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Designing healthy diets with computer analysis

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A new mathematical model for the interaction of bacteria in the gut could help design new probiotics and specially tailored diets to prevent diseases. The research, from Chalmers University of Technology in Sweden, was recently published in the journal *PNAS*.

"Intestinal bacteria have an important role to play in health and the development of diseases, and our new mathematical model could be extremely helpful in these areas," says Jens Nielsen, professor of systems biology at Chalmers, who led the research.

The new paper describes how the mathematical model performed when making predictions relating to two earlier clinical studies, one involving Swedish infants, and the other adults in Finland with obesity.

The studies involved regular measurements of health indicators, which the researchers compared with the predictions made from their mathematical model—the model proved to be highly accurate in predicting multiple variables, including how a switch from liquid to solid food in the Swedish infants affected their intestinal bacterial composition.

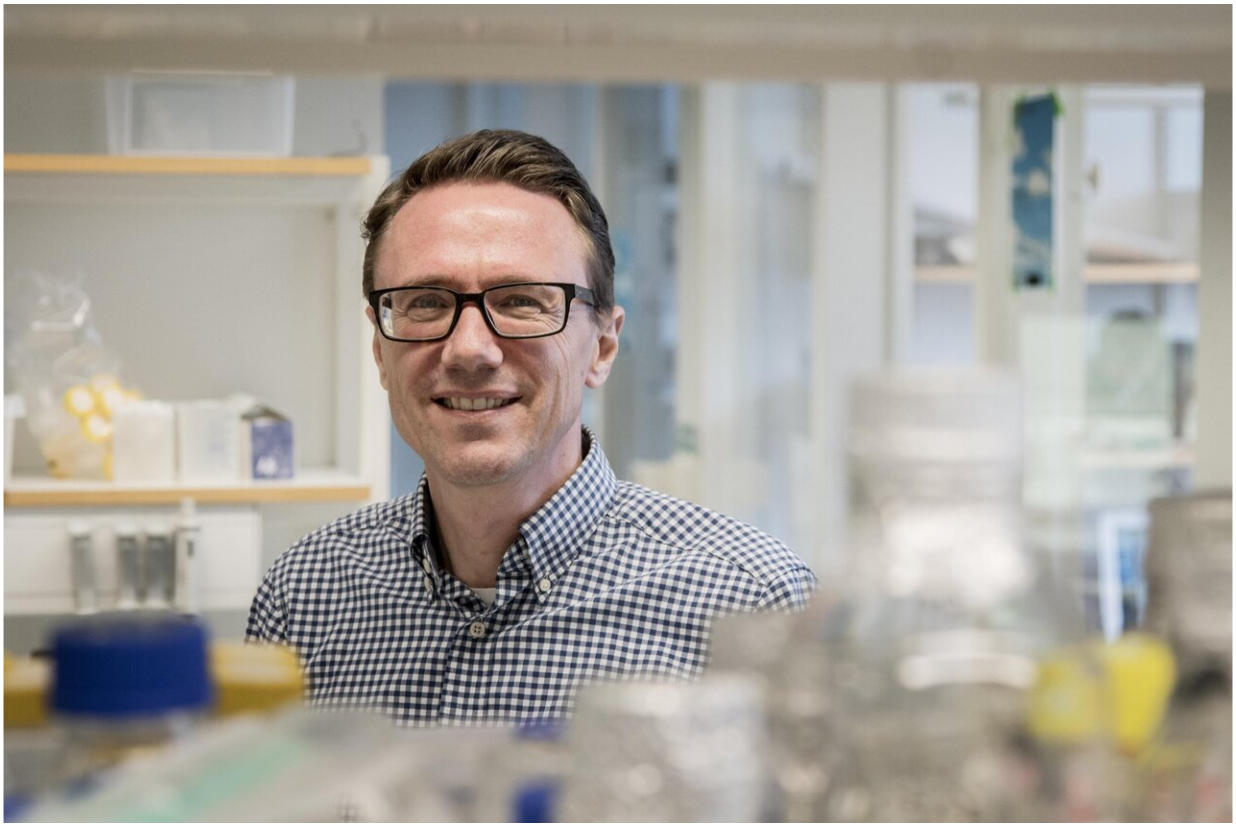
They also measured how the obese adults' intestinal bacteria changed after a move to a more restricted diet. Again, the model's predictions proved to be reliably accurate.

"These are very encouraging results, which could enable computer-based design for a very complex system. Our model could therefore be used to for creating personalized healthy diets, with the possibility to predict how adding specific bacteria as novel probiotics could impact a patient's health," says Jens Nielsen.

Many factors at play

There are many different things that affect how different bacteria grow and function in the intestinal system. For example, which other bacteria are already present and how they interact with each other, as well as how they interact with the host—that is to say, us. The bacteria are also further affected by their environmental factors, such as the diet we eat.

All of these variables make predicting the effect that adding bacteria or making dietary changes will have. One must first understand how these bacteria are likely to act when they enter the intestine or how a change in diet will affect the intestinal composition. Will they be able to grow there or not? How will they interact with and possibly affect the bacteria that are already present in the gut? How do different diets affect the intestinal microbiome?



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"The model we have developed is unique because it accounts for all these variables. It combines data on the individual bacteria as well as how they interact. It also includes data on how food travels through the gastrointestinal tract and affects the bacteria along the way in its calculations. The latter can be measured by examining blood samples and looking at metabolites, the end products that are formed when bacteria break down different types of food," says Jens Nielsen.

The data to build the model has been gathered from many years' worth of pre-existing clinical studies. As more data is obtained in the future, the model can be updated with new features, such as descriptions of hormonal responses to dietary intake.

A potential huge asset for future healthcare

Research on diet and the human microbiome, or intestinal bacterial composition, is a field of research that generates great interest, among both researchers and the general public. Jens Nielsen explains why:

"Changes in the bacterial composition can be associated with or signify a great number of ailments, such as obesity, diabetes, or cardiovascular diseases. It can also affect how the body responds to certain types of cancer treatments or specially developed diets."

Working with the bacterial composition therefore offers the potential to influence the course of diseases and overall health. This can be done through treatment with probiotics—carefully selected bacteria that are believed to contribute to improved health.

In future work, Jens Nielsen and his research group will use the model directly in clinical studies. They are already participating in a study together with Sahlgrenska University Hospital in Sweden, where older women are being treated for osteoporosis with the bacteria *Lactobacillus* *reuteri*. It has been seen that some patients respond better to treatment than others, and the new model could be used as part of the analysis to understand why this is so.

Cancer treatment with antibodies is another area where the model could be used to analyze the microbiome, helping to understand its role in why some patients respond well to immunotherapy, and some less so.

"This would be an incredible asset if our model can begin to identify bacteria that could improve the treatment of cancer patients. We believe it could really make a big difference here," says Jens Nielsen.

More information: Jun Geng et al, CODY enables quantitatively spatiotemporal predictions on in vivo gut microbial variability induced by diet intervention, *Proceedings of the National Academy of Sciences* (2021). DOI: 10.1073/pnas.2019336118

Provided by Chalmers University of Technology

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