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From a micro-biology perspective, directed evolution is a technique that uses controlled environmental pressures to select for a desired phenotype. Directed evolution has the distinct advantage over rational design of not needing extensive knowledge of the genome or pathways associated with a microorganism to induce phenotypes. However, there are currently limitations to the applicability of this technique including being time-consuming, error-prone, and dependent on existing assays that may lack selectivity for the given phenotype. The AADEC (Autonomous Adaptive Directed Evolution Chamber) system is a proof-of-concept instrument to automate and improve the technique such that directed evolution can be used more effectively as a general bioengineering tool.

A series of tests using the automated system and comparable by-hand survival assay measurements have been carried out using UV-C radiation and Escherichia coli cultures in order to demonstrate the advantages of the AADEC versus traditional implementations of directed evolution such as random mutagenesis. AADEC uses UV-C exposure as both a source of environmental stress and mutagenesis, so in order to evaluate the UV-C tolerance obtained from the cultures, a manual UV-C exposure survival assay was developed alongside the device to compare the survival fractions at a fixed dosage. This survival assay involves exposing E.coli to UV-C radiation using a custom-designed exposure hood to control the flux and dose. Surviving cells are counted then transferred to the next iteration and so on for several iterations to calculate the survival fractions for each exposure iteration.

This survival assay primarily serves as a baseline for the AADEC device, allowing quantification of the differences between the AADEC system over the manual approach. The primary data of comparison is survival fractions; this is obtained by optical density and plate counts in the manual assay and by optical density growth curve fits pre- and post-exposure in the automated case. This data can then be compiled to calculate trends over the iterations to characterize increasing UV-C resistance of the E.coli strains. The observed trends are statistically indistinguishable through several iterations from both sources.

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