Genetic algorithm for prediction of optimal nutrient combinations for cultivation of unknown bacteria

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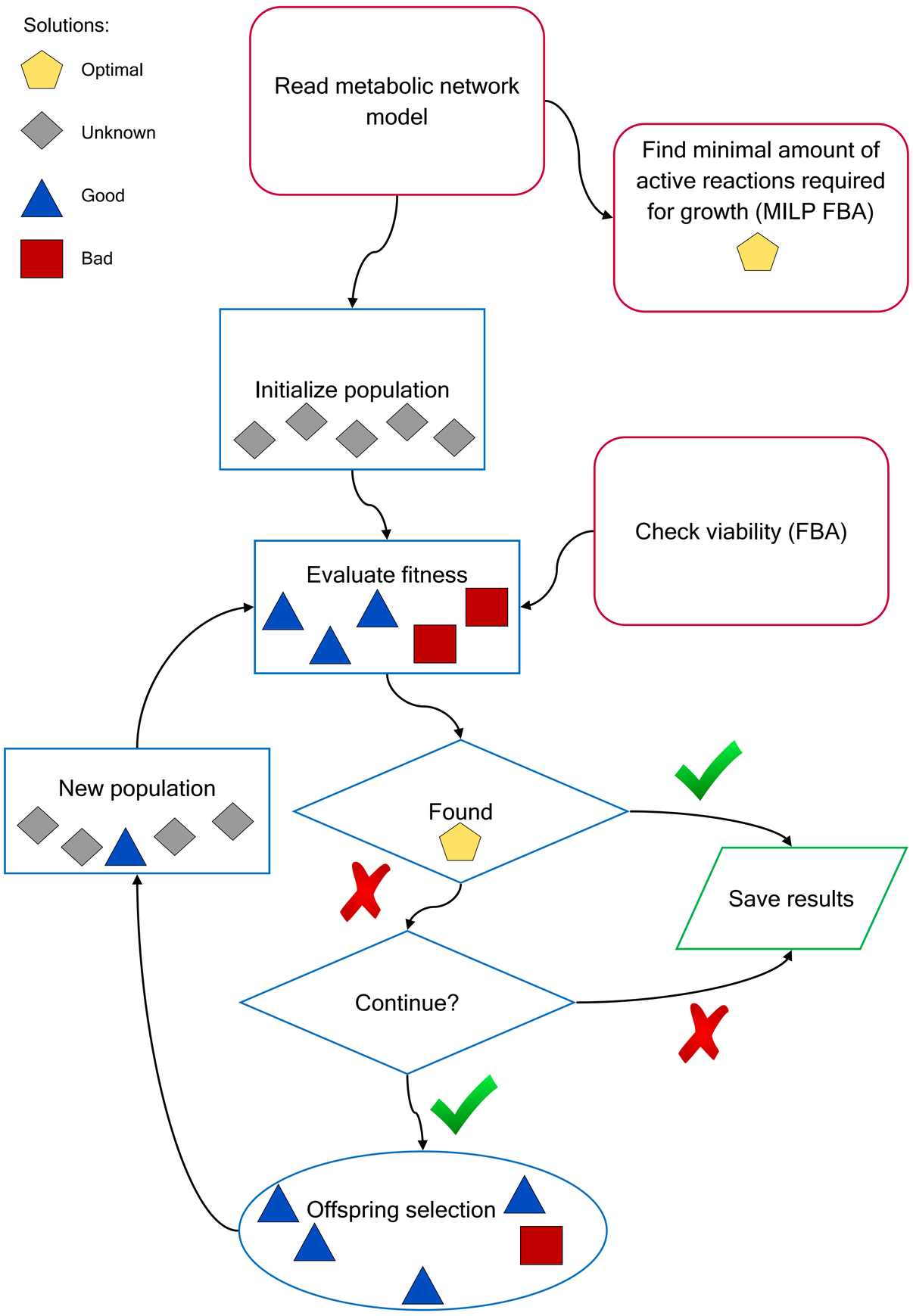
Introduction

One of the challenges when cultivating bacteria is choosing the best combination of nutrients in the growth medium. This challenge only becomes greater when the nutritional requirements of the bacteria to be cultivated are unknown. While many required nutrients and culture conditions can be inferred from the environment where the unknown bacterium is from, it would still require costly experimentation to find the best combination for cultivation.

