Continuous Game of Life

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The Game of Life is a famous cellular (discrete) automaton created by the mathematician J.H. Conway in 1970, which exhibit life-like patterns. We intend to define and study here a smooth version of this dynamic system. We show how the translation from a discrete definition to a smooth one highlights a chemicophysical interpretation of the system. An analysis strategy is sketched and observables are defined in order to explore numerically the "living" aspect of this dynamic system.

1 Definition

1.1 Discrete space-time

The Game of life is a two-dimensional grid whose square cells can take two different states : black or white ("dead" or "alive"). An evolution rule is applied to each cell at each time step, changing or conserving its state in function of its current state and its neighbourhood (the 8 surrounding cells) : any living cell *survives* if it has enough living neighbours (at least $s_1 = 2$) but not too much (less than $s_2 = 3$), and a dead one will be *born* if it has $b_1 = 3 = b_2$ neighbours. Otherwise the cell will die or stay dead [1].
This rule has been generalized for larger square neighbourhoods and formalized as (s_1, s_2) and (b_1, b_2), survival and birth intervals [2].

1.2 Smooth space

Based on this form of rule, a continuous version and its computer implementation has been exposed by Stephan Rafler in a 2011 article [3]. The grid is replaced by a continuous field $U : \mathbb{R}^2 \times \mathbb{N} \to [0, 1]$ and the domains of a cell and its neighbourhood are no squares anymore but a disk and a surrounding annulus.
This enlarge the symmetry around each cell from an order 4 rotational invariance to a polar symmetry. Cell's state $M(x, y, t)$ and population of their neighbourhood $N(x, y, t)$ are no longer computed by a counting process but by an integration over the cell-disk domain or the neighbourhood-annulus domain.
These averaged states are used to define the evolution rule. A cell state $M \in [0, 1]$ define a living interval (that matches with (s_1, s_2) if $M = 1$ and (b_1, b_2) if $M = 0$, intermediary otherwise). If the surrounding population of the cell at (x, y, t), N, is in the living interval computed from the cell state, then this point of the field will take the value 1 at $t + 1$.

1.3 Smoother space

Based on this, we have proposed a more natural definition of the cell state and its neighbourhood: the integration domain of the field is the full space in both cases, but the integration is weighted by a 2 dimensional Gaussian function, narrow for the cell domain, larger for its neighbourhood. This takes the form of a convolution of the field with the Gaussian function.

$$\begin{aligned} M(x,y,t) &= \int U(x',y',t) \cdot \frac{e^{-\frac{(x'-x)^2+(y'-y)^2}{2\sigma_M^2}}}{\sqrt{2\pi}\sigma_M} dx'dy' \\ &= U(t) * \mathcal{N}_{\sigma_M}(x,y) \\ N(x,y,t) &= \int U(x',y',t) \cdot \frac{e^{-\frac{(x'-x)^2+(y'-y)^2}{2\sigma_N^2}}}{\sqrt{2\pi}\sigma_N} dx'dy' \\ &= U(t) * \mathcal{N}_{\sigma_N}(x,y) \end{aligned}$$

where $\mathcal{N}_\sigma$ denotes the normalized Gaussian function of standard deviation σ.

This definition allows us to use the Fourier transform and the convolution theorem to compute these integrals. It is made espacially efficient by the use of the fast Fourier transform algorithm once discretized in its computer implementation.

1.4 Continuous time

The discrete time version of the system takes the form:

$$\begin{aligned} U(x,y,t+1) &= E[U(x,y,t)] \\ &= E(N(x,y,t), M(x,y,t); s_1, s_2, b_1, b_2) \end{aligned}$$

The evolution operator E can be represented by a two-dimensional function which takes N and M as arguments, and takes the value 1 in a certain region, 0 otherwise. This region can be define basically as two rectangles, "step rule", or more sophistically with a sigmoide function [3], "sigmoide rule" ; we also propose a single quadrangle version "slope rule". They can also have a continuous transition from 1 to 0. Here are plots, in there order of appearance, of these evolution functions over the unit square.

This can be turned into a differential equation by various means. One can consider the order 1 Taylor expansion of the above expression for $t + \tau$. This provide us the equation:

$$\frac{\partial U(x,y,t)}{\partial t} = \frac{E[U(x,y,t)] - U(x,y,t)}{\tau}$$

Assuming that $E[U(x,y,t)]$ is constant, we notice that this system behaves as an exponential decay of rate $\frac{1}{\tau}$ toward the values given by the operator E.

