TRACKING BACTERIA AND FUNGI DIVERSITY FROM NATURAL WATER SOURCES TO DRINKING WATER TREATMENT PLANTS AND DISTRIBUTION SYSTEMS – A REVIEW

MUDAU, K. L.[1] – KALU, C. M.[1] – MASINDI, V.[1,2] – MAPHANGWA, K. W.[1] – TEKERE, M.[1*]

[1]*Department of Environmental Science, College of Agriculture and Environmental Sciences, University of South Africa, Florida 1710, South Africa*

[2]*Research & Development Division, Scientific Services, Magalies Water, Brits, South Africa*

**Corresponding author*
e-mail: tekerm@unisa.ac.za; phone: +27-11-471-2270

(Received 5th Sep 2023; accepted 23rd Oct 2023)

Abstract. The complete removal of bacterial and fungal communities found in natural water sources by drinking water treatment plants (DWTPs) is a global issue of concern as many of these microbes are passed down to the end users through the drinking water distribution systems (DWDSs). An overview of the bacterial and fungal communities present in natural water sources is provided. The abundance of the bacterial and fungal communities in the final water exiting DWTPs and tap water from DWDSs provides an insight into the treatment plants' effectiveness. Information on the different technologies including artificial intelligence (AI) used in the water treatment plants was collated to elucidate their role in drinking water treatment. Based on previous studies, *Proteobacteria*, *Firmicutes*, *Nitrospirae*, and *Actinobacteria* are the predominant bacterial phyla while *Aspergillus*, *Cladosporium* and *Penicillium*, *Fusarium* and *Trichoderma* are the predominant fungal phyla identified in the final water and tap water. Information on the performance of advanced treatment shows the positive impact of the technology in bacteria and fungi removal. Furthermore, the application of AI in water treatment for the determination of coagulant dosages and prediction of the disinfectant is also promising. Research gaps were identified, and future studies were recommended to address water treatment concerns.

Keywords: *artificial intelligence, membrane technology, anthropogenic activities, coagulation-flocculation, disinfection stage*

Introduction

The availability of freshwater worldwide is an ongoing concern for people with/or without access to safe drinking water and basic human health services. With rising social-cultural and economic inequality, the security of safe drinking water has become of paramount importance to future generations and national security (Thom et al., 2022). According to the World Health Organization (2022), 2 billion people drink water from contaminated sources having poor sanitation. With cholera and Covid-19 outbreaks, the safety of water from microorganisms has become a greater concern (Perrin et al., 2019; Thom et al., 2022). Water service providers are responsible for managing, treating water, and distributing safe potable drinking water to end users. However, often end users receive contaminated tap water delivered from the DWDS (Potgieter et al., 2018; WHO, 2022). To address public health concerns associated with microorganisms in tap water and to develop efficient biological water quality management strategies, it is critical to explore origin of these bacterial and fungal communities especially the pathogenic, toxigenic, and allergenic ones and their survival through the treatment plants and the distribution system. Potentially, microorganisms in tap water may come from source water that has been polluted through various anthropogenic activities (Liu et al., 2018; Zhu et al., 2022), from the treatment process (Batista et al., 2022), and from the distribution network through biofilm detachment and loose resuspension (Lautenschlager et al., 2014). Tracking the source of bacterial and fungal communities from the source to DWTPs, treated sludge, and DWDS until the tap water still lack extensive systematic studies.

Existing studies on DWTPs and DWDS have revealed that bacterial communities are dominated by the Phyla Proteobacteria, Firmicutes, Nitrospirae, and Actinobacteria and fungal communities are dominated by Aspergillus, Cladosporium and Penicillium, Fusarium and Trichoderma (Zhang et al., 2018; Zhao et al., 2022). Most of these bacterial and fungal communities are pathogenic. Furthermore, different studies have found that Actinobacteria was the most abundant phyla in the treated water (after disinfection), suggesting the potential chlorine resistance in the bacterial group (Zhang et al., 2018; Perrin et al., 2019). To provide quality water that has good microbiological status and safety, there are different processes or stages of treatments (coagulation, flocculation, sedimentation, filtration, and disinfection) in the DWTPs that aim at removing organic matter, microorganisms, and total dissolved solutes (Bukhary et al., 2020). The presence of some bacterial and fungal communities with treatment progression is an indication of the selection and survival of the microbes in the different treatment stages. This creates serious challenges to the water treatment plants and water quality. There is a need to provide sustainable systems that can enhance proper removal of microbes and maintenance of requisite water quality parameters within the acceptable standard.

Various optimizations of the DWTPs processes have been done including the introduction of membrane technology (MT) and artificial intelligence (AI) which involve diverse machine learning models and deep learning models to determine coagulant dosages and prediction of the disinfectant and disinfection process (Zakhar et al., 2018; Safeer et al., 2022). The MT processes which include microfiltration (MF), nanofiltration (NF), ultrafiltration (UF), and reverse osmosis (RO) have shown to be effective in the removal of multivalent salts, organic molecules, and microorganisms (Puthai et al., 2017; Kang et al., 2020). Furthermore, the AI technology which includes artificial neural networks (ANN), support vector machine (SVM), and gene expression programming (GEP) has shown to be a promising tool in the prediction of coagulant dosages and disinfection by-products (DBPs) (Singh et al., 2012). However, research gaps still exist in these advanced approaches. This review tracked down some of the fungal diversity and bacterial diversities from the natural water sources as impacted by anthropogenic activities, treatment, and pollution for the DWTPs (final water) and DWDSs. It provides insight into the different advancements and technologies adopted in the DWTPs and DWDSs to enhance the removal of microbial contaminants and maintenance of water quality parameters within the acceptable standard for human consumption.

Bacterial and fungal diversity in natural water sources, DWTPs, and DWDSs

Natural water sources provide important ecological and economic values, including local climate regulation, a habitat that supports biodiversity, and resources for economic growth. Examples of natural water sources of concern are surface water systems (e.g., lakes, rivers, dams) and groundwater systems (e.g., aquifers)

(Lautenschlager et al., 2014; Luvhimbi et al., 2022). These natural water sources are important functional habitats that often contain the highest productivity and microbial communities depending on the changes in the environment, and the structure and function of the aquatic ecosystems (Wiese et al., 2016; Xu et al., 2017; Luvhimbi et al., 2022). Surface water, under river flow, groundwater and frozen water constitutes the fresh water sources treated by the drinking water treatment plants (DWTPs) and conveyed to the end users through drinking water distribution system (DWDS). These natural water sources are faced with the depletion challenge due to changes in the climate, drought, population growth, agricultural activities, urbanization, and industrialization (Barchiesi et al., 2021). Furthermore, pollution of the natural water sources is among the main problems faced globally and due to the vital role of water, there is a constant need to conserve it and prevent it from pollution (Prata, 2018; Kosuth et al., 2018).

In general, anthropogenic activities such as agriculture, mining and metal works, steel and metal alloys production, paint manufacturing, wood and paper processing, and dyeing are causes of rampant water pollution due to the release of diverse pollutants (Pellerin and Booker, 2000; Achmad et al., 2017; Ashraf et al., 2017; Kazakis et al., 2017; Jones et al., 2019; Brasili et al., 2020). The presence of these pollutants in the natural water causes diverse changes in the water ecosystems that influences the macro-and microbiota in the water system which when taken by the DWTPs poses some challenges in the removal of the contaminants including microorganisms.

In recent years, factors such as climate change and anthropogenic activities, including the construction of power stations, dams, aquaculture, and agriculture, have profoundly impacted the water regime of the natural water sources (Pinto et al., 2014; Batista et al., 2018; Liu et al., 2019).

Bacterial diversities in natural water sources

Water regime changes may strongly affect the natural water source’s microbial load and diversity and its biogeochemical cycling (Wiese et al., 2016; Ma et al., 2017). For example, upstream sources that include sewerage discharge and agricultural pollutants may influence bacterial diversity and composition due to organic and inorganic pollutant enrichment. The source water may contain high levels of organic and inorganic compounds that shape microbial population occurrence, abundance, and diversity (Lautenschlager et al., 2014; Carneiro et al., 2019). The characteristics and composition of bacterial communities in water treatment plants may be similar in natural water sources. Many studies have found that natural water sources are commonly dominated by the phyla Proteobacteria, Actinobacteria, and Bacteroidetes (Goecke et al., 2013; Zhu et al., 2022). ß-Proteobacteria *(Albidiferax, Deschloromanas, Polynucleobactar)* which belongs to the phylum Proteobacteria as well as some members of the phylum Actinobacteria have been reported as freshwater bacterioplankton which play diverse role in the maintenance of the freshwater ecosystem, but their abundance and diversities could be impaired by diverse environmental pollution (Taipale et al., 2009; Prest et al., 2016; Llirós et al., 2017; Batista et al., 2018; Hou et al., 2018; Batista et al., 2022). Beattie et al. (2020) observed the impact of agricultural activities (concentrated dairy cattle farming, manure fertilization, and associated agricultural runoff) in the river sediments of Kewaunee River surface water in Kewaunee County, U.S. state of Wisconsin. The authors identified genera *Thiobacillus*, *Methylotenera*, *Crenotrhix*, *Nitrospira*, and *Rhodoferax* and pathogens associated with cattle microbiome such as *Acinetobacer lwoffi* and *Arcobacter skirrowii* in abundance due to the impact of the agricultural activities. Furthermore, the proliferating abundance of some microbes commonly associated with agricultural pollution in fresh water such as *Arenimonas aquatica*, *Leptothrix cholodnii*, *Nitrospira defluvii*, *Flavobacterium flevense*, *Polaromonas naphthalenivorans*, *Zoogloea oleivorans*, F*lavobacterium psychrolimnae*, and *Flavobacterium xinjiangense* observed by the authors indicates the impact of agricultural activities microbiome of the fresh water (Kalyuzhnaya et al., 2012; Huang et al., 2017; Yu et al., 2017; Beattie et al., 2020). Sewage discharge and construction of a hydropower station in some rivers in China resulted in the selective growth and abundance of *Flavobacteria* and *Bacteroidia* (caused by sewage discharge) and *Cyanobacteria* (caused by hydropower station) (Wang et al., 2018).

The discharge of pollutant alters the natural functions of water system via the distortion of the normal physiochemical parameters of the water (Zhao et al., 2014). Changes in the physicochemical parameters influence the composition of the bacterial community of natural water sources (Pinto et al., 2014; Li et al., 2017). Understanding the correlation between water quality parameters and bacterial communities helps trace changes in microbial communities by monitoring water quality parameters (Li et al., 2017). Perrin et al. (2019) investigated the possible correlation between physicochemical parameters and bacterial diversity in the Paris distribution system. The results showed that variations in quantity and diversity of organic carbon compounds impact bacterial community structure and composition; sulphate and oxygen concentrations promote the growth of sulphate-reducing bacteria; deficiency in the trace metals can result in the bacterial growth limitations. Kaevska et al. (2016) found out that Actinobacteria are negatively correlated with phosphorus, sulfate, dissolved particles, and chloride levels. Proteobacteria positively correlated with sulfate, dissolved particles, chloride, dissolved oxygen, and nitrite levels. This implies that sulfate, dissolved particles, chloride, dissolved oxygen, and nitrite levels promotes the growth of bacteria belonging to the Proteobacteria and any pollutant that can increase their concentration in natural water will promote their growth. The availability of nutrients in the form of organic matter, nitrogen, and phosphorus can all influence bacterial regrowth and biofilm formation (Stutter et al., 2018; Wyatt and Rober, 2018). Studies have shown that the composition of dissolved organic matter is a key factor for the microbial dissolve organic matter consumption and degradation in stream ecosystems and an important driver for benthic microbial activities, e.g. assimilation, growth, and respiration (Hansen et al., 2016; Lupon et al., 2020).

Zhao et al. (2014) examined the changes in microbial diversity of river in Northeastern China under zinc and arsenic pollution. The authors observed that the pollutants select the microbes that could proliferate through denaturing gradient gel electrophoresis. Bacteria such as *Acinetobacter johnsonii*, *Clostridium cellulovorans*, and *Trichococcus pasteurii* and eukaryotes such as *Limnodrilus hoffmeisteri* which were resistant to the zinc and arsenic were dominant (Zhao et al., 2014). The massive growth of eukaryotes depleted the dissolved oxygen leading to the decline of aerobic bacteria. Also, the effects of exogenous pollution on the benthic microbial community structure in a large lake and river were studied in China (Zhang et al., 2020). The authors observed different bacterial community structures with different exogenous pollution such as *Arenimonas*, which belongs to the *Gammaproteobacteria*, was dominant in agricultural, industrial, and domestic waste polluted rivers while the genus *Micromonospora* was prominent in agriculturally polluted rivers. Furthermore, *Flavobacterium* and *Nitrospira* were observed to be abundant and play crucial role in nitrogen cycle in the watershed where the samples were collected (Zhang et al., 2020).

Nitrogen pollution in an urbanized city was reported to drive bacterial community shifts in river sediments (Lin et al., 2019). Proteobacteria, Firmicutes, and Bacteroidetes were the dominant bacterial phylum with Firmicutes and Nitrospirae being higher in suburban rivers than in urban rivers, while Bacteroidetes, Verrucomicrobia, and Spirochaetes were lower in suburban rivers than in urban rivers. This shows the impact of urbanization and the type of pollution on the microbial shift in the natural water sources like rivers. Jia et al. (2021) observed the abundance of diverse pathogenic bacteria such as *Prevotella* spp., *Enterobacter* spp., *Aeromonas hydrophila*, *Staphylococcus epidermidis*, *Serratia marcescens*, *Erysipelothrix* spp., *Acinetobacter lwoffii* and *Bacteroides fragilis* in Uberabinha River in south-eastern Brazil as impacted by domestic waste pollution.

