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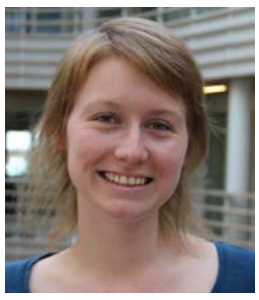
Monitoring chemical and microbial water quality by transcriptome analysis of single-cells



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Motivation

In the Netherlands, we are fortunate to have good drinking water facilities. The drinking water is of high quality and heavily monitored. It is distributed to households via a large and intricate distribution system. The challenge is to keep drinking water quality the same from where it enters the distribution system until the households. One important aspect is to maintain biological stability throughout the system [1]. In this project, we aim at using the indigenous bacteria in the drinking water as indicators of the water quality. Bacteria respond to their environment by switching certain genes on or off, which will lead to changes in mRNA levels [2]. Subsequently, this mRNA profile, or transcriptome, may be correlated to specific environmental stimuli. For example, the transcriptomic response could indicate biological instability or the presence of a certain compound in the distribution system. This may then, require action from the drinking water company (Figure 1). In other words, we propose to use the bacteria in drinking water as microbial sensors by investigating their transcriptomic response. They should potentially also be able to recognize and signal the presence of unknown impurities, which is not possible with the current standard methods.

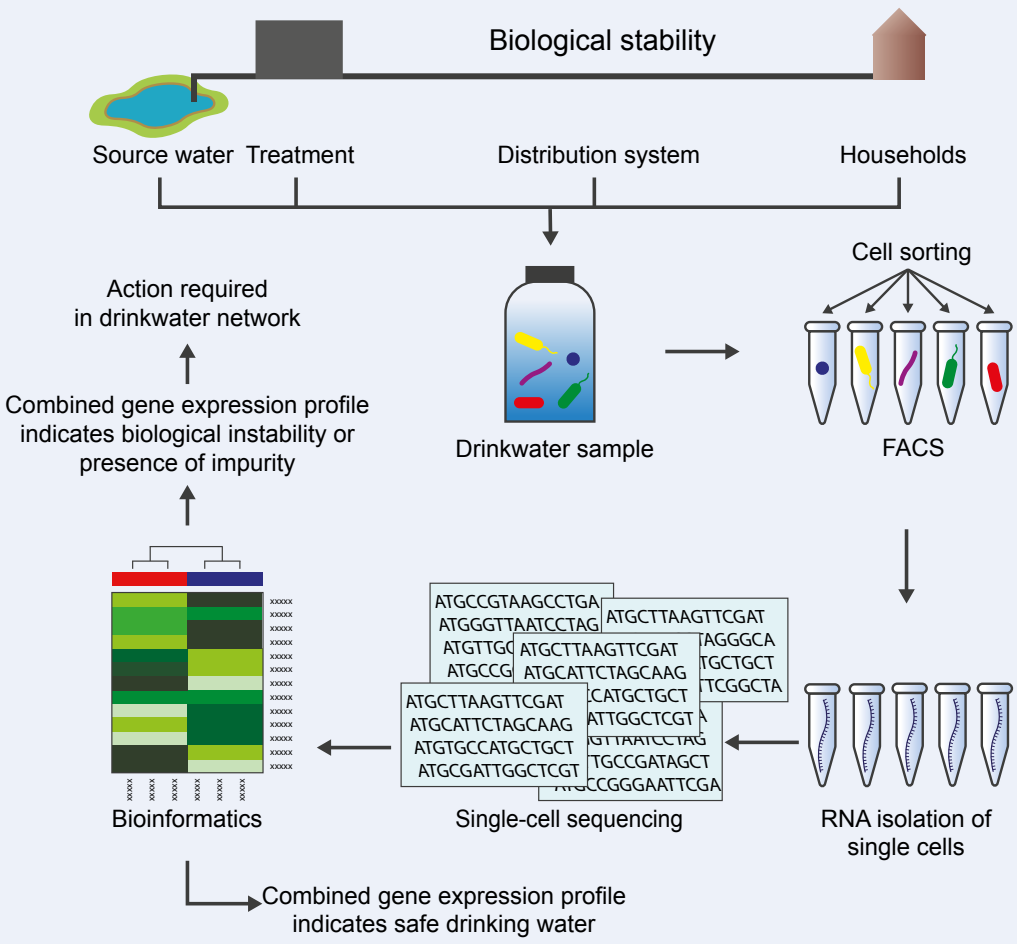

Figure 1: Project overview.

Technological challenge

- Sample preparation. mRNA is very unstable and just present for a short time in the cells. Therefore, sample processing and RNA isolation needs to be performed with care and speed; sample fixation may be necessary [2].
- Distinguishing between microbial subpopulations, such as the active and dormant fraction in drinking water, and sorting those with fluorescence-activated cell sorting (FACS).
- Performing single-cell analysis. We want to perform single-cell analysis to investigate the transcriptomic response in the individual cells instead of the average response of many cells. This is a relatively new and challenging technology, but would greatly improve using the indigenous bacterial cells as biological sensors.
- Data analysis. Analyzing the large amount of data and determining the transcriptomic profiles in relation to specific environmental stimuli will require a lot of bioinformatics and computational power.

Research goals

1. Establish a reliable workflow to distinguish between the microbial subpopulations in drinking water and for single-cell analysis.
2. Investigate what factors influence the biological stability in a full-scale water distribution system, in terms of community composition and bacterial transcriptomes.
3. Determine changes in the transcriptomic profile of microbial subpopulations and single-cells in response to known compounds.
4. Work towards an application that uses the transcriptomic profiles as an indicator for drinking water quality.

[1] Prest, E. I., Hammes, F., van Loosdrecht, M. C. M., & Vrouwenvelder, J. S. (2016). Biological stability of drinking water: Controlling factors, methods, and challenges. Frontiers in Microbiology, 7(FEB), 1–24. https://doi.org/10.3389/fmicb.2016.00045
[2] R. Farrel, RNA methadologies (2010; 4th edition)