

DNA fingerprinting in surface- and wastewater management

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Background

In surface- and wastewater management it is important to determine the origin of the water and of the potentially problematic substances/organisms it might contain. These are faecal contamination, nutrient-related questions, or malfunctioning wastewater treatment plants (WWTPs). This research examines the possible contribution of the DNA fingerprinting technique High Throughput Sequencing (HTS) in clarifying such questions.



Challenges

Questions related to various water types were tried to be answered with HTS:

1. Is WWTP effluent discharge into surface water traceable? And if so, how far from the source?
2. Is the influence of sewer overflow into surface water, and are the different origins of the overflow, traceable?
3. Is leakage of WWTP effluent into groundwater traceable?
4. Is the origin of surface water that flows into other surface water traceable?

These questions resulted in six research cases with Dutch water boards. One case is given as an example.

Results and discussion

- With HTS, we were able to distinguish sewage and WWTP effluent microbiomes (Figure 1).
- These microbiomes show characteristic OTUs for sewage and WWTP effluent (Figure 2).
- These microbiomes are sources that influence the microbial community on receiving waters. In our example case (Figure 3), the influence of these sources was traceable on the different sample locations and quantified using Source Tracker (Knight et al., 2011) (Figure 4).

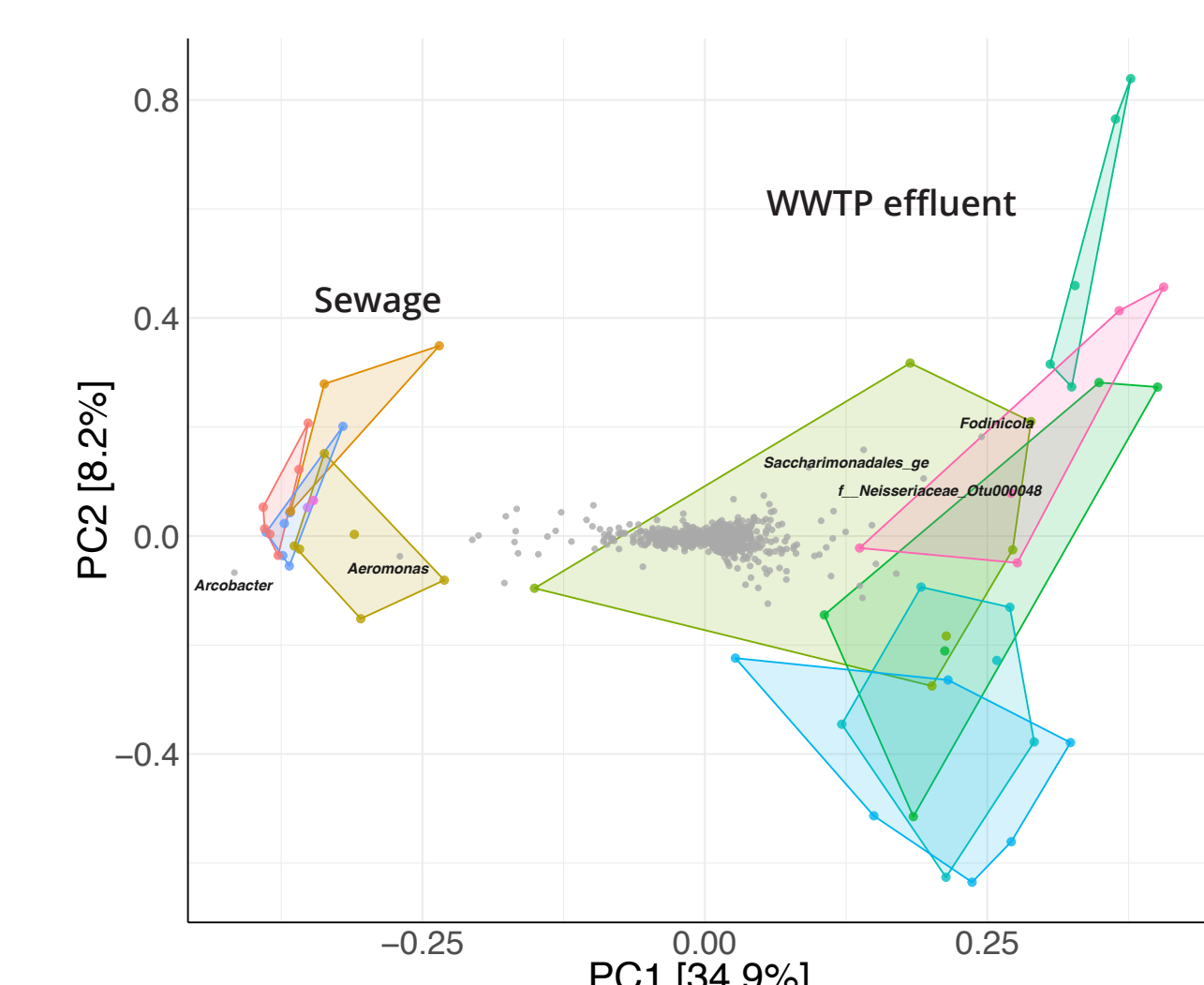


Figure 1: Principal Component Analysis of HTS data of all sewage and WWTP effluent samples from different sampling dates and different locations.

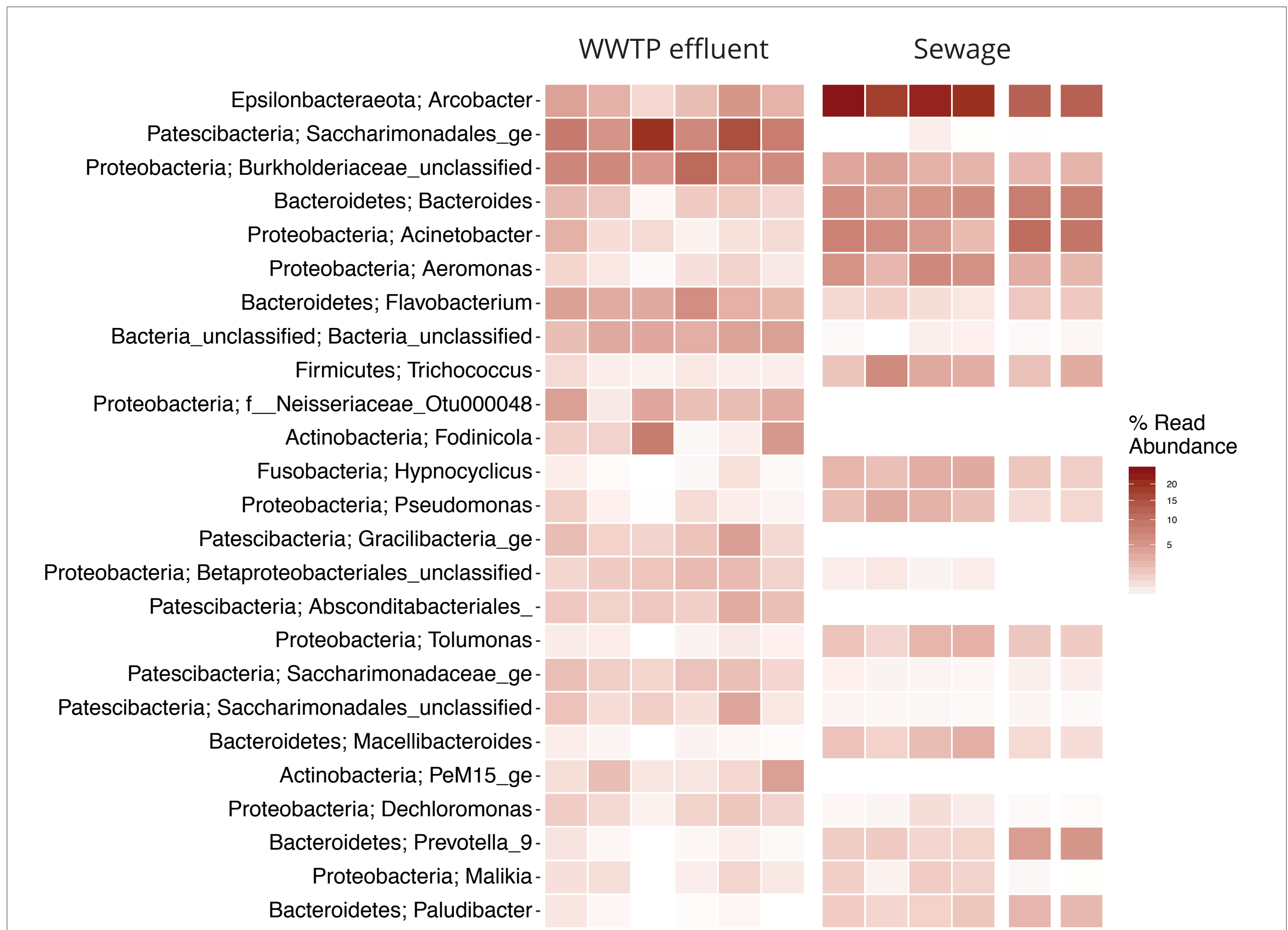


Figure 2: Heatmap of HTS data of all WWTPs effluent and sewage samples. Shown are the average relative abundances (%) of the top 25 most abundant OTUs with a minimum abundance of 0.1% in all samples per location. OTUs were classified at the genus level.

