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Artificial Intelligence Applications in Microbiome Research for Prostate Cancer: A Narrative Review

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Abstract

Introduction: *Prostate cancer is one of the most common malignancies in men worldwide and exhibits substantial biological heterogeneity, creating challenges in diagnosis, prognosis, and treatment selection. Artificial intelligence has emerged as a promising approach for analyzing complex microbiome datasets characterized by high dimensionality and biological variability.* ***Objective:*** *This narrative review aims to summarize current evidence regarding the application of artificial intelligence in microbiome research related to prostate cancer, with emphasis on biological insights, analytical approaches, current challenges, and future research directions.* ***Method:*** *A narrative review was conducted through a literature search of scientific databases using keywords related to prostate cancer, microbiome, microbiota, machine learning, artificial intelligence, and deep learning. Relevant original studies, review articles, and methodological papers were identified through database searching, citation tracking, and manual reference screening. The selected literature was synthesized narratively according to major thematic areas.* ***Result and Discussion:*** *Current evidence suggests that alterations in microbiome composition may be associated with prostate cancer through mechanisms involving immune modulation, microbial metabolites, inflammation, hormonal regulation, and host-environment interactions. Artificial intelligence, particularly machine learning, has been increasingly applied to microbiome analysis for feature selection, pattern recognition, biomarker discovery, and predictive modeling. Algorithms such as Random Forest, Least Absolute Shrinkage and Selection Operator, Extreme Gradient Boosting, and deep learning have* showed *potential for extracting biologically relevant information from complex datasets and supporting precision oncology approaches.* ***Conclusions:*** *The integration of artificial intelligence and microbiome research in prostate cancer represents a promising but still emerging field*

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Introduction

Prostate cancer is one of the most common malignancies affecting men worldwide and remains a major contributor to cancer-related morbidity and mortality. The disease is characterized by substantial biological and clinical heterogeneity, ranging from indolent tumors to aggressive metastatic forms, which complicates diagnosis, prognostic stratification, and treatment (Chang *et al.*, 2025; Goda & Abdel-Aziz, 2025; Hao *et al.*, 2026; McGale *et al.*, 2024). Despite advances in imaging, prostate-specific antigen (PSA)-based screening, and tissue biomarkers, current diagnostic and prognostic tools remain insufficient to accurately distinguish clinically significant from indolent disease, showing the need for improved biological understanding and more robust predictive approaches (Bazarkin *et al.*, 2026; Markowski *et al.*, 2025; Li *et al.*, 2026).

Recent evidence has increasingly showed the potential role of the microbiome in prostate cancer biology. Studies suggest that alterations in gut, urinary, and prostatic tissue microbiota may be associated with prostate cancer susceptibility, disease progression, and tumor aggressiveness, although most findings remain associative rather than causal (Cocomazzi *et al.*, 2025; Kim *et al.*, 2025; Pei *et al.*, 2025). The proposed “gut-prostate axis” provides a conceptual for understanding how intestinal microbiota may influence prostate carcinogenesis through systemic immune modulation, microbial metabolites, and endocrine signaling pathways (Fujita *et al.*, 2023; Romano *et al.*, 2024). In particular, microbial-derived metabolites such as short-chain fatty acids, as well as dysbiosis-associated chronic inflammation, have been implicated in pathways related to tumor growth, immune evasion, and androgen signaling regulation (Matsushita *et al.*, 2021; Y. Liu *et al.*, 2023). The microbiome may contribute to biological heterogeneity observed in prostate cancer and may hold potential as a source of non-invasive biomarkers for disease stratification, although clinical validation remains limited (Bazarkin *et al.*, 2026; Magashi Ali & Abdulkadir, 2025).

In parallel, growing interest has emerged in characterizing microbiome profiles across different biological sites relevant to prostate cancer, including fecal, urinary, and prostatic tissue samples. Although several studies have reported distinct microbial signatures in patients with prostate cancer compared to healthy controls, findings remain inconsistent due to differences in study design, sequencing methods, and population characteristics (Cocomazzi *et al.*, 2025; Kim *et al.*, 2025). Nevertheless, these observations collectively support the hypothesis that host-microbiome interactions may play in shaping prostate cancer development and progression, potentially through complex interactions involving host genetics, environmental exposures, and metabolic regulation (Lachance *et al.*, 2024; T. Liu *et al.*, 2025).

