

# Generation and robustness of Boolean networks to model *Clostridium difficile* infection

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One of the more common healthcare associated infection is Chronic diarrhea. This disease is caused by the bacterium *Clostridium difficile* which alters the normal composition of the human gut flora. The most successful therapy against this infection is the fecal microbial transplant (FMT). They displace *C. difficile* and contribute to gut microbiome resilience, stability and prevent further episodes of diarrhea. The microorganisms in the FMT their interactions and inner dynamics reshape the gut microbiome to a healthy state. Even though microbial interactions play a key role in the development of the disease, currently, little is known about their dynamics and properties. In this context, a Boolean network model for *C. difficile* infection (CDI) describing one set of possible interactions was recently presented. To further explore the space of possible microbial interactions, we propose the construction of a neutral space conformed by a set of models that diff