

New application of classic algorithm uniquely identifies individuals based on their bacterial 'companions'

May 11 2015



Image credit: Wikimedia.

A new study shows that the microbial communities we carry in and on our bodies—known as the human microbiome—have the potential to uniquely identify individuals, much like a fingerprint.

Harvard T.H. Chan School of Public Health researchers and colleagues demonstrated that personal microbiomes contain enough distinguishing features to identify an individual over time from among a research study population of hundreds of people. The study, the first to rigorously show

that identifying people from microbiome data is feasible, suggests that we have surprisingly unique microbial inhabitants, but could raise potential privacy concerns for subjects enrolled in [human](#) microbiome research projects.

The study appears online May 11, 2015 in the journal *PNAS*.

"Linking a human DNA sample to a database of human DNA 'fingerprints' is the basis for forensic genetics, which is now a decades-old field. We've shown that the same sort of linking is possible using DNA sequences from microbes inhabiting the human body—no human DNA required. This opens the door to connecting [human microbiome](#) samples between databases, which has the potential to expose sensitive subject information—for example, a sexually-transmitted infection, detectable from the microbiome sample itself," said lead author Eric Franzosa, research fellow in the Department of Biostatistics at Harvard Chan.

Franzosa and colleagues used publicly available microbiome data produced through the Human Microbiome Project (HMP), which surveyed microbes in the stool, saliva, skin, and other body sites from up to 242 individuals over a months-long period. The authors adapted a classical computer science algorithm to combine stable and distinguishing sequence features from individuals' initial microbiome samples into individual-specific "codes." They then compared the codes to microbiome samples collected from the same individuals' at follow-up visits and to samples from independent groups of individuals.

The results showed that the codes were unique among hundreds of individuals, and that a large fraction of individuals' microbial "fingerprints" remained stable over a one-year sampling period. The codes constructed from gut samples were particularly stable, with more than 80% of [individuals](#) identifiable up to a year after the sampling

period.

"Although the potential for any data privacy concerns from purely microbial DNA is very low, it's important for researchers to know that such issues are theoretically possible," said senior author Curtis Huttenhower, associate professor of computational biology and bioinformatics at Harvard Chan. "Perhaps even more exciting are the implications of the study for microbial ecology, since it suggests our unique microbial residents are tuned to the environment of our body—our genetics, diet, and developmental history—in such a way that they stick with us and help to fend off less-friendly microbial invaders over time."

More information: Identifying personal microbiomes using metagenomic codes, *PNAS*,

www.pnas.org/cgi/doi/10.1073/pnas.1423854112

Provided by Harvard School of Public Health

Citation: New application of classic algorithm uniquely identifies individuals based on their bacterial 'companions' (2015, May 11) retrieved 19 May 2024 from

<https://phys.org/news/2015-05-application-classic-algorithm-uniquely-individuals.html>

This document is subject to copyright. Apart from any fair dealing for the purpose of private study or research, no part may be reproduced without the written permission. The content is provided for information purposes only.