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## bioBakery Protocols

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Curtis Huttenhower

VERVE Net

Huttenhower Lab



Bahar Sayoldin

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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 in to 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 phylgenetically 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

### Protocol

NAME

**MetaPhlAn profiling of 20 HMP samples**

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### Protocol

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**MetaPhlAn output merge and visualization**

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### Protocol

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**GraPhlAn visualization of single and multiple samples**

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### Protocol

NAME

**Taxonomic biomarker discovery with LEfSe**

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## Protocol

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Metabolic profiling with HUMAnN

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