Deterministic modeling - project

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Project goal

The project aimes to model the characteristic **patterns on animal skin**. Let's imagine that the little kitten was born and its owners want to know how will the cat's fur look like. In this project we assume that the initial distribution of the pigment is random. To simulate the final distribution of the pigment which is responsible for the patterns we will use the **Gierer-Meinhardt model of reaction-diffusion**.

We will create the numerical finite difference numerical scheme for this model, next we will check the accuracy of the scheme. Finally, our aim is to compare the final patterns depending on the parameters of Gierer-Meinhardt model.

Framework

We assume that the animal which skin patterns we will analyze is a cat. We will use the Gierer-Meinhardt model on the following framework:

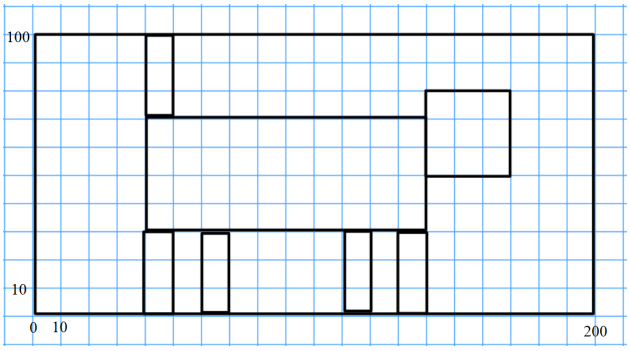

Figure 1: Framework

We can see that each body part is the rectangle. We will use the numerical scheme for each body part separately, because we assume that is no flow of the pigment between body parts. Moreover, the inital distribution of the pigment is random.

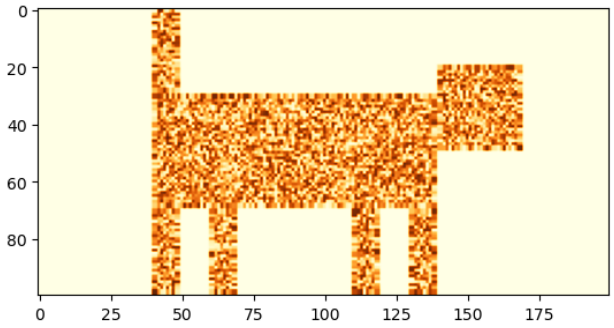

Figure 2: Initial distribution of the pigment

The above image comes from our implementation of the analyzing problem. We can see that in the inital (random) distribution of the pigment we actually can not distinguish any patterns.

Mathematical model

Alfred Gierer and Hans Meinhardt proposed in 1972 a molecularly plausible model for pattern formation, consisting of two partial differential equations of reaction-diffusion type. The model describes the concentration (values from 0 to 1) of a short-range autocatalytic substance, the activator, that regulates the production of its long-range antagonist, the inhibitor.

Gierer-Meinhardt model:

$$\frac{\partial a}{\partial t} = \frac{\rho \cdot a^2}{h(1 + c \cdot a^2)} - \mu_a a + D_a \Delta a + \rho_a$$

$$\frac{\partial h}{\partial t} = \rho a^2 - \mu_h h + D_h \Delta h + \rho_h,$$

where $\Delta f(x, y) = \frac{\partial^2 f}{\partial x^2} + \frac{\partial^2 f}{\partial y^2}$.

The above model is a reaction-diffusion system of the activator-inhibitor type.

Variables:

- a: a slowly diffusing *activator* - the substance responsible for the intensity of the pigment,
- h: a fast diffusing *inhibitor* - the antagonist which suppresses the value of a.

The first eqaution - change of activator concentration $\frac{\partial a}{\partial t}$:

- $\frac{\rho \cdot a^2}{h(1+c \cdot a^2)}$: the production rate (it depends in non-linear way of a and is slowed down by the inhabitor $1/h$ and by its own value),
- $-\mu_a a$: the number of molecules that decay per time unit (proportial to the decay rate μ_a and a),
- $D_a \Delta a$: the exchange (diffusion) of molecules,
- ρ_a: small activator-independent production rate.

The meaning of the second equation for $\frac{\partial h}{\partial t}$ is analogous.

We will assume that the initial pigment distribution is random and indepenedent in each part of the body (head, body, tail and legs).

