Quantum Helix: DNA Maze Solved!!

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This study aims to develop novel mathematical approaches for cancer treatment, specifically targeted gene therapy for cancer stem cells (CSCs) within tumors. CSCs, or ancestral cells, are targeted due to their persistent connections with the resulting colonies in the early stages. Initially, nanoballs targeting CD44 receptors are introduced into tumors to identify regions enriched in CSCs. The cellular subpopulations are then classified into ancestral, non-ancestral, or special cases; such as HeLa using either a microfluidic chip system, or AI-based image analysis of cell lines. Following classification, ancestral cells undergo DNA extraction and whole-genome sequencing, using two algorithms: “Operation Formula” for rapid sequencing (O(1) time complexity) and “Circular Loop” for higher accuracy (O(n) time complexity); these techniques minimize DNA fragmentation. The genomes are then analyzed using a UDRL algorithm; a customized gene editing program. This program employs pattern recognition to identify pathogenic mutations. It uses a mathematical framework of inverse nucleic acid base substitution to assess the optimal resolution; either by truncating the pathogenic genomic variant, or inducing targeted nucleotide remodeling through base exchange. Subsequently, the modified gene is reintroduced into the tumor microenvironment. The AI model demonstrated a high efficiency with a 99% accuracy rate, after processing data from 40,000 visual and non-visual files. The microfluidic chip also exhibited high accuracy in classifying 10 different samples. Additionally, the treatment algorithm achieved a high efficiency in 112 samples with 100% accuracy. This facet of the research holds promise; especially in the context of early-stage tumors exhibiting optimal effectiveness.