Unleashing the Power of Artificial Intelligence: Unraveling the Intricate Dynamics between Viral and Bacterial Infections, Immune Factors, COVID-19, and Cancer in Women's Health

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Abstract

The intricate interplay between viral and bacterial infections, immune factors, COVID-19, and cancer in women's health has garnered significant attention in recent research. This comprehensive study aimed to unravel the complex dynamics between these factors and provide valuable insights into their implications for women's health. Through meticulous analysis of available data, this study elucidated the prevalence of viral and bacterial infections in women, encompassing influential pathogens such as influenza, human papillomavirus, Staphylococcus aureus, Escherichia coli, and Streptococcus pneumoniae. Additionally, it explored the relationship between specific cytokine types, including Interleukin-6 (IL-6), Tumor Necrosis Factor-alpha (TNF-α), Interferon-gamma (IFN-γ), and Interleukin-10 (IL-10), and viral infections. The prevalence of various cancer types, such as breast cancer, lung cancer, colorectal cancer, ovarian cancer, and cervical cancer, was also assessed. Furthermore, this study examined the correlations between immune factors and viral infections, uncovering significant associations that shed light on the intricate interplay between immune responses and viral infections. Immune markers such as IL-6, TNF-α, IFN-γ, Interleukin-1beta (IL-1β), and Interleukin-12 (IL-12) exhibited diverse levels of correlation with specific viral infections. These findings hold promise for disease prognosis and treatment optimization. Additionally, the association between bacterial infections and women's health conditions was explored, revealing the impact of pathogens like Staphylococcus aureus, Escherichia coli, Streptococcus pneumoniae, Pseudomonas aeruginosa, and Enterococcus faecalis on gynecological infections, reproductive disorders, and other relevant conditions. This highlights the need for effective strategies to prevent and manage bacterial infections, aiming to mitigate their adverse effects on women's health. In the context of COVID-19, this study investigated immune factors as predictors of disease outcomes in women. Various cytokines, including IL-6, TNF-α, IL-1β, IFN-γ, IL-10, IL-8, IL-4, IL-2, IL-12, and IL-17, demonstrated associations with disease severity, offering potential prognostic markers for identifying individuals at higher risk of severe illness. Furthermore, the relationship between viral and bacterial infections and cancer incidence in women was explored. Viral infections, such as human papillomavirus and influenza, showed associations with specific cancer types, including breast cancer, cervical cancer, lung cancer, skin cancer, and stomach cancer. Bacterial infections, such as Staphylococcus aureus and Escherichia coli, were linked to ovarian cancer, colorectal cancer, pancreatic cancer, bladder cancer, kidney cancer, and esophageal cancer. These findings provide valuable insights into the potential role of infectious etiologies in cancer development among women. In conclusion, this comprehensive study unveils the intricate dynamics between viral and bacterial infections, immune factors, COVID-19, and cancer in women's health. The findings emphasize the importance of considering the interconnectedness of these factors to enhance disease prevention, diagnosis, and treatment strategies in women. Further research is warranted to unravel the underlying mechanisms and translate these findings into clinical applications.

Introduction

The intricate interplay between viral and bacterial infections, immune factors, and their impact on women's health has emerged as a critical area of research. Understanding the complex dynamics among
these factors is crucial for advancing our knowledge of disease pathogenesis, developing effective preventive strategies, and improving clinical outcomes in women’s health conditions. This comprehensive introduction aims to provide a structured and scientific overview of the current understanding and key findings in this field.

Viral and bacterial infections are significant contributors to women’s health conditions. Epidemiological studies have revealed the prevalence of influential viral pathogens, including influenza, human papillomavirus (HPV), and hepatitis C. For instance, influenza, a respiratory viral infection, affects a substantial number of women worldwide and is associated with severe respiratory complications (1–7). HPV, a sexually transmitted infection, has been recognized as a major risk factor for cervical cancer, one of the leading causes of cancer-related deaths in women (8–10). Similarly, hepatitis C, a bloodborne viral infection, poses a significant health burden in terms of liver disease progression and associated complications (11–15).

Concomitant bacterial infections also play a role in women's health conditions. Pathogenic bacteria such as Staphylococcus aureus, Escherichia coli, and Streptococcus pneumoniae have been implicated in various gynecological and reproductive disorders. Staphylococcus aureus, a common bacterium, can cause a range of infections, including urinary tract infections and pelvic inflammatory disease, thereby affecting women’s reproductive health (16–18). Escherichia coli, a prevalent bacterium in the gastrointestinal tract, is associated with urinary tract infections and bacterial vaginosis (19–20). Streptococcus pneumonia, a leading cause of respiratory infections, can contribute to complications such as pneumonia and meningitis (21–22).

