Cellular Automaton Modeling for Kidney Blood Vessel Dynamics: A Systems Engineering Approach to Microvascular Simulation

Juan David Buitrago Rodriguez
Systems Engineering Program
Universidad Distrital Francisco Jose De Caldas
Bogotá, Colombia
jdbuitragor@udistrital.edu.co

David Giovanni Aza Carvajal
Systems Engineering Program
Universidad Distrital Francisco Jose De Caldas
Bogotá, Colombia
dgazac@udistrital.edu.co

***Abstract*—This paper presents a cellular automaton (CA) simulation framework for modeling kidney blood vessel dynamics, addressing the complex vascular behaviors observed in histological kidney tissue. Building upon previous work in CNN-based histological image classification, we develop a discrete-time, grid-based simulation that captures emergent vascular phenomena including normal vessel propagation, pathological aneurysm formation, and tissue regeneration. The system integrates real histological images as initial conditions and demonstrates chaotic sensitivity to arterial distribution patterns. Key contributions include a novel pressure-driven vessel propagation model, pathological state transitions, and quantitative analysis of system stability under varying initial conditions. Results show that well-distributed arterial structures promote stable vascular networks, while sparse arterial configurations lead to chaotic dynamics and increased pathological events. This work provides a computational framework for understanding microvascular behavior and validates the application of cellular automata to biological tissue modeling.**

***Index Terms*—Cellular Automata, Blood Vessel Simulation, Kidney Vasculature, Chaos Theory, Systems Engineering, Microvascular Dynamics**

I. Introduction

The modeling of microvascular dynamics in kidney tissue represents a significant challenge in computational biology, requiring the integration of complex biological processes with mathematical frameworks capable of capturing emergent behaviors. This work addresses the development of a cellular automaton (CA) simulation system for kidney blood vessel dynamics, completing a comprehensive systems engineering pipeline that bridges theoretical design with practical implementation.

Kidney vascular networks exhibit intricate patterns of growth, adaptation, and pathological responses that are difficult to model using traditional mathematical approaches. The discrete nature of cellular automata, combined with their ability to generate complex global behaviors from simple local rules, makes them particularly suitable for simulating biological systems where emergent properties arise from local cellular interactions.

This research builds upon our previous work in histological image analysis and CNN-based classification systems, extending the pipeline to include dynamic simulation capabilities. The integration of real histological images as initial conditions provides a direct connection between observed tissue architecture and simulated vascular behavior, enabling validation of the computational model against biological ground truth.

The motivation for this work stems from the need to understand vascular arrangement patterns in kidney

tissues, particularly in the context of pathological conditions such as aneurysm formation and vessel degeneration. By implementing a cellular automaton framework, we can explore how local cellular rules give rise to global vascular patterns and investigate the sensitivity of these systems to initial conditions and parameter variations.

II. System Design and Architecture

A. Cellular Automaton Framework

The cellular automaton operates on a discrete 60×60 grid where each cell represents a spatial unit of kidney tissue. The system evolves through discrete time steps, with each cell updating its state based on its current state and the states of its neighbors according to predefined rules.

The CA framework addresses three key biological scenarios:

- **Normal Vasculature Growth**: Simulates vessel propagation from arterial sources and tests if generated networks match histological patterns
- **Pathological Responses**: Models aneurysm formation and rupture cascades, evaluating system stability under chaotic perturbations
- **Image-Driven Validation**: Processes real histological images into cellular automaton initial states and compares simulation outcomes with ground truth annotations

B. Cell Types and Behavioral Rules

The system defines seven distinct cell types, each with specific behavioral characteristics:

Artery (A): Constantly generates vessels in cardinal directions ($\uparrow \downarrow \leftarrow \rightarrow$) and always maintains adjacent vessels, representing the primary source of vascular flow.

Vessel (V): Propagates to empty adjacent cells with probability `PROPAGATION_CHANCE` (0.3). Dies if isolated and becomes aneurysm if `ANEURYSM_THRESHOLD` (5) vessel/artery neighbors are present.

Aneurysm (X): Explodes if `ANEURYSM_EXPLODE_NEIGHBORS` (2) aneurysm neighbors are present in cardinal directions, destroying nearby vessels within `EXPLOSION_RADIUS` (2). Cures if surrounded by ¡ `ANEURYSM_CURE_NEIGHBORS` (4) vessels.

Dead Cell (D): Revives into vessel if `REVIVE_DEAD_NEIGHBORS` (1) vessel/artery neighbors are present, representing tissue regeneration capacity.