In this case we assume that there is no flow at the edges - **homogeneous Neumann conditions**:

$$\frac{\partial a}{\partial n}(x,y,t) = \nabla a(x,y,t) \cdot n(x,y) = g(t) = 0,$$

$$\frac{\partial h}{\partial n}(x,y,t) = \nabla h(x,y,t) \cdot n(x,y) = g(t) = 0.$$

We will find the numerical scheme **for each part of the body separately** (for the rectangles: $[0,L] \times [0,M]$).

Finite difference numerical scheme

At the beginning we will approximate the value of Laplace operator:

$$\Delta a = a_{xx}(x,t) \approx \frac{a(x+h_x,t) - 2a(x,t) + a(x-h_x,t)}{h_x^2}.$$

We have:

$$\Delta a(x,y,t) \approx \frac{\partial^2 a(x,y,t)}{\partial x^2} + \frac{\partial^2 a(x,y,t)}{\partial y^2} \approx$$

$$\approx \frac{a(x+h_x,y,t) - 2a(x,y,t) + a(x-h_x,y,t)}{h_x^2} + \frac{a(x,y+h_y,t) - 2a(x,y,t) + a(x,y-h_y,t)}{h_y^2}.$$

We get the analogical formula for Δh.

- We have:

$$a_t = \frac{\rho \cdot a^2}{h(1+c \cdot a^2)} - \mu_a a + D_a \Delta a + \rho_a / \int_t^{t+h_t}$$

$$a(x,y,t+h_t) \approx a(x,y,t) + h_t \cdot \left(\frac{\rho \cdot a^2}{h(1+c \cdot a^2)} - \mu_a a + D_a \Delta a + \rho_a \right).$$

In matrix notation:

$$a_{i,j,k+1} \approx a_{i,j,k} + h_t \cdot \left(\frac{\rho \cdot a_{i,j,k}^2}{h_{i,j,k} \cdot (1 + c \cdot a_{i,j,k}^2)} - \mu_a a_{i,j,k} + D_a \Delta a_{i,j,k} + \rho_a \right).$$

- Similarly for the second equation:

$$h_t = \rho a^2 - \mu_h h + D_h \Delta h + \rho_h / \int_t^{t+h_t}$$

$$h(x,y,t+h_t) \approx h(x,y,t) + h_t \cdot (\rho a^2 - \mu_h h + D_h \Delta h + \rho_h).$$

In matrix notation:

$$h_{i,j,k+1} \approx h_{i,j,k} + h_t \cdot (\rho a_{i,j,k}^2 - \mu_h h_{i,j,k} + D_h \Delta h_{i,j,k} + \rho_h).$$

The above formulas are correct for $(x_i, y_j) \notin \partial\Omega$. Moreover, using the homogeneous Neumann conditions $(g(t) = 0)$ we get at the edge:

$$\mathrm{u}_{i,j,k+1} = \begin{cases} u_{L-1,j,k+1} + h_x g(t_{k+1}) & \text{if } x_i = L, 0 \leq y_j \leq M, \\ u_{1,j,k+1} + h_x g(t_{k+1}) & \text{if } x_i = 0, 0 \leq y_j \leq M, \\ u_{i,L-1,k+1} + h_x g(t_{k+1}) & \text{if } 0 \leq x_i \leq L, y_j = M, \\ u_{i,1,k+1} + h_x g(t_{k+1}) & \text{if } 0 \leq x_i \leq L, y_j = 0, \end{cases}$$

where $u = a$ or $u = h$.

Accuracy of the numerical scheme

Let's check if the above numerical scheme is good enough to use it in simulations. We don't know the theoretical solution of Gierer-Meinhardt model and we can't compare the numerical result with the theoretical one. For this reason, we can use the following procedure to check the accuracy of the model: we will calculate the solution (on the square $[0, 100]^2$) for time steps h_t and $\frac{h_t}{2}$. Next we will calculate the mean absolute errors in the common points for both time steps. If the numerical solution is stable, the errors for small time steps should be small.

We will calculate mean absolute errors for the following parameters:

$$h_x = 1, h_y = 1, h_t = 0.01, \rho = 1, \mu_a = 1, \mu_h = 1,$$
$$D_a = 0.02, D_h = 2.0, \rho_a = 0.02, \rho_h = 0, T_{max} = 100, c = 0.2.$$

The above set of parameters will be the basic one for the simualtions.

The diffusion for *activator* should be significantly less than the diffision for *inhibtor*. For this reason, we set $D_a = D_h/100$.