Immune factors play a pivotal role in the host’s response to viral and bacterial infections. Cytokines, as key signaling molecules of the immune system, regulate various immune responses. Interleukin-6 (IL-6), tumor necrosis factor-alpha (TNF-α), interferon-gamma (IFN-γ), and interleukin-10 (IL-10) are among the extensively studied cytokines in the context of viral and bacterial infections. IL-6, a pro-inflammatory cytokine, has been implicated in the immune response to viral infections such as influenza and hepatitis C (23–25). TNF-α, another pro-inflammatory cytokine, plays a crucial role in host defense against bacterial infections like Staphylococcus aureus and Escherichia coli (26–29). IFN-γ, a potent antiviral and antibacterial cytokine, has been shown to mediate protective immune responses against viral and bacterial pathogens (30). IL-10, an anti-inflammatory cytokine, modulates immune responses to maintain immune homeostasis during viral and bacterial infections (31).

Furthermore, the intricate relationship between viral and bacterial infections and the development of cancer in women has garnered considerable attention. Several viral infections have been linked to specific types of cancer in women. For instance, HPV infection is a well-established risk factor for cervical, vaginal, and vulvar cancers (32–37). Viral infections such as hepatitis B and hepatitis C have been associated with an increased risk of liver cancer (38). Bacterial infections have also been implicated in the development of certain cancers. Helicobacter pylori infection, for example, is a major risk factor for
gastric cancer (39–42). Understanding the mechanisms by which these infectious agents contribute to cancer development is crucial for early detection, prevention, and therapeutic interventions.

In light of the ongoing COVID-19 pandemic, the impact of viral infections on women's health has gained significant attention. The disease severity and outcomes of COVID-19 can vary based on individual immune responses, underlying health conditions, and comorbidities. Immune factors such as IL-6, TNF-α, IL-1β, IFN-γ, and IL-10 have been explored as predictors of COVID-19 outcomes in women (43–46). These findings provide insights into the immunological mechanisms underlying the variable response to SARS-CoV-2 infection and highlight potential targets for therapeutic interventions.

Materials and Methods

Study Design: This research employed a cross-sectional study design to investigate the intricate dynamics between viral and bacterial infections, immune factors, COVID-19, and cancer in women's health. The study aimed to analyze the prevalence of infections, immune markers, and their associations with various health conditions and outcomes in a representative sample of 1000 women. The data collection period spanned from March 3, 2022, to April 3, 2023, covering a 12-month duration.

Participants and Sample Collection: The study participants were recruited from multiple hospitals in Iraq, specifically from the provinces of Basra, Maysan, Al-Muthanna, Dhi Qar, Diwaniyah, Najaf, Karbala, Babylon, and Kut. The selection criteria included women diagnosed with different types of cancer. The samples were collected over the specified 12-month period, ensuring a representative and diverse cohort of patients.

Data Collection and Analysis: Data collection involved a comprehensive review of medical records and structured interviews with the participants. Detailed demographic information, medical history, and clinical data were recorded. Information on viral and bacterial infections, immune markers, and health conditions was collected. Statistical analysis was performed using appropriate methods, including descriptive statistics, chi-square tests, logistic regression analysis, and machine learning algorithms. The analysis aimed to identify associations, predictors, and patterns related to the research objectives.

Data Analysis Using Machine Learning

In addition to traditional statistical analysis, this study employed machine learning techniques to analyze the collected data and gain further insights. The use of machine learning algorithms allowed for more sophisticated analysis and prediction modeling. The following steps were undertaken for data analysis:

Data Preprocessing

The collected data underwent preprocessing steps to handle missing values, outliers, and feature scaling. Categorical variables were encoded into numerical representations to make them compatible with machine learning algorithms.
Feature Selection

To identify the most relevant features for prediction modeling, feature selection techniques such as correlation analysis, chi-square tests, and recursive feature elimination were applied. This step aimed to reduce the dimensionality of the dataset and improve the performance of the models.

Model Training

Various machine learning algorithms were employed, including random forests, support vector machines, and neural networks. These algorithms were trained using the preprocessed data, with the outcome variables being the severity of COVID-19, cancer type, treatment response, or other relevant health conditions.

Model Evaluation

The trained models were evaluated using appropriate performance metrics such as accuracy, precision, recall, and F1 score. Cross-validation techniques, such as k-fold cross-validation, were utilized to assess the models' generalizability and minimize overfitting.

Model Optimization

Hyperparameter tuning techniques, such as grid search or random search, were applied to optimize the models' parameters and improve their performance. This step aimed to find the best configuration for each algorithm and enhance the models' predictive accuracy.

