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Review

Mathematical and Artificial Intelligence Models for Zoonotic Foodborne Pathogens

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Abstract: Globally, zoonotic diseases have been on the rise in recent years. Predictive modelling approaches have been successfully used in the literature to identify the underlying causes of these zoonotic diseases. We examine the latest research in the field of predictive modeling that verifies the growth of zoonotic pathogens and assesses the factors associated with their spread. The results of our survey indicate that popular mathematical models can successfully be used in modeling the growth rate of these pathogens under varying storage temperatures. Additionally, some of them are used for the assessment of the inactivation of these pathogens based on various conditions. Based on the results of our study, machine learning models and deep learning are commonly used to detect pathogens within food items and to predict the factors associated with the presence of the pathogens.

Keywords: zoonotic pathogens; mathematical algorithms; machine learning; deep learning

1. Introduction

Bacterial, viral, parasitic or chemical contaminants are responsible for over 200 diseases, ranging from diarrhea to cancer (World Health Organization, 2022). According to World Health Organization (2015) report, foodborne diarrheal disease agents - primarily non-typhoidal *Salmonella enterica (NTS)* and *enteropathogenic Escherichia coli (EPEC)* - have caused a total of 18 million disability-adjusted life years (DALYs) worldwide. In the United States, 13,352 outbreaks of foodborne diseases caused 271,974 illnesses between 1998 and 2008 (Centers for Disease Control and Prevention, 2013). Between 2015 and 2020, outbreaks of foodborne diseases led to 82,811 illnesses, 6,093 hospitalizations, and 121 deaths Centers for Disease Control and Prevention (2020). According to Dewey-Mattia *et al.* (2018), *Listeria*, *Salmonella*, and *Shiga toxin-producing Escherichia coli (STEC)* account for the majority of hospitalizations and deaths associated with foodborne disease outbreaks between 2009 to 2015. In the European Union (27 member states), 3,086 outbreaks of foodborne disease led to 20,017 human cases, 1,675 hospitalizations, and 34 deaths (European Food Safety Authority and European Centre for Disease Prevention and Control, 2021). The majority of outbreaks are caused by bacteria, followed by bacterial toxins, viruses, and parasites.

In recent years, Artificial Intelligence models have proven valuable in studying zoonotic pathogens and their growth factors that pose a threat to global health (Carlson *et al.*, 2021). Mathematical algorithms are widely used to develop predictive models for kinetic processes such as bacterial growth, survival, and inactivation (Schiraldi and Foschino 2022, Adamczewski *et al.* 2022, Herron 2022). A modified Gompertz (Zwietering *et al.*, 1990) model, and the Baranyi and Roberts model (Baranyi and Roberts, 1994) are frequently used for analyzing the growth dynamics of bacteria in animals (Lanzl *et al.* 2020, Medvedova *et al.* 2021, Xiao *et al.* 2021, Guo *et al.* 2021). Logistic Regression (Cox, 1958) and Random Forest (Ho, 1995) algorithms are widely used for learning about zoonotic diseases and their transmission (Ntampaka *et al.* 2021, Kiambi *et al.* 2020, Acharya *et al.* 2019). The effectiveness of artificial neural networks in modeling zoonotic diseases and their causes have also been demonstrated in a number of studies (Boleratz and Oscar 2022, ZareBidaki *et al.* 2022, Denholm *et al.* 2020).

This review is an overview of the predictive models (since 2015) employed to study zoonotic food-borne pathogens. The review includes studies concerning pathogens and their relationships with package conditions, storage temperatures, food matrix, and so on. The literature review is based on UNEP and ILRI report (2020) and Dewey-Mattia *et al.* (2018) study of the recent popular causes of disease in the United States. As most previous studies have focused either on pathogens (Gaythorpe *et al.* 2018, Pexara and Govaris 2020) or animal models (de Souza *et al.*, 2022), we provide a summary of the modelling approaches that have been used for zoonotic diseases, pathogens, and the food categories associated with them. The scope of this study excludes the evolution and recent advancements in MRA methodologies (Joshi *et al.*, 2022), studies that utilize human or plant based samples (Buccioni *et al.*, 2022), or the effects of vaccination (Seekatz *et al.*, 2013).

The manuscript is organized as follows: Section 2 introduces some fundamental mathematical and machine learning concepts that are discussed in this paper. This survey's methodology and material are described in Section 3. In section 4, we examine studies utilizing mathematical and machine learning models to determine the etiology of a variety of diseases. In Section 5, the algorithms included in this manuscript are briefly summarized. Conclusions are offered in Section 6.

2. Background

2.1. Growth and Predictive Microbiology

The growth of microorganisms in foods goes through four phases: the lag phase in which microorganisms adjust to their surroundings, the log or exponential phase in which the population of microorganisms grows exponentially over time, the stationary phase in which the population stabilizes, and finally, the decline phase.

Predictive microbiology focuses on the growth dynamics of pathogenic microorganisms in food under a variety of environmental conditions. The objective is to determine the number of microorganisms in food at any given point in time in order to determine the minimum acceptable quality, to determine if the food is safe for consumption, or what treatment can be applied to inactivate the microorganisms. Microbiological laboratory testing is a time consuming process and is not suitable for making quick decisions in real time. In other words, predictive microbiology is beneficial for ensuring food safety, controlling risk, and predicting the shelf life of microorganisms.

Generally, predictive modelling is divided into two phases: primary and secondary. Primary models determine the isothermal growth rate, or isothermal survival rate, as a function of time. Secondary models determine the effects of temperature on the growth rate or survival rate. To understand microorganism growth, the primary focus is on determining the lag time, how fast the organism can grow, and the maximum cell densities. Inactivation learning, on the other hand, is concerned with determining how quickly microorganisms die off.

2.2. Mathematical Models

Mathematical models of population growth dynamics provide a firm basis for scientific understanding, making decisions based on the rate of growth, and testing the effect of changes to the system. Mathematical models are especially useful in scenarios where factors affecting growth can be modeled with a small number of parameters. Widely used primary models include the Baranyi and Roberts model, the Huang model, the reparamerized Gompertz model, and the Weibull model. Secondary models like the Ratkowsky square root model, the Huang square root model and the Arrhenius type model are frequently used in conjunction with primary models.

A brief summary of such models are as follows (Lihan Huang 2014, Lihan Huang 2017):

- **Baranyi Model** (Baranyi and Roberts 1994) is expressed as

  $$Y_t = Y_0 + \mu_{max} t + \ln(e^{-\mu_{max} t} + e^{-h_0}) - e^{-\mu_{max} t - h_0}$$

  where Y_0, Y_t, Y_{max} are bacterial population at times 0, t, and maximum, μ_{max} is the specific growth rate, and h_0 is the physiological state of the microorganism.
- **Modified Gompertz Model** (Zwietering *et al.* 1990) is expressed as

  $$Y_t = Y_0 + (Y_{max} - Y_0) exp\{-exp[\frac{Y_{max} e}{Y_{max} - Y_0}(\lambda - t) + 1]\}$$

  where λ is the lag phase duration.
- **Ratkowsky square-root model** (Ratkowsky *et al.* 1982) is represented as

  $$\sqrt{\mu} = a(T - T_0)$$

  where μ is the specific growth rate, and 'a' is a coefficient, T is the temperature, and T_0 is the nominal minimum temperature.
- **Nonlinear Weibull- Mafart model** (Mafart *et al.* 2002) is expressed as

  $$log(N) - log(N_0) = Y_0 - (\frac{t}{D})^K$$

  where $log(N)$ is the real time bacterial count, $log(N_0)$ is the initial bacterial count, and 'D' is the temperature condition.

2.3. Artificial Intelligence Models

In the real world, a small number of parameters are seldom sufficient. Models based on artificial intelligence are especially useful for predicting a wide range of outcomes of interest based on practically any number of parameters, as long as sufficient observations are available to construct such models. Machine learning approaches can be broadly classified into unsupervised approaches for clustering unlabeled data sets, and supervised algorithms for labeled datasets. More recently, with reduced cost of computation, it has been more useful to categorize them in to traditional machine learning algorithms, which are useful for numerical and category-based inputs, and computationally intensive deep learning algorithms, that can be applied to a wider range of input types, including images and audio.

A brief description of traditional machine learning algorithms widely used in the literature are as follows.

- **K-Nearest Neighbours (K-NN):** A KNN classifier is a non-parametric classifier that uses proximity to determine whether or not an individual data point belongs to a particular group. The nearest neighbors determine the class label by majority vote.
- **Logistic Regression:** It is a parametric, supervised algorithm that uses a logistic (sigmoid) function to model independent variables, viz.,

  $$Y = \frac{1}{1 + e^{-W_X}}$$

  where Y is the dependant variable, W_X is the linear combination of independent variables X and weights W.
- **Random Forest (RT):** A random forest is an ensemble learning technique that constructs an output class through a majority voting approach from a multitude of decision trees.
- **Naive Bayes (NB):** A Naive Bayes classifier is a probabilistic classifier that is based on Bayes' theorem and assumes that features are independent of one another.

- **Support Vector Machine (SVM):** Support vector machines are supervised classification algorithms that produce a hyperplane (decision boundary) that separates inputs into different categories.
- **eXtreme Gradient Boosting (XGBoost):** It is an ensemble-based boosting approach that consists of multiple decision trees that run sequentially and are aimed at minimizing the error from the previous model.

