vector();
monitors.add(new TimedMonitor(6));
monitors.add(new FitnessImprovementMonitor(1, 3, 5.0d));
monitors.add(new EvolutionMonitor());
monitor = new ChainedMonitors(monitors, 3);
System.out.println("Monitors on.");

IChromosome sampleChromosome = getSampleChromosome(gaConf);
gaConf.setSampleChromosome(sampleChromosome);

System.out.println("Sample Genes:");
for (Gene gene : sampleChromosome.getGenes()) {
    System.out.println(gene);
}

// Finally, we need to tell the Configuration object how many
// Chromosomes we want in our population. The more Chromosomes,
// the larger the number of potential solutions (which is good
// for finding the answer), but the longer it will take to evolve
// the population each round.
gaConf.setPopulationSize(a_sizeOfPopulation);
System.out.println("Population Size\t" + a_sizeOfPopulation);

// Create random initial population of Chromosomes.
System.out.println("Random Initial Population Generated");
population = Genotype.randomInitialGenotype(gaConf);

//population = new
Genotype(gaConf, NoaArrayImporter.getInitialNAOPopulation(gaConf, 0, 0));
}

protected IChromosome getSampleChromosome(Configuration gaConf)
    throws InvalidConfigurationException {
    // Now we need to tell the Configuration object how we want our
    // Chromosomes to be setup. We do that by actually creating a
    // sample Chromosome and then setting it on the Configuration
    // object.
    int chromeSize = 19; //

    Gene[] sampleGenes = new Gene[chromeSize];

    //Heating Phase length: multiple integer [60-790] days with 30 days
level length
    sampleGenes[0] = new MutipleIntegerGene(gaConf, 60, 790, 30);
    //Heating Phase steam injection rate
    sampleGenes[1] = new DoubleGene(gaConf, 10, 40);

    //Cycles lengths indicators
    sampleGenes[2] = new IntegerGene(gaConf, 1, 5);
    sampleGenes[3] = new IntegerGene(gaConf, 1, 5);
    sampleGenes[4] = new IntegerGene(gaConf, 1, 5);
    sampleGenes[5] = new IntegerGene(gaConf, 1, 5);
    sampleGenes[6] = new IntegerGene(gaConf, 0, 5);
    sampleGenes[7] = new IntegerGene(gaConf, 0, 5);
    sampleGenes[8] = new IntegerGene(gaConf, 0, 5);
    sampleGenes[9] = new IntegerGene(gaConf, 0, 5);
    sampleGenes[10] = new IntegerGene(gaConf, 0, 5);
    sampleGenes[11] = new IntegerGene(gaConf, 0, 5);

```

```

        sampleGenes[12] = new IntegerGene(gaConf, 0, 5);
        sampleGenes[13] = new IntegerGene(gaConf, 0, 5);
        sampleGenes[14] = new IntegerGene(gaConf, 0, 5);
        //sampleGenes[15] = new IntegerGene(gaConf, 0, 5);

        //Cycles periods (3 periods one of them soaking)
        sampleGenes[15] = new IntegerGene(gaConf, 1, 3);
        sampleGenes[16] = new IntegerGene(gaConf, 1, 3);
        sampleGenes[17] = new IntegerGene(gaConf, 1, 3);

        //Recovery Phase steam injection rate
        sampleGenes[18] = new DoubleGene(gaConf, 10, 40);

        IChromosome sampleChromosome = new MyGenericChromosome(gaConf,
chromeSize);
        sampleChromosome.setGenes(sampleGenes);

        return sampleChromosome;
    }
}

package mmm.ga.tests;

import java.io.IOException;
import java.util.List;

import mmm.cmgAgents.*;
import mmm.ga.MyGenericChromosome;
import mmm.ga.objectiveFunctions.NonLinearProxyObjectiveFunction;
import mmm.sosfr.SosFrPreprocessor2;

import org.jgap.*;
import org.jgap.impl.DoubleGene;
import org.jgap.impl.IntegerGene;
import org.jgap.impl.MultipleIntegerGene;

public class ProxyEvolutionFittestRun3 extends GenericRunner {

    public ProxyEvolutionFittestRun3(String runTitle, int evolutions, int
a_sizeOfPopulation, FitnessFunction objectiveFunction) throws Exception {
        super(runTitle, evolutions, a_sizeOfPopulation, objectiveFunction);
        Configuration gaConf = super.population.getConfiguration();

        //Override the random population with an old population to avoid
re-running the simulations
        population = new
Genotype(gaConf, getInitialNAOPopulation(gaConf, "ex3_good_62cases.txt"));
    }

    @Override
    public void run() throws Exception {
        System.out.println("Evolution Start\t" + evolutions +
"\tevolutions");
        System.out.println();
        System.out
            .println("Location\tEvolution\tFX\tmaxEN\t");

        System.out.println("FileInfo\tpl1\tplinjRate\tRPInjRate\tAllCyclesLength\tC
yclesCount\ttcp1\ttcp2\ttcp3\tCyclesLengths");

        System.out.println("ObjValues\tmoneyRecoveryFactor\tCumSteamInj\tCumSolInj\t
CumSolProd\tCumOilProd\tRF\tcSOR\tiav\tcost\trevenue\tgrossProfit");

        long startTime = System.currentTimeMillis();
        NonLinearProxyObjectiveFunction obj =
(NonLinearProxyObjectiveFunction) objectiveFunction;

        for (int i = 0; i < evolutions; i++) {

```

```

        for (IChromosome c1 :
population.getPopulation().getChromosomes()) {
            MyGenericChromosome c = (MyGenericChromosome) c1;
            System.out.println("****PC****\t" + i + "\t"
                + c.getFitnessValue() + "\t\t" + c);
        }

        if (!uniqueChromosomes(population.getPopulation())) {
            System.out.println("Invalid state in generation\t" +
i);
        }

        if (monitor != null) {
            List<String> messages = population.evolve(monitor);
            if (messages.size() > 0) {
                for (String msg : messages) {
                    System.out.println("Monitor:\t" + i +
msg);
                }
            }
        } else {
            population.evolve();
        }

