

Researchers team up with Illumina to speed-read your microbiome

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A screenshot of QIIME available in Illumina's BaseSpace app store. Credit: Illumina

The human microbiome—the total collection of bacteria, viruses and other microorganisms living in and on your body—has been linked to a variety of health and disease states, including obesity, allergies, asthma, and a rapidly growing list of other conditions. But as researchers try to sort out the complex relationship between microbial populations and human health and use that information to diagnose or treat disease, they are generating a deluge of microbial sequence data that first needs to be organized and analyzed.

To this end, University of California, San Diego School of Medicine's Rob Knight, PhD , and his team built a microbiome analysis platform called QIIME (pronounced "chime" and short for "Quantitative Insights Into Microbial Ecology"). This software will now be more readily

accessible to hundreds of thousands of researchers around the world through BaseSpace , a cloud-based app store offered by Illumina, a San Diego-based company that develops life science tools for the analysis of genetic variation.

"Previously, we relied on personal contacts and scientific publications to spread the word about QIIME, and then users needed to download several different software packages to their own computers. Users also needed some technical programming skills to use QIIME," said Knight, professor of pediatrics and computer science and engineering. "By working with Illumina, not only will many more researchers now be able to access QIIME from the cloud, the BaseSpace interface will make it much easier for non-technical researchers to analyze their data. This advancement will significantly ease the bottleneck in a variety of human and environmental microbiome studies."

Two high-profile microbiome studies that rely on QIIME are the Human Microbiome Project, a National Institutes of Health-led initiative akin to the Human Genome Project, and the [American Gut Project](#), a crowdsourced, crowdfunded project in which Knight's team is sequencing as many human microbiome samples as possible, from anyone who wants to participate.

"QIIME has proven to be a widely successful open-source project—the original paper our group published on it in 2010 has been cited by more than three thousand other papers since," said Yoshiki Vázquez-Baeza, an incoming UC San Diego Computer Science and Engineering graduate student in Knight's lab. "This collaboration, among many other things, will help us expand our user base and increase the availability of our methods." Like Knight and more than 25 other members of his lab, Vázquez-Baeza relocated from Colorado to UC San Diego this year, in part because of the collaborative spirit and innovative resources found in San Diego's life sciences research and biotechnology community.

"BaseSpace is a cloud solution for data repository and analysis options that help streamline the processing of the seemingly ubiquitous genomic and metagenomic sequence data that researchers generate every day," said Jay Patel, associate product manager of BaseSpace applications at Illumina. "QIIME is a highly utilized tool in metagenomics research and we are excited to make it part of the Illumina ecosystem."

Researchers are already eager to use QIIME in their own studies, including many at UC San Diego.

"We look forward to using QIIME on BaseSpace for our upcoming deep dive into the differences in the human gut microbiome in healthy people compared to people with inflammatory bowel disease," said Larry Smarr, PhD, professor and founding director of the California Institute for Telecommunications and Information Technology (Calit2) at UC San Diego.

Here's how Knight, Smarr and their teams plan to apply QIIME to determine if certain microbes are associated with [inflammatory bowel disease](#) (IBD). They will process fecal samples from a group of IBD patients and a control group of healthy people and send the microbial genetic material they collect to the UC San Diego School of Medicine's Institute for Genomic Medicine for sequencing. When complete, the researchers will receive an email from the facility director indicating that their data are available on BaseSpace. Once they log into BaseSpace and click on the QIIME app, the researchers will see their raw data and ask the program to generate a 3-D scatterplot of the differences and similarities between their IBD and healthy control samples. If there is a significant difference in the [microbial populations](#) present in the two groups, then the researchers will go back to the lab to further investigate those differences and what cause-or-effect roles they might play in IBD.

Eventually, Knight, Smarr and team hope they will be able to use this

information to develop new tests that predict a person's risk of developing IBD and new methods for treating the disease.

According to leading genomic and metagenomic assembly expert Pavel Pevzner, PhD, the Ronald R. Taylor Professor of Computer Science at UC San Diego and Howard Hughes Medical Institute, the addition of QIIME to BaseSpace adds to a growing collaboration between UC San Diego and Illumina on computational tools.

"Our own software—SPAdes Genome Assembler—has been available in the Illumina BaseSpace app store for some time, and has helped thousands of users assemble their genome data in a range of medical and scientific applications," said Pevzner, who also directs the NIH Center for Computational Mass Spectrometry. "Adding QIIME to the expanding toolbox of world-leading bioinformatics software for genomic and metagenomic analysis paves the way for future innovations and collaborations with Illumina in this space."

Provided by University of California - San Diego

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