Predicting the plasmidome content of *Enterococcus faecium*

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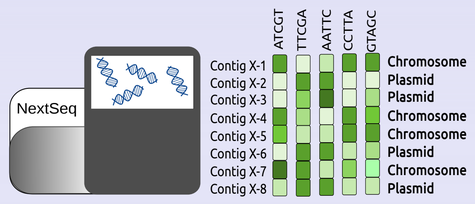


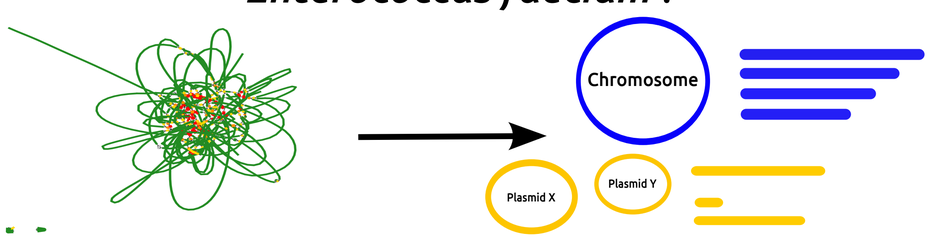
mlplasmids

UMC Utrecht

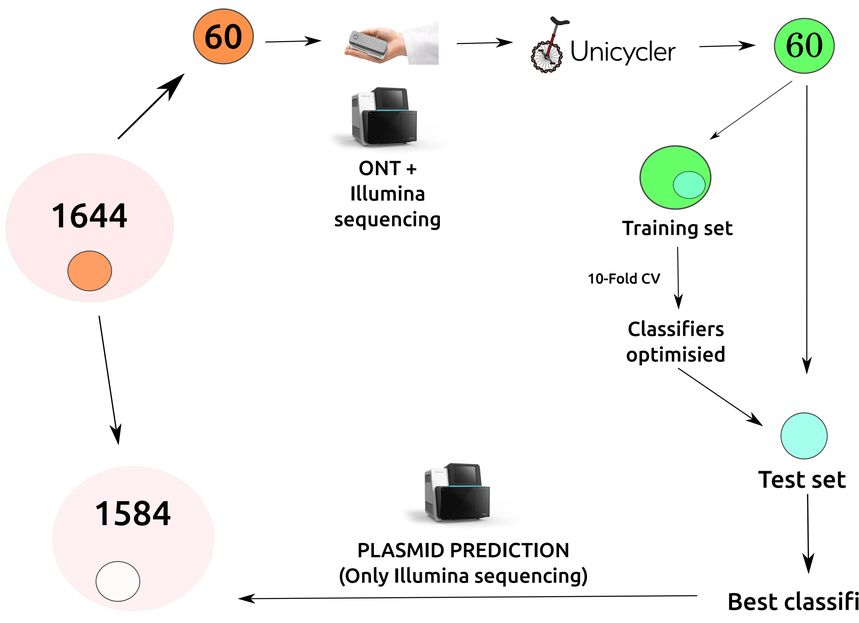
Introduction

Plasmid assembly from **short** whole-genome sequencing data **(WGS) results in an accurate but fragmented graph** consisting of hundreds of contigs. Determining whether a **contig is plasmid- or chromosome- derived is challenging** and error-prone with existing tools[1]. **Long-read sequencing** has emerged as a new solution to obtain complete plasmid sequences[2]. Information derived from **long-read sequencing can be used to label a dataset of short-read contigs** as chromosome- or plasmid- derived.

Can we accurately predict the plasmidome content of ***Enterococcus faecium*** ?



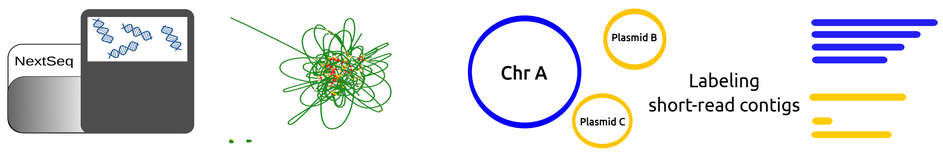
Predicting the plasmidome content of our collection



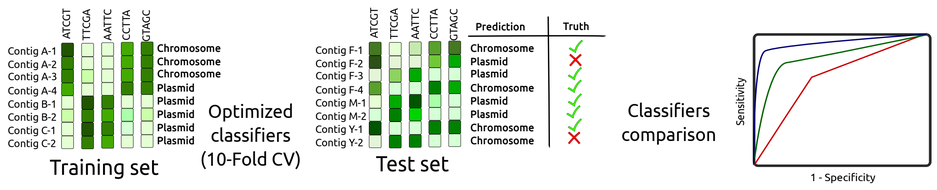
Developing a novel machine learning classifier

Hybrid assembly to obtain complete genome sequences (**Unicycler**[3])

Mapping short-read contigs against complete genomes (**bwa**[4] **+ samtools**[5])



Training and comparing different machine learning classifiers using **pentamer frequencies (R mlr package**[6]**)**



