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Review Article

Precision Metagenomics in Elder Care: Renovating Infection Diagnostics and Antimicrobial Stewardship

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Abstract: Antimicrobial resistance (AMR) remains a critical challenge in elder care, where frequent infections, polypharmacy, and immunosenescence contribute to poor outcomes. Traditional diagnostic methods, including culture-based and polymerase chain reaction assays, often fail to provide timely, comprehensive microbial identification, leading to prolonged empirical antibiotic use and worsening resistance trends. Precision metagenomics, a clinically refined application of next-generation sequencing, represents a transformative advancement in infection diagnostics and antimicrobial stewardship. By enabling culture-independent, high-resolution pathogen detection directly from clinical samples, precision metagenomics provides real-time identification of bacterial, viral, fungal, and parasitic pathogens, along with their antimicrobial resistance profiles. This approach facilitates early intervention, improves therapeutic precision, and minimizes unnecessary antibiotic exposure, particularly in long-term care facilities where multidrug-resistant organism outbreaks are prevalent. Additionally, the integration of non-invasive sample collection methods, such as diaper-derived urine and hydrogel-based wound dressings, enhances diagnostic accessibility for frail and cognitively impaired patients. As sequencing costs decline and bioinformatics pipelines become more efficient, the routine implementation of precision metagenomics in elder care settings will transition infection management from a reactive to a proactive paradigm. The synergy between precision metagenomics, artificial intelligence-driven clinical decision support systems, and real-time biosensors presents a novel framework for infection surveillance, offering a sustainable solution to combat AMR while optimizing patient outcomes. This paper explores the clinical applications, challenges, and future directions of precision metagenomics in elder care, emphasizing its role in redefining infection control and antibiotic stewardship.

Keywords: Precision Metagenomics, Antimicrobial Resistance, Infection Diagnostics, Elder Care, Next-Generation Sequencing, Antimicrobial Stewardship.

INTRODUCTION

Antibiotic resistance has emerged as a critical challenge in elder care, particularly within long-term care facilities and nursing homes, where older adults are highly susceptible to infectious diseases. This vulnerability is driven by multiple factors, including immunosenescence, the prevalence of chronic comorbidities, polypharmacy, and frequent hospitalizations [1, 2]. The consequences of antimicrobial resistance (AMR) in these settings are severe, as infections in older adults tend to be more frequent, prolonged, and resistant to standard treatments, increasing morbidity, mortality, and healthcare costs [3].

A recent longitudinal analysis of antibiotic use in U.S. nursing homes revealed a disturbing trend: despite antimicrobial stewardship efforts, antibiotic prescribing has remained persistently high, often without definitive microbiological evidence of bacterial infection [1]. Estimates suggest that 40–75% of antibiotic use in long-term care facilities is inappropriate, frequently initiated based on nonspecific symptoms rather than confirmed bacterial etiology [2, 3]. This practice fosters the proliferation of multidrug-resistant organisms and contributes to a rising incidence of Clostridioides difficile infections, further complicating patient management and increasing hospital readmissions [2].

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Challenges of Diagnosing Infections in the Elderly

Diagnosing infections in older adults presents unique challenges, particularly among those with cognitive impairments such as Alzheimer's disease or advanced dementia. Unlike younger adults, elderly individuals may not exhibit classical infection symptoms such as fever, leukocytosis, or localized pain. Instead, infections in this population often manifest as non-specific signs, including confusion, agitation, decreased mobility, or overall functional decline, making it difficult for clinicians to differentiate between infectious and non-infectious causes of deterioration [1]. Consequently, empirical antibiotic use is frequently initiated in the absence of definitive infection, reinforcing the cycle of resistance.

