Evaluating Quantum Game Theory as a Modeling Approach for Alectinib-Fibroblast Non-Small Cell Lung Cancer Evolutionary Dynamics

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This project aims to better predict cancer dynamics to mitigate the effects of drug resistance. This research project uses a dataset from Kaznatcheev et al., who created an evolutionary game assay to study dynamics in non-small cell lung cancer cultures. They examined interactions between Alectinib-sensitive parental and resistant strains across four environments, varying the presence of the drug and cancer-associated fibroblasts. While classical Evolutionary Game Theory (EGT) models used today rely on a simple frequency-dependent replicator dynamics equation for each strain, this project proposes a Quantum Game Theory (QGT) framework to capture the complex interactions underlying tumor evolution. The methodology begins by extracting the baseline dataset to replicate the original classical predictions. First, I used a Quantum-Inspired Radial Basis Function Kernel to test whether quantum fitness function fits could map raw data more accurately than classical function fits. Two different classical fitness functions are tested: affine and polynomial. Using Leave-One-Out Cross-Validation confirmed that classical functions remained optimal for preventing overfitting, directing the project's focus toward quantum dynamics rather than quantum fitness estimation and fitting. Singular Value Decomposition is then used to preprocess the classical polynomial fitness functions, and these fitness functions are used in the Lindblad Master Equation for actual dynamic calculation. The most advanced QGT model implements a leaky integrator and consistently outperforms all EGT models by 10-20% with a p-value of 0.0016, showing statistical significance. Overall, the project creates a novel QGT approach that is more accurate than baseline EGT models for simulating cancer dynamics.

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Fourth Award of $600

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