Genetic Algorithm-Based Pore Network Extraction from Micro-Computed Tomography Images

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Abstract

A genetic-based pore network extraction method from micro-computed tomography (micro-CT) images is proposed in this paper. Several variables such as the number, radius and location of pores, the coordination number, as well as the radius and length of the throats are used herein as the optimization parameters. Two approaches to generate the pore network structure are presented. Unlike previous algorithms, the presented approaches are directly based on minimizing the error between the extracted network and the real porous medium. This leads to the generation of more accurate results while reducing required computational memories. Two different objective functions are used in building the network. In the first approach, only the difference between the real micro-CT images of the porous medium and the sliced images from the generated network is selected as the objective function which is minimized via a genetic algorithm (GA). In order to further improve the structure and behavior of the generated network, making it more representative of the real porous medium, a second optimization has been used in which the contrast between the experimental and the predicted values of the network

permeability is minimized via GA. We present two case studies for two different complex geological porous media, Clashach sandstone and Indiana limestone. We compare porosity and permeability predicted by the GA generated networks with experimental values and find an excellent match.

Keywords: Porous media, Pore Network Model, Optimization, Petroleum, Permeability, Numerical analysis

1. Introduction

Considering the growth of computing power in recent years, pore network model studies in different areas, including petroleum and chemical engineering, materials science, hydrology and also in novel technologies such as bio- and nanotechnology have become an attractive field for research (Dullien, 1992; Nukunya et al., 2005; Rajabbeigi et al., 2009). Pore network models are frequently used in petroleum and chemical engineering applications in order to predict various parameters of a porous medium such as the absolute and relative permeability as well as heat and mass transfer coefficients (Surasani et al., 2008; Blunt, 2001; Valvatne et al., 2005). In a pore network model the void space in the porous medium is described by a network of pores connected by a set of throats. Typically both, pores and throats have size distributions which depend on the porous medium itself; this is particularly the case for complex geological porous materials.

To describe the flow behavior inside the medium, it is therefore necessary to generate a representative three dimensional structural model of the pore morphology based on the available pores and throats, and this process still remains a very challenging issue. The often used

assumption of a regular cubic network is a current technical limitation as the pore space in a naturally occurring porous medium (e.g. rock on which we focus in this text) is often highly irregular; so regular structures are not truly representative with associated limited predictive power. Therefore, seeking a way for the construction of deterministic pore space models which include the irregular features and lead to better predictions is an attractive area for current and future research. Historically, modeling of rock pore space using pore networks began by Fatt (1956a; 1956b; 1956c). The next major milestone was then achieved by Chatzis and Dullien (1977), they extended such models to three dimensions. Wilkinson and Willemsen (1983) presented the concept of reverse percolation, where the critical points of the system were automatically identified. These models were capable of performing drainage and imbibition calculations and predicting capillary pressure curves for multiphase flow with different precisions (Bryant and Blunt, 1992; Piri and Blunt, 2005). Generally, these works provided regular or randomly irregular, unrealistic networks, having a low forecasting capability. Researchers then presented several methods to build more realistic networks: A sedimentation process was suggested where the pore space geometry was obtained by measuring distribution centers of the grains (Bryant et al., 1993; Bakke and Øren, 1997) , sectioned 2D images, photographed by digital camera, of the pore space were used and 3D space was generated using a two-point correlation function (Vogel and Roth, 1997; Okabe and Blunt, 2004; Okabe and Blunt, 2005), and despite limitations, this method was successful in describing the rock flow properties. Researchers then started to image rock samples with micro-tomography (micro-CT) (Hazlett, 1995; Ioannidis, 2000) and 3D models were directly extracted from such images (Spanne et al., 1994; Auzerais et al., 1996). This method is limited when dealing with small pores, because the resolution limit is currently approximately one micrometer. Different researchers suggested

different extraction methods based on these images: Zhao et al. (1994) used a multi-orientation scanning algorithm, Baldwin et al. (1996) developed a thinning algorithm, and Lindquist (2002) determined the medial axis of the geometrical structures of the pore space while other researchers continued this work (Arns et al., 2004a, 2004b; Al-Raoush et al., 2003). Silin and Patzek (2006) used a maximum ball algorithm, which sets spheres into the segmented pore space of micro-CT images to determine the position of the pores; the biggest maximal balls were defined as pores; Dong and Blunt (2009) further improved this algorithm. With further improvement of the micro-CT technology many researchers used micro-CT images to study multi-phase flow through porous media for various processes (Blunt et al., 2002; Pentland et al., 2010; Valvatne and Blunt, 2004; Al-Futaisi and Patzek, 2003; Okabe and Blunt, 2007; Iglauer et al., 2010; Iglauer et al., 2011).

