A Novel Tensor Resistance-Based Pore-Network Model for Pore-Scale Flow in Porous Media

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Abstract. Pore-network models (PNMs) are powerful tools for simulating fluid flow and transport in porous media, with applications spanning petroleum engineering, hydrology, and materials science. Classical PNMs simplify porous media into interconnected pore-throat networks and model flow using empirical resistance relationships. This paper introduces the Tensor Resistance-Based Pore-Network Model (TR-PNM), a high-fidelity upscaling framework designed to overcome the limitations of classical pore-network models (C-PNM) in capturing anisotropic flow within complex porous media. By utilizing a natural domain decomposition process, the TR-PNM replaces idealized scalar resistances with $n \times n$ conductivity tensors derived from solving local Stokes flow problems on the actual 3D geometry of individual pore units. This approach bridges the gap between traditional "ball-and-stick" approximations and the high accuracy of Direct Numerical Simulation (DNS), by designating interface pressures at throat centers as the primary unknowns to ensure rigorous mass conservation. By providing a scalable and physically consistent characterization of high-fidelity flow behavior, the TR-PNM offers a robust tool for industrial applications in reservoir engineering, carbon sequestration, and groundwater remediation.

Keywords: Pore-network model · Tensor resistance · Domain decomposition · Anisotropic flow · Porous media · Computational hydraulics

1 Introduction

Porous media are ubiquitous across a vast array of natural and engineered systems, serving as the foundational structures for oil reservoirs, groundwater aquifers, fuel cells, and catalytic reactors. In these complex environments, understanding fluid flow at the pore scale is not merely a theoretical exercise but a

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critical necessity for accurately predicting macroscale transport behavior, effective permeability, and chemical dispersion [15, 16, 21, 10, 19]. While traditional laboratory experiments provide essential data, numerical modeling has become indispensable for gaining deeper insight into these hidden flow paths. Among these approaches, pore-network models (PNMs) [8, 4, 3, 2, 5] have emerged as a robust and highly cost-effective alternative to computationally demanding Direct Numerical Simulation (DNS) methods, such as the lattice Boltzmann method (LBM) [14, 13, 20], high-resolution finite volume/element methods (FVM/FEM) [1] or particle methods [9].

The **Pore-Network Model (PNM)** simplifies the pore space into a topologically equivalent graph of interconnected pore bodies (nodes) and pore throats (edges). For pore-scale incompressible single-phase flow of Newtonian fluid in porous media, the core of classical PNMs is the relationship between flow rate and pressure drop across a throat, derived from the Hagen-Poiseuille equation for laminar flow in a cylindrical tube:

$$q_{ij} = \frac{\pi r_{ij}^4}{8\mu L_{ij}}(p_i - p_j) = \frac{1}{R_{ij}}(p_i - p_j). \tag{1}$$

In this expression, r_{ij} and L_{ij} are the radius and length of throat ij, μ is the fluid viscosity, and $R_{ij} = \frac{8\mu L_{ij}}{\pi r_{ij}^4}$ defines the isotropic hydraulic resistance for that specific throat. For non-cylindrical throats (e.g., slit-shaped), the resistance is modified to: $R_{ij} = \frac{12\mu L_{ij}}{wh^3}$, where w is the width of the slit and h is the height of the slit. We note that here, in all cases, resistance is a *scalar* (isotropic) quantity. In our new TR-PNM to be introduced shortly, resistance will become a *tensor* (anisotropic) quantity.

The Hagen-Poiseuille equation (Equation (1)) alone is not closed and cannot be used to solve for both the pressure (at all nodes) and the flux (along all throats). We need to provide one additional equation at the network scale to close the system. For an incompressible fluid, the net flow into any pore i must be sources or sinks (no mass accumulation in time):

$$\sum_{j \in \mathcal{N}(i)} q_{ij} = Q_i, \tag{2}$$

where $\mathcal{N}(i)$ is the set of neighboring nodes to i, and Q_i is the external source/sink term at node i (zero for internal nodes).

Substituting the Hagen-Poiseuille equation (Equation (1)) into the mass balance Equation (2), we obtain a linear algebraic equation for each pore. These equations together form a system of linear equations: $\sum_{j \in \mathcal{N}(i)} \frac{1}{R_{ij}}(p_i - p_j) = Q_i$. In the matrix form, this is written as: $\mathbf{Ap} = \mathbf{Q}$. In this expression, $\mathbf{A}$ is an $N \times N$ conductance matrix with diagonal terms $A_{ii} = \sum_{j \in \mathcal{N}(i)} 1/R_{ij}$ and off-diagonal terms $A_{ij} = -1/R_{ij}$ for connected nodes, while $\mathbf{p}$ and $\mathbf{Q}$ represent the vectors of nodal pressures and source/sink terms, respectively.

