From the **pacmill** project

Written by consultants at www.sinclair.bio

Hosted at www.github.com/xapple/pacmill

Auto-generated taxonomy report

August 26, 2020

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1 Taxonomy report

1.1 General Information

This taxonomic classification report is based on the "silva" method. It is part of the project named "demo_project" which is described as "Demo project for the pacmill pipeline".

1.2 Processing

- This report and all the analysis was generated using the pacmill python pipeline.

- Documentation and source code is available at:

https://github.com/xapple/pacmill

- Version 0.3.3 of the pipeline was used.

- This document was generated at 2020-08-26 04:06:47 CEST+0200 on host bigmille.

1.3 Taxonomic classification

Relying on databases of ribosomal genes, we can attempt to classify each OTU and give it an approximative affiliation. This pairs OTU to predicted taxonomic names where possible. This is done using the "Mothur Version 1.42.1" method and "The Silva v138 database (mothur version)".

Out of our 6'164 OTUs some remain totally unclassified while others have predictions at different positions in the tree of life. The proportion of classified OTUs is summarized below:

Table 1. Classification summary for OTUs.

#	Rank	Classified	Unclassified
1	**Domain**	5677	487
2	**Phylum**	4213	1951
3	**Class**	3605	2559
4	**Order**	1992	4172
5	**Family**	1692	4472
6	**Genus**	1288	4876
7	**Species**	0	6164

1.4 Composition

We are now able to produce a bar-chart detailing the composition in terms of taxonomy of every one of our samples. Once again, this can be done at several ranks of classification ranging from *Domain*, down to *Species*. At levels that are too deep, such visualization become too crowded and unreadable. This of course depends on the complexity of the samples. Here are plotted different taxonomic levels in the following figures.
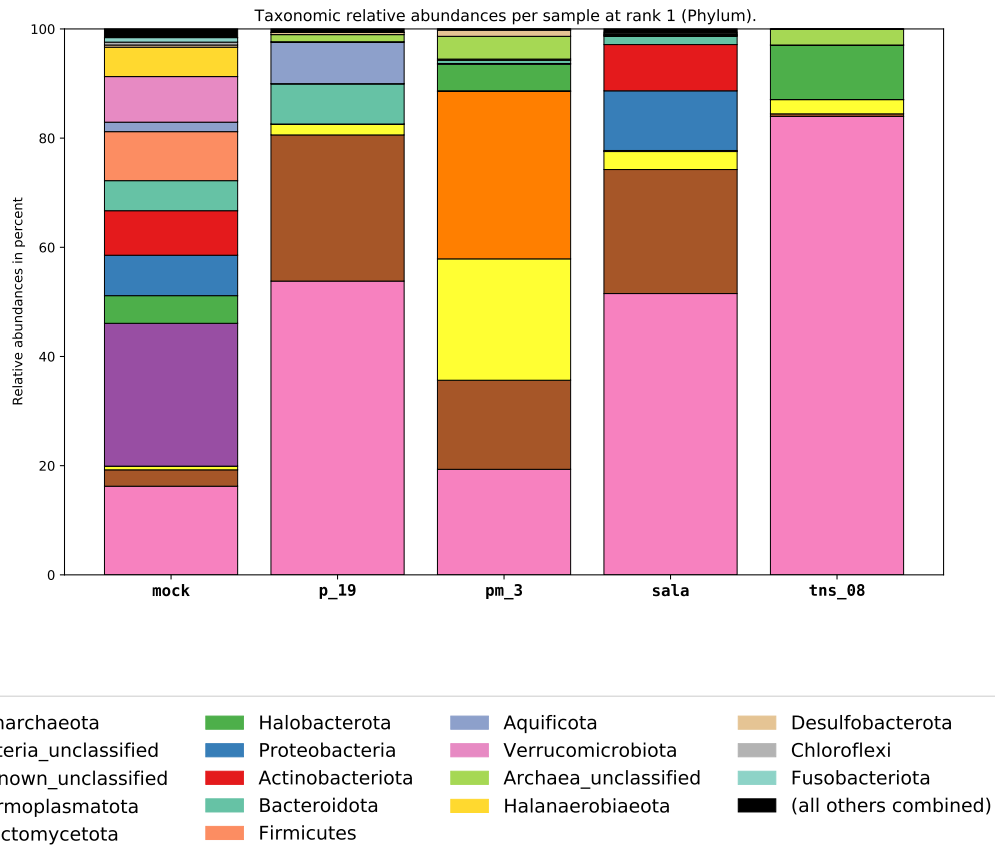
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Figure 1. Relative abundances per sample on the 'Phylum' level

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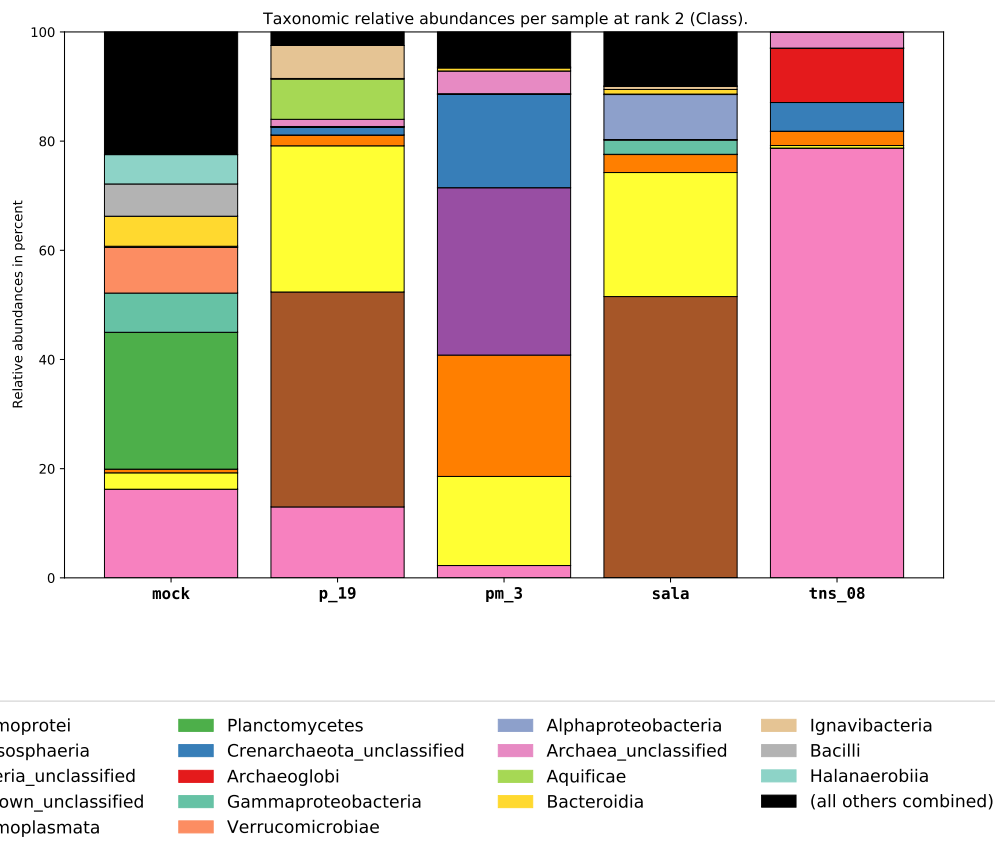
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Figure 2. Relative abundances per sample on the 'Class' level