Physarum

Slime mould computing simulation

Coppola Matteo 793329
Palazzi Luca 793556
Vivace Antonio 793509

Complex Systems: Models and Simulation,
July 2019

Abstract

We introduce and define the Cellular Automata mathematical model, used to describe the evolution of discrete systems. We give an overview of its relevancy and applications in different fields.

We use this tool to model the "intelligent" behavior of *Physarum polycephalum*, a slime mould extensively studied for its interesting characteristics:

Despite the protist not having a nervous system, it has the capacity to solve computational challenges such as the Shortest Path and instances of the Transportation Problem. It also exhibits a form of memory and creates efficient networks when given more than two food sources, being able to dynamically reallocate itself to maintain constant levels of different nutrients simultaneously.

We proceed to build a cross-platform software framework to run and visualize a simulation of the described model using modern tools. A UI exposes a series of control features, letting the user monitor and control the simulation.

Contents

List of Figures

Chapter 1

Introduction

Here we introduce and familiarise with the basic definitions and notations about Cellular Automata, a tool dating back to the late 1940s, when Stanislaw Ulam and John von Neumann defined it as a model for natural and biological processes.

1.1 Cellular Automaton

A cellular automaton (abbrev. CA) is a discrete dynamical system consisting of cells that change their states simultaneously according a local update rule. This update process is repeated at discrete time steps. Cellular automata are[2]

- discrete in space and time,
- homogeneous in space and time,
- local in their interactions.

Basics Let:

- $\mathbb{Z}^d$ be a d-dimensional cellular space, with $d \in \mathbb{N}^+$. Elements of this set are called *cells*.
- S be a finite state set. Elements of this set are called *states*.
- c be a *configuration* of a d-dimensional CA with a state set S, defined as the following function:

  $$c : \mathbb{Z}^d \to S$$

  that assigns a state to each cell.
- $c(\vec{n})$ the state of a cell $\vec{n} \in \mathbb{Z}^d$

Most frequently we consider one and two-dimensional spaces, in which cases the cells from a line are indexed by $\mathbb{Z}$ (line) or by $\mathbb{Z}^2$ (grid).

Denoting the set of functions from set A from B with B^A we can write that the set of all configurations is $S^{\mathbb{Z}^d}$.

A d-dimensional neighborhood vector of size m is a tuple

$$N = N = (\vec{n}_1, \vec{n}_2, ..., \vec{n}_m)$$

where each $\vec{n}_i \in \mathbb{Z}^d$ and $\vec{n}_i \neq \vec{n}_j$ for all $i \neq j$.

The *local update rule* of a CA with state set S and size m neighborhood is a fuction

$$f : S^m \to S$$

specifying the new state of the cell based on the old states of its neighborhood.

As we mentioned, all cells use the same rule, and this rule is applied simultaneously. Global configuration c becomes c' where for all $\vec{n} \in \mathbb{Z}^n$:

$$c'(\vec{n}) = f[c(\vec{n}, \vec{n}_1), c(\vec{n}, \vec{n}_2), ..., c(\vec{n}, \vec{n}_m)]$$

$c \mapsto c'$ is our *global transition function* $G : S^{\mathbb{Z}^d} \longrightarrow S^{\mathbb{Z}^d}$. Typically, G is iterated to produce a time evolution of the system.

$$c \mapsto G(c) \mapsto G^2(c) \mapsto G^2(c) \mapsto ..$$

Formal definition A CA is a 4-tuple $A = (d, S, N, f)$ where

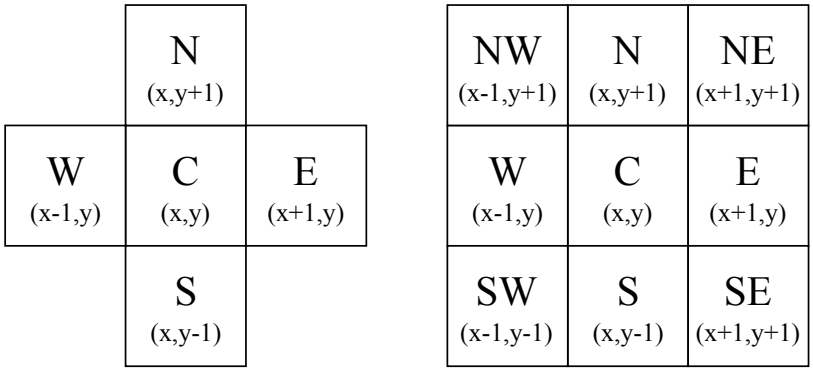
- d is the dimension,
- S is the finite state set,
- N is the neighborhood vector,
- f is the local update rule.

1.1.1 Neighborhoods

When considering two-dimensional CA, the *von Neumann* and the *Moore* neighborhoods (pictured in figure 1.1) are often used.