Limitation of Classical PNMs: Classical PNMs represent porous media as a network of pores (nodes or cells) and throats (bonds or edges or links)

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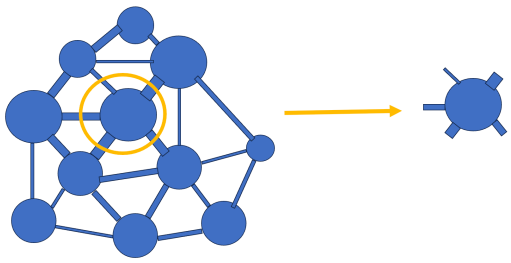

Fig. 1: The unit of TR-PNM

with simplified geometric and hydraulic properties. These models rely on empirical correlations (e.g., Hagen-Poiseuille for laminar flow) to compute flow resistance in throats, assuming isotropic resistance and homogeneous pore geometry [17]. While classical PNMs are computationally efficient, they fail to capture anisotropic flow behaviors [12, 18] in complex porous media (e.g., fractured rock or layered sediments). The classical PNMs are quite accurate for thin and small-radius pore throats, where the Hagen-Poiseuille solution is applicable, but they are not accurate for modeling thick "pore throats"; they are also satisfactory for describing a large pore body, where fluid flow resistance is negligible, but they incur pronounced modeling error for a large "pore body". In addition, the classical PNMs scale poorly for large networks ($>10^6$ pores) [6].

2 TR-Based PNM with Domain Decomposition

The fundamental difference between the Tensor Resistance-Based Pore-Network Model (TR-PNM) and the classic PNMs lies in how they partition the void space of the porous medium. The TR-PNM approach shifts the modeling paradigm from simplified geometric conduits to high-fidelity substructures, primarily through two key innovations: the transition from scalar to tensor-based resistance to capture directional anisotropy, and the implementation of domain decomposition [11] to partition the void space into specialized "pore units".

In the TR-PNM framework, the fundamental building block is the pore unit, a composite structure that departs significantly from the discrete "ball-and-stick" components used in a classic pore-network model (C-PNM). While a C-PNM distinguishes between pore bodies (storage nodes) and pore throats (resistive edges), the TR-PNM utilizes a more integrated geometry. As illustrated in Fig. 1, a pore unit is created by bisecting every connected pore throat at its exact geometric center to form "half-throats". These half-throats are then aggregated with their parent pore body to form a single, self-contained entity, which we call a TR-PNM pore unit or simply a TR-PNM unit. The entire TR-PNM is built using only these pore units as the fundamental building blocks. While the classic model treats pore bodies as zero-resistance nodes and isolates flow resistance within 1D throats defined by a single real number (implicitly assuming isotropic flow), the

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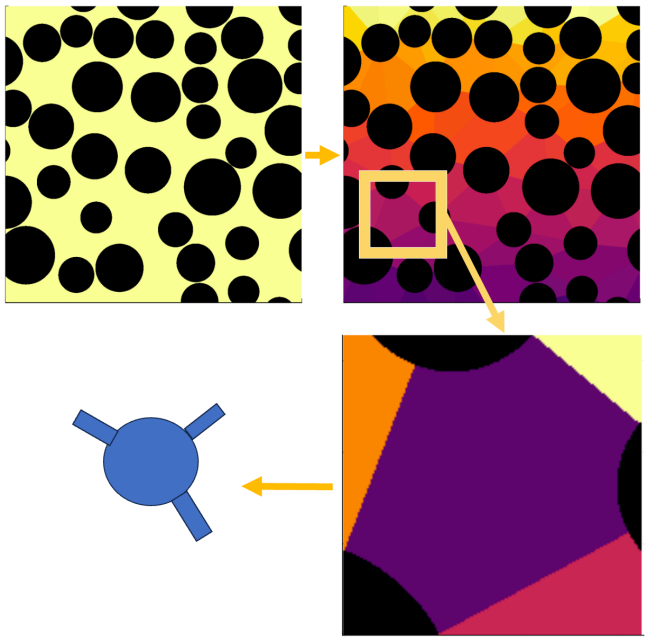