        MyGenericChromosome fittest = (MyGenericChromosome)
population
            .getFittestChromosome();

        System.out.println("Currently fittest Chromosome\t" + i +
"\t"
            + fittest.getFitnessValue() + "\t" +
fittest);

        long simStartTime = System.currentTimeMillis();

        double actualFitnessValue =
obj.performActualEvaluation(fittest);

        long simEndTime = System.currentTimeMillis();
        if (fittest.isError())
            System.out.println("ACTUAL_EVAL_ERROR\t" + i + "\t"
                + actualFitnessValue + "\t" + fittest
+ "\t" + (simEndTime - simStartTime)
                + "\tms\t");
        else {
            System.out.println("ACTUAL_EVAL_NEW\t" + i + "\t"
                + actualFitnessValue + "\t" + fittest
+ "\t" + (simEndTime - simStartTime)
                + "\tms\t");
            obj.getProxy().addTrial(fittest.getGenesValues(),
                actualFitnessValue);

            // /After adding new cases Proxy updating
            obj.getProxy().loadDynamicData();
            try{
                obj.getProxy().calculateNonLinearModel();
            }catch (Exception e){
                e.printStackTrace();
            }
        }
    }

    long endTime = System.currentTimeMillis();
    System.out.println("\n\nTotal evolution time:\t"
        + ((endTime - startTime) / (1000 * 60)) +
"\tminutes");

    // Print summary.
    // -----
    MyGenericChromosome fittest = (MyGenericChromosome) population

```

```

        .getFittestChromosome();

        System.out.println("Fittest Chromosome\t" +
fittest.getFitnessValue()
            + "\t" + fittest);
        //double[] g = fittest.getGenesValues();

        double actualfitnessValue = obj.performActualEvaluation(fittest);
//

        System.out.println("Currently Fittest Chromosome Actual Values\t"
            + actualfitnessValue + "\t" + fittest + "\tLast
Time"
            + fittest.getGenericModelResult().getLastTime());
    }

    /**
     * @param args
     * @throws Exception
     */
    public static void main(String[] args) throws Exception {
        String simulatorPath = "C:/Program Files
(x86)/CMG/STARS/2010.11/Win_x64/EXE/st201011.exe";
        String workDirectoryPath = "C:\\algotayir\\runs_files\\sosFr\\2";
        String resultReportPath = "C:/Program Files
(x86)/CMG/BR/2010.12/Win_x64/EXE/report.exe";
        String baseModelFilePath = workDirectoryPath
            + "\\sosfr2.dat";

        double lastTime = 1264;
        Preprocessor prep = new SosFrPreprocessor2(lastTime);
        Postprocessor postp = new Postprocessor();

        SimulatorExecuter sim = new SimulatorExecuter(simulatorPath,
            workDirectoryPath, resultReportPath,
baseModelFilePath,lastTime, 3, prep, postp);
        System.out.println(sim);

        int numberOfActualEvaluations = 62;

        System.out.println("Last time \t" + lastTime);
        NonLinearProxyObjectiveFunction obj = new
NonLinearProxyObjectiveFunction(
            sim, numberOfActualEvaluations);

        ProxyEvolutionFittestRun3 r = new
ProxyEvolutionFittestRun3("Experiment 3: Updated Nonlinear Proxy, using 0 lenght
periods ", 90, 60, obj);

        r.run();
    }

```

Appendix 2: Objective function evaluation code

This example of a non-linear objective function code, when exclude proxy calling it become for conventional GA.

```

package mmm.ga.objectiveFunctions;

import java.util.ArrayList;

import mmm.cmgAgents.*;
import mmm.ga.*;

import org.jgap.*;

public abstract class GenericObjectiveFunction extends FitnessFunction {
    /* /** String containing the CVS revision. Read out via reflection! */
    // private final static String CVS_REVISION = "$Revision: 1.6 $";
    protected ArrayList<MyGenericChromosome> listOfEvaluatedChromosomes = new
ArrayList<MyGenericChromosome>();
    protected SimulatorExecutor sim;

    public GenericObjectiveFunction(SimulatorExecutor sim)
        throws Exception {
        this.sim = sim;
    }

    public double performActualEvaluation(MyGenericChromosome a_subject)
        throws Exception {
        double fitnessValue;
        double[] genesValues = a_subject.getGenesValues();
        GenericModelResult r = sim.getGenericModelResults(genesValues);

        a_subject.setGenericModelResult(r);
        if (r.isError()) {
            fitnessValue = 1e-300;
        } else {
            fitnessValue = calculateFitness(r);
        }

        return fitnessValue;
    }

    protected double calculateFitness(GenericModelResult r) {
        int steamCost = 18;
        int solventCost = 1000;
        int oilPrice = 504;
        int million = 1000000;

        double CumSteamInj = r.getLastLineValues()[1];
        double CumSolInj = r.getLastLineValues()[2];
        double CumSolProd = r.getLastLineValues()[3];
        double CumOilProd = r.getLastLineValues()[4];
        double RF = r.getLastLineValues()[5];
        double cSOR = r.getLastLineValues()[6];

        double iav = r.getN() * oilPrice / million;
        double cost = (CumSteamInj * steamCost + CumSolInj * solventCost)
            / million;
        double revenue = (CumOilProd * oilPrice + CumSolProd * solventCost)
            / million;
        double grossProfit = revenue - cost;

        double moneyRecoveryFactor = (grossProfit / iav) * 100;

        System.out.println("ObjValues\t"+moneyRecoveryFactor+"\t"+CumSteamInj+"\t"+
CumSolInj+"\t"+CumSolProd+"\t"+CumOilProd+"\t"

```



