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Geospatial Modeling and Spatial Autocorrelation of Enteric Bacterial Contamination in Water Networks: A GIS-Based Risk Mapping of Al-Nidaa District, Najaf, Iraq

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النمذجة الجغرافية المكانية والارتباط المكاني لتلوث البكتيريا المعوية في شبكات المياه: رسم خرائط المخاطر باستخدام نظم المعلومات الجغرافية في منطقة النداء، النجف، العراق

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Abstract:
Geographic Information Systems (GIS) are considered an unconventional and effective tool for determining the spatial extent of pollutants and their impact on populated areas. Water quality is one of the most important factors for population stability, given its direct impact on human life and health. In this research, the study area was defined as the Al-Nidaa neighborhood, and the samples were specifically from filtered and tap water. The study area is one of the northern neighborhoods of Najaf Governorate and is a densely populated area. A total of (8) samples were taken for each type of water, for a total of (16) samples taken from different locations in the study, according to some established criteria. Pathogenic E. coli and Mirabilis Proteus bacteria were detected, as the samples were taken from the source at a rate of three replicates per location. Laboratory results obtained in this study revealed high levels of E. coli bacteria in samples taken from the identified sampling sites, as well as very high levels of Mirabilis Proteus botulism bacteria. These bacteria are primarily harmful to human health, as the water in these samples is considered unclean and contaminated with sewage and other sources such as domestic wastewater and fecal matter. Furthermore, spatial distribution maps were created for these samples, showing the areas with high, medium, and low concentrations of these types of bacteria.

Keywords: Geographic Information System, Water pollution, bacterial contamination, Escherichia coli, Mirabilis Proteus bacterium.

الملخص:
تُعتبر نظم المعلومات الجغرافية (GIS) أداةً غير تقليدية وفعّالة لتحديد النطاق المكاني للملوثات وتأثيرها على المناطق المأهولة بالسكان. وتُعدّ جودة المياه من أهم العوامل المؤثرة في استقرار السكان، نظرًا لتأثيرها المباشر على حياة الإنسان وصحته. في هذه الدراسة، حُدّدت منطقة الدراسة بحي النداء، وجُمعت العينات من المياه المُفلترة ومياه الصنبور. تقع منطقة الدراسة في أحد الأحياء الشمالية لمحافظة النجف، وهي منطقة ذات كثافة سكانية عالية. جُمع ما مجموعه 8 عينات من كل نوع من أنواع المياه، ليصبح المجموع 16 عينة جُمعت من مواقع مختلفة في منطقة الدراسة، وفقًا لمعايير مُحددة. تم الكشف عن بكتيريا الإشريكية القولونية الممرضة وبكتيريا المتقلبة المتغيرة، حيث جُمعت العينات من المصدر بمعدل ثلاث عينات لكل موقع. أظهرت نتائج المختبر التي تم الحصول عليها في هذه الدراسة مستويات عالية من بكتيريا الإشريكية القولونية في العينات المأخوذة من مواقع أخذ العينات المُحددة، بالإضافة إلى مستويات عالية جدًا من بكتيريا المتقلبة المتغيرة المسببة للتسمم الوشيقي. تُعدّ هذه البكتيريا ضارةً بشكل أساسي بصحة الإنسان، إذ تُعتبر المياه في هذه العينات غير نظيفة وملوثة بمياه الصرف الصحي ومصادر أخرى مثل مياه الصرف الصحي المنزلية والفضلات. علاوة على ذلك، تم إنشاء خرائط التوزيع المكاني لهذه العينات، تُظهر المناطق ذات التركيزات العالية والمتوسطة والمنخفضة من هذه الأنواع من البكتيريا.

الكلمات المفتاحية: نظام المعلومات الجغرافية، تلوث المياه، التلوث البكتيري، الإشريكية القولونية، بكتيريا المتقلبة البروتية.

