

Statistical Machine Learning for Foodborne Disease Source Attribution

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Overview

We developed a statistical machine learning classification model for Listeria monocytogene pathogen food source attribution based on a comparative analysis of Naïve Bayes and Random Forest algorithms.

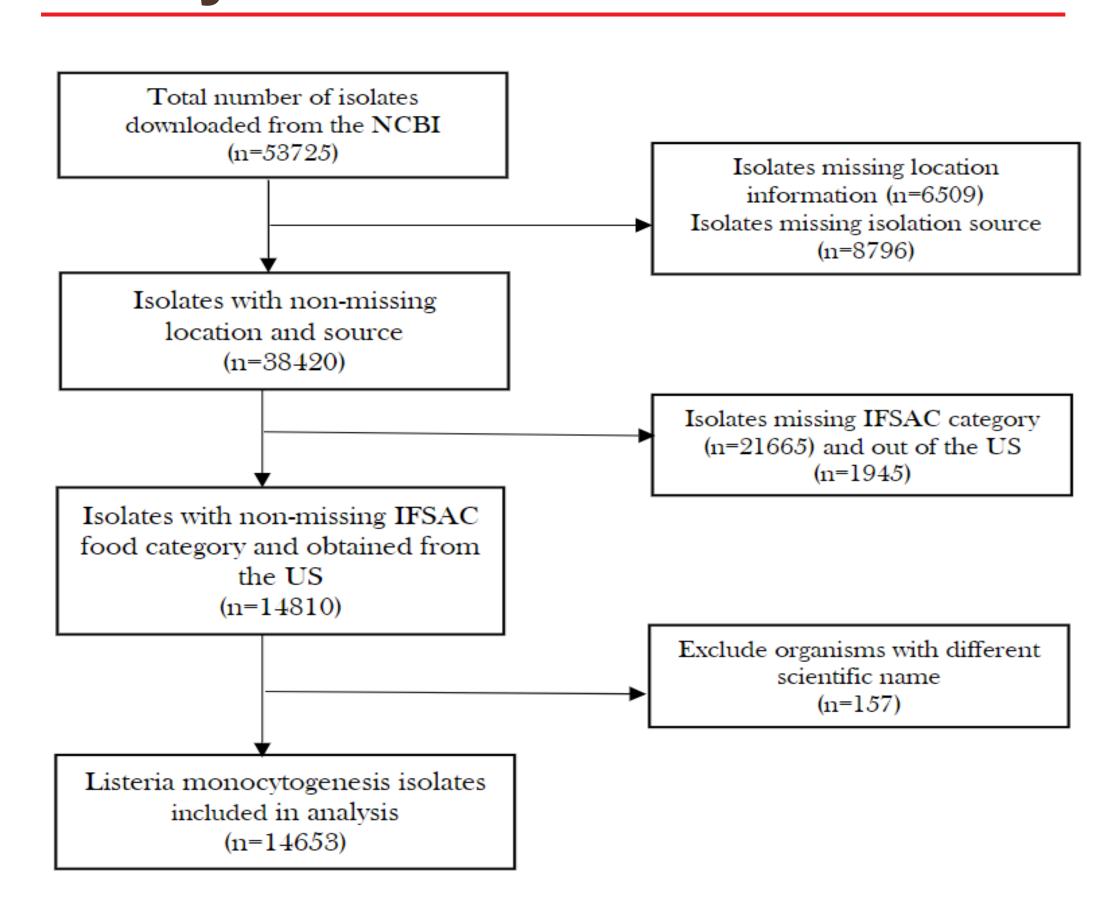
Background

- In the US, foodborne illnesses result in approximately 128,000 hospitalizations and 3,000 fatalities.
- The US Centers for Disease Control and Prevention (CDC) notes that approximately 1,600 cases of listeriosis are recorded annually with about 260 mortalities.
- Outbreak investigations have shown links between these pathogens and specific food sources.
- We compared the performance of Naïve Bayes and Random Forest algorithms to develop a model for foodborne-illness source attribution linked to L. monocytogene isolates.

