Modeling Mitotic Components as Neural Network Nodes in Minkowski Space: A Literature Review and Experimental Proposal

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Abstract

This literature review explores the feasibility and novelty of modeling the components of a 2-cell mouse embryo (e.g., chromosomes and centromeres) as nodes in a neural network, with their dynamics embedded in a Minkowski Space, as proposed in a recent perspective on X [darthur, 2025]. By synthesizing foundational knowledge from computational biology, machine learning, and theoretical physics, we assess whether this approach can realistically simulate mitotic processes and contribute to humanity's understanding of reality. We find that current imaging and computational technologies support the feasibility of this model, though significant challenges remain in scaling and validation. The perspective appears novel, bridging disparate fields to offer new insights into cellular dynamics and their computational underpinnings. We propose an experimental framework to validate this model, including mathematical foundations and practical steps for implementation, highlighting its potential to advance biological and physical understanding.

1 Introduction

Computational models have become essential in cell biology for simulating complex processes like mitosis, the mechanism by which cells divide to produce identical daughter cells. Traditional approaches, such as ordinary differential equations (ODEs) and agent-based models, have provided insights into the cell cycle [Tyson and Novák, 2001], but they struggle with the high-dimensional, spatiotemporal nature of biological data. Recent advances in machine learning and theoretical physics offer new paradigms, such as neural networks and Minkowski Space, to address these challenges.

A novel perspective, proposed by darthur [2025] on X, suggests modeling the nameable components of a 2-cell mouse embryo (e.g., chromosomes and centromeres) as nodes in a neural network, with their embedding space defined as Minkowski Space. This approach aims to simulate the dynamics of mitosis, capturing the forces and energy flows that drive chromosome movement, potentially revealing computational principles underlying cellular processes. This review evaluates the foundational knowledge required to design an experiment validating this perspective, assesses its feasibility and novelty, and proposes a method to implement it in reality.

2 Computational Models in Cell Biology

Computational modeling of the cell cycle and mitosis has evolved significantly since the 1950s, when early mathematical models linked cell growth to division [Mitchison, 1957]. Modern models incorporate detailed molecular interactions, such as the regulation of cyclin-dependent kinases (CDKs). For instance, Tyson and Novák [2001] used ODEs to model CDK dynamics, capturing transitions between cell cycle phases. Gérard et al. [2015] extended this with an

integrative model involving four cyclin/CDK modules, addressing processes like endoreplication and the G1 restriction point.

Genome-scale models have further advanced the field. Barberis and Ágoston [2023] developed a comprehensive model of the cell division cycle in *Saccharomyces cerevisiae*, simulating over 1,000 reactions to capture the molecular network controlling mitosis. These models demonstrate the power of computational approaches but are limited by their reliance on traditional mathematical frameworks, which struggle with high-dimensional, spatiotemporal data.

3 Neural Network Models in Biology

Neural networks have emerged as a powerful tool in computational biology, particularly for handling complex, high-dimensional data. In cellular processes, they have been applied to model intracellular signaling and gene regulatory networks. Nilsson et al. [2022] introduced LEMBAS, a recurrent neural network (RNN) framework for genome-scale simulations of intracellular signaling, predicting transcription factor activity from ligand concentrations with a Pearson correlation of 0.98 on synthetic data and 0.8 on macrophage experiments published in Nature Communications.

In mitosis, neural networks have been used for image analysis tasks, such as automatic detection of cell-cycle stages. Jose et al. [2024] proposed an RNN-based approach using Time Encoded ResNet18, achieving accuracies up to 99.57% on datasets like LiveCellMiner, as documented in PLOS ONE. However, these applications focus on pattern recognition rather than mechanistic modeling of cellular components as network nodes, highlighting a gap that the proposed perspective could address.

4 Minkowski Space and Its Applications

Minkowski Space is a four-dimensional mathematical framework used in special relativity to describe spacetime, combining three spatial dimensions and one temporal dimension with the metric:

$$ds^2 = -c^2dt^2 + dx^2 + dy^2 + dz^2,$$

where ds^2 is the spacetime interval, c is the speed of light, and t, x, y, z are time and spatial coordinates [Wikipedia, 2025]. This framework has been adapted for computational applications through the Minkowski Engine, a library for sparse tensor processing that operates in Minkowski Space, enabling efficient handling of high-dimensional data like 3D point clouds [Minkowski Engine, 2023].