1. Introduction

The deterioration of water networks and insufficient waste management systems in metropolitan locales such as Al-Nidaa often result in the decline of water quality. The major focus of this work is silent microbial proliferation. Potable water serves as a significant conduit for gastrointestinal diseases, although seeming satisfactory to the user. The fundamental premise posits a significant disparity between the perceived safety of filtered water and its real biological quality. Homeowners often use home filtration systems, which, if not meticulously maintained, transform from purifiers into active incubators for germs. Moreover, the closeness of municipal boundaries to sluggish sewage drains induces a "Cross-Contamination Effect" that circumvents established safety procedures. Access to potable water for consumption and everyday activities is important for the sustenance of life. (Kefyalew, 2018; Mohammed and Abdulrazzaq, 2021). Due to the increasing demand for water, the issue of drinking water quality has recently garnered significant attention. Water is an essential element of life and significantly influences evolution. Hazardous water contaminants detrimental to human health must be eradicated. Minerals, organic compounds, and pathogenic bacteria are among the pollutants, alongside the need to meet chemical, biological, and physical quality standards, thereby enabling water to be safely consumed, used for cooking, and employed in other domestic applications (Vigneswaran et al., 2009).

Bacteria are among the most important groups of microorganisms found in aquatic environments. Escherichia coli (E. coli) bacteria are relatively harmless microorganisms, as they live as normal flora in large numbers in the small intestine of humans and animals. The presence of E. coli bacteria in aquatic environments indicates contamination of the water with animal or human feces. This can indicate contamination with pathogenic bacteria, viruses, and other pathogens that can be excreted in feces, such as typhoid fever bacteria, hepatitis viruses, or bacteria that cause gastrointestinal infections. Fecal contamination is a serious matter for individuals using this water. E. coli bacteria are part of the normal microbiome in the intestinal tract of humans and animals. Furthermore, these bacteria can become pathogenic outside the digestive system. Thus, contamination of the surrounding environment can be attributed to the direct excretion of feces by these organisms. These specific bacterial species are identified because they are easy to detect, abundant in water, and always associated with pathogenic species. This gives a clear picture of the nature of the pathogenic microbes in the water and hence determines the different uses of the water body and identifies the treatment methods.

We can turn point data (e.g., water samples collected in the Al-Nidaa neighborhood) into continuous information surfaces using Geographic Information Systems (GIS). Using system tools like spatial interpolation, pollution levels and their distribution can be determined through mapping, which in turn reveals areas of high pollution concentration (Goodchild, 2011).

The Al-Nidaa neighborhood is located in the northern part of the holy city of Najaf and is considered an important gateway to the city. As shown in Figure 1, geographically it lies within the approximate coordinates of Najaf, Iraq, which are 32°01′44″N 44°20′23″E, and it is one of the most populous neighborhoods in the Middle Euphrates region. The samples used in this study were collected from 8 sites, as shown in Figure 1.

This research aims to detect the presence of enteric bacteria, such as Escherichia coli, which is an indicator of fecal contamination; assess water suitability; determine if drinking or filtered water is safe for human use; and identify sources of contamination. The importance of this research lies in determining the quality of water suitable for human drinking and monitoring water pollution in the study area due to the presence of human and animal waste in the study area.