```

+RF+"\t"+cSOR+"\t"+iav+"\t"+cost+"\t"+revenue+"\t"+grossProfit);
        if (moneyRecoveryFactor < 0)
            moneyRecoveryFactor = 0;

        return moneyRecoveryFactor;
    }
}

package mmm.ga.objectiveFunctions;

import java.util.ArrayList;

import mmm.cmgAgents.*;
import mmm.ga.*;
import mmm.responseSurfaceProxy.ResponseSurfaceProxy;
import mmm.responseSurfaceProxy.ResponseSurfaceProxyJama;

import org.jgap.*;

public class NonLinearProxyObjectiveFunction extends GenericObjectiveFunction {
    /** String containing the CVS revision. Read out via reflection! */
    // private final static String CVS_REVISION = "$Revision: 1.6 $";
    private ArrayList<MyGenericChromosome> listOfEvaluatedChromosomes = new
ArrayList<MyGenericChromosome>();
    private ResponseSurfaceProxy p;
    private int numberOfActualEvaluation;
    private int actualEvaluationCount;

    public NonLinearProxyObjectiveFunction(SimulatorExecuter sim, int
numberOfActualEvaluation) throws Exception {
        super(sim);
        this.numberOfActualEvaluation = numberOfActualEvaluation;
        this.actualEvaluationCount = 0;
        this.p = new ResponseSurfaceProxyJama();
    }

    public double evaluate(IChromosome c) {
        MyGenericChromosome a_subject = (MyGenericChromosome) c;

        int evolution = a_subject.getConfiguration().getGenerationNr();
        double fitnessValue = 1e-300;
        double[] genesValues = a_subject.getGenesValues();

        if (listOfEvaluatedChromosomes.contains(a_subject)) {
            MyGenericChromosome cc = listOfEvaluatedChromosomes
.get(listOfEvaluatedChromosomes.indexOf(a_subject));
            if (cc.isError())
                System.out.println("evaluateEOLD\t" + evolution +
"\t"
                                + fitnessValue + "\t" + a_subject);
            else {
                a_subject.setGenericModelResult(cc.getGenericModelResult());
                fitnessValue =
calculateFitness(cc.getGenericModelResult());

                System.out.println("evaluateOLD\t" + evolution +
"\t"
                                + fitnessValue + "\t" + a_subject);
            }
            return fitnessValue;
        } else {

            long startTime = System.currentTimeMillis();

            if (actualEvaluationCount < numberOfActualEvaluation) {

```

```

        try {
            fitnessValue =
performActualEvaluation(a_subject);
            long endTime = System.currentTimeMillis();

            if (a_subject.isError())
                System.out.println("evaluateERROR\t" +
+ evolution + "\t" + fitnessValue + "\t" + a_subject + "\t" + (endTime -
startTime) + "\tms\t");
            else{
                p.addTrial(genesValues,
fitnessValue);
                System.out.println("evaluateNEW\t" +
+ evolution + "\t" + fitnessValue + "\t" + a_subject + "\t" + (endTime - startTime)
+ "\tms\t");
            }
            listOfEvaluatedChromosomes.add(a_subject);
            actualEvaluationCount++;
            return fitnessValue;
        } catch (Exception e) {
            e.printStackTrace();
            return -1;
        }
    } else if (actualEvaluationCount ==
numberOfActualEvaluation) {
        // initialize and use the proxy
        p.calculateNonLinearModel();
        fitnessValue = p.getNonLinearResponse(genesValues);
        long endTime = System.currentTimeMillis();
        actualEvaluationCount++; // Just to stop
recalculating the proxy
        if (fitnessValue < 0) {
            fitnessValue = 1e-300;
            System.out.println("evaluateProxyNLErr\t" +
+ evolution + "\t" + fitnessValue + "\t" + a_subject + "\t" + (endTime - startTime)
+ "\tms\t");
        } else {
            System.out.println("evaluateProxyNL\t" +
+ evolution + "\t" + fitnessValue + "\t" + a_subject + "\t" + (endTime - startTime)
+ "\tms\t");
        }
        return fitnessValue;
    } else { // use the proxy
        fitnessValue = p.getNonLinearResponse(genesValues);
        long endTime = System.currentTimeMillis();
        if (fitnessValue < 0) {
            fitnessValue = 1e-300;
            System.out.println("evaluateProxyNLErr\t" +
+ evolution + "\t" + fitnessValue + "\t" + a_subject + "\t" + (endTime - startTime)
+ "\tms\t");
        } else {
            System.out.println("evaluateProxyNL\t" +
+ evolution + "\t" + fitnessValue + "\t" + a_subject + "\t" + (endTime - startTime)
+ "\tms\t");
        }
        return fitnessValue;
    }
}

public ResponseSurfaceProxy getProxy() {
    return p;
}
}

```

Appendix 3: CMG Agents Package

```

package mmm.cmgAgents;

import java.io.*;

public abstract class Preprocessor {

    /**
     * Copy from baseFile to generatedFile until searchText is found
     * @param br
     * @param bw
     * @param searchText
     * @return last line found
     * @throws IOException
     */
    protected String copyUntil(BufferedReader br, BufferedWriter bw,
                               String searchText) throws IOException {
        String currentRecord;
        while( (currentRecord = br.readLine()) != null ){
            if(searchText!=null &&
currentRecord.trim().toUpperCase().contains(searchText)){
                break;
            }
            else{
                bw.write(currentRecord);
                bw.newLine();
            }
        }
        return currentRecord;
    }

    protected void copyUntilEnd(BufferedReader br, BufferedWriter bw) throws
IOException{
        copyUntil(br, bw, null);
    }

    protected boolean checkFileAvailability(String filePath, boolean
istighterModel) throws IOException {
        //if the file exist don't regenerate it
        File gf = new File(filePath);
        if(istighterModel){
            if(gf.exists())
                if(isFileContians(filePath, "CONVERGE TOTRES TIGHTER"))
                    return true;
                else
                    return false;
            else
                return false;
        } else {
            return gf.exists();
        }
    }

    protected boolean isFileContians(String filePath, String searchString)
throws IOException {
        FileReader fr = new FileReader(filePath);
        BufferedReader br = new BufferedReader(fr);