The following is a brief description of deep learning models:

- **Artificial Neural Network:** Neuron networks are composed of layers of neurons that are processed in a forward direction. This method is intended to identify underlying relationships in a set of data. The system comprises three layers: the input layer that accepts the input, the hidden layer that consists of neurons that process based on an activation function, and the output layer that produces the output.
- **Recurrent neural network (RNN):** RNNs are a type of artificial neural network used to address ordinal or temporal problems. Their distinct characteristic is their ability to draw on information from previous inputs to influence current inputs and outputs.
- **Long Short Term Memory network (LSTM):** LSTMs are a special class of RNN with the ability to learn long-term relationships.

3. Materials and Methods

An extensive literature review was conducted in accordance with PRISMA guidelines in order to identify all available publications related to predictive modelling for foodborne diseases published between 2015 and 2022. Database searched in this study include PubMed, Google Scholar, ACM, IEEE Xplore, ScienceDirect, and BMC using three search strings given below. The search string identifies all predictive modelling studies that have been conducted with specified bacterium. Specifically, string 2 is intended to search for animal-based predictive models related to bacterium. String 3 identifies all studies related to specific predictive algorithms and a bacterium.

String 1: TITLE (bacterium name) AND TITLE (PREDICTIVE) AND TITLE (MODELLING)

String 2: TITLE (bacterium name) AND TITLE (ANIMAL OR MILK OR POULTRY OR CHEESE) AND TITLE (PREDICTIVE OR MATHEMATICAL)

String 3: TITLE (bacterium name) AND TITLE (BARANYI OR LOGISTIC REGRESSION OR SVM OR LINEAR REGRESSION)

Of the 638 publications, 271 papers were excluded on the basis of their title, 34 papers were excluded after reading their abstracts, and 183 papers were excluded after reading the methodologies. Exclusions were made for studies that used human or water samples. In particular, we excluded all studies that were not animal or zoonotic based. Lastly, eligible studies focusing on predictive modeling analysis of zoonotic foodborne diseases were included in this review (Figure 1).

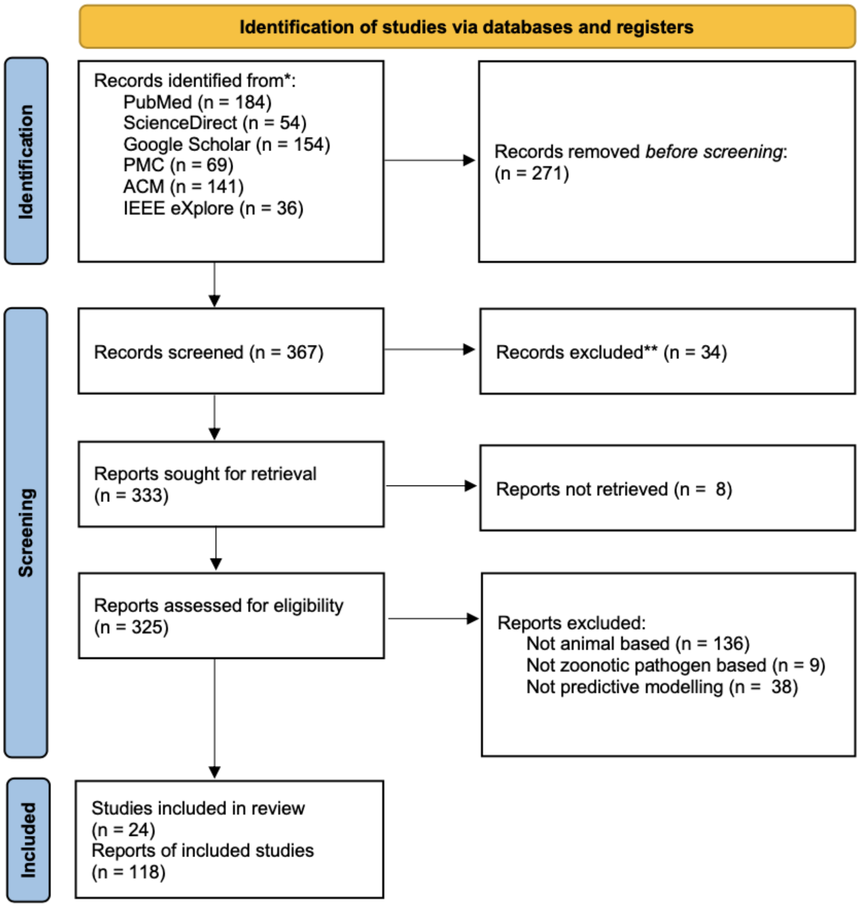

Figure 1. A flowchart illustrating how studies were selected for inclusion in this review based on Preferred Reporting Items for Systematic Reviews and Meta-Analyses (PRISMA).

4. Literature Review

This section provides a brief overview of zoonotic pathogen-based studies and their references. We review the studies based on bacterium (section 4.1), parasites (section 4.2), and virus (section 4.3). A summary of the literature review on bacterial and parasitic pathogens is provided in table 1.

Table 1. Etiology, Data source, and Reference

Etiology	**Data source**		**Reference**
	Animal	**Other**	
Salmonella	chicken liver		Dourou *et al.* 2021
		eggs	Park *et al.* 2020
		liquid egg whites	Kang *et al.* 2021
		scrambled egg mix	Li *et al.* 2017
		poultry farms	Hwang *et al.* 2020
Escherichia coli	human stool, cattle feces		Lupindu *et al.* 2015
		poultry farms	Xu *et al.* 2022
Escherichia coli, Shiga toxinproducing	beef		Amado *et al.* 2019
Campylobacter		poultry farms	Xu *et al.* 2021
	chicken, cattle, sheep, and wild birds		Arning *et al.* 2021
	meats, aquatic foods, eggs		Song *et al.* 2017
Clostridium perfringens	chicken		Sadeghi *et al.* 2015
	cooked ground pork		Juneja *et al.* 2021c
Clostridium botulinum	cooked pork		Juneja *et al.* 2022 Juneja *et al.* 2021b
	poultry meat		Juneja *et al.* 2021a
Staphylococcus aureus	beef		Amado *et al.* 2019
	beef		Yu *et al.* 2020
		eggs	Park *et al.* 2020
	cooked chicken		Hu *et al.* 2018
		chicken salad	Jafarpour *et al.* 2022
Staphylococcus spp.		swine farms	Mencía-Ares *et al.* 2021
	canine		Qekwana *et al.* 2017, Conner *et al.* 2018
*Shigella***	beef		Chai *et al.* 2016
		chicken salad	Jafarpour *et al.* 2022
Listeria monocytogenes	Mediterranean fish		Costa *et al.* 2019, Bolívar *et al.* 2018
	dairy, meat, poultry, seafood		Tanui *et al.* 2022
		dairy farm	Pang *et al.* 2017
Bacillus cereus	ready-to-eat boiled beef		Zhang *et al.* 2022
	dairy, meat		Ellouze *et al.* 2021
Vibrio parahaemolyticus	oyster		Ndraha *et al.* 2021, Liao *et al.* 2017
Vibrio vulnificus *Vibrio cholerae*	oyster		Ha *et al.* 2020a
	Raw whip-arm octopus		Oh *et al.* 2021
	sea squirts		Ha *et al.* 2020b
Vibrio vulnificus	oyster		Serment-Moreno *et al.* 2015
Vibrio alginolyticus	briny tilapia, shrimp, scallops oysters, pork, chicken freshwater fish, egg fried rice		Wang *et al.* 2021
Yersinia enterocolitica	mouse		Geißert *et al.* 2022
		milk from cows and goats	Bursová *et al.* 2017
		Camembert-type cheese	Kowalik and Lobacz 2015
		blue cheese	Zadernowska *et al.* 2015
Aeromonas hydrophila	chicken breasts		Yang *et al.* 2016
	raw tuna		Kim *et al.* 2022, Kim *et al.* 2021
	nigiri sushi or salmon		Hoel *et al.* 2018
	sardines		Bulat *et al.* 2020
Coxiella burnetti	dairy cattle herds		Pandit *et al.* 2016
	European rabbits		González-Barrio *et al.* 2015a
	dairy cow sheds		Boroduske *et al.* 2017
	cattle herds		Proboste *et al.* 2021
	sheep and goats		Valiakos *et al.* 2017
	red deer		González-Barrio *et al.* 2015b
Enterococcus faecalis	cow's milk		Ghalouni *et al.* 2018
Enterococcus faecalis *E. faecium, E. hirae* *E. durans*	raw milk pasturized milk		McAuley *et al.* 2015
Bovine tuberculosis	cow		Denholm *et al.* 2020
		cattle herd	Romero *et al.* 2020 Romero *et al.* 2021
Brucellosis		animal stock	Shen *et al.* 2022
Bacillus anthracis		animal density	Assefa *et al.* 2020
		elephant livestock	Walsh *et al.* 2019
Cryptosporidium		cattle and sheep feces	Ligda *et al.* 2020
	calf neonates		Delafosse *et al.* 2015
Giardia		cattle and sheep feces	Ligda *et al.* 2020
Trichinella Trichinella	pine martens pigs wild boars		Kirjušina *et al.* 2016 Franssen *et al.* 2017
African Trypanosomiasis			Bishop *et al.* 2021
Chagas disease			Eberhard *et al.* 2021

4.1. Bacterial Pathogens

Campylobacter: According to CDC, ***Campylobacter*** causes approximately 1.5 million illnesses a year (Centers for Disease Control and Prevention, 2020). Infection with *Campylobacter* can result in gastroenteritis, diarrhea, and sequelae such as Guillain-Barre syndrome. In order to predict *Campylobacter* prevalence on pastured poultry farms, Xu *et al.* (2021) developed a random forest predictive model that used farm practices and processing variables to identify variables that can reduce the prevalence of *Campylobacter* on pastured poultry farms.