Fungi diversities in natural water

Through various isolation methods including membrane filtration, centrifugation, direct plating, pipe coupons, pour-plating, swab applicators, glass, PVC and concrete coupons, diverse fungal genera in natural water sources which include *Aspergillus, Cladosporium, Epicoccum*, *Penicillium*, *Trichoderma*, *Fusarium*, *Phialophorahas Paecilomyces*, *Paraconiothyrium*, *Basiodobolus*, *Plectosphaerella*, and *Rhexocercosporidium* have been identified (Oliveira et al., 2013, 2016; Al-gabr et al., 2014; Hurtado-McCormick et al., 2016; Douterelo et al., 2016; Arroyo et al., 2019; Goralska et al., 2020). Novak et al. (2017, 2018) compiled information in review on the occurrence, ecology, and physiology of fungal contaminants in drinking water that includes surface water, groundwater, and tap water to elucidate the abundance of fungal communities.

Metagenomics approach which involves the application of different next generation sequencing (NGS) techniques have been employed in the detection of fungi in bulk water and biofilm (Moat et al., 2016; Novak et al., 2016; Del Olmo et al., 2021). The adoption of these NGS techniques has enhanced the detection of less abundant microorganisms which cannot be detected through cultural approach in DWTPs and DWDS. However, Douterelo et al. (2018) indicated the need for the development of new indicators of infrastructure or treatment failures through metagenomic approach and the understanding of their application in ensuring the protection and promotion of water with good quality and microbiological safety. In view of this, initiation and performance of a large-scale coordinated drinking water microbiome project starting from the natural water sources through the treated water from DWTPs to the DWDS becomes pertinent (Hull et al., 2019). More studies on the changes in the fungi diversity of surface raw water is summarized in *Table 1* together with data for bacterial changes. From the different studies, the diverse pollutants select the microbial communities that can proliferate in the polluted environment. In view of this, a proper selection of the different methods or techniques of treatment of the surface raw water by the DWTPs is pertinent to ensure proper removal of the pollutants as well as the microbes and promotion of the health of the end users.

Table 1. *Impacts of different pollutants on the microbial diversity of surface raw water*

Surface raw water type	Pollutants/pollution type	Abundant microbes (phyla/genera/species)	References
Rivers	Domestic and industrial	*Corynebacterium, Staphylococcus, Cutibacterium, Turicella, Acinetobacter, Micrococcus, Faecalibacterium, Shewanella, Escherichia, Klebsiella, Enterococcus, Prevotella, Legionella, Vibrio and Salmonella*	Odhiambo et al. (2023)
Surface water and ground water	Mining activities	Proteobacteria, Bacteroidetes and Actinobacteria	Zou et al. (2021)
River	Mining activities	Actinobacteria and Proteobacteria	Yan et al. (2020)
River	Heavy metal	Proteobacteria, Bacteroidetes, and Firmicutes	Chen et al. (2018a)
River	Sewage pollutant	Campylobacterales, Bacteroidales, Clostridiales, Aeromondales, Pseudomonadales, Flavobacteriales, Burkholderiales, Sphingobacteriales, Alteromonadales, Actinomycetales, Cyanobacteria and GN02; Tetrahymena (eukaryote); Blastocystis (Fungus)	Korajkic et al. (2015)
River	Hospital wastewater	Proteobacteria, Actinobacteria, Chloroflexi, Acidobacteria, Plantomycetes, and Bacteroidetes. Fungi: Ascomycota, Basidiomycota, and unclassified Eukarya_uc_p	Ogwugwa et al. (2021)
Freshwater lake, i.e. surface water, sediments and deepwater	Petroleum-hydrocarbons	Phyla: Proteobacteria, Bacteroidetes and Verrucomicrobia *Genera: Pseudomonas, Acinetobacter, Stenotrophomonas, Aeromonas, Sphingobacterium, Comamonas, Flavobacterium, and Enterobacter*	Phulpoto et al. (2021)
Freshwater lake	Mining activities	*Bacteroidetes, Gemmatimonadetes, Acidobacteria, Nitrospiraem Firmicutes and Alphaproteobacteria*	Chen et al. (2018b)
Freshwater lake	Microplastic and detergents	*Gammaproteobacteria (family Enterobacteriaceae)*	Varg and Svanbäck (2023)
Deep groundwater	Coal mining activities	Proteobacteria *(Gammaproteobacteria)*	Chen et al. (2023)
River	Heavy metal contamination	Proteobacteria (phylum), *Betaproteobacteria (class), Burkholderiales (order), Comamonadaceae (family), Hydrogenophaga (genus) and Chloroflexi bacterium OLB 14 (species)*	Raghav et al. (2022)
River	Sewage and industrial pollutant	*Proteobacteria, Bacteroidetes, Firmicutes, Actinobacteria and Chloroflexi phyla. Dechloromonas aromatica, Rhoopseudomonas palustris, Syntrophus aciditrophicus* and *Syntrophobacter fumaroxidans.* Fungi: *Nakaseomyces, Aspergillus, Schizosaccharomyces and Lodderomyces*	Parida et al. (2022)

Bacteria diversity in DWTPs and DWDS

DWTPs are designed with the purpose to produce drinking water that is acceptable aesthetically (acceptable color, odor, and taste), hygienically (free of opportunistic and true pathogenic microbial species), and operationally (limited corrosion and nitrification) (Pinto et al., 2014; Prest et al., 2016; Li et al., 2017). Before the final treated water is released into the distribution system, drinking water passes through different processes of treatment (coagulation, flocculation, sedimentation, filtration) with the last process called disinfection (ozonation, chlorination, chloramination, and UV treatment) (Bautista et al., 2016; Li et al., 2017; Douterelo et al., 2019). The disinfection process plays an important role in the inactivation of true pathogenic and opportunistic pathogenic microbial species and the introduction of disinfectant residuals which is key in the maintenance of biologically stable water (Bautista et al., 2016; Prest et al., 2016). *Table 2* provides a summary of the different treatment stages, their main objectives, effects on the microbiomes of the stage, advantages and disadvantages of the stages. Thom et al. (2022) observed that Proteobacteria (*Pseudomonas*, *Actinobacter*, and *Rheinheimera*) dominate water samples after disinfection, supporting the deterministic influence of the treatment. Although biofiltration defines taxa in drinking water treatment, disinfection has a stronger selective effect (Becerra-Castro et al., 2016). This is supported by the study comparing two identical treatment systems treating the same source of water, where chlorination and chloramination differentially select bacterial communities in the final water (Zhang et al., 2018; Potgieter and Pinto, 2019). Bautista et al. (2016) conducted a meta-analysis of microbial communities in bulk drinking water using all available 16S rRNA gene sequencing datasets. The result showed that Proteobacteria, particularly *Alpha*- and *Betaproteobacteria* dominate the drinking water bacteria communities irrespective of origin and presence or absence of disinfection residual type. This information highlights the need for extensive study on the factors within the water ecosystem that promotes the proliferation of the members of the phylum Proteobacteria.

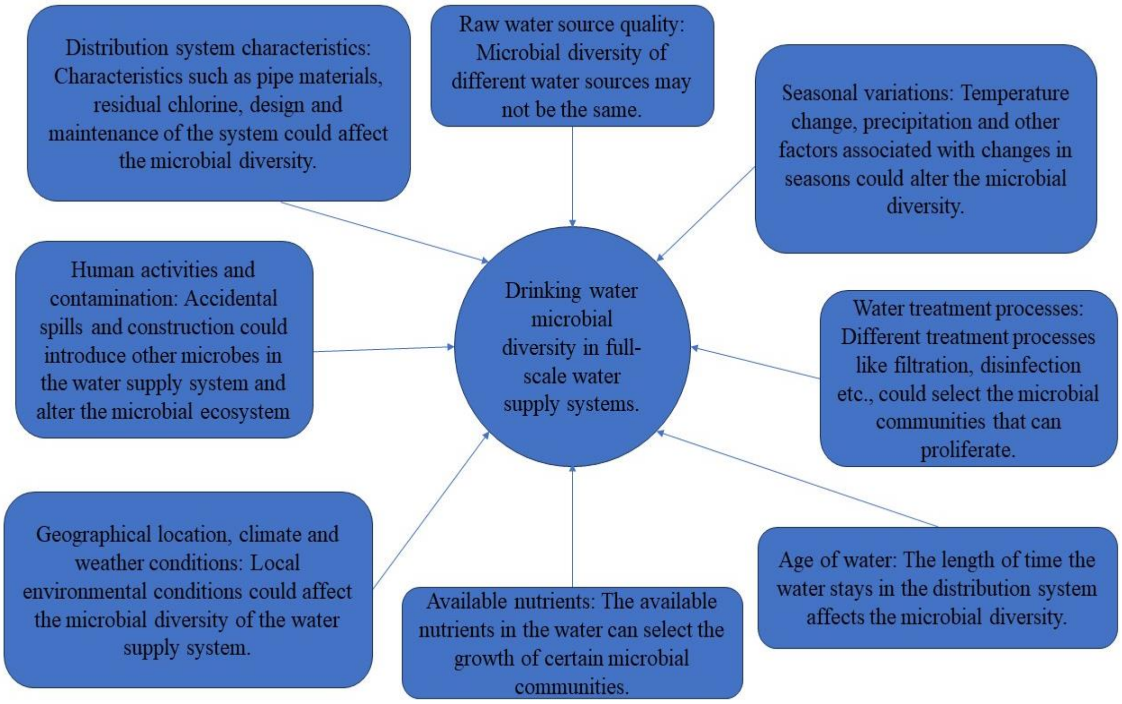
Table 2. *A summary of the effects of different drinking water treatment stages on the microbiome, purpose of the stage, advantages, and disadvantages*

Treatment processes	Primary purpose of the process	Effects on its microbiome	Advantages	Disadvantages	References
Coagulation/Flocculation and Sedimentation	The main objective of these processes is to remove suspended parties and other impurities	During suspended particles removal, organic nutrients can be removed leading to changes in the nutrient availability. Further, microbes can be removed as well. These could result in changes in the water quality in this stage and cause a shift in the microbial composition and dynamics in the water before moving to the next stage	Cost-effective. Rapid process that gives room for any emergency water treatment. Removal of certain microbes and antibiotic resistance genes	Alteration of microbial diversity and composition of water that could make it difficult for the next stage of treatment. The effectiveness of these stages is dependent on raw water quality and contaminants, temperature, pH, and the specific coagulants and flocculants used	Sun et al. (2018) Gomes et al. (2020)
Filtration	The main objective of this stage is to remove microorganisms from the water samples	It alters the microbial structure and composition of the water due to the removal of both beneficial and harmful microorganisms in the water. Furthermore, the process could lead to the removal of nutrients and creation of a nutrient-deficiency environment that could enhance the proliferation of other organisms including pathogenic ones	Enhanced removal of solid particles, pathogens, and chemicals as well as the improvement of taste and odor. It promotes reduction in chemical usage. It reduces the load of microbes that enter the next stage of water treatment	Limitation in the removal of dissolved contaminants. High initial capital cost especially for large-scale drinking water treatment plants. Filter fouling could contribute to deterioration of water quality due to the accumulation particles and pathogenic microbes	Cescon and Jiang (2020) Tang et al. (2018)
Disinfection	The main objective of this stage is to eliminate or deactivate microorganisms especially harmful ones	The toxic nature of the disinfectant could cause the death of the useful organisms that tends to maintain microbial balance within the water ecosystem. In addition, the disinfectant could select the microbes that proliferate especially, the resistant ones. The production of disinfectant by-products (DBPs) could also promote the growth of other pathogenic bacteria	This stage improves water quality. The elimination of pathogenic bacteria helps to protect the health of the public	The production of carcinogenic DBPs. The DBPs promotes the development of antibiotic resistant bacteria and biofilm formation	Lv et al. (2014) Mantilla-Calderon et al. (2019)

Chlorine-resistant bacteria have often been detected in final water which could result in biofilm formation and pipeline corrosion (Bautista et al., 2016; Prest et al., 2016; Li et al., 2017). Chao et al. (2013) have observed differential resistance of drinking water bacterial communities such as *Legionella*, *Escherichia*, *Geobactera* (in lab-scale system), *Mycobacterium*, *Siphingomonas*, and *Coxiella* (in full-scale system) increasing the relative abundance during monochloramine treatment. Studies have discovered that there are changes in the microbial community during the disinfection process, focusing mainly on improving the efficiency of disinfection and controlling costs (Huang et al., 2014; Potgieter et al., 2018). However, the disinfection process cannot destroy the microbial communities in the DWTPs, thus allowing bacteria into DWDS and potentially acting as a stress-based selecting pressure (Holinger et al., 2014; Wang et al., 2014). Ozone is reported to be a more powerful disinfectant than free chlorine and chlorine dioxide with its highest oxidation potential of 2.07 (Bautista et al., 2016; Fish and Boxall, 2018; Douterelo et al., 2019). Studies have found that double-layered gram positives such as *Mycobacterium* and *Legionella* survive and became predominant after ozonation (Roeselers et al., 2015; Becerra-Castro et al., 2016; Potgieter et al., 2018). Microbial communities are high in disinfection residual-free compared to the system with a disinfectant residual, indicating a greater taxonomic diversity of the bacterial community in the absence of a disinfectant residual. These disinfectant resistant bacteria are carried in the final water to the DWDS. Studies have shown that *alpha*- and *beta-proteobacteria* were dominant in chlorinated water as well as in the final treated water (Prest et al., 2016; Liu et al., 2018).