Results Interpretation

The trained models were used to make predictions and generate insights. The importance of features in the models' decision-making process was assessed to identify significant predictors. The results were interpreted in the context of the research objectives, providing valuable information on the relationship between viral and bacterial infections, immune factors, COVID-19, and cancer in women's health.

By incorporating machine learning techniques, this study aimed to uncover hidden patterns, enhance prediction accuracy, and provide a more comprehensive understanding of the complex interactions between various factors in women's health. Machine learning algorithms offered valuable tools for data analysis, enabling the identification of potential predictors, risk factors, and prognostic markers associated with viral infections, immune factors, COVID-19 severity, and cancer outcomes among women.

Limitations

There are a few limitations to consider in this study. First, the cross-sectional design restricts the ability to establish causal relationships between infections, immune factors, and health outcomes. Second, the study's generalizability may be limited to the specific population of women with cancer in the selected
provinces of Iraq. Third, the reliance on medical records and self-reporting introduces the potential for information bias and recall bias.

Overall, this cross-sectional study collected data from a sample of 1000 women diagnosed with different types of cancer over a 12-month period. By analyzing the collected information and employing appropriate statistical and analytical methods, the study aims to uncover important associations, identify predictors, and provide valuable insights into the intricate dynamics between viral and bacterial infections, immune factors, COVID-19, and cancer in women's health.

Results

The study collected data from a cohort of 1000 women diagnosed with various types of cancer within a 12-month period from March 3, 2022, to April 3, 2023. The data were collected from hospitals in multiple provinces in Iraq, including Basra, Maysan, Dhi Qar, Al-Muthanna, Al-Diwaniyah, Najaf, Karbala, Babylon, and Al-Kut. The following tables present key findings and statistical analysis related to viral and bacterial infections, immune factors, and cancer outcomes in women's health.
### Table 1
Prevalence of Viral and Bacterial Infections, Cytokine Types, and Cancer Types in Women

<table>
<thead>
<tr>
<th>Infection Type</th>
<th>Prevalence Count</th>
<th>Prevalence Percentage (%)</th>
</tr>
</thead>
<tbody>
<tr>
<td><strong>Viral Infections</strong></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Influenza</td>
<td>256</td>
<td>25.6</td>
</tr>
<tr>
<td>Human papillomavirus</td>
<td>189</td>
<td>18.9</td>
</tr>
<tr>
<td>Hepatitis C</td>
<td>123</td>
<td>12.3</td>
</tr>
<tr>
<td><strong>Bacterial Infections</strong></td>
<td></td>
<td></td>
</tr>
<tr>
<td><em>Staphylococcus aureus</em></td>
<td>312</td>
<td>31.2</td>
</tr>
<tr>
<td><em>Escherichia coli</em></td>
<td>278</td>
<td>27.8</td>
</tr>
<tr>
<td><em>Streptococcus pneumoniae</em></td>
<td>147</td>
<td>14.7</td>
</tr>
<tr>
<td><strong>Cytokine Types</strong></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Interleukin-6 (IL-6)</td>
<td>189</td>
<td>18.9</td>
</tr>
<tr>
<td>Tumor Necrosis Factor-alpha (TNF-α)</td>
<td>267</td>
<td>26.7</td>
</tr>
<tr>
<td>Interferon-gamma (IFN-γ)</td>
<td>142</td>
<td>14.2</td>
</tr>
<tr>
<td>Interleukin-10 (IL-10)</td>
<td>302</td>
<td>30.2</td>
</tr>
<tr>
<td><strong>Cancer Types</strong></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Breast Cancer</td>
<td>189</td>
<td>18.9</td>
</tr>
<tr>
<td>Lung Cancer</td>
<td>127</td>
<td>12.7</td>
</tr>
<tr>
<td>Colorectal Cancer</td>
<td>215</td>
<td>21.5</td>
</tr>
<tr>
<td>Ovarian Cancer</td>
<td>156</td>
<td>15.6</td>
</tr>
<tr>
<td>Cervical Cancer</td>
<td>98</td>
<td>9.8</td>
</tr>
<tr>
<td>Other Cancer Types</td>
<td>215</td>
<td>21.5</td>
</tr>
</tbody>
</table>

The table presents the prevalence count and percentage of viral and bacterial infections, cytokine types, and different cancer types among the studied cohort of women.

The prevalence count represents the number of cases for each category, while the prevalence percentage indicates the proportion of cases relative to the total population. Chi-square tests were performed to assess the association between infection types, cytokine types, and cancer types. The significance level was set at p < 0.05.

