

# The Diffusion Model for the Longitudinal Mixing of Microbes in Reservoir Beds of Finite Length

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**Abstract**—Microbial injection in petroleum reservoirs for enhancing oil recovery has recently been an area of intensive study in the oil and gas industry. Before the application of this non-expensive, environmental friendly method of recovery is employed, the comprehension of its modus operandi is paramount, most essential being its movement and transport techniques through tortuous porous media in petroleum reservoirs. This study reveals the patented process of microbial transport through advection within a finite length reservoir by development and Simulation of a mathematical model which when validated with microbial and reservoir parameters, showed a great degree of similarity with an already established model. Simulation of these models presented a visual description of the longitudinal mixing process of dispersing microbes in the reservoir using the SIMULINK program.

**Index Terms**—Diffusion, Dispersion, MEOR, Microbes.

## I. INTRODUCTION

The introduction of biotechnology for maximizing oil recovery has rapidly increased over time with quite a number of field and laboratory investigations also providing concrete comprehension of the entire recovery process. For effective microbial enhanced oil recovery on a field scale, the interaction of the microbes with its prevailing environment must be ascertained by critical investigation of some microbial transport modes down subsurface. It is most important to present visual-descriptive and mathematical approaches for a better understanding of these microbial transport methods. The relationship between advection and dispersion is employed in the determination of mass transport within the porous media. Generally, most bulk transport of fluids and solutes is dominated by advection and dispersion, with spatial and temporal variations in solute concentration [1]. Understanding solute transport in porous media is of central importance in most MEOR schemes. However, the difficulty in predicting transport properties subsurface is often encountered because of the geologic heterogeneity of the porous media under investigation. Early experimental evidences had shown that when a tracer is continuously injected into a slowly moving water, it spreads systematically from a point which it moves with the average velocity of the tortuous medium [2]. Prommer et al outlined that mechanical dispersion occurs by mixing as a result of local variations in velocity of flow. The variations in rates and direction of transport is traceable to the heterogeneity of the porous media of investigation. These heterogeneities are present in scales ranging from microscopic, macroscopic to megascopic systems [3].

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Dispersion is comprised to two components including molecular diffusion in the case of particles and mechanical dispersion resulting from mixing within the pores and tortuous paths. Blackwell in 1959 conducted an experiment to investigate the dispersion coefficient and its qualitative relevance in the molecular diffusion of transporting particles. [4]. Harvey in 1991 listed important processes and factors that constitute parameters for microbial transport in the porous media, such factors included pore straining, dispersion, detachment, growth and death, mobility and microbial chemotaxis [5]. In the study of Schottinget et al, studied the variations in fluid density and its effects on dispersion was also investigated [6]. Porous media properties either promote or retard dispersion, if the intrinsic permeability and porosity of the subsurface varies in order of magnitude in space, dispersion falls beyond the topic of interest [7]. This study aims at describing and understanding the subsurface processes undergoing longitudinal mixing of the microbes during Microbial enhanced oil recovery, not just relying solely on laboratory and field investigation, but with a descriptive mathematical and visual presentation of mixing and dispersion process of the injected microbes

## II. METHODOLOGY

Transport of microbes in a stream of fluid within a porous medium is not just governed by the complex physical, biological and chemical interaction between the microbes and nutrients but also the microscopic nature of the transport process. This transport isn't defined in a system of void space but a system whose flow path (tortuosity) is complex enough to cause turbulence, dispersion and mixing of the flowing phases. Longitudinal or axial mixing prevails for system where diffusive (dispersive) coefficient is high. The complex transport system leads to a careful attempt to model the diffusion of bacteria undergoing longitudinal mixing. The following assumptions are integral aspects of the development of a mathematical model of longitudinal mixing of microbes in a reservoir of finite length.

1. The porosity of the medium is constant before the MEOR process and remained unchanged after initialization, thus the tortuosity remained constant.
2. Isothermal condition is prevalent and a temperature effect on the rate of diffusion of microbes is considered negligible.
3. Microbial transport is based on diffusive and mixing process.
4. Transverse mixing is negligible.
5. Negligible gravity effects on capillary paths of the longitudinal flow path.
6. Flux of fluids on the axial axes is stronger than its counter gravitational forces.



