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## Use of flow cytometry and DNA sequencing as a proxy for characterising microbial communities during managed aquifer recharge

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Biological communities present in the subsurface are essentially involved in processes influencing the water quality. Characterising the temporal and spatial dynamics of microbial communities is key to understand processes in place and their influence on water quality – particularly when used for drinking water production. Due to limitations in automation of sampling and detection of conventional, cultivation-based microbial methods, a fully automatic flow cytometer (FCM) was employed in combination with sampling for DNA sequencing at a water works in Berlin, where drinking water is derived from groundwater recharged via infiltration basins. The DNA sequencing enables a complete "meta genomic" analysis and taxonomic profiling including bacterial, archaea, viral, eukaryotic DNA and the identification of antibiotic resistance genes. The FCM determines the total number of bacterial cells in a water sample (total cell count, TCC), the number of cells that have lost membrane integrity (defect cell count, DCC) and allows statements about the ratio of low nucleic acid content to cells with high nucleic acid content (LNA/HNA). In this study, FCM was installed in a continuously flowing sampling line measuring surface water (basin water) and groundwater (observation and abstraction well) along a flow path for high-frequency microbial monitoring. The combination of automatic FCM with DNA sequencing aims at i) optimizing monitoring strategies, and ii) developing a (quantitative) microbial risk assessment for managed aquifer recharge systems.