

## **Modelling the Diffusion Rate of Microbes in Porous Media during Microbial Enhanced Oil Recovery**

Chukwuma G.J. Nmegbu<sup>1</sup>

<sup>1</sup>*Department of Petroleum Engineering, Rivers State University of Science and Technology, Nigeria*

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**Abstract:-** Biotechnological advances have not only grown in chemical and biological industry but its application in oil and gas has completely followed an increasing trend. This work presents a study of the diffusion of microbes in one of such technologies. The models mathematically presented describe the transport of bacterial community through the pore throats of a porous system. Filtration loss control can be achieved using the formulated model mainly due to the plugging mechanism of biofilms. A computer program, written in JAVA code was used to run a simulation of the bacteria diffusion model. Three-Dimensional, areal, side and top views of the bacteria invasion environment are presented.

**Keywords:-** Diffusion, Microbe, MEOR, Biofilm, Simulation.

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### **I. INTRODUCTION**

Each reservoir is composed of a unique combination of geometry, rock properties, fluid characteristics and primary drive mechanism [1]. Notwithstanding, no two reservoir can be identical in all aspects, they can be grouped in accordance with the primary drive mechanism by which they produce. It has been observed that each drive mechanism has certain typical performance characteristics such as ultimate recovery factor, pressure decline rate, gas-oil ratio and water production often unique to it. These factors are of great importance because of the prevailing rock and fluid properties interaction. Alteration of these properties can thus lead to improvement or deterioration of these factors [2]. This is the aim of every Enhanced Oil Recovery (EOR) technology.

Microbial EOR is an aspect of biotechnology, utilizing the potentials of microbes to significantly influence oil flow and its recovery [3]. It involves the use of microorganisms to extract the remaining oil from the reservoirs [4]. These microbes are carefully selected considering prevalent reservoir conditions. Although certain types of microorganisms may grow prolifically at surface conditions and produce metabolic products that would obviously be beneficial to EOR, they may not be able to survive in a deep subsurface environment owing to conditions of temperature, pressure, salinity etc. [5], [6], [7].

The growth of microbes in-situ in the reservoir has a number of important interactions with the inorganic materials and the oil present in the formation. These microbes will produce biogenic gases which will mix with the oil and dissolve in the heavy crude and act as a mobilizing agent [8]. These fermentation and metabolic processes produce other useful products like polymer and surfactants downhole that aid further petroleum recovery. These result in modifications of the rock and fluid properties necessary for production, and may include permeability modification, viscosity reduction and provision of favourable mobility control.

The modeling of the behavior of bacteria used in MEOR and its activities in the reservoir has attracted interest of researchers [4]. Modeling of these processes often rely on conservation laws, incorporating growth and retention kinetics of biomass. A simplified model of this nature was presented by Knapp et al [6]. They predicted porosity reduction as a function of distance and time. Updegraff [9] used a filtration model in order to express bacteria transport as a function of pore entrance size. Similar models were used by Jang et al [10]. In a recent work, Jenneman et al [11] modified the filtration theory to relate permeability with the rate of bacteria penetration. Some of these models were found to show good agreement with experimental results. However none of these models incorporates fundamental laws of bacterial deposition, entrainment or adsorption of bacteria to the rock surface [12].

One-dimensional models and models extending to two and three dimensions have also been developed [9], [13]. Islam and Gianetto [14] derived a mathematical model for describing bacterial transport, nutrient propagation and microbial growth in porous media [15]. They used a successive over relaxation technique to solve the governing partial differential equations. Of these, they could not solve microbial transport and nutrient propagation directly because of the absence of numerical value of some constants [4]. This work models the transport of the injected bacteria using a simplified diffusion model which can be reduced to the Laplace equation.