Fig. 2: From domain decomposition to the TR-PNM unit

TR-PNM recognizes the entire pore unit as a complex, potentially anisotropic resistor. This behavior is rigorously captured by an $n \times n$ conductivity tensor, where n represents the number of half-throat inlets and outlets. The extraction of the pore unit in the Tensor Resistance-Based Pore-Network Model (TR-PNM) involves a clean and natural domain decomposition process that captures the full geometric fidelity of the pore space. As shown in Fig. 2, the complex void space of the porous medium is first partitioned into subdomains by assigning a number of cutting planes. The cutting planes are located at the center of throats and are perpendicular to the orientation of throats, so that the area of cutting planes is minimized. For pore geometries that differ from pore throats in their shape, the cutting planes can still be mathematically defined using the minimization process on the area of cutting planes. For a selected sub-domain (shortly later represented by a TR-PNM pore unit), the solid-fluid interfaces are designated as no-flow boundaries, while the N interfaces where throats were bisected are assigned as inflow/outflow boundaries (see the second step of Fig. 2).

We need to assign an effective resistance or conductivity tensor for each sub-domain. This tensor is algebraically represented by a square matrix, which relates the flow rates at each half-throat to the pressures at those boundaries. For a sub-domain with n half-throats (inlets/outlets), i.e., n inflow/outflow boundaries, the tensor is an $n \times n$ matrix. To numerically determine the conductivity tensor, a local problem of Stokes flow is solved by imposing a constant unit pressure ($P = 1$) on one specific boundary while setting all other $n - 1$ boundaries to

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zero pressure ($P = 0$), by using a conservative numerical method, such as the cell-centered finite difference (CCFD), a finite volume method, or a conservative finite element method. This process is repeated for each boundary to populate the $n \times n$ matrix.

3 Illustration through a Numerical Example

The transformation of a complex porous medium into a high-fidelity Tensor Resistance-Based Pore-Network Model (TR-PNM) follows a rigorous upscaling pipeline that preserves geometric realism while enabling computational efficiency. This process begins with the generation of the porous domain, as seen in the first plot of Fig. 2, where a synthetic medium is created using solid balls of varying radii and randomly generated locations. This initial 3D voxel-like representation serves as the basis for the domain decomposition, where the void space is partitioned into sub-domains through the strategic placement of cutting planes at the center of pore throats.

Once the global domain is partitioned, a specific sub-domain is isolated for detailed characterization, as illustrated in Fig. 3(left). In this example, the selected sub-domain features a central pore body connected to three neighboring half-throats. Unlike classic models that simplify this geometry into a zero-resistance sphere, the TR-PNM treats this sub-domain as a unique hydraulic unit. To prepare for numerical solving, a high-resolution mesh is applied to the unit, shown in Fig. 3(right), presenting the internal discretization that distinguishes between the fluid-occupied cells and the solid boundaries.

The core of the TR-PNM method is the solution of the local Stokes flow problem to derive a conductivity tensor. Because this sub-domain has three inlets/outlets ($N = 3$), three independent numerical experiments are performed. In each experiment, a unit pressure ($P = 1$) is applied to one half-throat interface while the others are set to $P = 0$, and the solid boundaries are treated as no-flow zones. The resulting pressure distributions across the unit for these three scenarios are captured in Fig. 4(left), Fig. 5,(left) and Fig. 6(left), showing how the pressure gradient develops specifically according to the irregular internal morphology. The corresponding fluid velocity fields, as shown in Fig. 4(right), Fig. 5,(right) and Fig. 6(right), allow for the calculation of the volumetric flow rates exiting and entering each of the three interfaces.

By integrating the flux data from these three local simulations, we construct the 3×3 conductivity tensor for the TR-PNM unit. For this specific example, the resulting tensor is: $\mathbf{C} = \begin{bmatrix} -0.0015507 & 0.0011285 & 0.00042218 \\ 0.0011276 & -0.0014306 & 0.00030297 \\ 0.00042309 & 0.00030205 & -0.00072514 \end{bmatrix}$. This matrix acts as the "fingerprint" of the pore unit, mathematically relating boundary pressures to volumetric flow rates. The off-diagonal terms represent the cross-coupling between different throats, while the diagonal terms represent the primary resistance along each path. Finally, these characterized sub-domains are reassembled into a global network. Each pore unit, represented by its central

