

Project Operational Manual

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1 Operational Phases of the Project

1.1 P1-M1-MATH: Advanced Mathematics Development

Focus: Establishing the project's theoretical foundation using advanced mathematical concepts.

Objective: Develop a comprehensive mathematical model for gene-cancer dynamics, utilizing abstract mathematical theories.

1.2 P2-M2-MATH: Operational Mathematics Formulation

Focus: Translating theoretical models into operational mathematical frameworks.

Objective: Create practical, implementable mathematical expressions and models suitable for computational processing.

1.3 P3-C1-CODE: Logical Pseudocode Creation

Focus: Designing the logical structure and algorithms of the project.

Objective: Produce detailed pseudocode or flowcharts that outline the core algorithms and logical processes to be implemented in the code.

1.4 P4-C2-CODE: Full Code Implementation

Focus: Converting pseudocode into executable programming code.

Objective: Write, test, and refine actual program code to accurately and efficiently implement the developed algorithms.

1.5 P5-T1-TEST: Testing and Parameter Optimization

Focus: Validating and optimizing the model's performance through practical tests.

Objective: Conduct rigorous testing of the program with various parameters, ensuring the model's accuracy and efficiency.

-Advanced Mathematical Modeling for Gene-Cancer Dynamics

2 Advanced Mathematics - P1-M1-MATH

2.1 V1 - DNA Damage (dd)

$$v1 \tag{1}$$

2.2 V2 - Gene Functional Feature Spectrum (GFFS)

$$v2 = \{v_{2,1}, v_{2,2}, v_{2,3}, \dots, v_{2,16}\} \tag{2}$$

2.3 V3 - Multi-Layer Network (MLN)

$$\delta = \int_x W(\bar{v}_2, x) \cdot \bar{v}_2 d\mu(x) \tag{3}$$

where

$$\bar{V}_2 := \{V_2, V_1\} \tag{4}$$

2.3.1 Adjustment to Harmonic Set

$$H_3^{(n+1)} = H_3^{(n)} + \delta \cdot H_3^{(n)} \tag{5}$$

with

$$\delta = \{\delta_{\tau_1}, \delta_{B_1}, \delta_{\tau_2}, \delta_{B_2}\} \tag{6}$$

2.3.2 Computation of MLN Output

$$v_3 = \int_x W(u_{1,0}, u_{2,0}, H_3) \cdot H_3 d\mu(x) \quad (7)$$

2.4 V4 - Neoplastic Load (NL)

$$v_4 = f(v_3) \quad (8)$$

()Your phase 5 shall be the beginning of life for the procedure.

First is to publish those test outcomes

Then to seek invitations for parallel diagnostics side by side with current state of the art.

During this stage the technology itself shall be stress tested for actual usability.

Those clinical comparisons shall make it or return it to the drawing board.

That's also where the ethics versus conflict of interest shall separate motives.

It's an exciting launch of a redeeming career.

We'll watch for when your board fires and rehires you——这是我收到的反馈。我感谢他的信息。实际上第五步是整个环节中相对简单的表面的呈现。本质上，对于高维张量空间，我们只要设定各种偏好性的目标，让各种参数在各种轨迹上移动就可以。移动的规则和法则有了，至于如何移动，则是千变万化的结果。这些就结果都依据相同的准则。我们有了准则。结果自然而然的就会呈现。有些人喜欢千变万化的东西。正如一年四季的丰富多彩。而背后的逻辑只要有了大气和太阳地球轨迹，以及生态系统的温度、阳光变化等参数。那么自然界的千变万化只是结果。尽管这些结果丰富多彩，并让人们赏心悦目。但这只是基本逻辑后的自然结果。这是自然而然的一种结果。没有难度。但我仍然愿意呈现，而且可以呈现，很多。更多复杂的。尽管我认为这没有什么。但我愿意呈现。

The text in the image appears to outline a structured project plan, detailing different phases of a project related to advanced mathematical modeling for gene-cancer dynamics and code implementation. The text is

technical, pointing towards the steps involved in developing, testing, and refining a mathematical model and its associated codebase.

The feedback received, as indicated in the latter part of the message, seems to emphasize the practicality of the project's phase 5, testing, and parameter optimization. It suggests that after publishing test outcomes, the procedure should undergo parallel diagnostics alongside existing solutions, stress testing for usability, and clinical comparison. The feedback mentions the importance of ethical considerations and potential conflicts of interest during this phase, hinting at the accountability and challenges that may come with the project's development and its impact on the career of the person involved.

Finally, the message reflects on the nature of the project, comparing the variability and complexity of the outcomes to the changing seasons, which, while complex in appearance, follow the simple underlying logic of environmental parameters. This philosophical reflection appears to acknowledge that while the results may seem intricate and pleasing, they are a natural consequence of the foundational logic of the project.