In general, several studies have shown that final treated water from the DWTPs is laden with diverse bacterial communities such as *Aeromonas spp., Sphingomonadaceae, Klebsiella, Raoultella. Enterobacter, Citrobacter, Pseudomonas, Massilia, Acinetobacter, Sphingomonas, Methylobacterium*, and *Brevundimonas*; *Bacillus* sp., *Shigella* spp., *Sinorhizobium* sp., *Bradyrhizobiaceae* sp., *Comamonadaceae* sp., *Sphingomonas* sp., *Ensifer* sp. *Escherichia, Acinetobacter, Bacteroides Mycobacterium frederiksbergense, Brevundimonas mediterranea* mostly belonging to the phyla Proteobacteria, Bacteroidetes, Firmicutes, Actinobacteria and Chloroflexi, (Bai et al., 2015; Lu et al., 2018; Jia et al., 2019; Dias et al., 2020; Maguvu et al., 2020; Siedlecka et al., 2021; Ma et al., 2022; Thom et al., 2022; Yu et al., 2022; Ke et al., 2023). The presence of these diverse bacterial communities both pathogenic and antibiotic resistant bacteria in the final treated water which are being channel to the end users through the DWDS create a major concern in the effectiveness of the treatment plants and health implication.

DWDS is designed and managed to maintain the biostability of drinking water from treatment to tap, thereby safeguarding the water quality and protecting public health (Fish and Boxall, 2018). Drinking water from the DWDS leaving the consumers' tap is expected to be void of microbes. However, drinking water leaving the consumer tap is estimated to contain millions of microbial cells per liter (Li et al., 2017; Zhu et al., 2020). This is traced to diverse factors including planktonic microbial regrowth and contamination during distribution due to decline in the residual chlorine (Prest et al., 2016). Other factors such as formation of suspended particles, dispersal of unconsolidated sediments from the DWTPs, long retention time, the nature of the pipe, oligotrophic environment, age of water, and biofilm formation contributes to the proliferation of diverse microorganism within the DWDS system (Wang et al., 2012, 2022; Pinto et al., 2014; Bergeron et al., 2015; Deuterelo et al., 2018; Fang et al., 2018; Yu et al., 2021; Chen et al., 2022; Zhuang et al., 2021). *Figure 1* provides a summary of influencing factors of drinking water microbial diversity in a full-scale water supply system. Studies have shown that long retention time of water in the distribution system cause the domination of water by the members of bacteria belonging to the phyla Proteobacteria, Actinobacteria, Firmicutes and Bacteroidetes despite the quality of water from the DWTPs and disinfection type adopted (Wang et al., 2014; Li et al., 2017; Cui et al., 2020). A study by Proctor et al. (2015) showed that residual chlorine decreased with the water age resulting in the increase in dissolved organic matter, total organic carbon, and bacterial diversity.



Distribution system characteristics: Characteristics such as pipe materials, residual chlorine, design and maintenance of the system could affect the microbial diversity.

Raw water source quality: Microbial diversity of different water sources may not be the same.

Seasonal variations: Temperature change, precipitation and other factors associated with changes in seasons could alter the microbial diversity.

Human activities and contamination: Accidental spills and construction could introduce other microbes in the water supply system and alter the microbial ecosystem

Drinking water microbial diversity in full-scale water supply systems.

Water treatment processes: Different treatment processes like filtration, disinfection etc., could select the microbial communities that can proliferate.

Geographical location, climate and weather conditions: Local environmental conditions could affect the microbial diversity of the water supply system.

Available nutrients: The available nutrients in the water can select the growth of certain microbial communities.

Age of water: The length of time the water stays in the distribution system affects the microbial diversity.

Figure 1. *Influencing factors of the drinking water microbial diversity in full-scale water supply systems*

Biofilm formation in the DWDS system promote the proliferation of diverse microbial communities and increase microbial biomass (Huang et al., 2014). This is attributed to the development of extracellular polymeric substances (EPS) within the biofilm creating microenvironment on the inner surface of the pipeline systems that enhance the growth and regrowth of microbes (Mi et al., 2015; Liu et al., 2017a; Fish and Boxall, 2018). To date, the influences of the material and design of DWTPs and DWDS on the biofilm growth on the pipeline walls have also been widely investigated, and these studies have been deepened step by step with the innovation of detection technology (Wang et al., 2014; Dueterelo et al., 2017). It is increasingly recognized that biofilms can degrade water quality as they are mobilized from the pipe wall into the water column, causing poor aesthetic quality and potential public health risks (Liu et al., 2017b).

Fungi diversity in DWTP and DWDS

Several mycological analyses of the final treated water from the DWTPs have been done and filamentous fungi belonging to the genera *Aspergillus*, *Cladosporium* and

Penicillium, Fusarium and *Trichoderma* has been reported to be predominate among the identified fungal communities (Zhao et al., 2022). The identified fungal communities in the treated water from the DWTPs include *Alatospora, Aspergillus, Penicillium, Taphrina* and *Tuber* (Ma et al., 2017); *Aspergillus* and *Cladosporium* (Bai et al., 2017); *Aspergillus* and *Penicillium* (Doggett, 2000); *Aspergillus* and *Penicillium* (Arvanitidou et al., 2000); *Aspergillus, Cladosporium* and *Fusarium* (Grabinska-Łoniewska et al., 2007); *Aspergillus, Cladosporium, Fusarium* and *Penicillium* (Sammon et al., 2010); and *Aspergillus, Cladosporium* and *Penicillium* (Sammon et al., 2011). In addition, Mhlongo et al. (2019) provided a comprehensive review on the prevalence of mycotoxigenic fungi found in DWDS as well as the health risk associated with their occurrence. The processes of water treatment including the disinfection of the water is expected to inhibit the growth and regrowth of the fungi as well as the spread from the DWTPs to DWDS. Their ability to withstand the stress associated with the different treatment processes was highlighted by Sonigo et al. (2011) as follows:

- The ability of the filamentous fungi to secret melanin that provides protection to the produced spores and enhance their competitive potential against other microorganisms.
- The hydrophobic nature of spores provides an addition protection against various disinfectant used in disinfection stage of water treatment due to their ability to form aggregates with each other and other particles either suspended particles or unconsolidated segments.

The presence of pathogenic, allergenic, and toxigenic filamentous fungi isolated from final water and their association with hospital water systems creates a great concern (Mesquita-Rocha et al., 2013; Schiavano et al., 2014; Ma et al., 2015). Hospital water system is believed to create a conducive environment for the proliferation of pathogenic fungi due to the continuous isolation and identification pathogenic filamentous fungi such as *Aspergillus fumigatus, Fusarium solani* (Ma et al., 2015). Allergenic potentials in many of these pathogenic fungi belonging to the genera *Aspergillus, Penicillium, Cladosporium* and *Alternaria* gave them the ability to cause many allergic diseases such as asthma and other respiratory problems in human (Paterson and Lima, 2005; Denning et al., 2006; Zhao et al., 2022). Zhao et al. (2022) indicated the that the concentration of *Aspergillus* in municipal and hospital water ranged from 16 to 63.8 CFU/100 mL. This information is an indication of the health risk associated with drinking water present in such areas and highlights the need for creating adequate control strategy to reduce the proliferation of the pathogenic fungi in the drinking water. Furthermore, Mhlongo et al. (2019) highlighted the treated water quality legislation and the need for inclusion in treated drinking water quality regulations to ensure the protection of the human health.

Naturally, DWDS are not known as habitat for the proliferation of filamentous fungi. Their presence in the DWDS is traceable to cracks in the pipelines, penetration through maintenance processes, physical openings in storage facilities, treatment breakthroughs, and leaking joints and adapters (Afonso et al., 2021). Another source of filamentous fungi in the DWDS is the spores. Because of the nature of the spores, they can be carried by air and deposited in the DWDS through the crack pipelines, leaking joints, and adapters, etc. (Sammon et al., 2011; Zhao et al., 2022). One striking characteristics of the filamentous fungi is their potential to mitigate the oligotrophic conditions in the DWDS through scavenging of nutrients from the colonized substrate or surrounding water. Their proliferation creates an additional problem to the quality of water distributed to the end users and the health of the populace (Sonigo et al., 2011; Oliveira et al., 2018; Afonso et al., 2021).

Filamentous fungi develop a hyphal mat that aid in biofilm formation and enhance their nutrient uptake in the oligotrophic condition of the DWDS and alongside with their absorptive nutrition mode, secretion of extracellular enzymes mechanisms, they can digest complex molecules and promotes the development of the biofilms for the sustainable proliferation (Simoes et al., 2015). This information indicates the survival of fungi in the DWDS is biofilm-formation dependent (Simoes et al., 2015). Zhao et al. (2022) reported that *Aspergillus* concentrations in DWDSs biofilm ranged from 1.9 to 3.6 colony-forming units (CFU)/cm^2. Fungal-bacteria interaction has been reported to play crucial role in the formation of biofilm in the DWDS (Afonso et al., 2021). In the complex nature of biofilms, co-inhabitation of microbes exists leading to a diverse complex interaction between organisms of the same or different species (Douterelo et al., 2016, 2018a, b). Kastman et al. (2016) indicated the crucial role played by the interaction between the microbes of the same species in the biofilm growth but the regulation of these microbial communities in biofilm is observed in the biotic interactions between distantly related organisms across the kingdoms. Inter-kingdom biofilms involving fungi and bacteria embedded within the extracellular matrix can be regarded as bacterial-fungal interaction. Frey-Klett et al. (2011) highlighted the needed for more exploration on the bacterial-fungal inter-kingdom interaction within the biofilm in the DWDS.

A good system of communication between the bacterial-fungal interaction is one of the major factors that enhance their growth and the community behavior. Quorum-sensing (QS) is a communication mechanism which involves the release of signaling molecules that when detected by the interacting microbial community tend to coordinate their behavior through modification of gene expression (Rasmussen et al., 2005). Reviews that compiled diverse QS molecules for both gram positive and negative bacteria were provided by Cook and Federle (2014) and Papenfort and Bassler (2016). Furthermore, Afonso et al. (2021) reviewed the bacterial-fungal interaction in detail and provided few examples on how the bacterial-fungal interaction promoted the development of biofilms although negative interaction may be observed between them. The authors further highlighted the need for further research to elucidate diverse correlations between fungi and bacteria as well as the inherent interacting factors that promote their co-existence.

Advances in the DWTPs’ technologies for improved water treatment

Coagulation-flocculation and sedimentation (CFS)

Due to population growth and climate change, DWTPs are faced with the challenge of processing raw waters from the natural sources to potable water that complies with more strict regulations for the protection of public health (Li et al., 2021). Coagulation is a critical process in DWTPs for the actualization of the good quality and microbiological safety. It aggregates colloidal particles which settles as flocs in the subsequent process (Bukhary et al., 2020). Among the challenge faced in coagulation process is the determination of the type of coagulants to be used and the adequate dosage for the actualization of the expected outcome. Heddam (2021) indicated that the coagulant dosage determination is time-consuming because of the aggregation of different factors that come into play for effective coagulation process to occur. Among the factors considered include raw water quality, quick mixing potential of the coagulants, hydraulic factors, and environmental condition (Zhang et al., 2013; Sohrabi et al., 2018). It is imperative to put into consideration all the necessary factors in the determination of the accurate coagulant dosage as inaccurate dosage could result in inadequate particle settling and removal, clogging of the filters, and high cost of subsequent treatment processes (Narges et al., 2021).

Different models for the determination of the coagulation dosage have been developed and adopted by researchers. Mathematical models have been the old model previously adopted to determine the coagulant dosage (Bazer-Bachi et al., 1990; Van Leeuwen et al., 1999). It gave a base-line information on the coagulant dosage determination however, the inclusion of factors that are based on assumptions making the application in practice challenging is one of the model's limitations (Haghiri et al., 2018). The deficiency in the knowledge of the inclusive dynamics of the water treatment processes in the mathematical models create a difficult situation in the management of nonlinear relationships among factors common in the coagulation process (Li et al., 2021). Hence, many DWTPs depended on the manual determination of the coagulant dosage according to the knowledge of the operator. In view of the challenge faced in the adoption of mathematical models, new models that involve data-driven techniques using machine learning have been introduced because of its lesser restrictions on the assumptions (Yin et al., 2016). It helped to proffer solution to the flaws of the mathematical models by managing complex and complicated nonlinear relationships among the factors common in the coagulation process which enhanced the monitoring and prediction of water quality as well as determination of coagulation dosage (Li et al., 2021). Examples of machine learning models adopted include Artificial Neural Networks (ANNs). This model has been adopted by Griffiths and Andrews (2011) and Shi et al. (2022) to determine the coagulant dosage in water treatment with good outcomes. However, due to the trapping of local minima that reduces the coagulation dosage determination ability of ANN, an adaptive neuro-fuzzy inference system (ANFIS) was introduced and adopted with an improved performance accuracies (Kim and Parnichkun, 2017; Narges et al., 2021). Despite the positive outcomes of ANN and ANFIS, the use of short-term data that do not provide enough information that can indicate the influence of weather and climate change in the determination of coagulation dosage- becomes the major limitation.

This propelled the introduction of deep learning which is a component of machine learning to augment and remedy the shortcomings of the previously developed machine learning models (LeCun et al., 2015; Goodfellow et al., 2016). Li et al. (2021) highlighted the strong features of the deep learning in data mining ability, however, its application in the coagulation dosage determination is minimal due to the lack of a large amount of data for training. Examples of deep learning models adopted with success in the coagulant dosage determination include convolutional neural network (CNN) (Yamamura et al., 2020), recurrent neural networks (RNN), Long short-term memory (LSTM) (Goodfellow et al., 2016), Gated recurrent unit (GRU) (Huang and Ku, 2018; Zhang et al., 2018; Liu et al., 2019; Zhou et al., 2019). Because of the change in the raw water characteristics used by DWTPs due to changes in time and season, development of a model that employ timeseries datasets for the prediction of coagulant dosages becomes necessary. A solution to this need is the development of an attention-based mechanism deep learning model (Godoy-Rojas et al., 2022). According to Zhao et al.