In theoretical physics, Vanchurin [2020] explores the idea that the universe could be modeled as a neural network, with space-time, including Minkowski Space, emerging from its dynamics. This concept, published in Entropy, suggests that neural networks can inherently capture spatiotemporal relationships, providing a theoretical basis for modeling biological systems in Minkowski Space.

5 Modeling Mitotic Components as Neural Networks in Minkowski Space

The perspective proposed by darthur [2025] involves modeling the components of a 2-cell mouse embryo, such as chromosomes and centromeres, as nodes in a neural network, with their dynamics embedded in Minkowski Space. This approach aims to simulate mitotic processes, capturing the forces and energy flows driving chromosome movement. The idea is grounded in the concept of emergent space-time from neural network dynamics [Vanchurin, 2020], where interactions between subsystems give rise to structured space-time.

The X post by darthur references a 2-cell mouse embryo image showing chromosome missegregation, where fluorescent markers highlight chromosomes (blue) and centromeres (orange),

capturing a 1-hour process of cellular division. Fluorescence microscopy provides the necessary 4D data (3D space + time) to track chromosome positions during mitosis. By estimating the mass of components, which remains fixed due to conservation of mass, forces can be inferred using Newton's second law, $F = ma$, where F is the force, m is the mass, and a is the acceleration derived from positional data:

$$a = \frac{d^2x}{dt^2},$$

with $x(t)$ as the position over time t.

The "natural transformation" referenced by darthur likely involves mapping the forces driving chromosome movement (e.g., mitotic spindle forces) to neural network weights, simulating how energy dynamics during cell division could be represented as changes in an embedding space. The Minkowski Engine [Minkowski Engine, 2023] supports sparse tensor operations, making it feasible to handle the high-dimensional data of the embryo. Forces can be mapped to neural network weights, simulating how energy dynamics drive structural changes, as noted by Picard [2025] in the quoted X post.

6 Feasibility and Novelty Assessment

6.1 Feasibility

Current imaging technologies, such as fluorescence microscopy, can provide detailed 4D data on chromosome positions during mitosis [darthur, 2025]. By inferring forces from positional data and mass estimates, the need for direct force measurements is eliminated, addressing a key challenge in measuring forces at the pico-Newton scale [Dumont et al., 2009]. The Minkowski Engine supports the computational requirements, though scaling to the entire embryo would require significant resources, potentially achievable within 5–10 years given current trends in computing technology [Minkowski Engine, 2023].

As the second document points out, it seems likely that this approach is feasible with today's technology, though short-term implementation would likely involve proof-of-concept models for subsets of the embryo rather than the entire system. The feasibility assessment is supported by advances in both imaging techniques and computational frameworks, though challenges remain in scaling and integration.

6.2 Novelty

This approach is novel because it combines neural networks with Minkowski Space to model biological systems, a departure from traditional ODE-based models [Tyson and Novák, 2001]. It aligns with theoretical frameworks suggesting that complex systems may be computational at their core [Vanchurin, 2020], offering a new paradigm for understanding cellular dynamics and their relationship to physical principles.

The novelty lies in bridging biology, machine learning, and physics, as emphasized in the second document, providing a holistic view of cellular processes as part of a larger computational framework. This interdisciplinary approach represents a significant shift in how we conceptualize and model biological systems, potentially leading to new insights across multiple fields.

6.3 Contribution to Understanding Reality

By simulating mitosis as a neural network in Minkowski Space, this perspective could reveal how energy flow shapes cellular structures, potentially leading to applications in drug discovery and synthetic biology. It bridges biology, machine learning, and physics, contributing to a holistic understanding of reality as a computational system [Vanchurin, 2020].