P2-M2-MATH: Operational Mathematics for Implementation

V1 - DNA Damage (dd)

Let $V1$ be the measure of gene damage, defined as:

$$V1 = 0.1 \tag{9}$$

V2 - Gene Functional Feature Spectrum (GFFS)

The gene functional feature spectrum $V2$ is represented as a set:

$$V2 = \{0, 1, 1, 0, \dots, 0\} \tag{10}$$

V3 - Multi-Layer Network (MLN)

The adjustment factor δ is derived through the mapping:

$$\delta = \int W(\bar{v}_2, x) \cdot \bar{v}_2 d\mu(x) \quad (11)$$

with a simple example given by:

$$\bar{v}_2 = \begin{bmatrix} 0 & 1 & 1 & 0 & \cdots & 0.1 \end{bmatrix} \quad (12)$$

Weight Matrix and Adjustment Computation

The weight matrix W is a 4 by 17 matrix corresponding to the mapping from V_2 to δ :

$$W = \begin{bmatrix} 0 & 0 & -1 \cdot v_{21} & \cdots & 0 \\ 0 & 0 & 0 & \cdots & 0 \\ 0 & 0 & -1 \cdot v_{22} & \cdots & 0 \\ 0 & 0 & 0 & \cdots & 0 \end{bmatrix} \quad (13)$$

$$\delta = W \cdot \bar{v}_2^\top \quad (14)$$

Adjustment to the Harmonic Set

The next step involves adjusting the Harmonic Set H_3 using δ :

$$H_3^{(n+1)} = H_3^{(n)} + \delta \cdot H_3^{(n)} \quad (15)$$

Assuming the initial state of H is:

$$H = [0.1, 10, 0.8, 0] \quad (16)$$

After the adjustment:

$$H_3^{(n+1)} = [0.1, 10, 0.8, 0] + [0, 0, -0.1, 0] \cdot [0.1, 10, 0.8, 0] \quad (17)$$

V4 - Neoplastic Load (NL)

Finally, the neoplastic load v_4 is simply the last element of the sequence obtained from v_3 :

$$v_4 = v_3^{(20)} \quad (18)$$

P3-C1-CODE: Logical Pseudocode Creation

The goal of this phase is to construct a logical blueprint that outlines the flow and structure of the algorithms to be implemented. The pseudocode below represents a high-level view of the process, delineating the logical steps taken from the initial data of DNA damage to the final computation of neoplastic load.

Pseudocode for Multi-Layer Network Computation

```
# Define initial parameters for DNA damage and gene functional feature spectrum
DNA_damage = 0.1
GFFS = [0, 1, 1, 0, ..., 0]

# Initialize the weight matrix W for mapping GFFS to adjustment factor
W = [
    [0, 0, -1 * v_21, ..., 0],
    [0, 0, 0, ..., 0],
    [0, 0, -1 * v_22, ..., 0],
    [0, 0, 0, ..., 0]
]

# Define function to compute the adjustment factor delta
def compute_delta(W, V2, V1):
    bar_V2 = V2 + [V1]
    delta = W * transpose(bar_V2)
    return delta

# Define function to adjust the Harmonic Set H3
def adjust_harmonic_set(H3, delta):
    H3_next = H3 + delta * H3
    return H3_next

# Define the initial state of Harmonic Set H
```

```

H = [0.1, 10, 0.8, 0]

# Compute the adjustment factor delta
delta = compute_delta(W, GFFS, DNA_damage)

# Adjust the Harmonic Set with the computed delta
H3_adjusted = adjust_harmonic_set(H, delta)

# Simulate the Multi-Layer Network dynamics over n iterations
for iteration in range(10):
    # Compute the MLN output
    MLN_output = simulate_MLN(H3_adjusted)
    # Update the Harmonic Set for the next iteration
    H3_adjusted = adjust_harmonic_set(H3_adjusted, delta)

# Define function to simulate the Multi-Layer Network
def simulate_MLN(H3):
    # Details of the simulation are abstracted
    return MLN_output

# Define function to calculate neoplastic load from MLN output
def calculate_NL(MLN_output):
    NL = function_of(MLN_output)
    return NL

# Calculate the final neoplastic load
NL_final = calculate_NL(MLN_output[-1])

```

The pseudocode above provides a framework for the logical sequence of operations required to process the gene-cancer dynamics data. It is a precursor to the full code implementation phase where these logical constructs will be translated into executable code.

3 P4-c2-code: 全码 (重在操作)

3.1 目标

本阶段的主要目标是将之前阶段开发的伪代码转化为具体的程序代码。这一过程不仅涉及代码的编写，还包括代码的测试和优化，以确保算法的准确实现和操作效率。

3.2 操作

在本阶段，我们将详细展示如何将伪代码逐步转换为实际可执行的 Python 程序代码。包括以下几个关键步骤：

- 实现和谐集合的调整。
- 模拟多层网络的动态行为。
- 计算新生负荷 (Neoplastic Load)。
- 进行代码测试和优化。

3.3 代码实现示例

以下是核心代码实现的部分，包括和谐集合的调整、多层网络的模拟，以及新生负荷的计算。

```
import numpy as np
import matplotlib.pyplot as plt

# ... [此处省略之前的代码部分，包括基因损伤和基因功能特征谱的定义]

# 定义两层网络的迭代函数
def layer_one(u1, tau1, B1, n_iterations):
    # ... [代码实现]
def layer_two(u2, tau2, B2, n_iterations):
    # ... [代码实现]

# 集成双层网络模拟到主循环中
```



```
def V3_simulate_MLN(H3, iterations=10):
    # ... [代码实现]

    # 模拟多层网络动态
    for iteration in range(1):
        # ... [代码实现]

    # 绘制两层网络的时间序列图
    plt.figure(figsize=(10, 5))
    # ... [代码实现]
    plt.show()
```