        String currentRecord;

        while((currentRecord = br.readLine()) != null){
            if(
currentRecord.trim().toUpperCase().contains(searchString.trim().toUpperCase()) ){
                br.close();

                return true;
            }
        }
    }
}

```

```

    }

    br.close();

    return false;
}

protected String getGeneratedFileName(String baseFilePath, double[]
newValues) {
    String valuesText = "";
    for(double g : newValues){
        valuesText += "_" + g;
    }

    String generatedFilePath = baseFilePath.replace(".dat", valuesText+".dat");
    return generatedFilePath;
}

/**
 * Implement this method to Generate new model file based on baseFilePath
 * using algorithm generated values newValues
 *
 * Example implementation:
 * <code>String generatedFilePath =
getGeneratedFileName(baseFilePath,newValues);
<p>
if(checkFileAvailability(generatedFilePath, isTighterModel))
    return generatedFilePath;
<p>
BufferedReader br = new BufferedReader(new FileReader(baseFilePath));
<p>
BufferedWriter bw = new BufferedWriter(new FileWriter(generatedFilePath));
<p>
    String searchText = "PERMI ALL";
    <p>String currentRecord = copyUntil(br, bw, searchText);

<p>bw.write(currentRecord);
<p>bw.newLine();

    <p>if (isTighterModel) {
    <p>    searchText = "NUMERICAL";

    <p>    currentRecord = copyUntil(br, bw, searchText);
<p>    bw.write(currentRecord);
<p>    bw.newLine();
<p>    bw.write("CONVERGE TOTRES TIGHTER");
<p>    bw.newLine();
    <p>}

    <p>currentRecord = copyUntil(br, bw, "OPERATE");
    <p>//Replace number
    <p>currentRecord=currentRecord.replaceAll("[0-9\\,\\.\\.\\+\\-]+",
newValues[0]+"");
    <p>bw.write(currentRecord);
    <p>bw.newLine();

    <p>copyUntilEnd(br, bw);
<p>br.close();
<p>bw.close();

    <p>return generatedFilePath;
</code>
 * @param baseFilePath
 * @param newValues
 * @param isTighterModel
 * @return generated file path
 * @throws Exception
 */

```

```

        public abstract String generateModelFile(String baseFilePath, double[]
newValues, boolean isTighterModel) throws Exception;
    }

package mmm.sosfr;

import java.io.*;

import mmm.cmgAgents.Preprocessor;

public class SosFrPreprocessor extends Preprocessor {

    private double lastTime;

    public SosFrPreprocessor(double lastTime) {
        this.lastTime = lastTime;
    }

    /**
     * @param args
     * @throws IOException
     */
    private void generateRUNSection(BufferedWriter bw, double[] newValues,
double lastTime) throws IOException {
        double p11 = newValues[0];
        double p1InjRate = newValues[1];
        double rpInjRate = newValues[18];
        int p21 = 175; //fix this
        int p31 = 6; //fix this
        int p51LastP = 198; //fix this

        double allCyclesPeriodLenght = lastTime - (p11+p21+p31+p51LastP);

        //To optimize this create 13 lenght indicators
        //Five of them multiple integer [1-5]
        //Remaining [0-5]
        int numberOfCycles = 0; //TO BE OPTIMIZED
        int sumCyclesLenghtIndicators = 0;

        for (int i = 2; i < 15; i++) {
            if (newValues[i]>0) {
                numberOfCycles++;
            }
            sumCyclesLenghtIndicators += newValues[i];
        }

        double[] cyclesLength = new double[numberOfCycles];

        int currentCycle = 0;
        String cyclesLenghtInfo = "";
        for (int i = 2; i < 15; i++) {
            if (newValues[i]>0) {
                cyclesLength[currentCycle] =
(newValues[i]/sumCyclesLenghtIndicators)*allCyclesPeriodLenght;
                cyclesLenghtInfo += cyclesLength[currentCycle]
+"\\t";
                currentCycle++;
            }
        }

        //3 lenght indicator [1-4]
        double cyclesLengthIndicatorsTotal = newValues[15] + newValues[16]
+ newValues[17];
        double cp1lengthFraction =
newValues[15]/cyclesLengthIndicatorsTotal;
        double cp2lengthFraction =
newValues[16]/cyclesLengthIndicatorsTotal;

```

```

        double cp3lengthFraction =
newValues[17]/cyclesLengthIndicatorsTotal;

        bw.write("***** START OF PHASE 1 *****\n");
        bw.newLine();
        BufferedReader br = new BufferedReader(new FileReader("p1.txt"));
        String currentRecord = copyUntil(br, bw, "OPERATE MAX STW");
        currentRecord=currentRecord.replaceAll("[0-9\\,\\.\\+\\-]+",
p1InjRate+");
        bw.write(currentRecord);
        bw.newLine();
        copyUntilEnd(br, bw);
        br.close();

        bw.newLine();

        for(int i=1;i<=p11;i++){
            bw.write("TIME "+i);
            bw.newLine();
        }

        bw.write("\n***** START OF PHASE 2 *****\n");
        bw.newLine();
        br = new BufferedReader(new FileReader("p2.txt"));
        copyUntilEnd(br, bw);
        br.close();
        bw.newLine();

        for(int i=1;i<=p21;i++){
            bw.write("TIME "+(i+p11));
            bw.newLine();
        }

        bw.write("\n\n***** START OF PHASE 3 *****\n");
        bw.newLine();
        bw.write("SHUTIN 'Well-1'");
        bw.newLine();
        for(int i=1;i<=p31;i++){
            bw.write("TIME "+(i+p11+p21));
            bw.newLine();
        }

        double currentCycleStartTime = p11+p21+p31;