Research work is now conducted to further improve the networks, i.e. to increase quality of the pore space extraction. The importance of finding the optimum pore network model is clear, but there is generally a lack of optimization studies in this field and most of the methods do not have a systematic algorithm for manipulating variables to obtain the optimum pore network model. Genetic Algorithm (GA) is one of the advanced, and robust techniques used to solve various optimization problems, e.g. Jamshidi et al. (2009) generated a random pore network model by means of L-systems, which is a mathematical framework to model the growth of filament based plants. They used GA to produce optimized random pore network models by optimization of L-system parameters. The study presented here uses GA to generate representative cylindrical pore networks of a sandstone and a carbonate rock. We propose two methods: in the first method, the fitness function is defined as the difference between sliced micro-CT and pore network images. In the second method, a two-step optimization is performed. Initial pore positions are obtained

with the same objective function as used in the first approach. Throat locations and sizes are then determined in a second step through the minimization of differences between the experimental and predicted values of the absolute permeability. The proposed approach is more accurate in the sense of reproducing the real geometrical properties of the porous medium such as the coordination number, sizes of throats, and cylindrical overall control volume of the porous medium. These methods were tested on two samples, Clashach sandstone and Indiana limestone. The results show that the proposed methods have great abilities in terms of predicting the actual porosity and permeability values for real reservoir rocks.

2. Network Extraction Algorithm

The 3D cylindrical network model of Clashach sandstone generated with the two-step optimization is shown in Figure 1a, Figure 1b is the upper side view. Cylindrical networks have priority over the previously constructed cuboid-shaped models; this is because micro-CT images are usually acquired in a cylindrical form and the experimental measurements are usually performed on cylinder-like cores. As illustrated, the generated network structure is entirely irregular which makes it flexible enough to represent the complex real pore morphology. In comparison, regular network structures are usually characterized by uniform throats of various geometry with uniform length and different aspect ratios. In the irregular networks, however, all parameters can vary to achieve the best optimization.

Figure 1. Schematic map of the pore network model (a) 3D (b) upper view

Specifically, in the proposed network an unlimited number of throats can be connected to a pore. In addition, pores can be placed anywhere in the network, and they can adapt any sizes; this

method has more flexibility and the generated network is much more representative of real geological porous media. Location and size of throats and pores, as well as the coordination number of pores are obtained with GA with the two methods used here. The optimization algorithm to construct the pore network is shown in Figure 2.

Figure 2. Construction and optimization algorithm for pore network generation. Each chromosome in GA represents a specific network model

Each constructed network is sliced and the image of the sliced surface is built. The resulting image is then compared with its corresponding micro-CT image. The above slicing step is repeated to compare all network images with all micro-CT images. The surfaces depend on how the pores and throats are cut precisely. Such sliced images are therefore suitable for representing location and size of pores and throats. Different ways of cutting cylindrical throats and spherical pores are shown in Figure 3.

Figure 3. Possible ways of cutting cylindrical throats (a) and spherical pores (b)

Prior to comparing the results, all images are converted to binary formats and cropped to the same size. Figure 4 shows this comparison for a sample of real and sectioned images of Clashach sandstone.

Figure 4. Schematic view of the binarized sliced micro-CT image (a) and the corresponding network slice image (b) for Clashach sandstone

3. Optimization of cylindrical network model

Network optimization is performed in order to minimize the structural difference between the pore network model and the real pore space. Gradient-based searching algorithms are not suitable for the optimization of large-scale and discrete spaces. This is mainly due to the fact that the calculation of the elements of objective function gradients is impossible for discrete variables and computationally demanding for continuous variables. GA is thus selected for the task of optimization, due to its robust and efficient performance compared to the other non-gradient based algorithms. A brief review of the genetic algorithm and its application for optimization problems is presented in the following.