Moore neighborhood The d-dimensional radius-r Moore neighboorhood, containing $(2r+1)^d$ elements is defined as follows:

$$M_r^d = (k_1, K_2, ..., k_d) \in \mathbb{Z}^d \text{ where } |k_i| \leq r \ \forall i = 1, 2, ..., d$$



(a) Von Neumann (b) Moore

Figure 1.1: Moore and Von Neumann neighborhoods for Cellular Automata

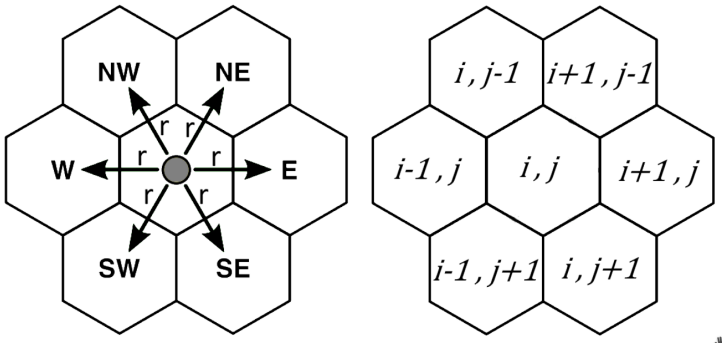


Figure 1.2: Hexagonal neighborhod for Cellular Automata[1]

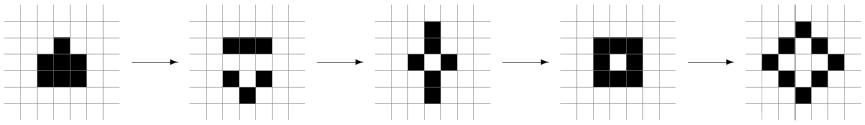


Figure 1.3: Five steps of a time evolution in Conway's Game-of-life[2]

Von Neumann neighboorhood

$$V_r^d = (k_1, K_2, ..., k_d) \in \mathbb{Z}^d \text{ where } \sum_{i=1}^{d} |k_i| \leq r$$

1.1.2 Examples

The most known CA in the scientific literature is *Game of Life*, devised by the John Horton Conway in 1970 with the intention of producing a simple model of von Neumann's idea of the machine capable of reproducing itself and simulate a Turing machine.

In the universe of *Game of Life* each cell is in one of two possible states, alive or dead (or populated and unpopulated, respectively). Every cell interacts with its eight neighbours, which are the cells that are horizontally, vertically, or diagonally adjacent. At each step in time, the following transitions occur:

- Any live cell with fewer than two live neighbours dies, as if by underpopulation
- Any live cell with two or three live neighbours lives on to the next generation
- Any live cell with more than three live neighbours dies, as if by overpopulation
- Any dead cell with exactly three live neighbours becomes a live cell, as if by reproduction

The initial pattern constitutes the seed of the system. The first generation is created by applying the above rules simultaneously to every cell in the seed; births and deaths occur simultaneously, and the discrete moment at which this happens is sometimes called a tick. Each generation is a pure function of the preceding one. The rules continue to be applied repeatedly to create further generations.

1.2 Physarum

Physarum polycephalum [4], [5] is a species of order Physarales, subclass Myxogastromycetidae, class Myxomecetes, division Myxostelida, commonly known as

a true slime mould. It is a single celled protist that is visible to the naked eye. Slime mold inhabits shady, cool and moist areas that exist on decaying leaves and logs in forest areas.

It exhibits a very wide repertoire of pattern formation behaviors used for growth, movement, food foraging, nutrient transport, hazard avoidance, and shape maintenance.

Physarum thrives in favorable environmental conditions, particularly when the right combinations of humidity, temperature and nutrient presence are found. If the conditions are not adequate for development, Physarum behaves like a single-celled organism that does not demonstrate organizational skills. In appropriate conditions, it joins together to create particularly efficient filamentary nets in physical distribution.

1.2.1 Life Cycle

Spores, released from mature fruiting bodies, germinate into mononuclear amoebae (n), which propagate by mitosis. At high population density, amoebae are able to mate, to form a zygote (2n). This diploid cell later develops into a multinuclear plasmodium (2n), through multiple nuclear divisions. Following starvation, the plasmodium can be induced to sporulation by visible light. Later, the plasmodial mass develops into individual fruiting bodies, which will subsequently yield haploid spores (n) [3].

It is common to refer to the Physarum by the name of its vegetative (resting) life cycle phase, the plasmodium. The Physarum plasmodium is a single yellow cytoplasmic mass that can range in size from a few mm^2 to over half a m^2. The organism will typically be composed of a network of protoplasmic veins that can contain more than 100,000 nuclei.

It is during this stage that the organism searches for food. Multiple sources state that the plasmodium is both predatory and saprophytic: its natural foodstuffs include fungal spores, bacteria, smaller amoebae and decaying matter, the latter of which may be digested extracellularly through the secretion of enzymes.

To find its prey, slime mould is able to explore its environment by spontaneous and self-organised oscillatory contractions [6]. This means that the slime mould is able to contract its body in an organized way, allowing the organism to slowly push itself in all directions. When a slime mould encounters a new food source, it is able to connect the new food source to its pre-existing ones. To conserve mass, the slime mould gradually funnels the link between the food sources to a single protoplasmic tube.

