17(2) 351-366, Summer 2025

Journal of Animal Environment

(E-ISSN 2717-1396, ISSN 2717-1388)

Journal homepage: http://www.aejournal.ir

Original Research Paper

Impact Of Waterborne Pathogens on Gastrointestinal Diseases in People and Wildlife Populations in Areas with Poor Sanitation

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Key Words

Waterborne pathogens, Gastrointestinal diseases, Poor sanitation, Public health, Microbial contamination, Disease transmission, Environmental health.

Abstract

Inadequate sanitation has continued to contribute immensely to the distribution of waterborne pathogens as well as the burden of gastrointestinal diseases among vulnerable human populations. The paper will look at how gastrointestinal disease is caused by contaminated water in a society without proper sanitation facilities due to the source of the pathogens. Water samples of drinking and domestic-use were tested to determine any major bacteria, viral, and protozoan pathogens, and household surveys were carried out to establish the level of disease prevalence, hygienic practices, and patterns of exposure. The results reveal that the contamination of microbes is high, and E. coli, Vibrio, rotavirus, and Giardia were found in different sites. Accordingly, gastrointestinal symptoms comprising diarrhoea, vomiting, and abdominal pains were significantly more common in those places that had the highest pathogen loads. The statistical analysis revealed that the association between the concentration of microbes and the presence of the disease was very strong, and all the factors were the products of the effects of unsafe water, low levels of hygiene, and poor sanitation. It has also been observed that the impact of the waterborne pathogens on domestic and wild animals, including livestock and wildlife species, are also affected since they also come into contact with the same sources of contaminated water, and they may be the cause of further spreading the disease to humans. This finding has been supported by the evidence around the globe that water and sanitation quality are significant determinants of health, particularly in low-resource settings. In this paper, the significance of specific measures, including improved water treatment, improvements in sanitation systems, and the community level of hygiene education, is emphasized to minimize disease transmission and protect vulnerable populations.

Introduction

Waterborne pathogens still pose a significant burden on people's overall health, particularly in areas where safe water and sanitary sewerage are not readily available. These microbes include bacteria, viruses, and protozoa, and they remain in water contamination in the surface waters, shallow wells, and poorly guarded distribution systems. They may easily cause gastrointestinal

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Received: 15 May 2025; Reviewed: 20 June 2025; Revised: 13 August 2025; Accepted: 29 August 2025
(DOI): 10.70102/AEJ.2025.17.2.34

infections of varying severity once they enter domestic water used for consumption or food preparation (Ashbolt, 2004). Vibrio cholerae, Escherichia coli, rotavirus, and Giardia are common pathogens regularly reported in poorly managed water sources, and their presence indicates broader failures of the environmental health infrastructure (Forstinus et al., 2016). Recurrent diarrheal episodes, growth retardation, and immunosuppression in children in many low-income environments where such organisms are routinely encountered have been associated with the problem; thus, it is not only acute but also chronic in nature (Islam et al., 2020). Environmental stressors such as increased precipitation, uncontrolled flooding, and rising temperatures also promote pathogen spread by destabilizing sanitation facilities and enhancing the movement of fecal contaminants (Cissé, 2019).

Along with people, domestic animals, livestock, and wildlife species in such regions are prone to waterborne pathogens. Most of these animals consume similar sources of contaminated water, thus contracting similar gastrointestinal diseases (Lobna & Metawea, 2013). Moreover, the animals may serve as a reservoir or vectors and transmit the pathogens to humans, particularly in rural and peri-urban environments. The One Health approach to the issue of human and animal health highlights the connection between human health and animal health within the framework of the transmission of waterborne diseases. Such need encompasses the incorporation of the treatment of human and animal waste in the sanitation strategies as a means of minimizing the spread of microorganisms (Sobsey et al., 2006). Consequently, waterborne pathogens have remained the primary focus of health organizations in nations seeking to reduce the prevalence of preventable gastrointestinal illnesses.

Neighborhoods without adequate sanitation facilities face a distinct cluster of hazards that increase their susceptibility to gastrointestinal illnesses. Sanitation in most informal settlements and peri-urban areas is loosely controlled, or not at all, and fecal matter can reach groundwater and streams, as well as domestic storage and storage vessels. Research indicates that open defecation, leaky pit latrines, and sewage discharge lead to direct entry of microbial pollution into the environment, eventually weakening the water sources on which the population depends daily (Atemoagbo, 2024). Inadequate waste management, stagnant waste and living in overcrowded environments are all that enhance the chances of pathogens dispersing using different routes of exposure (Kulshrestha & Mittal, 2003). Studies conducted in urban slums show that viral and bacterial pollution is often above established limits, and household wells are too close to sanitation facilities, which leads to recurrent illnesses, particularly among children and the elderly (Katukiza et al., 2014). As a result, people in these settings end up in a spiral of poor sanitation, which is directly linked to increased rates of gastrointestinal diseases and outbreaks. The impact of waterborne pathogens on gastrointestinal diseases in human populations in areas with poor sanitation is a critical public health issue, highlighting the urgent need for effective water treatment strategies and health interventions in underserved regions (Rajan, 2024**).**

