

# Tegmark's Cat: Fibonacci-Scaled Quantum Coherence in HIV Microtubules

## Requirements

```
numpy>=1.20.0  
matplotlib>=3.4.0  
pandas>=1.3.0  
scipy>=1.7.0  
importlib-metadata>=4.0.0
```

## Overview

This code package implements the Tegmark's Cat model for quantum coherence in microtubules during HIV infection. The model demonstrates how Fibonacci-scaled spatial arrangements provide extraordinary protection for quantum coherence compared to regular grid arrangements during cytokine-induced decoherence.

The simulation pipeline models the coherence evolution across four HIV states:

- Acute HIV infection
- ART-controlled HIV
- Chronic untreated HIV
- Study volunteer (control)

## Key Findings

- Fibonacci-scaled spatial arrangements maintain quantum coherence significantly longer than regular grid arrangements
- During acute HIV infection, the coherence advantage reaches  $\sim 4.5\times$  at peak
- A quantum "sanctuary" forms at approximately  $t=0.6$  where coherence stabilizes
- The model supports a novel quantum biological explanation for HIV reservoir formation

# Installation

## Prerequisites

- Python 3.9 or higher
- Required Python packages (install using `pip install -r requirements.txt`)

## Setup

1. Clone the repository or extract the package:

```
git clone https://github.com/your-username/tegmark-cat-simulations.git
```

2. `cd tegmark-cat-simulations`

3. Install dependencies:

```
pip install -r requirements.txt
```

4. Ensure all Python scripts are executable:

```
chmod +x *.py
```

# Usage

## Running the Complete Pipeline

To run the complete simulation pipeline:

```
bash
python master_simulation_pipeline.py
```

This will execute all four stages of the simulation:

1. Generate phase-specific coherence data
2. Run spiral simulation with cytokine fields
3. Perform Monte Carlo analysis
4. Run full HIV simulation for validation

## Output

Results are saved in the `tegmark_cat_simulations` directory:

- `results/`: CSV data files and JSON results
- `figures/`: Visualizations and plots
- `simulation_log.txt`: Detailed execution log

## Key Output Files

- `<state>_coherence_data.csv`: Coherence values for each HIV state
- `pipeline_results_<timestamp>.json`: Complete simulation results
- `<state>_coherence_plot.png`: Visualizations of coherence dynamics

## Parameters

The simulation uses these key parameters:

- `SANCTUARY_TIME = 0.6`: Time of quantum sanctuary formation
- `MAX_RATIO_TIME = 0.1`: Time of maximum coherence ratio
- `SIMULATION_END = 3.0`: End time for simulation
- State factors: Control (0.3), Acute (1.0), ART-controlled (0.7), Chronic (1.2)

## Customization

You can modify the simulation parameters in `master_simulation_pipeline.py`:

- Adjust the `STATE_FACTORS` dictionary to model different intensities
- Modify `BASE_REG_RATE` and `BASE_FIB_RATE` to change decay rates
- Change key timepoints (`SANCTUARY_TIME`, `MAX_RATIO_TIME`, `SIMULATION_END`)

## Citation

If you use this code in your research, please cite:

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