A practical simplification consists in replacing $-U(x,y,t)$ by -0.5 to get an evolution at constant rate. But we have to make sure that the field's values stay in the range $[0,1]$.

Those differential equations are discretized again in the computer implementation with the Euler method:

$$U(x,y,t+1) \simeq U(x,y,t) + \frac{\partial U(x,y,t)}{\partial t}$$

2 Chemicophysical interpretation

2.1 Gaussian convolution and the diffusion equation

Our proposition of "Gaussian neighbourhood" puts into evidence a strong link between our dynamic system and a diffusion process. Indeed, the resolution of the diffusion equation by the Fourier method express the solution at an arbitrary time as the Gaussian convolution (or Gaussian blurring) of the initial field. In the 1-dimensional case:

$$\begin{aligned}
\frac{\partial U(x,t)}{\partial t} &= D\frac{\partial^2 U(x,t)}{\partial x^2} \\
\frac{\partial \widetilde{U}(k,t)}{\partial t} &= D(-k^2)\widetilde{U}(k,t) \\
\widetilde{U}(k,t) &= e^{-k^2 Dt}\widetilde{U}(k,0) \\
\Rightarrow U(x,t) &= e^{Dt\frac{\partial^2}{\partial x^2}}U(x,0) \\
&= U(t=0) * \mathcal{N}_{\sqrt{2Dt}}(x)
\end{aligned}$$

We have used the convolution theorem in the last part of the resolution, and the solution can be written as above with the Weierstrass operator $e^{\frac{\sigma^2}{2}\Delta}$ which expresses the Gaussian convolution with standard deviation σ [4].

2.2 Derivation of the reaction-diffusion equation

Let's denote $U_\sigma = e^{\frac{\sigma^2}{2}\Delta}U \ \forall\sigma \geq 0$, then $U = U_0$. Using the time translation operator $e^{\tau\frac{\partial}{\partial t}}$, the discrete time evolution takes the form:

$$\begin{aligned}
e^{\tau\frac{\partial}{\partial t}}U_0 &= E(U_{\sigma_N}, U_{\sigma_M}) \\
e^{\tau\frac{\partial}{\partial t}}e^{-\frac{\sigma^2}{2}\Delta}U_\sigma &= E(U_{\sigma_N}, U_{\sigma_M})
\end{aligned}$$

We can now make appear explicitly the diffusion process in our system writting the exponential operators as series expansions. Assuming that τ and σ^2 are small enough, we will linearize these series. Note that, because of the presence of differential operators in the expansion, this would not be possible if the field were not regular enough . However, $U_\sigma = U_0 * \mathbb{N}_\sigma$ is of class C^∞, which is inherited from the Gaussian function by the differentiation property of the convolution. Then, for τ and σ^2 small enough we obtain a reaction-diffusion equation:

$$\begin{aligned}
\tau\frac{\partial U_\sigma}{\partial t} - \frac{\sigma^2}{2}\Delta U_\sigma + U_\sigma &= E(U_{\sigma_N}, U_{\sigma_M}) \\
\frac{\partial U_\sigma}{\partial t} &= D\Delta U_\sigma + \frac{E(U_{\sigma_N}, U_{\sigma_M}) - U_\sigma}{\tau} \\
\text{where } D = \frac{\sigma^2}{2\tau} &\text{ diffusion coefficient}
\end{aligned}$$

We find back the continuous time version of the system for $\sigma = 0$.

2.3 Interpretation

This provides us an interpretation of the evolution function E as the source term of the reaction part of the equation, independent of σ contrary to the loss term U_σ. Then, the time discreteness parameter $\frac{1}{\tau}$ is also a creation and decay rate.

If we think of U_σ as the concentration of a chemical, σ determines its diffusion coefficient. Then, the creation of any chemical species (any σ) is driven by two of them, caracterized by the diffusion coefficients $D_M = \frac{\sigma_M^2}{2\tau}$ and $D_N = \frac{\sigma_N^2}{2\tau}$. Then the ratio between surfaces of the cell and its neighbourhood corresponds to the ratio of the diffusion coefficient of this two chemicals. In the following, we will use the following coefficient:

$$R = \frac{\sigma_N}{\sigma_M} = \sqrt{\frac{D_N}{D_M}}$$

$R = 3$ in the original Game of Life model.

