

AMRflows: Antimicrobials And Resistance From Manufacturing Flows To People: Joined Up Experiments, Mathematical Modelling And Risk Analysis

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Overview

Experimentally, we are working with two rivers or watersheds in India, near Hyderabad and Chennai. We sample river water and sediments to measure water quality, extract DNA for qPCR and sequencing, count sensitive and resistant *E. coli* and heterotrophs growing on a sewage mimicking medium, etc. We are not yet ready with the LC/MS methods to quantify antibiotics. We have constructed mesocosms to generate time series data that can be used to infer degradation kinetics and other parameters for the mathematical modelling of AMR dynamics. We also use bioreactor mesocosms to study plasmid fate, again to parameterize the model.

Mesocosms: incubating 'clean' or polluted river water samples without them flowing away: monitor dynamics over time



Using digital elevation maps, climate data, river cross-sections and reservoir discharge data we have been constructing mathematical models of water flow (hydrological and hydraulic models). Combining water flow models with AMR dynamics models will allow us to predict the fate of AMR in the aquatic environment. This will feed into assessing mitigation strategies and risk analysis to ultimately inform environmental standards and policy.





(FACS) Flow cytometry + cell sorting



Infection Risk Model: Zebrafish

Bayesian Network – Risk model draft

Summary

It has been challenging but we have made progress. Mesocosms have been constructed and preliminary data obtained. The plasmid donor, an isolate from wastewater, has been sequenced, cured of a resident plasmid and tagged. The Zebrafish survive incubation in polluted river water. The Bayesian Network for risk analysis is being developed. Sampling sites have been chosen and sampled several times. Analytic methods are being developed but are lagging behind. Mathematical modelling has focused on adding exchange between planktonic and sediment attached bacteria to an existing model and setting up the microbial population dynamics coupling to water and sediment transport. Coding to numerically solve the equations has begun. Watershed and river models have been set up but need refinement and more detailed parameterization. Tasks dependent on output from others have not begun. We are looking forward to presenting the data and results in EDAR7.









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