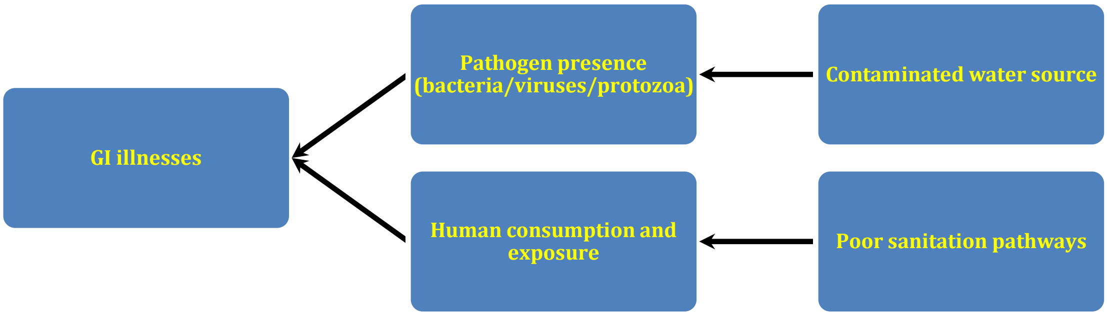

Figure 1(a): Conceptual Overview of Waterborne Pathogen Exposure

This (Figure 1(a)) illustrates the key pathways through which polluted water may lead to gastrointestinal illnesses among human beings. It shows how a polluted water source might turn in a source of pathogens (bacteria, viruses, and protozoa) due to poor sanitation, and then be ingested or contacted by humans, and hence cause GI diseases. The diagram is graphically used to demonstrate the connection between environmental pollution, hygiene, and human health, and to point out the key areas, where the interventions can reduce the risk of the disease.

The former aims to evaluate microbial contamination in drinking and domestic-use water sources and to determine how this assessment relates to the incidence of reported health symptoms. The second aim is to analyze factors related to sanitation, including waste disposal, water-holding habits, and environmental hygiene, that can promote the spread of pathogens. In low-resource communities, the study seeks to identify the pathways that expose residents to increased risk. Experiences of the previous literature point to the fact that low sanitation, poor hygiene, and unsafe water are the factors that increase the disease outcomes, and that integrated analysis is the necessary condition to create effective intervention planning (Pal et al., 2018; Praveen et al., 2016; Nwabor et al., 2016). The research will give a comprehensive view of the interaction between water quality and gastrointestinal disease using environmental sampling and health data analysis hence will provide evidence to guide the policy makers and health practitioners to formulate particular solutions at the community level. The spread of waterborne pathogens in areas with poor sanitation contributes significantly to gastrointestinal diseases, underscoring the need for urgent public health interventions and preventive strategies, as highlighted by similar research (Ismail & Ahmad, 2024).

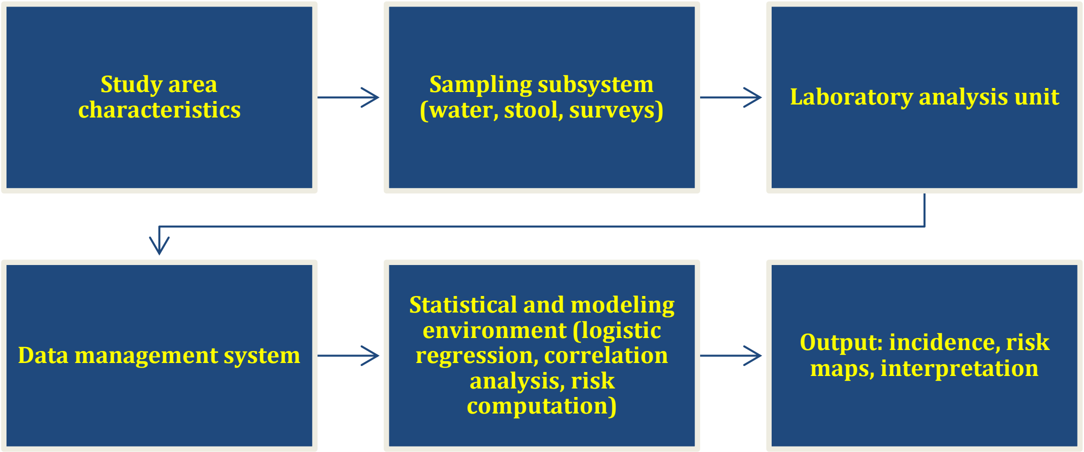

Figure 1(b): Research Workflow for Waterborne Pathogen Assessment

Figure 1(b) illustrates the whole research procedure, which will start with the characterization of the study area, collection of samples (water, stool and surveys) and laboratory assessments. This leads to data management which is systematic and statistical modeling (logistic regression, correlation analysis, risk calculation) and lastly, results would be incidence rates, risk maps, and their interpretation. It gives a simple step-by-step demonstration of the flow of data between the collection stage and analysis into useful information.