The parameters b_1, b_2, s_1, s_2 don't have other physical significance that threshold concentrations of the two previous chemicals for a positive reaction term. They allow a self-regulation when well adjusted.

However, this chemical interpretation is not sufficient. Indeed, while a simple diffusion equation allows for global conservation of chemical species, here the conservation is not guaranted. Instead, the global amount of any chemical varies in time but stays the same for all chemicals at a given time (according to their averaging relation by a Gaussian convolution). In fact, the fundamental quantity U_0, which is not diffusing, behaves like the spatial source of all other chemicals and drives their production. The concentrations of the two essential chemicals are retroacting on it.

We finally argue that the biological interpretation of the fondamental field $U_0(x,y,t)$ as a "life" property, although heuristical, still makes sense since it characterizes the places where new chemicals are continuously produced and where the concentrations of the two essential chemicals stay in a certain proportion.

The observation of organic-like patterns, their stability and reproductive property for certain parameters agrees with this interpretation.

3 Numerical analysis

3.1 Overview of the implementation

The numerical analysis of this system is based on its C++ implementation, developped in a previous work [5]. The field is discretized into a large matrix of values between 0 and 1, and the Euler method is used to discretize the time parameter. A specific features of this implementation is the use of the fast Fourier transform (FFT) and the convolution theorem to compute the convolutions. The space has the topology of a torus, which is automatically provided by the periodicity property of the FFT. In this way, we avoid border effects. Further optimizations has been provided for this study, such as single-precision floating-point values. The size of the matrix is also minimized for heavy computation in a way that it remains large enough compared to the size of a neigbourhood (which is also the characteristic scale of the produced patterns). The initial empty matrix is partially filled with white squares of this characteristic scale, set in a uniform random way in the matrix. We have added a coloration of the living cells pattern according to their position in the survival interval : the bluer the more populated and the redder the less populated is the neighbourhood.

We will try to develop strategies and algorithms to figure out the possible outcomes of the system and to attempt to characterize it.

3.2 A vector-field-like approach

The analysis of this dynamic system is not common because of the unusual form of the evolution function. The time derivative of the field at a certain position cancels out when it reaches the value given by the evolution function at this point (0 or 1). However, this value is dependent of neighbouring points, which are themselves dependent of neighbouring points, etc. Then, we can't describe locally in space the behaviour of the system, because of the presence of convolutions in the equation which extends the usually infinitesimal domain of influence around each point of the field to a large domain.

We can consider a kind of phase space if we plot the trajectories of the points of the field along three axis $(U_0, U_{\sigma_M}, U_{\sigma_N})$ (see Appendix). Choosing a small decay rate parameter, we can visualize the trajectories in this space. However, the points are not following a constant vector field since we can only predict the displacement of the points along the U_0 axis for the same reason than above. Even though, we can clearly observe in time that the flow is cycling, which is specific to the self-regulated configurations.

3.3 Observations

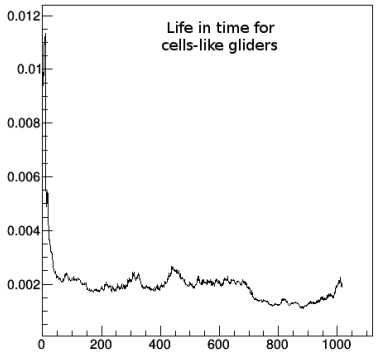
It is obvious that an empty (dead) space is a stable steady state of the system. We call it the "global death" configuration. However, non-trivial ones are observed in various versions of the evolution rule.
Their are static and stable configurations, such as "crystals" that is to say isolated and usually symmetric patterns, or filling ones. Their are also non-static patterns at a dynamic equilibrium, such as "oscillators" (periodically transforming crystals), "gliders" (or "bugs" [2]) or filling dynamic patterns.
Gliders are metastable moving pattern. Some are really stable (although moving) if isolated, others will split in two gliders after a certain time. For a small time discreteness parameter, this structure is strickingly analog to a cell division, with apparent membrane and nucleus (see Appendix).