7. Darcy's law is applicable.

Recalling microscopic conservation principle of mass balance to the finite region of the 3-D system

$$[\text{Mass of bacteria in}] - [\text{Mass of bacteria}] = [\text{Mass accumulation}] \quad (1)$$

Recalling density = mass/volume

$$M = \rho V \quad (2)$$

Derivative of the above, we have

$$\frac{\partial}{\partial t}(m) = \frac{\partial}{\partial t}(\rho v) \quad (3)$$

Density of bacteria community is considered constant. This holds on the basis that growth and decay of microbes are not considered, thus

$$\frac{\partial}{\partial t}(\text{mass}) = (\text{density}) \frac{\partial}{\partial t}(\text{volume}) \quad (4)$$

Rate volumetric transformation ie volume flow rate

$$\text{Thus, } \frac{\partial v}{\partial t} = q \quad (5)$$

$$\text{And } \frac{\partial}{\partial t} = (\rho q) \quad (6)$$

Where

m = mass of bacteria

ρ = density of bacteria

q is the volumetric flow rate of the microbes.

For a system of multiple species of microbes undergoing longitudinal mixing, (6) now becomes

$$\sum_{i=1}^{i=n} \frac{\partial m}{\partial t} = q \sum_{i=1}^{i=n} \rho \quad (7)$$

In constitutive form, we have

$$\frac{\partial m_1}{\partial t} + \frac{\partial m_2}{\partial t} \dots \dots \dots \frac{\partial m_n}{\partial t} = q[\rho_1 + \rho_2 + \dots \dots \dots \rho_n] \quad (8)$$

Presenting the above in vector form to reveal the essence of a three dimensional rate of mass transformation

$$\left( \frac{\partial m_1}{\partial t} + \frac{\partial m_2}{\partial t} \dots \dots \dots \frac{\partial m_n}{\partial t} \right)_{i,j,k} + \left( \frac{\partial m_1}{\partial t} + \frac{\partial m_2}{\partial t} \dots \dots \dots \frac{\partial m_n}{\partial t} \right)_{j,i,k} + \left( \frac{\partial m_1}{\partial t} + \frac{\partial m_2}{\partial t} \dots \dots \dots \frac{\partial m_n}{\partial t} \right)_{k,i,j} + q[(\rho_1 + \rho_2 + \dots \dots \dots \rho_n)_{i,j,k}] + [(\rho_1 + \rho_2 + \dots \dots \dots \rho_n)_{j,i,k}] + [(\rho_1 + \rho_2 + \dots \dots \dots \rho_n)_{k,i,j}] \quad (9)$$

The above represents the spatial mass conservation for multiple mass of microbe at a given time t.

In vector notation, (7) can be written as

$$\sum_{i=1}^{i=n} \frac{\partial m}{\partial t} \Big|_{i,j,k} = (q \sum_{i=1}^{i=n} \rho) \Big|_{i,j,k} \quad (10)$$

In terms of "mass in" and "mass out" for (10)

$$\left( q \sum_{i=1}^{i=n} \rho \right) \Big|_{i,j,k} \Big|_{in} - \left( \left( q \sum_{i=1}^{i=n} \rho \right) \Big|_{i,j,k} \right) + \Delta \left[ \left( q \sum_{i=1}^{i=n} \rho \right) \Big|_{i,j,k} \right] \Big|_{out} = \text{Mass accumulation of microbes} \quad (11)$$

For a porous media of porosity  $\phi$ , permeability, k and bacteria slurry viscosity  $\mu$ ,

$$\text{Mass accumulation of microbes} = \phi \frac{\Delta c}{\Delta t} \Big|_{\Delta x, \Delta y, \Delta z} \quad (12)$$