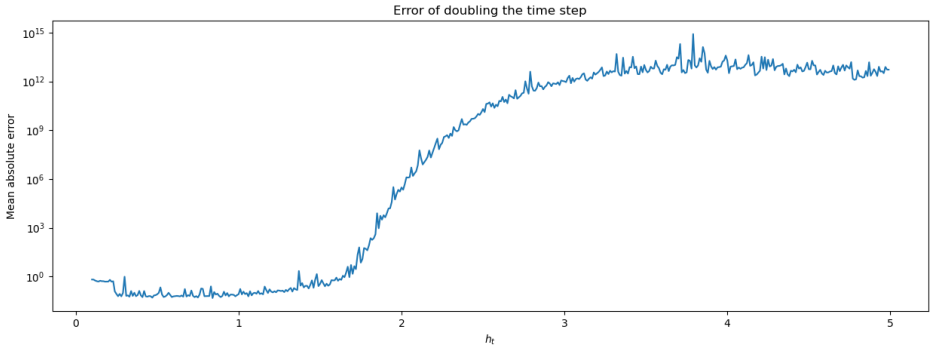

Figure 3: Error of doubling the time step

The above plot shows us that:

- the mean absolute error increase with the growth of time step h_t,
- the mean absolute error for $h_t \leq 1$ are close to zero,
- the numerical scheme for $h_t \approx 0$ is good enough to use it in simulations.

Simulations

Let's use the above numerical scheme for Gierer-Meinhardt model to simulate the final patterns on the cat's skin for a few different sets of parameters.

Patterns depending on the parameters c and D_h:

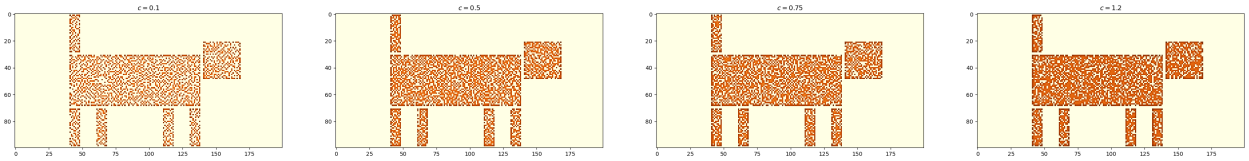

Figure 4: $D_h = 0.5$

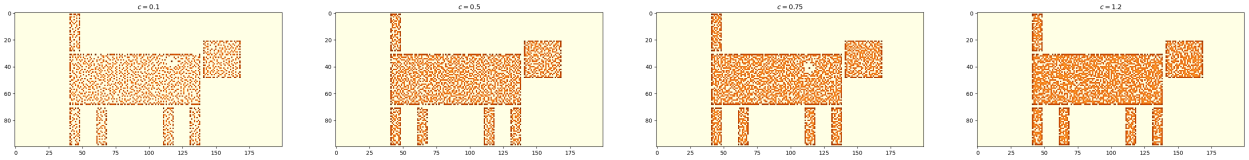

Figure 5: $D_h = 1$

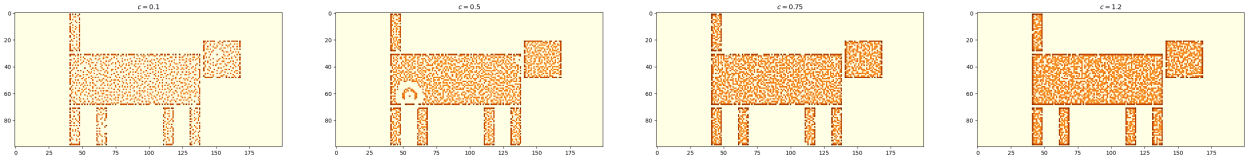

Figure 6: $D_h = 2$

The above results show us that:

- The final pattern for each set of investigating parameters is differente.
- The value of parameter c which is responsible for the pigment production rate has strong impact on the final pattern.
- For $c = 0.1$ the patterns could be described as the separate points of the pigment concentration. This kind of pattern is especially visible for the high inhibitor diffusion rate $D_h = 2$.
- When $c \geq 0.5$ the patterns are different: we can see the joined patterns (leopard-like pattern).
- With the growth of the value of parameter c the patterns are more intensive: there is more strong pigment. For this reason, the patterns are getting more uniformly strong.
- The growth of the value of the parameter D_h - which is responsible for the diffusion of inhibtor (we assume that $D_a = D_h/100$, so the change of paremeter D_h means also the change of the parameter D_a) - causes the increase of the intensity of the pigment. The patterns for the smallest value of the parameter D_h have the most strong pigment.
- In same cases we can the interesting circular concentration of the pigment which causes the round spots on the fur.

