Systems Biology & Neurobiology

Homework Report

Simon Chardin, Émile Sabatier, Samuel Diebolt

Teachers: Philippe Nghe, Andrew Griffiths

Abstract

Deep mutational scanning (DMS) makes use of large-scale mutagenesis to reveal intrinsic protein properties, functions and the consequences of genetic variation. Recently, the CRISPR/Cas9-mediated genomic error-prone editing (CREPE) technology was developed as a high-throughput method for mutating essential genes of *Escherichia coli* [1]. Its authors applied the technology to target *rpoB*, the gene encoding the β subunit of bacterial RNA polymerase, and used deep sequencing to study resistance against the antibiotic rifampicin. In particular, the authors studied epistastis effects by comparing fitness of double mutants in *rpoB* with those from the respective single mutations in the presence of rifampicin. In this report, we replicated the aforementioned epistasis study using a simplified dataset provided by A. Choudhury.

Motivations & Hypotheses

State of the Art

Methods & Results of the Supporting Article

Effects of Epistasis in Double Mutants

In this section, we replicated the analyses performed by the authors of the article supporting this report to better understand the impact of epistasis on rifampicin resistance. In particular, we were interested in comparing the fitness of double mutants, compared to the sum of fitness from the respective single mutations.

Next Steps

References

[1] A. Choudhury, J. A. Fenster, R. G. Fankhauser, J. L. Kaar, O. Tenaillon, and R. T. Gill, "Crispr/cas9 recombineering-mediated deep mutational scanning of essential genes in escherichia coli," *Molecular Systems Biology*, vol. 16, no. 3, p. e9265, 2020.