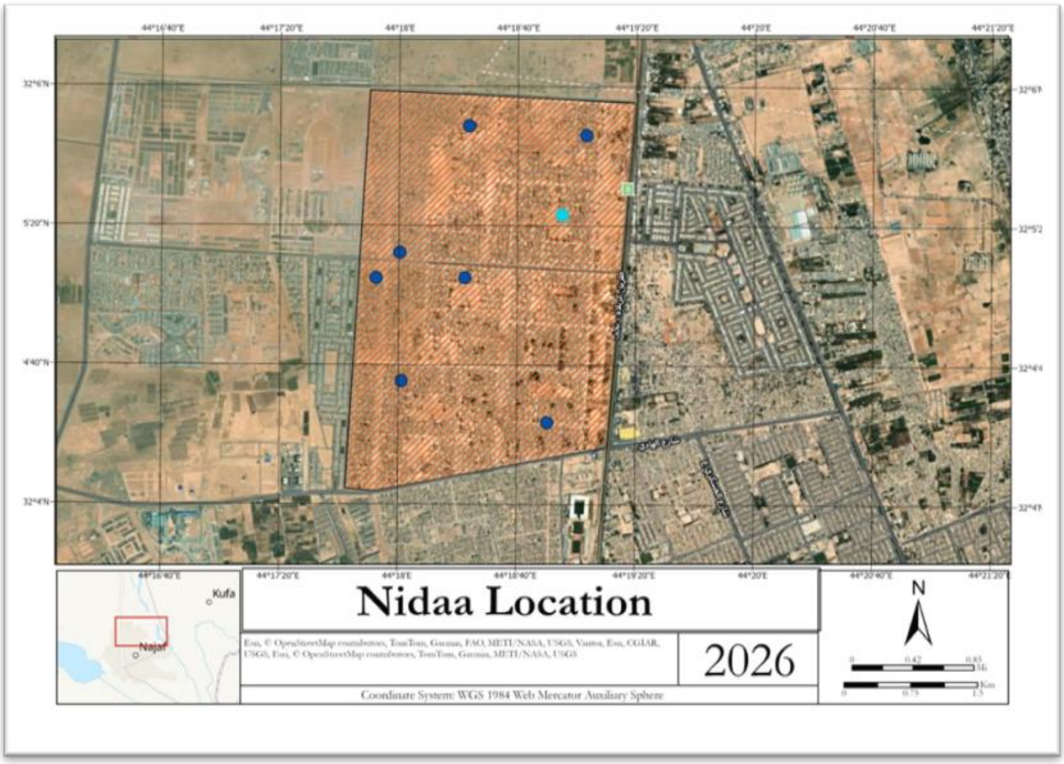

Figure 1: Administrative boundaries of the Al-Nidaa neighborhood with sample locations

Materials and Methods

A set of samples was collected from the locations shown in Figure 1, with two samples from each location (one sample of the area's main water supply and one sample of household filtered water). In case of biological assays, bacteria were enumerated by the Total Plate Count (TPC) method by inoculating 1 ml of the first dilution of the water sample directly onto the nutrient agar medium in triplicate, using the formula: Number of bacteria = Number of colonies x Dilution factor. The total coliform and fecal coliform bacteria were estimated using the Most Probable Number (MPN) method in a multitube system, in which a series of dilutions were inoculated onto MacConkey Broth medium (Garrido-Perez et al., 2008). Laboratory analyses were performed on the samples at the College of Science, University of Kufa. This study transcends conventional descriptive statistics, positioning GIS as a pivotal catalyst for environmental monitoring. Goodchild (2011) said that epidemiology should not be limited to pinpointing locations on a map; instead, it must include a thorough understanding of the fundamental spatial dynamics that regulate disease dissemination. Spatial analysis capabilities inside GIS software were used to bridge the gap between laboratory findings and the environmental conditions in the research region. The research used this method to convert the interpretation from a one-dimensional point-based analysis to a two-dimensional framework, facilitating the prediction of pollution levels in unsampled regions (Boulos, 2004). Eight sampling locations within the Al-Nidaa landscape were identified; two samples were collected from each site, one for tap water and the other for filtered water. The research employed spatial interpolation methods, such as Inverse Distance Weighting, to generate continuous risk surfaces, thereby converting discrete microbial counts into visual "Risk Maps" that illustrate the dynamics of contamination in relation to the district's topography and sewage discharges. The integration of GIS allows urban planners to see the "invisible threat," showing that biological degradation of water is a spatially predictable outcome of environmental neglect and infrastructure proximity to pollution sources.

Results

Filtered Water Analysis

The results of the laboratory analysis of E. coli bacteria appeared as shown in Table 1. Based on this data, a spatial modeling map of E. coli bacteria was drawn in Figure 2. By observing the map of the studied area of filtered water samples, it was found that they varied from one area to another, where the concentrations of these colonies were divided into (high, medium, and low). The bacterial colonies with high concentration were represented by two sites (7w-8w), and the concentrations at these sites were (234-245) bacterial cells (for the third dilution 10) per 100 ml. Meanwhile, the bacterial concentrations with medium concentration were represented by these sites (w1-w2-w3-w4-w5), where the concentrations at these sites were (189-134-120-124-120) bacterial cells (for the third dilution 10) per 100 ml. The lowest concentration was represented by site (w6), where the concentration at this site was 100 bacterial cells. (For the third dilution, 10) 100ml.

