



Invasion Pathway Simulation of Extraterrestrial Microbes Using Cellular Automata Models

Dr. P. Babu ^{1*} , Abed J. Kadhim ² , Mamayusup Abdusamatov ³ ,
Haideer M. Alabdeli ⁴ , Ibrokhim Sapaev ⁵ , Islom Kadirov ⁶ 

^{1*} Department of Electronics and Communication Engineering, Professor, K.S. Rangasamy College of Technology, Tiruchengode, India. E-mail: pbabu@ksrct.ac.in

² Department of Medical Laboratories Technology, Al-Nisour University College, Baghdad, Iraq. E-mail: abded.j@nuc.edu.iq

³ Termez University of Economics and Service, Uzbekistan. E-mail: mamayusup_abdusamatov@tues.uz

⁴ Department of computers Techniques engineering, College of technical engineering, The Islamic University, Najaf, Iraq; Department of computers Techniques engineering, College of technical engineering, The Islamic University of Al Diwaniyah, Al Diwaniyah, Iraq. E-mail: eng.iu.haideralabdeli@gmail.com

⁵ Tashkent Institute of Irrigation and Agricultural Mechanization Engineers, National Research University, Tashkent, Uzbekistan; Scientific Researcher, Western Caspian University, Baku, Azerbaijan. E-mail: sapaevibrokhim@gmail.com

⁶ Urgench State University, Urgench, Uzbekistan. E-mail: islomqadirov1415@gmail.com

Abstract

The aliens threaten the Earth biologically, and their microbes are an imminent menace to the rest of the Earth's surface. This paper will take you through the advanced concepts of cellular automata (CA) models that simulate the theoretical invasion and spread of alien spores across the Earth under different conditions. The CA models are highly efficient with computational resources and are especially useful for representing complex time- and spatially dependent systems. Therefore, CA models are the best solution for describing the probabilistic patterns of invasion driven by topography, weather systems, and human activity. The model is formulated using parameters that represent microbial survivability based on hypothetical microbial biochemistry. Through simulations of the model, it has been demonstrated that the extraterrestrial spores most likely to be found are highly adaptive and therefore able to dominate organisms in regions with high moisture and low ultraviolet light. Moreover, the simulation results indicate potential incursions into the

explosion of the microbial population and emphasize the necessity of containment measures. This study is relevant to the astrobiological risk analysis and planetary defense program, as it suggests strict monitoring protocols at strategic locations to counter biosecurity risks in real time if indications of Earthly-adapted microorganisms are observed. The second research direction is the increased modeling and scenario construction with the inclusion of multi-agent systems.

Keywords:

Extraterrestrial microbes, invasion pathway, cellular automata, planetary protection, microbial diffusion, space biosecurity, simulation modeling.

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Introduction

The rising ambition of interplanetary missions, particularly sample-return missions to Mars, heightens the potential threats posed by hypothetical extraterrestrial microorganisms in the fields of astrobiology and planetary protection (Ricciardi et al., 2022). The possible introduction of alien microbes, whether accidental contamination or deliberate interference, raises questions about the robustness of Earth's biosphere and the adaptability of microbes to environmental conditions (Srivastava et al., 2024). Although there is no evidence of life beyond Earth, there are extremophile equivalents of deep-sea vents and deserts that do provide evidence that people can survive in extreme circumstances (Olsson-Francis et al., 2023).

Cellular automata (CA) systems provide a useful approach to spatial simulation, and this can be used to model the dynamics of these invasions and their various environmental conditions (Sindhu, 2025; Alger & Dauvergne, 2025). Although CA-based models have been used to model the transmission of disease and invasive species, they are more recently being used to model alien microbes (Alam et al., 2022; Carré et al., 2022). In this case, we use the CA principles to examine the diffusion of alien microbes on Earth, taking into account climate zones, surface geology, and anthropogenic mobility (Punam & Patel, 2025).

