Re-purposing software for functional characterization of the microbiome

Laura-Jayne Gardiner

Niina Haiminen

Filippo Utro

Laxmi Parida

Ed Seabolt

Ritesh Krishna

James H. Kaufman

Video Byte

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Abstract

Solving problems doesn't always require an entirely new fix – or new software. A team at IBM recently demonstrated that repurposed software offers improved functional characterization of microbiomes at a fraction of the development time. Currently, microbial functional profiling is typically done by classifying sequencing reads taxonomically, followed by computationally demanding functional analysis. But in a clever twist, researchers opted instead to directly compare sequencing reads to a functionally annotated database. The group developed a tree-shaped functional hierarchy and repurposed taxonomic bioinformatics tools to do the functional annotation. The method was applied to soil samples taken across the globe. This revealed, for example, that antioxidant activity was much higher in polar regions compared with equatorial areas. Next, the team plans to use the technique on other biological samples to further probe the secret lives of microbes. The scientists also suggest developers should repurpose software more often when tackling other problems, especially when this can improve a computationally inefficient task.