Comparison & Analysis of Local Environmental Metagenomics and Diversity Sequencing Data Sets

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Metagenomics is the rapidly advancing field that studies genetic material extracted directly from environmental samples. Recent advances in computational and sequencing methodologies now give an array of options to biologists who seek to analyze their samples; however, these new technologies are often run independently with little comparison of the results obtained between methods on the same sample. Prior to this study, field work by local biology instructors in conjunction with the labs of Drs. Marisa Pedulla and Alysia Cox made use of two such techniques to analyze the DNA of a locally-obtained soil sample. One

technique, "shotgun," or metagenomic sequencing, sequenced all of the DNA molecules in the sample; the second technique, "diversity" sequencing, only sequenced the molecules amplified from a single gene, the 16S ribosomal subunit rRNA gene, of the prokaryotic DNA in the sample. Because the 16S gene is highly recognizable and species-specific, the latter method also provided a count of the occurrences of each prokaryotic species. Due to this feature, the use of the 16S diversity sequencing approach is commonly utilized for studies aiming to understand prokaryotic species representation in samples. When metagenomics DNA sequences are known, represented species and their number of occurrences in a sample may also be derived computationally by comparison to procured databases of known sequences of organisms. This exploratory study compared the commercially obtained results of bacteria proportions in our sample by the diversity method, along with two experimental computational methods using these sequences compared to the public databases. Our hypothesis was that metagenomics data would provide the most accurate portrayal of bacteria in the sample at the phylum taxon. Results found significant disparities in results between each method, with implications in microbiome studies of the environment and human gut.