The second document reinforces this, suggesting that the approach could provide a deeper understanding of reality by showing how complex systems might be fundamentally computational in nature. For example, simulating mitosis as a neural network could reveal how perturbations affect chromosome segregation, aiding in the development of cancer therapies. However, as noted in the second document, this is largely uncharted territory, and more research is needed to fully validate these potential contributions.

7 Proposed Experimental Methods

To validate the perspective, we propose the following experimental framework to build and test the system in reality.

7.1 Data Collection

1. **Time-Lapse Imaging**: Use fluorescence microscopy to collect 4D data (3D space + time) on chromosome and centromere positions in a 2-cell mouse embryo during mitosis, as in darthur [2025]. Employ light-sheet microscopy for high-resolution imaging (sub-micrometer spatial resolution, sub-minute temporal resolution) over 1 hour.

2. **Mass Estimation**: Estimate the mass of chromosomes and centromeres using biological data. For a mouse chromosome, approximate the mass as:

$$m \approx \frac{\text{DNA mass per cell}}{\text{number of chromosomes}} \times (1 + \text{histone mass fraction}),$$

   where DNA mass per cell is 6 pg (diploid), with 40 chromosomes, yielding 0.15 pg per chromosome, adjusted to 0.2 pg with histones.

7.2 Neural Network Design

1. **Nodes and Features**: Represent each chromosome and centromere as a node in the neural network, with features including position $x(t)$, velocity $v = \frac{dx}{dt}$, acceleration $a = \frac{d^2x}{dt^2}$, and mass m.

2. **Embedding in Minkowski Space**: Embed the nodes in Minkowski Space using the Minkowski Engine [Minkowski Engine, 2023], with coordinates (t, x, y, z). Use sparse tensors to handle localized interactions.

3. **Force-to-Weight Mapping**: Infer forces using $F = ma$, where a is computed from positional data. Map forces to weights w_{ij} between nodes i and j:

$$w_{ij} \propto F_{ij},$$

   where F_{ij} is the force between components (e.g., chromosome to spindle pole), approximated as a spring-like force:

$$F_{ij} = -k(x_i - x_j),$$

   with k as the spring constant.

7.3 Training and Simulation

1. **Training Data**: Use the 4D positional data to compute velocities, accelerations, and forces. Split the data into training (80%) and validation (20%) sets.

2. **Loss Function**: Train the neural network to predict the next position $x(t+1)$ given current state, minimizing the mean squared error:

$$\text{Loss} = \frac{1}{N}\sum_{i=1}^{N} \|x_i(t+1) - \hat{x}_i(t+1)\|^2,$$

where $\hat{x}_i(t+1)$ is the predicted position.

3. **Simulation**: Use the trained model to simulate chromosome movements over the 1-hour period, comparing predicted trajectories with experimental data.

7.4 Validation and Iteration

1. **Validation**: Compare simulated trajectories with experimental observations, using metrics like root mean squared error (RMSE).

2. **Iteration**: Refine the model by incorporating additional interactions (e.g., stochasticity, motor protein forces) and adjusting hyperparameters.

7.5 Expected Outcomes

A successful experiment would demonstrate that the neural network can accurately predict chromosome movements, validating the perspective. This would provide insights into energy flow in mitosis and establish a new computational framework for biological modeling.

7.6 Collaboration Requirements

As highlighted in the second document, this experimental approach would require collaboration between biologists, physicists, and computer scientists. The interdisciplinary nature of the project necessitates expertise in multiple areas, including advanced imaging techniques, computational modeling, and theoretical physics. Such collaboration would be essential for addressing the challenges in data collection, model development, and validation.

8 Expected Implementation and Practical Applications

8.1 Concrete Implementation

The concrete implementation of the proposed model would consist of several key components working together to create a functional system:

1. **Imaging Platform**: A dedicated light-sheet microscope equipped with multiple fluorescence channels to simultaneously track chromosomes and centromeres. This would be integrated with an automated stage and environmental control system to maintain viable embryos during the 1-hour imaging period.

2. **Data Processing Pipeline**: A computational pipeline for processing raw microscopy data, including image segmentation to identify individual chromosomes and centromeres, tracking algorithms to follow their movements through time, and data transformation tools to convert pixel coordinates to physical positions in 3D space.