Medical management has seen the benefits of deep learning in the prediction of morbidity. Song *et al.* (2017) developed a deep denoising autoencoder to discover relationship between the gastrointestinal diseases and the contaminants. Data was collected from four counties in China that included meat, aquatic foods, and eggs. Despite incomplete and imperfect information, their analysis showed that deep learning approaches are effective for building predictive models to detect diseases. Their neural network architectures were found to be effective in finding the source of *Campylobacteriosis*, a foodborne illness caused by *Campylobacter jejuni*.

In Arning *et al.* (2021), popular neural networks such as the recurrent neural network and the long short-term memory network have been used effectively to determine the source of transmission of *Campylobacteriosis* from a variety of food sources such as chicken, cattle, sheep, and wild birds. They concluded that tree-based ensemble methods for machine learning classification using bacterial genomic data are useful for determining the source of human *Campylobacteriosis*.

Listeriosis: The CDC estimates that 1,600 people contract ***Listeriosis*** each year, and approximately 260 of them die from the disease (https://www.cdc.gov/listeria/index.html). Immunocompromised individuals and pregnant women and their newborns are susceptible to infection. Using the core genomes of *L. monocytogenes*, Tanui *et al.* (2022) proposed machine learning models to attribute sources of human *Listeriosis*. The isolates from dairy, fruits, leafy greens, meat, poultry, seafood, and vegetables were analyzed to identify the source of the disease. The authors employed supervised classification algorithms, including the random forest algorithm, the support vector machine radial kernel algorithm, the stochastic gradient boosting algorithm, and the logistic boost algorithm in their study. Their analysis found that 17.5% of human clinical cases were caused by dairy products, 32.5% by fruits, 14.3% by leafy greens, 9.7% by meat, 4.6% by poultry, and 18.8% by vegetables. Furthermore, they demonstrated that genomic data combined with machine learning-based models can greatly enhance the ability to track *L. monocytogenes*.

The Baranyi model is found to be effective in detecting *L. monocytogenes* in Mediterranean fish species when packaged under different atmospheric conditions (Costa *et al.* 2019, Bolívar *et al.* 2018)). Pang *et al.* (2017) used logistic regression and random forest to analyze the association between meteorological factors and *Listeria spp.*. in a mixed produce and diary farm. This study collected fresh cow feces from a dairy barn, cow feed, cow drinking water, and bird feces, and water from the lagoon. Temperature, precipitation, and wind speed were included in the meteorological samples. According to their findings, wind speed and precipitation have a significant role in the transmission of *Listeria spp.*.

Salmonella: Dourou *et al.* (2021) investigated the potential for combining Fourier-transform infrared spectroscopy and machine learning algorithms in order to verify the quality of meat and poultry. This study focused on ***Salmonella***'s ability to survive and proliferate during extended refrigerated storage, and provides valuable information since there is limited research on chicken liver microbiological quality. They combined tree-based ensemble methods with support vector regression (SVR) to estimate the microbial populations in chicken samples. A combination of *Salmonella*-inoculated and non-inoculated chicken liver samples was used for food quality evaluation. Tree-based ensemble approach is used to extract the critical features that best represent the samples, and SVR with radial kernel function is used to estimate *Salmonella* levels. Overall, the results indicated that *Salmonella* was capable of both surviving and growing at refrigeration temperatures.

Salmonella enteritidis outbreaks that were reported in eleven U.S. states in October, 2018 listed shell eggs as a possible contributing factor (Centers for Disease Control and Prevention, 2018). Based on Monte Carlo simulation, Park *et al.* (2020) developed a predictive model for *Salmonella spp.* and *S. aureus* growth in fresh eggs under isothermal and non-isothermal conditions. However, it has been estimated that there is no likelihood of infection from ready-to-eat egg products due to *Salmonella spp.* or *S. aureus*. Using square root Ratkowsky *et al.* (1982) and Davey linear models, Kang *et al.* (2021) developed a predictive model to detect *Salmonella spp.* growth in pasteurized liquid egg whites (LEW) as a function of temperature. The researchers found that *Salmonella spp.* multiplied much more rapidly in LEW than in egg white under certain refrigerating conditions. Li *et al.* (2017) used a nonlinear baranyi model (Baranyi and Roberts, 1994) as the primary model and a modified Ratkowsky model (Zwietering *et al.*, 1991) as the secondary model to predict *Salmonella spp.* growth in scrambled egg mix as a function of temperature changes at the time of liquid egg processing. In their study, *Salmonella spp.* reached their maximum growth at 47 °C temperature for scrambled egg mix.

A random forest-based predictive model was developed by Hwang *et al.* (2020) to quantify the relationship between meteorological factors and the presence of *Salmonella* on pastured poultry farms. According to their analysis, the soil model identified humidity as the most significant meteorological variable associated with *Salmonella* prevalence, while the feces model identified high wind gust speed and average temperature as the most significant.

Escherichia Coli: In order to detect bacteria such as ***Escherichia Coli*** and ***Staphylococcus Aureus*** in raw meat (beef), Amado *et al.* (2019) employed a variety of machine learning algorithms (K-Nearest Neighbors (KNN), Support Vector Machine (SVM), Random Forest (RF), Naive Bayes Classifier (NB), and Artificial Neural Network (ANN))). The dataset inputs were derived from the emitted gases of meat. The Random Forest predictive model demonstrated the highest level of performance (more than 95% accuracy) in this multi-classification task.

Efforts to understand the impact of livestock farming practices on the transmission of zoonotic pathogens are always of interest to the health care sector. Using samples collected from 100 household clusters that kept cattle in close proximity to humans, Lupindu *et al.* (2015) studied the transmission of fecal microorganisms between cattle, humans, water and soil inside and outside livestock farms, as well as the transfer from livestock farms to the neighborhood. Ampicillin- and tetracycline-resistant *Escherichia coli* isolates were detected using logistic regression analysis from cow feces, human stools, soil, and water samples. Using such modeling provides a framework for improving livestock management practices to reduce fecal pollution and the spread of pathogens from livestock manure to humans and the environment. *E. coli* infections associated with foodborne pathogens like *Campylobacter*, *Salmonella*, and *Listeria* were studied by Xu *et al.* (2022) in pastured poultry farms. For fecal, soil, ceca and whole carcass rinse processing and chilling samples, a logistic regression model was developed. In their analysis, the amount of *E. coli* in the soil was significantly associated with the predicted presence of *Salmonella*, and the percentage of *Campylobacter* in feces and ceca decreased as *E. coli* concentration increased.

Staphylococcus aureus: Another Gram-positive bacterium, ***Staphylococcus aureus***, can cause nausea, vomiting, shock and shallow breathing (Millette *et al.*, 2007). In the United States, *S. aureus* has been reported in beef and beef products, posing a threat to food safety (Jackson *et al.*, 2013). Yu *et al.* (2020) assessed the growth or survival characteristics of *S. aureus* based on temperature, time, and packaging systems, and proposed statistical metrics for microbial risk assessment in beef. The researchers analyzed raw beef samples from wrapped packages (WP), modified atmosphere packages (MAP), vacuum packages (VP), and vacuum skin packages (VSP) to predict microbial growth based on the type of packaging. They used two primary models (modified Gompertz model and re-parameterized Gompertz survival model) and two secondary models (polynomial equation and Davey model) in the study. Their predictive model is validated using three factors: bias factor

(Bf), accuracy factor (Af), and RMSE. According to to their findings, the population of *S. aureus* increased in wrapped packaging beef and modified atmosphere packaging beef at 10 °C, whereas it decreased in vacuum packaging beef and vacuum skin packaging beef. To model the time to detect *Staphylococcal enterotoxins* produced by *Staphylococcus aureus* in cooked chicken products, Hu *et al.* (2018) proposed linear polynomial regression analysis. The high correlation coefficient of the regression equation indicated the validity of their methodology. Their study concluded that temperature is the most significant environmental factor that influences the detection of *S. enterotoxins*. *Staphylococcus aureus* and ***Shigella flexneri*** inactivation rates were evaluated in association with temperature variation when Vitex pseudo-negundo extract (VE) is added to chicken salad (Jafarpour *et al.*, 2022). A Baranyi inactivation model showed that higher concentrations of VE markedly promoted thermal inactivation of pathogens. This evaluation suggested that the predictive models can be used to select the best heat treatment for reducing pathogens without adversely affecting the quality of the product.

Shigella sonnei is an anaerobic, facultative, gram-negative pathogen that is commonly found in water, vegetables, and meat. By using a modified Gompertz model, Chai *et al.* (2016) examined *Shigella sonnei* in beef at different temperatures and predicted growth characteristics from quantitative real-time polymerase chain reaction (qRT-PCR). Their results indicated that as temperature increased, the lag time decreased and the maximum growth rate of *S. sonnei* in beef increased. This study presented a promising method for analyzing *Shigella sonnei* growth in food.

Bacillus cereus, a Gram-positive rod bacterium belonging to the prokaryotic group, is an aerobic, facultative human pathogen. In animal feeds and human foods, *Cinnamaldehyde* has demonstrated broad-spectrum antibacterial properties (Friedman, 2017). In Zhang *et al.* (2022), *Cinnamaldehyde* was investigated for its effects on the growth and germination of *Bacillus cereus* spores in boiled ready-to-eat ground beef. To predict the lag time and maximum growth rate, the Huang model was used as the primary model, while Cubic polynomial models were used as the secondary model. They used statistical measures such as the coefficient of determination (R2), the accuracy factor , the bias factor , and RMSE to evaluate the performance of the regressed model. In this study, *Cinnamaldehyde* was found to be a useful antimicrobial agent in ready-to-eat boiled ground beef that inhibited the germination and growth of *Bacillus cereus*. In another study, Ellouze *et al.* (2021) estimated the growth of *Bacillus cereus* and the synthesis of cereulides in cereal-, dairy-, meat-, and vegetable-based food matrices. Their experiments were conducted using the Baranyi model as the primary model and the Ratkowsky model as the secondary model. Based on the results of the study, both growth and toxin production were influenced by the food matrix and the environment.