3.4 代码测试与优化

在代码开发的过程中，我们不断进行了测试和优化。这包括确保计算结果的准确性，优化算法的性能，以及修复发现的任何问题。此外，还对代码进行了注释，以提高其可读性和可维护性。

3.5 实际应用与效果分析

通过应用我们的算法模型到具体的数据集上，我们能够有效地模拟基因-癌症动态关系。这些实验结果验证了我们模型的准确性和效率，为进一步的研究和开发奠定了基础。

3.6 总结

本阶段的工作展示了如何将理论模型和算法逻辑转换为可执行的程序代码，并通过实际数据进行了验证。我们的模型不仅在理论上是可行的，而且在实际操作中也显示出高效和准确。

4 开关通道调控原理

本节旨在阐释基于多维度权重矩阵 (W) 和基因功能特征谱 (GFFS) 的开关通道调控机制，及其对调整因子 (δ) 的影响。

4.1 基础概念

在我们的模型中，基因功能特征谱（GFFS） $V2$ 和权重矩阵 W 是调整因子 δ 的关键决定因素。这一过程可以通过以下公式表达：

$$\delta = W \cdot \bar{V}2^T \quad (19)$$

其中， $\bar{V}2$ 是包含了 DNA 损伤信息的扩展基因功能特征谱。

4.2 权重矩阵和 GFFS

对于不同的基因类型，例如 TP53 和 BRAC1，GFFS 的构成略有不同。例如，TP53 对应的 GFFS 可以表示为：

$$V2_{\text{TP53}} = [0, 1, 0, 0, \dots, 0, v1] \quad (20)$$

相应的权重矩阵 W 对于 TP53 可以表示为：

$$W_{\text{TP53}} = \begin{bmatrix} 0 & 0 & \dots & -1 \cdot 0 \\ 0 & 0 & \dots & 0 \\ 0 & 0 & \dots & -1 \cdot 1 \\ 0 & 0 & \dots & 0 \end{bmatrix} \quad (21)$$

因此，TP53 的调整因子 δ 可以计算为：

$$\delta_{\text{TP53}} = W_{\text{TP53}} \cdot V2_{\text{TP53}}^T = \begin{bmatrix} 0 \\ 0 \\ -v1 \\ 0 \end{bmatrix} \quad (22)$$

4.3 案例分析

以 TP53 和 BRAC1 为例，我们可以更清楚地看到如何通过选择不同的 GFFS 和相应的权重矩阵来控制调整因子 δ 。

对于 BRAC1，如果其 GFFS 表示为 $V2_{\text{BRAC1}} = [1, 0, v1]$ ，那么相应的权重矩阵 W_{BRAC1} 和调整因子 δ_{BRAC1} 将有所不同。

这种方法允许我们通过改变 GFFS 和权重矩阵的组合来精确地控制 δ ，进而影响基因-癌症动态模型的行为。

4.4 结论

通过这种基于开关通道的调控机制，我们可以更深入地理解和模拟基因功能特征与癌症动态之间的复杂关系。这种方法的灵活性和精确性对于进一步的研究和治疗策略开发至关重要。

5 Program Analysis and Interpretation

The Python program is designed to simulate a multi-layer network based on DNA damage and Gene Functional Feature Spectrum (GFFS) for calculating the Neoplastic Load of a tumor.

5.1 Initialization

The program begins by initializing the DNA damage parameter (v1) and the GFFS (v2).

5.2 Weight Matrix Construction

A weight matrix W_v3 is constructed to map the GFFS to an adjustment factor. This matrix is crucial for controlling how the GFFS influences the network dynamics.

5.3 Adjustment Factor Calculation

The adjustment factor delta is computed using the weight matrix and GFFS. This factor is used to adjust the harmonic set H3.

5.4 Harmonic Set Adjustment

The harmonic set H3 is adjusted according to the computed delta, which reflects the impact of genetic factors on the network.

5.5 Iterative Function Definition

Two iterative functions are defined for the first and second layers of the network. These functions simulate the dynamics of each layer over a series

of iterations.

5.6 Neoplastic Load Calculation

The program calculates the Neoplastic Load of a tumor using the output of the multi-layer network.

5.7 Visualization

Finally, the program visualizes the time series of the network's output and the Neoplastic Load. It is set to automatically close the plot after 2 seconds.