

# Comparative analysis of taxonomies for metagenomics analyses

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May 16, 2016

The basis of metagenomic reaserch is assigning sequenced reads to certain taxonomic units. This is mostly done using one of the four taxonomies NCBI, RDP, SILVA or Greengenes and a classifier based either on read alignments or k-mer spectra. The outcome of this crucial step depends on the chosen taxonomy as well as on the tool.

We present a visual comparison of the four taxonomies and contrast the specificity of different tools used in 16s RNA analysis (with different taxonomies). Differences are presented in a very concise visual way exploiting the nice hierarchical structure of taxonomic classifications.