Final Report Beatrice Bonato

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Evolution of Metabolic Networks

Contributions

In this project, I was primarily responsible for coming up with the main idea and programming the solution. I thought it would be beneficial to combine the major concepts we've covered in class, specifically genetic algorithms, Flux Balance Analysis (FBA), and stoichiometric matrices, into an interesting and meaningful project. Therefore, I mainly wrote the code and additionally prepared few slides about our work's results for the class presentation.

Take home messages

This project was a great learning experience. I was fascinated by how we could integrate different concepts from the course to address a complex scientific question. The most interesting question for me was whether it's possible to find an evolutionary pathway between two different organisms with distinct metabolites and reactions. This question is significant because understanding the transformation of organisms or bacteria over time could lead to interesting biological insights. We represented the organisms using their stoichiometric matrices, which not only added biological relevance but also helped us meet one of our project's objectives: to find a feasible evolutionary pathway at each step. To ensure the viability of these pathways, we calculated Flux Balance Analysis (FBA) at each generation step for every individual, discarding those with insufficient biomass growth. Choosing the best fitness function definition was an important part of the process. We experimented with two main definitions but in the end, we decided to use FBA as a threshold to eliminate individuals with insufficient growth, focusing on the similarity to the target for the fitness value. Both approaches tried allowed for convergence but with different behaviors over the generations.

Among the most interesting results was observing how slight changes in the mutation rate significantly affected the population's evolutionary behavior, with only a mutation rate of 0.001 allowing us to reach convergence. The heatmaps visualization was particularly useful since they showed the transitions in the population's reactions over generations. It was interesting to see a possible pattern in the order of appearance and disappearance of reactions while aiming for convergence. Running the evolution simulation many times and

analyzing the resulting heatmaps, suggested potential patterns in these transitions, which could be worth exploring in the future. This also relates to the result of the heatmap columns clustering, indicating that there may be a possible correlation among different reactions over time.

Overall, the most fascinating part of the course for me was learning about stoichiometric matrices and discovering how modifications to reactions can influence the flow of metabolites. In our project, we applied this concept to explore what happens when reactions are added or removed from an organism's metabolic network. This not only helped me understand how theoretical concepts are applied in practice, but also highlighted the dynamic and complex nature of biological systems.