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Background

- In traditional chemotherapy, large doses of drugs are applied for fixed lengths of time, having the side effect of cells developing drug resistance.
- Adaptive therapy is an effective alternative that treats for stability by adjusting drugs, doses, and timing to maintain competition between drug-resistant and drug-sensitive cells. However, the sheer number of regimens and the costs of clinical trials make it prohibitively expensive to try every adaptive therapy.
- **Research question:** In this project, the research team uses genetic algorithms and CancerSim, a 3D tumor simulator, to efficiently explore large spaces of adaptive therapies, identifying promising candidates for further study in clinical trials.

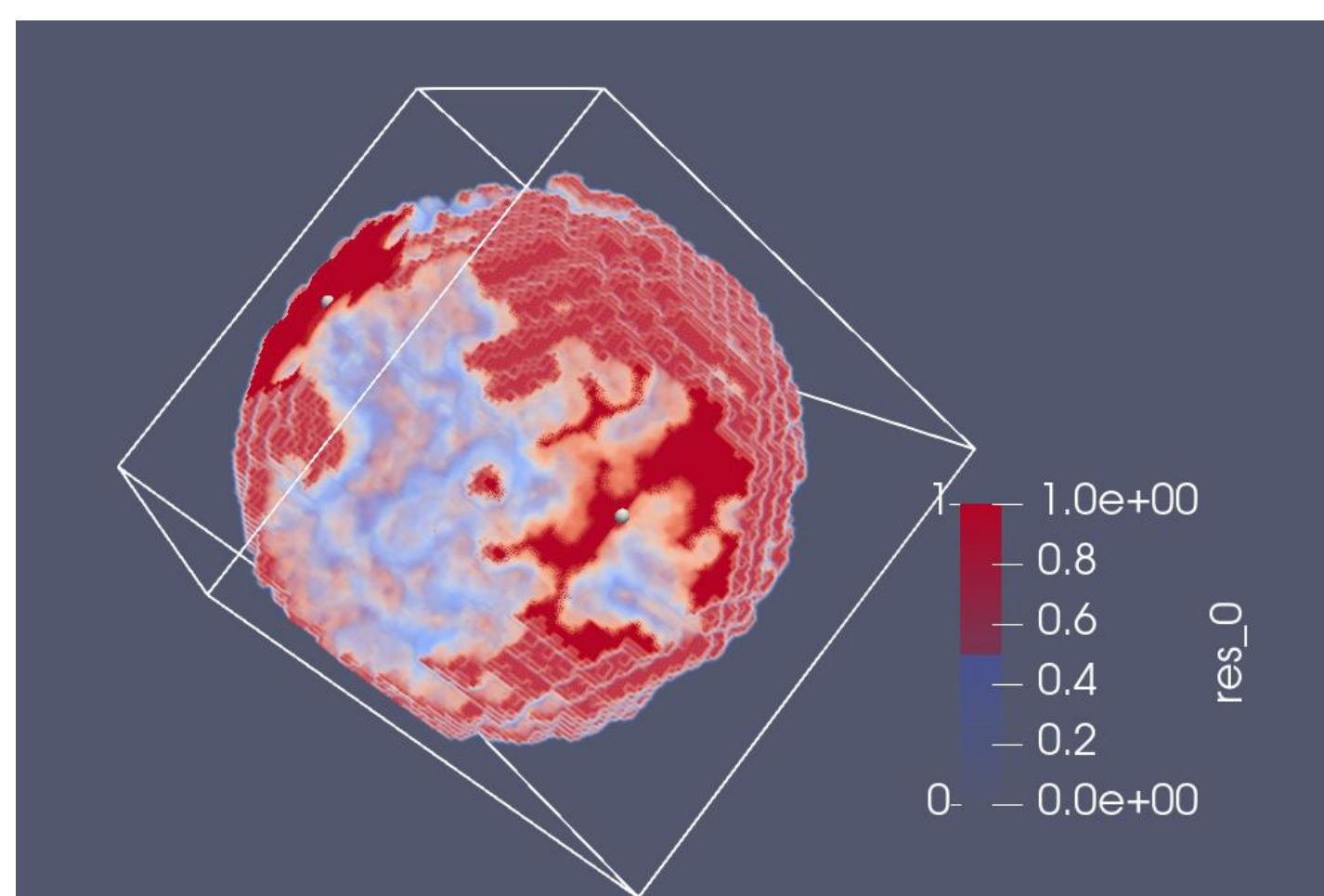


Figure (1): CancerSim modeling of a tumor including drug-resistant cells and drug-sensitive cells

Methods

Algorithm design:

- Genome representation of drug routines
- Genetic operators:
 - Initialization: random within constraints
 - Selection: tournament selection of three
 - Crossover: two-point crossover
 - Mutation: add/remove/update at finetuned probability
- Fitness evaluation: longest time until cell death

After initial algorithm design and setup, the GA is run against random fitness functions before plugging into CancerSim for comprehensive analysis. Quantitative methods were implemented to finetune code and parameters.