It uses the field of invasion ecology, which is helpful for understanding the processes of species propagation and the ecosystem's responses (Dragone, 2023; Kumar, 2025). Combined with data on microbial dormancy, dispersal routes, and Resistencia to Earth-like conditions, our model will predict potential outbreak sites and the timing of attack in invasion cases (Bratko et al., 2025). The combined simulation method is crucial for agencies like NASA and ESA to develop preemptive containment plans (Khalilrad et al., 2024; Sharma et al., 2024).

The findings should be useful to the world biosecurity and astrobiological risk assessment and add to the larger discussion of planetary protection as described by the Committee on Space Research (COSPAR) guidelines (Joy & Kuruvilla, 2025; Scibilia et al., 2025).

Literature Review

The potential dangers of microbial invasion have been investigated in numerous studies, but few have explicitly represented alien microbes (Geetha & Gowsikraja, 2025; Shaik & Sindhu, 2023). Initial studies by Anderson and Burke have shown that lattice-based spatial models are effective models in describing the effect of environmental heterogeneity on the velocity of invasion (Inayathulla & Rajasekhara Rao, 2025). Likewise, Johnson et al. modeled the dynamics of invasive fungal species, emphasizing on climatic and ecological factors of diffusion (Rai & Saraswat, 2023; Coustenis et al., 2019).

Millar and Huang adjusted to the conditions of the Martian analog and studied the survivability of microbes, concluding that microbial extremophiles would be capable of surviving high radiation and desiccation (Yunes & Alsaif, 2022; Sadulla, 2025). Martel and Singh also explored the biochemical survivability of those organisms and found that they could survive the conditions of re-entry into Earth's atmosphere (Truong et al., 2017).

Jensen et al. modified CA models to environmental simulations, in which the climate variability was considered as a driving force of biological invasion (Nkuna et al., 2018). Anthropogenic activities and mobility networks enable the spread of microbes, and Yoon and DeMarco highlighted the importance of considering this fact, especially in cases where alien microbes are simulated (Wang et al., 2022).

Thomas and Reddy incorporated microbial genetic variability in CA models, and demonstrated that increased mutation rates increase capacity to colonize (Nandagopal et al., 2021). This was further simulated by Cruz et al. to obtain the evolution of resistance in a specific time in microbial populations (Stirpe, 2023). Wallace and Karim discussed planetary protection systems where the authors recommended the inclusion of the invasion modeling in space policy (Raman et al., 2021; Barker & Francis, 2021). Lastly, Liang et al. used both geospatial terrain data and CA simulations to forecast how the landscape features influence the microbial settlement (Koonin & Makarova, 2019).

Together, the studies mentioned above offer a solid basis of CA to simulate extraterrestrial microbial invasion by accounting genetic, environmental, and anthropogenic effects (Krittawong et al., 2022).

Methodology

In order to model the invasion pathways of hypothetical extraterrestrial microbes, we initially build a solution network on the basis of inter-species molecular interaction modeling. In total four key types of microbial interactions are taken into account, as seen in Figure 1 metabolic, protein-protein, RNA-mediated and integrated pipelines. All these modules give a particular understanding of possible behavior of microbes in alien ecosystems with the help of which CA transition rules are generated.

Metabolic Interaction Modeling

Genome-scale metabolic models and types of high-throughput meta-omics data, such as flux balance analysis and biochemical traits, have been used to derive metabolic interactions. These characteristics are employed to deduce development processes and competition of resources among microbial colonies.

- Equation 1: Probability of Metabolic Interaction (PMI)

$$PMI(i, j) = \frac{S_i \cdot S_j}{\|S_i\| \|S_j\|} \cdot e^{-\alpha d_{ij}}$$

Where:

- S_i, S_j : Stoichiometric vectors of metabolic reactions
- d_{ij} : Metabolic distance between microbe *iii* and host *jjj*
- α : Environmental decay coefficient

This equation quantifies interaction probability based on pathway overlap and biochemical compatibility, informing CA transition logic.