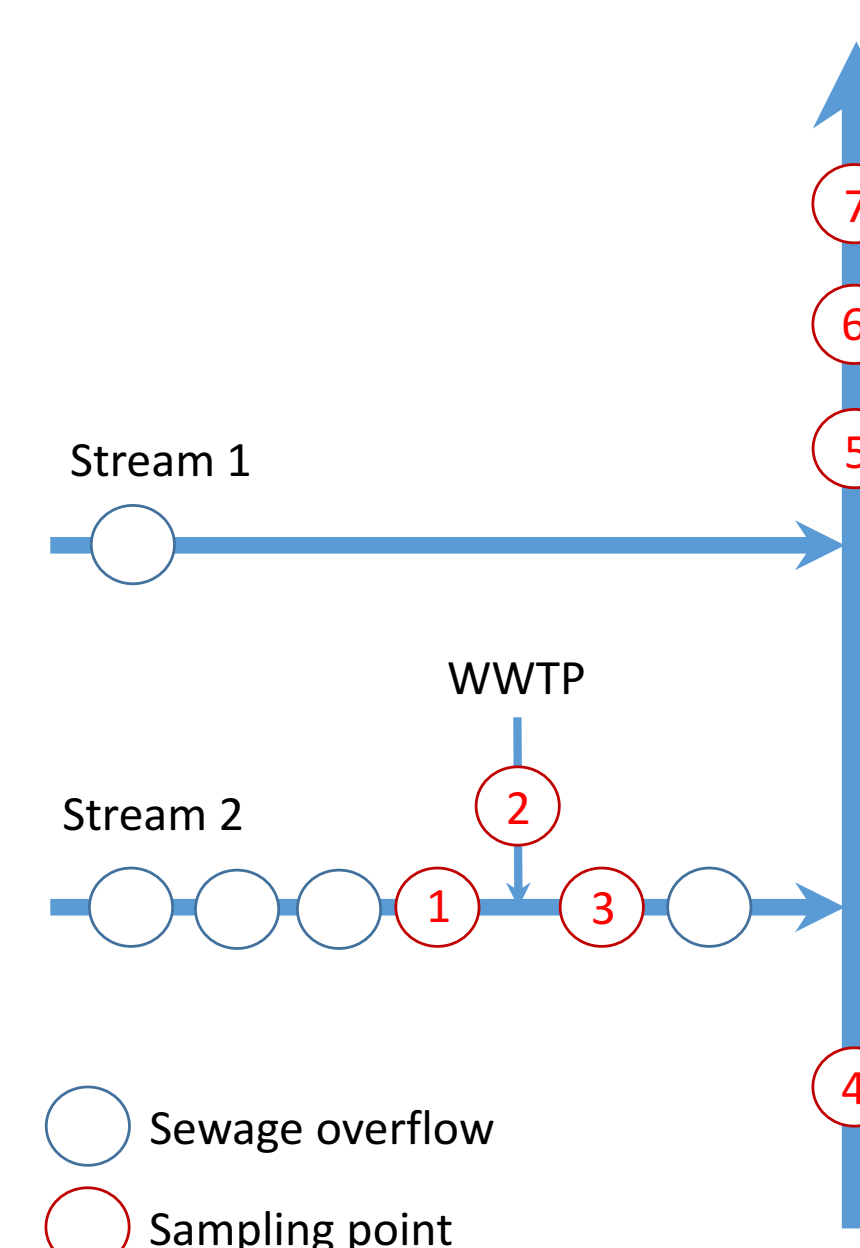


Figure 3: Schematic representation of an example where we applied HTS as a tool to track changes in surface waters. Stream 2 receives sewage overflow water and WWTP effluent discharge. It is expected that the water of stream 2 shows a different microbial profile before (sampling point 1) than after WWTP discharge (sampling point 3). This effect should also be measurable in stream 3, where we compared the microbial profile before (sampling point 4) and after (sampling points 5, 6 and 7) inflow of stream 2.