The remainder of this paper is structured in a way that the development of the context to conclusions is understandable and clearly structured. The literature review follows the introduction that presents the significance of waterborne pathogens and the conditions in low-sanitation facilities, which predisposes people to the development of the disease. The next part (methodology) describes the region of the study, the way of sampling, the laboratory procedure and the measures of the analyses to determine the contamination and health outcomes. This is preceded by the findings which are the integration of the laboratory findings, the disease incidences, and statistical correlations that show the relationship between water quality and gastrointestinal illness. These are addressed in the context of the whole study and with specific attention paid to convergent and distinct findings. Finally, a conclusion will summarize the main results, limitations of the study, and propose the further research and ways to enhance the sanitation.

Literature Review

Waterborne pathogens represent a wide category of microorganisms that may lead to gastrointestinal infections in case they are ingested as contaminated water or food. Bacterial agents are also one of the most widely studied and identified, and these are Vibrio, Salmonella, and pathogenic E. coli that are frequently present in sewage-contaminated environments. The high load of bacteria is caused by runoff, poor drainage, and degraded infrastructure in some localities, which enables fecal contamination of the distribution systems (Arnone & Walling, 2007). Viral pathogens i.e., norovirus, hepatitis A virus and rotavirus are also important due to their low infectious doses and have a longer persistence in water. It has been determined that the changes in water temperature and salinity induced by the climate influence the viral survival and seasonality, which in turn cause changes in the pattern of the infection of the exposed population (Nichols et al., 2018). Other major causes of persistent diarrheal disease are the protozoa (such as Giardia and Cryptosporidium). The outcome of meta-analyses shows that the lack of sanitation and water treatment can also be considered a good predictor of protozoan infection and that these factors are pronounced in rural and peri-urban populations, where there are no protective measures against contaminants (Speich et al., 2016). The synergistic relationship between these groups of pathogens shows the multifaceted microbiological image of the spread of waterborne diseases. The issue of waterborne pathogens in unsanitary areas is a major contributor to gastrointestinal disease burden hence the need to create new methods of diagnosing and treating it just like in the case of medical diseases.

There are a few ways through which fecal pathogens can access the human body in places where there are incomplete or poorly constructed sanitation systems. The major sources of pathogen transmission are usually contaminated surface water and shallow ground water, especially in cases where households rely on untreated water sources to drink or wash their clothes. The discharge of sewage in the Ganges river indicates that, along with the culturally-based bathing, it provides uniform exposure routes making the pathways more vulnerable to enteric infections (Hamner et al., 2006). The absence of proper hygiene, as well as other aspects that reduce the number of handwashing stations, further endangers disease transmission at the domestic level, particularly among children, who are highly susceptible to fecal-oral transmission (Brown et al., 2013). The proliferation of pathogens in drinking-water supplies and the introduction of disease risk in settlements with an inadequate drainage infrastructure are also caused by flooding, runoff, and seasonal changes (Fenta & Kebede, 2019). Other activities like livestock watering and poor handling of animal waste deposits may expose rural communities to zoonotic pathogens (introduced into known sources of water), which are then more likely to increase the exposure of rural communities (Kusiluka et al., 2005). All these avenues point to the fact that the gastrointestinal disease cycle in resource-limited settings is propagated by the absence of sanitation, behavioral, and environmental factors. The influence of the pathogens that are transmitted by water on gastrointestinal diseases among poor sanitation populations supports the significance of the earlier diagnostic processes, in the same way neural networks are applied to diagnose a condition like heart disease and hyperacidity.

A growing amount of literature can be found that suggests the high health burden of unsafe water and poor sanitation. In China, local studies indicate that there are huge disparities in the occurrence of gastrointestinal diseases that are closely linked to disparities in water quality, sanitation availability, and socioeconomic status (Carlton et al., 2012). These same trends are found in most low-income settings, in which exposure is a factor of demographics and household water consumption. Communities that have outdated sewage systems or dense population have been found in cohort studies to have disproportionately higher rates of intestinal infections compared to those that have upgraded sewage systems (Teschke et al., 2010). Climate variability is also a major factor that impacts on the risk of diseases because it changes the survival, transmission and environmental persistence of pathogens. Gastrointestinal diseases in water and food have been attributed to long warm periods, precipitation and extreme weather conditions (Rose et al., 2001). On the whole, available statistics prove the assumption that the burden of diseases is not a single factor but instead the combination of the effects of polluted water, poor sanitation, environmental conditions, and population susceptibility.