This protoplasmic tube has the ability to exchange not only nutrients, but also information throughout the entire network the slime mold creates. This allows the slime mould to conduct a logical and efficient search of its surroundings to decide what the most efficient method of utilizing its resources is. In early stages of slime mold development, the Physarum exists in a feeding phase, in which the slime mold remains on an already discovered food source, and increases in mass. The organism will then gradually transition into a more

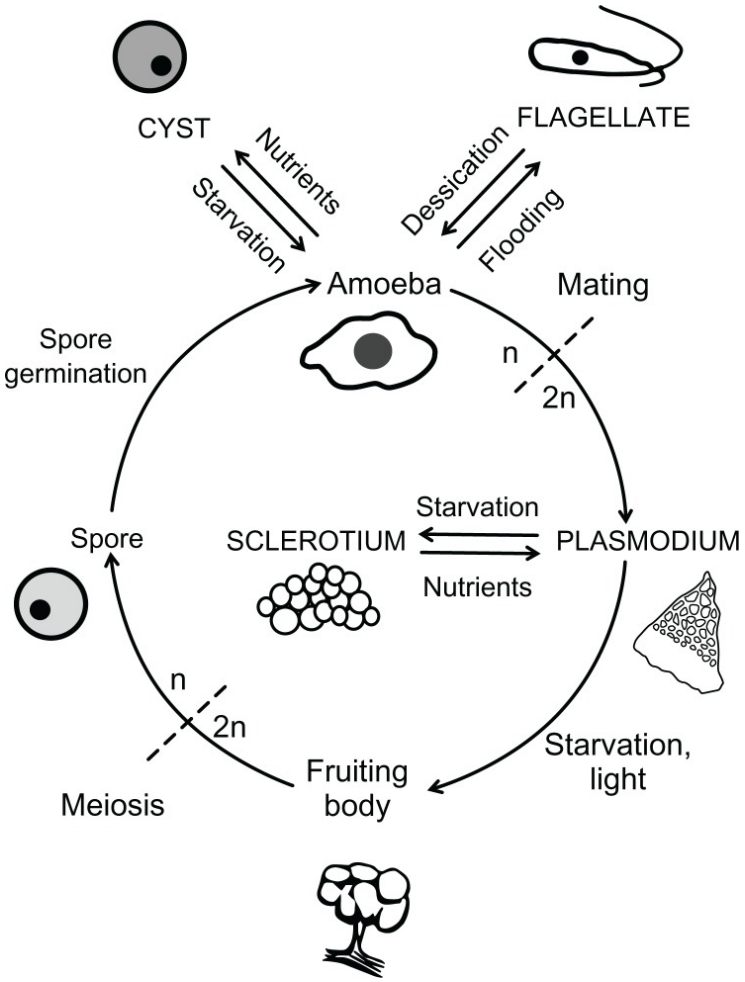


Figure 1.4: The life cycle of Physarum polycephalum[3]

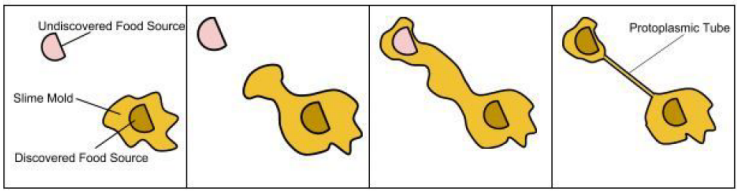


Figure 1.5: Physarum protoplasmic tube formation

explorative phase, where it discovers new sources of food and prepares to create fruiting bodies, which eventually create more slime mould.

If environmental conditions cause the plasmodium to desiccate during feeding or migration, Physarum will have another life cycle phase called the sclerotium. The sclerotium is basically highly resistant desiccated tissue that serves as a dormant stage, protecting Physarum for long periods of time. The organism will assume it if environmental conditions become too unfavourable. Once favorable conditions resume, a sclerotium can be revert back to a viable plasmodium that reappears to continue its quest for food.

As the food supply runs out, the plasmodium stops feeding and begins its reproductive phase. Stalks of sporangia form from the plasmodium. It is within these structures that meiosis occurs and spores are formed. Sporangia are usually formed in the open spaces so that the spores they release will be spread by wind currents.

Spores can remain dormant for years if needed. However, when environmental conditions are favorable for growth, the spores germinate and release either flagellated or amoeboid swarm cells (motile stage). The swarm cells then fuse together to form a new plasmodium.

DA INTEGRARE?

The plasmodium is an aggregate of protoplasm with a network of tubular elements through which nutrients and chemical signals circulate, the geometry of which is related to internal communication. Moreover, the tubes act as "legs", allowing the organism to navigate around its environment, and can be disassembled and reassembled within a few hours in response to changes in external conditions [7].

DA INTEGRARE?

This, in turn, drives tip growth in the direction of the highest nutrient density by initiating pseudopodium formation (directed actin cytoskeleton assembly, membrane synthesis, etc.). Plasmodial sensing is continuous, pandirectional, and multisensorial (optical, temperature, etc.) and the actions of each receptor occur concurrently. Via the combined action of amoeboid tip-growth and contraction of muscle proteins which shuttle the contents of the cytoplasm in the direction of movement, the plasmodium forms a network of tubular structures between all NSs, as illustrated in Figure 2, which typically assumes a highly optimised topology. When being at rest, the fluid contents of the cytoplasm oscillate rhythmically, distributing internalised food, organelles, and intraplasmodial chemical signalling compounds.Thus, fluid movements within the plasmodium are subjected to dynamically optimizing alternations.

DA INTEGRARE?

