Researchers develop tool to rapidly determine phylogenetic makeup of large microbial communities

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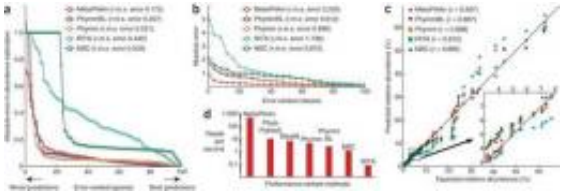

Comparison of MetaPhlAn to existing methods. Image: *Nature Methods* (2012) doi:10.1038/nmeth.2066 . For more details, please see the original publication.

(Phys.org) -- A team of researchers has developed a new tool that can be used to profile the metagenome of large microbial communities such as those that live in the human gut. Using the new tool, researchers can discover in mere hours what used to take months for a supercomputer to calculate, perhaps leading to new discoveries about the mysteries leading to such ailments as Crohn's Disease and diabetes.

The new tool, called MetaPhiAn (metagenomic phylogenetic analysis), is already being used to begin building a profile of the myriad of bacteria that live in the human gut. The tool, the team explains, in their paper published in the journal *Nature Methods*, essentially gives the medical community, for the first time, a means to truly understand what bacteria are present in the gut, which hopefully, will lead to studies that describe what each does and what its role is in human health.

The human gut, as most know, has a lot of bacteria in it, mostly the good kind. Different bacteria do different things of course and researchers are just now starting to understand what a few of them do and how they contribute to our overall health. Being able to identify all of them though would go a long way towards providing researchers with a much better picture of what is going on inside of us, which is exactly what MetaPhiAn is promising to do.

There is a downside of course, despite reducing the time it takes to identify different bacteria in the gut, researchers still have to contend with a really huge number of them; scientists estimate that there are ten times as many bacteria in us than there are our own cells. And identifying them is just the first step. Each must then be studied to see what it does and hopefully, work out whether it's good for us, or harmful. Fortunately, it's not as hit and miss as it sounds, researchers do have some idea of which types of bacteria they'd like to look at first, and they already know some of the kinds that cause us problems. What's most problematic are the bacteria that are normally good for most people, but cause problems in a select few. Figuring out what is going in these cases might boil down to seeing which other bacteria are involved, and that's where the speed of MetaPhiAn might really help.

More information: Metagenomic microbial community profiling using unique clade-specific marker genes, *Nature Methods* (2012) doi:10.1038/nmeth.2066

Abstract

Metagenomic shotgun sequencing data can identify microbes populating a microbial community and their proportions, but existing taxonomic profiling methods are inefficient for increasingly large data sets. We present an approach that uses clade-specific marker genes to unambiguously assign reads to microbial clades more accurately and >50× faster than current approaches. We validated our metagenomic phylogenetic analysis tool, MetaPhlAn, on terabases of short reads and provide the largest metagenomic profiling to date of

the human gut. It can be accessed at huttenhower.sph.harvard.edu/metaphlan/