Clostridium botulinum: Using Baranyi model as a primary model and modified Ratkowsky model as a secondary model, Juneja *et al.* (2021a) established a model of ***Clostridium botulinum*** inactivation in poultry meat when subjected to temperature variation. The same models were used to analyze the growth rates of *Clostridium botulinum* in cooked pork (Juneja *et al.* 2021b, Juneja *et al.* 2022). Juneja *et al.* (2021c) also developed a quadratic polynomial model and a Baranyi model to predict ***Clostridium perfringens*** growth in cooked ground pork supplemented with salt and sodium pyrophosphate at different temperatures. By using vocalization, Sadeghi *et al.* (2015) proposed a neural network method to detect and classify chickens infected with *Clostridium perfringens*. The five most important and effective vocal features of the poultry were selected based on Fisher Discriminate Analysis (FDA). It was then applied to detect signals and classify healthy and unhealthy chickens using the neural network pattern recognition (NNPR) structure.

Vibrio spp. are facultative, Gram-negative bacteria that survive in marine environments (Tsai *et al.*, 2009). ***Vibrio parahaemolyticus***, ***Vibrio vulnificus***, and ***Vibrio cholerae*** can cause dehydration, shock, sepsis, and even death when it is consumed raw or improperly heated (Gauthier 2015, Yan *et al.* 2019). Ha *et al.* (2020a) investigated that the likelihood of foodborne illnesses with raw oysters contaminated with *Vibrio vulnificus* and *Vibrio cholerae*.

The study analyzed *Vibrio spp.* growth bioaccumulation, and the concentration of bacteria that can be ingested through the consumption of oysters. Risk assessment results indicated that neither *V. vulnificus* nor *V. cholerae* were detected in the samples. Additionally, a dose response model using the Beta-Poisson model has been developed to calculate the probability of food poisoning occurring based on the exposure dose to pathogenic bacteria. They concluded that frequency of consumption is the most significant factor in the development of foodborne illnesses.

Oh *et al.* (2021) examined the growth rate and risk of food-borne illnesses with *V. vulnificus* and *V. cholerae* in South Korea from consumption of raw whip-arm octopus. To predict maximum specific growth and lag phase duration at different storage temperatures, the Baranyi model was used as the primary model and the polynomial model as the secondary model. Root Mean Square Error (RMSE), bias factor, and accuracy factor were used to measure the differences between predicted and observed values and parameters were compared to a pairwise t-test at $\alpha = 0.05$. In addition, a Beta-Poisson model was used to estimate *V. vulnificus* and *V. cholerae* dose response. The results indicated that consumption of raw whip-arm octopus in South Korea does not pose a high risk of infection with *Vibrio spp.*.

Ha *et al.* (2020b) evaluated the risk of foodborne illness with *V. vulnificus* and *V.cholerae* due to sea squirt consumption in South Korea. Beta-Poisson models were used to develop dose response, and the results indicate that the risk of pathogenic *Vibrio spp.* in sea squirt in South Korea is low. A curved, rod-shaped Gram-negative bacterium, *Vibrio parahaemolyticus*, found in the marine environment, is transmitted through undercooked seafood. Researchers have investigated the effect of oyster environmental parameters on the concentration of *Vibrio parahaemolyticus*.

Ndraha *et al.* (2021) examined the effect of sea surface temperature (SST), precipitation (Precp), wind speed (WS), wind gust (WS_gust), salinity (Sal), and acidity (pH) on *Vibrio parahaemolyticus* using machine learning and statistical metrics. An extreme gradient boosting machine learning algorithm (XGBoost) was used to build a prediction model for *Vibrio parahaemolyticus*. According to the results obtained, XGBoost is capable of modeling the pathogen in oysters and seawater, but not in sediments. As part of this study, partial dependence plots (PDPs) were generated by SHapley Additive exPlanations (SHAP) (Lundberg and Lee, 2017)[1] methods to determine the relationship between environmental variables and the level of *V. parahaemolyticus*. According to the relative importance variable analysis, variations in SST influence the concentration of *V. parahaemolyticus* in oysters.

Liao *et al.* (2017) analysed the survival of *V. parahaemolyticus* in Eastern oysters under a variety of temperature conditions. To determine the viability of *V. parahaemolyticus*, reverse transcription-PCR (RT-PCR) assay are used as input for the Baranyi function model. In another study, Wang *et al.* (2021) examined ***V. alginolyticus*** growth rate and hemolysin production in briny tilapia, shrimp, scallops, oysters, pork, chicken, freshwater fish, and egg fried rice. According to their analysis, the modified Gompertz model is a more effective model for predicting the growth of *V. alginolyticus* in food than the logistic model. They found that *Vibrio* growth was comparable in all food samples at the stationary phase while hemolysin activity and hemolytic titers were higher in some non-seafoods, and that raw and cooked foods did not differ in terms of growth or hemolytic activity. Upon analysis of raw oyster consumption risk along the northern coast of the Gulf of Mexico between 1994 and 1995, Serment-Moreno *et al.* (2015) found that quantification variability of *V. vulnificus* has a significant effect on the estimation of raw oyster consumption risk. To determine the probability of developing septicemia based on the load of *V. vulnificus*, a Beta-Poisson model was used. Monte Carlo analysis was performed with variables such as *V. vulnificus* counts at harvest, ambient temperatures during transportation, meat weight per oyster, Beta-Poisson model parameters, and high-pressure processing decimal reductions. According to their findings, raw oyster sampling and *V. vulnificus* quantification methods should be rigorously

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[1] SHAP dependancy plot demonstrates how a single feature impacts the model's output.

evaluated prior to implementing treatment and handling recommendations based on a risk analysis.

Antimicrobial resistance (AMR) is recognized as a global problem, but its magnitude has not yet been fully quantified. To evaluate the antimicrobial resistance of *Campylobacter*, *Salmonella*, and *Staphylococcus*, the most common zoonotic pathogens in pig populations, Mencía-Ares *et al.* (2021) assessed antimicrobial use on swine farms. In this study, the phenotypic resistance of *Campylobacter spp.*, *Staphylococcus spp.*, and *Salmonella spp.* isolates recovered from intensive and organic/extensive Spanish swine farms was investigated. Univariate mxed-effects logistic regression was used to assess the influence of production system type, sample type, antimicrobial consumption on the occurrence of multidrug resistant (MDR) phenotypes. Feces, slurry, and environmental variables were sampled for *Campylobacter*, environmental, oral fluid for *Staphylococcus*, and feces, slurry, environmental, oral fluid for *Salmonella*. Multivariate mixed effects analysis is applied to the predictor variables with a $p \leq 10$ in the likelihood ratio test (LRT) and is ranked using the Akaike information criterion (AIC). The odds ratio (OR) is reported as the influence factor along with its 95% confidence interval in the final model. This study demonstrated the link between antimicrobial consumption and resistance and concluded that AMR development in *Campylobacter spp.* and *Staphylococcus spp.* is influenced by the production system, with antimicrobial usage as a major factor.

Qekwana *et al.* (2017) studied patterns and predictors of AMR among *Staphylococcus spp.* isolates from clinical samples of canines submitted to the University of Pretoria bacteriology laboratory for routine diagnostic evaluation between 2007 and 2012. The dataset contained 334 confirmed *Staphylococcus* isolates, composed of *S. aureus* and *S. pseudointermedius*, with variables such as the site of collection, breed, sex, age, and the antimicrobial agent used for testing. They explored predictors of AMR in *S.aureus* (98% isolates) and *S. pseudintermedius* (77%) using logistic regression models. Chi-square or Fisher's Exact tests are used to find associations between categorical variables. An analysis of the trends in the proportion of samples resistant to each antimicrobial agent is performed using the Cochran-Armitage trend tests. A binary logistic regression model is used as an initial model to identify antimicrobial resistance predictors from variables such as age, sex, breed. In the second step, a multivariate logistic regression is conducted using variables that received a p-value less than 0.2 in the first step. Based on the Wald Chi-Square Test, predictor variables with p-values less than 0.05 were considered statistically significant. More than 50% of the *S. aureus* isolates tested in their study were resistant to *ampicillin*, *penicillin*, *lincospectin*, and *clindamycin*. Similarly, more than half of the isolates of *S. pseudointermedius* were resistant to both *ampicillin* and *penicillin*.

Conner *et al.* (2018) examined AMR predictors among *Staphylococcus spp.* isolated from canine specimens submitted to the University of Kentucky Veterinary Diagnostic Laboratory (UKVDL) between 1993 and 2009. In this study, 4,972 *Staphylococcus* isolates were assessed with variables including the year, *Staphylococcus spp.*, geographic region, dog breed, age group, sex, and specimen source. Cochran-Armitage trend tests were used to analyze the temporal trends for each antimicrobial. AMR and MDR were investigated using logistic regression models. This study found 80 isolates of *Staphylococcus spp.* to be resistant to 50% of the antimicrobials tested, while eight isolates were resistant to 75% of the antimicrobials tested.