The plasmodium of Physarum is a membrane-bound syncytium of nuclei within a cytoplasm composed of a complex gel-sol network. The gel phase is composed of a spongelike matrix of contractile actin and myosin fibers through which the protoplasmic sol flows. Local oscillations in the thickness of the plasmodium spontaneously appear with approximately 2-min duration. The spatial and temporal organization of the oscillations has been shown to be ex-

tremely complex and affects the internal movement of sol through the network by assembly and disassembly of the local actin-myosin structures. The protoplasm moves backward and forward within the plasmodium in a characteristic manner known as shuttle-streaming. The plasmodium is able to sense local concentration gradients, and the presence of nutrient gradients appears to alter the structure of external membrane areas. The softening of the outer membrane causes a flux of protoplasm in the general direction of the gradient in response to internal pressure changes caused by the local thickness oscillations. The strong coupling between membrane contraction and streaming movement is caused by the incompressibility of the fluid, requiring a constant volume—the weakening of the membrane provides an outlet for the pressure. When the plasmodium has located and engulfed nearby food sources, protoplasmic veins appear within the plasmodium, connecting the food sources. The veins transport protoplasm among the distributed extremes of the organism. The relative simplicity of the cell and the distributed nature of its control system make Physarum a suitable subject for research into distributed computation substrates. [8]

The mechanisms used to fulfil these requirements are growth, movement, and area reduction. During the growth-and-foraging stage the plasmodium exhibits a default, broadly reticulated outward growth patter - albeit one that is influenced by substrate and gradient quality. Once nutrients have been located, the topology of the pattern is influenced by the nutrient distribution - the connectivity patterns (the protoplasmic tube network) evolve to achieve a compromise between minimal transport costs and fault tolerance. Since the plasmodium obviously cannot have any global knowledge about the initial or optimal topology, the network must evolve by physical forces acting on the protoplasmic transport.

Chapter 2

State of the Art

An increasing number of researchers have conducted studies concerning the Physarum to explore its intelligence in the field of optimal problems. This happened due to some biological experiments observed in laboratory conditions in which the Physarum exhibited complex patterning, adaptive behavior and extraordinary capacities to build efficient networks.

It is very important to remember that the slime mould is a puzzling organism because it possesses no neural tissue yet, despite this, are known to exhibit complex biological and computational behavior: it is not explicitly trying to solve computational problems. So the idea served by several researchers was how to take advantage of Physarum's to survive in order to solve complex problems.

In the laboratory experiments that demonstrate these computing capabilities, small food sources - agar blocks containing ordinary oat flakes - are presented at various positions to a starved plasmodium, it endeavours to reach them all; as a consequence, only a few tubes are in contact with each individual food source. The organism attempts to optimize the shape of the network to facilitate effective absorption of the available nutrients. However, this might be difficult to achieve when multiple food sources are presented because of the limited body mass of the organism.

This network shape of the body enables certain physiological requirements to be met [7]:

- absorption of nutrients from food souces as efficiently as possible because almost all the body mass stays at the food sources to enable absorption
- maintenance of the connectivity and intracellular communication throughout the organism
- meeting the constraint of limited resource of body mass. The network shape is regarded as a solution for the organism's survival problems.

Contrary to this, if food is plentiful, the organism finally splits into two pieces on two food sources.

The organism requires a well hydrated substrate. All true slime moulds reproduce by sporulation. Certain factors, such as starvation, light irradiation and dehydration will prompt the plasmodium to irreversibly transform into a multitude of black, globulose structures known as sporangia that harbour the organism's spores.

The name Physarum refers to the fact that multiple apparently autonomous leading edges may exist in one plasmodium. This is an observation of note as some of the first work on slime mould was based on the principle that Physarum can "choose" the most efficient path between food sources.

The biological basis for this involves the Physarum identifying chemical gradients with multiple advancing margins before deciding to navigate along the strongest gradient. This has been interpreted as slime mould undertaking problem solving and network optimization, such as demonstrated in the following ground-breaking experiments.

Maze solving Nakagaki et al. [9] were the first to observe that the plasmodium of the slime mould changes its shape as it crawls over a plain agar gel. If food is placed in two certain spots, it puts out pseudopodia that connect those food spots. The most interesting part is that the plasmodium had the ability to find the minimum-length solution between two points in a maze. This happens because Physarum reduces its mass, from the paths of the maze that is far from the minimum distance, and strengthens its tubes that belong to the minimum distance.

Network formation In 2010 Tero et al. [10] compared the actual rail network in Japan with a Physarum network consisted by 36 nutrients sources (NSs) that represented the geographical locations of cities in Tokyo area. The Physarum was planted on Tokyo and from there started its foraging and exploration for NSs until it filled much of the available land space. Then the organism started to concentrate on the NSs by thinning out the network to leave a subset of larger interconnecting tubes. The topology of many Physarum networks appeared similar to the rail network. The conclusion was that Physarum networks showed characteristics with comparable qualities to those of the rail network in terms of cost, transport efficiency and fault tolerance.

AGGIUNGERE MODELLO MATEMATICO?
SEZIONE SEPARATA?

In the recent years, computer scientists have been inspired by biological systems for computational approaches, in particularly with respect to complex optimization and decision problems [11]. In this context, Physarum emerged as a model organism which has attracted substantial interest. The aforementioned experiments require expensive and specialized equipment and some experience on basic biological laboratory techniques. However, the majority of scientists are unfamiliar with such methods and the experiments on a living organism may last a lot of hours or maybe some days to provide data.

A commonly proposed alternative alleviating these difficulties is software models that simulate the behavior of the plasmodium and provide similar results. The advantages of a software model over the real slime mould are repeatability and faster productions of results.

As slime mould has no brain or any central processing system, its distributed control can be perfectly described by the local rule of CAs. It is noteworthy that CAs are known for emerging global behavior from local interactions. The CA model was firstly proposed to design high-quality networks [12]. In this model, the optimization process is consistent with the properties of real cells.

