

## Data Analysis for Taxonomy Prediction and Annotation of 16S rRNA Gene Sequences from Metagenome Data

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**Abstract :** Skin metagenomics has a wide range of applications with direct relevance to the health of the organism. It gives us insight to the diverse community of microorganisms (the microbiome) harbored on the skin. In the recent years, it has become increasingly apparent that the interaction between skin microbiome and the human body plays a prominent role in immune system development, cancer development, disease pathology, and many other biological implications. Next Generation Sequencing has led to faster and better understanding of environmental organisms and their mutual interactions. This project is studying the human skin microbiome of different individuals having varied skin conditions. Bacterial 16S rRNA data of skin microbiome is downloaded from SRA toolkit provided by NCBI to perform metagenomics analysis. Twelve samples are selected with two controls, and 3 different categories, i.e., sex (male/female), skin type (moist/intermittently moist/sebaceous) and occlusion (occluded/intermittently occluded/exposed). Quality of the data is increased using Cutadapt, and its analysis is done using FastQC. USearch, a tool used to analyze an NGS data, provides a suitable platform to obtain taxonomy classification and abundance of bacteria from the metagenome data. The statistical tool used for analyzing the USearch result is METAGENassist. The results revealed that the top three abundant organisms found were: Prevotella, Corynebacterium, and Anaerococcus. Prevotella is known to be an infectious bacterium found on wound, tooth cavity, etc. Corynebacterium and Anaerococcus are opportunist bacteria responsible for skin odor. This result infers that Prevotella thrives easily in sebaceous skin conditions. Therefore it is better to undergo intermittently occluded treatment such as applying ointments, creams, etc. to treat wound for sebaceous skin type. Exposing the wound should be avoided as it leads to an increase in Prevotella abundance. Moist skin type individuals can opt for occluded or intermittently occluded treatment as they have shown to decrease the abundance of bacteria during treatment.

**Keywords :** bacterial 16S rRNA , next generation sequencing, skin metagenomics, skin microbiome, taxonomy

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