(2020), the breakthrough in this model is identification of the important input sequence data enhance prediction in the target time series. It has been applied in the monitoring of industrial processes, surface water quality, and hydrology (Fang et al., 2021; Godoy-Rojas et al., 2022; Noor et al., 2022; Li and Li, 2023). Lin et al. (2023) employed graph attention-based multivariate time series forecasting model (GAMTF) which is a newly developed attention-based mechanism deep learning model using long-term data to improve performance in water treatment processes. In comparison to conventional machine learning and deep learning models, the authors observed that GAMTF model improved the prediction accuracy in coagulant dosage taking into consideration the effect of weather conditions. However, the author highlighted the need for future studies to combine the supervisory control and data acquisition (SCADA) system in the determination of suitable and economical coagulant dosage in actual DWTPs.

Although the determination of coagulant dosage is important, determination of other factors that could contribute to the better performance of CFS stage in the water treatment is also crucial to ensure the effectiveness of the treatment stage. Extreme weather conditions could also paly crucial role in the efficiency of this stage. Heat waves and drought has been reported as a factor that could affect the CFS process (Ritson et al., 2014). These two factors can alter the hydrophilicity of natural organic matter (NOM) and dissolved organic matter (DOM) in water sources (Ritson et al., 2014). Increase in their hydrophilicity during coagulation process has been reported to decrease the efficiency in the removal of DOM (Liu et al., 2022). This can result in the increase in the concentration of NOM and DOM in water sources. Hence, the DWTPs will need to optimize the CFS process to enhance pollutant removal efficiency (Sillanpaa et al., 2018; Qui et al., 2019). According to Tafvizi et al. (2022), water pH adjustment, variation in the coagulant type and dosage used, mixing increment, and extension of the sedimentation time are among the optimization procedures that can considered and applied in the CFS stage to enhance coagulation and sedimentation.

Xiao et al. (2023) highlighted that optimized CFS process in DWTPs have the tendency to increase removal efficiency of both the organic matter and bacteria. Zhang et al. (2020) compared the bacteria removal efficiency of poly aluminum chloride (PAC) and poly dimethyl diallyl ammonium chloride (PDMDAAC) applied individual and in combination. The authors observed the bacteria removal percentage of poly aluminum chloride (PAC) and poly dimethyl diallyl ammonium chloride (PDMDAAC) to be 46.3% and 19.5%, respectively when applied individually, but the removal efficiency accelerated to 94.0% when applied in combination. This implied that optimization of the CFS process through the adoption of effective measures could play a crucial role in the mitigation of the effect of heat waves and drought in coagulation process as well reduce the risk associated with the presence of microbes in the source water.

Extreme precipitation is another factor that could affect the performance efficiency of CFS processes because of its tendency to alter the quality of water sources in a short time leading to the increase in the concentration of total suspended solids (TSS), other pollutants, and microbial communities. Hence, there is a need to enhance the CFS process to accommodate the impact of extreme precipitation. Most enhanced CFS focused on treating high turbid water induced by precipitation. Moreira et al. (2023) evaluated the CFS enhancement by organic coagulant in the removal of water turbidity and observed the reduction of turbidity of water source within the range of 201 to 26 NTU on application of $FeCl_3$ while the organic coagulant reduced the turbidity of water source within the range of 36 to 11 NTU. Furthermore, Hu et al. (2013) observed the combination of chitosan and low dosage of aluminum salt caused a reduction of the turbidity of high turbid water to 10 NTU with a minimal sludge production. Increase proliferation and increase in the abundance of bacteria caused by the extreme precipitation can also be mitigated through enhanced CFS process. Shàarani et al. (2019) observed the reduction of Gram-positive and Gram-negative bacteria through the application of natural coagulant with variation in the level of reduction for the two bacterial community. Although the enhancement/or optimization of the CFS using improved coagulant both natural and chemical is promising, the microbial community imbalance that could be caused by the CFS through the selection of the bacterial community that can proliferate by the selected coagulant is a critical challenge as IT may affect the biofilm formation and microbial community structures in the filter (Solano et al., 2014; Ruhal and Kataria, 2021).

Filtration

Filtration process in DWTPs removes the flocs formed during the CFS stage through the aid of suitable filter membrane. The filter membrane is a porous membrane that provides a barrier that prevent the passage of the contaminant as molecules flow through it. In water treatment systems, the filter membrane is categorized into polymeric (PM) and inorganic membranes (IM) based on the nature of the constituent materials. In view of the cost of production between the two categories of filter membrane, Algieri et al. (2021) indicated that the cost of manufacturing the PM less than the manufacturing cost of IM. The most preferred PMs in the filtration stage are cellulose acetate (CA), polycarbonate (PC), polyethersulfone (PES), polysulfone (PSf), polyetherimide (PEI) polyvinylidene fluoride (PVDF), polyamide (PA), polyacrylonitrile (PAN), and polytetrafluoroethylene (PTFE) because of their quality and superior properties (Acarer, 2023a).

Alumina (Al_2O_3), silica (SiO_2), silicon carbide (SiC), zirconia (ZrO_2), silicon nitride, titania (TiO_2), and zeolite are the major constituent of IM. According to Kayvani Fard et al. (2018), each IM are made up of three layers such as supporting layer (bottom), intermediate layer (middle), and the separation layer (top). The IMs can withstand harsh environment than the PMs because of their ability to withhold the thermal, chemical, and mechanical resistance as well as better separation efficiency and antibacterial attribute, high flux due to high hydrophilicity (Hofs et al., 2011; He et al., 2019). Furthermore, the membrane has a longer lifespan than PM, it serves longer treatment periods. However, due to IMs’ high cost of production and brittleness, their production posed a little more challenge making the PM to be widely used today in large-scale application (including DWTPs) and small-scale application (including laboratory studies) (Acarer, 2023a). Acarer (2023a) highlighted that the quality of membrane to be used in DWTPs should have a minimal cost of production, a strong resistance to chemical agents, heat application and mechanical agitations as well as low fouling tendencies. This prompted the need for the optimization of PM to enhance better performance in adequate amount of polymer to be used (Alvi et al., 2019), quantity and type of solvent needed (Acarer, 2022; Yin et al., 2022), and number of pore-forming agents required (Gebru and Das, 2017) in the production of PM.

Recent studies have focused on the addition of different inorganic nanoparticles into PM matrix to enhance the membrane properties, increase the flux, and improve separation performance (Polisetti and Ray, 2021; Srivastava and Raval, 2022).

DOI: http://dx.doi.org/10.15666/aeer/2201_507537

Furthermore, the impact of the nanomaterials optimization (including the type and amount as well as production conditions) on the membrane efficiency and properties have been investigated with a promising result (Nikita et al., 2019; Poon et al., 2023). Hence, Acarer (2023a) encouraged more studies on the production and in-depth characterization of PM to enhance the determination of appropriate composition of the membrane as well as bringing the beneficial aspects of ceramic membranes to low-cost PMs.

Nano-filtration (NF), micro-filtration (MF), ultra-filtration (UF), and reverse osmosis (RO) are the four basic forms of membrane technology (Zakhar et al., 2018). NF membrane technology operates at 5–15 bar and has a pore size of 1–10 nm. They are used to remove multivalent salts and organic molecules with molecular weight cut-off of 200 Da from water sources (Puthai et al., 2017; Kang et al., 2020). NF is a process between RO and UF with high-quality effluent, low energy demand, more salt rejection, higher flux performance, and smooth operation and maintenance advantage over the two other membrane technology (RO and UF) (Abid et al., 2012; Cooray et al., 2019). It has been applied in industries and water treatments in the removal of micro-pollutants, disinfection by-products and viruses and treatment of dissolved salt (Cooray et al., 2019). Furthermore, NF has been used in the treatment of water containing microplastics and heavy metals like arsenic with positive outcomes (Figoli et al., 2019; Barbier et al., 2022; Kara et al., 2023). However, the small pore size and the associated high pressure need when employed in water purification limits their widespread application. Abdel-Fatah (2018) indicated that the use of NF in water treatment caused an increase in the energy need by 60–150%. This can make the application of NF to be cost-intensive.

The pore size of UF is between 1nm to 100 nm and operates at a pressure of 1–10 bar making it suitable for removing suspended solids, colloids, bacteria, viruses, and high molecular weight organic compounds from water (Tomaszewska and Mozia, 2002; Karimi et al., 2019; Jacquet et al., 2021). Ma et al. (2019) reported the effective removal of microplastic from deionized water using UF. This can be attributed to the smaller pore size associated with UF membrane. Ferrer et al. (2015) reported that direct UF efficiently removed bacterial indicators to a greater extent than the conventional process. However, the removal of viruses is lower when compared to the conventional pre-treatment. The authors highlighted the need for the optimization of the UF membrane technology to ensure the removal of viruses as well as unculturable bacterial communities. Polymer (chitosan)-enhanced ultrafiltration was applied in the sand filter backwash water (SFBW) of the DWTP to evaluate its ability to remove cyanobacteria and the microcystin toxin in drinking water and overall removal of > 99% of the toxin and cyanobacteria was observed (Akyol et al., 2021). Delphos et al. (2016) reported the removal of pathogenic microbes such as *Cryptosporidium* and *Giardia cysts* using UF membrane technology. Efstratiou et al. (2017) highlighted that although the disinfection stage in full-scale DWTP is indispensable, the use of UF membranes could minimize the consumption of disinfectant.

MF membranes have a pore size of 0.1–10 μm and operates at a pressure between 0 bar and 2 bar (Moradihamedani, 2022). MF membrane technology is employed to enhance the removal of suspended solids, colloids, and bacteria from water source. Polymer(chitosan)-enhanced microfiltration enhanced the removal of cyanobacteria and the microcystin toxin in drinking water (Akyol et al., 2021). RO membranes have a pore size of 1 nm and operates at a pressure that is greater than 20 bar to enhance water passage through the pores (Acarer, 2023b). Licona et al. (2018) indicated that the RO membrane technology undergoes a process that is based on sorption-diffusion mechanism. They are used in desalination of seawater and brackish water, as well as drinking water and can remove monovalent ions as well as pathogens (Antony et al., 2012; Ansari et al., 2021; Indika et al., 2021). However, one of the flaws is the high energy requirement that could make the technology cost intensive.

According to Safeer et al. (2022), artificial intelligent (AI) based models have been developed in membrane technology for membrane filtration performance prediction based on water flux, membrane fouling, and the removal of organic matter and nutrients. Membrane fouling performance parameter is complex making simulation and prediction challenging because of several operating parameters that are involved. In view of this, ANN model was developed to predict membrane fouling potentials in NF membranes used in municipal water treatment plant and full-scale water treatment plants based on the following parameters: flow rates, pH, UV254, and TDS as input; NOM as the most influential parameter (Shetty and Chellam, 2003). With the incorporation of Long short-term memory (LSTM), the model can remember past events and apply it in the prediction of future events using time-series datasets. Evaluation of the fouling phenomenon in NF membrane based on the performance parameters was done by Shim et al. (2021). The authors observed R^2 values with high estimation accuracy of the model for training and validation sets with regression coefficients of > 0.98 and > 0.97, respectively. Schmitt et al. (2018) reported a very high accuracy of ANN prediction of trans-membrane pressure in an anoxic aerobic membrane bioreactor (MBR) for domestic wastewater treatment. Interfacial interaction is a determining factor in the adhesion and membrane fouling caused by pollutants. Hence, Shi et al. (2021) highlighted the importance of determining effective method for quantifying the interfacial interactions to improve the performance of ANN in membrane technology.

Disinfection

Disinfection is the final barrier to ensuring drinking water’s biological safety; its influence on microbial diversity is greatest in the DWT process, determining the microbial communities in the processing unit. Most microorganisms are inactivated by disinfection, but those that can withstand the disinfection stress are transported to distribution networks and proliferate even at low organic nutrient concentrations (Li et al., 2017). Recent research has found that filtration and disinfection have a greater impact on the microbial community than other processes such as coagulation and sedimentation and that the biofiltration process may influence the downstream microbiome (Choi et al., 2019; Liu et al., 2019). Collivignarelli et al. (2017) provided an overview of different disinfectants and disinfection processes in WWTPs and DWTPs. The authors explore the conventional processes applied in full-scale WWTPS and DWTPs (including action mechanisms, possible formation of DBPs, operative conditions, advantages, and disadvantages) as well as the advance processes and natural disinfection technologies (including action mechanism). The authors pinpointed the need for multi-step disinfection concept meaning the application of disinfection process in different stages of treatment processes and not only at the final stage to enhance the removal of microbes.

AI technologies has been introduced in the disinfection process for the prediction of diverse DBPs in the disinfection process. For the detection of the formation of DBPs such as trihalomethanes (THMs) in chlorine treated water using the AI technology, ANN, support vector machine (SVM), and gene expression programming (GEP) was developed (Singh et al., 2012). The authors observed that the models predicted the non-linear relationship between the condition of disinfection and the production of THM with good values for training and validation sets. Furthermore, the sensitivity analysis showed that initial pH, contact time, and temperature influences THM formation during chlorination. Genetic algorithm (GA) was proposed by Moradi et al. (2017) for detecting another DBPs known as N-nitrosodi-methylamine (NDMA) in chlorinated water. Safeer et al. (2022) provided a comprehensive review on the different AI technologies developed for the prediction and detection of diverse DBPs in chlorinated water. Although the models showed positive performance in the prediction of diverse DBPs, evaluation of the models in the detection of anticipated novel DBPs in chlorinated water is required.