The analysis of microbiome data presents significant methodological challenges, particularly due to its high dimensionality, compositional nature, sparsity, and interindividual variability. These characteristics complicate traditional statistical modeling and increase the risk of overfitting, especially in studies with relatively small sample sizes (Papoutsoglou *et al.*, 2023; Rahman *et al.*, 2025). Additionally, complex microbial interactions and non-linear relationships between biological variables further limit the applicability of conventional analytical approaches (Freitas *et al.*, 2023). These limitations show the need for more advanced computational methods capable of capturing complex biological patterns.

Artificial intelligence (AI), particularly machine learning, has emerged as a promising approach to address these challenges by enabling high-dimensional data integration, feature selection, and predictive modeling in microbiome research. Machine learning algorithms such as Random Forest, Least Absolute Shrinkage and Selection Operator (LASSO), Extreme Gradient Boosting (XGBoost), and deep learning methods have demonstrated the ability to identify microbial signatures associated with disease phenotypes and clinical outcomes (Li *et al*., 2026; Raber *et al*., 2026). In the context of prostate cancer, AI-based approaches have the potential to integrate microbiome data with genomic, transcriptomic, metabolomic, and clinical variables, thereby improving risk stratification and supporting precision oncology strategies (Freitas *et al*., 2023; Marouf *et al*., 2025; Wei *et al*., 2023; McGale *et al*., 2024).

However, despite this potential, the integration of artificial intelligence with microbiome research in prostate cancer remains in an early stage of development. Existing studies are limited in number, often exploratory in design, and characterized by methodological heterogeneity, small sample sizes, and limited external validation (Liss *et al*., 2026; Novielli *et al*., 2024). There is currently no standardized analytical framework, and findings remain fragmented across different populations and study designs (Papoutsoglou *et al*., 2023; Rahman *et al*., 2025). Compared with other cancer types, translation of AI-driven microbiome research into clinically applicable tools for prostate cancer remains particularly limited (Bautista *et al*., 2025; Freitas *et al*., 2023).

Given the rapid expansion of both microbiome science and artificial intelligence, there is a need to synthesize current evidence specifically within the context of prostate cancer. A focused and structured review is required to clarify current biological insights, evaluate analytical approaches, identify methodological limitations, and show future research directions. Therefore, this narrative review aims to summarize and critically discuss the application of artificial intelligence in microbiome research related to prostate cancer, with emphasis on biological mechanisms, computational methodologies, existing challenges, and potential clinical implications.

Method

This study was conducted as a narrative review to provide a comprehensive overview of the current evidence regarding the application of artificial intelligence (AI) in microbiome research related to prostate cancer. The review aimed to summarize and discuss existing knowledge concerning the biological relationship between the microbiome and prostate cancer, the role of artificial intelligence in microbiome data analysis, current methodological approaches, and future research opportunities in this emerging field. Relevant literature was identified through searches of scientific databases, primarily PubMed, using combinations of keywords related to prostate cancer, the microbiome, and artificial intelligence. The search strategy included terms such as "prostate cancer," "microbiome," "microbiota," "machine learning," "artificial intelligence," and "deep learning." Additional relevant publications were identified through citation tracking and manual searches of references from key articles. Priority was given to peer-reviewed articles published in English that addressed the relationship between prostate cancer and the microbiome, as well as studies discussing the application of artificial intelligence, machine learning, bioinformatics, or computational approaches in microbiome-related cancer research.