Traditional diagnostic modalities, including blood cultures, urine cultures, and syndromic polymerase chain reaction (PCR) panels, are inadequate in many elder care settings [4]. Cultures, the current gold standard, are time-consuming, often requiring 48–72 hours for pathogen identification, and may yield false negatives in patients who have received prior antibiotic therapy [5, 6]. PCR-based tests, while faster, can only detect pre-specified pathogens, missing rare or emerging organisms and failing to provide a comprehensive microbial landscape [7]. This diagnostic uncertainty often leads to the unnecessary use of broad-spectrum antibiotics, which accelerate AMR and negatively impact patient outcomes.

The Case for Advanced Diagnostics: Next-Generation Sequencing

Given these diagnostic complexities, integrating advanced molecular technologies such as next-generation sequencing (NGS) into elder care settings is promising [8]. Metagenomic next-generation sequencing (mNGS) has demonstrated significant potential as a culture-independent, unbiased pathogen detection tool that can simultaneously identify bacteria, viruses, fungi, and parasites in clinical samples with unprecedented speed and accuracy [8-13]. Unlike conventional methods, mNGS enables the detection of polymicrobial infections, characterization of antimicrobial resistance genes, and identification of novel or difficult-to-culture pathogens, all within a single assay [14]. However, traditional mNGS approaches generate vast amounts of sequencing data, which can be challenging to interpret in real-time clinical settings. The high background noise from host DNA, the complexity of bioinformatics pipelines, and the time required for data analysis can limit the clinical utility of mNGS in acute care scenarios [15]. To address these challenges, precision metagenomics has emerged as a refined, clinically actionable version of mNGS, selectively enriching for clinically relevant microbial DNA/RNA while filtering out non-informative background sequences [16].

Precision Metagenomics: A Transformative Approach for Antimicrobial Stewardship

Precision metagenomics has potential to offer noteworthy advantages in the diagnosis and management of infections in elder care, particularly by enhancing diagnostic yield, enabling the rapid identification of multidrug-resistant organisms, and integrating seamlessly into antimicrobial stewardship programs. One of the most compelling benefits of precision metagenomics is its ability to detect **r**are, novel, or polymicrobial infections that may be missed by conventional culture-based or PCR diagnostic methods [7-12]. Traditional culture techniques often fail to identify fastidious or slow-growing organisms, while PCR is limited to detecting only pre-specified pathogens. In contrast, precision metagenomics provides unbiased, high-throughput sequencing, allowing for the comprehensive identification of all microbial DNA/RNA present in a clinical sample. Research has shown that precision metagenomics can detect a greater diversity of pathogens in suspected urinary tract infections (UTIs) than traditional culture methods [7]. This diagnostic superiority is particularly vital in elder care settings, where asymptomatic bacteriuria is prevalent, and distinguishing between colonization and true infection is critical to prevent unnecessary antibiotic exposure.

Beyond pathogen identification, precision metagenomics also facilitates the real-time detection of AMR genes**,** allowing for rapid identification of multidrug-resistant organisms [17]. Unlike conventional susceptibility testing, which can take days, precision metagenomics can immediately profile resistance determinants, such as extended-spectrum beta-lactamases, carbapenemases, and methicillin resistance [18]. This ability to rapidly detect resistance mechanisms enables clinicians to tailor antibiotic therapy at the point of care, ensuring that patients receive the most effective treatment while avoiding the use of ineffective or unnecessarily broad-spectrum antibiotics. Such precision is particularly crucial in long-term care facilities, where multidrug-resistant organism outbreaks can have devastating consequences, increasing hospitalization rates, morbidity, and mortality. By enabling earlier escalation or de-escalation of therapy, precision metagenomics help curb the spread of resistant pathogens, reducing the overall burden of antibiotic resistance in these high-risk environments [19, 20].

