Metagenomic Vs 16s Dna Sequencing for Identifying Bacterial Populations

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Next Generation Sequencing (NGS) technology has launched immense growth of DNA sequence databases, paving the way to better categorize the genetic diversity of the biosphere. Bioinformaticians curate and analyze this massive amount of DNA sequence data for applications that range from science and medicine to forensics and commercial ancestry services. The DNA sequences provided by NGS can be analyzed to profile bacterial communities within environmental niches. Experimental approaches for assessing these communities vary widely between labs. Our goal was to compare two common methods to test for cohesion between these approaches' results. We obtained DNA sequences from both metagenomic ("shotgun") and bacterial 16S gene sequencing for five DNA samples (two soil and three human microbiome). We developed a custom software pipeline in conjunction with the program BLAST, processed hundreds of thousands of DNA sequence reads produced by each sequencing method (metagenomic or 16S) and, for each sample, compared the two resulting bacterial profiles. For all five samples, community taxonomic profiles produced from the two methods were distinctly different. Explanations for these disparities may include sampling bias in databases or the reliability of the 16S gene as a species identifier. These results highlight the importance of establishing a common methodology to accurately infer bacterial communities from DNA sequence data.