Combining (12) and (11)

$$\left( q \sum_{i=1}^{i=n} \rho \right) \Big|_{i,j,k} \Big|_{in} - \left( \left( q \sum_{i=1}^{i=n} \rho \right) \Big|_{i,j,k} \right) + \Delta \left[ \left( q \sum_{i=1}^{i=n} \rho \right) \Big|_{i,j,k} \right] \Big|_{out} = \phi \frac{\Delta c}{\Delta t} \Big|_{\Delta x, \Delta y, \Delta z} \quad (13)$$

Where C is the mass concentration of microbes in a finite volume

From Darcy's law,

$$q = \frac{KA}{\mu} \frac{\partial c}{\partial L} \quad (14)$$

$$\text{Microbial velocity } U_b = \frac{q}{A} \frac{K}{\mu} \frac{\partial c}{\partial L} \quad (15)$$

The above can be written in I, j and k directions.

Replacing the summation of microbial density with  $\rho_t$ , for a bacteria concentration in a control volume, for. (14) we have

$$-\frac{\partial}{\partial x} \left( \frac{k_i}{\mu} \frac{\partial c}{\partial x} \rho_t \right) \Big|_{i,j,k} - \frac{\partial}{\partial y} \left( \frac{k_j}{\mu} \frac{\partial c}{\partial y} \rho_t \right) \Big|_{i,j,k} - \frac{\partial}{\partial z} \left( \frac{k_k}{\mu} \frac{\partial c}{\partial z} \rho_t \right) \Big|_{i,j,k} = \phi \frac{\Delta c}{\Delta t} \quad (16)$$

Applying the assumption of constant density and viscosity of bacteria slurry, the equation reduces

$$-\left( k_i \frac{\partial^2 c}{\partial x^2} + \frac{\partial c}{\partial x} \frac{\partial k_i}{\partial x} \right) \Big|_i - \left( k_j \frac{\partial^2 c}{\partial y^2} + \frac{\partial c}{\partial x} \frac{\partial k_j}{\partial x} \right) \Big|_j - \left( k_k \frac{\partial^2 c}{\partial z^2} + \frac{\partial c}{\partial x} \frac{\partial k_k}{\partial x} \right) \Big|_k = \frac{\phi \mu}{\rho_t} \frac{\Delta c}{\Delta t} \quad (17)$$

The derivative  $\frac{\partial k}{\partial L}$  is traceable to the flow by mixing. For any direction, it is important to outline the permeability is not same. On the assumption that it is constant, we can say;

$$\frac{\partial k_k}{\partial z} > \frac{\partial k_i}{\partial x} \approx \frac{\partial k_j}{\partial y}$$

Bacteria reaction = multiplicity rate – decomposition rate

Setting A to be the advective coefficient, we can writ

$$-k \left[ \frac{\partial^2 c}{\partial x^2} - \frac{\partial^2 c}{\partial y^2} \right] - k_i \frac{\partial^2 c}{\partial z^2} - A_i \frac{\partial c}{\partial x} - A_j \frac{\partial c}{\partial y} - A_k \frac{\partial c}{\partial z} = \frac{\phi \mu}{\rho_t} \frac{\partial c}{\partial t} \quad (18)$$

$R_b = R_m + R_d$

Note that multiplicity rate and decomposition rates are integral components of microbial diffusion

there exist a positive microbial displacement, we can define rates as;

$R_m$  = positive displacement/time

$R_d$  = negative displacement/time

$$\text{Thus, } R_b = \frac{\text{positive displacement} - \text{negative displacement}}{\text{time}} = \frac{\text{net displacement}}{\text{time}} = \frac{V_b}{t} \quad (19)$$

where  $V_b$  is the microbial reaction velocity.

Substituting the above into (18)

$$-k \left[ \frac{\partial^2 c}{\partial x^2} - \frac{\partial^2 c}{\partial y^2} \right] - k_i \frac{\partial^2 c}{\partial z^2} - A_i \frac{\partial c}{\partial x} - A_j \frac{\partial c}{\partial y} - A_k \frac{\partial c}{\partial z} + \frac{V_b}{t} = \frac{\phi \mu}{\rho_t} \frac{\partial c}{\partial t} \quad (20)$$

In a single dimension, (20) can be written as

$$-k \frac{\partial^2 c}{\partial x^2} - A \frac{\partial c}{\partial x} + \frac{V_b}{t} = \frac{\phi \mu}{\rho_t} \frac{\partial c}{\partial t} \quad (21)$$

The above will be employed in accounting for the longitudinal mixing of microbes in a finite porous media.