Moreover, the integration of precision metagenomics into antimicrobial stewardship programs represents a critical advancement in infection control and antibiotic optimization. Antimicrobial stewardship programs aim to reduce inappropriate antibiotic use, optimize treatment duration, and improve clinical outcomes, all of which align with the core capabilities of precision metagenomics [3]. By providing early, targeted identification of both pathogens and their resistance profiles, precision metagenomics minimizes the need for empirical broad-spectrum antibiotics, thereby reducing selective pressure for resistance and decreasing adverse drug events. In practice, facilities that have incorporated metagenomics-guided antimicrobial stewardship have reported a 30% reduction in inappropriate antibiotic use and a significant decrease in hospital-acquired infections [21]. This precision-based approach ensures that antimicrobial therapies are rational, effective, and tailored to individual patients, ultimately improving patient outcomes while mitigating the escalating threat of AMR in elder care settings.

Novel Matrices for Precision Metagenomics

One of the most significant barriers to implementing precision metagenomics in elder care is the challenge of obtaining high-quality clinical samples from frail, immobile, or cognitively impaired patients. Traditional sample collection methods, such as midstream urine collection, blood draws, and bronchoalveolar lavage, can be invasive, uncomfortable, and impractical for elderly patients, particularly those in long-term care facilities or with advanced dementia. Expanding precision metagenomics applications to novel, non-invasive sample matrices, such as sodium polyacrylate-based diapers for urine collection, represents a groundbreaking innovation in infection diagnostics and antimicrobial stewardship.

Diaper-Based Urine Collection for Non-Invasive precision metagenomics testing

The development of non-invasive sample collection methods is a crucial advancement in the application of precision metagenomics for elder care. A recent study validated the use of sodium polyacrylate-based diapers as an effective matrix for PCR-based detection of uropathogens, demonstrating that urine samples extracted from these diapers could be successfully analyzed for microbial content with minimal loss of diagnostic sensitivity [22]. The study optimized urine extraction methods from diaper matrices and confirmed that diaper-derived urine samples retained high concordance with traditional urine samples, with only a modest reduction in PCR sensitivity ($\Delta Ct = -1.65$). Importantly, molecular diagnostic tools, including quantitative PCR (qPCR) and NGS, could be applied to diaper-extracted samples to detect a wide range of uropathogens, fungal species, and AMR genes. Additionally, the diaper matrix itself did not interfere with pathogen detection, ensuring that urine samples collected through this method could be used for high-fidelity microbial characterization [22]**.** This innovation is particularly relevant to elder care settings, where many residents suffer from incontinence or cognitive impairments that make traditional midstream urine collection challenging or impossible**.** The ability to reliably analyze urine samples extracted from absorbent materials represents a paradigm shift in diagnostic accessibility, ensuring that patients who previously lacked feasible testing options can now be included in routine infection surveillance and antimicrobial stewardship efforts.

Expanding precision metagenomics applications to diaper-derived urine samples could reform infection diagnostics in elder care by providing reliable, real-time infection surveillance for conditions that are often misdiagnosed or overtreated. For example, UTIs in elderly patients frequently lead to unnecessary antibiotic prescriptions, particularly when asymptomatic bacteriuria is mistaken for an active infection. Precision metagenomics sequencing of diaper-collected urine samples could enable differentiation between colonization and true infection, ensuring that antibiotic therapy is reserved for clinically relevant infections rather than reflexively prescribed based on bacterial presence alone. Furthermore, diaper-based sampling could be used for longitudinal surveillance of AMR genes in long-term care facilities, enabling the early detection of emerging resistance patterns and providing stewardship teams with actionable data to guide targeted interventions.

By integrating precision metagenomics-based sequencing into routine diaper-collected urine samples**,** elder care facilities could implement real-time infection surveillance, significantly reducing delays in treatment, minimizing hospital readmissions, and optimizing antimicrobial stewardship programs. This approach could serve as a model for expanding non-invasive metagenomics-based diagnostics beyond UTIs, potentially transforming infection monitoring and antimicrobial resistance surveillance in vulnerable populations. As the field of precision diagnostics evolves, leveraging novel sampling matrices such as sodium polyacrylate-based diapers will be instrumental in improving accessibility, accuracy, and timeliness of infection detection in elder care settings.

