

Study looks beyond averages to track variability in a bacterial population

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As a result of the variable nature of gene expression, genetically identical cells inhabiting the same environment can vary significantly in their numbers of key enzymes, which in turn results in strikingly different cellular behaviors. This cell-to-cell variability can manifest in the form of anything from differences in growth rate, to the specific biochemical pathways used and the types of metabolic byproducts produced by each cell.

Incorporating data from studies of gene regulation and protein distributions in single cells, the research group of University of Illinois chemistry professor Zaida Luthey-Schulten was able to identify several behavioral subtypes within a modeled population. The researchers' computer model predicts emissions of metabolic byproducts and pathway selection to balance energy (glycolysis pathway) and protein costs (ED pathway) as a function of growth. The research also suggests that tracking the behavior of a few genes "may be sufficient to capture most of the metabolic variability of the entire population," the authors wrote.

"Our investigations provide the first calculations linking variation in specific pathway usages to the growth rate distribution of a microbial population," Luthey-Schulten said. "By looking beyond the average growth rate of a colony, our work provides insight into the different strategies used by bacteria for survival. "

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The paper, "Heterogeneity in protein expression induces metabolic variability in a modeled *Escherichia coli* population," is available to the media from the [University of Illinois News Bureau](#).

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