PREDICTING THE IMPACT OF ENVIRONMENTAL STRESSORS ON CELL POPULATION DYNAMICS

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Understanding how cell populations respond to environmental stressors—such as nutrient limitation, salt stress, heat shock, and UV exposure—is vital to both basic biology and applied fields like biotechnology and environmental health [1,2]. This project employs a structured Before–During–After workflow to link quantitative modeling and laboratory validation. Before experimentation, we mathematically extend classical population-growth equations—the Verhulst (logistic) and Gompertz models—to include an "environmental stress level" parameter that dynamically adjusts intrinsic growth rate (r) and carrying capacity (K) based on stress intensity. Implemented as ordinary differential equations in Python, these models are numerically solved to produce predicted growth curves, allowing us to identify critical timepoints and stress thresholds for sampling [4,5]. During the laboratory phase, *Escherichia coli* cultures are subjected to controlled gradients of NaCl (0–5 %), heat shock at 42 °C, and UV radiation at 254 nm. Optical density at 600 nm (OD_{600}) is recorded hourly for 12 hours, generating high-resolution growth datasets that capture the onset, exponential, and stationary phases under each stress condition. After data collection, we perform nonlinear regression to fit both the standard and stress-augmented models to the observed OD_{600} curves. Sensitivity analyses quantify how each stress parameter influences r and K, while model selection metrics (R^2, AIC/BIC) and Bayes factors assess predictive accuracy and parsimony [6]. Residual analysis highlights systematic deviations, directly testing our hypothesis that environmental stressors induce parameter-specific, quantitatively predictable shifts in population dynamics. This integrative approach—combining mathematical theory, computational simulation, and empirical assays—advances mechanistic understanding of stress-driven population dynamics with quantitative biology approach.

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