Characterisation and Identification of STEC O157:H7 Pathogenicity using Machine Learning

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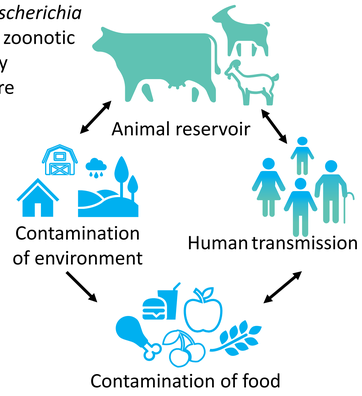
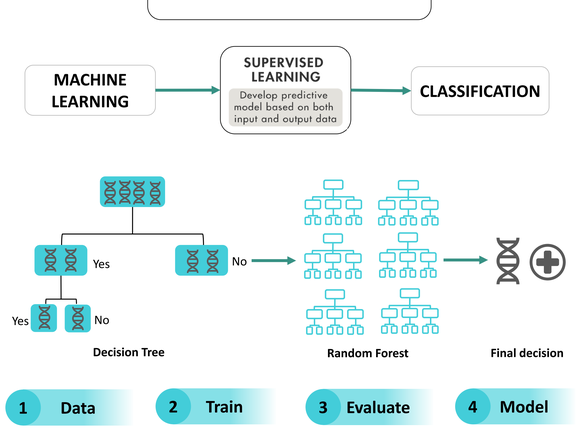
Introduction

Shiga toxin-producing *Escherichia coli* O157:H7 (STEC) is a zoonotic pathogen that is globally dispersed, causing severe gastroenteritis when transmitted from ruminants to humans.

Is there any **association** between STEC **k-mer sequence** and the observed **clinical outcome**?

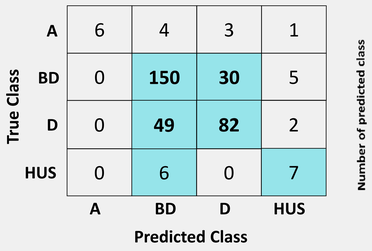


Method

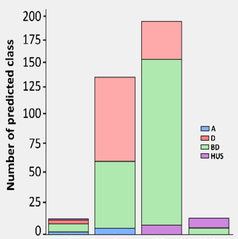


- **1148** STEC O157:H7 isolated from human cases in 2017 and 2018.
- DNA sequence of each isolate were sub-sequenced into k length of ***k-mers*** (9-100).
- **1 million randomly selected *k-mers*** were used to train the Random Forest classifier.
- *k*-mers copy number was **normalised**.
- Symptoms classed into*:* ***Asymptomatic (A), Diarrhoea (D), Bloody Diarrhoea (BD), Hemolytic uremic syndrome (HUS)***
- Recursive feature elimination with **10-fold cross validation** performed.

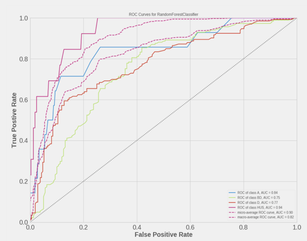
Results



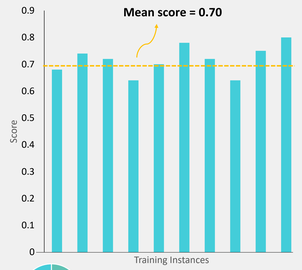
72% Precision, Recall and F1 score



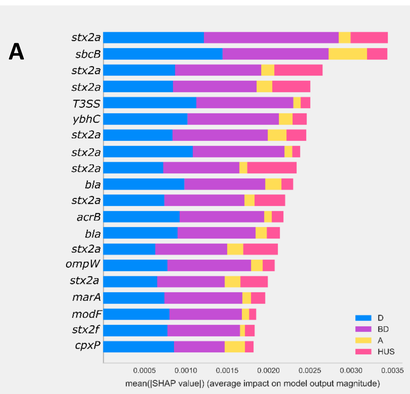
>70% Correct classification

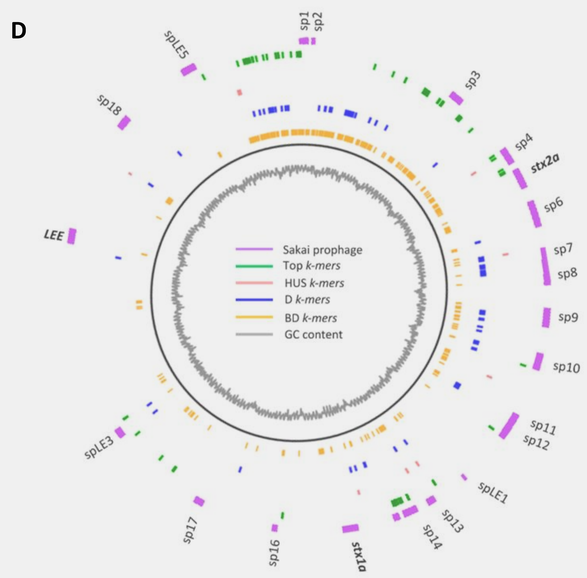


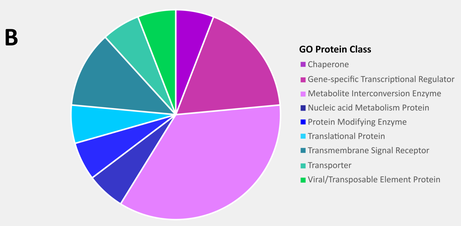
0.90 Area Under the ROC Curve

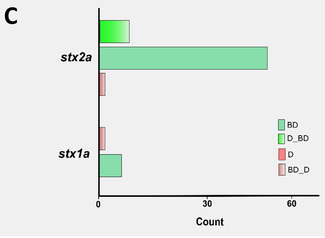


0.70 10-fold cross validation









A. Contribution of D, BD, A, HUS related *k-mers* to model learning and their impact on learning a true prediction.
B. GO Protein Class of Top *k-mers.*
C. Difference in the abundance of BD and D *k-mers* associated with Shiga toxins.
D. Distribution of *k-mers* across the Sakai genome.

Conclusion

1. **Association between STEC genome and clinical outcome learnt using Random Forest classifier. Association found to be linked to specific *k-mer* profile.**
2. **BD specific *k-mers* and *k-mers* associated with Shiga toxins had greater impact on models learning.**
3. **Pathogenicity highly dependent on the presence of specific types of Shiga toxin.**
4. **Severity of clinical outcome is strongly correlated to the lineage of STEC O157:H7 isolate.**

Acknowledgement

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