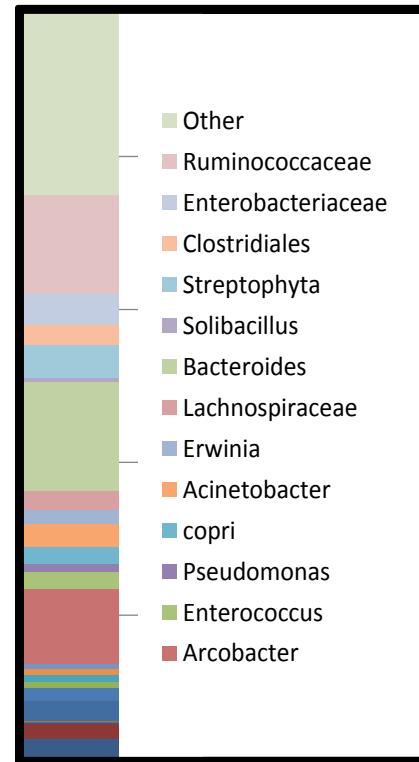
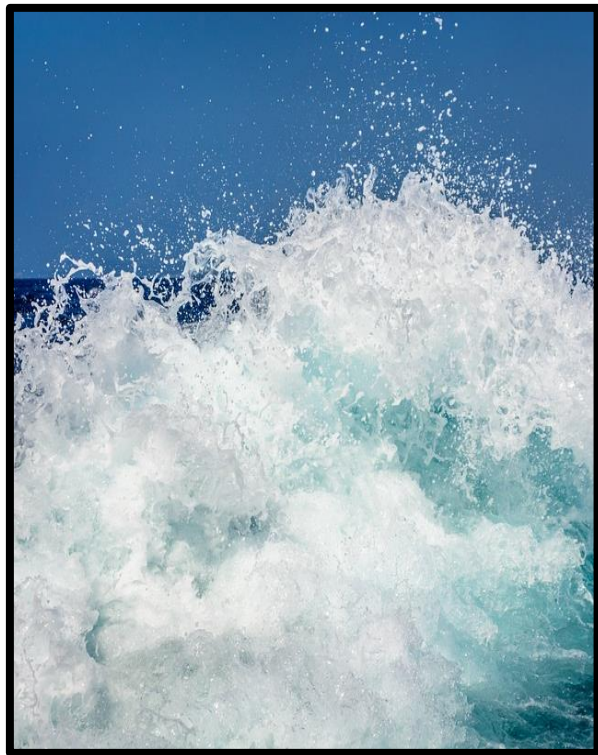




Which point source represents the greatest risk?

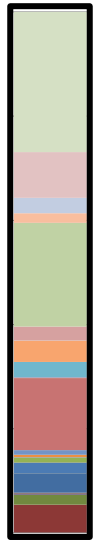
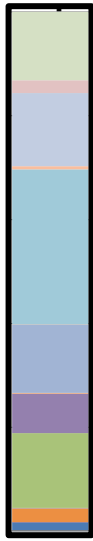


Using microbial populations to define source contributions



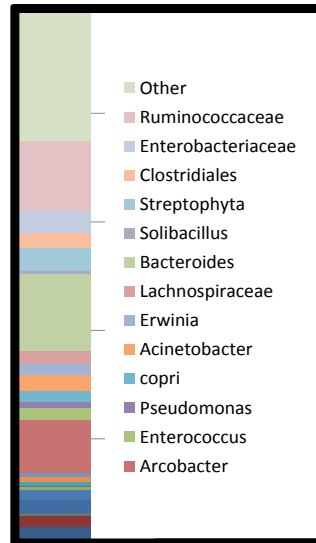
Sink Community

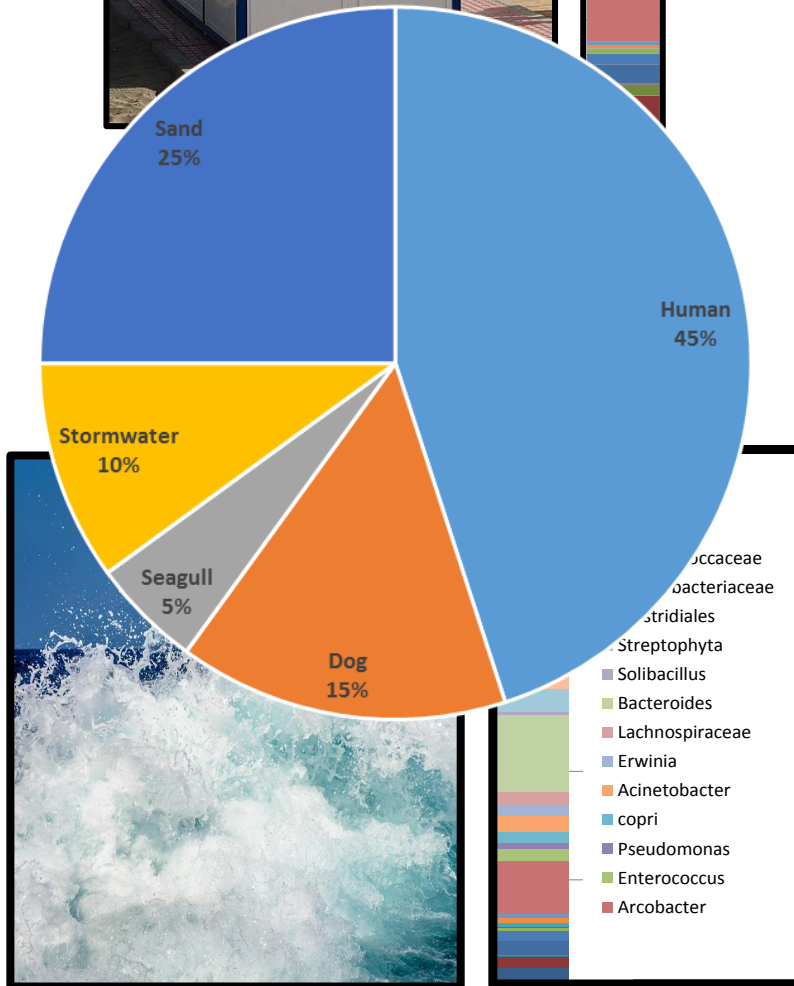
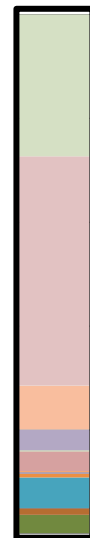
- Environments have unique microbial fingerprints
- Sink environments
 - Act as reservoirs for multiple sources
 - Microbial fingerprints change with source inputs
 - Can be applied to track and identify major point source contributors



So what are the contributions?

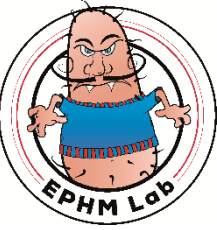
Total microbial community sequencing and Bayesian modelling





- ...baccaceae
- ...bacteriaceae
- ...stridiales
- ...Streptophyta
- ...Solibacillus
- ...Bacteroides
- ...Lachnospiraceae
- ...Erwinia
- ...Acinetobacter
- ...copri
- ...Pseudomonas
- ...Enterococcus
- ...Arcobacter





Further Analysis Available from EPHM

- Industry water monitoring standards
 - *E. coli*
 - *Enterococci*
 - *Bacteroides*
 - *Salmonella*
 - *Campylobacter*
- Integrated community source tracking and hydrodynamic modelling
- In depth investigation of source specific bacterial risks
 - Typing and virulence profiling of source and sink microbes
 - i.e. Water and avian associated *Campylobacter*