Expanding precision metagenomics to Other Absorbent Matrices for Respiratory and Wound Infection Diagnostics

While sodium polyacrylate-based diapers have demonstrated feasibility for non-invasive urine collection and UTI diagnostics [22], the potential for expanding precision metagenomics applications to other absorbent matrices could significantly enhance infection surveillance in elder care settings. Many elderly patients, particularly those who are immobile, frail, or cognitively impaired, experience recurrent respiratory infections and chronic wounds, yet traditional diagnostic methods for these conditions are often invasive, delayed, or inaccurate. By adapting precision metagenomics-based sequencing to alternative absorbent materials, clinicians could gain rapid, high-resolution insights into microbial colonization and resistance patterns in these vulnerable populations, allowing for earlier interventions and more targeted antimicrobial stewardship efforts. Several absorbent matrices could be optimized for precision metagenomics-based detection of respiratory and wound infections, including (1) absorbent nasal swabs for non-invasive metagenomic analysis of pneumonia-causing pathogens [12], (2) hydrogel-based wound dressings to monitor chronic wound infections and biofilm-associated pathogens [23], and (3) saliva-absorbing pads (e.g., Oracol, OraSure, etc.) for rapid detection of viral and bacterial respiratory infections[24].

Preliminary research on respiratory tract infections has demonstrated that saliva and nasal swabs can be successfully used for metagenomic sequencing, providing a less invasive alternative to bronchoalveolar lavage, which is often required for deep lung infection diagnosis [25]. The ability to detect pathogens and AMR genes in nasal and saliva samples could be transformative for elderly patients with pneumonia, chronic obstructive pulmonary disease, or aspiration-related infections, where early and precise identification of bacterial, viral, or fungal contributors could significantly improve clinical outcomes and reduce unnecessary antibiotic use [12]. Similarly, the application of precision metagenomics to hydrogel-based wound dressings presents a major opportunity for improving chronic wound management in long-term care facilities. Elderly patients with pressure ulcers, diabetic foot infections, or post-surgical wounds are at high risk for multidrug-resistant organism colonization, yet current wound culture methods often fail to capture the full complexity of microbial biofilms. By integrating precision metagenomics sequencing into hydrogel dressings, clinicians could detect multidrug-resistant organisms at an earlier stage, monitor shifts in microbial populations over time, and tailor antibiotic or debridement strategies accordingly. This approach could enhance precision wound care, prevent systemic infections, and reduce hospitalizations due to complicated soft-tissue infections.

By validating additional non-invasive matrices for precision metagenomics-based diagnostics, infection surveillance in elder care could be expanded beyond UTIs to encompass respiratory and wound infections, two of the most significant drivers of antibiotic overuse and resistance in aging populations [26, 27]. A holistic approach that integrates precision metagenomics sequencing across multiple sample types would transform infection prevention strategies, ensuring that elderly patients receive the most appropriate, targeted treatments while minimizing the risks associated with empirical antibiotic therapy. The ability to leverage absorbent matrices for precision diagnostics represents a scientifically rigorous and clinically actionable advancement that could redefine infection control and antimicrobial stewardship in elder care settings.

Integration of Wearable Biosensors with Precision Metagenomics for Continuous Infection Monitoring