Yersinia, belonging to the family Enterobacteriaceae, is a Gram-negative, rod-shaped, asporogenic facultative anaerobe. ***Yersinia enterocolitica (Ye)*** has been extensively investigated in host pathogen interaction studies (Dave *et al.* 2016, Deuschle *et al.* 2016). Geißert *et al.* (2022) examined the dynamics of bacterial population during gastrointestinal infection in murine models of oral infection with *Ye*. Using a computational model based on ordinary differential equations (ODE), analysis of scenarios where colonization resistance mediated by the microbiome is lacking, or where the immune response is partially compromised, was carried out. The ODE model with seven dimensions predicted *Ye* population dynamics and optimized it using maximum log-likelihood. This study demonstrated how computational modeling can help understand infection course across a variety of host environments. Identifying the microbiological risks associated with the production and distribution of food is critical to determining its shelf life and health benefits.

Bursová *et al.* (2017) used *Ye* growth dynamics to assess at the impact of storage conditions in pasteurized cow and goat milk. Based on the Baranyi-Roberts model, the paper examined the effects of proper and improper storage conditions on inoculated milk samples that were stored at 8°C and at 24°C for 14 days. This model predicted the time required for *Ye* to reach a critical mass in order to cause yersiniosis in humans. Modeling results indicated that, depending on the storage temperature, even low quantity of Ye can multiply to an infectious dose within a short period of time.

Kowalik and Lobacz (2015) conducted an evaluation of the growth rate of *Ye* at temperatures ranging from 3 to 15°C in Camembert-type cheese using mathematical models. Camembert-type cheese stored at 3-15°C showed a significant increase in *Ye*, according to the Baranyi and Gompertz model. This study summarized that the growth of *Y. enterocolitica* to a high level in Camembert-type cheese poses a health risk. In a similar study, Zadernowska *et al.* (2015) examined the possibility of *Ye* growing in blue cheese with and without a probiotic (Lactobacillus acidophilus LA-5®) at 3, 6, 9, 12 and 15°C. To determine whether there were significant differences, a one-way analysis of variance (ANOVA) and Duncan's multiple range test were performed. There was a systematic increase in cells at lower temperatures, as opposed to the stationary and die-off phases at higher temperatures. Study results showed that at every stage of the experiment, *Ye* cells were lower in the presence of the probiotic in the blue cheese.

Aeromonas hydrophila is a Gram-negative, facultative anaerobe that can cause a range of human infections, including gastrointestinal inflammation (on Microbiological Specifications for Foods, 1996). Hoel *et al.* (2018) discussed the increased consumption of ready-to-eat seafood and its food safety concerns regarding the presence of potentially pathogenic *Aeromonas spp.* in stored raw seafood products. A predictive model for *A. hydrophila*, however, was not sufficient to predict growth of nigiri sushi or salmon at different temperatures. Using the Baranyi model and nonlinear regression analysis, Kim *et al.* (2022) analyzed the function of *A. hydrophila* in raw tuna in relation to temperature. Bulat *et al.* (2020) measures the differences between microbial load and bacterial shell life of *A. hydrophila* with respect to storage of sardines at different temperatures , using a one-way analysis of variance (ANOVA) to determine differences in daily measures. Sardines' gills, skin, meat, and intestines were analyzed using statistical prediction models to estimate their shelf-life and quality. A post hoc Tukey test was used to determine whether there were any differences between the groups. Using the Levene test, homogeneity of variance was checked for dependent variables. A normal distribution was evaluated using the Kolmogorov-Smirnov and Shapiro-Wilk tests. Whenever the assumption of normality could not be achieved, Kruskal-Wallis and Mann-Whitney tests were used to determine the differences between the group means. The Friedman S test was used for the sensory analysis. According to their findings, sardines stored in the refrigerator had a longer shelf life than those stored at the temperature used for seafood processing. The sardines stored at the temperature used for seafood processing, however, contained higher microbial loads than those stored in the refrigerator. Yang *et al.* (2016) used modified Gompertz equations and nonlinear regression to model the growth rate of *A. hydrophila* as a function of changes in cold temperature. Based on their evaluations, the models were found to be useful for predicting the growth of *A. hydrophila* in chicken breasts.

Coxiella burnetii is an intracellular Gram-negative bacterium that causes Q fever in humans (Reeves *et al.*, 2017). Pandit *et al.* (2016) investigated the spread of *C. burnetii* across dairy herds of dairy cattle and quantified the contribution of airborne transmission and livestock exchange to pathogen spread.A Gaussian dispersion model with meteorological data was used to model the airborne dispersion. A Poisson model with a null hypothesis that the number of cases in each area would be proportional to the size of its population, a spatial cluster analysis for predicted positive herds was performed to identify regions with a high risk of incidence. According to their analysis, 92% of all new herd infections were caused by airborne transmission, while the remainder was associated with cattle trade. Furthermore, they report relatively small and ephemeral outbreaks in herds due to airborne transmission. Conversely, disease-free herds that acquired an infected cow showed a significantly higher prevalence within the herd.

González-Barrio *et al.* (2015a) examined the role of European rabbits in the Iberian region as a reservoir for *C. burnetii*. Islands. Serum, spleen, uterus, mammary glands, as well as vaginal, sex, weight, and presence/absence of ruminants and uterus swabs are among the variables examined. The risk of exposure to *C. burnetii* was analyzed by logistic regression models. The results show that rabbit density plays a major role in the ecology of *C. burnetii*, and the higher risk of exposure observed during the summer may be the result of increased indirect interactions with *C. burnetii* shed by coexisting ruminants.

Boroduske *et al.* (2017) investigated the prevalence and spatial distribution as well as risk factors contributing of *C. burnetii* infections in dairy cow sheds in Latvia. A Bernoulli probability model was used to predict high and low rates of occurence and antibody in clusters of cattle sheds infected with *C. burnetii*. By assessing the geographical distribution of *C. burnetii* seroprevalence in the cattle herds of Jimma town, Proboste *et al.* (2021) examined the ecological risk factors. Using a semivariogram via spatial correlations, the study investigated the geographical clustering of *Coxiellosis* seropositive farms and the strength of the clusters. The authors quantify the risk factors associated with Q fever and predicted its prevalence in Jimma using the binomial generalized linear method. A MaxEnt model is used by Valiakos *et al.* (2017) to determine the spatial distribution of exposure, identify environmental parameters, and to identify high exposure risk areas for sheep and goats to *C. burnetii* in central Greece. Based on environmental, host, and management factors, González-Barrio *et al.* (2015b) assesses red deer exposure to *C. burnetii* using multivariate logistic regression models and analyzes the influence of different potential risk factors.

Enterococcus faecalis: Baranyi growth model is also used by Ghalouni *et al.* (2018) to determine ***Enterococcus faecalis*** maximum cell density and growth rate in fermented cow's milk. Using Baranyi and Robert's model, McAuley *et al.* (2015) investigated the growth of ***E. faecalis, E faecium, E hirae, and E. durans*** present in raw milk and pasteurized milk. According to the study findings, *enterococci* in pasteurized milk are not associated with higher counts of *enterococci* in raw milk.

Bovine tuberculosis (bTB) is a slowly progressive and debilitating zoonotic disease caused by ***mycobacterium bovis*** infection in tissues primarily associated with respiratory tracts and lymph nodes. Denholm *et al.* (2020) used an artificial neural network architecture to predict the bTB status of UK dairy cows by using their mid-infrared spectral profiles, their single intradermal comparative cervical tuberculin (SICCT) skin-test results, their culture, and the presence of lesions. The architecture they developed enabled them to identify cows that are likely to fail the SICCT skin test, which allows farmers to make early management decisions concerning potential reactor cows. Romero *et al.* (2020) evaluated potential herd-level predictors of *bovine tuberculosis* using decision trees and multivariable logistic regression in high, edge, and low risk areas in England. This dataset contained information regarding demographic characteristics of the herd, the history of bTB, cattle movements, badger density, and land class. Using their models, they were able to analyze how bTB risk factors were interrelated in order to determine the likelihood of an incident occurring in high-risk groups of herds. In addition, Romero *et al.* (2021) conducted studies using random forest and LASSO regression models on the same dataset in order to identify high-risk farms and develop a targeted disease control strategy

Brucellosis is an infectious disease caused by ***brucellae*** bacteria that infects the human body and causes symptoms of fatigue, muscle aches and joint pains. Convolution-based LSTM recurrent neural networks were employed by Shen *et al.* (2022) to understand how machine learning can be applied to epidemic disease prediction using animal stock, food supply information, population, and GDP data. They devised an effective decision support system for controlling *brucella* .

Bacillus anthracis, a soil-borne spore-producing neglected bacterium, is responsible for ***anthrax***, an archetypal animal disease. With the use of artificial neural networks, surface range envelopes, flexible discriminant analysis, general linear models, general boosted models, classification tree analysis, multiple adaptive regression splines, random forests, and maximum entropy approaches, Assefa *et al.* (2020) developed a prediction analysis for *anthrax* using bioclimatic variables, soil characteristics variables, and livestock density variables. Based on their evaluation, the model was influenced by a variety of precipitation factors and animal density factors. Walsh *et al.* (2019) evaluated *anthrax*'s geographical suitability in India using a maximum entropy (Maxent) machine learning approach that considered both biotic and abiotic factors. There was a significant impact of water–soil balance, soil chemistry, and historic forest loss on the model, and the elephant-livestock interface played a crucial role in the cycle of *anthrax*.