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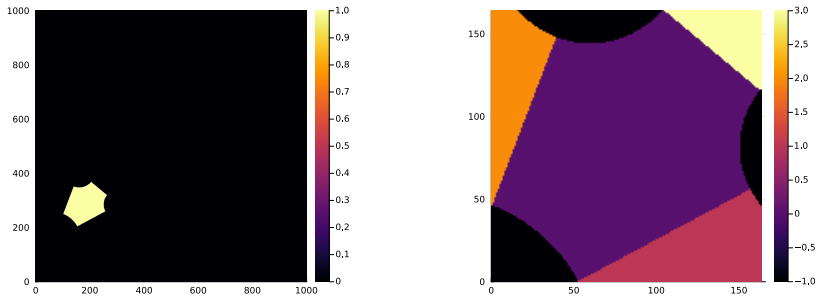
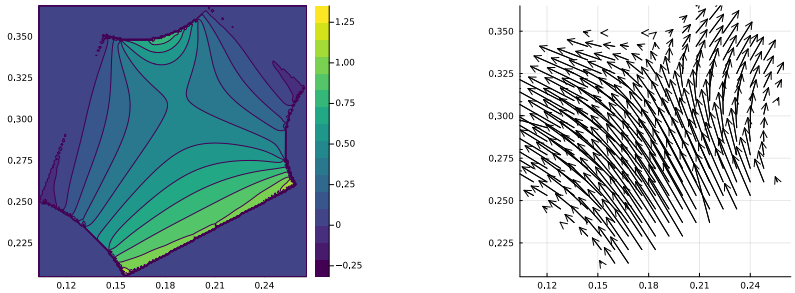
body and associated half-throats, is connected to its neighbors at the throat interfaces. By enforcing mass conservation at these interfaces, where the flux leaving one unit must equal the flux entering the next, a global sparse linear system is formed.



(a) Location of the selected subdomain (b) Zoomed-in panel of the subdomain

Fig. 3: A selected subdomain in the domain-decomposion of the porous medium



(a) The computed pressure profile (b) The computed velocity plot

Fig. 4: CCFD solution of the first sub-problem in the selected subdomain

4 Conclusion

We presented the Tensor Resistance-Based Pore-Network Model (TR-PNM) as a high-fidelity alternative to C-PNM, which fails to capture complex anisotropic flow in fractured/layered porous media. Using domain decomposition, it replaces scalar resistances with 3D geometry-derived conductivity tensors, balancing DNS accuracy and simulation speed, with applications in oil recovery, groundwater remediation and carbon sequestration. TR-PNM combines network efficiency and

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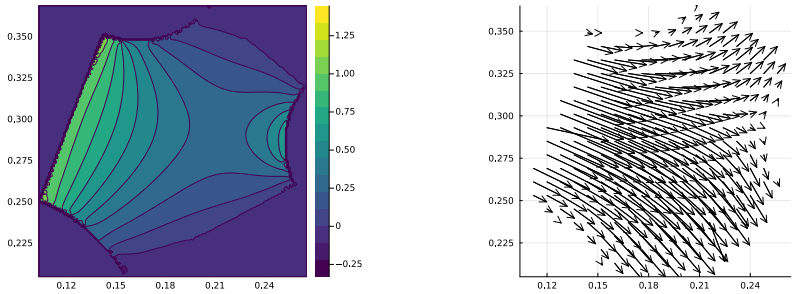
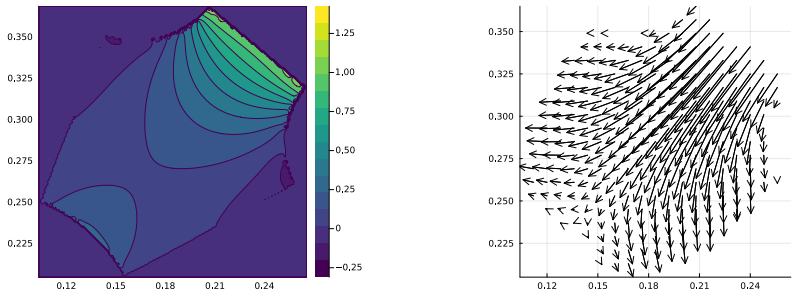


(a) The computed pressure profile (b) The computed velocity plot

Fig. 5: CCFD solution of the second sub-problem in the selected subdomain



(a) The computed pressure profile (b) The computed velocity plot

Fig. 6: CCFD solution of the third sub-problem in the selected subdomain

DNS rigor, scales to large systems, and supports non-linear extensions. Future work will improve interface accuracy, automate network extraction via machine learning, and extend to multiphase flow.

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