Prospects

While water is essential for the sustenance of human life and it covers about three quarters of the earth surface, about 1% of the water comprises of freshwater sources that needs to be treated and used for human consumptions. Ng et al. (2015) predicted that demand of water globally is going to increase from 4200 Bm^3 in 2015 to 6900 Bm^3 by 2030. This creates serious challenge to both DWTPs and DWDSs as industrial and other anthropogenic activities increasingly introduce many impurities (including diverse bacterial and fungal communities) and hazardous materials of variable compositions and nature into freshwater sources (Dubey et al., 2015). Furthermore, extreme weather condition (heat waves, droughts, and extreme precipitation) alters both microbial and physiochemical properties of freshwater sources and drinking water quality thereby affecting the whole drinking water production chain (Xiao et al., 2023). Hence, there is the need to develop a system or technology that can provide adequate information on the nature of pollutants, sources of pollution, and variability in the microbial indicators and physiochemical parameters of the freshwater sources before entering the DWTPs channel for purification. This will provide adequate guide on the treatment methods needed to ensure adequate removal of the pollutants. Water quality index (WQI) which considers dissolved oxygen (DO), temperature, turbidity, TSS, BOD, calcium, COD, and pH (water quality variable) is the most used indicator to determine the performance of water treatment plants (Yaseen et al., 2018). According to Safeer et al. (2022), diverse AI models that include ANN, multilinear regression (MLR), GA, radial basis function (RBF), particle swarm optimization (PSO), and SVM have been used to monitor and predict water quality parameters with positive outcomes. Surface water quality has been monitored and assessed using neural networks (NNs) (Safeer et al., 2022). However, future studies could take consideration the microbiological indicators present in freshwater sources using the AI models of monitoring and prediction as well as adoption of multidisciplinary approach that cut across molecular docking technology, computational chemistry, and epidemiological approach.

Diverse advancement in the water treatment technology has been adopted in different stages of treatment. Membrane technology, machine learning approach, and deep learning techniques are among the advancement in the drinking water treatment processes that have been adopted in coagulation-flocculation, sedimentation, filtration, disinfection stages as well as in DWDS with promising outcomes. However, the continuous presence of microbial communities both pathogenic and antimicrobial resistance microbes in the final treated water and along the distribution system indicates that more advancement and optimization is needed. For example, Lahaye et al. (2016) treated DWDS of a pig farm using essential oils and observed the growth of a positive bacterial biofilms. According to the authors, the initial biofilms were colonized by hyphenated fungi and the addition of the essential oil promoted the decay of fungal population and caused the proliferation of new bacterial population. Another striking observation by the authors on the application of the essential oil is the improvement of the pigs' health with antibiotics application. This implied that application of natural products like the essential oil enhanced the development of a positive biofilms in the water network (Lahaye et al., 2016). Another alternative evaluated was the use of extracts from the seed of *Moringa oleifera* as a disinfectant in water treatment to ascertain their ability to inhibit the growth of fungal spores (Zakaria et al., 2022). The authors observed the decline in the spore growth from 71% to 60% from day two until day seven. In view of this information, alternatives including application of more plant extracts in the disinfection stages could be a promising tool in combination with other advanced water treatment techniques.

Concluding remarks

Bacterial and filamentous fungal communities are cosmopolitan, and DWTPs and DWDSs are no exception to their proliferation. Several studies have highlighted their presence including pathogenic species in natural water sources as impacted by diverse anthropogenic activities and pollutions which pose critical challenge to the DWTPs and DWDSs. In this study, overview of the bacterial and fungal diversity in natural water sources with an indication of some of the pollution types that contribute to their abundance were provided. Further, emphasis was given on their diversity in DWTPs (final treated water) and DWDS (tap water) and contributing factor to their proliferation which include biofilm formation as well as extreme weather conditions. Advanced treatment approaches in the different stages of water treatment plant were also provided. This review therefore is unique as it combines information on advanced treatment and fungi and bacterial diversity in DWTP and DWDS in a way that offers future perspectives to efficient treatment and safeguard of drinking water amidst increased microbial changes with intensive anthropogenic pollution among others.

Identification of bacterial communities and filamentous fungal communities as well as the novel pathogens in the natural water is pertinent to provide direction on the appropriate treatment approach to be adopted. However, studies on fungal identification have shown that the approach in their identification is not uniform. Further studies are recommended in methodology of fungi identification in natural water, DWTPs, and DWDSs which includes culture-dependent and culture-independent methods in complement of each other. In addition, bacterial-fungal interaction in biofilm formation is reported to play crucial role in the deterioration of water quality in DWTPs and DWDSs. In view of this role, further investigation of the factors that enhanced the interaction as well as the detailed composition of the diversity of fungal and bacterial communities through NGS techniques, molecular approach, and deep machine learning approach is required.

Extreme weather conditions impact on natural water sources, DWTPs, and DWDSs leading to significant change in the quality of the water and the microbial composition.

The weather decreases the efficiency of the coagulation, sedimentation, and disinfection stages in the DWTPs and cause an increase in the filter overload. This will alter the water quality that enters the DWDSs as there will be increase in the microbial proliferation due to decrease in the residual chlorine concentration. In the quest to proffer solutions to the improvement of the water treatment process, AI was introduced was encompassed diverse machine learning and deep learning models. AI has shown increasingly superior performance in many water treatment processes especially in the determination of coagulant dosages and other physicochemical parameters of water prediction. However, further studies are recommended in the development of models that analyze the whole treatment plants taking into consideration the microbiological aspect of the water, extreme weather conditions, and real-world process that is constantly fluctuating.

Acknowledgements. The authors wish to acknowledge the Water Research Commission (South Africa) for funding under the research grant 2022/2023-00801.

REFERENCES

[1] Abdel-Fatah, M. A. (2018): Nanofiltration systems and applications in wastewater treatment. – Ain Shams Engineering Journal 9(4): 3077-3092.
[2] Abid, M. F., Zablouk, M. A., Abid-Alameer, A. M. (2012): Experimental study of dye removal from industrial wastewater by membrane technologies of reverse osmosis and nanofiltration. – Iranian Journal of Environmental Health Science and Engineering 9: 1-9.
[3] Acarer, S. (2022): Effect of different solvents, pore-forming agent, and solubility parameter differences on the properties of pes ultrafiltration membrane. – Sakarya University Journal of Science 26(6): 1196-1208.
[4] Acarer, S. (2023a): A review of microplastic removal from water and wastewater by membrane technologies. – Water Science and Technology 88(1): 199-219.
[5] Acarer, S. (2023b): Microplastics in wastewater treatment plants: sources, properties, removal efficiency, removal mechanisms, and interactions with pollutants. – Water Science and Technology 87(3): 685-710.
[6] Achmad, R. T., Budiawan, Auerkari, E. I. (2017): Effects of chromium on human body. – Australia Road Research Board 13: 1-8.
[7] Afonso, T. B., Simões, L. C., Lima, N. (2021): Occurrence of filamentous fungi in drinking water: their role on fungal-bacterial biofilm formation. – Research in Microbiology 172(1): 103791.
[8] Akyol, Ç., Ozbayram, E. G., Accoroni, S. et al. (2021): Monitoring of cyanobacterial blooms and assessing polymer-enhanced microfiltration and ultrafiltration for microcystin removal in an Italian drinking water treatment plant. – Environmental Pollution 286: 117535.
[9] Al-gabr, H. M., Zheng, T., Yu, X. (2014): Occurrence and quantification of fungi and detection of mycotoxigenic fungi in drinking water in Xiamen City, China. – Science of the Total Environment 466-467: 1103-1111.
[10] Algieri, C., Chakraborty, S., Pal, U. (2021): Efficacy of phase inversion technique for polymeric membrane fabrication. – Journal of Phase Change Material 1(1).
[11] Alvi, M. A. U. R., Khalid, M. W., Ahmad, N. M. et al. (2019): Polymer concentration and solvent variation correlation with the morphology and water filtration analysis of polyether sulfone microfiltration membrane. – Advances in Polymer Technology 2019: 8074626.

[12] Ansari, M., Al-Obaidi, M. A., Hadadian, Z. et al. (2021): Performance evaluation of a brackish water reverse osmosis pilot-plant desalination process under different operating conditions: experimental study. – Cleaner Engineering and Technology 4: 100134.

[13] Antony, A., Blackbeard, J., Leslie, G. (2012): Removal efficiency and integrity monitoring techniques for virus removal by membrane processes. – Critical Review in Environmental Science and Technology 42: 891-933.

[14] Arroyo, M. G., Frota, O. P., Peresi, J. T. M. et al. (2019): Wide diversity of fungal species found in wellwater for human consumption: an analytical cross-sectional study. – Sao Paulo Medical Journal 137: 512-516.

[15] Arvanitidou, M., Spaia, S., Velegraki, A. et al. (2000): High level of recovery of fungi from water and dialysate in haemodialysis units. – Journal of Hospital Infection 45(3): 225-230.

[16] Ashraf, A., Bibi, I., Niazi, N. K. et al. (2017): Chromium (VI) sorption efficiency of acid-activated banana peel over organo-montmorillonite in aqueous solutions. – International Journal of Phytoremediation 19: 605-613.

[17] Bai, X., Ma, X., Xu, F. et al. (2015): The drinking water treatment process as a potential source of affecting the bacterial antibiotic resistance. – Science of the Total Environment 533: 24-31.

[18] Bai, X., Zhang, T., Qu, Z. et al. (2017): Contribution of filamentous fungi to the musty odorant 2,4,6-trichloroanisole in water supply reservoirs and associated drinking water treatment plants. – Chemosphere 182: 223-230.

[19] Barbier, J. S., Dris, R., Lecarpentier, C. et al. (2022): Microplastic occurrence after conventional and nanofiltration processes at drinking water treatment plants: preliminary results. – Frontiers in Water 4: 886703.

[20] Barchiesi, M., Chiavola, A., Di Marcantonio, C., Boni, M. R. (2021): Presence and fate of microplastics in the water sources: focus on the role of wastewater and drinking water treatment plants. – Journal of Water Process Engineering 40: 101787.

[21] Batista, A. M. M., Meynet, P., Garcia, P. P. et al. (2018): Microbiological safety of a small water distribution system: evaluating potentially pathogenic bacteria using advanced sequencing techniques. – Water Supply 18(2): 391-398.

[22] Batista, A. M. M., de Siqueira, J. C., Meynet, P. et al. (2022): Diversity and dynamics of bacterial communities in the drinking water distribution network of a mid-sized city in Brazil. – Journal of Water Health 20(12): 1733.

[23] Bautista-de los Santos, Q. M., Schroeder, J. L., Sevillano-Rivera, M. C. et al. (2016): Emerging investigators series: microbial communities in full-scale drinking water distribution systems—a meta-analysis. – Environmental Science and Water Research Technology 2: 631-644.

[24] Bazer-Bachi, A., Puech-coste, R., Probst, J. (1990): Mathematical modelling of optimal coagulant dose in water treatment plant. – Revenue Des Sciences De L'eau Journal of Water Science 3: 377-397.

[25] Beattie, R. E., Bandla, A., Swarup, S., Hristova, K. R. (2020): Freshwater sediment microbial communities are not resilient to disturbance from agricultural land runoff. – Frontiers in Microbiology 1: 539921.

[26] Becerra-Castro, C., Macedo, G., Silva, A. M. T. et al. (2016): *Proteobacteria* become predominant during regrowth after water disinfection. – Science of the Total Environment 573: 313-323.

[27] Bergeron, S., Boopathy, R., Nathaniel, R. et al. (2015): Presence of antibiotic resistant bacteria and antibiotic resistance genes in raw source water and treated drinking water. – International Biodeterioration and Biodegradation 102: 370-374.

[28] Brasili, E., Bavasso, I., Petruccelli, V. et al. (2020): Remediation of hexavalent chromium contaminated water through zero-valent iron nanoparticles and effects on tomato plant growth performance. – Scientific Report 10: 1920.

[29] Bukhary, S., Batista, J., Ahmad, S. (2020): Design aspects, energy consumption evaluation, and offset for drinking water treatment operation. – Water 12(6): 1772.

[30] Carneiro, Z. A., Lima, J. C., Lopes, C. D. et al. (2019): Heterobimetallic nickel (II) and palladium (II) complexes derived from S-benzyl-N- (ferrocenyl) methylenedithiocarbazate: Trypanocidal activity and interaction with *Trypanosoma cruzi* Old Yellow Enzyme (TcOYE). – European Journal of Medicinal Chemistry 180: 213-223.

[31] Cescon, A., Jiang, J. Q. (2020): Filtration process and alternative filter media material in water treatment. – Water 12(12): 3377.

[32] Chao, C. M., Lai, C. C., Tsai, H. Y. et al. (2013): Pneumonia caused by *Aeromonas* species in Taiwan, 2004–2011. – European Journal of Clinical Microbiology and Infectious Disease 32: 1069-1075.

[33] Chen, J., Li, W., Tan, Q. et al. (2022): Effect of disinfectant exposure and starvation treatment on the detachment of simulated drinking water biofilms. – Science of the Total Environment 807: 150896.

[34] Chen, J., Gui, H., Guo, Y., Li, J. (2023): Spatial distributions of microbial diversity in the contaminated deep groundwater: a case study of the Huaibei coalfield. – Environmental Pollution 318: 120866.

[35] Chen, X. P., Chen, H. Y., Sun, J. et al. (2018b): Shifts in the structure and function of the microbial community in response to metal pollution of freshwater sediments in Finland. – JSS 18: 3324-3333.

[36] Chen, Y., Jiang, Y., Huang, H. et al. (2018a): Long-term and high-concentration heavy-metal contamination strongly influences the microbiome and functional genes in Yellow River sediments. – Science of the Total Environment 637: 1400-1412.

[37] Choi, Y., Cha, Y., Kim, B. (2019): Characteristics of bacterial communities in biological filters of full-scale drinking water treatment plants. – Journal of Microbiology and Biotechnology 29: 91-104.

