

## **Correcting bias in genetic source attribution for zoonotic infections**

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Source attribution methods attempt to identify the animal reservoir responsible for human infections from the information contained in the pathogen's genome. These methods are used for a wide range of zoonotic infections (infections that are spread from animals to humans). This would give the potential for wide impact, especially if the student developed a good quality accessible implementation.

Existing source attribution methods that use just 7 genes are known to be biased, so the first step is to develop methods to correct for these biases. Preliminary results show that increasing the number of genes used for source attribution may actually increase the bias, and so more generally we would like to develop an unbiased approach.

The initial MSc project will use techniques from Bayesian statistics and will involve post-processing output from Markov chain Monte Carlo algorithms. This work would use substantial datasets from Food Standards Agency funded research and global datasets. To extend the project to a PhD the student would work directly on genomic source attribution methods using whole genome data. It would be interesting to compare the performance of machine learning approaches against biologically informed models of genetic evolution. This will be in collaboration with Public Health England with access to national data.