

# bioBakery Protocols

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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: [MetaPhlAn](#), [GraPhlAn](#), [LEfSe](#), and [HUMAnN](#). Our last addition to the PhlAn tools is [PhyloPhlAn](#) 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](#)).

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## Collection

### PROTOCOLS

#### 1. [MetaPhlAn profiling of 20 HMP samples](#)

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#### 2. [MetaPhlAn output merge and visualization](#)

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#### 3. [GraPhlAn visualization of single and multiple samples](#)

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#### 4. [Taxonomic biomarker discovery with LEfSe](#)

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#### 5. [Metabolic profiling with HUMAnN](#)

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