Chapter 3

Model

Consider only the plasmodium stage of its life cycle, there is no single model that can describe exactly the behavior of Physarum. So far, there is a variety of modeling approaches which also are implemented by a variety of tools [13], [12], [14].

In this project the behaviour of slime mould during the laboratory experiments have been simulated by a model based on Cellular Automata. Using CA can be justified by the emergence of global behaviour from local interactions, a rule that applies also on the real slime mould.

All of the biological studies indicated above, like solving a maze and designing a transport network, have observed the optimization behaviour of the plasmodium with the experimental setups roughly consisting of three steps [14]:

- First step: the plasmodium fully searches the given space
- Second step: some sources of attractant or repellent stimuli are given to the plasmodium that is fully and homogeneously spreading in the space
- Third step: the plasmodium optimizes the connection between the sources

The majority of the studies focus on the behaviour of the plasmodium in a closed space. However, few studies have been done for the plasmodium that is exploring an open space.

INIZIO CONSIDERAZIONI

We believe that we can find more enhanced biological characteristics of the biological entities by observing the behaviours of them in an open and unknown environment. In this study, we thus tried to investigate the exploratory behaviour of the plasmodium in an open space and to understand how the organism makes its decision in exploration.

FINE CONSIDERAZIONI

The CA based model that inspired us [13] mimics the foraging strategy and tubular network formation. In particular, the model is based on the representation of diffusion of chemical attractants by NSs and the attraction of the

plasmodium, which initiates its exploration from the starting point (SP), by these chemicals.

However, this model consideres only slime mould foraging behaviour and also - with the only information in the paper - seems not to follow the true behavior of slime mould; the main problems encountered can be summarized in the following points:

- No mass conservation. Map flooding
- Tube's creation dependent on the mass gradient. A tube is seen as a separate entity
- No shrinking of the mass towards the tube despite in the Physarum exploitation phase the organism tends to shrink and collect its body mass to move towards resource of attraction

For this reason we have proposed an alternative model - starting from the model Tsompanas et al. [13] - that aims at a more faithful exploration of slime mould.

3.1 Paper model

The plasmodium is first starved and then introduced to an exploring region in a SP. Moreover, some NSs which produces chemo-attractants are located at characteristic points.

The plasmodium starts searching for nutrients, exhibiting pattern of guided movement towards/away from sources of stimulation; it explores the available area, encapsulates the NSs and creates a tubular network that connects all these NSs by a nature-inspired, cost effective and risk avoiding manner. Typically, slime mould is stimulated in experimental situations by providing a number of spatially distributed chemoattractant nutrient NSs towards which it will migrate (chemotaxis).

To note the geometry of the network created by the plasmodium depends on the positions of the NSs. Moreover, further parameters can play key role in determining exact structure of plasmodium network.

In order to imitate and simulate a biological laboratory experiment, the entire area is divided into a matrix of squares with identical areas - that constitutes a set defined as E - and each square of the surface is represented by a CA cell. This area can be categorized as available area (a set of cells defined as A) and unavailable area (a set of cells defined as U) for the development of the plasmodium. Also some cells that are included in the available area set of cells, represent the oat flakes that are considered as NSs for the plasmodium (a set of cells defined as N) and one cell represents the place where the plasmodium is initially introduced to the experimental environment or the SP (a set of one cell defined as S). The neighbourhood type used for the model is Moore

neighbourhood and the state of the $c_{(i,j)}$ cell at time step t ($ST^t_{(i,j)}$) is defined as:

$$ST^t_{(i,j)} = [AA_{(i,j)}, PM^t_{(i,j)}, CHA^t_{(i,j)}, TE^t_{(i,j)}] \tag{3.1}$$

where:

- AA stands for Available Area for the exploration by the plasmodium. It assumes a boolean value:

$$AA_{(i,j)} = \begin{cases} \text{True}, & \forall i,j : c_{(i,j)} \in A \\ \text{False}, & \forall i,j : c_{(i,j)} \in U \end{cases}$$

- PM (Physarum Mass) is a floating-point variable. It indicates the volume of the cytoplasmic material of the plasmodium located on a specific cell. This parameter can have any value in the continuous space of [0–100]
- CHA (CHemoAttractant) is a floating-point variable. It represent the concentration of chemo-attractants that are located on a specific cell. This parameter can have any value in the continuous space of [0–100]
- TE stands for Tube Existence and represents the participation of a cell in the tubular network inside the body of the slime mould

The initial values for parameters PM and CHA are defined as:

$$PM^t_{(i,j)} = \begin{cases} 100, & \forall i,j : c_{(i,j)} \in S \\ 0, & \text{else} \end{cases} \tag{3.2}$$

$$CHA^t_{(i,j)} = \begin{cases} 100, & \forall i,j : c_{(i,j)} \in N \\ 0, & \text{else} \end{cases} \tag{3.3}$$

Taking into consideration the assumptions made for the way the Physarum develops through an available area, which were confirmed by laboratory experiments, it is determined that the plasmodium is "amplified" at a NS and then searches for other NSs, considering the recently encapsulated NS as a new SP. Also, when a NS is covered by the plasmodium, the generation of chemoattractant substances is ceased. In the model the NSs are turned into SPs when the plasmodium encapsulates them with a sufficient amount of mass. Furthermore, it is realized that the plasmodium is propagating away from the most recently captured NS by taking a semi-circular form.

