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Metagenomics : beyond the horizon of current implementations and methods

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Stellingen behorend bij het proefschrift getiteld

“Metagenomics: Beyond the horizon of current implementations and methods”

1. The widely held opinion that 16S data is sufficient for the analysis of metagenomic samples is outdated; good practices for the analysis of microbial communities should recommend the Whole Genome Sequencing data type, especially when correct inhabitant abundances are required (Chapters 1 and 2).
2. Reference-free approaches open the way to a more accurate and unbiased determination of the complexity of microbial communities (Chapter 3).
3. *k*-mer-based reference-free approaches may be used for a wide range of applications, such as forensic DNA fingerprinting, due to its sensitivity to temporal changes in skin microbiomes (Chapter 4).
4. The pathogenicity of a clinical sample can (and probably should) be determined using Whole Genome Sequencing data approaches (Chapter 5).
5. Since the percentage of “dark matter” in metagenomic data remains significantly high, the area of reference-free approaches for the analysis of microbial communities should be expanded.
6. The concept of metagenome as being one genomic entity should be widely accepted.
7. A simple taxonomic determination of microbiome inhabitants might not be adequate, especially when analyzing clinical samples as two similar metagenomic communities might carry functionally different alleles.
8. Microbial communities “personalize” the inhabited environment and thus metagenomics analysis should be a routine procedure prior to treatments that change that environment.
9. A fair balance is vital to any healthy living community.
10. Many data scientists believe that “If you torture data long enough, it will confess to anything” (Ronald Coase, early 1960s). However, if you tackle data from all angles the truth will always come out.