### III. RESULTS AND DISCUSSION

The deduced model was observed to be similar to that of the Fickian law. From the 1-D equation above, the rate  $\frac{V_b}{t}$  is positive because there exists a positive difference between microbial multiplicity and decomposition rate. Reaction rate is zero because the outlined rates are considered the same, and microbial concentration within a finite length is constant.

$$\frac{k}{\mu} \frac{\partial^2 c}{\partial x^2} + \frac{V_b}{t} = \frac{\phi \mu}{\rho_t} \frac{\partial c}{\partial t}$$

The transmissibility term is given as  $\frac{k}{\mu} \frac{\partial^2 c}{\partial x^2}$  in the equation above, serving as a diffusion coefficient.

The simulation results of the developed model are presented below.



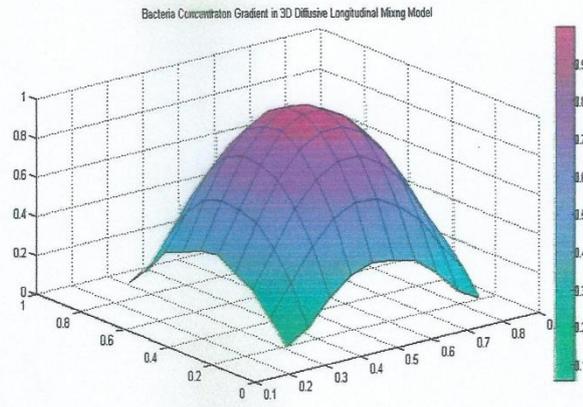


Fig 1. Showing the front view of microbial diffusion undergoing longitudinal mixing in 3D

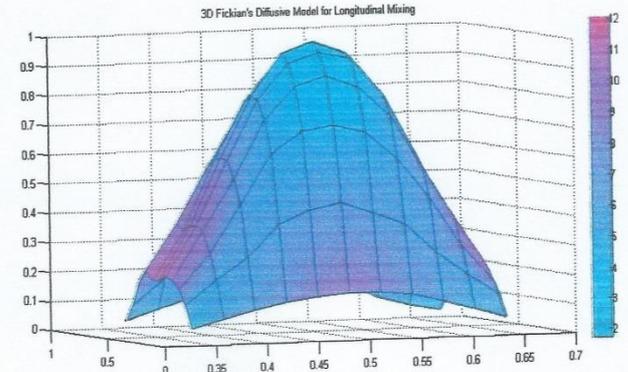


Fig 5. Showing Fickian side view of microbial diffusion undergoing longitudinal mixing

