Background

Antibiotic resistance is one of the top threats to human health, according to the WHO [1], and bacterial antimicrobial resistance (AMR) is estimated to have caused 1.14 deaths in 2021 [2]. The number of antibiotic resistant bacterial infections are rising exponentially, highlighting the need for better understanding of their cause and potential treatments. It is estimated that by the year 2050 resistant infections will lead to 10 million deaths annually, if the current trend continues [3].

Pathogens can confer antibiotic resistance by chromosomal mutations. It has been shown that microplastics enrich potentially pathogenic bacteria that carry a great number of antibiotic resistance genes (ARGs) [4].

In a previous study [5], the question whether the acquisition of ARGs is greater in the plastisphere compared to free-living phases was raised. Additionally there is also a clear knowledge gap regarding the extent to which genetic changes from mutations can contribute to the development of AMR in the plastisphere.

Aim

By utilizing publicly available (meta)genomic data, this study aims to assess the presence of ARGs in the plastisphere and identify genetic changes (e.g., point mutations) which can lead to altered susceptibility of bacteria to antibiotics. To do so, bioinformatic methods will be applied to screen antibiotic resistance genes in microorganisms which colonize microplastics, compared to those inhabiting natural substrates and/or free-living bacteria. Thereafter, the project aims to estimate point mutations of plastisphere bacteria, and compare their levels with those estimated for bacteria inhabiting various other substrates such as glass and wood. For this, the application of a bioinformatic tool, called Mumame [6], is planned that was specifically developed to detect such genetic changes.

Machine learning could potentially be used to identify features that could increase the likelihood of point mutations, or to find if the substrate type is a key feature for the incidence of point mutations. The machine learning algorithm XGBoost could be used as a starting point, it has previously been used to identify the plastic degrading potential from protein sequences and could be modified to suit the needs of the project [7].

The findings from the current project, as well as any potential methodological developments, would aid in enhancing the current knowledge base regarding AMR, as well as improving the ability for us to monitor the presence of AMR in the future.

Method

- Literature search and Data collection, publicly available, for example from International Nucleotide Sequence Database Collaboration and recent data publications.
- Quality control and filtering, using tools such as Trim Galore! or similar.
- Using Mumame to identify point mutations.
- Improve Mumame, especially the database building step it includes. This could involve other sources for mutation lists, or potentially the method by which it is built.

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