The literature considered in this review included original research articles, review articles, and relevant methodological studies that contributed to understanding the biological, computational, and clinical aspects of artificial intelligence-based microbiome analysis in prostate cancer. Studies focusing on microbiome-host interactions, the gut-prostate axis, microbiome-associated biomarkers, machine learning applications, multi-omics integration, and precision oncology were considered particularly relevant to the objectives of this review. The selected literature was critically examined and synthesized narratively. The discussion was organized into several thematic areas, including the biological relationship between the microbiome and prostate cancer, the analytical challenges of microbiome data, the role of artificial intelligence and machine learning in microbiome research, current evidence regarding AI applications in prostate cancer, methodological limitations of existing studies, and future directions for research and clinical translation.

Result and Discussion

Biological Interpretation of the Microbiome-Prostate Cancer Relationship

Accumulating evidence suggests that the gut microbiome may be associated with prostate cancer (PCa) through complex biological mechanisms involving interactions between host genetics, environmental exposures, immune regulation, and metabolic pathways. Although current evidence does not establish direct causality, several studies have reported associations between microbial composition and prostate cancer susceptibility, progression, and clinical heterogeneity. Mendelian randomization analyses have suggested that specific microbial taxa may have genetic associations with prostate cancer risk, supporting the possibility that host genetic factors influence both microbiome composition and disease susceptibility (Li *et al.*, 2026).

One of the most widely discussed biological frameworks is the gut-prostate axis, which proposes that gut microbiota may influence prostate tissue through systemic immune signaling, microbial metabolites, and endocrine pathways (Fujita *et al.*, 2023; Romano *et al.*, 2024). Gut dysbiosis has been associated with chronic low-grade inflammation and alterations in the prostate microenvironment that may support tumor development and progression (Dovey *et al.*, 2026; Pei *et al.*, 2025). Furthermore, microbial metabolites such as short-chain fatty acids have been reported to influence cell proliferation, immune responses, and metabolic regulation, suggesting potential mechanisms linking microbial communities to carcinogenesis (Y. Liu *et al.*, 2023; Matsushita *et al.*, 2021).

The microbiome has increasingly been recognized as a factor that may contribute to the biological heterogeneity of PCa. Several studies have reported associations between specific microbial profiles and aggressive disease phenotypes, treatment response, and tumor behavior (Alum, 2025; Bazarkin *et al.*, 2026). In addition, microbial communities may influence oncogenic pathways through interactions with host metabolism and immune regulation, further supporting the hypothesis that microbiota contribute to the biological environment associated with tumor progression (Hao *et al.*, 2026; Magashi Ali & Abdulkadir, 2025).

Host genetics and environmental exposures appear to interact in shaping microbiome composition in PCa. Factors such as dietary habits, obesity, hormonal status, and genetic variation have been associated with alterations in gut microbial communities and prostate cancer risk (Lachance *et al.*, 2024; T. Liu *et al.*, 2025). Interactions between microbiota and androgen metabolism have attracted particular attention because androgen signaling plays a central role in prostate cancer biology (Romano *et al.*, 2024; Sandeep, 2026). These observations support the concept that the microbiome may function as an intermediary between environmental exposures and prostate tumor biology (Fujita *et al.*, 2023; Lachance *et al.*, 2024).

Dietary factors represent important determinant of microbiome composition. Studies involving prostate cancer survivors have reported associations between dietary patterns and microbial diversity, indicating that environmental factors may substantially influence microbiome profiles in individuals affected by PCa (Raber *et al*., 2026). These findings further show the dynamic nature of microbiome-host interactions and their potential relevance to disease development and progression.

Variations in microbial composition have been observed across fecal, urinary, and prostate tissue samples from patients with PCa, although findings remain inconsistent among studies (Cocomazzi *et al*., 2025; Kim *et al*., 2025). Several reports have described enrichment of specific bacterial taxa accompanied by reductions in potentially beneficial microorganisms, suggesting dysbiotic states associated with chronic inflammation and tumor-promoting environments (Matsushita *et al*., 2023; Pei *et al*., 2025). However, differences in study design, sampling procedures, sequencing methods, and population characteristics limit direct comparisons across studies and prevent definitive conclusions regarding causal mechanisms (Hao *et al*., 2026; Magashi Ali & Abdulkadir, 2025).

