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Abstract

This tutorial focuses on performing a comprehensive metagenomic analysis from whole-genome shotgun sequencing data for microbiome studies. It is divided into different steps that use the following metagenomic, computational tools: [MetaPhiAn](#), [GraPhiAn](#), [LEfSe](#), and [HUMAN](#). Our last addition to the PhiAn tools is [PhyloPhiAn](#) that can be used in metagenomics for phylogenetically and taxonomically place contigs assembled from whole metagenomic sequencing samples. This tutorial is also a step-by-step description of the metagenomic pipeline we used in our review paper about [computational meta'omics](#) (specifically [Figure 4](#)).

Files

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Protocol



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MetaPhlAn profiling of 20 HMP samples

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MetaPhlAn output merge and visualization

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GraPhlAn visualization of single and multiple samples

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Taxonomic biomarker discovery with LEfSe

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Metabolic profiling with HUMAnN

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