Table 1 Laboratory results for types of enteric bacteria in filtered water for Al−Nidaa neighborhood

Sample no.	E. coli bacteria	Mirabilis Proteus bacteria
w1	189	243
w2	134	200
w3	120	234
w4	124	237
w5	120	248
w6	100	239
w7	234	214
w8	245	285

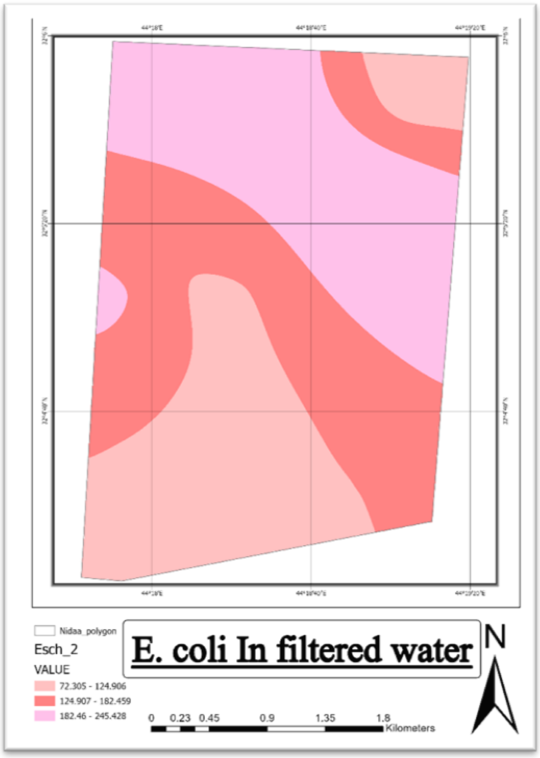

Figure 2 Spatial modeling map of E. coli bacteria in filtered water using ArcGIS Pro

While the concentration of Mirabilis Proteus bacteria also varied from one location to another, as observed in Table (1) and the spatial modeling map (Figure 3), it was very high across all locations. The colors in the modeling map indicate the variation in concentration levels.

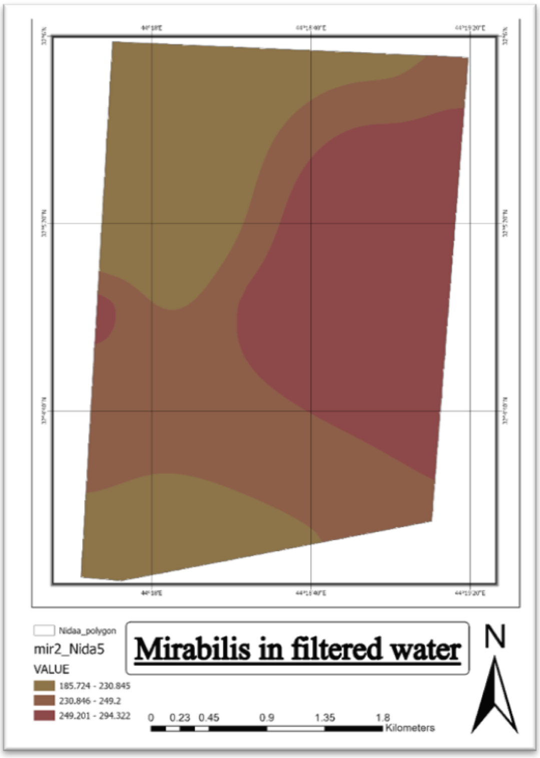

Figure 3 Spatial modeling map of Mirabilis Proteus bacteria in filtered water using ArcGIS

There are several reasons for the contamination of filtered water with enteric bacteria in homes, including: failure to change the purification filters regularly; the filter becoming a breeding ground for bacteria; filter blockage; the accumulation of organic matter, which encourages bacterial growth; incorrect filter installation; allowing leakage of untreated water; failure to disinfect the filter during maintenance; bacteria remaining and multiplying inside the device; storing water in the filter for extended periods; and stagnation, which promotes the growth of bacteria such as Proteus. This indicates that the presence of E. coli is a strong indicator of fecal contamination (a serious health risk). Similarly, Mirabilis Proteus grows in stagnant water and indicates poor hygiene. These bacteria can cause health problems in the human digestive and urinary systems (Aaron, W.T., 2001).