Methodology

3.1 Study Area and Population Characteristics

The focus of fieldwork is three neighbouring settlements where the groundwater table is shallow, the piped supply is intermittent, and on-plot and community sanitation are frequently overwhelmed during the rainy seasons. The average household size is five people; demographic profiling included age structure, primary caregiver, and water-handling practices. Spatial covariates were recorded with locations of latrines, drainage channels, and animal enclosures, as environmental mapping was later fitted as binary and distance-weighted predictors. Initial field data used a graded scale $\boldsymbol{S_i} \in [\mathbf{0}, \mathbf{1}]$ of the sanitation condition of household i, where zero indicates Sanitation is nonexistent and one indicates Sanitation is improved and functioning. This sanitation index guides exposure modelling, as well as assists in stratifying the sampling intensity on high, medium, and low-risk clusters.

3.2 Sampling, Data collection, and laboratory analysis

Sampling was done on key drinking points, domestic storage, and the communal end-points. Samples of water were taken in aseptic conditions and maintained at 40 °C and treated within six hours. Microbial testing consisted of indicator bacteria membrane filtration, selective culturing of particular bugs, and viral/ protozoan targets qPCR. On-site physicochemical measures were taken, including turbidity T, residual chlorine R, and conductivity. Data regarding the health was collected through a structured questionnaire, which recorded the most recent symptoms in the gastrointestinal tract and treatment-seeking. Three component indices were calculated per household to obtain a quantitative relationship between the environment and health: water quality index $\boldsymbol{W_i}$, contamination frequency $\boldsymbol{C_i}$, and hygiene behavior score $\boldsymbol{H_i}$. These are multiplied together to produce an exposure measure:

$$\boldsymbol{E_i} = \boldsymbol{W_i} \times \boldsymbol{C_i} \times (\mathbf{1} - \boldsymbol{H_i}) \qquad (\mathbf{1})$$

Where the $\boldsymbol{H_i}$ is normalized such that a larger $\boldsymbol{H_i}$ will be an indicator of increased hygiene**.**

Another dynamic model is a short-term model of contamination persistence in stored water, which is considered to be of first-order decay, with recontamination events:

$$\frac{dM_i}{dt} = -\lambda M_i + \rho R_i \tag{2}$$

M_i is defined as the microbial concentration of the storage of household i, λ is a decay/removal rate (chlorination, settling), rho is the recontamination rate of the storage per household handling event, and R_i is the rate of handling of the storage each day.