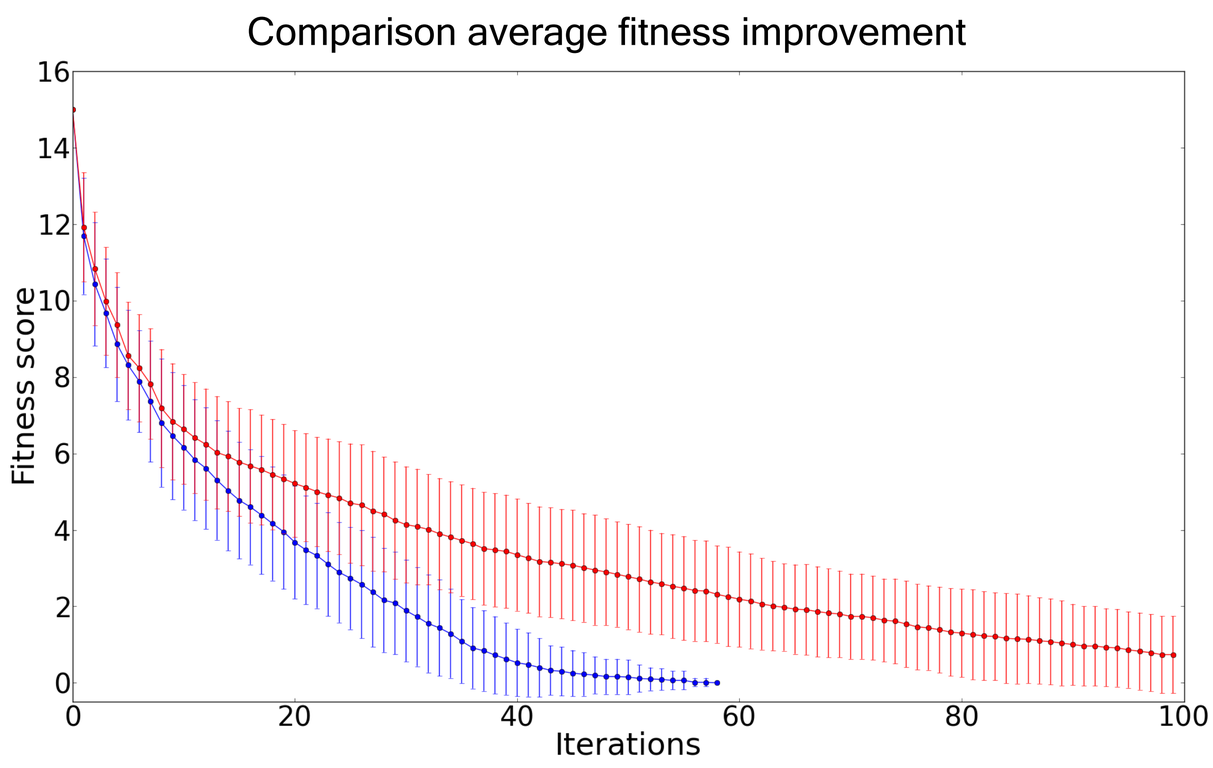
In order to minimize the cost of this experimentation we are developing a genetic algorithm (GA) approach to find a viable combination of as few nutrients and culture conditions as possible in as few experimental iterations as possible. The creation of this GA will be done *in silico* where flux balance analysis (FBA) will mimic a lab test. The final aim of the project is to develop a wet-lab protocol in which a good growth medium can be identified with a minimal number of lab tests.

