

FunOMIC: Pipeline with built-in Fungal Taxonomic and Functional Databases for Human Mycobiome Profiling

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While analysis of the bacterial microbiome has become routine, that of the fungal microbiome is still hampered by the lack of robust databases and bioinformatic pipelines. Here, we present FunOMIC, a pipeline with built-in taxonomic (1.6 million marker genes) and functional (3.4 million non-redundant fungal proteins) databases for the identification of fungi. Applied to more than 2,600 human metagenomic samples, the tool revealed fungal species associated with geography, body sites, and diseases. Correlation analysis provided new insights into inter-kingdom interactions. With this pipeline and two of the most comprehensive fungal databases, we foresee a fast-growing resource for mycobiome studies.