The next frontier in precision metagenomics applications lies in the integration of non-invasive sampling matrices with real-time wearable biosensors, enabling continuous infection monitoring in elder care settings. This is similar to the current use of metabolomics-driven approaches for identifying therapeutic targets in drug discovery [28]. Traditional diagnostics rely on episodic testing, meaning that infections are often detected late, when symptoms become severe or when empirical antibiotic treatment has already begun, limiting the ability to tailor therapy based on precise microbial and resistance profiling. By embedding precision metagenomics-driven biosensors into wearable medical devices, real-time infection surveillance could become a proactive, rather than reactive, strategy, allowing for earlier interventions, improved infection control, and optimized antimicrobial stewardship efforts. Potential innovations in wearable precision metagenomics biosensors include: (1) smart diapers with embedded biosensors capable of detecting bacterial metabolites or AMR gene signatures in real time, enabling the early differentiation of UTIs from asymptomatic bacteriuria [29], (2) bio-integrated wound sensors that track microbial biofilm formation and antibiotic resistance markers in chronic wounds, allowing clinicians to detect infections before they progress to severe soft-tissue or systemic infections [30], and (3) smart respiratory patches that collect exhaled breath condensates for continuous monitoring of respiratory pathogens, providing real-time insights into pneumonia progression or viral-bacterial co-infections in high-risk elderly patients [31].

By linking these wearable biosensors to cloud-based precision metagenomics analytics, clinicians and antimicrobial stewardship teams could receive instant infection alerts, facilitating real-time decision-making based on dynamic microbial profiles. This would drastically reduce the time-to-diagnosis, eliminating the delays associated with culture-dependent methods and allowing for preemptive interventions before severe infections escalate. Additionally, this technology could be integrated into electronic health record systems, ensuring that historical infection patterns and antimicrobial resistance trends are continuously monitored and factored into patient management strategies.

For elderly patients in long-term care facilities, hospitals, and home-based elder care, precision metagenomics-integrated wearable biosensors could revolutionize infection surveillance and response, providing clinicians with unprecedented precision in tracking disease progression. By shifting from passive, symptom-driven diagnostics to an active, real-time infection monitoring system, elder care facilities could significantly reduce hospitalization rates, prevent outbreaks, and advance personalized antimicrobial stewardship approaches. As biosensor technology continues to evolve, its synergy with precision metagenomics-driven diagnostics has the potential to reshape elder care infection management, offering a novel, proactive approach to combating AMR and optimizing patient outcomes. By advancing precision metagenomics into non-invasive diagnostics, elder care facilities could transition from reactive infection management to a proactive, precision-driven approach, ultimately reducing hospitalizations, preventing outbreaks, and improving patient outcomes in aging populations.

Integrating Precision Metagenomics with AI-Driven Clinical Decision Support Systems

A major limitation of traditional infectious disease diagnostics is the delay in obtaining actionable results, which often forces clinicians to initiate empirical broad-spectrum antibiotics before definitive pathogen identification. This reactive approach contributes to AMR, increased healthcare costs, and patient morbidity, particularly in elder care settings where infections frequently present atypically. While precision metagenomics significantly reduces diagnostic turnaround time, its full clinical potential can only be realized when seamlessly integrated into real-time decision-making workflows. By embedding precision metagenomics within clinical decision support systems powered by artificial intelligence (AI) and machine learning, infection management in elder care could transition from delayed, empirical treatments to precision-guided, real-time interventions.

A precision metagenomics-driven clinical decision support system could function as an automated, scalable system that provides real-time analysis of sequencing data, offering critical insights into pathogen identification, antimicrobial resistance markers, and infection trends. The system could: (1) compare metagenomic sequencing results against global AMR surveillance databases, allowing for the early detection of emerging resistance patterns, (2) automatically flag multi-drug-resistant organisms and recommend narrow-spectrum antibiotic alternatives, ensuring that treatment choices are optimized based on the patient's infection profile rather than relying on broad-spectrum empiricism, (3) integrate with electronic health records to track longitudinal infection patterns in elderly patients, enabling proactive infection control strategies and personalized antimicrobial stewardship efforts, and (4) facilitate automated alerts for antimicrobial stewardship program teams, notifying them immediately when resistant pathogens are detected or when inappropriate antibiotic prescriptions are initiated. And there is scientific justification. AI-enhanced antimicrobial stewardship is an emerging field, with studies demonstrating 30-50% reductions in inappropriate antibiotic use when real-time AI-based diagnostics are combined with stewardship teams [32, 33]. By positioning precision metagenomics within a clinical decision support system framework, it becomes a scalable, automated solution for combating AMR in elder care settings. This system would not only improve patient outcomes but also optimize healthcare resource utilization, ensuring that elderly patients receive targeted, evidence-based treatments while reducing unnecessary antibiotic exposure.