## II. METHODOLOGY

### A. Modelling

Consider the statement of mass balance below.

$$\left[ \begin{array}{c} \text{Net rate of accumulation} \\ \text{of microbes in system} \end{array} \right] = \left[ \begin{array}{c} \text{Microbes flow rate} \\ \text{into the system} \end{array} \right] - \left[ \begin{array}{c} \text{Microbes flow rate} \\ \text{out of the system} \end{array} \right] + \left[ \begin{array}{c} \text{Rate of production} \\ \text{of microbes} \end{array} \right] - \left[ \begin{array}{c} \text{Rate of consumption} \\ \text{of the microbes} \end{array} \right] \quad (1)$$

For a 3-dimensional unit vector system, variation of microbe concentration with time in space is given as:

$$\frac{\partial c}{\partial t} = -\frac{\partial j_x}{\partial x} - \frac{\partial j_y}{\partial y} - \frac{\partial j_z}{\partial z} + R \quad (2)$$

where

t = Time,

C = Concentration of microbes

j = Unit vector microbes flux

R = Net generation rate

Assuming that the in-situ microbial concentration is determined primarily by a diffusion process, Equation (2) can be written as:

$$\frac{\partial c}{\partial t} = \frac{\partial}{\partial x} \left( D \frac{\partial c}{\partial x} \right) + \frac{\partial}{\partial y} \left( D \frac{\partial c}{\partial y} \right) + \frac{\partial}{\partial z} \left( D \frac{\partial c}{\partial z} \right) - r \quad (3)$$

Equation (3) is a second degree Partial differential equation accounting for the diffusion of the microbes in the porous medium. It can be written as:

$$\frac{\partial c}{\partial t} = D \left[ \frac{\partial^2 c}{\partial x^2} + \frac{\partial^2 c}{\partial y^2} + \frac{\partial^2 c}{\partial z^2} \right] - r \quad (4)$$

Equation (4) is a weighted form of Laplace equation in spatial coordinates. If a steady state process (i.e.  $\frac{\partial c}{\partial t} = 0$ ) with no net generation ( $r=0$ ) were assumed, the traditional Laplace equation is obtained. Thus, Equation (4) can be readily adapted to specific model conditions.

### B. Adaptive Solution

For a 1D steady state problem, Equation (4) can be written as:

$$\frac{\partial^2 c}{\partial x^2} = 0 \quad (5)$$

Consider the grid system shown below.

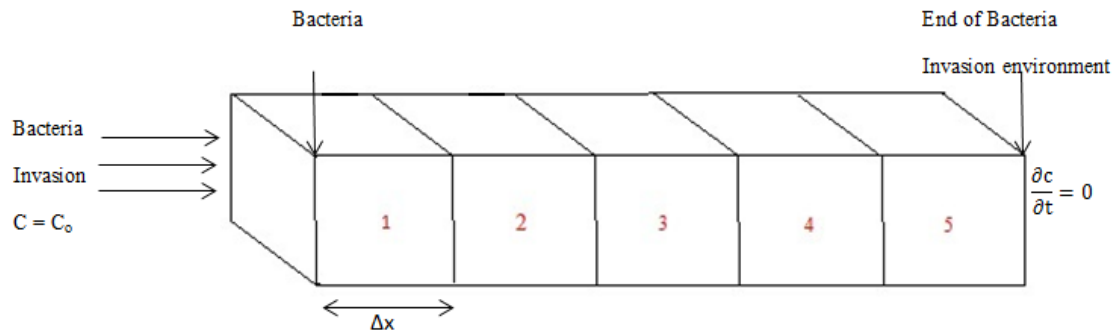


Fig. 1: Block centered grid of bacteria invasion environment

Implementing a numerical solution to Equation (5) for a finite element form of the bacterial invasion environment by applying the central difference approximation gives:

$$\frac{c_{i-1} - 2c_i + c_{i+1}}{(\Delta x)^2} \quad (6)$$

where 'i' represents the position of the grid.