[38] Collivignarelli, M. C., Abbà, A., Benigna, I. et al. (2017): Overview of the main disinfection processes for wastewater and drinking water treatment plants. – Sustainability 10(1): 86.

[39] Cook, L. C., Federle, M. J. (2014): Peptide pheromone signaling in *Streptococcus* and *Enterococcus*. – FEMS Microbiology 38: 473-492.

[40] Cooray, T., Wei, Y., Zhang, J. et al. (2019): Drinking-water supply for CKDu affected areas of Sri Lanka, using nanofiltration membrane technology: from laboratory to practice. – Water 11(12): 2512.

[41] Cui, H., Huang, X., Yu, Z. et al. (2020): Application progress of enhanced coagulation in water treatment. – RSC Advances 10: 20231-20244.

[42] Del Olmot, G., Husband, S., Sanchez Briones, C. et al. (2021): The microbial ecology of a Mediterranean chlorinated drinking water distribution systems in the city of Valencia (Spain). – Science of the Total Environment 754: 142016.

[43] Delphos, P. J. (2016): Microfiltration and Ultrafiltration Membranes for Drinking Water. Manual of Water Supply Practices M53. – Water Works Association, Denver, CO.

[44] Denning, D. W., O'Driscoll, B. R., Hogaboam, C. M. et al. (2006): The link between fungi and severe asthma: a summary of the evidence. – European Respiratory Journal 27: 615-626.

[45] Dias, M. F., da Rocha Fernandes, G., de Paiva, M. C. et al. (2020): Exploring the resistome, virulome and microbiome of drinking water in environmental and clinical settings. – Water Research 174: 115630.

[46] Ding, H., Zhao, D., Gao, Y. (2016): Response surface optimization of cholesterol extraction from lanolin alcohol by selective solvent crystallization. – Chemical Papers 71(1): 1-79.

[47] Doggett, M. S. (2000): Characterization of fungal biofilms within a municipal water distribution system. – Applied Environmental Microbiology 66: 1249-1251.

[48] Douterelo, I., Jackson, M., Solomon, C., Boxall, J. (2016): Microbial analysis of in situ biofilm formation in drinking water distribution systems: implications for monitoring and control of drinking water quality. – Applied Microbiology and Biotechnology 100: 3301-3311.

[49] Douterelo, I., Jackson, M., Solomon, C., Boxall, J. (2017): Spatial and temporal analogies in microbial communities in natural drinking water biofilms. – Science of the Total Environment 581-582: 277-288.

[50] Douterelo, I., Fish, K. E., Boxall, J. B. (2018a): Succession of bacterial and fungal communities within biofilms of a chlorinated drinking water distribution system. – Water Research 141: 74-85.

[51] Douterelo, I., Calero-Preciado, C., Soria-Carrasco, V., Boxall, J. B. (2018b): Whole metagenome sequencing of chlorinated drinking water distribution systems. – Environmental Science: Water Research and Technology 4: 2080-2091.

[52] Douterelo, I., Sharpe, R. L., Husband, S. et al. (2019): Understanding microbial ecology to improve management of drinking water distribution systems. – Wiley Interdisciplinary Reviews: Water 6: e01325.

[53] Dubey, R., Bajpai, J., Bajpai, A. K. (2015): Green synthesis of graphene sand composite (GSC) as novel adsorbent for efficient removal of Cr (VI) ions from aqueous solution. – Journal of Water Process Engineering 5: 83-94.

[54] Efstratiou, A., Ongerth, J. E., Karanis, P. (2017): Waterborne transmission of protozoan parasites: review of worldwide outbreaks—an update 2011-2016. – Water Research 114: 14-22.

[55] Fang, M., Tang, L., Yang, X. et al. (2021): FTPG: a fine-grained traffic prediction method with graph attention network using big trace data. – IEEE Transactions on Intelligent Transportation System 23(6): 5163-5175.

[56] Fang, T., Cui, Q., Huang, Y. et al. (2018): Distribution comparison and risk assessment of free-floating and particle-attached bacterial pathogens in urban recreational water: implications for water quality management. – Science of the Total Environment 613: 428-438.

[57] Ferrer, O., Casas, S., Galvañ, C. et al. (2015): Direct ultrafiltration performance and membrane integrity monitoring by microbiological analysis. – Water Research 83: 121-131.

[58] Figoli, A., Fuoco, I., Apollaro, C. et al. (2019): Arsenic-contaminated groundwaters remediation by nanofiltration. – Separation and Purification Technology 238: 116461.

[59] Fish, K. E., Boxall, J. B. (2018): Biofilm microbiome (Re)growth dynamics in drinking water distribution systems are impacted by chlorine concentration. – Frontiers in Microbiology 9: 2519.

[60] Frey-Klett, P., Burlinson, P., Deveau, A. et al. (2011): Bacterial-fungal interactions: hyphens between agricultural, clinical, environmental, and food microbiologists. – Microbiology and Molecular Biology Reviews 75: 583-609.

[61] Gebru, K. A., Das, C. (2017): Effects of solubility parameter differences among peg, PVP and ca on the preparation of ultrafiltration membranes: impacts of solvents and additives on morphology, permeability, and fouling performances. – Chinese Journal of Chemical Engineering 25(7): 911-923.

[62] Godoy-Rojas, D. F., Leon-Medina, J. X., Rueda, B. et al. (2022): Attention-based deep recurrent neural network to forecast the temperature behaviour of an electric arc furnace side-wall. – Sensors 22(4): 1418.

[63] Goecke, F., Thiel, V., Wiese, J. et al. (2013): Algae as an important environment for bacteria–phylogenetic relationships among new bacterial species isolated from algae. – Phycologia 52: 14-24.

[64] Gomes, I. B., Maillard, J. Y., Simões, L. C. and Simões, M. (2020): Emerging contaminants affect the microbiome of water systems—strategies for their mitigation. – NPJ Clean Water 3(1): 39.

[65] Goodfellow, I., Bengio, Y., Courville, A. (2016): Deep Learning. – MIT Press, Cambridge, MA. http://www.deeplearningbook.org.

[66] Goralska, K., Błaszkowska, J., Dzikowiec, M. (2020): The occurrence of potentially pathogenic filamentous fungi in recreational surface water as a public health risk. – Journal of Water and Health 18: 127-144.

[67] Grabinska-Łoniewska, A., Koniłłowicz-Kowalska, T., Wardzynska, G., Boryn, K. (2007): Occurrence of fungi in water distribution system. – Polish Journal of Environmental Studies 16: 539-547.

[68] Griffiths, K., Andrews, R. (2011): The application of artificial neural networks for the optimization of coagulant dosage. – Water Science and Technology 11: 605-611.

[69] Haghiri, S., Daghighi, A., Moharramzadeh, S. (2018): Optimum coagulant forecasting by modeling jar test experiments using ANNs. – Drinking Water Engineering and Science 11: 1-8.

[70] Hansen, A. M., Kraus, T. E. C., Pellerin, B. A. et al. (2016): Optical properties of dissolved organic matter (DOM): Effects of biological and photolytic degradation. – Limnology and Oceanography 61: 1015-1032.

[71] He, Z., Lyu, Z., Gu, Q. et al. (2019): Ceramic-based membranes for water and wastewater treatment. – Colloids and Surfaces A: Physicochemical and Engineering Aspects 578: 123513.

[72] Heddam, S. (2021): Extremely Randomized Tree: A New Machines Learning Method for Predicting Coagulant Dosage in Drinking Water Treatment Plant. – In: Samui, P. et al. (eds.) Water Engineering Modeling and Mathematic Tools. Elsevier, Amsterdam, pp. 475-489.

[73] Hofs, B., Ogier, J., Vries, D. et al. (2011): Comparison of ceramic and polymeric membrane permeability and fouling using surface water. – Separation and Purification Technology 79: 365-374.

[74] Holinger, E. P., Ross, K. A., Robertson, C. E. et al. (2014): Molecular analysis of point-of-use municipal drinking water microbiology. – Water Residual 49: 225-235.

[75] Hou, L., Zhou, Q., Wu, Q. et al. (2018): Spatiotemporal changes in bacterial community and microbial activity in a full-scale drinking water treatment plant. – Science of the Total Environment 625: 449-459.

[76] Hu, C. Y., Lo, S. L., Chang, C. L. et al. (2013): Treatment of highly turbid water using chitosan and aluminum salts. – Separation and Purification Technology 104: 322-326.

[77] Huang, C. J., Kuo, P. H. (2018): A deep CNN-LSTM model for particulate matter (pm2. 5) forecasting in smart cities. – Sensors 18: 2220.

[78] Huang, K., Zhang, X. X., Shi, P. et al. (2014): A comprehensive insight into bacterial virulence in drinking water using 454 pyrosequencing and illumina high-throughput sequencing. – Ecotoxicology and Environmental Safety 109: 15-21.

[79] Huang, W., Chen, X., Jiang, X., Zheng, B. (2017): Characterization of sediment bacterial communities in plain lakes with different trophic statuses. – Microbiology Open 6: e00503.

[80] Hull, N. M., Ling, F., Pinto, A. J. et al. (2019): Drinking water microbiome project: is it time? – Trends in Microbiology 27: 670-677.

[81] Hurtado-McCormick, S., Sanchez, L., Martínez, J. et al. (2016): Fungi in biofilms of a drinking water network: occurrence, diversity, and mycotoxins approach. – Water Science and Technology: Water Supply 16: 905-914.

[82] Indika, S., Wei, Y., Hu, D. et al. (2021): Evaluation of performance of existing RO drinking water stations in the north central province, Sri Lanka. – Membranes 11: 383.

[83] Jacquet, N., Wurtzer, S., Darracq, G. et al. (2021): Effect of concentration on virus removal for ultrafiltration membrane in drinking water production. – Journal of Membrane Science 634: 119417.

[84] Jambeck, R. J., Geyer, R., Wolcox, C. et al. (2015): Plastic waste inputs from land into the ocean. – Science 347(6223): 768-771.

[85] Jia, J., Gomes-Silva, G., Plath, M. et al. (2021): Shifts in bacterial communities and antibiotic resistance genes in surface water and gut microbiota of guppies (*Poecilia reticulata*) in the upper Rio Uberabinha, Brazil. – Ecotoxicology and Environmental Safety 211: 111955.

[86] Jia, S., Wu, J., Ye, L. et al. (2019): Metagenomic assembly provides a deep insight into the antibiotic resistome alteration induced by drinking water chlorination and its correlations with bacterial host changes. – Journal of Hazardous Materials 379: 120841.

[87] Jones, A. S., Marini, J., Solo-Gabriele, H. M. et al. (2019): Arsenic, copper, and chromium from treated wood products in the U.S. disposal sector. – Waste Management 87: 731-740.

[88] Kaevska, M., Videnska, P., Sedlar, K., Slana, I. (2016): Seasonal changes in microbial community composition in river water studied using 454-pyrosequencing. – SpringerPlus 5: 409.

[89] Kalyuzhnaya, M. G., Beck, D. A. C., Vorobev, A. et al. (2012): Novel methylotrophic isolates from lake sediment, description of *Methylotenera versatilis* sp. nov. and emended description of the genus *Methylotenera*. – International Journal of Systemic Evolution and Microbiology 62: 106-111.

[90] Kamboj, N., Kamboj, V. (2019): Water quality assessment using overall index of pollution in riverbed-mining area of Ganga-River Haridwar, India. – Water Science 33(1): 65-74.

[91] Kang, Y., Jang, J., Kim, S. et al. (2020): PIP/TMC interfacial polymerization with electrospray: novel loose nano filtration membrane for dye wastewater treatment. – ACS Applied Materials and Interfaces 12: 36148-36158.

[92] Kara, N., Sari Erkan, H., Onkal Engin, G. (2023): Characterization and removal of microplastics in landfill leachate treatment plants in Istanbul, Turkey. – Analytical Letter 56(9): 1535-1548.

[93] Karimi, A., Khataee, A., Vatanpour, V., Safarpour, M. (2019): High-flux PVDF mixed matrix membranes embedded with size-controlled zıf-8 nanoparticles. – Separation and Purification Technology 229: 115838.

[94] Kastman, E. K., Kamelamela, N., Norville, J. W. et al. (2016): Biotic interactions shape the ecological distributions of *Staphylococcus* species. – mBio 7: 1-13.

[95] Kayvani Fard, A., Mckay, G., Buekenhoudt, A. et al. (2018): Inorganic membranes: preparation and application for water treatment and desalination. – Materials 11: 74.

[96] Kazakis, N., Kantiranis, N., Kalaitzidou, K. et al. (2017): Origin of hexavalent chromium in groundwater: the example of Sarigkiol Basin, Northern Greece. – Science of the Total Environment 593-594: 552-566.

[97] Ke, Y., Sun, W., Jing, Z. et al. (2023): Antibiotic resistome alteration along a full-scale drinking water supply system deciphered by metagenome assembly: regulated by seasonality, mobile gene elements and antibiotic resistant gene hosts. – Science of the Total Environment 862: 160887.

[98] Kim, C. M., Parnichkun, M. (2017): Prediction of settled water turbidity and optimal coagulant dosage in drinking water treatment plant using a hybrid model of k-means clustering and adaptive neuro-fuzzy inference system. – Applied Water Science 7: 3885-3902.

[99] Korajkic, A., Parfrey, L. W., McMinn, B. R. et al. (2015): Changes in bacterial and eukaryotic communities during sewage decomposition in Mississippi river water. – Water Research 69: 30-39.

[100] Kosuth, M., Mason, S. A., Wattenberg, E. V. (2018): Anthropogenic contamination of tap water, beer, and sea salt. – PLoS ONE 13: 1-18.