Current workflow of the GA



Preliminary results

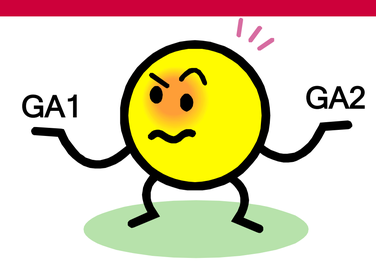
The metabolic network model used for FBA is a genome-scale model of *Escherichia coli* K-12 (iJR904 [1]). Fitness of a solution is the difference between the number of active reactions of the solution and the objective. Two GA's with differing mutation methods were run 80 times, the graph below shows the average and standard deviation of the results.



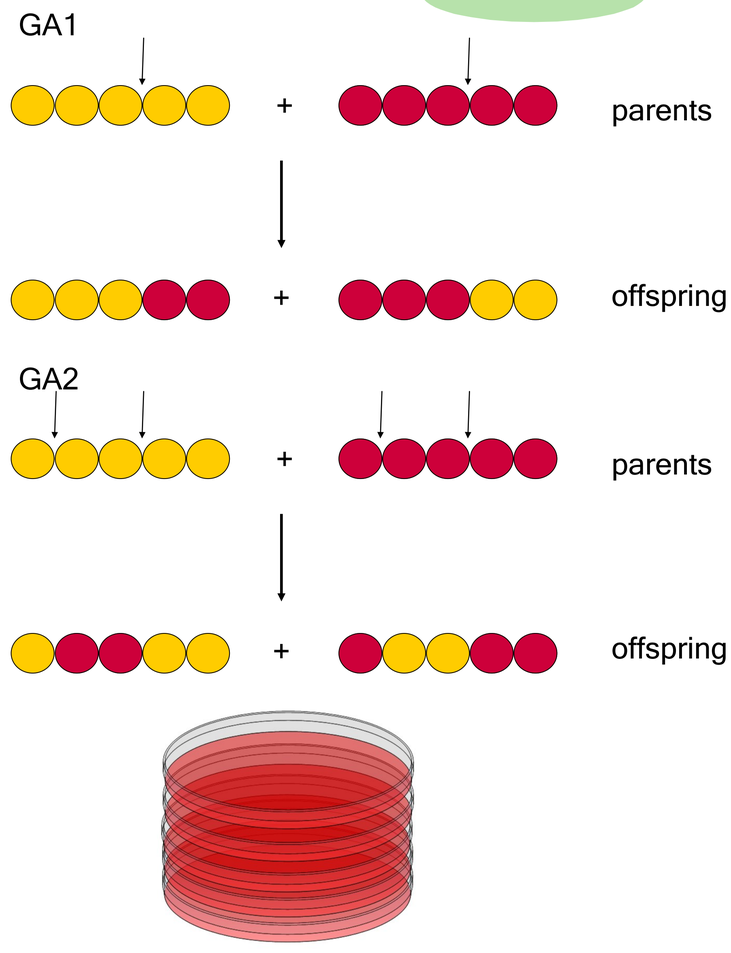
The GA with preferential mutation method (blue line) finds the objective faster than the GA with simple mutation method (red line). The faster method would require fewer experiments in the lab.

Next steps

Finding the methods for offspring selection, crossover and mutation that cause the GA to reach the objective the fastest will be done through experimentation and comparison.



Use of FBA with Molecular Crowding [2] might allow for better checking of viability of nutrient combinations and culture conditions.



It is expected that the final GA can be used in a wet lab to minimize the number of experiments required to find a suitable growth medium for cultivating

References

[1] Reed, J. L., et al. (2003). An expanded genome-scale model of *Escherichia coli* K-12 (iJR904 GSM/GPR). *Genome biology*, *4*(9), R54.

[2] Beg, Q., & Vazquez, A. (2007). Intracellular crowding defines the mode and sequence of substrate uptake by *Escherichia coli* and constrains its metabolic activity. *PNAS, 104*(31), 12663-12668.

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