As AI and machine learning models continue to evolve, a precision metagenomics-integrated clinical decision support system could revolutionize infectious disease management, transitioning elder care facilities from a reactive model of infection control to a predictive, precision-driven approach. This transformation could have far-reaching implications, reducing hospitalizations, minimizing AMR-related complications, and ensuring that antimicrobial stewardship remains a dynamic and data-driven discipline in aging populations.

Using precision Metagenomics for Early Detection of Infection-Associated Cognitive Decline and Sepsis Risk in Elderly Patients

A unique and high-impact extension of precision metagenomics research involves investigating how metagenomic sequencing can be leveraged for the early detection of infections that exacerbate cognitive decline and increase sepsis risk in elderly patients with neurodegenerative diseases. Research increasingly suggests that chronic low-grade infections and persistent inflammation contribute to accelerated cognitive decline in patients with Alzheimer's disease and other dementias [34]. Additionally, elderly individuals who experience sepsis are at significantly higher risk of long-term cognitive impairment, highlighting the urgent need for early pathogen detection and intervention before infections progress to systemic inflammation or neurodegeneration. Precision metagenomics could play a pivotal role in key areas related to infection-driven cognitive and systemic deterioration in aging populations. For example, by identifying chronic low-level infections (e.g., gut dysbiosis, urinary tract colonization, or periodontal pathogens) that are associated with neuroinflammation and cognitive decline. Emerging evidence suggests that oral and gastrointestinal microbial dysbiosis may exacerbate neurodegenerative processes, making longitudinal monitoring of microbial signatures an essential tool in dementia research [35]. Also, detecting bloodstream infections (bacteremia) at an early stage, allowing for preemptive interventions before sepsis develops. Sepsis-related neuroinflammation has been implicated in acute and long-term cognitive impairment, making rapid, metagenomics-based pathogen detection a potential game-changer in preventing severe neurological sequelae in elderly patients [36]. Furthermore, precision metagenomics provides a distinct advantage by detecting pathogenic bacterial DNA fragments in blood or cerebrospinal fluid (CSF) well ahead of conventional diagnostics. This early detection enables timely intervention in infection-driven neuroinflammation, which is particularly crucial given its association with cognitive decline [37]. By integrating metagenomics-based infection profiling into geriatric medicine, clinicians could shift from reactive treatment of cognitive and systemic decline to a proactive, precision-driven approach, ultimately reducing hospitalizations, preventing rapid cognitive deterioration, and improving long-term quality of life in aging populations (Table 1).

Table 1: ***Comparison of Traditional Diagnostics vs. Precision Metagenomics in Elder Care Infection Management***

Feature	Traditional Diagnostics	Precision Metagenomics
Pathogen Identification	Culture-based, requires 48-72 hours; PCR-based, limited to pre-specified pathogens	Detects all microbial DNA/RNA, including rare and emerging pathogens in a single assay
Turnaround Time	Delayed (days to weeks)	Rapid (hours to a day)
Sensitivity & Specificity	Prone to false negatives, particularly in pre-treated patients	High sensitivity, detects low-abundance pathogens
Detection of Polymicrobial Infections	Limited, often misses co-infections	Comprehensive, captures entire microbial landscape
Antimicrobial Resistance Profiling	Culture-dependent susceptibility testing takes days	Real-time AMR gene detection, allows for immediate antibiotic adjustments
Impact on Antimicrobial Stewardship	Empirical broad-spectrum antibiotic use due to diagnostic uncertainty	Targeted therapy based on real-time resistance profiling, reducing unnecessary antibiotic exposure
Sample Collection Challenges	Invasive (blood draws, BAL, catheterized urine)	Non-invasive (diaper-derived urine, saliva, wound swabs, breath condensates)
Implementation in Elder Care	Limited utility due to diagnostic delays and sample collection challenges	Ideal for frail or cognitively impaired patients, enabling proactive infection surveillance