4.2. Parasitic Pathogens

Cryptosporidium and ***Giardia*** are globally recognized as parasites that often cause waterborne diseases. *Giardia* cysts and *Cryptosporidium* oocysts cause gastrointestinal problems through direct and indirect transmission. Using fecal samples from cattle and sheep farms, Ligda *et al.* (2020) estimated the contribution of farms to surface water contamination and identified interactions between biotic/abiotic factors as a basis for developing models of risk assessment. To analyze microbiological, physicochemical, and meteorological parameters, this study developed a predictive model based on mixed effect zero-inflated negative binomial models and linear discriminant function analysis (LDFA). LDFA was successfully used as a machine-learning classification method to predict (oo)cyst concentrations from the input parameters. Delafosse *et al.* (2015) conducted studies on calf neonates living on dairy farms to determine the prevalence of *Cryptosporidium* infection and the risk factors associated with it. During the study, feces were microscopically examined for (oo)cysts and data about *C. parvum* oocyst shedding, calf-level care and management practices, and mortality rates were collected. They conducted both bivariate and multivariate analyses of the potential risk factors for *C. parvum* oocyst shedding. It was found that diarrhea in calves was strongly correlated with the amount of *C. parvum* (oo)cysts shed. According to their findings, calves with high diarrhea and shedding scores had a significantly higher mortality rate.

Trichinella parasites are cosmopolitan nematodes that infect mainly wild animals. Kirjušina *et al.* (2016) evaluated the larval biomass of naturally infected pine martens (Martes martes) of Latvia to investigate the transmission patterns of *Trichinella spp.* from animals to humans. From pine martens that had been infected with ***T. britovi***, muscles were collected from the abdomen, the back, the diaphragm, the intercostal muscles, the muscles of the head, the shoulders, the lower and upper parts of the forelimbs and hind limbs, the neck, the rump and tail, and the base and tip of the tongue. Using linear regression, the larval burden of muscles was evaluated to determine the total larval burden of an animal. Their results indicated that the estimated biomass was subject to substantial variation owing to the uncertainty of the parameters used to calculate the biomass. (Franssen *et al.*, 2017) utilized quantitative microbiological risk assessment (QMRA) methods in their paper to assess the risk of human *trichinellosis* associated with the consumption of meat from infected pigs, wild boars, and pigs raised in uncontrolled housing. In order to assess the risk model, *Trichinella* muscle larve (ML), edible muscle types, heat inactivation by cooking and portion sizes, and sensitivity at carcass control are taken into account. To estimate the number of larvae in an animal's diaphragm, a negative binomial distribution is used with maximum likelihood parameter estimation. The beta binomial distribution is used to model the variability associated with *Trichinella* ML detection. According to the analysis, testing for *Trichinella* in pigs that are kept under controlled housing does not add any value to the protection of human health.

Tsetse flies (family ***Glossinidae*** and genus ***Glossina***), which are obligate parasites and biological vectors of ***trypanosomes***, cause human sleeping sickness and *animal trypanosomi-*

asis. Bishop *et al.* (2021) used a random forest regression algorithm to construct a model for learning about ***Glossina pallidipes*** habitat suitability across Kenya and northern Tanzania based on genetic data and remotely sensed environmental data. Based on the research, they concluded that vector control will be most successful in the Lake Victoria Basin, and *G. pallidipes* should be managed as a single unit in most of eastern Kenya.

An ***American trypanosomiasis***, or ***Chagas disease***, is a neglected tropical disease caused by the flagellated protozoa ***Trypanosoma cruzi***. This disease is transmitted by *haematophagous triatomines* of the family *Reduviidae*, subfamily *Triatominae*. In order to detect differences in the intestinal metabolome of the *triatomine Rhodnius prolixus* and predict whether the insect had been exposed to *T. cruzi*, Eberhard *et al.* (2021) used logistic regression, random forest classifiers, and gradient boosting algorithms. The study uncovered complex interactions between the *triatomine* vector and parasite, including effects on metabolic signatures.

4.3. Viral Pathogens Based

This section provides a brief overview of viral pathogen-based studies and their references. A summary is provided in table 2

Table 2. Etiology, Data source, and Reference

Etiology	**Data source**		**Reference**
	Animal	**Other**	
Newcastle disease	chicken		Cuan *et al.* 2022
Norovirus	oyster deli meat		McMenemy *et al.* 2018 Hunt *et al.* 2020, Chenar and Deng 2021 Bozkurt *et al.* 2015a
Hepatitis A	deli meat clam		Bozkurt *et al.* 2015a Bozkurt *et al.* 2015b
Rotavirus *Astrovirus*		molecular sequencing	Mollentze *et al.* 2021
Rabies virus, Hepeviridae *Coronaviridae , Reoviridae* *Astroviridae, Picornaviridae*	vampire bats		Bergner *et al.* 2021
Avian influenza		poultry farm wild bird wild bird poultry farm	Yoon *et al.* 2020, Yoo *et al.* 2022 Yoo *et al.* 2021 Walsh *et al.* 2019 Schreuder *et al.* 2022
Mad cow disease	cows		Bhakta and Byrne 2021
Crimean-Congo haemorrhagic fever			Ak *et al.* 2020, Ak *et al.* 2018
Ebola virus	mice		Price *et al.* 2020
Japanese encephalitis		mosquitoes ardeid birds and pig density	Tu *et al.* 2021 Walsh *et al.* 2021
Rift Valley fever		wildlife	Walsh *et al.* 2017 Tumusiime *et al.* 2022
West Nile virus			Wieland *et al.* 2021 Chinnathambi *et al.* 2020
Zika virus			Evans *et al.* 2017
SARS-CoV-2			Ali *et al.* 2022 Fischhoff *et al.* 2021 Brierley and Fowler 2021

Noroviruses are a genus within the ***Caliciviridae*** family that causes acute gastroenteritis (AGE) worldwide. Shellfish consumption has been identified as a potential entry point for *norovirus* into the human population, and depuration is one method to reduce microbiological risk. In depuration, harvested shellfish are submerged in clean water, where they remain for a period of time sufficient for the animals to expel any microbiological

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contaminants. To explain how shellfish depuration affects *norovirus* levels, McMenemy *et al.* (2018) proposed a mathematical model based on a log-normal distribution. According to their analysis, *norovirus* and *FRNA+ bacteriophages* required substantially longer depuration times than *Escherichia coli*. For the purpose of risk assessment analysis, Hunt *et al.* (2020) used a lognormal and gamma distribution to estimate the distribution of *norovirus* copies per oyster. The weight of oyster digestive tissues had been multiplied by these distributions and is provided to three compound Poisson distributions: Poisson-lognormal, Poisson-gamma, and Poisson-K, in order to estimate the *norovirus* count. In their study, they concluded that no model fit better than the others, and that all three could be used in future risk assessments. Another research based on a hybrid PCA-ANN model, Chenar and Deng (2021) successfully predicted the 10 years of historical outbreaks of oyster *norovirus* along the northern Gulf of Mexico coast. Remote sensing data from the Moderate Resolution Imaging Spectroradiometer (MODIS) satellite, which are gathered at the center of each oyster harvesting area, were used as input to this system. In order to reduce the size of the MODIS Aqua data, PCA was utilized. They trained a Artificial Neural Network model using the first four years of data, and successfully predicted six additional years data.

Studies on the kinematics of thermal inactivation for microorganisms are essential for designing pasteurization conditions for foods in order to inactivate or control microorganisms. A Weibull-based mathematical model was used by Bozkurt *et al.* (2015a) to determine the thermal inactivation kinetics of Human *noroviruses (HNoV)* surrogates and ***hepatitis A*** virus in turkey deli meat in order to reduce the risk of foodborne illness outbreaks. According to their findings, *HNoV* surrogates and *HAV* are more resistant to heat than many vegetative bacteria found in food. Using similar method, Bozkurt *et al.* (2015b) developed thermal inactivation kinetics for *HAV* in order to design adequate thermal processes to control clam-associated outbreaks of *HAV*.

Researchers use molecular sequencing data (Mollentze *et al.*, 2021) to evaluate zoonotic potential by ranking the likelihood of human infection. Bergner *et al.* (2021) collected metagenomic sequences of feces and saliva from common vampire bats and evaluated their zoonotic potential using XGBoost. An analysis of variation in feature importance was performed using SHAP, and gradient boosted machines (GBMs) trained on virus taxonomy were used to rank phylogenetic proximity to human-infecting viruses. Based on their findings, 58 viruses were detected as having a higher zoonotic potential, which includes ***rabies virus, Hepeviridae, Coronaviridae, Reoviridae, Astroviridae, and Picornaviridae***.

Avian influenza virus (HPAI) is a highly contagious virus that belongs to the family *Orthomyxoviridae* and genus *influenza virus A*. Using poultry farm management variables, the visit records of livestock-related vehicles, and environmental variables, Yoon *et al.* (2020) presented a deep learning model to assess *avian influenza* risk at the farm level. As a result of their study, preemptive control measures were taken to prevent the spread of disease, enhancing risk management activities. Yoo *et al.* (2021) employed Random Forest, Gradient Boosting Machine (GBM), and eXtreme Gradient Boosting models to predict *avian influenza* using environmental, on-farm biosecurity, meteorological, vehicle movement, and HPAI wild bird surveillance data. Eight to ten of the 19 premises infected during the infected period were predicted to be at high risk in advance by these models. Based on wild bird samples, Walsh *et al.* (2019) used gradient boosted trees to predict *avian influenza viruses*. Analysis of sample features, including bird age, sex, bird type, geographic location, and rRT-PCR results, revealed that geographic location and rRT-PCR results are predictive factors. Schreuder *et al.* (2022) predicted spatial patterns associated with HPAI outbreak risk on Dutch poultry farms based on wild bird density and land cover data. Random forest prediction evaluation identified 20 best explaining predictors, of which 17 are water-associated bird species, 2 are birds of prey, and 1 is agricultural cover. Similarly, Yoo *et al.* (2022) used a Bayesian logistic regression and an extreme gradient boosting model to predict the risk of HPAI occurrence at poultry farms using 12 spatial variables. According to their study, domestic duck farms and the minimum distance to live bird markets were the leading risk factors for outbreaks.