Tap Water Analysis

The table 2 shows the laboratory results for enteric bacteria types in tap water, and figure 4 shows the spatial modeling of E. coli sample locations. The concentrations varied from one location to another, and these samples were divided according to the concentration of each bacterial colony: high, medium, and low. Location (w5) was represented by (200) bacterial cells (for the third dilution, 10) per 100 ml. The locations had medium concentrations : (w1-w4-w6-w8), with concentrations of (120-130-199-130) bacterial cells (for the third dilution 10) per 100 ml. The locations with low concentrations were (w2-w3-w7), where the concentration was (100) bacterial cells (for the third dilution 10) per 100 ml.

Table 2 Laboratory results for types of intestinal bacteria in the tap water of Al-Nidaa neighborhood

Sample no.	E. coli bacteria	Mirabilis Proteus bacteria
w1	120	300
w2	100	213
w3	100	200
w4	130	234
w5	200	253
w6	199	287
w7	100	200
w8	130	112

This indicates very high levels of pollution were observed in most of the studied sites, whether for filtered or tap water, with a significant presence of bacterial activity in both types.

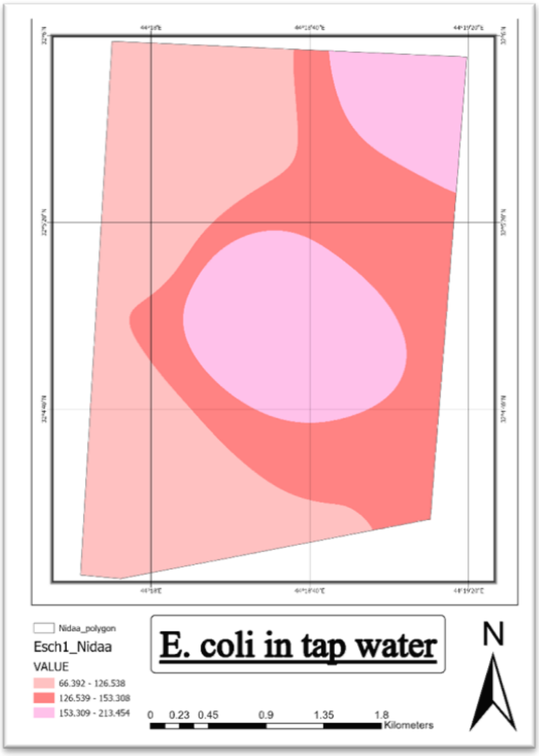

Figure 4 Spatial modeling map of E. coli bacteria in tap water using ArcGIS Pro

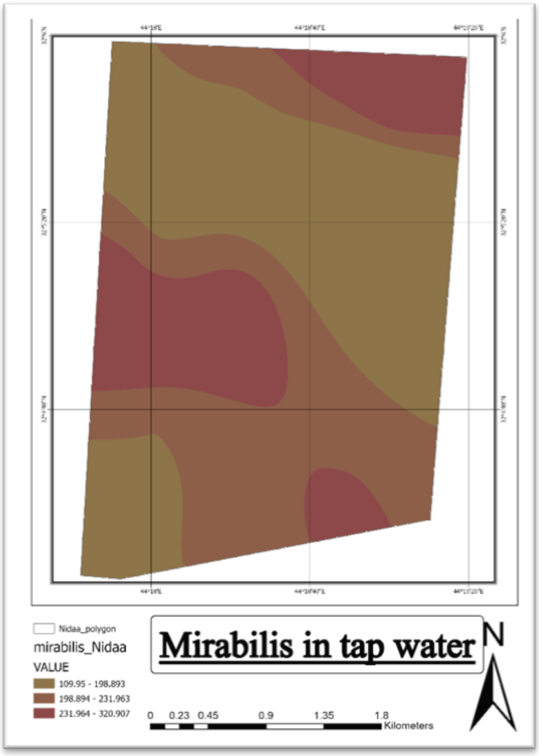

Figure 5 Spatial modeling map of Mirabilis Proteus bacteria in tap water using ArcGIS Pro