Challenges and Future Directions

Despite the transformative potential of precision metagenomics in elder care settings, several challenges must be addressed before its widespread clinical implementation. One of the most significant barriers is cost and accessibility. Although the costs of sequencing have steadily declined over the past decade, precision metagenomics remains more expensive than traditional diagnostic methods, such as culture-based techniques and syndromic PCR panels. The financial burden includes not only the direct costs of sequencing but also the infrastructure needed for high-throughput data processing and storage [38]. However, it is essential to recognize that precision metagenomics long-term benefits, including reduced hospitalizations, decreased reliance on empiric antibiotic use, and improved AMR management, may ultimately offset these costs by lowering the economic burden associated with multidrug-resistant infections**.**

Another major challenge is the complexity of data interpretation and the need for standardization. Unlike conventional diagnostics, which provide binary positive or negative results, precision metagenomics generates large volumes of sequencing data that require sophisticated bioinformatics pipelines to accurately identify pathogens, differentiate between colonization and true infection, and detect antimicrobial resistance genes [39]. The variability in sequencing methodologies, analytical tools, and reference databases can lead to inconsistent results across different institutions, limiting precision metagenomics clinical utility. Ongoing research is focused on leveraging AI and machine learning algorithms to automate data analysis, improve the accuracy of microbial identification, and provide clinically relevant, real-time decision support for physicians.

Furthermore, regulatory approval and clinical validation remain critical hurdles for precision metagenomics' integration into routine infectious disease diagnostics. While early studies have demonstrated promising diagnostic accuracy, more extensive clinical trials are required to establish precision metagenomics efficacy across diverse infection types, patient populations, and healthcare settings. The development of standardized protocols, quality control measures, and regulatory frameworks is essential to ensure reproducibility, reliability, and compliance with existing clinical guidelines [40, 41]. Without clear regulatory pathways, the adoption of precision metagenomics in elder care facilities and hospitals may be hindered, limiting its potential impact on antibiotic stewardship and patient care. Looking ahead, technological advancements will likely play a pivotal role in expanding the accessibility and clinical feasibility of precision metagenomics. Innovations such as real-time portable sequencing platforms could allow for point-of-care diagnostics, eliminating the need for centralized laboratories and long turnaround times. Additionally, the integration of precision metagenomics with electronic health records could facilitate automated clinical decision support, enabling physicians to receive real-time pathogen identification and resistance profiles directly within their workflow. These developments have the potential to revolutionize infection management in elder care, ensuring that diagnoses are accurate, treatments are targeted, and antibiotic use is optimized to combat the growing threat of antimicrobial resistance**.**

CONCLUSION

Precision metagenomics has potential to reform infection diagnostics and antimicrobial stewardship in elder care settings. By enabling rapid, high-resolution pathogen detection and real-time antimicrobial resistance profiling, this approach minimizes reliance on broad-spectrum antibiotics, curbing antimicrobial resistance and improving patient outcomes. Its integration into non-invasive sampling methods and AI-driven clinical decision support systems enhance diagnostic accessibility, particularly for frail and cognitively impaired patients. As sequencing technologies become more cost-effective and bioinformatics pipelines more streamlined, the routine implementation of precision metagenomics will transition elder care facilities from reactive infection management to a proactive, precision-driven paradigm. Future advancements in wearable biosensors and electronic health record integration will further solidify its role in real-time infection surveillance, ensuring targeted, data-driven interventions that enhance both individual patient care and public health outcomes.

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