Cuan *et al.* (2022) found an effective deep learning method based on a bidirectional long short term memory neural network for detecting ***Newcastle disease Virus***. They extracted complex vocalizations from a specific pathogen-free chicken (SPF) poultry and used them to develop a predictive model to distinguish sick vocalizations from healthy vocalizations.

Creutzfeldt-Jakob disease (CJD), also called ***mad cow disease***, is a fatal neurodegenerative disease resulting in lesions, cell damage, gliosis, and neuron loss. A popular variant of CJD is caused by consumption of cattle products contaminated with bovine *spongiform encephalopathy (BSE)*. With the use of elastic net regression, recurrent neural networks, and random forests, Bhakta and Byrne (2021) learned the predictive causes of the CJD epidemic in the United States. Their results indicated that beer consumption, obesity, and tobacco use are strongly associated with CJD.

Crimean-Congo haemorrhagic fever (CCHF) is a highly virulent human disease caused by a single-stranded, negative sense RNA virus belonging to the genus ***Nairovirus*** in the family ***Bunyaviridae***. Using a structured Gaussian approach, Ak *et al.* (2020) identified risky geographic regions for the CCHF (Ak *et al.*, 2018). The dataset included information on climate, land use, and animal and human populations at risk in order to capture spatiotemporal transmission dynamics. According to their analysis, CCHF is primarily driven by geographical dependence and climate effects on ticks.

Ebola virus disease (EVD) is a rare and deadly disease affecting humans and non-human primates. Using clinical, virologic, and transcriptomic features that distinguish tolerant from lethal outcomes, Price *et al.* (2020) studied host responses to the *Ebola virus* infection in mice. Based on their analysis, the random forest model was found to be capable of accurately predicting disease outcome.

Japanese encephalitis virus (JEV) is a zoonotic disease spread by mosquitoes, particularly ***Culex tritaeniorhynchus***. Using a long short-term memory model, Tu *et al.* (2021) assessed the relationship between meteorological factors and population density of *Culex tritaeniorhynchus*. Using their analysis, they found that mean air temperature and relative humidity had a positive effect on outbreak risk and intensity. Using wildlife-livestock interfaces, Walsh *et al.* (2021) examined the landscape epidemiology of JEV outbreaks in India. A poisson point process was used to model outbreak risk, which was strongly influenced by habitat suitability of ardeid birds and pig density.

Rift Valley fever is a severe viral hemorrhagic fever caused by ***RVF virus*** (genus *Phlebovirus*, order *Bunyavirales*). Utilizing a maximum entropy machine learning model, (Walsh *et al.*, 2017) examined the ecological role of wildlife reservoirs and surface water features in the increasing risk of RVF outbreaks. A correlation between RVF outbreaks and wetlands, bovidae species richness, and sheep density was found in their validation study. Using Bayesian models with Laplace approximations, Tumusiime *et al.* (2022) estimated the risk of RVF based on animal level factors and meteorological factors. Based on their analysis, it was concluded that low precipitation seasonality, haplic planosols, and low cattle density were highly associated with the risk of mortality.

West Nile virus is an emerging arthropod-borne virus that causes ***West Nile fever***, which is most commonly transmitted by mosquitoes. An analysis of climate factors and regional data was conducted by Wieland *et al.* (2021) for predicting the distribution of native mosquito species as vectors of the *West Nile virus*. An XGboost machine learning algorithm was used for the evaluation model, and the SHAP library was used for the identification of explanatory variables. They concluded that regional characteristics play a larger role in the habitat of native mosquitoes than climatic conditions. Using a hybrid support vector machine and partial least square regression model, Chinnathambi *et al.* (2020) effectively forecasted trap counts of *Culex Tarsalis*, female mosquitoes that transmit *West Nile Virus*, based on meteorological data, dead birds, WNV cases, and human deaths.

Aedes mosquitoes (A. aegypti and A. albopictus) are the primary vectors of the ***Zika virus***, which belongs to the *Flaviviridae* virus family. Using an ecological network that links *flaviviruses* and their mosquito vectors, Evans *et al.* (2017) developed a predictive model using gradient boosted regression treed to identify associations between vector species and the *Zika virus*. According to their model, 35 species, including *Culex quinquefasciatus* and *Cx. pipiens*, might be capable of transmitting the disease.

COVID-19 is caused by ***severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2)***, a *coronavirus*. While the origin of *COVID-19 (SARS-CoV-2)* in humans is unknown, using feature vectors derived from spike protein sequences using a position weight matrix (PWM), Ali *et al.* (2022) assessed the host specificity of *coronaviruses* in birds, bats, camels, swine, humans, and weasels. Using boosted regression algorithms, Fischhoff *et al.* (2021) combined ecological traits with biological traits in an attempt to predict the zoonotic potential of *SARS-CoV-2* in greater than 5000 mammals. Based on their evaluations, 540 species belonging to 13 orders were predicted to have a high zoonotic potential for *Corona virus*. Based on sequencing of 511 whole genome nucleotide sequences and 650 spike protein sequences, Brierley and Fowler (2021) developed a random forest model to predict the host animal for *SARS-CoV-2*. According to their analysis, human sequences of *SARS-CoV-2* were predicted to have been acquired from bats (suborder *Yinpterochiroptera*), supporting bats as the probable source of the current pandemic.

5. Discussion

Neural network and machine learning models used in the detection of zoonotic pathogens, along with their references, are presented in Table 3 and 4.

Table 3. Neural network learning approaches, Etiology, and References

Neural Learning Models	Etiology	Reference
Artificial neural network	*Escherichia coli, Shiga toxinproducing*	Amado *et al.* 2019
	Clostridium perfringens	Sadeghi *et al.* 2015
	Staphylococcus aureus	Amado *et al.* 2019
	Norovirus	Chenar and Deng 2021
	Avian influenza	Yoon *et al.* 2020
	Bacillus anthracis	Assefa *et al.* 2020
	Mad cow disease	Bhakta and Byrne 2021
	Bovine tuberculosis	Denholm *et al.* 2020
Long short-term memory RNN	*Campylobacter*	Arning *et al.* 2021
Long short-term memory	*Newcastle disease*	Cuan *et al.* 2022
	Brucellosis	Shen *et al.* 2022
	Japanese encephalitis virus	Tu *et al.* 2021
Auto-Encoder	*Campylobacter*	Song *et al.* 2017

In our survey, neural network (deep learning) methods have been found to be effective for detecting animal diseases. In particular, the use of LSTM, RNN, and Auto-Encoder neural network models have been found to be effective in modelling various zoonotic pathogens. Machine learning algorithms such as logic regression, support vector machines, gradient boosting algorithms, and random forest models are commonly used to predict pathogens and their associated risks. In our literature review, these methods, along with linear regression, Naive Bayes, and K-Nearest Neighbors, have been used to identify popular food attributions to diseases. A number of popular food choices, such as chicken, beef, pork, dairy products, and seafood, have been found to pose a potential risk factor for various zoonoses based on their prediction models.

Table 4. Machine learning approaches, Etiology, and References

Machine Learning Models	Etiology	Reference
Support Vector Machine	*Salmonella*	Dourou *et al.* 2021
	Escherichia coli, Shiga toxinproducing *Staphylococcus Aureus*	Amado *et al.* 2019
	Listeria monocytogenes	Tanui *et al.* 2022
	West Nile virus	Chinnathambi *et al.* 2020
Logistic Regression	*Listeria monocytogenes*	Pang *et al.* 2017
	Staphylococcus spp.	Mencía-Ares *et al.* 2021 Qekwana *et al.* 2017 Conner *et al.* 2018
	Coxiella burnetti	González-Barrio *et al.* 2015a González-Barrio *et al.* 2015b
	*** *E. coli*	Lupindu *et al.* 2015, Xu *et al.* 2022
	Avian influenza	Yoo *et al.* 2022
	Bovine tuberculosis	Romero *et al.* 2020, Romero *et al.* 2021
	Chagas disease	Eberhard *et al.* 2021
Linear Regression	*Trichinella*	Kirjušina *et al.* 2016
Random Forest	*Salmonella*	Dourou *et al.* 2021
	Escherichia coli, Shiga toxinproducing *Staphylococcus Aureus*	Amado *et al.* 2019
	Salmonella	Hwang *et al.* 2020
	Campylobacter	Xu *et al.* 2021
	Staphylococcus aureus	Amado *et al.* 2019
	Listeria monocytogenes	Tanui *et al.* 2022, Pang *et al.* 2017
	African trypanosomiasis	Bishop *et al.* 2021
	Avian influenza	Yoo *et al.* 2021
	Avian influenza	Schreuder *et al.* 2022
	Bacillus anthracis	Assefa *et al.* 2020
	Mad cow disease	Bhakta and Byrne 2021
	Bovine tuberculosis	Romero *et al.* 2020, Romero *et al.* 2021
	Chagas disease	Eberhard *et al.* 2021
	Ebola virus	Price *et al.* 2020
	SARS-CoV-2	Brierley and Fowler 2021
Gradient Boosting	*Listeria monocytogenes*	Tanui *et al.* 2022
	Vibrio parahaemolyticus	Ndraha *et al.* (2021)
	Rabies virus *Hepeviridae* *Coronaviridae* *Reoviridae* *Astroviridae* *Picornaviridae*	Bergner *et al.* 2021
	Avian influenza	Yoo *et al.* 2021
	Avian influenza	Walsh *et al.* 2019
	Avian influenza	Yoo *et al.* 2022
	Bacillus anthracis	Assefa *et al.* 2020
	Chagas disease	Eberhard *et al.* 2021
	West Nile virus	Wieland *et al.* 2021
	Zika virus	Evans *et al.* 2017
	SARS-CoV-2	Fischhoff *et al.* 2021
K-Nearest Neighbors	*Escherichia coli, Shiga toxinproducing*	Amado *et al.* 2019
	Staphylococcus aureus	Amado *et al.* 2019
NaïveBayes	*Escherichia coli, Shiga toxinproducing*	Amado *et al.* 2019
	Staphylococcus aureus	Amado *et al.* 2019
	Rift Valley fever	Tumusiime *et al.* 2022
Linear Discriminant Function Analysis	*Cryptosporidium*	Ligda *et al.* 2020
Polynomial regression	Salmonella	Park *et al.* 2020
	Staphylococcus aureus	Hu *et al.* 2018
Monto Carlo Simulation	*Salmonella*	Park *et al.* 2020
Gaussian Process	*Crimean-Congo haemorrhagic fever*	Ak *et al.* 2020, Ak *et al.* 2018
Poisson Point Process	*Japanese encephalitis virus*	Walsh *et al.* 2021