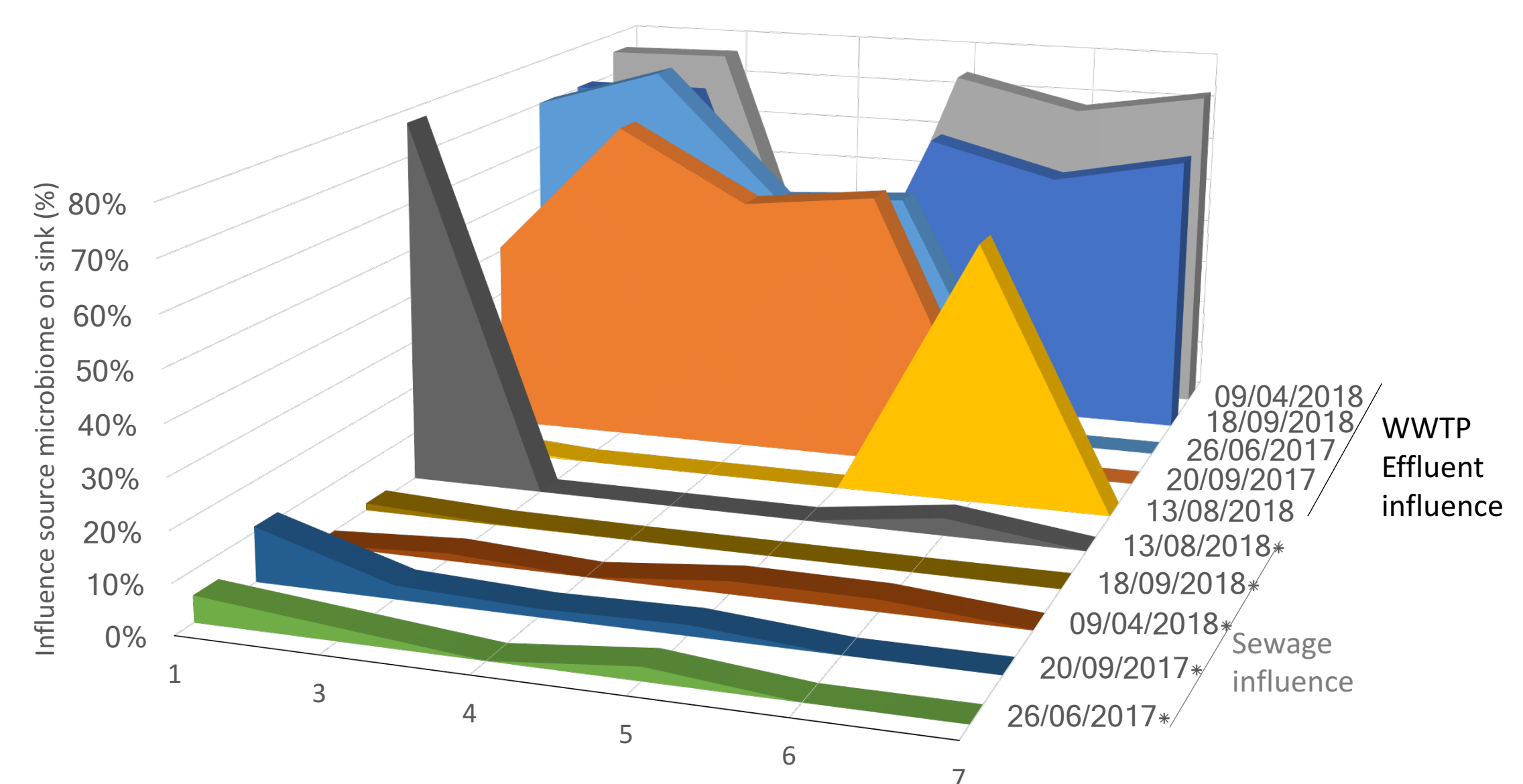


Figure 4: Source tracker analysis of the relative amount (%) of influence of sewage or WWTP effluent on the different sampling locations (sample numbers from Fig 3). Samples were taken on different dates.

Conclusion

HTS is a powerful technique that can distinguish different sources that have a specific microbial fingerprint. These fingerprints can be detected specifically and with high sensitivity in sinks. This gives the opportunity to apply HTS to answer complex questions related to water management, where it is important to know the origin of different water bodies.

Acknowledgements

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References

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