The model is analyzed in the following flowchart: TODO inserire flowchart.

The initialization step includes the definition of parameters that have a great impact on the results of the model. These parameters include:

- The length of the CA grid

- The parameters for the diffusion equation for the cytoplasm of the plasmodium (PMP1, PMP2)
- The parameters for the diffusion equation of the chemo-attractants substances (CAP1, CAP2)
- The consumption percentage of the chemo-attractants substances by the plasmodium (CON - Consumption)
- The attraction of the slime mould by chemoattractant substances (PA - Physarum Attraction)
- The threshold of Physarum Mass that encapsulates a NS (ThPM).

After the initialization and for 50 time steps, diffusion equations are used to calculate the values for CHA and PM for every cell in the grid. Every cell uses the values of its neighbours at time step t to calculate the value of the CHA and PM parameter for time step t + 1.

The contribution to the diffusion of the Physarum Mass of the von Neumann neighbours ($PMvNN$) of the $c_{(i,j)}$ cell is defined as:

$$\begin{aligned} PMvNN^t_{(i,j)} = {} & (1 + PA^t_{(i,j),(i-1,j)}) \times PM^t_{(i-1,j)} - AA_{(i-1,j)} \times PM^t_{(i,j)} + \\ & (1 + PA^t_{(i,j),(i,j-1)}) \times PM^t_{(i,j-1)} - AA_{(i,j-1)} \times PM^t_{(i,j)} + \\ & (1 + PA^t_{(i,j),(i+1,j)}) \times PM^t_{(i+1,j)} - AA_{(i+1,j)} \times PM^t_{(i,j)} + \\ & (1 + PA^t_{(i,j),(i,j+1)}) \times PM^t_{(i,j+1)} - AA_{(i,j+1)} \times PM^t_{(i,j)} \end{aligned} \tag{3.4}$$

Moreover, the contribution to the diffusion of the Physarum Mass of the exclusively Moore neighbours ($PMeMN$) of the $c_{(i,j)}$ cell is defined as:

$$\begin{aligned} PMeMN^t_{(i,j)} = {} & (1 + PA^t_{(i,j),(i-1,j-1)}) \times PM^t_{(i-1,j-1)} - AA_{(i-1,j-1)} \times PM^t_{(i,j)} + \\ & (1 + PA^t_{(i,j),(i+1,j-1)}) \times PM^t_{(i+1,j-1)} - AA_{(i+1,j-1)} \times PM^t_{(i,j)} + \\ & (1 + PA^t_{(i,j),(i-1,j+1)}) \times PM^t_{(i-1,j+1)} - AA_{(i-1,j+1)} \times PM^t_{(i,j)} + \\ & (1 + PA^t_{(i,j),(i+1,j+1)}) \times PM^t_{(i+1,j+1)} - AA_{(i+1,j+1)} \times PM^t_{(i,j)} \end{aligned} \tag{3.5}$$

The total PM for a cell $c_{(i,j)}$ for time t + 1 is a sum of the contributions of its neighbours with appropriate weights and is defined as:

$$PM^{t+1}_{(i,j)} = PM^t_{(i,j)} + PMP1 \times [PMvNN^t_{(i,j)} + PMP2 \times PMeMN^t_{(i,j)}] \tag{3.6}$$

The equation represents the exploration of the available space by the plasmodium which is affected by chemoattractants. The values PMP1 and PMP2 depict that the von Neumann and the exclusively Moore neighbours have different contributions on the diffusion of these parameters. If a neighbouring cell is representing unavailable area, there is no contribution to the diffusion.

The parameter $PA_{(i,j),(k,l)}$ represents the attraction of the plasmodium - in cell $c_{(i,j)}$ - by the chemo-attractants towards the direction of an adjacent cell

$c_{(k,l)}$, modeling the attraction of the organism towards the higher gradient of chemoattractants. It is equal to a predefined constant (PAP) for the neighbour with the higher concentration of chemo-attractants and equals to the negative value of the parameter PAP for the neighbour across the neighbour with the higher value of chemoattractant, in order to simulate the non-uniform foraging behavior of the plasmodium. For the other neighbours in an area that has no chemo-attractants, then the foraging strategy of the plasmodium is uniform and these parameters are equal to zero.

INSERIAMO LA FORMULAZIONE DI PA?

The PA parameter for cell $c_{(i,j)}$ towards its north neighbour $c_{(i-1,j)}$ is defined as:

$$PA^t_{(i,j),(k,l)} = \begin{cases} PAP, & if CHA_{(i-1,j)} = MAX(CHA_{(k,l)} \forall k,l : i-1 \leq k \leq i+1 \\ and j-1 \leq l \leq j+1) & \\ -PAP, & if CHA_{(i-1,j)} = MAX(CHA_{(k,l)} \forall k,l : i-1 \leq k \leq i+1 \\ and j-1 \leq l \leq j+1) & \\ 0, & \text{else} \end{cases} \tag{3.7}$$

The contribution to the diffusion of the chemoattractants for the plasmodium of the von Neumann neighbours ($CHAvNN$) of the $c_{(i,j)}$) cell is defined as:

$$\begin{aligned} CHAvNN^t_{(i,j)} = (CHA^t_{(i-1,j)}) - AA_{(i-1,j)} \times CHA^t_{(i,j)} + \\ (CHA^t_{(i,j-1)}) - AA_{(i,j-1)} \times CHA^t_{(i,j)} + \\ (CHA^t_{(i+1,j)}) - AA_{(i+1,j)} \times CHA^t_{(i,j)} + \\ (CHA^t_{(i,j+1)} - AA_{(i,j+1)} \times CHA^t_{(i,j)} \end{aligned} \tag{3.8}$$