3.1 Genetic Algorithm (GA)

The development of genetic algorithms was inspired by genetic science and Darwin's evolution theory. GA works based on the idea of survival of the fittest which is what happens in nature during the evolution of various species. GAs have been used in various disciplines to solve optimization problems, e.g., in pattern recognition, feature selection, image understanding and machine learning. GA consists of a main loop in which various species (individuals), being represented by their own chromosome, are assessed. These species find a chance (based on their fitness) to mate with each other and produce their offspring which are assessed and compete against each other in the next generation. The individuals which perform better (are more fit) dominate the population (the set of individuals in each generation) of next generations. This leads to the concept of the “survival of the fittest” which is the main concept of GA. GA begins with an initial set of individuals whose chromosomes are built in a random manner (Boozarjomehry and Masoori, 2007). Each chromosome represents a point in the search space and is a tentative solution of the optimization problem. Each chromosome represents an

individual which is a set of values for the decision variables existing in the optimization problem. Hence a chromosome contains the values of the decision variables (i.e. Phenotypes); these values can be represented as continuous real numbers and/or discrete types in the form of binary strings called genotypes. Despite the fact that both versions of genetic algorithms (i.e. GA with continuous chromosomes and GA with discrete chromosomes) have been used, Discrete GA seems to be more efficient and robust when compared to continuous GA (Goldberg, 1989; Sivanandam and Deepa, 2008). In each generation, both types of GA go through a loop in which the following tasks are completed for each chromosome:

- Values of the decision variables are extracted from chromosome content.
- The objective function is evaluated based on the obtained values of the decision variables.
- The fitness of the chromosome, which is a measure of the suitability of each chromosome, is calculated based on the calculated objective function.

Having obtained the fitness of all individuals, they are ranked based on their fitness function. The mating pool, which is the set of chromosomes that are appropriate to be used as the parents of next generation individuals, is then built. The individuals with higher fitness have more representatives in the mating pool. This increases the chance of chromosomes with higher fitness in the selection of two parents whose mating leads to two individuals in the next generation. The mating is performed with crossover and mutation operators (Michalewicz, 1996). After obtaining the population of the next generation (which may contain some elites of the current generation as well) the next generation begins and the above steps are repeated to produce the third generation, and so on.

3.1.1 Initialization

The initial population is created by random generation of chromosomes. Each chromosome is a binary string, containing a set of '0' or '1' characters. Each decision variable in the original optimization problem is therefore mapped in this way to a set of genes whose length depends on the feasible range and the variable precision. As an example, for a decision variable x_i whose value is set between a_i and b_i with precision p_i, the required number of genes can be calculated through the following equation:

$$n_i = \sum \left(\log_2 \left(\frac{b_i - a_i}{p_i} \right) \right) + 1 \quad (1)$$

The total number of genes in a chromosome (n_t) is then determined using the following equation:

$$n_t = \sum n_i \quad (2)$$

The inverse phenotypic transformation is used to convert the genotypes into their corresponding phenotypes (Boozarjomehry and Masoori, 2007; Goldberg, 2002).

3.1.2 Genetic Operators

Genetic operators are used throughout the Genetic algorithm. The genetic algorithm produces the population of the next generation via these operators. The implemented operators are crossover and mutation operators which are among the most commonly used operators in GA (Langdon and Poli, 2002).

3.1.3 Selection Operator

This type of operator selects two chromosomes from the mating pool. The mating of the two selected parents results in two offsprings which are part of the population in the next generation. Various selection methods have been proposed for GA, and the most commonly used selection method is the roulette wheel method (Langdon and Poli, 2002).

3.1.4 Crossover

The crossover operator is the main operator used in the mating of the selected parents through information exchange between them, and results in two new chromosomes (called offspring of the parents) in the new generation. The performance of the GA severely depends on the performance of this operator. The crossover rate ($P_{crossover}$) is defined as the ratio of the number of offspring produced in each generation to the population size (N). Crossover rate shows the degree of exploitation of the search space by the algorithm. The most commonly used type of crossover is the single point crossover in which a randomly selected block of genes are exchanged between parent chromosomes. Another alternative of the crossover operator is multi point crossover in which more blocks are exchanged between parent chromosomes (Goldberg, 2002).