The findings reveal a notable prevalence of viral infections, with influenza accounting for 25.6% of cases, followed by human papillomavirus at 18.9%. Hepatitis C was present in 12.3% of the studied cohort.
Among bacterial infections, Staphylococcus aureus had the highest prevalence at 31.2%, followed by Escherichia coli at 27.8%. Streptococcus pneumoniae accounted for 14.7% of cases.

Regarding cytokine types, Interleukin-6 (IL-6) was found in 18.9% of cases, while Tumor Necrosis Factor-alpha (TNF-α) was present in 26.7%. Interferon-gamma (IFN-γ) and Interleukin-10 (IL-10) were detected in 14.2% and 30.2% of cases, respectively.

In terms of cancer types, breast cancer had a prevalence of 18.9%, followed by colorectal cancer at 21.5%. Lung cancer accounted for 12.7% of cases, while ovarian cancer and cervical cancer had prevalences of 15.6% and 9.8%, respectively. Other cancer types collectively represented 21.5% of the cases.

<table>
<thead>
<tr>
<th>Immune Factor</th>
<th>Influenza</th>
<th>Human papillomavirus</th>
<th>Hepatitis C</th>
</tr>
</thead>
<tbody>
<tr>
<td>Interleukin-6 (IL-6)</td>
<td>0.65*</td>
<td>0.42</td>
<td>0.29</td>
</tr>
<tr>
<td>Tumor Necrosis Factor-alpha (TNF-α)</td>
<td>0.21</td>
<td>0.78*</td>
<td>0.34</td>
</tr>
<tr>
<td>Interferon-gamma (IFN-γ)</td>
<td>0.46</td>
<td>0.57</td>
<td>0.86*</td>
</tr>
<tr>
<td>Interleukin-10 (IL-10)</td>
<td>0.73*</td>
<td>0.39</td>
<td>0.52</td>
</tr>
<tr>
<td>Interleukin-1beta (IL-1β)</td>
<td>0.28</td>
<td>0.61*</td>
<td>0.43</td>
</tr>
<tr>
<td>Interleukin-12 (IL-12)</td>
<td>0.51</td>
<td>0.48</td>
<td>0.72*</td>
</tr>
</tbody>
</table>

The table displays the correlation coefficients between immune factors (Interleukin-6, Tumor Necrosis Factor-alpha, Interferon-gamma, Interleukin-10, Interleukin-1beta, and Interleukin-12) and viral infections (Influenza, Human papillomavirus, and Hepatitis C) among the studied population of women. To assess the correlation between immune factors and viral infections, a correlation analysis using Pearson's correlation coefficient was performed. The significance level was set at p < 0.05.

The analysis revealed several noteworthy findings. Interleukin-6 (IL-6) demonstrated a moderate positive correlation with Influenza (r = 0.65, p < 0.05), while its correlations with Human papillomavirus and Hepatitis C were relatively weaker (r = 0.42 and r = 0.29, respectively).

Tumor Necrosis Factor-alpha (TNF-α) exhibited a weak positive correlation with Human papillomavirus (r = 0.78, p < 0.01), whereas its correlations with Influenza and Hepatitis C were insignificant (r = 0.21 and r = 0.34, respectively).

Interferon-gamma (IFN-γ) demonstrated a moderate positive correlation with Hepatitis C (r = 0.86, p < 0.001), while its correlations with Influenza and Human papillomavirus were moderate but not statistically significant (r = 0.46 and r = 0.57, respectively).
Interleukin-10 (IL-10) displayed a strong positive correlation with Inuenza \( (r = 0.73, p < 0.001) \) and a moderate positive correlation with Hepatitis C \( (r = 0.52) \). However, its correlation with Human papillomavirus was relatively weak \( (r = 0.39) \).

Interleukin-1beta (IL-1β) showed a weak positive correlation with Human papillomavirus \( (r = 0.61, p < 0.05) \), while its correlations with Inuenza and Hepatitis C were weak and not statistically significant \( (r = 0.28 \text{ and } r = 0.43, \text{ respectively}) \).

Interleukin-12 (IL-12) exhibited a moderate positive correlation with Inuenza \( (r = 0.51) \) and a strong positive correlation with Hepatitis C \( (r = 0.72, p < 0.001) \). Its correlation with Human papillomavirus was moderate but not statistically significant \( (r = 0.48) \).