[101] Lahaye, E., Renaux, J. J., Le Tilly, V., Sire, O. (2016): Evolution of a fungal ecosystem in a water distribution system to a positive bacterial biofilm subsequent to a treatment using essential oils. – Comptes Rendus Chim 19: 505-510.

[102] Lautenschlager, K., Hwang, C., Ling, F. et al. (2014): Abundance and composition of indigenous bacterial communities in a multi-step biofiltration-based drinking water treatment plant. – Water Research 62: 40-52.
[103] LeCun, Y., Bengio, Y., Hinton, G. (2015): Deep learning. – Nature 521: 436-444.
[104] Li, J., Liu, H., Paul Chen, J. (2018): Microplastics in freshwater systems: a review on occurrence, environmental effects, and methods for microplastics detection. – Water Research 137: 362-374.
[105] Li, L., Rong, S., Wang, R., Yu, S. (2021): Recent advances in artificial intelligence and machine learning for nonlinear relationship analysis and process control in drinking water treatment: a review. – Chemical Engineering Journal 405: 126673.
[106] Li, Q., Yu, S., Li, L. et al. (2017): Microbial communities are shaped by treatment processes in a drinking water treatment plant and their contribution and threat to drinking water safety. – Frontiers in Microbiol 8.
[107] Li, Y., Li, R. (2023): Predicting ammonia nitrogen in surface water by a new attention based deep learning hybrid model. – Environmental Research 216(3): 114723.
[108] Licona, K. P. M., Geaquinto, L. R. D. O., Nicolini, J. V. et al. (2018): Assessing potential of nanofiltration and reverse osmosis for removal of toxic pharmaceuticals from water. – Journal of Water Process and Engineer 25: 195-204.
[109] Lin, S., Kim, J., Hua, C. et al. (2023): Coagulant dosage determination using deep learning-based graph attention multivariate time series forecasting model. – Water Research 232: 119665.
[110] Lin, W., Yu, Z., Zhang, H., Thompson, I. P. (2014): Diversity and dynamics of microbial communities at each step of treatment plant for potable water generation. – Water Research 52: 218-230.
[111] Lin, X., Gao, D., Lu, K., Li, X. (2019): Bacterial community shifts driven by nitrogen pollution in river sediments of a highly urbanized city. – International Journal of Environmental Science 16(20): 3794.
[112] Liu, G., Tao, Y., Zhang, Y. et al. (2017a): Hotspots for selected metal elements and microbes' accumulation and the corresponding water quality deterioration potential in an unchlorinated drinking water distribution system. – Water Research 124: 435-445.
[113] Liu, G., Zhang, Y., Knibbe, W. J. et al. (2017b): Potential impacts of changing supply-water quality on drinking water distribution: a review. – Water Research 116: 135-148.
[114] Liu, H., Li, Y., Yang, H. et al. (2022): The characters of dissolved organic matters from litter-mimic with the different humification states and their effects on drinking water treatment processes. – Science of the Total Environment 861: 160470.
[115] Liu, P., Wang, J., Sangaiah, A. K. et al. (2019): Analysis and prediction of water quality using LSTM deep neural networks in IoT environment. – Sustainability 11: 2058.
[116] Liu, S., Huang, W., Shu, W. et al. (2018): Performance of L-493 macroprous resin for adsorption of trihalomethanes from water. – Water, Air, and Soil Pollution 229: 1-12.
[117] Llirós, M., Inceoglu, O., Garcia-Armisen, T. et al. (2017): Bacterial community composition in three freshwater reservoirs of different alkalinity and trophic status. – PLoS One 9(12): e116145.
[118] Lu, J., Tian, Z., Yu, J. et al. (2018): Distribution and abundance of antibiotic resistance genes in sand settling reservoirs and drinking water treatment plants across the Yellow River, China. – Water 10(3): 246.
[119] Lupon, A., Catalan, N., Marti, E., Bernal, S. (2020): Influence of dissolved organic matter sources on in-stream net dissolved organic carbon uptake in a Mediterranean stream. – Water 12: 1722.
[120] Luvhimbi, N., Tshitangano, T. G., Mabunda, J. T. et al. (2022): Water quality assessment and evaluation of human health risk of drinking water from source to point of use at Thulamela municipality, Limpopo Province. – Scientific Report 12: 605.

[121] Lv, L., Jiang, T., Zhang, S., Yu, X. (2014): Exposure to mutagenic disinfection byproducts leads to increase of antibiotic resistance in *Pseudomonas aeruginosa*. – Environmental Science and Technology *48*(14): 8188-8195.

[122] Ma, B., Xue, W., Hu, C. et al. (2019): Characteristics of microplastic removal via coagulation and ultrafiltration during drinking water treatment. – Chemical Engineering Journal 359: 159-167.

[123] Ma, L., Jiang, X. T., Guan, L. et al. (2022): Nationwide biogeography and health implications of bacterial communities in household drinking water. – Water Research 215: 118238.

[124] Ma, X., Baron, J. L., Vikram, A. et al. (2015): Fungal diversity, and presence of potentially pathogenic fungi in a hospital hot water system treated with on-site monochloramine. – Water Research 71: 197-206.

[125] Ma, X., Vikram, A., Casson, L., Bibby, K. (2017): Centralized drinking water treatment operations shape bacterial and fungal community structure. – Environmental Science and Technology 51: 7648-7657.

[126] Maguvu, T. E., Bezuidenhout, C. C., Kritzinger, R. et al. (2020): Combining physicochemical properties and microbiome data to evaluate the water quality of South African drinking water production plants. – PLoS One 15(8): e0237335.

[127] Mantilla-Calderon, D., Plewa, M. J., Michoud, G. et al. (2019): Water disinfection byproducts increase natural transformation rates of environmental DNA in *Acinetobacter baylyi* ADP1. – Environmental Science and Technology 53(11): 6520-6528.

[128] Mesquita-Rocha, S., Godoy-Martinez, P. C., Gonçalves, S. S. et al. (2013): The water supply system as a potential source of fungal infection in paediatric haematopoietic stem cell units. – BMC Infectious Diseases 13: 1-8.

[129] Mhlongo, N. T., Tekere, M., Sibanda, T. (2019): Prevalence and public health implications of mycotoxigenic fungi in treated drinking water systems. – Journal of Water and Health 17(4): 517-531.

[130] Mi, Z., Dai, Y., Xie, S. et al. (2015): Impact of disinfection on drinking water biofilm bacterial community. – Journal of Environmental Science 37: 200-205.

[131] Moat, J., Rizoulis, A., Fox, G., Upton, M. (2016): Domestic shower hose biofilms contain fungal species capable of causing opportunistic infection. – Journal of Water and Health 14: 727-737.

[132] Moradi, S., Chow, C. W., Cook, D., Newcombe, G., Amal, R. (2017): Estimating NDMA formation in a distribution system using a hybrid genetic algorithm. – Journal of American Water Works Associations 109(6): E265-272.

[133] Moradihamedani, P. (2022): Recent advances in dye removal from wastewater by membrane technology: a review. – Polymer Bulletin 79: 2603-2631.

[134] Moreira, V. R., Guimarães, R. N., Moser, P. B. et al. (2023): Restrictions in water treatment by conventional processes (coagulation, flocculation, and sand-filtration) following scenarios of dam failure. – Journal of Water Process and Engineering 51: 103450.

[135] Narges, S., Ghorban, A., Hassan, K., Mohammad, K. (2021): Prediction of the optimal dosage of coagulants in water treatment plants through developing models based on artificial neural network fuzzy inference system (ANFIS). – Journal of Environmental Health Science and Engineering 19: 1543-1553.

[136] Ng, K. C., Thu, K., Oh, S. J., Ang, L., Shahzad, M. W., Ismail, A. B. (2015): Recent developments in thermally-driven seawater desalination: energy efficiency improvement by hybridization of the MED and AD cycles. – Desalination 356: 255-270.

[137] Nikita, K., Karkare, P., Ray, D. et al. (2019): Understanding the morphology of MWCNT/pes mixed-matrix membranes using sans: interpretation and rejection performance. – Applied Water Science 9: 154.

[138] Noor, F., Haq, S., Rakib, M. et al. (2022): Water level forecasting using spatiotemporal attention-based long short-term memory network. – Water 14: 612.

[139] Novak Babic, M., Zalar, P., Zenko, B. et al. (2016): Yeasts and yeast-like fungi in tap water and groundwater, and their transmission to household appliances. – Fungal Ecology 20: 30-39.
[140] Novak Babic, M., Gunde-Cimerman, N., Vargha, M. et al. (2017): Fungal contaminants in drinking water regulation? A tale of ecology, exposure, purification, and clinical relevance. – International Journal of Environmental Research and Public Health 14(6): 636.
[141] Novak Babic, M., Zupancic, J., Brandao, J., Gunde-Cimerman, N. (2018): Opportunistic water-borne human pathogenic filamentous fungi unreported from food. – Microorganisms 6: 79.
[142] Odhiambo, K. A., Ogola, H. J. O., Onyango, B. et al. (2023): Contribution of pollution gradient to the sediment microbiome and potential pathogens in urban streams draining into Lake Victoria (Kenya). – Environmental Science and Pollution Research 30(13): 36450-36471.
[143] Ogwugwa, V. H., Oyetibo, G. O., Amund, O. O. (2021): Taxonomic profiling of bacteria and fungi in freshwater sewer receiving hospital wastewater. – Environmental Research 192: 110319.
[144] Oliveira, B. R., Barreto Crespo, M. T., San Romao, M. V. et al. (2013): New insights concerning the occurrence of fungi in water sources and their potential pathogenicity. – Water Research 47: 6338-6347.
[145] Oliveira, B. R., Mata, A. T., Ferreira, J. P. et al. (2018): Production of mycotoxins by filamentous fungi in untreated surface water. – Environmental Science and Pollution Research 25: 17519-1728.
[146] Oliveira, H. M. B., Santos, C., Paterson, R. R. M. et al. (2016): Fungi from a groundwater-fed drinking water supply system in Brazil. – International Journal of Environmental Research and Public Health 13(3): 304.
[147] Papenfort, K., Bassler, B. L. (2016): Quorum sensing signal-response systems in Gram-negative bacteria. – Nature Review Microbiology 14: 576-588.
[148] Parida, P. K., Behera, B. K., Dehury, B. et al. (2022): Community structure and function of microbiomes in polluted stretches of river Yamuna in New Delhi, India, using shotgun metagenomics. – Environmental Science and Pollution Research 29(47): 71311-71325.
[149] Paterson, R. R. M., Lima, N. (2005): Fungal Contamination of Drinking Water. – In: Lehr, J., Keeley, J., Lehr, J., Kingery III, T. B. (eds.) Water Encyclopedia. Wiley, New York, pp 1-7.
[150] Pellerin, C., Booker, S. M. (2000): Reflections on hexavalent chromium: health hazards of an industrial heavyweight. – Environmental Health Perspect 108: A402-A407.
[151] Perrin, Y., Bouchon, D., Delafont, V. et al. (2019): Microbiome of drinking water: a full-scale spatio-temporal study to monitor water quality in the Paris distribution system. – Water Research 149: 375-385.
[152] Phulpoto, I. A., Hu, B., Wang, Y. et al. (2021): Effect of natural microbiome and culturable biosurfactants-producing bacterial consortia of freshwater lake on petroleum-hydrocarbon degradation. – Science of the Total Environment 751: 141720.
[153] Pinto, A. J., Schroeder, J., Lunn, M. et al. (2014): Spatial-temporal survey and occupancy-abundance modeling to predict bacterial community dynamics in the drinking water microbiome. – mBio 5.
[154] Polisetti, V., Ray, P. (2021): Nano SiO_2 and TiO_2 embedded polyacrylonitrile/polyvinylidene fluoride ultrafiltration membranes: improvement in flux and antifouling properties. – Journal of Applied Polymer and Science 138: e49606.
[155] Poon, Y. K., Enche, A., Rahim, S. K. et al. (2023): Synthesis, and characterisation of self-cleaning TiO_2/pes mixed matrix membranes in the removal of humic acid. – Membranes 13: 373.
[156] Potgieter, S. C., Pinto, A. J. (2019): Reproducible microbial community dynamics of two drinking water systems treating similar source waters. – bioRxiv Microbiology 678920.

[157] Potgieter, S., Pinto, A., Sigudu, M. et al. (2018): Long-term spatial and temporal microbial community dynamics in a large-scale drinking water distribution system with multiple disinfectant regimes. – Water Research 139: 406-419.

[158] Prata, J. C. (2018): Airborne microplastics: consequences to human health? – Environmental Pollution 234: 115-126.

[159] Prest, E. I., Hammes, F., Kotzsch, S. et al. (2016): A systematic approach for the assessment of bacterial growth-controlling factors linked to biological stability of drinking water in distribution systems. – Water Science and Technology: Water Supply 16: 865-880.

[160] Proctor, C. R., Hammes, F. (2015): Drinking water microbiology—from measurement to management. – Current Opinion in Biotechnology 33: 87-94.

[161] Przydatek, G., Kanownik, W. (2019): Impact of small municipal solid waste landfill on groundwater quality. – Environmental Monitoring and Assessment 191: 1-14.

[162] Puthai, W., Kanezashi, M., Nagasawa, H., Tsuru, T. (2017): Development, and permeation properties of sio2-zro2 nanofiltration membranes with a MWCO of 200. – Journal of Membrane Science 535: 331-341.

[163] Qiu, F., Lv, H., Zhao, X., Zhao, D. (2019): Impact of an extreme winter storm event on the coagulation/flocculation processes in a prototype surface water treatment plant: causes and mitigating measures. – International Journal of Environmental Research and Public Health 16: 2808.