Moreover, the contribution to the diffusion of the chemoattractants for the plasmodium of the exclusively Moore neighbours ($CHAeMN$) of the $c_{(i,j)}$ cell is defined as:

$$\begin{aligned} CHAeMN^t_{(i,j)} = (CHA^t_{(i-1,j-1)}) - AA_{(i-1,j-1)} \times CHA^t_{(i,j)} + \\ (CHA^t_{(i+1,j-1)}) - AA_{(i+1,j-1)} \times CHA^t_{(i,j)} + \\ (CHA^t_{(i-1,j+1)}) - AA_{(i-1,j+1)} \times CHA^t_{(i,j)} + \\ (CHA^t_{(i+1,j+1)}) - AA_{(i+1,j+1)} \times PM^t_{(i,j)} \end{aligned} \tag{3.9}$$

As a result, the total CHA for a $c_{(i,j)}$ cell for time t + 1 is defined as:

$$CHA^{t+1}_{(i,j)} = CON \times CHA^t_{(i,j)} + CAP1 \times (CHAvNN^t_{(i,j)} + CAP \times CHAeMN^t_{(i,j)}) \tag{3.10}$$

The equation represents the diffusion of chemoattractants from the NSs in the available space. The values CAP1 and CAP2 depict that the von Neumann and

the exclusively Moore neighbours have different contributions on the diffusion of these parameters. The multiplication with the parameter CON provides the imitation of the consumption of the chemoattractant substances by the plasmodium. Also in this case as in the diffusion of PM, if a neighbouring cell is representing unavailable area there is no contribution to the diffusion.

After every 50 time steps of calculating the diffusion equations in the available area, the operation of designing the tubular network takes place. If any NS is covered with over the predefined PM (ThPM), each NS cell is connected to a SP cell by a tubular path from the NS cell to the SP cell, following the increasing gradient of parameter PM of neighboring cells. More specifically, starting from the cell representing the encapsulated NS, the adjacent cell with the higher PM value is selected to participate to the tubular network. Then the cell selected to participate to the tubular network selects the next cell from its neighbours with the higher PM value to participate to the tubular network and so on, until a SP is reached.

Finally, the NS cell is transformed to a SP, which means changing its parameters as illustrated in the following equations:

$$PM^{t}_{(i,j),(k,l)} = \begin{cases} 0, & \forall i,j : c_{(i,j)} \in U \\ 100, & \forall i,j : c_{(i,j)} \in S \\ 100, & \forall i,j : c_{(i,j)} \in NandPM^{t}_{(i,j)} \geq ThPM \end{cases} \tag{3.11}$$

$$CHA^{t}_{(i,j),(k,l)} = \begin{cases} 100, & \forall i,j : c_{(i,j)} \in NandPM^{t}_{(i,j)} < ThPM \\ 0, & \forall i,j : c_{(i,j)} \in NandPM^{t}_{(i,j)} \geq ThPM \end{cases} \tag{3.12}$$

If more NSs are covered with the ThPM, each is connected to the nearest SP and they are all transformed to SPs.

DA INSERIRE ?

A logical question that comes to mind is why procedures (2) to (5) are executed for a second time. As identified in some laboratory experiments [44], after a seemingly random and not certain amount of time the plasmodium seems to change the formation of its protoplasmic networks and abandon some NSs. Then it seems to regenerate in a manner and re-colonize some NSs, meaning it forms new tubular edges that connect NSs that were already connected to other NSs. As the CA model is designed without the use of probabilistic equations, it uses a second starting point to regenerate and explore the available area once more. That point will be a point of interest (NS), which is empirically chosen to be away from the initial SP

DA INSERIRE ?

The second to last NS to be encapsulated was chosen, based on the fact that it is far enough from the initial SP and it is less likely to be a point of interest surrounded by unavailable area that would cause difficulties for the growth of the plasmodium. Finally, the time period of 50 time steps for the diffusion equations, was also empirically chosen, although the alternation of that will cause little difference to the results of the model.

3.2 Experimental model

We introduced a new rule on the Physarum diffusion process to imitate the natural process of Physarum shrinkage, where if a Physarum cell is not contributing to the path towards food resource for a certain time (number of iterations), the whole Physarum mass is migrated to the nearest neighbour cell contributing to the path of food resource attraction.

Chapter 4

Implementation

4.1 Software Stack

4.2 Simulation framework

Fading colors Assuming colors are given as triples (r_1, g_1, b_1) and (r_2, g_2, b_2) in the RGB color system, we can fade between them with a simple *linear interpolation*:

$$r' = (1-t) \cdot r_1 + t \cdot r_2 \tag{4.1}$$
$$g' = (1-t) \cdot g_1 + t \cdot g_2 \tag{4.2}$$
$$b' = (1-t) \cdot b_1 + t \cdot b_2 \tag{4.3}$$

This gives a blended color (r', g', b') for all $t \in [0, 1]$. For $t = 0$ it will give the first color, for $t = 1$ the second color.

$$C_1 = \begin{pmatrix} r_1 \\ g_1 \\ b_1 \end{pmatrix}, \qquad C_2 = \begin{pmatrix} r_2 \\ g_2 \\ b_2 \end{pmatrix}$$

The blended color is given as the vector $C'(t) = (1-t) \cdot C_1 + t \cdot C_2$.