3.4 Observables

In order to rationalize the exploration of the parameters and quantify these different structures, we define observables, and compute them at different times. Their are many possibilities ; the simplest one is the spatial average (or the sum-integral) of the field, which is useful to detect "global death" and stop the computation. To capture the velocity information, we use another observable defined as the sum of variations squared of all points of the field between two successive time steps. We have finally choosen to work with a combination of these two; we called this observable the *"life"* L of the system:

$$L(t) = \frac{\int (U(x,y,t-1) - U(x,y,t))^2 dxdy}{\int U(x,y,t) dxdy}$$

This observable is especially suitable for the study because it characterizes the velocity of the system while being independent of the necessarily finite size of the space for the simulation (when large enough). Moreover, it is a really stable observable for the study of gliders. Indeed, their number can vary a lot and L is independent of their number (which is proportionnal to the integral of the field). After a transitory period from the arbitrary initial state to $t =$, the life observable become quite steady. It is very likely that its mean converges and characterizes this glider.

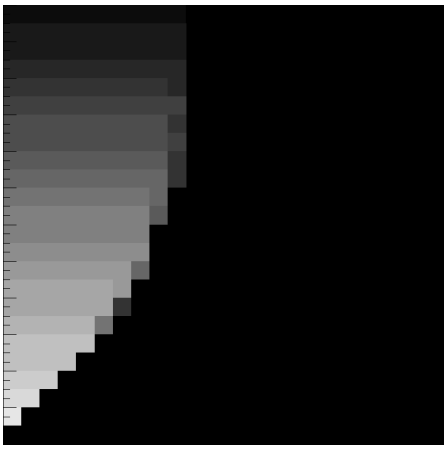


3.5 Map of the parameters space

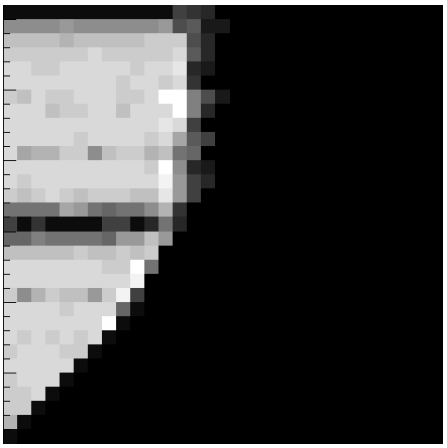
Two kinds of glider where found, each in a very narrow range of parameters of the complete model: one for discrete time ($\frac{1}{\tau}$=1) and the "slope rule" or the "step rule", the other (cells-like) for continuous time ($\frac{1}{\tau}$ small) and the "sigmoid rule" [6]. The difficulty to study these models comes from the 6 and 8 parameters respectively. Even

removing the time discreteness parameter (which slow down the motion but don't change the pattern) and the size of the cell (which rescale the pattern without changing it), a 5 or 6-dimensional parameter space is hard to explore.

We have achieved a partial (1-dimensional) exploration determining the presence of discrete-time gliders for different scale ratio parameter R, for fixed and suitable other parameters. R holds the information about the diffusion coefficients for the two essential chemicals in the chemicophysical interpretation. An new observable has been used to estimate the number of glider and distinguish them from a space filling pattern: this is the number of connected (non-black) pieces in space. This yield a presence of gliders for R between 2.95 and 3.45, with steadier but also less gliders for smaller R and more gliders splitting and multiplicating for larger R. Even smaller R leads to "global death" whereas even larger R leads to a dynamic filling (connected) pattern. The algorithm to compute this observable is, however, quite slow. We decided to map the parameters space of a simplified system : we take the same values for the birth interval and for the survival interval, and we put the cell scale to zero (that we could also understand as just one essential chemical). In this way, we just have the two threshold values of the evolution function, plus the time-discreteness parameter. We draw the histogram of the averaged "life" observable for a long time as shades of gray. The x-axis is the lower threshold for a birth or survival, the y-axis is the upper one. The time-discreteness is fixed to 0.1 (quite continuous time).



Note that the domain $y < x$ can't lead to a living configuration by definition of the evolution fonction. We clearly observe two domains: the black one leads to "global death", and the other region of is "alive" with a gradient of the "life" value. A discrete-time (parameter equal 1) yield to a similar nearly parabolic division between two "phases", and a shot of the patterns for different parameters suggest that patterns are richer around the phase transition ("oscillators" and spanning membranes).
We can reasonably assume that gliders occurs around a similar phase transition in the complete model since "global death" and filling patterns configurations are found for close parameters.



