

Abstract Submitted  
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**A Computational Approach to Competitive Range Expansions**

MARKUS F. WEBER, GABRIELE POXLEITNER, ELKE HEBISCH, ERWIN FREY, MADELEINE OPITZ, Ludwig-Maximilians-Universität München — Bacterial communities represent complex and dynamic ecological systems. Environmental conditions and microbial interactions determine whether a bacterial strain survives an expansion to new territory. In our work, we studied competitive range expansions in a model system of three *Escherichia coli* strains. In this system, a colicin producing strain competed with a colicin resistant, and with a colicin sensitive strain for new territory. Genetic engineering allowed us to tune the strains' growth rates and to study their expansion in distinct ecological scenarios (with either cyclic or hierarchical dominance). The control over growth rates also enabled us to construct and to validate a predictive computational model of the bacterial dynamics. The model rested on an agent-based, coarse-grained description of the expansion process and we conducted independent experiments on the growth of single-strain colonies for its parametrization. Furthermore, the model considered the long-range nature of the toxin interaction between strains. The integration of experimental analysis with computational modeling made it possible to quantify how the level of biodiversity depends on the interplay between bacterial growth rates, the initial composition of the inoculum, and the toxin range.

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