Assuming that the initial bacteria count (i.e., concentration), ready for diffusion is  $C_0 = 200$  (mass unit/volume unit) and applying the boundary conditions as indicated on the diagram results in the set of simultaneous equations given in the matrix below.

$$\begin{bmatrix} -2 & 1 & 0 & 0 \\ 1 & -2 & 1 & 0 \\ 0 & 1 & -2 & 1 \\ 0 & 0 & 1 & -1 \end{bmatrix} \begin{bmatrix} C_2 \\ C_3 \\ C_4 \\ C_5 \end{bmatrix} = \begin{bmatrix} -200 \\ 0 \\ 0 \\ 0 \end{bmatrix} \quad (7)$$

### III. RESULTS

Resolution of the equation, irrespective of the unavailability of data, leads to a conclusion on the bacterial diffusion that more concentration exists at the inner boundary and diffuses into the pore until the outer boundary is reached. This conclusion is better revealed in the dimensionless plots below generated from computer simulation. It is worth mentioning that concentration gradient (x and y axes) and concentration is the parameter in the z-axis. This is because bacteria concentration gradient is responsible for bacteria transport and at each point in time, the z-axis is indicating bacteria mass/population for any unit thickness, thus denoting cross-sectional volume. The simulations are given below.

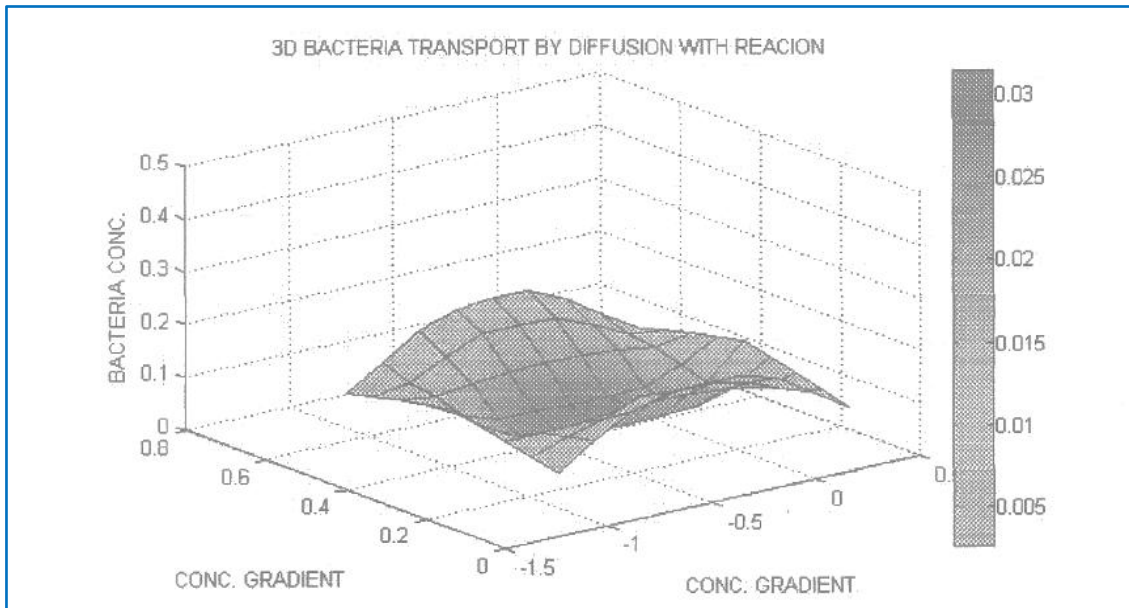


Fig. 2: Angular side view of bacteria transport due to diffusion and reaction

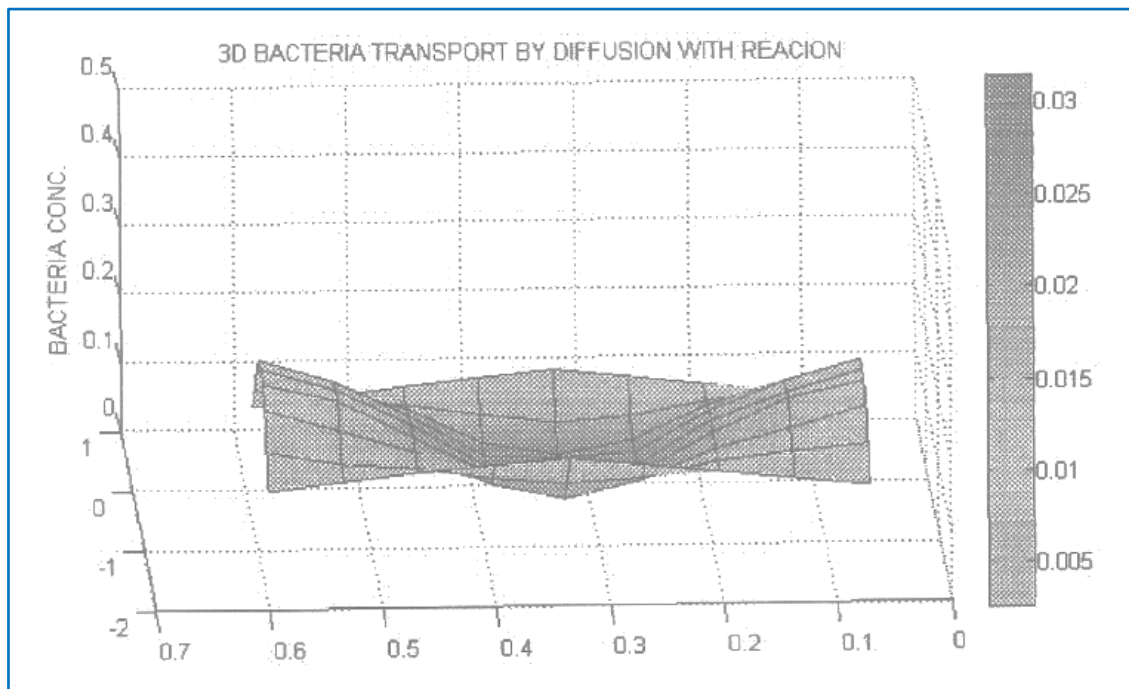


Fig. 3: Elevated side view of bacteria transport due to diffusion and reaction

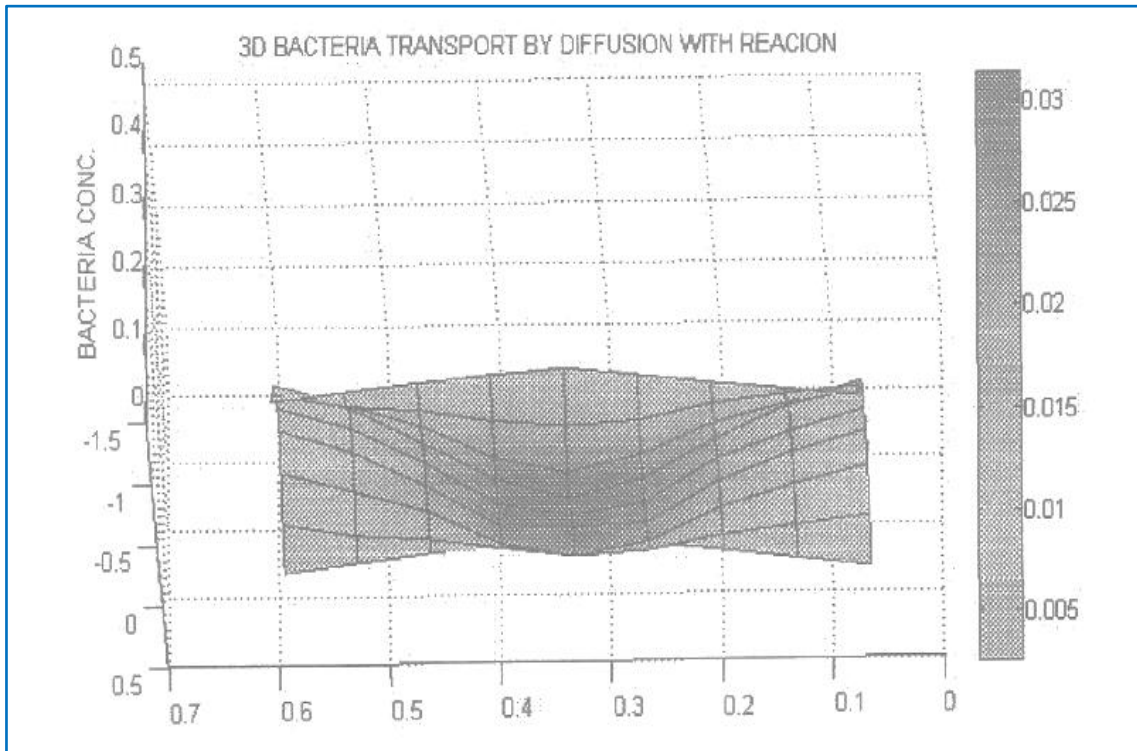


Fig. 4: Top side view of bacteria transport due to diffusion and reaction