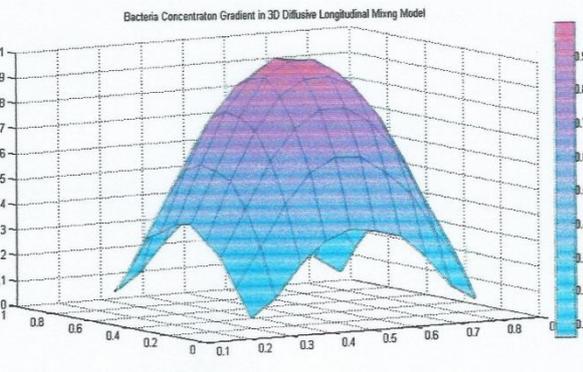


Fig 2. Showing Side view of microbial diffusion undergoing longitudinal mixing

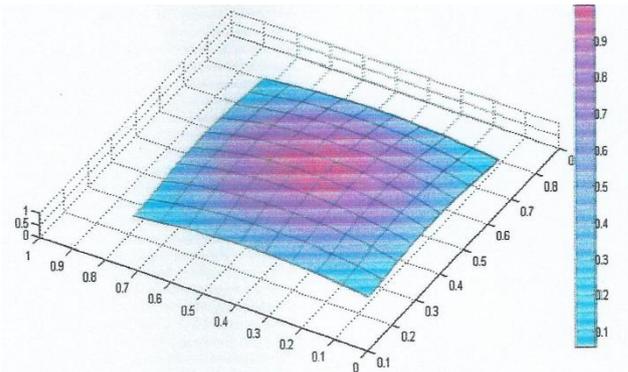


Fig 6. Showing Fickian near-top view of microbial diffusion undergoing longitudinal mixing

Fig 3. Showing near-top view of microbial diffusion undergoing longitudinal mixing

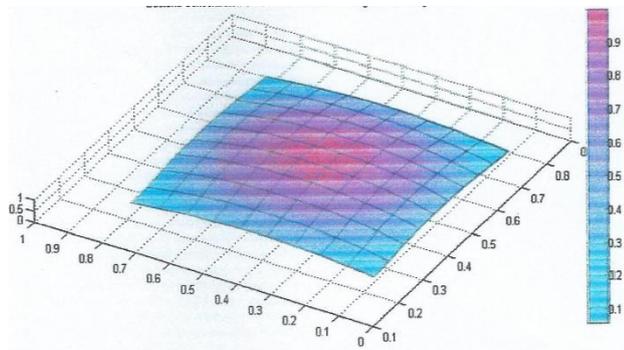
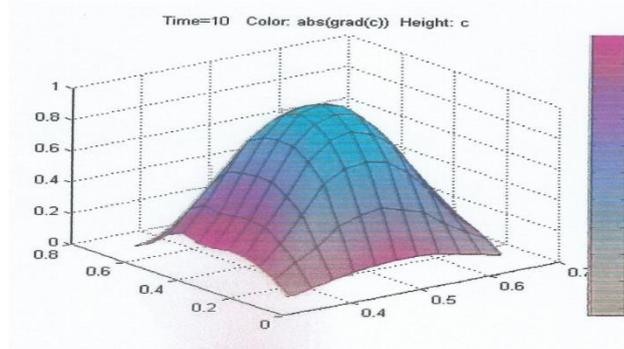


Fig 4. Showing Fickian front view of microbial diffusion undergoing longitudinal mixing



Figures 1, 2 and 3 are simulations of the deduced model in 3-dimensions, each being views of the simulation from different angles. Fig 4, 5 and Fig 6 presents the Fickian model for diffusion of microbes with inclusion of advective flow (mixing), and both simulations showed similar representation with the application of unaltered parameters used for validation. The model showed a greater value in the k-direction than that of the Fickian model traceable to the variation in the diffusion coefficient. The diffusion coefficient was not certain for the Fickian model, but the transmissibility coefficient was used for that of the deduced model. Another reason for this variation could be tortuosity assumption in the z-axis. It is also observed that the mixing and diffusive process was not dominant in the x and y directions during the simulation. This is as a result of the boundary conditions denoting no microbial influx at the boundaries. The microbial reaction term was not an integral component of the simulation because it was assumed a zero value (multiplicity rate = decomposition rate). Displacement rate of the microbe was constant, this assumption holds for finite lengths, whereas, it doesn't for infinite lengths of changing values of concentration and velocity profiles. For this study, a differential length was considered to be the finite length of the system. The limitation of this study lies on the extent to which these assumptions hold for other reservoir geometries.

#### IV. CONCLUSION

Mathematical approach has proved instrumental in revealing the true longitudinal mixing of microbes during their transportation/diffusion with a pictorial representation, with so much of the microbial transport in respect to the z-direction. The model validated with the SIMULINK computer program showed a credible correlation to that of Fickian model which takes into account both transverse and longitudinal mixing. The condition of poor tortuosity in the x and y directions was the limiting factor for the consideration of only longitudinal mixing in this study. This study is thus open for investigation for both neglected axis.

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