Patterns depending on the parameters μ_a and μ_h:

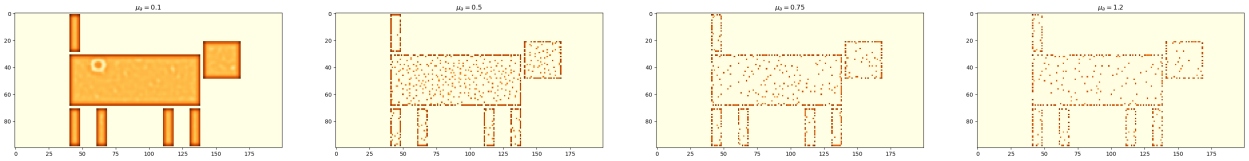

Figure 7: $\mu_h = 0.3$

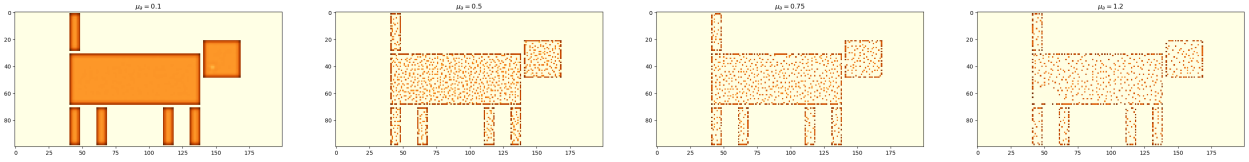

Figure 8: $\mu_h = 0.5$

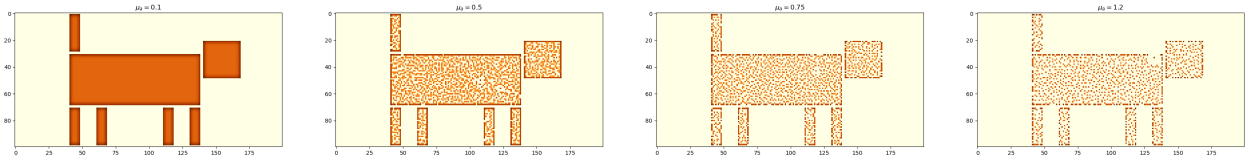

Figure 9: $\mu_h = 1$

Let's remind that the parameters μ_a, μ_h are responsible for the decay of the molecules of *activator* and *inhibitor* respectively.

We can see that:

- The small value $\mu_a = 0.1$ causes that there is a very strong concentration of the pigment (which doesn't decay significantly). For this reason, the final pattern has uniformly strong pigment.
- The growth of the parameter μ_a causes the faster decay of the *activator*. We can see that the patterns have smaller conctration of the pigment. For the highest value of μ_a (especially for small μ_h) the fur of the cat is almost completely devoid of pigment.
- The growth of the value of the parameter μ_h causes that the *inhibitor* decays very rapidly and the concentration of the pigment is higher.
- The patterns are: uniform for $\mu_a = 0.1$, separately dotted for the most of cases and joined (leopard-like pattern) when $\mu_a = 0.5, \mu_h = 1$.

Measuring diversity

We have seen above that there are very different final patterns depending on the parameters. In this paragraph we will calulate how the **diveristy of patterns** depends on the parameters of the Gierer-Meinhardt model.

We have to compare the resulting patterns in terms of diversity.

We will use the following method:

1. We get the results matices for each body parts.
2. We rewrite matrices as vectors.
3. We count the variance of each vector.
4. We set the result variance as the weighted arithmetic mean of variances with weights equal to the area of the appropriate body part (result matrix).

Using weighted mean allows us to retain information about the animal's proportions.

We don't count for example the covariances of matrices, because we compare just a value of function $a(x, y, T_{max})$ (pigment concentration) and we are interested to calculate the diversity of this value - we would use the corresponding method also in 1D or 3D cases.