Empty Tissue (T): Can be converted into vessels by arteries or through propagation, representing available space for vascular growth.

Glomerulus (G): Static biological filters marked as healthy when well vascularized, representing kidney filtration units.

Glomerulus Failing (GF): Degrades from healthy glomerulus state when lacking support from nearby vessels or arteries.

C. Image Integration and Classification

The system integrates real histological images through a pixel-intensity classification function that maps grayscale values to biological cell types:

Listing 1: Pixel classification rule

```
def classify_pixel(value):
    if value < 90: return "A"
# Artery
    elif value < 130: return "V"
# Vessel
    elif 130 <= value < 140: return "G"
# Glomerulus
    else: return "T"
# Empty tissue
```

This classification enables direct initialization of the cellular automaton from histological images, providing biologically relevant starting conditions for simulation.

III. Implementation and Technical Framework

A. Core Architecture Components

The implementation consists of several integrated modules:

Grid Management: Implements a 60×60 grid with 10-pixel cells, optimized for real-time visualization and computational efficiency.

Visualization System: Utilizes Tkinter canvas with dynamic coloring based on cell types and neighbor relationships, providing real-time feedback on system evolution.

Image Processing: Employs PIL-based pixel classification for converting grayscale histological images into cellular automaton initial states.

Simulation Engine: Implements the discrete-time update logic with parallel processing of all cell state transitions.

B. Update Algorithm

The simulation follows a five-step update process executed at each time step:

1) **Arterial Generation**: All artery cells convert adjacent empty or dead cells to vessels
2) **Vessel Dynamics**: Vessels check neighborhood conditions for death, aneurysm formation, or propagation
3) **Aneurysm Processing**: Aneurysms evaluate explosion or healing conditions based on neighbor counts
4) **Tissue Regeneration**: Dead cells assess revival conditions based on vascular support
5) **Glomerular Assessment**: Glomeruli update their functional status based on local vascularization

C. Systems Engineering Considerations

The design incorporates several systems engineering principles:

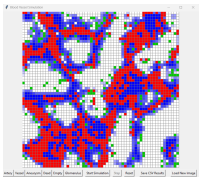
Constraints: Discrete 2D grid with fixed size, real-time rendering requirements, and fixed time-step update logic.

Resource Management: Memory usage scales as $O(n^2)$ with grid size, requiring careful optimization for larger simulations.

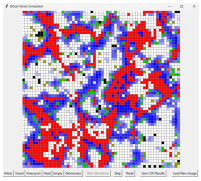
Performance-Accuracy Tradeoff: Grid size selection balances anatomical detail against computational performance, with optimal size determined by available system resources.

IV. Experimental Results and Analysis

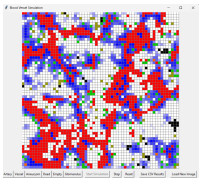
Fig. 1: Case 1



Iteration #1



Iteration #50



Iteration #100

Fig. 2: Case 1 Metrics

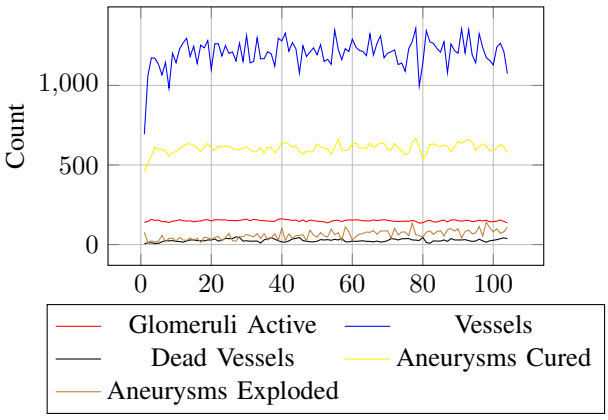
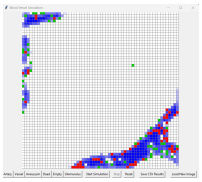
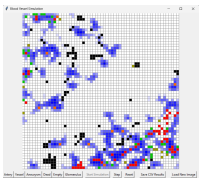