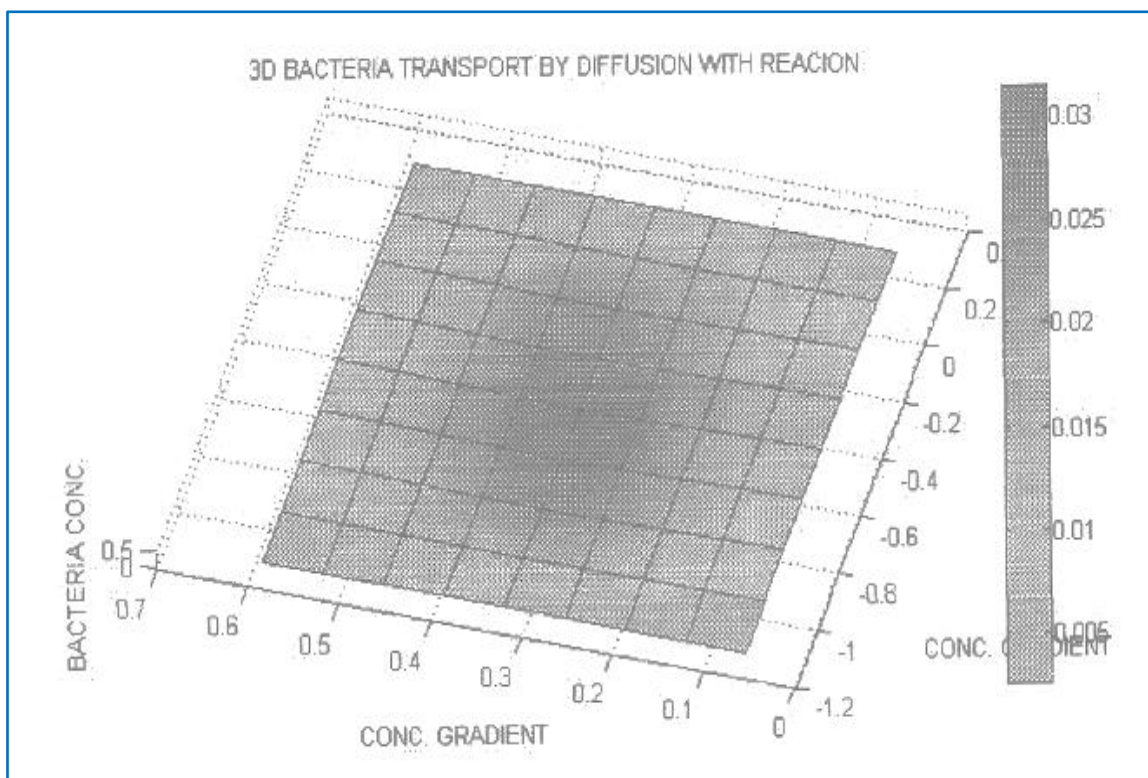
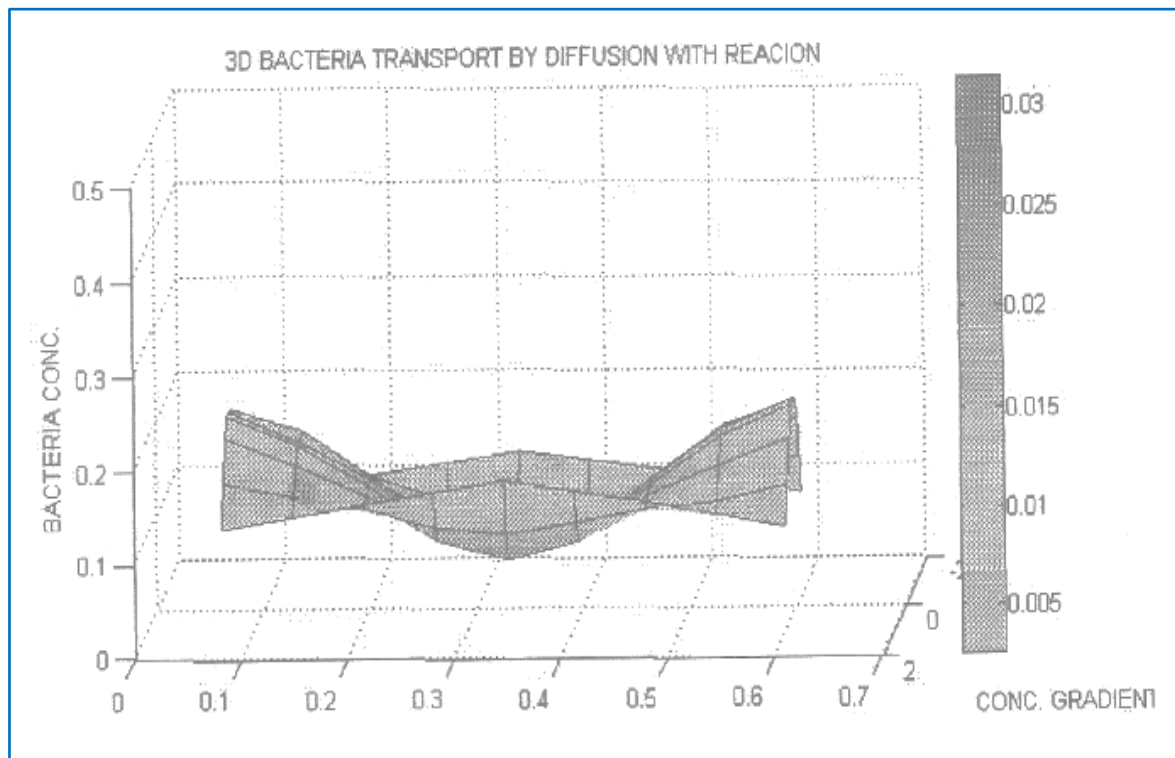


Fig. 5: Top view of bacteria transport due to diffusion and reaction

Figure 5 above gives, perhaps, the best view of the diffusion process, marked by the darker regions in the center of the bacteria invasion environment.



**Fig. 6: Side view of bacteria transport due to diffusion and reaction**

The simulation views show a discontinuity in the process, one characterized by a sink (negative net generation) owing to the fact that the death rate will be greater than the growth rate and the transport of bacteria into the z-direction which is the bacteria concentration axis.

#### IV. CONCLUSIONS

Bacterial diffusion rate has been clearly defined in this theoretical and mathematical research. The model equation and simulation can provide a conclusive answer to the change in bacteria concentration from borehole to the interior of a porous medium undergoing MEOR process or similar biotechnological process. The transiency of concentration and possible automated or controlled bacteria incubation during the process can be effectively used to control fluid loss but it should be noted that an uncontrolled process can lead to very serious permeability damage and this may not serve the purpose of this research.

It should be noted however, that the diffusion has been studied for just an instantaneous influx of bacteria. Any other influx other than the initial will experience the same process of diffusion but with less constant diffusing values.

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