Let's remind that the basic set for the above simulations is equal to:

$$h_x = 1, h_y = 1, h_t = 0.01, \rho = 1, \mu_a = 1, \mu_h = 1,$$
$$D_a = 0.02, D_h = 2.0, \rho_a = 0.02, \rho_h = 0, T_{max} = 100, c = 0.2.$$

We will calculate the variance for the final patterns for the same set of parameters with the parameters $D_h = 1, D_a = 0.01, c = 0.1$ to show all the results on one chart.

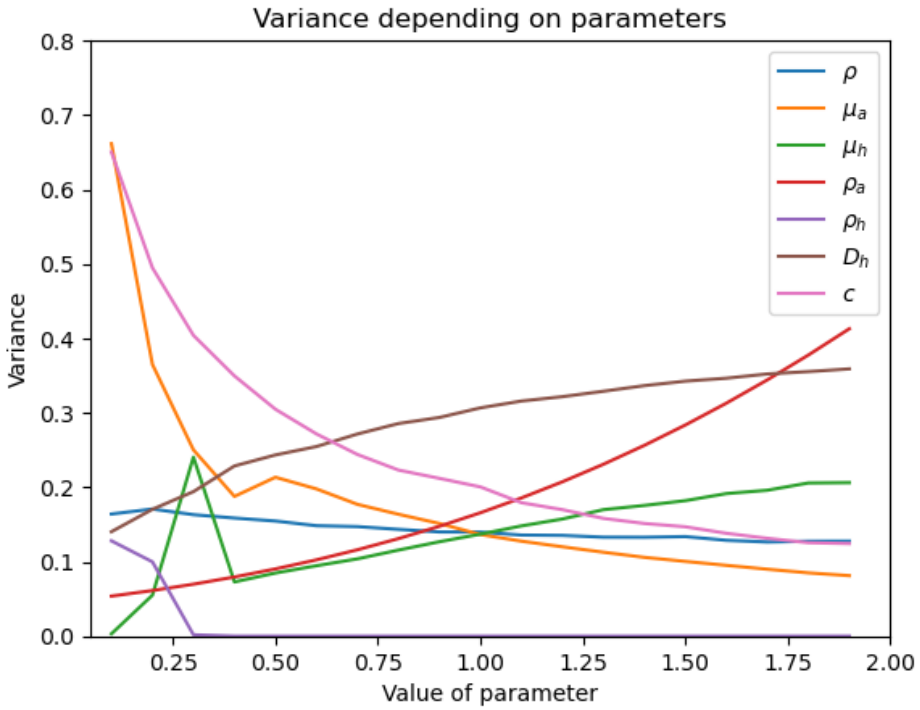

Figure 10: Weighted variance for the final patterns

The above results show us that:

- Parameter ρ which controls the production rate of *activator* and *inhibitor* doesn't have the significant impact on the diversity of final patterns.
- Parameters μ_a, μ_h are responsible for the decay of the molecules of *activator* and *inhibitor* respectively. We can see the natural results: the growth of μ_a causes the decrease of the diversity of final patterns. On the other hand, the growth of μ_h causes the increase of the diversity.
- Parameters ρ_a, ρ_h cause the independent production rate and should be small enough so as not to disturb the model. The growth of the value of ρ_a causes the very rapid growth of the variance of patterns. This means that there is very strong production of the *activator*. On the other hand, the growth of the parameter ρ_h causes that the variance is rapidly equal to zero. Too much value of the independent production rate for *inhibitor* causes that there is approximately no pigment and for this reason the variance of patterns is close to zero.
- Let's remind that we assume that $D_a = D_h/100$. So the growth of the value D_h causes also the growth of D_a. We can see that due to that growth the variance of patterns is increasing. That's the natural reason, because the higher diffusion (D_a, D_h - parameters of diffusion) causes that the pigment is quickly distributed and the patterns could be diverse.
- Parameter c is responsible for the production rate of the *activator* and has the strong impact on the diversity for the final patterns. The weighted variance for the final patterns increases rapidly with the growth of the value of the paramterer c.

Summary

In this project we have analyzed the pattern formation on the animal's (especially cat's) skin using the reaction-diffusion Gierer-Meinhardt model. We created the numerical scheme for this model, checked its accuracy and then we performed simulations.

The simulations showed us how diverse patterns we can get depending on the parameters of the model. We have seen for example separate dots, joined or uniform patterns.

Last but not least, we have calculated the weighted variance of the final patterns to investigate how the diversity of patters depends on the parameters of Gierer-Meinhardt model.