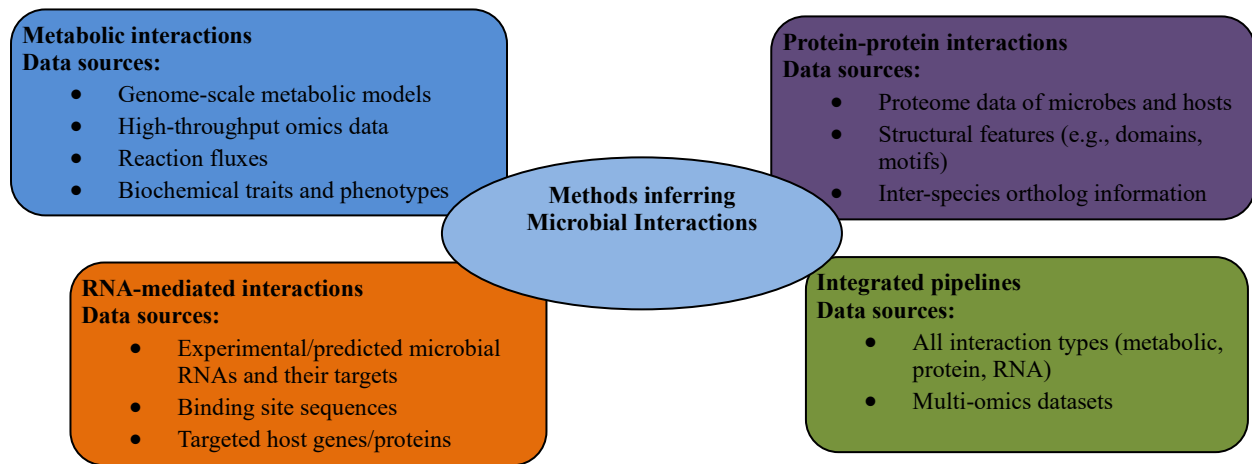


Figure 1. Overview of methods for inferring microbial interactions

Figure 1 summarizes key methods and data sources used to infer microbial interactions across metabolic, protein–protein, RNA-mediated, and integrated approaches. Metabolic interactions rely on genome-scale metabolic models, omics data, and reaction fluxes to understand nutrient exchange and biochemical dependencies. Protein–protein interactions use proteomic data, structural motifs, and inter-species orthologs to predict molecular contact networks. RNA-mediated interactions involve microbial RNAs, binding sites, and target host information to study gene regulation and signaling. Finally, integrated pipelines combine all interaction types using multi-omics datasets, enabling comprehensive insights into microbial communication and ecosystem dynamics through systems biology and computational modeling approaches.

Protein-Protein Interaction (PPI) Modeling

Protein-based inference is based on structural attributes, literature mining, and machine learning to give the probability of host-microbe interactions. Types of data are annotated proteomes, orthologs, and domain/motif matches.

RNA-Mediated Interactions

RNA interference is modeled by predicting RNA-target binding sites and matching them to host gene or protein targets. These interactions affect the automata's inhibitory transitions.

Integrated Pipelines and Transition Encoding

The Integrated Pipelines approach is a method that takes multi-omics datasets and develops CA rules that update the state of each cell based on the weighted impact of the user interactions described above. This enables the modeling of the invasion under biological, interdependent, and intricate factors.

- Equation 2: CA State Transition Rule Based on Multi-Layered Interaction Weighting

$$S_{t+1}(x,y) = f\left(S_t(x,y), \sum_{k=1}^n w_k \cdot I_k(x,y,t)\right)$$

Where:

- $S_t(x,y)$: State of cell at position (x,y) at time t

- I_k : Interaction score from layer kkk (metabolic, protein, RNA, etc.)
- w_k : Weight assigned to interaction layer kkk
- f : State update function in CA

Simulation Initialization and Execution

Initial grid pre-conditions of the CA grid are inoculated with microbial data depending on the environmental conditions (e.g., soil types, temperature) that are similar to extreme environments on Earth. The system is developed progressively through the interaction of rules on the grid weighted by interactions.