[164] Raghav, N., Saraswat, P., Srivastava, J. N., Ranjan, R. (2022): Metagenomics study of bacterial communities from Yamuna River water of city of Taj. – Agra bioRxiv 2022-03.

[165] Rasmussen, T. B., Skindersoe, M. E., Bjarnsholt, T. et al. (2015): Identity and effects of quorum-sensing inhibitors produced by *Penicillium* species. – Microbiology 151: 1325-1340.

[166] Ritson, J. P., Graham, N. J., Templeton, M. R. et al. (2014): The impact of climate change on the treatability of dissolved organic matter (DOM) in upland water supplies: a UK perspective. – Science of the Total Environment 473: 714-730.

[167] Roeselers, G., Coolen, J., van der Wielen, P. W. J. J. et al. (2015): Microbial biogeography of drinking water: patterns in phylogenetic diversity across space and time. – Environmental Microbiology 17: 2505-2514.

[168] Ruhal, R., Kataria, R. (2021): Biofilm patterns in gram-positive and gram-negative bacteria. – Microbiological Research 251: 126829.

[169] Safeer, S., Pandey, R. P., Rehman, B. et al. (2022); A review of artificial intelligence in water purification and wastewater treatment: recent advancements. – Journal of Water Process and Engineering 49: 102974.

[170] Sammon, N. B., Harrower, K. M., Fabbro, L. D., Reed, R. H. (2010): Incidence and distribution of microfungi in a treated municipal water supply system in sub-tropical Australia. – International Journal of Environmental Research and Public Health 7: 1597-1611.

[171] Sammon, N. B., Harrower, K. M., Fabbro, L. D., Reed, R. H. (2011): Three potential sources of microfungi in a treated municipal water supply system in sub-tropical Australia. – International Journal of Environmental Research and Public Health 8: 713-732.

[172] Schiavano, G. F., Parlani, L., Sisti, M. et al. (2014): Occurrence of fungi in dialysis water and dialysate from eight haemodialysis units in central Italy. – Journal of Hospital Infection 86: 194-200.

[173] Schmitt, F., Banu, R., Yeom, I. T., Do, K. U. (2018): Development of artificial neural networks to predict membrane fouling in an anoxic-aerobic membrane bioreactor treating domestic wastewater. – Biochemical Engineering Journal 133: 47-58.

[174] Shàarani, S., Azizan, S. N. F., Md Akhir, F. N. et al. (2019): Removal efficiency of Gram-positive and Gram-negative bacteria using a natural coagulant during coagulation,

flocculation, and sedimentation processes. – Water Science and Technology 80: 1787-1795.
[175] Shen, M., Zhu, Y., Zhang, Y. et al. (2019): Micro (nano) plastics: unignorable vectors for organisms. – Marine Pollution Bulletin 139: 328-331.
[176] Shetty, G. R., Chellam, S. (2003): Predicting membrane fouling during municipal drinking water nanofiltration using artificial neural networks. – Journal of Membrane Science 217: 69-86.
[177] Shi, F. N., Yang, H., Liu, X. W. et al. (2022): Spatial-temporal distribution of phytoplankton in Waihai of Dianchi Lake and its nonlinear correlation analysis with environmental indicators. – Acta Hydrobiologica Sinica 46: 1070-1079.
[178] Shi, Y., Wang, Z., Du, X. et al. (2021): Recent advances in the prediction of fouling in membrane bioreactors. – Membranes 11(6): 381.
[179] Shi, Z., Chow, C. W., Fabris, R. et al. (2022): Determination of coagulant dosages for process control using online UV-VIS spectra of raw water. – Journal of Water Process and Engineering 45: 102526.
[180] Shim, J., Park, S., Cho, K. H. (2021): Deep learning model for simulating influence of natural organic matter in nanofiltration. – Water Research 197: 117070.
[181] Siedlecka, A., Wolf-Baca, M. J., Piekarska, K. (2021): Antibiotic and disinfectant resistance in tap water strains—insight into the resistance of environmental bacteria. – Polish Journal of Microbiology 70(1): 57-67.
[182] Sillanpaa, M., Ncibi, M. C., Matilainen, A., Vepsalainen, M. (2018): Removal of natural organic matter in drinking water treatment by coagulation: a comprehensive review. – Chemosphere 190: 54-71.
[183] Simoes, L. C., Simoes, M., Lima, N. (2015): Kinetics of biofilm formation by drinking water isolated *Penicillium expansum*. – Biofouling 31: 349-362.
[184] Singh, K. P., Gupta, S. (2012): Artificial intelligence-based modeling for predicting the disinfection by-products in water. – Chemometric and Intelligent Laboratory Systems 114: 122-131.
[185] Sohrabi, Y., Rahimi, S., Nafez, A. H. et al. (2018): Chemical coagulation efficiency in removal of water turbidity. – International Journal of Pharmaceutical Research 10: 188-194.
[186] Solano, C., Echeverz, M., Lasa, I. (2014): Biofilm dispersion and quorum sensing. – Current Opinion in Microbiology 18: 96-104.
[187] Sonigo, P., De Toni, A., Reilly, K. (2011): Defra A review of fungi in drinking water and the implications for human health. – Review: Literature and Arts of the Americas 33: 100-107.
[188] Srivastava, A., Raval, H. D. (2022): Investigating the role of copper and zinc oxide nanomaterials in abatement of biofouling of ultrafiltration membrane in dynamic conditions. – Journal of Applied Polymer and Science 139: e51879.
[189] Stutter, M. I., Graeber, D., Evans, C. D. et al. (2018): Balancing macronutrient stoichiometry to alleviate eutrophication. – Science of the Total Environment 634: 439-447.
[190] Su, H. C., Liu, Y. S., Pan, C. G., Chen, J., He, L. Y., Ying, G. G. (2018): Persistence of antibiotic resistance genes and bacterial community changes in drinking water treatment system: from drinking water source to tap water. – Science of the Total Environment 616: 453-461.
[191] Tafvizi, H., Husain, T. (2022): Enhanced coagulation for removal of natural organic matter and disinfection byproducts: multivariate optimization. – Environmental Engineering and Science 39: 156-167.
[192] Taipale, S., Jones, R. I., Tiirola, M. (2009): Vertical diversity of bacteria in an oxygen-stratified humic lake, evaluated using DNA and phospholipid analyses. – Aquatic Microbial Ecology 55: 1-16.

[193] Tang, X., Cheng, X., Zhu, X. et al. (2018): Ultra-low pressure membrane-based bio-purification process for decentralized drinking water supply: improved permeability and removal performance. – Chemosphere 211: 784-793.

[194] Thom, C., Smith, C. J., Moore, G. et al. (2022): Microbiomes in drinking water treatment and distribution: a meta-analysis from source to tap. – Water Research 212: 118106.

[195] Tomaszewska, M., Mozia, S. (2002): Removal of organic matter from water by PAC/UF system. – Water Research 36: 4137-4143.

[196] Van Leeuwen, J., Chow, C., Bursill, D., Drikas, M. (1999): Empirical mathematical models and artificial neural networks for the determination of alum doses for treatment of southern Australian surface waters. – Journal of Water Supply: Research Technology-Aqua 48: 115-127.

[197] Varg, J. E., Svanbäck, R. (2023): Multi stress system: microplastics in freshwater and their effects on host microbiota. – Science of the Total Environment 856: 159106.

[198] Wang, H., Masters, S., Hong, Y. et al. (2012): Effect of disinfectant, water age, and pipe material on occurrence and persistence of *Legionella*, *Mycobacteria*, *Pseudomonas aeruginosa*, and two amoebas. – Environmental Science and Technology 46(21)11566-11574.

[199] Wang, H., Masters, S., Edwards, M. A. et al. (2014): Effect of disinfect, water age, and pipe materials on bacterial and eukaryotic community structure in drinking water biofilm. – Environmental Science and Technology 48(3): 1426-1435.

[200] Wang, H., Yu, P., Schwarz, C. et al. (2022): Phthalate esters released from plastics promote biofilm formation and chlorine resistance. – Environmental Science and Technology 56(2): 1081-1090.

[201] Wang, L., Zhang, J., Li, H. et al. (2018): Shift in the microbial community composition of surface water and sediment along an urban river. – Science of the Total Environment 627: 600-612.

[202] Weise, L., Ulrich, A., Moreano, M. et al. (2016): Water level changes affect carbon turnover and microbial community composition in lake sediments. – FEMS Microbiology and Ecology 92(5): fiw035.

[203] World Health Organization (WHO) (2022): Drinking Water. – who.int.

[204] Wyatt, K. H., Rober, A. R. (2018): Warming enhances the stimulatory effect of algal exudates on dissolved organic carbon decomposition. – Freshwater Biology 1-10.

[205] Xiao, X., Fu, J., Yu, X. (2023): Impacts of extreme weather on microbiological risks of drinking water in coastal cities: a review. – Current Pollution Reports 9(2): 259-271.

[206] Xu, D., Xiao, E., Xu, P. et al. (2017): Bacterial community and nitrate removal by simultaneous heterotrophic and autotrophic denitrification in a bioelectrochemical-assisted constructed wetland. – Bioresource and Technology 245.

[207] Yamamura, H., Putri, E. U., Kawakami, T. et al. (2020): Dosage optimization of polyaluminum chloride by the application of convolutional neural network to the floc images captured in jar tests. – Separation and Purification Technology 237: 116467.

[208] Yan, C., Wang, F., Liu, H. et al. (2020): Deciphering the toxic effects of metals in gold mining area: microbial community tolerance mechanism and change of antibiotic resistance genes. – Environmental Research 189: 109869.

[209] Yaseen, Z. M., Ramal, M. M., Diop, L., Jaafar, O., Demir, V., Kisi, O. (2018): Hybrid adaptive neuro-fuzzy models for water quality index estimation. – Water Resource Management 32: 2227-2245.

[210] Yin, J. Y., Boaretti, C., Lorenzetti, A. et al. (2022): Effects of solvent and electrospinning parameters on the morphology and piezoelectric properties of PVDF nanofibrous membrane. – Nanomaterials 12: 962.

[211] Yin, S., Wang, G., Gao, H. (2016): Data-driven process monitoring based on modified orthogonal projections to latent structures. – IEEE Transport Control System and Technology 24(4): 1480-1487.

[212] Yu, Q., Feng, T., Yang, J. et al. (2022): Seasonal distribution of antibiotic resistance genes in the Yellow River water and tap water, and their potential transmission from water to human. – Environmental Pollution 292: 118304.

[213] Yu, S. X., Pang, Y. L., Wang, Y. C. et al. (2017): Spatial variation of microbial communities in sediments along the environmental gradients from Xiaoqing River to Laizhou Bay. – Marine Pollution Bulletin 120: 90-98.

[214] Yu, Y., Li, G., Chen, R., Shi, B. (2021): Trihalomethanes formation enhanced by manganese chlorination and deposition in plastic drinking water pipes. – Water Research 204: 117582.

[215] Zakaria, S. N. S., Ku, C. K. M. F. C., Yahya, N. Y. (2022): The potential of Moringa oleifera seeds for fungal disinfection in water. – Mate Today: Proceedings 57: 1369-1372.

[216] Zakhar, R., Derco, J., Cacho, F. (2018): An overview of main arsenic removal technologies. – Acta Chim Slovaca 11: 107-113.

[217] Zhang, D., Lindholm, G., Ratnaweera, H. (2018): Use long short-term memory to enhance internet of things for combined sewer overflow monitoring. – Journal of Hydrology (Amst) 556: 409-418.

[218] Zhang, K., Chari, G., Li, H. et al. (2013): Machine learning approaches to predict coagulant dosage in water treatment plants. – International Journal System Assurance Engineering and Management 4: 205-214.

[219] Zhang, L., Zhao, F., Li, X., Lu, W. (2020): Contribution of influent rivers affected by different types of pollution to the changes of benthic microbial community structure in a large lake. – Ecotoxicology and Environmental Safety 198: 110657.

[220] Zhang, S., Zheng, H., Tang, X. et al. (2020): Sterilization by flocculants in drinking water treatment. – Chemical Engineering Journal 382: 122961.

[221] Zhao, H., Wang, Y., Duan, J. et al. (2020): Multivariate time-series anomaly detection via graph attention network. – 2020 IEEE International Conference on Data Mining (ICDM), Sorrento, Italy, 17-20 November 2020, pp. 841-850.

[222] Zhao, H. X., Zhang, T. Y., Wang, H. et al. (2022): Occurrence of fungal spores in drinking water: a review of pathogenicity, odor, chlorine resistance and control strategies. – Science of the Total Environment 853: 158626.

[223] Zhao, J., Zhao, X., Chao, L. et al. (2014): Diversity change of microbial communities responding to zinc and arsenic pollution in a river of northeastern China. – Journal of Zhejiang University of Science B 15(7): 670-680.

[224] Zhou, X., Xu, J., Zeng, P., Meng, X. (2019): Air pollutant concentration prediction based on GRU method. – Journal of Physics: Conference Series. IOP Publishing 032058.

[225] Zhu, W. B., Gao, L., Zhang, Y. K. et al. (2022): Insight into the liquid adsorption of tobacco specific nitrosamines on ZIF-8. – Microporous Mesoporous Material 333: 111730.

[226] Zhu, Z., Shan, L., Hu, F. et al. (2020): Biofilm formation potential and chlorine resistance of typical bacteria isolated from drinking water distribution systems. – RSC advances 10(52): 31295-31304.

[227] Zhuang, Y., Qin, X., Li, Y. et al. (2021): Structural property and risk assessment of loose deposits in drinking water distribution systems. – Journal of Water Supply: Research and Technology - Aqua 70(6): 811-821.

[228] Zou, H. Y., He, L. Y., Gao, F. Z. et al. (2021): Antibiotic resistance genes in surface water and groundwater from mining affected environments. – Science of the Total Environment 772: 145516.