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Title of Poster Presentation: Modeling Bacterial Conjugation

Abstract:

Bacterial conjugation, part of three types of horizontal gene transfer, occurs via an extra-chromosomal DNA molecule called a plasmid through direct cellular contact between a donor and a recipient. Ecologically, the spread of genetic information by engineered microorganisms (GEM), as well as the transfer and distribution of natural plasmids has generated interest in mathematically modeling conjugation. Mathematical modeling of microbial populations not only serves to reflect a general pattern, but also quantifies through its constants, a system's characteristics. Thus, by continuously improving and/or modifying the models used to parallel observed conjugation data, we ameliorate the methods for accounting attributions to conjugation. The data used here fit an alternated use of a simple modified mass action model and an additive Fermi-logistic equation. We use a differential form of the logistic or Verhulst equation, to model conjugation accounting for both the growth and decay of populations. We used nonlinear regressions to find parameters, such as growth and decay rates. We expect to improve upon the previous models of the data used by providing one equation as opposed to the two above to determine the conjugation rate constant.