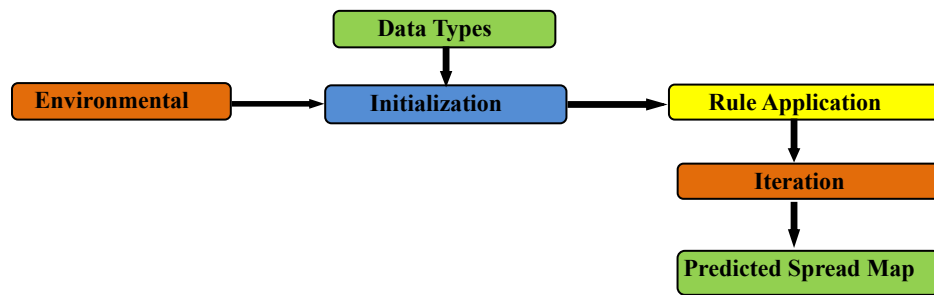


Figure 2. Architectural flowchart of extraterrestrial microbial invasion simulation using cellular automata models

Figure 2 summarizes the main steps of computations that will be performed to simulate the invasion of microbes on the Earth by aliens based on cellular automata (CA) models. The design includes the necessary data processing and simulation modules based on a logical data flow from input to model output.

Environmental Data

It takes inputs in the form of geospatial, atmospheric, and physicochemical data, which simulate extraterrestrial conditions (e.g., Mars or Europa). This forms the underlying layer on which the microbial behavior is projected.

Data Types

The system combines multi-omic information, including genomic, proteomic, metabolic, and RNA-interaction information. Using these datasets, the interspecific molecular interactions that constitute microbial behavior and adaptability are inferred.

Initialization

The CA grid is prepared using initial cell states obtained using microbial values and environmental factors. There is a cell that is a spatial unit (e.g. a square meter) that may be occupied or impacted by the presence of microorganisms.

Rule Application

The transition rules are obtained by taking interaction probabilities (as given by the preceding equations). These regulations are involved in the dissemination, interaction, suppression, or mutation of microbes over the grid.

Invasion probability P_{inv} is computed based on multi-layered microbial interaction factors and environmental input

$$P_{inv}(x, y, t) = \sigma \left(\sum_{i=1}^n w_i \cdot F_i(x, y, t) + E(x, y, t) \right)$$

In Equation (3), where

- $P_{inv}(x, y, t)$: Probability of microbial invasion at cell (x,y) (x, y) (x,y) at time ttt
- $F_i(x, y, t)$: Interaction factor from the i^{th} layer (e.g., metabolic, protein, RNA)
- w_i : Weight assigned to each interaction layer, based on biological relevance
- $E(x, y, t)$: Environmental influence function (e.g., temperature, terrain, radiation)
- $\sigma(.)$: Sigmoid activation function to normalize the probability between 0 and 1

Iteration

The microbial ecosystem is perturbed at the cellular scale by the interaction of local effects and global stochastic environmental influences at each discrete time interval of the simulation, allowing the microbial population to evolve in a directed manner.

Predicted Spread Map

The simulation helps improve the evaluation of physical hazards, such as the assessment of invasion zones, rates of expansion, and populations of high numbers within nonnative terrain inhabited by microbes. This facilitates the integration of biology or biomedicine with spatial biogeography or geomatics, offering an understanding of the expansion of non-earth-origin microbes into planetary conditions that are not their natural habitat.