4.3 User Interface

TODO: citare la funzione unity che fa questa cosa

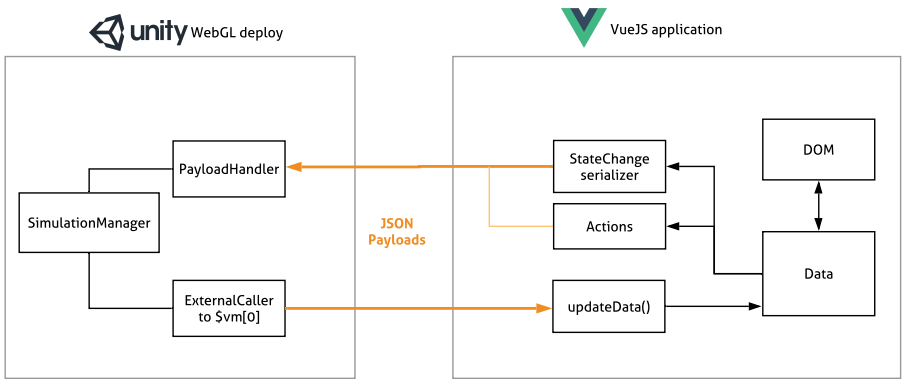


Figure 4.1: Overview of the implemented VueJS - Unity bidirectional comunication

Chapter 5

Simulations

The most thoroughly studied laboratory experiment that the plasmodium of Physarum is subjected to, is the imitation and optimization of human-made transport networks.

Adamatzky proposed another approach of the same problem. The main difference can be found in the initial conditions. Adamatzky placed the plasmodium in one place of the maze and, simultaneously, placed one FS in another place of the maze, before the plasmodium covers all the maze. The biological experiments show that the plasmodium spreads its pseudopodia trying to reach the food. Simultaneously, the food, releases the chemo-attractants to any direction in the maze. When the plasmodium finds those chemo-attractants, it follows them to the source food forming the minimum distance path between its initial site and the food site. So the plasmodium solves the maze in one pass because it is assisted by a gradient of chemo-attractants propagating from the target food. This approach, is modeled in this paper.

Chapter 6

Analysis of the results

Chapter 7

Conclusions

Bibliography

[1] Abubakr Awad, Wei Pang, David Lusseau, and George M. Coghill. A hexagonal cell automaton model to imitate physarum polycephalum competitive behaviour. In *Proceedings of the 2019 Conference on Artificial Life*, 4 2019.

[2] Jarkko Kari. *Cellular Automata notes*. University of Turku, 2013.

[3] Ignacio Barrantes, Jeremy Leipzig, and Wolfgang Marwan. A next-generation sequencing approach to study the transcriptomic changes during the differentiation of physarum at the single-cell level. *Gene regulation and systems biology*, 6:127–37, 10 2012.

[4] Yahui Sun. Physarum-inspired network optimization: A review. *arXiv preprint arXiv:1712.02910*, 2017.

[5] Richard Mayne. Biology of the physarum polycephalum plasmodium: preliminaries for unconventional computing. In *Advances in Physarum Machines*, pages 3–22. Springer, 2016.

[6] Jeff Dale Jones. Exploiting environmental computation in a multi-agent model of slime mould. In *AIP Conference Proceedings*, volume 1648, page 580006. AIP Publishing, 2015.

[7] Toshiyuki Nakagaki, Ryo Kobayashi, Yasumasa Nishiura, and Tetsuo Ueda. Obtaining multiple separate food sources: behavioural intelligence in the physarum plasmodium. *Proceedings of the Royal Society of London. Series B: Biological Sciences*, 271(1554):2305–2310, 2004.

[8] Jeff Jones. Characteristics of pattern formation and evolution in approximations of physarum transport networks. *Artificial life*, 16(2):127–153, 2010.

[9] Toshiyuki Nakagaki, Hiroyasu Yamada, and Ágota Tóth. Intelligence: Maze-solving by an amoeboid organism. *Nature*, 407(6803):470, 2000.

[10] Atsushi Tero, Seiji Takagi, Tetsu Saigusa, Kentaro Ito, Dan P. Bebber, Mark D. Fricker, Kenji Yumiki, Ryo Kobayashi, and Toshiyuki Nakagaki. Rules for biologically inspired adaptive network design. *Science*, 327(5964):439–442, 2010.

[11] Martin Grube. Physarum, quo vadis? In *Advances in Physarum Machines*, pages 23–35. Springer, 2016.

[12] Yukio-Pegio Gunji, Tomohiro Shirakawa, Takayuki Niizato, and Taichi Haruna. Minimal model of a cell connecting amoebic motion and adaptive transport networks. *Journal of theoretical biology*, 253(4):659–667, 2008.

[13] Michail-Antisthenis I. Tsompanas, Georgios Ch. Sirakoulis, and Andrew Adamatzky. *Cellular Automata Models Simulating Slime Mould Computing*, pages 563–594. Springer International Publishing, Cham, 2016.

[14] Tomohiro Shirakawa, Hiroshi Sato, and Shinji Ishiguro. Construction of living cellular automata using the physarum plasmodium. *International Journal of General Systems*, 44(3):292–304, 2015.