

Abstract

Software and pipelines for taxonomic assignment in metagenomics

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The classification of next generation sequencing reads from a metagenomic sample using a reference taxonomy is usually based on first mapping the reads to the reference sequences and then, classifying each read at a node under the lowest common ancestor of the candidate sequences in the reference taxonomy with the least classification error. In this lecture, we will discuss potential biases of this approach, current software implementing taxonomic annotation, and their integration in some of the most widely used pipelines for metagenomic analysis.