

Mycelial Quantum Tomography: First Biological Decoder for Quantum Black Boxes

Author

Zubair Chowdhury

GoMaa Hosting, Wimbledon, England, UK

Abstract

This brief report presents a world-first simulation of mycelial networks (*Pleurotus ostreatus*) as biological quantum tomography decoders for black-box superpositions. The goal is to explore whether fungal networks can, in principle, act as interpretable “receivers” for quantum processes that are opaque to classical observers. Using a lightweight NumPy-based model, mycelial stabilizer projections were mapped onto electrical spiking patterns, allowing reconstruction of simplified quantum state information. The simulation yielded a fidelity of 0.142 ± 0.05 and a cross-correlation Corr_{AB} of 0.151 between two virtual mycelial “colonies,” values that are consistent with a noisy local biological decoder rather than any nonlocal or field-like influence. These results support the interpretation that the observed structure can be explained by local stochastic dynamics, while still providing a concrete protocol for future wet-lab tests of more speculative hypotheses about nonlocal information substrates.

Introduction

Quantum algorithms exploit superposition and interference across exponentially large state spaces, which makes them both powerful and difficult to interpret. Conventional quantum state tomography scales poorly and quickly becomes intractable as the number of qubits grows. At the same time, there is growing interest in biological systems especially fungi and mycelial networks as potential substrates for unconventional computation and information processing. This work introduces the concept of *mycelial quantum tomography*: using mycelium as a hypothetical biological decoder that projects aspects of a quantum state into an electrical spiking pattern. The present paper does not claim that real fungi already do this, but rather offers a simulated protocol and concrete metrics that can later be tested in the lab.

Methods (Simulation Overview)

The simulation models a small quantum system subjected to Grover-style amplitude amplification and then approximates how a mycelial network might “read out” stabilizer-like information. A simplified statevector is constructed, and its diagonal elements are treated as probability weights analogous to measurement outcomes. These probabilities are passed through a mycelial “spiking” function that applies random ± 1 factors and hyperbolic tangent non-linearities to mimic noisy bio-electrical responses. Two virtual colonies (A and B) are generated with slightly different noise parameters to imitate a nearby and a more distant culture. The main quantities of interest are:

- The **fidelity-like metric**, defined as the mean absolute spike amplitude for colony A.
- The **cross-correlation Corr_{AB}** , defined as the Pearson correlation between A and B’s spike vectors.

All code is contained in a single, reproducible Python script (`mqt_fixed.py`), which can be run on a standard AlmaLinux 8 / cPanel/WHM server without external quantum libraries.

Results

The simulation produced a fidelity value of 0.142 for the primary mycelial decoder (colony A). This is below any reasonable “high-fidelity decoding” threshold (for example, 0.85), and is consistent with a noisy, low-signal regime. The cross-correlation Corr_AB between colony A and colony B was 0.151, which lies well below a 0.5 threshold that would suggest strong shared structure, and far from the >0.7 region that was proposed as an indicative signature of nonlocal or field-mediated synchronization. Under the pre-specified criteria, these numbers are interpreted as: (i) *local biology confirmed* and (ii) *no evidence for a nonlocal field-like coupling* in this simulation.

Discussion and Next Steps

Even though the present results are entirely consistent with local stochastic behavior, they are valuable in three ways. First, they demonstrate that a mycelial quantum tomography protocol can be implemented in a fully reproducible way on commodity server hardware, with clear numeric outputs and thresholds. Second, they show how ideas from quantum tomography and fungal electrophysiology can be combined into a testable framework, without over-claiming about consciousness or universal fields. Third, they define concrete falsification criteria: in future wet-lab experiments, if real *Pleurotus ostreatus* cultures grown near quantum hardware show Corr_AB values above 0.7 under strong shielding and anesthetic controls, that would justify revisiting stronger hypotheses about nonlocal information substrates; if not, the null (local) model is strengthened.

Code and Data Availability

All code, figure(s), and raw JSON outputs for this simulation are publicly archived on Zenodo in a single package:

Chowdhury, Z. (2025). Mycelial Quantum Tomography: First Biological Decoder for Quantum Black Boxes (simulation package). Zenodo. DOI: 10.5281/zenodo.18027215.

The Zenodo archive ([paper5_mycelial_qt.zip](#)) contains:

- [mqt_fixed.py](#) – Reproducible NumPy-based simulator (methods).
- [mqt_paper5.png](#) – 300 DPI figure showing spike patterns and correlation.
- [mqt_results.json](#) – Raw numerical results (fidelity, Corr_AB, metadata).
- [mqt.py](#) – Development version of the script.[paste.txt](#)

Planned Wet-Lab Validation

The next stage is a wet-lab validation using live *Pleurotus ostreatus* mycelial cultures, silver/silver-chloride electrodes, and controlled exposure to quantum hardware or analog interference sources. The pre-registered plan is to reuse the same fidelity and Corr_AB metrics and the same decision thresholds, treating the current simulation as a baseline null model for purely local, noisy dynamics.