The subsequent development of next generation sequencing technologies has led metagenomics studies to become a powerful tool for the analysis of microbial communities from various environments. To date, high-throughput sequencing of PCR-amplified conserved genes such as 16S rRNA gene remains the most accessible and widely used approach to describe bacterial organisms in a community. Nevertheless, these approaches generate huge amount of data that needs to be processed for the extraction of relevant information. Although several tools are now available, their use and configuration remains complicated to implement and require knowledge in bioinformatics and computer science. To make these analytical tools available to all, we developed a fully automatic tool implemented with a user-friendly web interface.

We will focus on the improvements to the steps of reads preprocessing that are necessary for the management of MiSeq 2×300bp sequencing data.

**APPLICATIONS**

Metabiote Online and its high-quality assembly and preprocessing steps was developed to monitor complex microbial communities based on their taxonomic profiling. Metabiote Online was initially developed on 16S rDNA gene (A) but it could be used to survey as well prokaryotic and eucaryotic microbial communities based on 18S rDNA gene (B) and Nuclear ribosomal internal transcribed spacer ITS (C) within complex environments.

**CONCLUSION**

Metabiote Online:

- Computation of high-throughput sequencing datas
- Taxonomic affiliation of full length and high-quality dataset for 454 and Illumina sequencing technologies
- Fully automated analysis and available on a web interface for 16S rDNA sequences
- Implementation on various taxonomic biomarkers and dedicated database
- Suitable for microbial taxonomic profiling within complex environments

*Contact:* Frédéric Texier frederic.texier@genoscreen.fr