Novel Insights into Microbial and Viral Complexity

Fully characterize complete microbial genomes and populations affordably with SMRT® Sequencing, simultaneously detailing base modifications and mobile elements, quantifying low-level variants and achieving strain-level resolution within communities.

Complete Microbial Characterization in a Single Experiment

“We can now do it [investigate plasmid transfer] in the context of fully sequenced genomes because we now know every plasmid and what it carries. We’re now doing a study that I think is fully informed.”

- Julie Segre, NHGRI

Investigate Viral Population Dynamics

- De-convolute complex mixtures of unique haplotypes
- Track evolution and phylogeny of viral populations
- Identify and quantify minor variants

“To understand within-host viral evolution, long high-quality sequences are absolutely necessary. PacBio is the only NGS technology that hits the sweet spot for length, accuracy and depth.”

- Ben Murrell, UCSD CFAR

Long-read sequencing can resolve complete plasmids in order to track the dissemination of antimicrobial-resistance genes among pathogenic bacteria.

HIV env sequences expand and diversify throughout infection.
Detailed Examination of Microbial Communities

“SMRT Sequencing is a single molecule technique that can generate long reads (10-15 kb), is highly accurate and can distinguish methylated bases from the normal A,C,G,T. This latter property is unique as no other method can do that for N6-methyladenine or N4-methylcytosine without additional chemistry being involved.”

- Rich Roberts, New England Biolabs

- Discover novel genes with longer reads and contigs
- Identify and assign functions to community members with better genome assemblies
- Leverage epigenomic data to cluster contigs, including those from closely related strains

Full-length 16S

Whole-Genome Shotgun

Species-level resolution of soil sample

Key References