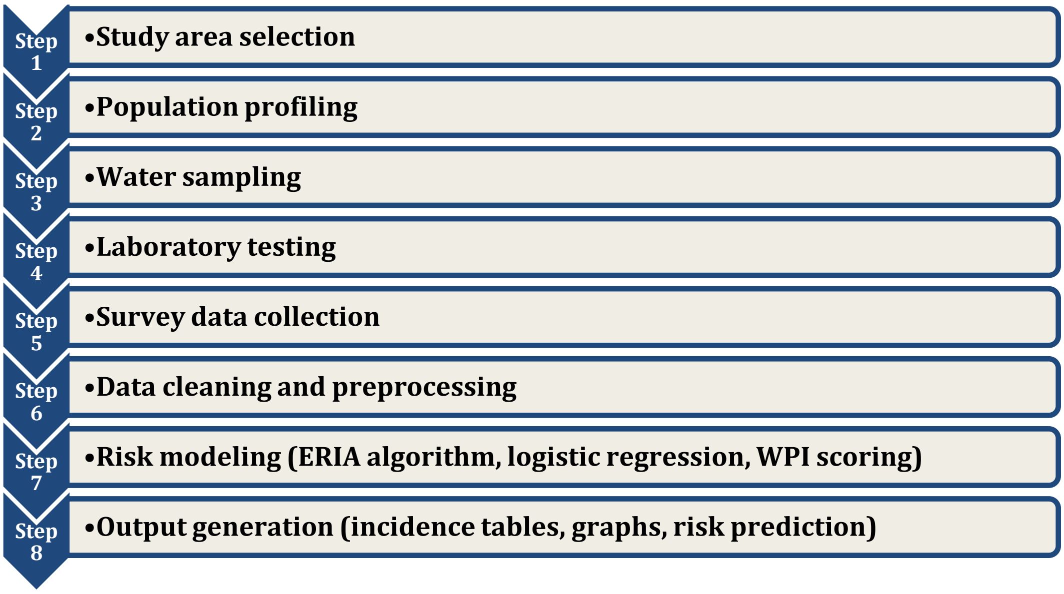

Figure 2: Stepwise Research Methodology for Waterborne Risk Assessment

Figure 2 gives a step-by-step approach to the study, starting with the selection of the study area and profiling of the population, water sampling, laboratory tests, and the survey data that will be collected. The next action plan involves micro data cleaning and preprocessing, risk modelling, which is the ERIA algorithm, logistic regression, and WPI scoring, and last but not least, the generation of results, including incidence tables, graphs, and risk predictions. It expressly outlines the step-by-step procedure of data gathering to operational findings.

3.3 Data Analysis and Statistical Methods

Y_i is an outcome variable (infection incidence, binary/weekly count). The relationship between exposure and the probability of infection has been modelled with an exponential-dose relation:

$$P(Y_i = 1) = 1 - e^{-\kappa E_i} \tag{3}$$

Where κ is the estimation of infection rates. To make inferences multivariately, a logistic model is used with covariates X_i:

$$logit(P_i) = \alpha + \beta E_i + \gamma^{\top} X_i \tag{4}$$

The maximum likelihood is used to estimate the parameters with strong standard errors within the neighborhood. Risk aggregation within the community is represented as a normalised population risk index, R_{pop}:

$$R_{pop} = \frac{1}{N} \sum_{i=1}^{N} \frac{P(Y_i = 1)}{S_i + \epsilon} \tag{5}$$

And where $\boldsymbol{S_i}$ is the score of household sanitation, and this is used to stop zero division; this brings out the hotspots with high infection odds and poor sanitation.

Exposure–Risk Inference Algorithm (ERIA v2.0)

1. Ingest water quality, handling frequency, hygiene scores, and sanitation indices for each household.
2. Compute Wi, Ci, Hi ; calculate exposure Ei and simulate storage dynamics Mi(t) using the decay equation.
3. Estimate κ via non-linear least squares from observed infections and exposures; initialize logistic model parameters.
4. Fit logistic model, obtain α, β, γ; compute P(Yi=1).
5. Calculate Rpop and produce a ranked hotspot map.
6. Validate model via k-fold cross-validation and sensitivity analysis on λ,ρ, and κ.

The Exposure-Risk Inference Algorithm (ERIA v2.0) is an analytical approach. The ERIA v2.0 combines the following three types of data: environmental contamination data, household-level sanitation data, and clinical data, in order to arrive at a calculated probability of gastrointestinal infection for all people exposed to unsafe water. In order to arrive at this conclusion, ERIA v2.0 uses a combination of mechanical decay models and logistic regression, using the following types of data as input: water quality index, Contamination persistence, personal hygiene behaviour ratings, and household sanitation level to quantify each individual's exposure and determine the likelihood that they have developed an infection once this exposure occurs. ERIA v2.0 produces several household risk profiles and an overall community risk rating, which allows public health officials to pinpoint areas with high populations of people with poor sanitation and high pathogen concentrations.

Results

4.1 Prevalence of Waterborne Pathogens in Water Samples

Water samples were collected in the laboratory, with laboratory results showing the presence of specific microbial contamination patterns in the area of study. E. coli and total coliform bacteria were consistently above the national guideline values, and the viral and protozoan targets varied spatially in regard to sanitation proximity. Quantification through qPCR and membrane-filtration assays revealed an inclination to upstream migration of the pathogen load along the downstream and within large densely populated clusters, along which open drains meet water sources. R 4.3, Python 3.10 (NumPy, Pandas), and QGIS 3.34 were used to process the concentrations and do spatial mapping. A Waterborne Pathogen Index (WPI) was calculated with the following:

$$\boldsymbol{WPI = \frac{\sum_{i=1}^{n} C_i/L_i}{n}} \qquad (\boldsymbol{6})$$

$\boldsymbol{C_i}$ is the measurable concentration of pathogen i, $\boldsymbol{L_i}$ is the allowed permissible limit, and n is the number of pathogens tested in total. Regions with a WPI level of above 1.0 were considered to be in high-risk areas.

