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The problem of aging as a problem of the appearance of unstable components when detailing the system

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***Abstrac t*— Recently, interest in Physical Informed Neural Network (PINN) has grown. But the process of implementing these models in the field of mathematical biology is still in its infancy. For this area, the question of finding a region of stability is both very difficult and important. There are many models for disease, aging, and carcinogenesis, but they all rely on the concept of an attractor of human health and resilience. But if you teach Artificial Intelligence to maintain the region of stability of a healthy state, it will inevitably face entering the region of instability, in which there is great sensitivity to changes in parameters, which will give exponentially large gradients. But when it comes to critical processes, organisms have a fairly good set of ways to maintain short-term stability that they have acquired through the process of evolutionary selection. Thus, all factors that affect aging are dynamics with slow exponential growth throughout life, similar to DNA mutations. Therefore, a hypothetical rough model that could directly suppress all such deep problems in their infancy may be an interesting first approximation, although most likely, due to excessive suppression, it will simplify the structure of the organism itself and possibly make its tissues and coordination of cellular reprogramming more similar to the tissues of the immortal jellyfish Turritopsis dohrnii. This abstract approximation model has long-term stability, and from there we can view aging as a problem of unstable components emerging in the detailing of the organism that we must solve.**

***Keywords – PINN*; mathematical biology; perturbation theory; life extension;**

I. INTRODUCTION

One of the most advanced models for simulating the structure of complex patterns of embryo development , organs and tissues is a multicomponent nonlinear partial differential equation.

The most famous of these is the reaction-diffusion equation, here is its usual form:

$$\frac{\partial u(t,X)}{\partial t} - \Big(f\big(u(t,X)\big) + \Delta u(t,X)\Big) = 0, X \epsilon B,$$

$$X = (x,y),$$

where $u(t,X) = \big(u_1(t,X), u_2(t,X), \dots, u_n(t,X)\big)$.

Or if we write down the components for each, then we have: $\frac{\partial u_i(t,X)}{\partial t} = \Big(f_i\big(u_1(t,X), \dots u_n(t,X)\big) + \Delta u_i(t,X)\Big)$

$$i \in \overline{1,n}$$

$$\frac{\partial u}{\partial n} = b = 0, X \epsilon \partial B$$

There were attempts to generalize this differential equation using different coefficients for diffusion [7] :

$$\frac{\partial u_i(t,X)}{\partial t} = \Big(f_i\big(u_1(t,X), \dots u_n(t,X)\big) + d_i \Delta u_i(t,X)\Big)$$

$$i \in \overline{1,n}.$$

In the framework of which the theory of how to build models of complex biological processes on the basis of differential equations was built.

But this theory did not give an answer how to find the equation in a more general form:

$$\frac{\partial u(t,X)}{\partial t} - \Big(f\big(u(t,X)\big) + D\Delta u(t,X)\Big) = 0.$$

Where $D$is the matrix$n \times n$ diffusion coefficients.

As it turns out, it is not enough to search for a matrix only in the form in which it is positive definite ($x^T D x \geq 0$) . And therefore simple theories may not give all the models that can be in nature.But recently, Google Research started working on Differentiable Self-organizing Systems[5], which made it possible to try to expand the area of searching for models for patterns [6] .

In this way, a more qualitative model of how the skin of the gopher (Ictidomys tridecemlineatus) and the patterns on it are formed. It was compared with existing methods [8] and theories [7] and it was shown that it is more effective for modeling complex patterns.

II. LIFE QUALITY OPTIMIZATION TASK

Let's consider the case when the algorithm built a mathematical model that is able to extend the life of an organism by maintaining the stability of the state $u_{healthy}$under some simplified conditions.

That is, a vector of optimal parameters c was found for the following problem with a operator: T_c:

$$u_t = T_c(u) = A(u, \Delta u, c),$$

$$\left(u_{healthy}\right)_t = T_c\left(u_{healthy}\right)$$

$$F(u_0, c) = \int dist\left(u(t,X), u_{healthy}(X)\right) dt \to min$$

where $u(t,X) = \left(u_1(t,X), u_2(t,X), \ldots, u_n(t,X)\right)$ - vector of spatio-temporal distribution of metabolic processes and epigenetic configurations.

Now if we need to get the model parameters for a bit of a pain detailed model.

$$u_t = A_\epsilon(u, \Delta u, c),$$

$$A_0 = A.$$

We can get a problem that even with a small step, an eigenvalue may appear in the linear expansion of the operator $A_\epsilon(u, \Delta u, c)$ at the point $u_{healthy}$ which has a real part equal to or greater than 0.

III. Using the Template

We obtain a linearized equation for δ - a small deviation from $u_{healthy}$:

$$\delta_t = a_{\epsilon, u_{healthy}}(\delta, \Delta\delta, c).$$

Let 's take the maximum eigenvalue by its real part for $a_{\epsilon, u_{healthy}}$ - λ_ϵ.

We have what $\Re(\lambda_\epsilon) = ln\left(\left\|e^{a_{\epsilon, u_{healthy}}}\right\|_2\right)$.

From what we have that if $a_{\epsilon, u_{healthy}}$ - changes continuously according to the norm $\|.\|_2$ over the variable ϵ we have $\Re(\lambda_\epsilon)$- changes continuously. And therefore, in the case of the appearance of instability in pattern formation during growth ϵ will be the minimum value ϵ_1 for which $\Re\left(\lambda_{\epsilon_1}\right) = 0$.

Suppose we chose ϵ in such a way that λ_ϵ the only egenvalue with $\Re(\lambda) \geq 0$.

For this eigenvalue, consider the eigenvector $u_{\lambda_\epsilon}(X)$.

Then, with initial values u_0 close to $u_{healthy}$ we will have a problem close to a linearized one:

$$\delta_t = a_{\epsilon, u_{healthy}}(\delta, \Delta\delta, c).$$

Which $\delta(t,X) = k(t)u_{\lambda_\epsilon}(X)$ at

$$k'(t) = \lambda_\epsilon k(t).$$

$$k(t) = k(0)e^{\lambda_\epsilon t}.$$

$$\delta(t,X) = k(0)e^{\lambda_\epsilon t}u_{\lambda_\epsilon}(X)$$

We have that $\delta(t,X) = k(0)e^{\lambda_\epsilon t}u_{\lambda_\epsilon}(X)$ - the main long-term component that takes you out of the health zone and leads to death.

It is worth emphasizing that this component is not necessarily a visible process, it may be some kind of invisible process that takes the system out of the stability zone, within which normal reactions become inadequate or lead to the creation of cancerous tumors.

For this model it is enough to study:

$$FailComponent(t) = \frac{u(t,X) - u_{healhy}(t,X)}{\|u - u_{healhy}\|_B}$$

To supervisedly train our system to avoid this component without having huge random steps due to finite growth and high sensitivity, we can use gradient descent with gradient normalization and exponential smoothing:

$$g_i = \frac{grad_c F(u_0, c_i)}{\|grad_c F(u_0, c_i)\| + \epsilon}$$

$$G_i = \beta g_i + (1-\beta)G_{i-1}$$

$$\bar{g}_i = \frac{1}{1-\beta^{i+1}}G_i$$

$$c_{i+1} = c_i - \alpha\bar{g}_i$$

If we look at this procedure as a specific approach, it focuses on a deeper understanding of the processes during a healthy state, deep enough to analyze small long-term changes and find the accumulating and increasing components and optimize the dynamics of the body to eliminate this instability.

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