

A new tool for forecasting the behavior of the microbiome

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A team of investigators from Brigham and Women's Hospital and the University of Massachusetts have developed a suite of computer algorithms that can accurately predict the behavior of the microbiome - the vast collection of microbes living on and inside the human body. In a paper published in *Genome Biology*, the authors show how their algorithms can be applied to develop new treatments for serious diarrheal infections, including *Clostridium difficile*, and inflammatory bowel disease. The team also shows how to identify bacteria most crucial for a healthy and stable microbial community, which could inform the development of probiotics and other therapies.

The open source software package the researchers have designed, known as Microbial Dynamical Systems INference Engine (MDSINE), uses advanced machine learning technologies to accurately predict how microbial communities in the gut will grow and interact over time. The team validated MDSINE using extensive computational simulations, and also applied the software to infection experiments to evaluate the dynamics of *C. difficile*, a bacterial species that is the most common cause of infection in the hospital and can cause serious illness and even death in patients. The team also analyzed the effects of a "probiotic cocktail" of various bacterial strains that is being developed to treat inflammatory diseases, predicting the contributions of each member of the cocktail to maintain the stability of the bacterial community when diet was altered.

"Every person has their own bacterial ecosystem living within them.

There's a lot of exciting new evidence that giving patients bacteriotherapies, or cocktails of bacteria, may be effective in treating or preventing a variety of major diseases including infections, arthritis, [inflammatory bowel disease](#), and cancer. MDSINE is the first tool we've developed under the new BWH Precision Medicine Initiative, and we're releasing it as open source software in that hope that it will help to advance the bacteriotherapy field," said senior author Georg Gerber, MD, PhD, MPH, Assistant Professor in Computational Pathology at BWH and Co-Director of the Massachusetts Host-Microbiome Center at BWH.

"Advanced computational methods like MDSINE are essential for understanding how to design and evaluate bacteriotherapies or 'bugs as drugs,' and to tailor them to individual patients since everyone's [microbiome](#) is different. Our results have given us insights into new bacteriotherapies for *C. difficile* infection and inflammatory bowel disease, and moreover suggest general strategies for developing these therapies for many other diseases," said Vanni Bucci, PhD, first author of the study and an assistant professor at the University of Massachusetts at Dartmouth.

More information: Vanni Bucci et al, MDSINE: Microbial Dynamical Systems INference Engine for microbiome time-series analyses, *Genome Biology* (2016). [DOI: 10.1186/s13059-016-0980-6](https://doi.org/10.1186/s13059-016-0980-6)

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