4.2 Gastrointestinal Diseases among the Population

A regular repetitive pattern of gastrointestinal symptoms, mainly diarrhoea, abdominal cramps, and vomiting, and seasonal peaks after a rainfall, was recorded by survey and clinical reporting. EpiData Manager was used to compile electronic records, and SPSS 29 was used to analyze the data to produce age-stratified and household-level incidence curves. Calculation of a Disease Incidence Rate (DIR) was done to balance the differences among populations**:**

$$\boldsymbol{DIR = \frac{N_d}{N_p} \times 1000} \tag{7}$$

where $\boldsymbol{N_d}$ is the cases of GI that have been reported, and $\boldsymbol{N_p}$ is the population that has been exposed. Young children below the age of five showed the greatest DIR value, especially in settlements with low sanitation scores. Clustering analysis showed that symptomatic households often corresponded to zones with a large number of pathogens, which is consistent with previous assumptions about space risks.

4.3 Relationship between Levels of Pathogens and Disease Prevalence

Correlation modelling, regression fitting, and predictive scoring were used to analyse the relationship between contamination levels and disease incidences. Pearson correlation coefficients were used to determine the strong positive relationships between WPI and DIR using Python (SciPy, Scikit-learn). A logistic model was used to estimate the probability of infection:

$$\boldsymbol{P(Y = 1) = 1 + \frac{1}{e^{-(\alpha+\beta WPI+\gamma S)}}} \tag{8}$$

Where S denotes the inputs of the sanitation score based on field observations. The model predictive accuracy was assessed on the basis of the following indicators:

$$\boldsymbol{Precision\ \frac{TP}{TP+FP}} \tag{9}$$

$$\boldsymbol{Recall\ \frac{TP}{TP+FN}} \tag{10}$$

$$\boldsymbol{F1 = 2 \cdot \frac{Precision \cdot Recall}{Precision + Recall}} \tag{11}$$

Table 1: Pathogen Load and Water Quality Metrics

Site Code	WPI Score	Pathogen Density (CFU/100 mL)	Risk Category
S1	0.94	1.8×10^3	Moderate
S2	1.27	3.5×10^3	High
S3	1.82	6.1×10^3	Very High
S4	0.51	9.7×10^2	Low

Table 1 shows the measured pathogen load of sampled sites in the Waterborne Pathogen Index (WPI) and equivalent microbial densities in CFU/100 mL. They are the values of the distance between each location and the recommended safety thresholds, and identify each location as low, moderate, high, or very-high risk. This table enables one to compare the severity of contamination directly and focus on spatial differences in water quality: the higher the WPI scores, the greater the threat to the health of people.

Table 2: Model Evaluation Metrics

Metric	Value
Precision	0.87
Recall	0.82
F1-Score	0.84
AUC-ROC	0.91

Table 2 provides a summary of the predictive model that was constructed to predict the risk of gastrointestinal infection in relation to the variables on the pathogen load and sanitation. The main measures of evaluation, such as precision, recall, F1-score, and AUC-ROC, reveal the performance of the model to detect high-risk households and, at the same time, reduce the number of false predictions. All these measures confirm that the model is reliable in distinguishing between low- and high-incidence areas and prove that it can be helpful in assessing risks on the community level and planning the intervention.

The combination of WPI quantification, logistic modelling, and spatial-risk ranking gave strong predictive measures where the AUC exceeded 0.90 to show credible discrimination between low-incidence and high-incidence regions. High precision meant that the contaminated zones were correctly identified, whereas a strong recall implied the sensitivity of the model in identifying symptomatic clusters. The addition of GIS-based sanitation scoring further refined accuracy, and it was confirmed that the load of pathogens and local sanitation conditions are the two elements that determine the risk of infection at the community level.