The Role and Potential of Artificial Intelligence in Prostate Cancer Microbiome Research

Artificial intelligence (AI), particularly machine learning approaches, has emerged as a promising analytical tool for addressing the complexity of microbiome datasets. Microbiome data are characterized by high dimensionality, compositionality, sparsity, and substantial interindividual variability, creating analytical challenges that often exceed the capabilities of conventional statistical methods (Papoutsoglou *et al*., 2023; Rahman *et al*., 2025). Machine learning techniques have been increasingly applied to identify meaningful patterns within genomic, microbiome, metabolomic, and clinical datasets. These methods facilitate feature selection, biomarker discovery, and predictive modeling by identifying variables that are most strongly associated with disease-related outcomes (Li *et al*., 2026). Beyond prostate cancer, AI approaches have been utilized to analyze complex biological datasets and identify patterns associated with tumor aggressiveness, prognosis, and therapeutic response (Alum, 2025; Bazarkin *et al*., 2026; Hsu *et al*., 2026).

Feature selection represents one of the most important contributions of AI in microbiome research. Algorithms such as Random Forest and LASSO can identify microbial taxa, metabolites, or environmental variables that contribute most strongly to observed biological patterns (Raber *et al*., 2026). These approaches are particularly valuable because they can accommodate nonlinear relationships and complex interactions that are common in microbiome-host systems (Papoutsoglou *et al*., 2023; Rahman *et al*., 2025). More advanced techniques, including XGBoost and deep neural networks, have also been reported in microbiome and oncology research for predictive modeling and multi-omics integration (Freitas *et al*., 2023; Marouf *et al*., 2025; Wei *et al*., 2023). The integration of AI with microbiome analysis has significant implications for precision oncology. By combining microbiome information with genomic and clinical data, AI-based models may facilitate the identification of biologically distinct patient subgroups and support risk stratification strategies (Chang *et al*., 2025; Far, 2023; Goda & Abdel-Aziz, 2025; Markowski *et al*., 2025; McGale *et al*., 2024). Such approaches may ultimately contribute to more personalized diagnostic, prognostic, and therapeutic strategies.

Despite these opportunities, AI applications in PCa microbiome research remain at an early stage of development. Compared with several other cancer types, studies integrating microbiome analysis and machine learning in prostate cancer remain relatively limited, and large multicenter validation studies are still lacking (Freitas *et al*., 2023; Liss *et al*., 2026; Novielli *et al*., 2024; Rahman *et al*., 2025). Consequently, AI currently serves primarily as an exploratory tool for identifying biological patterns and generating hypotheses regarding microbiome-cancer interactions (Bautista *et al*., 2025; Magashi Ali & Abdulkadir, 2025). Figure 1 shows artificial intelligence can facilitate microbiome analysis through feature selection, pattern recognition, biomarker identification, and predictive modeling in prostate cancer research.