Table 5 summarizes the popular mathematical models and their references.

Table 5. Mathematical Models, Etiology, and References

Mathematical Model	**Etiology**	**Reference**
Baranyi and Roberts model	*Salmonella*	Li *et al.* 2017
	Staphylococcus aureus *Shigella***	Jafarpour *et al.* 2022
	Listeria monocytogenes	Costa *et al.* 2019, Bolívar *et al.* 2018
	Bacillus cereus	Ellouze *et al.* 2021
	Clostridium perfringens	Juneja *et al.* 2021c
	Clostridium botulinum	Juneja *et al.* 2021a Juneja *et al.* 2022 Juneja *et al.* 2021b
	Vibrio parahaemolyticus	Liao *et al.* 2017
	Vibrio vulnificus *Vibrio cholerae*	Oh *et al.* 2021
	Yersinia enterocolitica	Bursová *et al.* 2017, Kowalik and Lobacz 2015
	Aeromonas hydrophila	Kim *et al.* 2021, Kim *et al.* 2022
	Enterococcus faecalis *E. faecium* *E. hirae* *E. durans*	McAuley *et al.* 2015
	Enterococcus faecalis	Ghalouni *et al.* 2018
Gompertz model	*Staphylococcus aureus*	Yu *et al.* 2020
	*Shigella***	Chai *et al.* 2016
	Yersinia enterocolitica	Kowalik and Lobacz 2015
	Vibrio alginolyticus	Wang *et al.* 2021
	Aeromonas hydrophila	Yang *et al.* 2016
Ratkowsky model	*Clostridium botulinum*	Juneja *et al.* 2021a Juneja *et al.* 2022 Juneja *et al.* 2021b
	Salmonella	Li *et al.* 2017
	Bacillus cereus	Ellouze *et al.* 2021
Polynomial models	*Staphylococcus aureus*	Yu *et al.* 2020
	Bacillus cereus	Zhang *et al.* 2022
	Clostridium perfringens	Juneja *et al.* 2021c
	Vibrio vulnificus *Vibrio cholerae*	Oh *et al.* 2021
Beta-Poisson Model	*Vibrio vulnificus, Vibrio cholerae*	Ha *et al.* 2020a, Ha *et al.* 2020b
	V. vulnificus	Serment-Moreno *et al.* 2015
Square root linear model	*Salmonella*	Kang *et al.* 2021
Gaussian dispersion model	*Coxiella burnetti*	Pandit *et al.* 2016
Bernoulli probability model	*Coxiella burnetti*	Boroduske *et al.* 2017
Binomial model	*Coxiella burnetti*	Proboste *et al.* 2021
	Cryptosporidium	Ligda *et al.* 2020
	Trichinella	Franssen *et al.* 2017
Maximum entropy model	*Coxiella burnetti*	Valiakos *et al.* 2017
	Bacillus anthracis	Assefa *et al.* 2020
	Bacillus anthracis	Walsh *et al.* 2019
	Rift Valley fever	Walsh *et al.* 2017
Huang Model	*Bacillus cereus*	Zhang *et al.* 2022
Davey linear model	*Salmonella*	Kang *et al.* 2021
	Staphylococcus aureus	Yu *et al.* 2020
Weibull model	*Norovirus* *Hepatitis A*	Bozkurt *et al.* 2015a
	Hepatitis A	Bozkurt *et al.* 2015b

Mathematical models have been widely used in research pertaining to bacterial growth, survival, and inactivation. Baranyi and Roberts' model is one of the most popular choices for testing the dynamics of bacterial growth in response to temperature changes. Together with the modified Ratkowsky model, the Baranyi model was successfully used to verify the bacterial growth potential in *Bacillus cereus, Salmonella, and Clostridium botulinum*. Our

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literature search suggests that combining Baranyi with Gompertz or polynomial models can be useful for detecting bacterial contamination. In addition, the modified Gompertz model has proven to be an effective method for modeling bacterial growth, survival, and inactivation. Several researchers have demonstrated that Gompertiz models are effective for detecting bacteria such as *Staphylococcus aureus, Shigella, Vibrio alginolyticus, Yersinia enterocolitic*, and *Aeromonas hydrophila* in response to temperature changes. The use of polynomial functions in combination with other primary models for determining the quantity of bacteria in different foods also appears to be beneficial. The literature has identified numerous mathematical equations for the classification of bacteria, parasites, and viruses, including the beta-poisson equation, Bernoulli equation, Binomial equation, Davey equation, Huang equation, and Weibull equation.

A quantitative representation of predictive algorithms in the literature is presented in Figure 2.

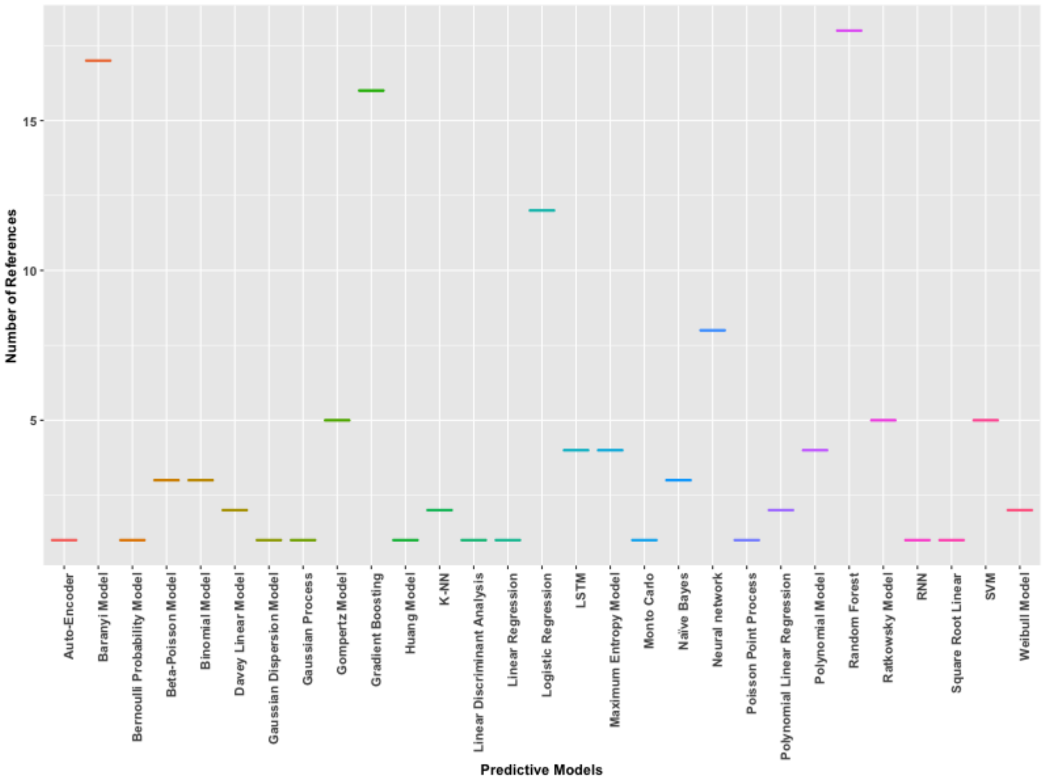

Figure 2. Predictive algorithms and their representation in etiology based studies.

6. Conclusion

We aimed to synthesize and analyze available mathematical, machine learning, and deep learning approaches related to zoonotic pathogens in this study. Our review findings will assist researchers and risk managers in better understanding the predictive modeling research on zoonosis and in identifying research gaps. By using the tools described in this study, it is possible to identify the risks in the food chain and the methods that can be used to eliminate them. The study revealed that mathematical algorithms and traditional machine learning models are widely used in this field. However deep learning methods have tremendous potential for identifying appropriate protective measures. Application of deep learning techniques, such as segmentation and classification of images, can enhance research into diagnosing irregularities caused by infections. While the resources in this field are limited, transfer learning (Jeremy *et al.*, 2005) where we reuse a previously trained model as the basis for training a new model or zero-shot based learning (Chang *et al.*, 2008) that classifies data based on very few or even no labeled examples have the potential to make learning more efficient.

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