A pan genome catalog of the human respiratory tract microbiome

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A dysbiotic airway microbiome is associated with various disorders of the human respiratory system, including chronic obstructive pulmonary disease (COPD) and chronic rhinosinusitis. The nature and dynamics of the airway microbiome are still not fully understood. This information is crucial for addressing the disease causality and potential mechanisms of disease progression with microbial dysbiosis.

To tackle this knowledge gap, we want to assemble a pan-genome catalog of microorganisms associated with the human respiratory tract. We can elucidate the complex microbial genomic inventory within an ecosystem with whole genome metagenomic sequencing. In particular, the reconstruction of metagenome-assembled genomes (MAGs) from these samples can provide species- and strain-specific insights into the functional and pathogenic potential of the human microbiome.

Therefore, we retrieved public metagenomic datasets from data archives like NCBI-SRA to perform a MAG de novo assembly, to compile a representative set of genomes specific to the human respiratory system. This catalog will be supplemented with the microbial genomes retrieved in-house after sequencing clinical samples and isolates.

We present some summary statistics from the public metagenomic datasets downloaded and analyzed, and some preliminary insights into the diversity of respiratory microbiome; after an initial screening of human lung explants with 16S rRNA gene amplicon sequencing. We get an initial estimate for the number of bacterial taxa and contaminant taxa present in the lung sample.

The final catalog of microbial genomes will enable us to leverage the whole gene content information for a multitude of purposes, including improved taxonomic classification, functional capacity prediction, or metabolic modeling of dysbiosis in the human respiratory system.