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*Challenges in the modeling of antibiotic effects on gut flora*

The experimental study of gut microbiota often uses laboratory reactors that mimic the ecological conditions in the large intestine. Such reactors can be described by large chemostat-like models. We review one such model that is based on the International Water Association's Anaerobic Digestion Model No. 1, and we extend it to account for the side effect of bacteriostatic antibiotics on gut processes. We present some first results and point out modelling challenges due to the mathematical and microbial complexity that are unique to this setting vis-a-vis more traditional chemostat model applications.