Rapid resistome mapping using nanopore sequencing

The emergence of antibiotic resistance in human pathogens has become a major threat to modern medicine. The outcome of antibiotic treatment can be affected by the composition of the gut. Accordingly, knowledge of the gut resistome composition could enable more effective and individualized treatment of bacterial infections. Yet, rapid workflows for resistome characterization are lacking. To address this challenge we developed the poreFUME workflow that deploys functional metagenomic selections and nanopore sequencing to resistome mapping. We demonstrate the approach by functionally characterizing the gut resistome of an ICU (intensive care unit) patient. The accuracy of the poreFUME pipeline is with >97% sufficient for the annotation of antibiotic resistance genes. The poreFUME pipeline provides a promising approach for efficient resistome profiling that could inform antibiotic treatment decisions in the future.

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Contributors: van der Helm, E., Imamovic, L., Ellabaan, M. M. H., van Schaik, W., Koza, A., Sommer, M. O. A.
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