I. Motivation

II. Methodology

III. Results

A. Bacterial Community Composition (BCC) varied with site and land use within Kranji Reservoir and catchment

B. Sewage-associated taxa (SAT) in samples from concrete-lined drainages in Kranji Reservoir Catchment

C. Diversity and distribution of pathogen-like sequences (PLS) varied with abundance of potential sewage indicator groups (FIB and sewage associated taxa (SATs))

D. Sites sampled twice revealed microbial communities with higher similarity. The abundance of E. coli and HF183 explained significant variation in BCC and subgroups (SAT) and (PLS) among samples

IV. Conclusions

V. Acknowledgements

VI. Bibliography