A subtler transition is found inside the living domain of the simplified model among the patterns. It has been captured by mapping in the same way another observable, an estimate of the entropy of the field values distribution (for a continuous-time model). The entropy gives an information about the diversity of the shades of gray in the field. We observe here that a line around the value 0.5 for the upper threshold span the living domain and separates two domaines of different pattern "texture" by a quite monochromatic pattern (the low entropy line).

Conclusion

We stop here our numerical exploration, but many directions remains open : since the system is deterministic, how chaotics are the patterns ? The phases of the many-dimensional parameter space are not determined yet.
The Continuous Game of Life model turns out to be a really rich dynamic system. Among the great diversity of patterns that can be observed, we recognize strong similarities with other pattern producing systems where diffusion is also present: we can quote the Belousov-Zhabotinsky reaction (moving wavefront patterns of the simplified model), magnetic domain patterns and Turing patterns (still filling pattern of the continuous time complete model).

References

[1] *Conway's Game of Life*, Wikipedia

[2] Kellie Michele Evans, *Larger than Life: It's so non-linear*, Ph.D. Thesis, University of Wisconsin Madison, 1996. `www.csun.edu/~kme52026/thesis.html`

[3] Stephan Rafler, *Generalization of Conway's "Game of Life" to a continuous domain - SmoothLife*, december 2011, `arxiv.org/pdf/1111.1567v2.pdf`

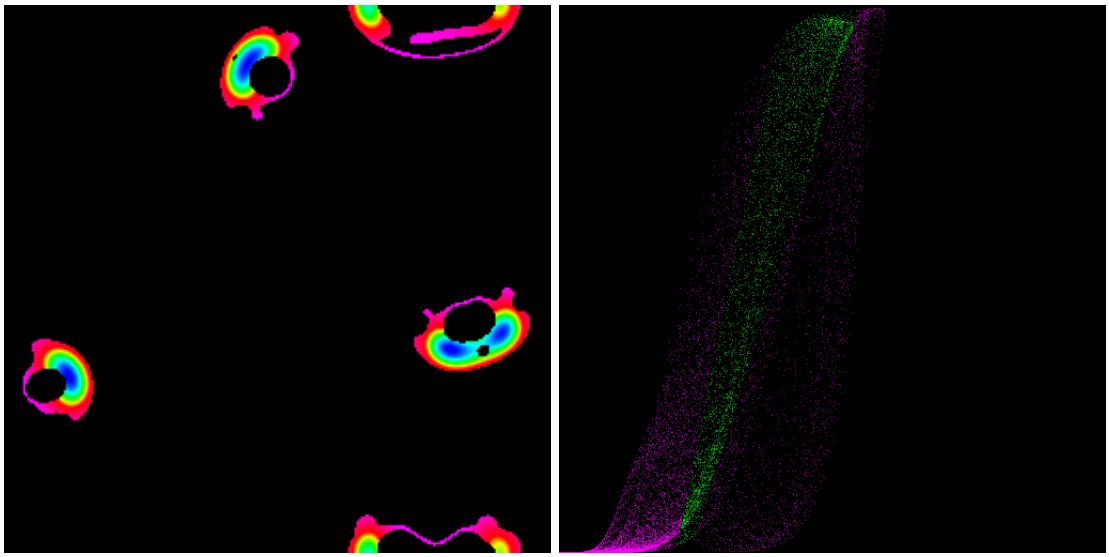
[4] *Weierstrass transform* - Generalizations, Wikipedia

[5] Théotime Girardot, Alexandre Guillet, Projet de Physique numérique, december 2016

