LoopSeq: Ultra-accurate microbial amplicon sequencing

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Abstract

Amplicon sequencing has made the business of identifying bacteria directly from environmental samples routine work, but there's much room for improvement. Long-read sequencing technologies have helped cover the information gaps that plague short-read sequencing, but obtaining accurate results from complex metagenomes remains a challenge. A new study reports how LoopSeq can help boost microbial detection accuracy. Building on previous synthetic long-read (SLR) technologies, LoopSeq uses barcode-based molecular counting to construct accurate long reads from short-read sequences. Experiments confirmed that LoopSeq produces long reads with low error rates. In fact, LoopSeq produced more error-free reads of different lengths compared with other commercially available long-read technologies, and in a real-world test of six samples of US retail meat. LoopSeq could differentiate between strains within species of bacteria identified by the CDC as potential foodborne pathogens. While synthetic long reads still tend to be more expensive than short reads on a per-read basis, LoopSeq's ability to generate accurate microbiome reads from short-read sequencers is expected to accelerate the advancement of microbial genomics.