Benchmarking resulting classifier

Results

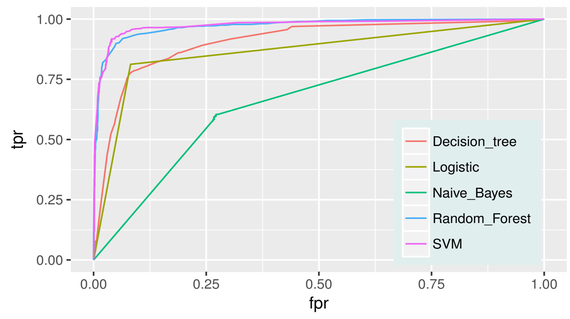


Figure 1. ROC Curves obtained for the tested machine learning algorithms

Support vector machine (SVM) was selected as **best classifier** (AUC = 0.97 ; F1-score = 0.95) using our test set (n = 2,010 contigs). Resulting model was **implemented in mlplasmids (Figure 1)**

Plasmidome prediction resulted in an **average of 58 plasmid contigs (~ 254,700 bp) and 119 chromosomal contigs (~ 2,632,470 bp)** with an associated average **posterior probability of 0.95 and 0.91** of belonging to the plasmid and chromosome class **(FIgure 2)**

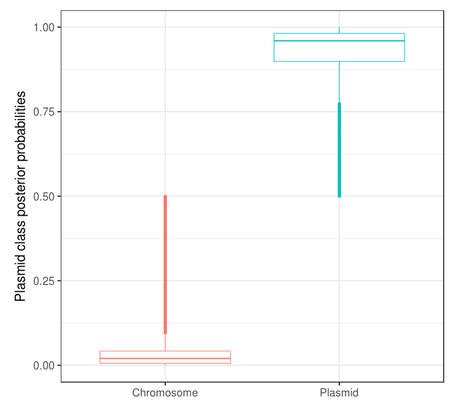


Figure 2. Boxplot showing the posterior probabilities distribution of belonging to the plasmid class

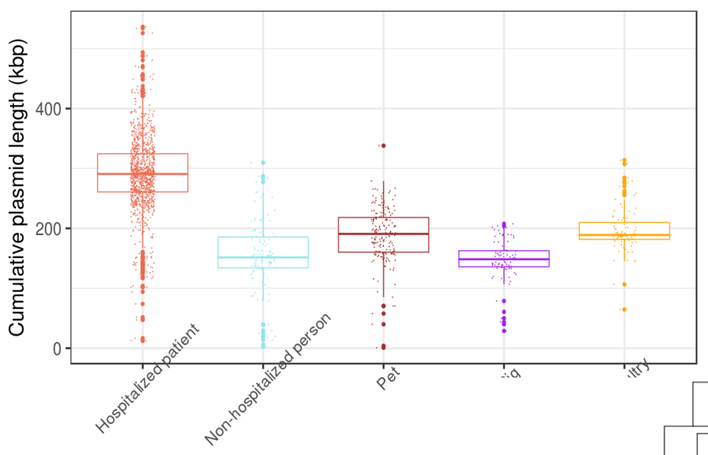


Figure 3. Box plot showing the distribution of the predicted cumulative plasmid length (kbp) per isolation source

Predicted cumulative plasmid length is higher in hospitalized patients (average 290.51 kbp vs 174.46 kbp) **(Figure 3)**

Plasmid DNA coding capacity differs between **hospitalized patients** and other isolation sources **(Figure 4)**

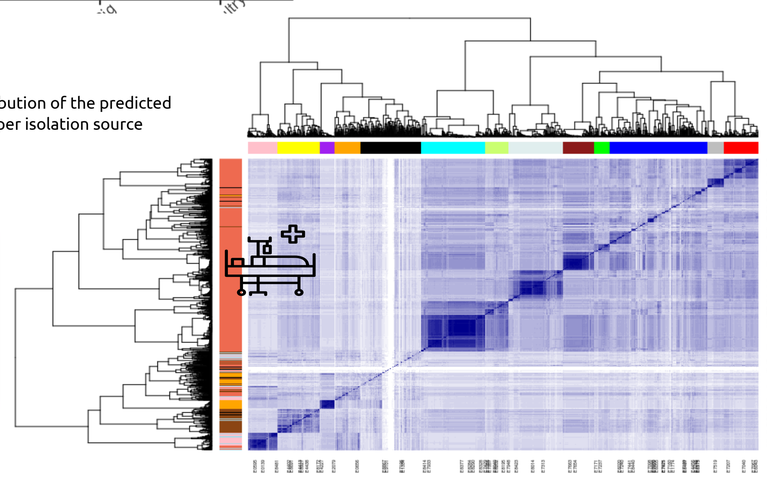


Figure 4. Heatmap showing the distance similarity between strains based on their predicted plasmid gene content (mlplasmids + Prokka[6]+ Roary[7]). Isolation sources are indicated on the left-vertical bar using the same colours defined in Figure 3. We defined 13 plasmid clusters (top-horizontal bar) to represent all the plasmid subpopulations present in our collection.

Conclusions

Genomic structure information resolved by ONT sequencing can be used to build a model capable to accurately classify plasmid sequences in *E. faecium*

E. faecium hospital isolates have a different pool of plasmid genes than isolates from other sources

mlplasmids is publicly available and allows the assignment of a particular contig/gene of interest as plasmid- or chromosome- encoded

References

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GitLab

https://gitlab.com/sirarredondo/mlplasmids

Shiny by RStudio

Future releases

Escherichia coli and *Klebsiella pneumoniae* models