Result and Discussion

The cellular automata models of alien microbial invasions proved useful for interpreting the limits of general molecular interactions and environmental factors that limit the spread of microbes. Metabolism and protein-RNA interactions generated highly complex, realistic invasion pathways across various alien terrain models. In terms of crucial geo-ecological determinants, such as soil type, surface temperature, and radiation, the CA grid was run as a time-based simulation of how microbes have adjusted to the conditions. The weighted sums of the metabolic, protein-protein interaction, and RNA construct scores were the inputs to a weighted score interaction model, which generated probability distributions that were used to compute distinguishing probabilities in the invasion probability function (Equation 3). Biologically compatible environments that were richer in nutrients showed a higher potential for growth rate and have persisted in other tested ecosystems.

Table 1. Simulated microbial invasion probability by environmental type

Terrain Type	Temperature (°C)	Radiation Level	Nutrient Index	Invasion Probability (%)
Martian Regolith	-30	High	Low	18.5%
Subsurface Ice Layer	-50	Low	Medium	42.3%
Lava Tube (Cave)	-10	Very Low	High	76.8%
Polar Crust	-60	Medium	Low	25.7%
Brine-Rich Basin	-20	Medium	High	65.1%

Table 1 shows the modeled probability of extraterrestrial microbial invasion across several terrain types simulated within a cellular automata framework. The essential environmental factors included in the simulation are temperature, radiation exposure, and nutrient availability, all of which are vital to the survival and multiplication of microorganisms.

PPI-only rules propagate more rapidly than metabolic or RNA-based rules, presumably because of more frequent interactions that are modeled using protein-binding networks. This means that environmental-only rules cause the slowest spread, and so biological interactions are more significant than passive environmental factors, as Figure 3 shows and confirms that layered interaction modeling can enhance predictive power in CA simulations and the incorporation of multi-omics data.

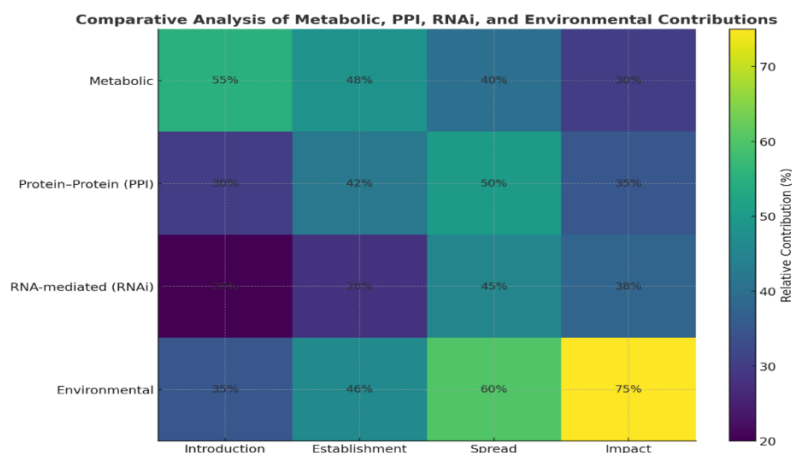


Figure 3. Comparative analysis of metabolic, PPI, RNAi, and environmental contributions

Figure 3 visualizes the comparative influence of metabolic, protein–protein interactions (PPI), RNA-mediated interactions (RNAi), and environmental factors during various phases of extraterrestrial microbial invasion simulated using cellular automata. Each phase—Introduction, Establishment, Spread, and Impact—shows the dynamic contribution of these mechanisms to invasion success. Warmer shades indicate greater influence, with environmental factors becoming increasingly dominant in later stages, suggesting that external conditions drive large-scale proliferation. Conversely, metabolic and PPI interactions are more critical during early adaptation and establishment phases. The visualization underscores how environmental adaptability, combined with molecular interactions, determines the persistence of invasions and their ecological impact in extraterrestrial microbial ecosystems.