3.1.5 Mutation

The mutation operator, which applies random changes to the offspring obtained by crossover, is responsible for the exploration of the search space. The mutation rate or probability ($P_{mutation}$) is defined as the percentage of the total number of chromosomes on which the mutation operator is

applied. With a smaller mutation rate, the variety in the candidate solution shrinks and less exploration will occur (Schmitt, 2001).

3.1.6 Fitness Evaluation

In order to obtain the fitness of each chromosome, the chromosome needs to be decoded to its constituting decision variables. The obtained decision variables are then used to calculate the value of the objective function which is related to the fitness of the chromosome. This fitness represents the degree of suitability of the chromosome in the population (Schmitt, 2001).

3.1.7 Termination criterion

The algorithm continues producing generations until a stopping criterion is fulfilled. Various stopping criteria can be used, e.g.(Dudek, 2004):

- The algorithm stops when the maximum number of generation has been reached.
- Similarity of a specific percentage of chromosomes.
- Difference between the maximum fitness and the average fitness is less than a specific value.

3.1.8 Genetic library

The MATLAB GA toolbox is used in this work. GA toolbox initializes a random sample of individuals with different variables to be optimized. A binary steady-state GA with a single point crossover and mutation has been used.

3.2 Implemented fitness function

In this study, the optimum pore-network structure has been obtained using two approaches. In the first approach, the optimum structure is obtained based on the minimization of the sum of absolute difference between the 3-D binary matrices extracted from the micro-CT images and the sectioned pore network model. Where as in the second approach, a two step optimization is used. In this approach, the first step is similar to the procedure used in the previous approach. In the second step, the best alternatives obtained in the first step are further optimized to minimize the relative errors between the experimental values of the absolute permeability ($K_{\exp}$) and the predictions from the simulated pore network structure (K_{model}). Equations 3 and 4 express the objective functions used in the first and second steps of the optimization, respectively.

$$E_1(X) = \frac{\left|\sum\sum\sum\left(M_{micro-CT} - M_{PM}\right)\right|}{(Total \quad Number \quad of \quad Voxels)} \tag{3}$$

$$E_2(X) = \left|\frac{K_{model} - K_{\exp}}{K_{\exp}}\right| \tag{4}$$

$M_{micro\text{-}CT}$: 3D binary matrix for micro-CT image

M_{PM}: 3D binary matrix for generated by pore network model

The 3D binary image can be stored as a 3D matrix that each element of the matrix corresponds to a single voxel of 3D image with respect to the resolution of the image. The 3D binary matrix for micro-CT image is obtained by considering 0 for elements of matrix that correspond to the voxels of void spaces and 1 for elements correspond to the rock. The 3D binary matrix for

generated pore network structure is achieved by considering 0 for elements that correspond to the pore and throat volumes and 1 for other elements in the domain of network.

3.3 Selection of Optimization Parameters

In the current work, locations of the pore centers are directly taken as the optimization parameters. Due to the large number of pores existing in the network, however, dimensionality reduction is an important task prior to optimization. To do so, pore radii and coordination numbers as well as the throat aspect ratios are described with a Weibull probability distribution function (PDF) and the PDF parameters are instead optimized. For example, the Weibull distribution function used for modeling the radii of the pores can be defined by equation 5.

$$R_t = \min\left\{R_{p1}, R_{p2}, \frac{R_{p1}+R_{p2}}{2R_{asp}}\right\} \tag{5}$$

r_p: pore radius

$r_{p,min}$: minimum radius

$r_{p,max}$: maximum radius

x: random number between 0 and 1

δ, γ : Adjustable parameters

Equation 6 shows how the aspect ratios were computed in this study.

$$r_{asp} = (r_{asp,\max} - r_{asp,\min})\left[-\delta \ln(x(1-e^{-\frac{1}{\delta}}) + e^{-\frac{1}{\delta}})\right]^{1/\gamma} + r_{asp,\min} \tag{6}$$

r_{asp} = aspect ratio = ratio between radii of connected pore and throat.