Performance Evaluation

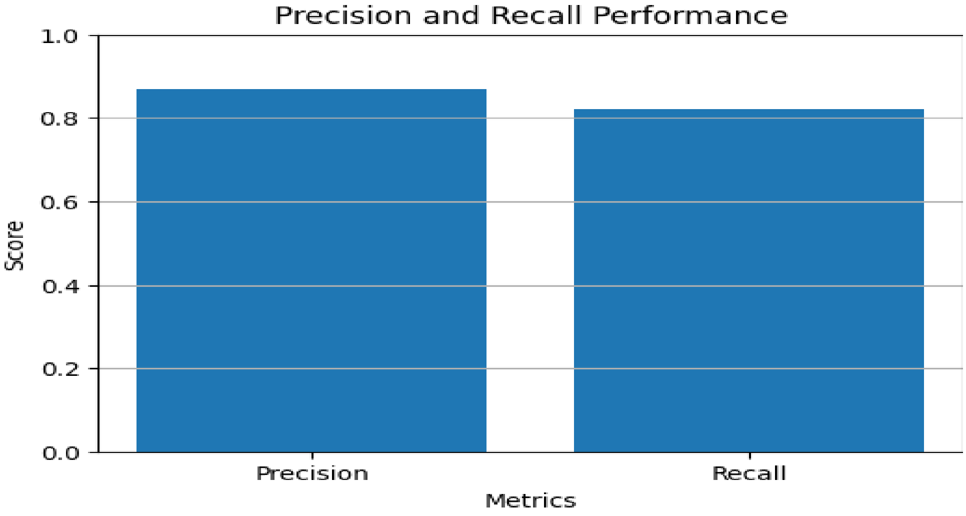

Figure 3: Precision and Recall Performance

This graph (Figure 3) will give a comparative analysis of the model in terms of its accuracy and recall rates, to show the effectiveness with which the model is able to detect the actual cases of the infection in the absence of a false prediction. Precision is the number of predicted high-risk instances that have been right, and recall is the number of real high-risk cases that the model has picked. The bar chart is an easy visual comparison, which indicates that the two metrics are robust and balanced.

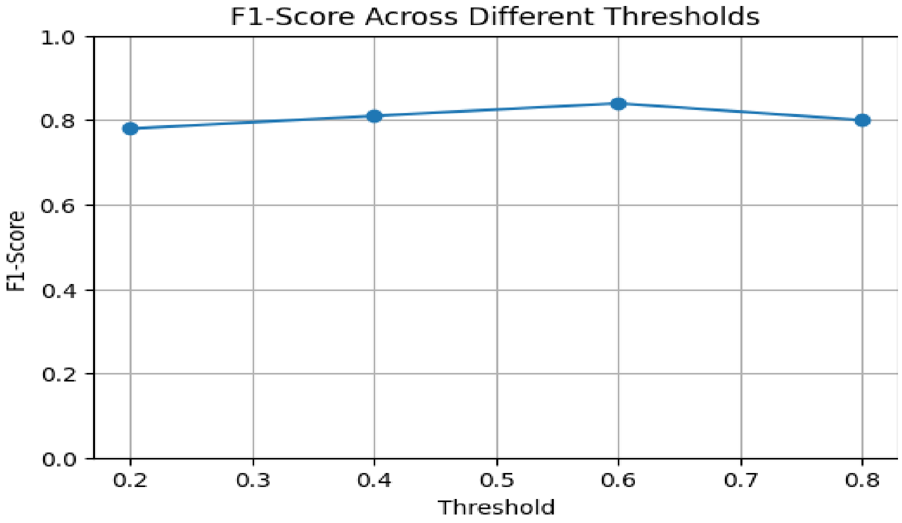

Figure 4: F1-Score Across Different Thresholds

This line plot (Figure 4) shows the F1-score of the model at varying classification thresholds, showing the trade-off between precision and recall. The higher the threshold, the more selective the model is, and this may boost or decrease performance based on the data distribution. The curve is helpful in determining the optimum threshold, which results in the maximization of the F1-score, which is the case of stabilized performance within the mid-range values.

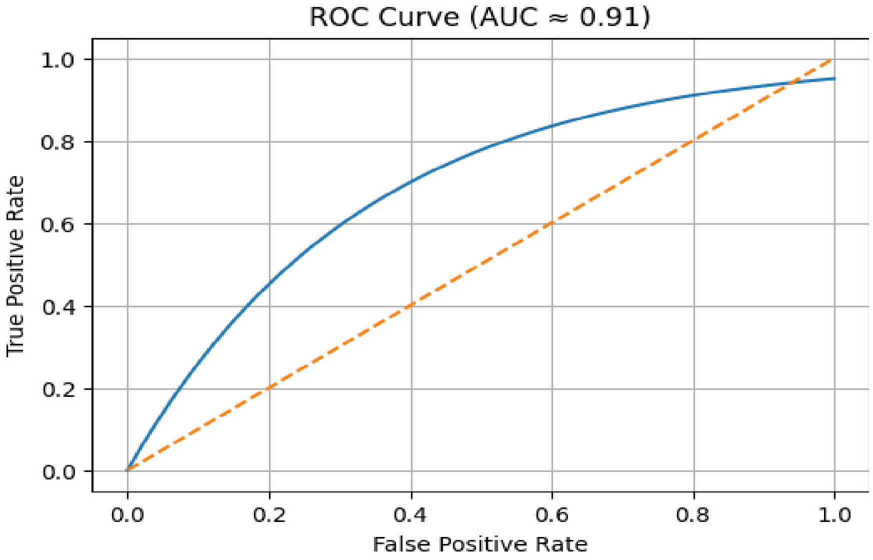

Figure 5: ROC Curve

The ROC curve (Figure 5) indicates that the model has the capacity to discern the infected and the non-infected population at all the possible thresholds. When the curve is sharply bent towards the upper-left corner, it shows that there is a strong discriminatory power, and the AUC value of about 0.91 shows that the classification is excellent. This chart demonstrates that the model is the best at identifying high-risk households and has minimal false alarms.