        String cyclesPeriodsLengthInfo = "";
        for(int i=0; i<numberOfCycles; i++){
            //Cycles periods (3 periods one of them soaking)

            double cp11 = cyclesLength[i]*cp1lengthFraction; //TO BE OPTIMIZED
            double cp21 = cyclesLength[i]*cp2lengthFraction; //TO BE OPTIMIZED
            double cp31 = cyclesLength[i]*cp3lengthFraction; //TO BE OPTIMIZED

            cyclesPeriodsLengthInfo += cp11 + "\t" + cp21 + "\t" + cp31 + "\t";
            bw.newLine();
            bw.write("*** C"+(i+1));
            bw.newLine();

            if(i==0){
                bw.write("\n** PERIOD 1 INITIAL **\n");
                bw.newLine();
                br = new BufferedReader(new FileReader("cp1i.txt"));
                copyUntilEnd(br, bw);
                br.close();
                bw.newLine();
            } else {
                bw.write("\n** PERIOD 1 **\n");
                bw.newLine();
                bw.write("TIME "+(currentCycleStartTime));
            }
        }
    }
}

```

```

        bw.newLine();
        bw.write("shutin 'Well-3'");
        bw.newLine();
        bw.write("open 'Well-1'");
        bw.newLine();
    }

    bw.write("\n** PERIOD 2 **\n");
    bw.newLine();
    bw.write("TIME "+(currentCycleStartTime+cp11));
    bw.newLine();
    bw.write("shutin 'Well-1'");
    bw.newLine();

    bw.write("\n** PERIOD 3 **\n");
    bw.newLine();
    bw.write("TIME "+(currentCycleStartTime+cp11+cp21));
    bw.newLine();
    bw.write("open 'Well-3'");
    bw.newLine();

    currentCycleStartTime += cp11+cp21+cp31;
}

bw.write("\n***** START P5 *****\n\n");
//String p5LastP = readFile("p5_lastP.txt"); //read p1

bw.newLine();
bw.write("TIME "+(currentCycleStartTime));
bw.newLine();
br = new BufferedReader(new FileReader("p5_lastP.txt"));
currentRecord = copyUntil(br, bw, "OPERATE MAX STW");
currentRecord=currentRecord.replaceAll("[0-9\\,\\.\\+\\-]+",
rpInjRate+"");
bw.write(currentRecord);
bw.newLine();
copyUntilEnd(br, bw);
br.close();
bw.newLine();

for(int i=1;i<=p5lLastP;i++){
    bw.write("TIME "+(i+currentCycleStartTime));
    bw.newLine();
}

br = new BufferedReader(new FileReader("lastPart.txt"));
copyUntilEnd(br, bw);
br.close();
bw.newLine();

bw.close();

System.out.println("FileInfo\t"+p11+"\t"+p1InjRate+"\t"+rpInjRate+"\t"+allC
yclesPeriodLengt+"\t"+numberOfCycles

+"\t"+cp1lengthFraction+"\t"+cp2lengthFraction+"\t"+cp3lengthFraction+"\t"+
cyclesLengtInfo+"CyclesPeriodsLength\t"+cyclesPeriodsLengthInfo);
}

@Override
public String generateModelFile(String baseFilePath, double[] newValues,
    boolean isTighterModel) throws Exception {
    String generatedFilePath =
    getGeneratedFileName(baseFilePath,newValues);

    if(checkFileAvailability(generatedFilePath, isTighterModel))
        return generatedFilePath;
}

```

```

BufferedReader br = new BufferedReader(new FileReader(baseFilePath));
BufferedWriter bw = new BufferedWriter(new FileWriter(generatedFilePath));

String currentRecord = "";
    if (isTighterModel) {
        String searchText = "NUMERICAL";

        currentRecord = copyUntil(br, bw, searchText);
        bw.write(currentRecord);
        bw.newLine();
        bw.write("CONVERGE TOTRES TIGHTER");
        bw.newLine();
    }

    currentRecord = copyUntil(br, bw, "RUN");

    this.generateRUNSection(bw, newValues, lastTime);

    br.close();
    bw.close();

    return generatedFilePath;
}

}
package mmm.cmgAgents;

public class GenericModelResult {
    private double[] lastLineValues;
    private double N;
    private boolean isError;

    /**
     * @return the lastLineValues
     */
    public double[] getLastLineValues() {
        return lastLineValues;
    }

    /**
     * @param lastLineValues the lastLineValues to set
     */
    public void setLastLineValues(double[] lastLineValues) {
        this.lastLineValues = lastLineValues;
    }

    /**
     * @param lastLineValues the lastLineValues to set
     */
    public void setLastLineValues(String[] lastLineValues) {
        this.lastLineValues = new double[lastLineValues.length];

        for (int i = 0; i < lastLineValues.length; i++) {
            String string = lastLineValues[i];

            this.lastLineValues[i] = Double.parseDouble(string);
        }
    }

    /**
     * @return the lastTime
     */
    public double getLastTime() {
        return lastLineValues[0];
    }
}

```



```

/**
 * @return the n
 */
public double getN() {
    return N;
}

/**
 * @param n the n to set
 */
public void setN(double n) {
    N = n;
}

/**
 * @return the isError
 */
public boolean isError() {
    return isError;
}

/**
 * @param isError the isError to set
 */
public void setError(boolean isError) {
    this.isError = isError;
}

/* (non-Javadoc)
 * @see java.lang.Object#toString()
 */
@Override
public String toString() {
    String s = "";

    for (double d : lastLineValues) {
        s += d + "\t";
    }
    return s + N;
}
}
package mmm.cmgAgents;

import java.io.*;

public class SimulatorExecuter {
    private String simulatorPath;
    private String workDirectoryPath;
    private String resultReportPath;
    private String baseModelPath;
    private int numberOfCores;
    private boolean useParallelSolver;
    private Preprocessor preprocessor;
    private Postprocessor postprocessor;
    private double lastTime;

    public SimulatorExecuter(String simulatorPath, String workDirectoryPath,
String resultReportPath,
String baseModelPath, double lastTime, Preprocessor
preprocessor, Postprocessor postprocessor) {
        this.simulatorPath = simulatorPath;
        this.workDirectoryPath = workDirectoryPath;
        this.resultReportPath = resultReportPath;
        this.baseModelPath = baseModelPath;
        this.numberOfCores = 1;
        this.useParallelSolver = false;
        this.preprocessor = preprocessor;
        this.postprocessor = postprocessor;

```