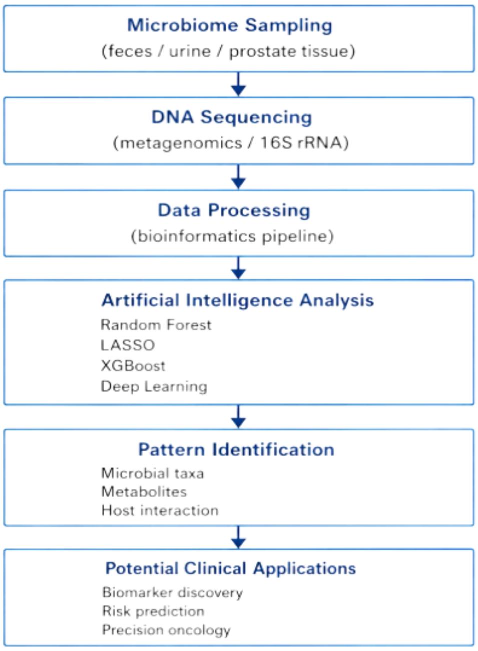

Figure 1. AI in Facilitate Microbiome Analysis

Current Challenges and Future Directions

Although interest in AI-driven microbiome research continues to grow, several important challenges remain. One major limitation is the substantial heterogeneity observed across microbiome studies. Differences in sampling protocols, sequencing technologies, bioinformatic pipelines, population characteristics, and analytical methodologies can lead to inconsistent findings and limit reproducibility (Papoutsoglou *et al*., 2023; Rahman *et al*., 2025). Another challenge involves the relatively small sample sizes commonly encountered in microbiome studies, which may increase the risk of overfitting and reduce model generalizability. External validation remains uncommon in many AI-based microbiome studies, limiting confidence in the broader applicability of reported findings (Li *et al*., 2026; Raber *et al*., 2026). Table 1, shows current study AI applications in prostate cancer-microbiome research.

Table 1
AI Applications in Prostate Cancer-Microbiome

No	Authors & Year	Microbiome	AI Method	Sample	Finding and Clinical Validity
1	Li *et al.,* 2026	Gut	ML, Mendelian randomization, bioinformatics (GEO, GWAS integration; multi-model feature selection, nomogram)	Large-scale GWAS, transcriptomic datasets (GEO validation cohort)	Identified 16 gut microbial taxa causally associated with PCa (7 risk, 9 protective). Integrated analysis revealed 144 associated genes, with key feature genes (PLCL1, VSNL1, ROR2, NRXN3, TEAD1) contributing to a predictive nomogram. Mechanistically, genes were linked to epithelial-mesenchymal transition, proliferation, migration, and invasion pathways. No external clinical implementation
2	Raber *et al.,* 2026	Gut	Random Forest, LASSO, multivariate statistical modeling (PERMANOVA, MaAsLin2)	n = 79 prostate cancer survivors (diet and exercise intervention cohort)	Diet quality scores (MEDAS, HEI-2015, MIND) significantly associated with gut microbiome diversity and beta diversity patterns. Identified 129 taxa associated with diet and host factors. Interaction effects observed between diet, exercise intervention, APOE genotype, and testosterone levels, suggesting multi-factorial modulation of microbiome composition in PCa survivors. No external validation / exploratory cohort only

The integration of multiple biological data layers represents important area for future investigation. Although microbiome research has increasingly moved toward multi-omics approaches, studies combining microbiome data with genomics, transcriptomics, metabolomics, and clinical information remain limited in prostate cancer (Freitas *et al*., 2023; Marouf *et al*., 2025; Wei *et al*., 2023). Such integrative approaches may provide a more comprehensive understanding of tumor biology and facilitate the development of clinically relevant predictive models.

Additional research is also needed to investigate microbiomes beyond the gastrointestinal tract. While most available evidence focuses on the gut microbiome, urinary and prostate tissue microbiomes may offer biologically relevant insights because of their closer anatomical relationship to the prostate (Cocomazzi *et al*., 2025; Kim *et al*., 2025). Exploration of these microbial ecosystems using advanced AI methodologies may provide new perspectives on prostate cancer pathogenesis and biomarker development. The convergence of microbiome science, artificial intelligence, and precision oncology represents a promising but still emerging research area. Continued interdisciplinary collaboration among microbiologists, clinicians, bioinformaticians, and data scientists will be essential to advance the field and translate emerging discoveries into meaningful clinical applications (Li *et al*., 2026; Raber *et al*., 2026).

Conclusion

Artificial intelligence-based analysis of the microbiome in prostate cancer shows a promising but still early-stage area within precision oncology. Although emerging evidence suggests potential associations between microbiome alterations and prostate cancer through genetic, metabolic, immune, and environmental pathways, these relationships remain largely associative without established causality. Machine learning approaches offer useful tools for handling high-dimensional microbiome data and identifying potential microbial signatures, however, current studies are predominantly exploratory and lack robust external validation. The limitations such as small sample sizes, methodological heterogeneity, and insufficient multicenter or longitudinal data continue to restrict clinical translation. Therefore, further standardized, well-validated, and collaborative studies are required before AI-driven microbiome approaches can be applied in routine prostate cancer management.

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