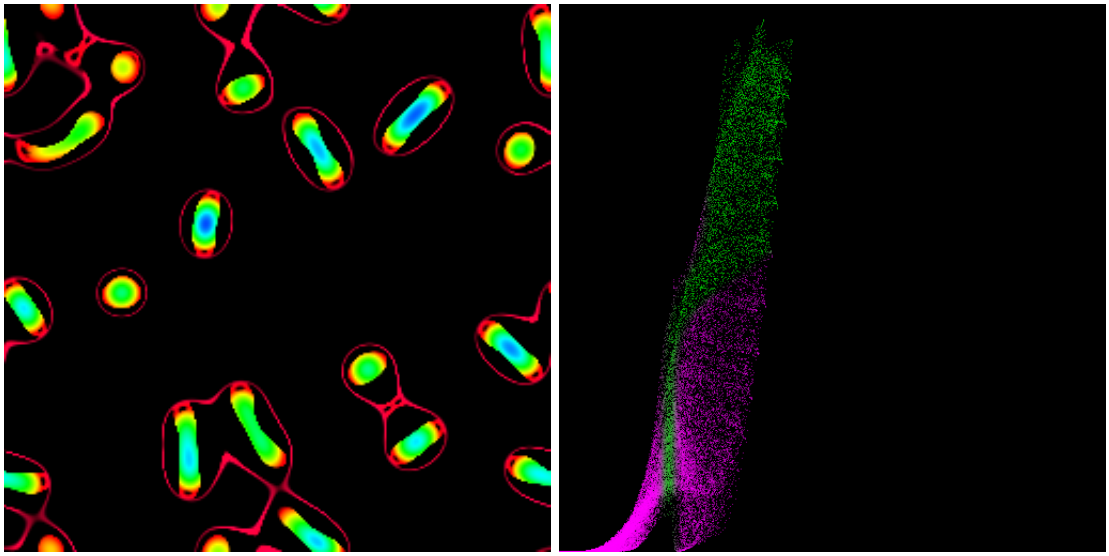
[6] "Cornus Ammonis", *Smoother Life*, Youtube, march 2015, & Tim Hutton's *Ready*, software.

Appendix A

Field and its plot in the $(U_0, U_{\sigma_M}, U_{\sigma_N}) \in [0,1]^3$ space, projected on the plane $(U_{\sigma_N}, U_{\sigma_M})$. Green points have increasing value and magenta ones have decreasing value along the U_0-axis.



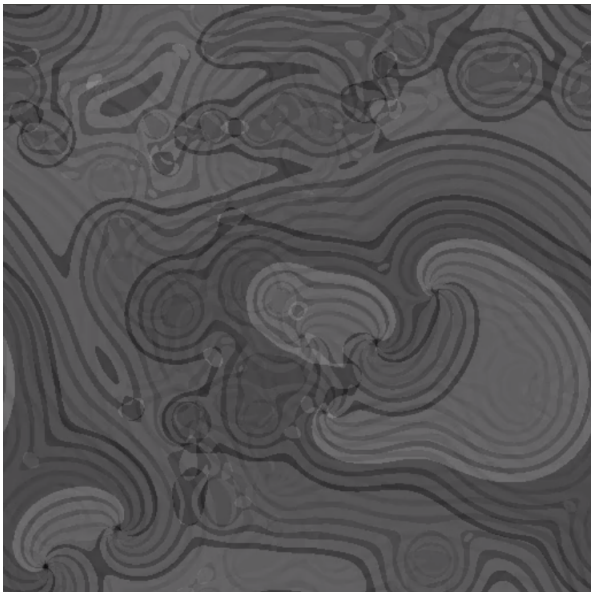
Gliders for the "slope rule", discrete time, intervals (0.213, 0.24) and (0.41, 0.55), R=3.15



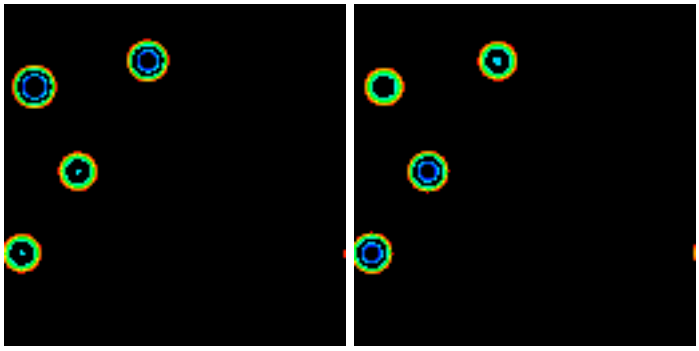
Gliders for the "sigmoide rule", continuous time, intervals (0.19, 0.21) and (0.27, 0.44), R=3.15, λ_1=0.0048, λ_2=0.038

Appendix B

Other patterns.



Belousov-Zhabotinsky analog patterns for the "simplified model", $\frac{1}{\tau}$=0.125, intervals (0.26, 0.32)



Oscillators of period 2 for the "simplified model", discrete time, interval (0.3, 0.5)

Turing analog patterns for the "slope rule", $\frac{1}{\tau}$=0.1, intervals (0.169, 0.188) and (0.388, 0.487), R=3, λ=0.002