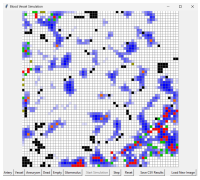
Fig. 3: Case 2



Iteration #1

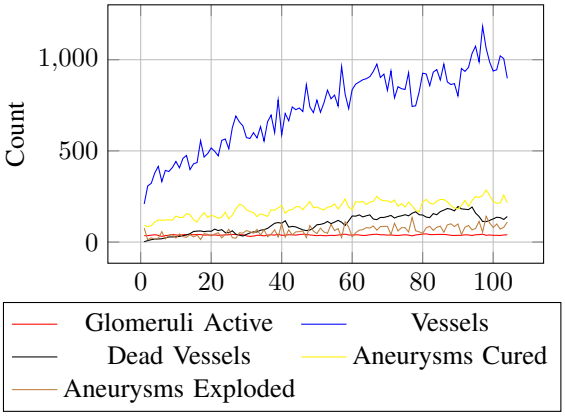


Iteration #50



Iteration #100

Fig. 4: Case 2 Metrics



A. Chaos Analysis and Sensitivity

The system demonstrates strong sensitivity to initial conditions, a hallmark of chaotic dynamics. Four distinct test cases were analyzed to evaluate system behavior under varying arterial distributions:

Case 1 & 2: Comparison of sparse versus dense arterial distributions showed that well-distributed arterial networks promote stable vessel growth, while sparse configurations lead to chaotic behavior and vascular instability.

Case 1: Structured arterial input resulted in steady vessel generation, stable aneurysm cure rates, and maintained arterial pressure within expected ranges over 100 iterations.

Case 2: Poorly structured arterial input caused erratic vessel generation, continuously increasing arterial pressure, and higher numbers of dead vessels despite overall pressure increases.

B. Quantitative Metrics

The simulation tracks multiple quantitative metrics over time:

- Vessel count and spatial distribution
- Aneurysm formation and cure rates
- Glomerular function status (healthy vs. failing)
- Dead cell counts and regeneration rates
- Arterial pressure dynamics

Results demonstrate that initial arterial configuration serves as a critical determinant of long-term vascular performance and system stability.

C. Emergent Behaviors

Several emergent behaviors were observed:

- **Stable Propagation**: Dense arterial structures promote smooth vessel propagation and maintain glomerular function
- **Chaotic Patterns**: Sparse arterial inputs generate chaotic patterns with frequent aneurysm formation and cell death
- **Clustering Effects**: Aneurysms tend to cluster in overpopulated vessel zones, creating chain reactions of damage
- **Regeneration Dynamics**: Dead zones can revive under specific conditions, but require precise vascular support

V. Discussion and Validation

A. Biological Relevance

The simulation successfully captures key aspects of renal microvascular behavior:

- Vessel branching patterns consistent with histological observations
- Pathological responses including aneurysm formation and rupture cascades
- Tissue regeneration capabilities under appropriate conditions
- Glomerular function dependence on vascular support

B. Model Limitations

Several limitations were identified:

- Vessel stagnation or regression under insufficient arterial support
- High sensitivity of aneurysm thresholds to neighbor counts
- Narrow conditions required for dead zone revival
- Limited representation of three-dimensional vascular architecture

C. Sensitivity and Robustness

The system demonstrates deterministic chaos characteristics:

- **Initial Condition Sensitivity**: Small changes in arterial placement produce vastly different outcomes
- **Nonlinear Feedback**: Local interaction rules create amplifying or suppressive feedback loops
- **Parameter Control**: Threshold adjustments can transition the system between stable and unstable regimes
- **Emergent Complexity**: Simple local rules generate complex global vascular patterns

VI. Conclusions and Future Work

This work presents a novel cellular automaton framework for simulating kidney blood vessel dynamics, successfully demonstrating the emergence of complex vascular behaviors from simple local rules. The system's strong dependency on initial arterial configuration and its chaotic sensitivity to parameter variations enhance biological realism while providing insights into vascular system stability.

Key contributions include:

- A comprehensive cellular automaton model for kidney vascular dynamics
- Integration of histological images as biologically relevant initial conditions
- Quantitative analysis of system stability under varying arterial distributions
- Demonstration of emergent pathological behaviors including aneurysm formation and tissue degeneration

The results highlight the potential of cellular automata as tools for exploring vascular phenomena and underscore the critical importance of precise initial condition design in computational models of biological tissue.

Future work should focus on:

- Extension to three-dimensional vascular architecture
- Integration of additional biological factors such as metabolic demands
- Development of parameter optimization techniques for specific pathological conditions
- Validation against larger datasets of histological images
- Implementation of machine learning approaches for automatic parameter tuning

This understanding of microvascular behavior offers potential applications in medical diagnosis, treatment planning, and drug development.