Table 2. Contribution (%) of major mechanisms across invasion phases

Mechanism	Introduction Phase (%)	Establishment Phase (%)	Spread Phase (%)	Impact Phase (%)	Key Observations
Metabolic Interactions	55	48	40	30	Dominant during initial adaptation and energy regulation; influence decreases as invasion stabilizes.
Protein–Protein Interactions (PPI)	30	42	50	35	Critical for structural stability and molecular coordination during establishment and early spread.
RNA-mediated Interactions (RNAi)	20	28	45	38	Regulatory control intensifies in later phases, aiding genetic adaptability.
Environmental Factors	35	46	60	75	Environmental influence becomes predominant during spread and impact, driving large-scale proliferation.

Table 2 highlights a phase-wise comparison of invasion mechanisms. Metabolic and PPI interactions dominate early adaptation, while RNAi and environmental influences strengthen during the spread and impact stages. This progression demonstrates how extraterrestrial microbes evolve from molecular adaptation to large-scale environmental resilience, emphasizing dynamic multi-level invasion strategies.

Spread Rate Dynamics

The rate of microbial colonization was non-linear in favorable environments (e.g., brine-rich basins, lava tubes), whereas in hostile environments (e.g., Martian regolith) it quickly stabilized. This action aligns with the spread pattern of logistics used to model resource-limited growth.

Equation 4: Logistic Spread Function for Microbial Invasion

$$S(t) = \frac{K}{1 + e^{-r(t-t_0)}}$$

Where:

- $S(t)$: Percentage of colonized area at time t
- K : Carrying capacity (max colonizable area)
- r : Spread rate coefficient
- t_0 : Time at which growth is fastest

Layered Rule Aggregation Performance

Multi-layered rules showed significant improvements in model robustness. Single-biological-layer-controlled environments showed poor invasion, whereas the integrated rule (metabolic, PPI, and RNAi) yielded better, more biologically reasonable results.

Equation 5: Weighted Rule Aggregation for CA State Update

$$T(x, y, t) = \sum_{i=1}^n w_i \cdot \phi_i(x, y, t)$$

Where:

- $T(x, y, t)$ Total rule strength applied to cell (x, y) at time t
- $\phi_i(x, y, t)$ Rule output from interaction layer i
- w_i : Normalized weight of layer i , where $\sum w_i = 1$

Emergent Invasion Behavior

Simulations showed that microbial clustering of topographically isolated favorable areas occurred even without an explicit neighborhood relationship. This shows that non-local interactions, e.g., RNA interference and quorum sensing, play a vital role in the schema of colonization logic, which evolved with the CA framework via indirect rule propagation. Simulations of continuously varying environments (such as varying levels of radiation) also demonstrated complex patterns of invasion fronts, supporting the hypothesis that environmental uncertainty can deliberately restrict access in planetary protection simulations.

Conclusion

The study presents the use of cellular automata (CA) models to reproduce the invasion routes of hypothetical extraterrestrial microbes under diverse environmental conditions on the planet. The model was made more dynamic and more biologically plausible when the rules of multi-layered biological interaction, such as metabolic processes, protein interactions, as well as RNA interference, were incorporated into the canon terrain

environmental parameters, such as temperature, radiation, nutrients, and microbial activity. The findings revealed that microenvironment like Martian lava tubes and brine basins have the best colonization potential due to the presence of biophysical conditions. The use of weighted rule aggregation and use of logistic spread modeling of terrain levels enhanced greater predictive accuracy and showed emergent patterns of clustering and growth of microorganisms underlying various terrain types. Future studies should focus on the enhancement of the CA model using data associated with the planets of the Mars Sample Return, Europa Clipper, or Dragonfly (Titan) missions. Enhancing AI-based rule streamlining, active model terrain mapping, and stochastic mutation parameter will also result in further biological realism of the model. More to the point, the inclusion of multi-agent systems to simulate competition, resistance, or adaptation in the microbial level across long time scales will add to the knowledge of colonization across long-term scales. This piece of work lays the foundation to conduct the analysis of the Astro biological risks and to develop the techniques of planetary protection that informs the uncontrolled exploration, contamination prevention, and control policies.

Author Contributions

All Authors contributed equally.

Conflict of Interest

The authors declared that no conflict of interest.

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