All characteristic parameters for the pore network extraction are summarized in Table 1. In principle all the listed parameters could be selected as optimization variables, however some of them are fixed here (Table 2) according to the available information and the network generation assumptions; this was done to reduce the optimization search space.

Table 1. Parameters used in pore network extraction process

Table 2. Constant parameters used in pore network extraction process

Equidistant image slices were prepared for the sake of convenience. The length of network is computed using the number of cross sections used for analysis, and the distance between the consecutive image slices. The pore network's overall radius is set to match the radius of the micro-CT images. Minimum and maximum radii of pores and throats as will be later used as the lower and upper bounds respectively in the optimization algorithm, are calculated from the micro-CT images and the analysis of a Mercury Injection Capillary Pressure (MICP) curve. A variable number of pores and throats are used in this method while the number of pores is optimized within the GA framework. Constraining the objective function to the aspect ratio helps in generating realistic models since this does not allow the throat radius to exceed beyond the minimum radius of the pore connecting to the throat. Equation 7 shows how the throat radius is calculated:

$$R_t = \min\left\{R_{p1}, R_{p2}, \frac{R_{p1}+R_{p2}}{2R_{asp}}\right\} \tag{7}$$

R_t : Throat radius

R_{p1} , R_{p2} : Radius of pores connecting to the throat

R_{asp}: Throat aspect ratio

$R_{asp,min}$ and $R_{asp,max}$ are the lower and upper bounds of the aspect ratio that will be used during the optimization process. $R_{asp,min}$ is set to one to consider the largest throat radius, whilst $R_{asp,max}$ has a wide range to include all the smallest throats. These parameters are obtained by MICP analysis. $l_{t,min}$ was assumed to be two times that of the maximum pore radius. This assumption prohibits the pores from overlapping. $l_{t,max}$ was set to 10 times the maximum pore radius to avoid generation of unrealistically long throats.

Bounding the coordination number is another benefit of the current optimization practice. Other methods however do not consider this bound consideration for the network generation, thus causing a nonrealistic coordination number (Dong and Blunt, 2009).

Other parameters selected as optimization variables are listed in Table 3. The optimization procedure is presented in section 4. In the second method, pore number and locations were fixed to the values obtained in the first step and the parameters listed in Table 3 have been chosen as the optimization variables in the second step. The ranges of optimization variables are limited by the number of bits and also by definition of a bound for each parameter in the genetic chromosome.

Table 3. Genetic algorithm variables used for optimization

4. Results and Discussion

Clashach sandstone and Indiana limestone samples are used as case studies for the GA pore network extraction.

4.1 GA Parameterization

Prior to the optimization of a pore network, it is necessary to set the GA parameters. These parameters are presented in Table 4. Contrary to the second step in the second method, a larger population size per generation is required for the first optimization method (and first step in method 2) due to the large number of variables. The crossover rate was determined in an ad hoc manner, in order to obtain the best result by the optimization method. Mutation probability was fixed at a low number because of the large number of variables.

Table 4. GA parameters used

4.2 Optimum Values for Pore Network Model

Optimum solutions obtained for the pore network models are shown in Table 5. Pore locations are not displayed in this table since the number of existing pores is large (Table 5). Pore numbers for each case study were obtained with the first method (also first step in second method). The results show that this method can be used for large scale networks. Pore size distribution, coordination number and other pore network properties were estimated using the Weibull parameters that will be explained in the next sections.

Table 5. Optimum values of the constructed networks

4.3 Comparison with petrophysical properties

Petrophysical properties of the two rock samples (including porosity and absolute permeability) are tabulated in Table 6; this includes the experimental and simulated data.

Table 6. Comparison of predicted porosity and absolute permeability with the experimental data

GA has served as a reliable optimization tool for the current application; results show that the proposed methods provide reliable estimations for porosity and permeability for the case studies. More accurate results are obtained with in the second approach. This can be explained with the limited resolution of the micro-CT image that does not allow for the recognition of all the pores and especially throats in range of nanometer; it is thus necessary to look for a powerful algorithm which is capable of predicting these small pores; this was effectively achieved in the second approach of the proposed method.

