

## **Genomics**

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**Diskussion am X. Dezember 2013**

1. We are interested in the abundances of certain species in a metagenomic experiment. Give reasons why it is not sufficient to only count reads that have matches against reference sequences and why it is not sufficient to concentrate on reads with unique hits.
2. Outline a possible approach to estimate the relative abundance of species contained in the sample assuming that the genomes of the species are all given and possibly very similar.