**Introduction**

The mycobacteriophage population represents an incredibly large and diverse set of genomic sequences. Traditional alignment-based methods for comparative analysis and phylogenetic reconstruction may be ineffective on populations with significant horizontal gene transfer and are relatively difficult to compute computationally. Alignment-free sequence analysis methods, such as measures that compute the usage of oligonucleotides (k-mers) in the genome, require less computational time and show potential to infer relationships between significantly diverged sequences. We applied methods