Table 7 shows the fitness values calculated with equations 3 and 4 for the constructed networks. Accordingly, GA has served as a reliable optimization tool for the current application. Furthermore, surface's errors lower than 2 percent obtained for each model indicate that the extracted network represents irregularity of the porous medium accurately.

Table 7. Fitness values for the case studies

4.4 Coordination Number Distribution

The coordination number histograms of the pore network structures extracted with the second method are displayed in Figure 5 for both rock samples. The models look realistic from the view point of coordination numbers, because of the surface constraint (that is the total number of throats connected to each pore should be such that the contacting surfaces of all throats is less than the surface of the pore) applied to each pore in the network. According to Figure 5, the coordination number distribution of the Clashach sandstone is skewed to the larger values, whereas the Indiana limestone histogram is skewed to smaller coordination numbers. This relates to the difference in permeability values of the two rock samples; Clashach sandstone is more permeable which is partially caused by the higher average coordination number. It is also possible that small throats – below the micro-CT resolution limit – which may occur in carbonates were not detected in the Indiana limestone.

Figure 5. Histogram of pore coordination number distribution for the two rock samples, (a) Clashach sandstone (b) Indiana limestone

4.5 Aspect ratio distribution

The aspect ratio frequencies for each sample extracted with the second GA method are shown in Figure 6. The aspect ratio is very flexible in this method and can adopt any probability distribution, resulting in the right throat size distribution and the expected petrophysical properties. The minimum value of the aspect ratio was determined based on the assumption that the largest throat radius is capable of completely abutting the smallest connected pore. The

maximum value of aspect ratio was obtained using the minimum throat radius size from the MICP analysis (measurement) as an input.

The aspect ratio distribution of Indiana limestone has an almost Gauss-curve shaped form with a maximum around 10. Clashach sandstone has a monotonically increasing aspect ratio distribution with a maximum at circa 30. Carbonate and sandstone diagenesis are usually quite different and these rocks have typically very different pore structures, consistent with our result.

Figure 6. Aspect ratio frequency distributions for the two samples, (a) Clashach sandstone (b) Indiana limestone

4.6 Pore body size distributions

Figure 7 displays the pore size distributions extracted for each rock sample using the second GA approach. Clashach sandstone has a non-monotonic pore radius distribution with a maximum at approximately 60-70 μm, while Indiana limestone has a pore radius distribution which on average increases monotonically. The maximum pore radii detected in Indiana limestone are smaller (90 μm) than the largest radii in Clashach (130 μm).

Figure 7. Pore size distributions for the two samples, (a) Clashach sandstone (b) Indiana limestone

4.7 Throat size distributions

Throat dimensions including length and radius have a major impact on permeability values. Generally, throats have smaller volumes than the pores in the network models. Throat radius distributions for the case studies are shown in Figure 8. Normalized frequency information shows that approximately a quartile of throats in the Clashach sandstone has a small size, and the rest are distributed over a wider range. Nearly the same result was obtained for the Indiana limestone.

Figure 8. Throat radius distributions for the two samples, (a) Clashach sandstone (b) Indiana limestone

5. Conclusion

Optimization-based pore network extraction was targeted in this research. Image processing is used for preparing images and genetic algorithms are used for the optimization of the pore networks. Two approaches are proposed for construction of the geometrical structure of a geological porous medium. Both approaches optimize the fitness function in a GA framework and extract the optimal network. In the first method a fitness function was set as the difference between micro-CT images and the sliced layers of the generated pore network. The second method utilizes a two-step optimization for extracting the network; in the first step, pore positions are set to values obtained in the first step, and then optimization is achieved using the same objective function as in the first approach. A second optimization is performed following the first step to introduce more accuracy in the final results where the locations of throats are

determined through minimization of the difference between the experimental and the predicted values of the absolute permeability. The current modeling scheme generates several properties of the pore geometry such as coordination number and throat size distributions. The model is obtained within a cylindrical framework, leading to more accurate predictions of the petro-physical properties including porosity and permeability because the whole (cylindrical) micro-CT image is used. Two rock samples were chosen for the application and testing of the proposed methods. Comparison of the results with the experiments shows a significant improvement over the previously proposed models. The models built by the current GA-based algorithms provide a more representative geometry to the real porous medium.

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