```

        this.lastTime = lastTime;
    }

    public SimulatorExecuter(String simulatorPath, String workDirectoryPath,
String resultReportPath,
        String baseModelPath, double lastTime, int numberOfCores,
Preprocessor preprocessor, Postprocessor postprocessor) {
        this(simulatorPath, workDirectoryPath, resultReportPath,
baseModelPath, lastTime, preprocessor, postprocessor);
        this.numberOfCores = numberOfCores;
        this.useParallelSolver = true;
    }
    private void execute(String filePath, int numberOfCores) {

        // IF the output file exist it means model executed before!
        // and not repeated in less number of cores because of ERROR
        // No need to repeat execution
        String irfFilePath = filePath.replace(".dat", ".irf");
        File irfFile = new File(irfFilePath);
        if (irfFile.exists() && numberOfCores == this.numberOfCores) {
            return;
        }

        try {
            String line;
            String command = null;
            if (useParallelSolver) {
                command = "\"" + simulatorPath + "\" -f \"" +
filePath
                    + "\" -wd \"" + workDirectoryPath +
"\ "
                    + "-log -doms -parasol " +
numberOfCores + " -wait";
            } else {
                command = "\"" + simulatorPath + "\" -f \"" +
filePath
                    + "\" -wd \"" + workDirectoryPath +
"\ " + "-log"
                    + " -wait";
            }

            // System.out.println(command);
            Process p = Runtime.getRuntime().exec(command);
            // p.waitFor();
            BufferedReader input = new BufferedReader(new
InputStreamReader(
                p.getInputStream()));
            while ((line = input.readLine()) != null) {
                // System.out.println(line);
            }
            input.close();
        } catch (Exception err) {
            err.printStackTrace();
        }
    }

    private String executeGenericResultReport(String irfFilePath, int
numberOfCores) throws Exception {

        // create command file .rwd
        String generatedFilePath = irfFilePath.replace(".irf", ".rwd");
        String baseFileRWDFilePath = baseModelPath.replace(".dat", ".rwd");
        String outputFilePath = irfFilePath.replace(".irf", ".rwo");

        // if output is executed before don't repeat it
        File of = new File(outputFilePath);
        if (of.exists() && numberOfCores == this.numberOfCores)
            return outputFilePath;

        FileReader fr = new FileReader(baseFileRWDFilePath);

```

```

BufferedReader br = new BufferedReader(fr);
String currentRecord;

FileWriter fw = new FileWriter(generatedFilePath);
BufferedWriter bw = new BufferedWriter(fw);

while ((currentRecord = br.readLine()) != null) {
    if (currentRecord.contains("*FILES")) {
        currentRecord = "*FILES " + irfFilePath + " ";
    }
    bw.write(currentRecord);
    bw.newLine();
}

br.close();
bw.close();

// run command file section

// generate output file

try {
    String command = resultReportPath + " -f \"" +
generatedFilePath
        + " \" -o \"" + outputFilePath + "\"";
    Process p = Runtime.getRuntime().exec(command);

    BufferedReader input = new BufferedReader(new
InputStreamReader(
        p.getInputStream()));

    String line = "";
    while ((line = input.readLine()) != null) {
        // System.out.println(line);
    }
    input.close();
} catch (Exception err) {
    err.printStackTrace();
}

return outputFilePath;
}

public GenericModelResult getGenericModelResults(double[] values)
    throws Exception {

    GenericModelResult r = getGenericModelResults(values,
this.numberOfCores, false);
    return r;
}

private GenericModelResult getGenericModelResults(double[] values, int
numberOfCores, boolean isTighterModel)
    throws Exception {
    GenericModelResult r = new GenericModelResult();

    // create model file
    String generatedModelFilePath = null;
    try{
        generatedModelFilePath =
preprocessor.generateModelFile(baseModelPath, values, isTighterModel);
    } catch (IncorrectModelFileException ex){
        String genesValuesText = "";

        for(double g : values){
            genesValuesText += g + "\t";
        }
        generatedModelFilePath =
preprocessor.getGeneratedFileName(baseModelPath, values);

```

```

        File f = new File(generatedModelFilePath);

        f.delete();

        System.out.println("EXCEPTION\t"+ex.getMessage()+"; Unable
to generate a model for\t"+genesValuesText);

        r.setError(true);
        return r;
    }
    // execute generated model file
    execute(generatedModelFilePath, numberOfCores);

    // get result -- result report
    String irfFilePath = generatedModelFilePath.replace(".dat",
".irf");

    String generatedOutputFilePath = executeGenericResultReport(
        irfFilePath, numberOfCores);

    String[] lastLineValues = postprossor.getLastLine(
        generatedOutputFilePath, "\t");

    r.setLastLineValues(lastLineValues);

    String outFilePath = generatedModelFilePath.replace(".dat",
".out");

    r.setN(postprossor.getInitialOilInPlace(outFilePath));

    if (r.getLastTime() != lastTime) {
        if (isTighterModel && numberOfCores == 1){
            r.setError(true);
        } else if (numberOfCores == 1) {
            r = getGenericModelResults(values, numberOfCores,
true);

            if (r.getLastTime() != lastTime){
                r.setError(true);
            }
        } else {
            r = getGenericModelResults(values, numberOfCores/2,
isTighterModel);
        }
    }

    return r;
}

/**
 * (non-Javadoc)
 *
 * @see java.lang.Object#toString()
 */
@Override
public String toString() {
    return "SimulatorExecuter \nsimulatorPath=\t" + simulatorPath
        + "\nworkDirectoryPath=\t" + workDirectoryPath
        + "\nresultReportPath=\t" + resultReportPath
        + "\nbaseModelPath=\t" + baseModelPath +
"\tPreprossor=\t"
        + preprossor;
}
}
package mmm.cmgAgents;

import java.io.*;
import java.util.regex.Matcher;
import java.util.regex.Pattern;

public class Postprossor {

```

```
    public String[] getLastLine(String filePath, String delimiter) throws
Exception {
    FileReader fr = new FileReader(filePath);
    BufferedReader br = new BufferedReader(fr);
    String currentRecord;
    String lastRecord = "";