- Data collection from test runs
- Data analysis
- Literature review to identify relevant details such that implementations align with current cancer research

Results

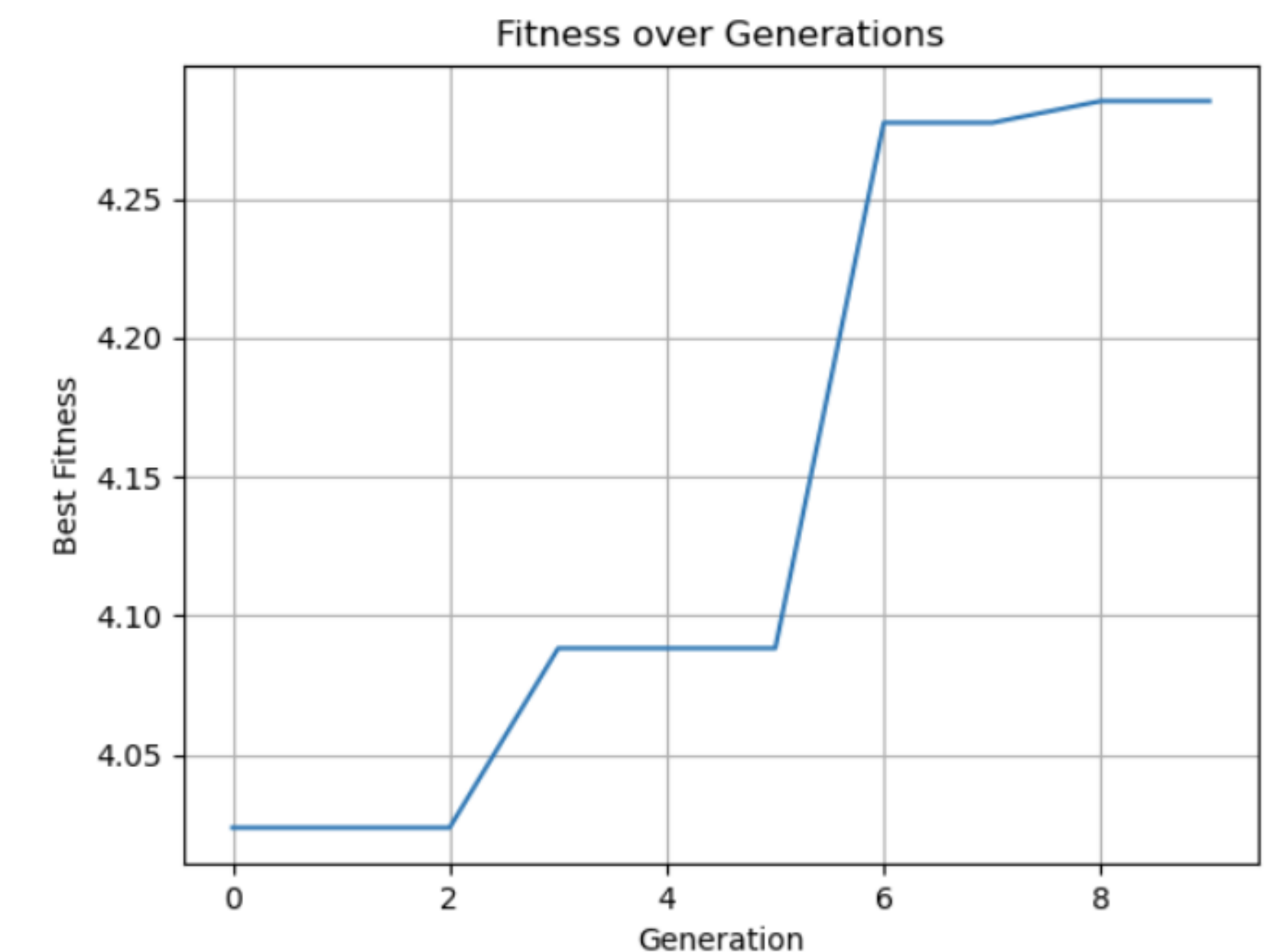


Figure (2): Implementation of GA and drug routines

Future Experimentation

- Implement parallelization for efficient execution on the lab workstations and ASU supercomputers.
- Run full-scale experiments. Further implement a more adaptive genome representation of drug routines.