3. **Force Inference Engine**: A physics-based module that calculates velocities and accelerations from positional data, then infers forces using Newton's laws. This would include calibration with known biophysical parameters, such as viscosity of the cytoplasm and estimated masses of cellular components.

4. **Minkowski Network Architecture**: A specialized neural network architecture implemented using the Minkowski Engine, with sparse tensorial operations optimized for 4D data. The network would consist of:
    - An input layer representing the current state of each component (position, velocity)
    - Hidden layers structured to capture spatial relationships in Minkowski Space
    - Weights initialized to correspond to the physical forces between components
    - An output layer predicting the next state of each component
5. **Interactive Visualization Tool**: A graphical interface allowing researchers to visualize both experimental data and simulated predictions in 3D space, with options to animate time evolution, toggle between different views (e.g., physical space vs. network representation), and explore the network weights as force vectors.

In practice, a researcher would begin by collecting microscopy data of a 2-cell mouse embryo undergoing mitosis. This data would be fed into the processing pipeline, which would extract the positions of chromosomes and centromeres over time. The force inference engine would calculate the forces acting on these components, which would then be mapped to weights in the neural network. The network would be trained on a portion of the time series data and validated on the remainder. Once trained, the network could simulate mitotic processes, with the visualization tool allowing researchers to explore the results.

8.2 Practical Applications as a Tool

The completed system would serve as a powerful tool with several practical applications:

1. **Drug Discovery**: Pharmaceutical researchers could use the model to predict how potential drugs might affect mitosis. By simulating perturbations to specific forces or interactions, they could identify promising candidates for anticancer drugs that target mitotic processes.
2. **Developmental Biology Research**: Developmental biologists could use the tool to explore how variations in initial conditions or physical parameters affect chromosome segregation and cell division. This could provide insights into developmental disorders caused by mitotic errors.
3. **Educational Platform**: The visualization component could serve as an educational tool, allowing students to observe and manipulate mitotic processes in an intuitive way, bridging the gap between microscopy images and theoretical understanding.
4. **Personalized Medicine**: With patient-specific data, the system could potentially model how genetic variations affect mitotic processes in different individuals, enabling more personalized approaches to treating conditions like cancer.
5. **Synthetic Biology Design**: Synthetic biologists could use the tool to design and test artificial chromosomes or modified cell division mechanisms, predicting their behavior before experimental implementation.
6. **Theoretical Physics Research**: Physicists could explore how biological systems implement computation through physical processes, potentially revealing new insights into the relationship between information processing and physical dynamics.
7. **Algorithmic Inspiration**: Computer scientists could draw inspiration from how biological systems organize computation, potentially leading to new architectures for artificial neural networks that more efficiently handle spatiotemporal data.

The primary workflow would involve iterative cycles of experiment, simulation, and refinement. Researchers would collect data on mitotic processes, use the model to simulate these processes, compare the simulations to experimental results, refine the model based on discrepancies, and then use the refined model to make predictions about untested conditions. This cycle would progressively improve both the model's accuracy and our understanding of the underlying biological processes.

Ultimately, this tool would bridge the gap between observational biology and theoretical physics, providing a concrete implementation of the idea that biological systems can be understood as computational networks operating according to physical principles in spacetime.

9 Conclusion

This review synthesizes the foundational knowledge required to validate the perspective of modeling mitotic components as neural network nodes in Minkowski Space. Existing literature supports its feasibility, with current technologies enabling data collection and computation, though challenges in scaling remain. The approach is novel, bridging biology, machine learning, and physics, and could significantly contribute to understanding reality by revealing computational principles underlying cellular processes. The proposed experimental framework provides a practical path to implementation, with potential applications in medicine and synthetic biology.

The integration of information from the second document reinforces these conclusions, highlighting that while there are no direct precedents for this specific approach, the existing literature in computational biology, neural networks, and theoretical physics provides a strong foundation for exploring this idea. As noted in the second document, further research is needed to develop and validate such a model, but the potential rewards in terms of scientific understanding and technological innovation make it a worthwhile pursuit, with significant implications for advancing humanity's understanding of reality.

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