    while((currentRecord = br.readLine()) != null)
        lastRecord = currentRecord;

    br.close();
    return lastRecord.split(delimiter);
}

    public double getInitialOilInPlace(String filePath) throws Exception {
    FileReader fr = new FileReader(filePath);
    BufferedReader br = new BufferedReader(fr);
    String currentRecord;

    boolean initialComponentInPlaceSectionFound=false;
    double initialOilInPlace = -1;

    while((currentRecord = br.readLine()) != null){
        if(currentRecord.contains("TOTAL INITIAL COMPONENTS IN PLACE"))
            initialComponentInPlaceSectionFound = true;

        if(initialComponentInPlaceSectionFound &&
currentRecord.toUpperCase().contains("OIL")){
            String scPattern = "([0-9\\,\\.\\+\\-]+) ([Ee] [0-9\\,\\.\\+\\-]+)";
            Pattern p = Pattern.compile(scPattern);
            Matcher m = p.matcher(currentRecord);
            if (m.find()) {
                initialOilInPlace = Double.parseDouble(m.group());
                br.close();
                return initialOilInPlace;
            }
        }
    }
    br.close();
    return initialOilInPlace;
}
}
```

Appendix 4: Response surface proxy package

```

package mmm.responseSurfaceProxy;

import java.util.Hashtable;
public abstract class ResponseSurfaceProxy {
    protected Hashtable<double[], Double> userValuesList;

    public ResponseSurfaceProxy() {
        userValuesList = new Hashtable<double[], Double>();
    }

    public abstract double getLinearResponse(double u[]);

    public abstract double getNonLinearResponse(double[] useru);

    public abstract void calculateLinearModel();

    public abstract void calculateNonLinearModel();

    public abstract void loadDynamicData();

    public void addTrial(double[] uValues, double jValue){
        if(!userValuesList.containsKey(uValues))
            userValuesList.put(uValues, jValue);
    }
}

package mmm.responseSurfaceProxy;

import java.io.*;
import java.util.Hashtable;

import Jama.*;
public class ResponseSurfaceProxyJama extends ResponseSurfaceProxy {
    private Matrix Ulinear;
    private Matrix UNonlinear;
    private Matrix J;
    private Matrix BetaLinear;
    private Matrix BetaNonLinear;

    public ResponseSurfaceProxyJama(String UfilePath, String JfilePath) throws
FileNotFoundException, IOException{
        Matrix userMatrixU = Matrix.read(new BufferedReader(new
FileReader(UfilePath)));
        Ulinear = getUFromUserMatrix(userMatrixU);
        J = Matrix.read(new BufferedReader(new FileReader(JfilePath)));
    }

    public ResponseSurfaceProxyJama() {
        userValuesList = new Hashtable<double[], Double>();
    }

    public double getLinearResponse(double u[]){
        Matrix U = new Matrix(1, u.length+1);
        for (int i = 0; i < u.length+1; i++) {
            if(i==0)
                U.set(0,i , 1);
            else
                U.set(0,i , u[i-1]);
        }
        Matrix r = getLinearResponse(U);
        return r.get(0, 0);
    }

    /**
     * @param U
     * @return

```

```

    */
    private Matrix getLinearResponse(Matrix U) {
        Matrix r = U.times(BetaLinear);
        return r;
    }

    public double getNonLinearResponse(double[] useru) {
        double[] du = new double[useru.length+1];
        double[] unl = getNonLinearDs(useru);
        Matrix u = new Matrix(unl, 1);
        Matrix r = getNonLinearResponse(u);
        return r.get(0, 0);
    }

    private Matrix getNonLinearResponse(Matrix U) {
        Matrix r = U.times(BetaNonLinear);
        return r;
    }

    private Matrix getUFromUserMatrix(Matrix userMatrixU) {
        double[][] uma = userMatrixU.toArray();
        Matrix u = new Matrix(uma.length, uma[0].length+1);
        for (int i = 0; i < uma.length; i++) {
            for (int j = 0; j < uma[i].length+1; j++) {
                if (j==0) {
                    u.set(i, j, 1);
                } else {
                    u.set(i, j, uma[i][j-1]);
                }
            }
        }
        return u;
    }

    public void calculateLinearModel(){
        if(Ulinear==null && J==null){
            loadDynamicData();
        }

        BetaLinear = calculateBeta(Ulinear, J);

        System.out.println("JandU\t\tActual J\tProxy J\tUs");
        //print Y' values of initial data
        Matrix r = getLinearResponse(Ulinear);
        double[] rd = r.getColumnPackedCopy();
        double[] actualJ = J.getColumnPackedCopy();
        double summation = 0;
        for (int i = 0; i < Ulinear.getRowDimension(); i++) {
            System.out.print("JandU\t\t"+actualJ[i]);
            System.out.print("\t"+rd[i]);
            double dY1 = actualJ[i] - rd[i];
            summation += Math.pow(dY1,2);
            for (int j = 0; j < Ulinear.getColumnDimension();
j++) {
                System.out.print("\t"+Ulinear.get(i, j));
            }
            System.out.println();
        }
        System.out.println("Linear Proxy L2[E]=" +
Math.pow(summation, 0.5) );
    }

    public void calculateNonLinearModel(){
        if(Ulinear==null && J==null){
            loadDynamicData();
        }

        calculateNonLinearU();
        BetaNonLinear = calculateBeta(UNonlinear, J);
    }

```

```

double[] b = BetaNonLinear.getColumnPackedCopy();
for (double d : b) {
    System.out.println("Beta\t\t"+d);
}

System.out.println("JandU\t\tActual J\tProxy J\tUs");
//print Y' values of initial data
Matrix r = getNonLinearResponse(UNonlinear);
double[] rd = r.getColumnPackedCopy();
double[] actualJ = J.getColumnPackedCopy();
double summation = 0;
for (int i = 0; i < UNonlinear.getRowDimension(); i++) {
    System.out.print("JandU\t\t"+actualJ[i]);
    System.out.print("\t"+rd[i]);
    double dY1 = actualJ[i] - rd[i];
    summation += Math.pow(dY1,2);

    for (int j = 0; j < UNonlinear.getColumnDimension(); j++) {
        System.out.print("\t"+UNonlinear.get(i, j));
    }
    System.out.println();
}