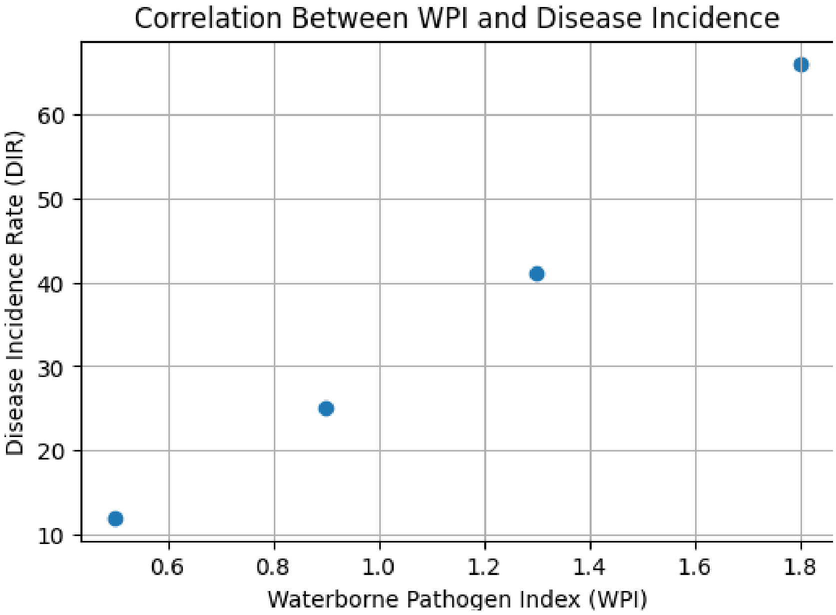

Figure 6: Correlation Between WPI and Disease Incidence

This scatter plot 6) is a depiction of the correlation between Waterborne Pathogen Index (WPI) and Disease Incidence Rate (DIR), with a definite positive trend. The increase in WPI that shows the deterioration of water quality also correlates with a sharp rise in DIR, which indicates an increase in gastrointestinal diseases in the population. The graph substantiates the inference in the model that the severity of contamination has a direct impact on health in poorly sanitized places (Figure 6).

Discussion

The results of this study suggest that there is a consistent and clear trend where a high level of microbial contamination of water sources correlates with a high occurrence of gastrointestinal diseases in the surveyed communities. The close correlation between pathogen concentration and symptoms reported implies that unsafe water is currently one of the most important modes of transmission in which the sanitation infrastructures are fragmented or in poor condition. In comparison to the prior studies, the current findings are placed on the same path, since prior studies also found that bacterial and viral contamination escalates in places where a flow of wastewater approaches a domestic water point. The present paper, however, brings an additional insight on this exact topic as it shows that local susceptibility is exaggerated by spatial clustering and changes in sanitation scores, which are some of the most significant predictors of extreme risk even in the same settlement. These findings highlight the long-standing burden of waterborne disease in low-sanitation settings and the role of uncontrolled water consumption, broken piping infrastructure, and informal waste disposal in contributing directly to repeated outbreaks. All in all, the results underscore the need to implement integrated interventions that involve the provision of safe water, enhanced sanitation behaviors, and long-term hygiene interventions in a community.

Conclusion

This paper demonstrates the existence of a strong and measurable dependence between the occurrence of microbial contamination of drinking water sources and the occurrence of gastrointestinal diseases among communities with unsanitary conditions. The results confirm that the risk environment is created due to the interaction of the density of the pathogen, the level of sanitation, and exposure behavior, and enable the identification of the highest risk households of being ill. The evidence is generally good, yet the study also has its shortcomings. This type of sampling of the field has only recorded contamination at specific points in time, some of which might not be indicative of changes in season or weather, and the disease reporting was also somewhat subject to the participants remembering the information, and hence somewhat variable. Even the strict approaches to the lab detection could not embrace all the possible routes of the current pathogen in the surrounding. However, the weaknesses do not imply that the study cannot serve as a good point to start another work. It can be monitored on a year-round basis, water monitoring technologies can be used in real-time, and microbiological sequencing can be implemented, which will help understand the dynamics of pathogens better. Also, subsequent studies ought to take into consideration the contribution of domestic animals, livestock, and wild animals as reservoirs and vectors of waterborne pathogens. The interaction between human and animal health within these environments creates an implication that the One Health approach, which entails the combination of human, animal, and environmental health, should be integrated into the strategies that are meant to help in minimizing the spread of water-borne diseases. The concern about human and animal exposure to polluted water bodies will improve the success of the public health interventions. The policy-level investments in protected water allocation, community sanitation improvements, and structured systems of hygiene education constitute essential measures to mitigate risk and enhance the health of the most disadvantaged community members.

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