

Supplementary File 1. Full list of benchmark papers

Question 1:

1. Søråas A, Sundsfjord A, Sandven I, Brunborg C, Jenum P. Risk factors for community-acquired urinary tract infections caused by ESBL-producing enterobacteriaceae—a case–control study in a low prevalence country. *PloS One*. 2013; 8:e69581. (<https://doi.org/10.1371/journal.pone.0069581.g001>)
2. Mughini-Gras L, Dorado-García A, van Duijkeren E. Attributable sources of community-acquired carriage of Escherichia coli containing beta-lactam antibiotic resistance genes: a population-based modelling study (vol 3, pg e357, 2019). *Lancet Planet Health*. 2019; 3:E408-. ([https://doi.org/10.1016/S2542-5196\(19\)30130-5](https://doi.org/10.1016/S2542-5196(19)30130-5))
3. Schijven J, Blaak H, Schets F, de Roda Husman A. Fate of extended-spectrum β -lactamase-producing Escherichia coli from faecal sources in surface water and probability of human exposure through swimming. *ES&T*. 2015; 49:11825-33. (<https://doi.org/10.1021/acs.est.5b01888>)
4. O'Flaherty E, Solimini A, Pantanella F, Cummins E. The potential human exposure to antibiotic resistant-Escherichia coli through recreational water. *Sci Total Environ*. 2019; 650:786-95. (<https://doi.org/10.1016/j.scitotenv.2018.09.018>)

Question 2:

1. Amos G, Gozzard E, Carter C, Mead A, Bowes M, Hawkey P, Zhang L, Singer A, Gaze W, Wellington E. Validated predictive modelling of the environmental resistome. *ISME J*. 2015; 9:1467-76. (<https://doi.org/10.1038/ismej.2014.237>)
2. Amos G, Hawkey P, Gaze W, Wellington E. Waste water effluent contributes to the dissemination of CTX-M-15 in the natural environment. *J Antimicrob Chemother*. 2014; 69:1785-91. (<https://doi.org/10.1093/jac/dku079>)
3. Amos G, Ploumaki S, Zhang L, Hawkey P, Gaze W, Wellington E. The widespread dissemination of integrons throughout bacterial communities in a riverine system. *ISME J*. 2018; 12:681-91. (<https://doi.org/10.1038/s41396-017-0030-8>)
4. Amos G, Zhang L, Hawkey P, Gaze W, Wellington E. Functional metagenomic analysis reveals rivers are a reservoir for diverse antibiotic resistance genes. *Vet Microbiol*. 2014; 171:441-7. (<http://dx.doi.org/10.1016/j.vetmic.2014.02.017>)
5. Daramola B, Williams R, Dixon R. In vitro antibiotic susceptibility of Vibrio parahaemolyticus from environmental sources in northern England. *Int J Antimicrob Agents*. 2009; 34:499-500. (<https://doi.org/10.1016/j.ijantimicag.2009.06.015>)
6. Dhanji H, Murphy N, Akhigbe C, Doumith M, Hope R, Livermore D, Woodford N. Isolation of fluoroquinolone-resistant O25b: H4-ST131 Escherichia coli with CTX-M-14 extended-spectrum β -lactamase from UK river water. *J Antimicrob Chemother*. 2011; 66:512-6. (<https://doi.org/10.1093/jac/dkq472>)
7. Gaze W, Abdousslam N, Hawkey P, Wellington E. Incidence of class 1 integrons in a quaternary ammonium compound-polluted environment. *Antimicrob Agents Chemother*. 2005; 49:1802-7. (<https://doi.org/10.1128/AAC.49.5.1802-1807.2005>)

8. Hargreaves K, Colvin H, Patel K, Clokie J, Clokie M. Genetically diverse *Clostridium difficile* strains harboring abundant prophages in an estuarine environment. *AEM*. 2013; 79:6236-43. (<https://doi.org/10.1128/AEM.01849-13>)
9. Song Y, Cui L, López J, Xu J, Zhu Y, Thompson I, Huang W. Raman-Deuterium Isotope Probing for in-situ identification of antimicrobial resistant bacteria in Thames River. *Sci Rep*. 2017; 7:1-0. (<https://doi.org/10.1038/s41598-017-16898-x>)