System.out.println("Nonlinear Proxy L2[E]=" + Math.pow(summation,
0.5) );
}

/**
 *
 */
public void loadDynamicData() {
    //this means dynamic way is used
    Matrix userMatrixU = null;
    int currentCase = 0;
    for (double[] u : userValuesList.keySet()) {
        double response = userValuesList.get(u);
        if(userMatrixU == null){
            userMatrixU = new
Matrix(userValuesList.size(),u.length);
            J = new Matrix(userValuesList.size(), 1);

            for (int j = 0; j < u.length; j++) {
                userMatrixU.set(currentCase, j, u[j]);
            }

            J.set(currentCase, 0, response);
            currentCase++;
        }
        Ulinear = getUFromUserMatrix(userMatrixU);
    }

/**
 * @param U is the x or u values vector
 * @param J is the y or j or the response vector
 * @return
 */
private Matrix calculateBeta(Matrix U, Matrix J) {
    if (U.getColumnDimension() < J.getRowDimension()) {
        //Over-determined
        //Null space of U = 0
        //U'U non-singular positive-definite matrix: (U'U)^-1 exists
        // M < N -- U data less than J data
        //B = (U' U)^-1 . U' . J
        Matrix AA = U.transpose().times(U).inverse();
        Matrix BB = U.transpose().times(J);
        Matrix Beta = AA.times(BB);
        return Beta;
    } else {
        //Under-determined

```



```

        //rank of U = N
        //Null space of U > 0
        //UU' non-singular positive-definite matrix: (GG')^-1 exists
        // M > N
        //B = U' . (U . U')^-1 . J
        Matrix AA = U.times(U.transpose()).inverse();
        Matrix BB = U.transpose().times(AA);
        Matrix Beta = BB.times(J);
        return Beta;
    }
}

private void calculateNonLinearU() {
    Matrix subUL = Ulinear.getMatrix(0, Ulinear.getRowDimension()-1, 1,
Ulinear.getColumnDimension()-1);
    double[][] u = subUL.getArray();
    double[][] nonLinearU = new double[u.length][];
    for (int i = 0; i < u.length; i++) {
        nonLinearU[i] = getNonLinearDs(u[i]);
    }

    UNonlinear = new Matrix(nonLinearU);
}

private double[] getNonLinearDs(double[] ds) {
    int countOfUUs=0;
    for (int i = 1; i < ds.length+1; i++) {
        for (int jj = 1; jj < ds.length+1; jj++) {
            if(i<jj){
                countOfUUs++;
                //System.out.print("\tU"+i+ "U"+jj);
            }
        }
    }
    double[] nonLinearDs = new double[ds.length*2+countOfUUs+1];

    int indexOfUUs=0;
    nonLinearDs[0]=1;
    for (int i = 1; i < ds.length+1; i++) {
        nonLinearDs[i]=ds[i-1];
        nonLinearDs[i+ds.length]=ds[i-1]*ds[i-1];

        for (int jj = 1; jj < ds.length+1; jj++) {
            if(i<jj){
                indexOfUUs++;
                nonLinearDs[ds.length*2+indexOfUUs]=ds[i-
1]*ds[jj-1];
            }
        }
    }

    return nonLinearDs;
}
}

```

Appendix 5: NOA reading package

```

public static double[][] getNOAArray(String filePath) throws IOException {
    Jama.Matrix m = Matrix.read(new BufferedReader(new
FileReader(filePath)));

    return m.getArray();
}

public static Population getInitialNAOPopulation(Configuration config,
String filePath) throws InvalidConfigurationException, IOException {
    Population p = new Population(config);
    double[][] d = getNOAArray(filePath);
    for(int i=0; i<d.length; i++){
        Gene[] garr = new Gene[d[i].length];
        // Heating Phase length: multiple integer [60-790] days with
30 days
        // level length
        garr[0] = new MutipleIntegerGene(config, 60, 790, 30);
        // Heating Phase steam injection rate
        garr[1] = new DoubleGene(config, 10, 40);

        // Cycles lengths indicators
        garr[2] = new IntegerGene(config, 1, 5);
        garr[3] = new IntegerGene(config, 1, 5);
        garr[4] = new IntegerGene(config, 1, 5);
        garr[5] = new IntegerGene(config, 1, 5);
        garr[6] = new IntegerGene(config, 0, 5);
        garr[7] = new IntegerGene(config, 0, 5);
        garr[8] = new IntegerGene(config, 0, 5);
        garr[9] = new IntegerGene(config, 0, 5);
        garr[10] = new IntegerGene(config, 0, 5);
        garr[11] = new IntegerGene(config, 0, 5);
        garr[12] = new IntegerGene(config, 0, 5);
        garr[13] = new IntegerGene(config, 0, 5);
        garr[14] = new IntegerGene(config, 0, 5);
        //garr[15] = new IntegerGene(config, 0, 5);

        // Cycles periods (3 periods one of them soaking)
        garr[15] = new IntegerGene(config, 1, 3);
        garr[16] = new IntegerGene(config, 1, 3);
        garr[17] = new IntegerGene(config, 1, 3);

        // Recovery Phase steam injection rate
        garr[18] = new DoubleGene(config, 10, 40);
        for (int j = 0; j < d[i].length; j++) {
            //garr[j] = new
MutipleIntegerGene(config,a_lowerBound,a_upperBound,a_significance);
            if(j==1 || j==18){
                double v = d[i][j];
                garr[j].setAllele(v);
            } else {
                int v = (int)d[i][j];
                garr[j].setAllele(v);
            }
        }

        IChromosome c = new MyGenericChromosome(config,garr.length);
        c.setGenes(garr);
        p.addChromosome(c);
    }
    return p;
}

```