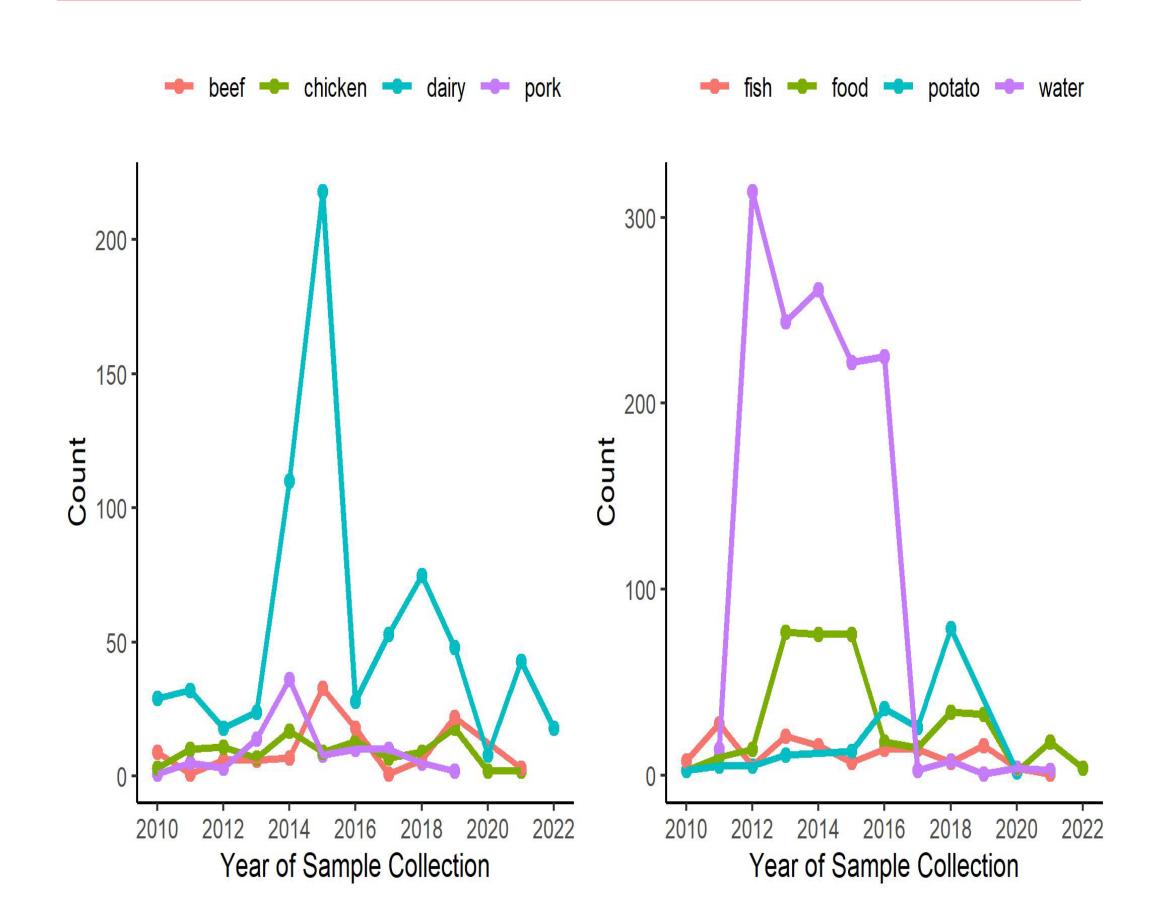
Study Design and Methods

- Given strains of L. Monocytogenes isolates sampled from the National Centers for Biotechnology Information's (NCBI) Pathogen Detection database, Naïve Bayes and Random Forest modeling were used to predict food sources.
- There were 66 isolates from human listeriosis patients, 5696 from environmental sources, 1967 from food sources and 618 isolates from other sources.
- Food sources included dairy (624), fruits (258), leafy greens (70), meat (267), poultry (254), sea food (198) and vegetables (296).
- Data was split into training and test sets (75% and 25% respectively).
- A 10-fold cross validation and minority class up-sampling was employed to develop the Naïve Bayes and Random Forest (RF) machine learning algorithms in the training data.
- Final tuning parameters were; α=1 Laplace smoothing for the Naïve Bayes; mtry=2 for the Random Forest model.
- The developed models were evaluated against the test set and performance assessed based on model accuracy, Kappa values and other confusion matrix statistics.
- The final model was developed by the training the best algorithm; the Random Forest model on the full training data.

Study Flowchart



Trends of L. monocytogenes counts by top isolation sources



Results

Table 1. Performance measures across 10 folds with resampling for Naive Bayes and random forest classification algorithms

Metric	Naïve Bayes		Random Forest	
	Estimate	Standard error (SE)	Estimate	Standard error (SE)
Accuracy	0.2577	0.0065	0.8727	0.0033
Jaccard's Index	0.2831	0.009	0.6519	0.0103
Карра	0.1398	0.0046	0.7438	0.0055
AUC	0.7961	0.0057	0.9453	0.0028
Sensitivity	0.3633	0.0092	0.6771	0.0105
Specificity	0.9198	0.0007	0.9748	0.0006

Table 2. Naïve Bayes and RF
Performance measures on test data

Performance measures on test data					
Metric	Naïve Bayes	Random Forest			
Accuracy	0.2496	0.8625			
Jaccard's Index	0.2515	0.5533			
Карра	0.132	0.7194			
AUC	0.7597	0.9265			
Sensitivity	0.3324	0.5813			
Specificity	0.9191	0.972			

Table 3. Performance measures of Random Forest on the full data

Metric	Random Forest		
Wellic	Estimate	Standard error (SE)	
Accuracy	0.884	0.0036	
Jaccard's Index	0.6874	0.0116	
Карра	0.7687	0.0043	
AUC	0.958	0.0019	
Sensitivity	0.7098	0.0115	
Specificity	0.9776	0.0004	

• The performance of Naïve Bayes and Random forest differed significantly from one another with an average accuracy of 0.258 and 0.873, respectively.

Conclusion

- The Random forest model had a very good ability to discriminate between the different food sources, with an area under the curve (AUC) of 0.945 compared to the Naïve Bayes model that had moderately good discriminatory ability, AUC of 0.796.
- Statistical machine learning methods promise efficiency in food source attribution of L. monocytogenes isolates, which can substantially enhance investigation of outbreak cases and reduce the pool of food sources targeted by intervention policies.
- The study was restricted to a complete case analysis due to high percentage of missing data. Categorization of the isolation source variable may have introduced bias and loss of efficiency in the results.

References

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