Discussion

The regional study undertaken in the Al-Nidaa district demonstrates a severe divergence between the supposed safety of home water sources and their actual biological integrity. This study effectively visualises the fundamental dynamics of microbial contamination by transitioning from conventional point-source data to continuous predictive risk surfaces using Geographic Information Systems (GIS). The resulting prediction maps indicate that bacterial degradation in these local networks is not arbitrary; instead, it is a spatially predictable outcome influenced by the convergence of ageing hydraulic infrastructure and proximity to raw sewage discharges. An especially troubling finding emerges from the study of point-of-use household filtration systems. In contrast to typical consumer assumptions about cleanliness, household filtered water exhibited high concentrations of both Escherichia coli and Proteus mirabilis. Rather of serving as protective sanitary barriers, these living units often transform into active bacterial incubation chambers. This paradoxical impact is mostly associated with end-user behavioural problems, particularly the recurrent neglect to replace purification cartridges and perform routine maintenance. Extended water stagnation inside these devices, together with the accumulation of organic debris, creates an optimal environment for biofilm development, facilitating the aggressive proliferation of opportunistic bacteria such as Proteus. The municipal tap water exhibited significant geographical variation in enteric contamination. The highest pathogenic concentrations were significantly concentrated in areas susceptible to untreated domestic sewage and municipal wastewater discharges. The ongoing biological degradation of essential river sources, exacerbated by the lack of regular dredging and inadequate localised administrative oversight, facilitates the persistent conveyance of faecal contaminants directly into the domestic plumbing system. Moreover, the proximity of municipal distribution lines to inefficient drainage routes creates a substantial "cross-contamination effect" that severely harms the local aquatic ecosystem. Prolonged exposure to these specific gastrointestinal indicators has urgent and significant public health implications. The presence of E. coli serves as a definitive biomarker for recent faecal contamination, whereas the overall bacterial load is strongly linked to acute clinical manifestations. Inhabitants dwelling inside the indicated high-risk spatial zones suffer greater probabilities of getting severe watery diarrhea, resulting to fast dehydration and consequent malnourishment, particularly in pediatric demographics. Additionally, exposure to such extensively polluted effluents might cause complicated systemic diseases, including hemorrhagic complications and acute renal failure. The biological hazard is distinctly amplified for at-risk populations, including pregnant women since the natural suppression of their immune system can lead to localized bacterial colonization in a rather rapid fashion. Overall, these spatial and laboratory observations underscore a pressing need to better address public understanding of household water storage hygiene alongside reforms to the wider district wastewater management systems.

Climate pressure alters both the abundance and quality of water. Drought can intensify the same load of pollution. Elevation of temperature can accelerate biological processes and deplete oxygen. Pollutants are washed from land into rivers during flooding. Freshwater ecosystem loss is driven by climate change, land-use change and water pollution (IPCC AR6II; Caretta et al., 2022). This result reinforces the ensemble method we used in this paper. Existing policy weakens under climate pressure as well. A wastewater plant may comply with normal flow conditions. It could still lead to bad river quality in drought. Runoff may be acceptable during dry weather at a farm field. It can also deliver large nutrient inputs during storm events. For this reason, weather and flow context should be taken into account while measuring water quality. Without flow data, a pollutant measurement is not complete. A trend in the absence of drought and flood data might mislead decision makers. by SDG 6.3.2 reporting at Level 1. These should be included to future surveillance in high-risk areas.

Conclusion

In conclusion, this analysis shows that Geographic Information Systems (GIS) provide an essential analytical framework for environmental epidemiology, efficiently converting localised sample data into dynamic, actionable maps of biological risk. The geospatial models obtained here clearly indicate the structural deterioration of the area water resources due to insufficient dredging of the rivers and direct inflow of untreated sewage facilitating extensive transmission of microbes across the municipal grid. The alarming resurgence of Escherichia coli and Proteus mirabilis at dangerously elevated levels in both tap and home-filtered water indicates a persistent cycle of faecal contamination that significantly jeopardises household water security. This systemic sanitary failure presents a significant localised health issue, strongly associated with fast paediatric dehydration, severe gastrointestinal distress, and potential renal complications. The situation is further worsened by the double vulnerability: the ignorance of the people about the need of the maintenance of the residential filtration systems and the absence of proactive inspection by the governments. Such a rising public health concern necessitates swift, localised administrative measures to restore aquatic infrastructure and extensive community awareness efforts on domestic water cleanliness.

Data Availability

The data presented is derived from field sample analysis conducted in the labs of the College of Science, University of Kufa. This study only utilises data acquired from a series of water samples, with no further data included. The specimens were examined at the labs of the College of Science at the University of Kufa.

Ethics Statement

The data presented in this research were only acquired via fieldwork involving a set of water samples, with no further data included.

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