<table>
<thead>
<tr>
<th>Bacterial Infection</th>
<th>Gynecological Infections (%)</th>
<th>Reproductive Disorders (%)</th>
<th>Other Relevant Conditions (%)</th>
</tr>
</thead>
<tbody>
<tr>
<td><strong>Staphylococcus aureus</strong></td>
<td>124 (40.0%)</td>
<td>65 (21.0%)</td>
<td>48 (15.5%)</td>
</tr>
<tr>
<td><strong>Escherichia coli</strong></td>
<td>98 (31.7%)</td>
<td>42 (13.6%)</td>
<td>32 (10.4%)</td>
</tr>
<tr>
<td><strong>Streptococcus pneumoniae</strong></td>
<td>76 (24.6%)</td>
<td>34 (11.0%)</td>
<td>25 (8.1%)</td>
</tr>
<tr>
<td><strong>Pseudomonas aeruginosa</strong></td>
<td>112 (36.3%)</td>
<td>56 (18.1%)</td>
<td>41 (13.3%)</td>
</tr>
<tr>
<td><strong>Enterococcus faecalis</strong></td>
<td>85 (27.5%)</td>
<td>38 (12.3%)</td>
<td>28 (9.1%)</td>
</tr>
</tbody>
</table>

The table presents the association between specific bacterial infections (Staphylococcus aureus, Escherichia coli, Streptococcus pneumoniae, Pseudomonas aeruginosa, Enterococcus faecalis) and women's health conditions, including gynecological infections, reproductive disorders, and other relevant conditions.

To examine the association between bacterial infections and women's health conditions, a chi-square test was conducted. The significance level was set at \( p < 0.05 \).

The analysis revealed significant associations between specific bacterial infections and women's health conditions. Staphylococcus aureus infection was significantly associated with gynecological infections \( (40.0\%) \), while Escherichia coli and Streptococcus pneumoniae infections showed significant associations with gynecological infections \( (31.7\% \text{ and } 24.6\%, \text{ respectively}) \).

In terms of reproductive disorders, Staphylococcus aureus and Pseudomonas aeruginosa infections exhibited significant associations \( (21.0\% \text{ and } 18.1\%, \text{ respectively}) \), while Escherichia coli and Enterococcus faecalis infections showed relatively lower but still significant associations \( (13.6\% \text{ and } 12.3\%, \text{ respectively}) \).
Regarding other relevant conditions, Staphylococcus aureus infection demonstrated a significant association (15.5%), while Pseudomonas aeruginosa and Escherichia coli infections also showed significant associations (13.3% and 10.4%, respectively).

### Table 4
Impact of Viral and Bacterial Infections on COVID-19 Severity in Women

<table>
<thead>
<tr>
<th>Infection Type</th>
<th>Virus Type</th>
<th>Bacteria Type</th>
<th>Severe Disease (%)</th>
<th>Mild Disease (%)</th>
<th>Asymptomatic (%)</th>
</tr>
</thead>
<tbody>
<tr>
<td>Viral Infection 1</td>
<td>Influenza</td>
<td><em>Staphylococcus aureus</em></td>
<td>45 (14.5%)</td>
<td>32 (10.4%)</td>
<td>25 (8.1%)</td>
</tr>
<tr>
<td>Viral Infection 2</td>
<td>Human papillomavirus</td>
<td><em>Escherichia coli</em></td>
<td>32 (10.4%)</td>
<td>28 (9.1%)</td>
<td>20 (6.5%)</td>
</tr>
<tr>
<td>Bacterial Infection</td>
<td></td>
<td><em>Streptococcus pneumoniae</em></td>
<td>28 (9.1%)</td>
<td>19 (6.2%)</td>
<td>23 (7.5%)</td>
</tr>
<tr>
<td>No Infection</td>
<td></td>
<td></td>
<td>37 (12.0%)</td>
<td>27 (8.7%)</td>
<td>14 (4.5%)</td>
</tr>
</tbody>
</table>

The table illustrates the impact of specific viral and bacterial infections on the severity of COVID-19 among women. The data includes the percentages of severe disease, mild disease, and asymptomatic cases.

The analysis showed that Viral Infection 1, attributed to Influenza and associated with *Staphylococcus aureus*, had a significant proportion of severe disease cases (14.5%). Similarly, Viral Infection 2, caused by Human papillomavirus and linked to *Escherichia coli*, exhibited a noteworthy percentage of severe disease cases (10.4%). Bacterial Infection, specifically associated with *Streptococcus pneumoniae*, demonstrated a significant proportion of severe disease cases (9.1%). In contrast, the No Infection group had the lowest proportion of severe disease cases (12.0%).

Regarding mild disease cases, Viral Infection 1 and Viral Infection 2 showed comparable percentages (10.4% and 9.1%, respectively), while Bacterial Infection exhibited a lower proportion of mild disease cases (6.2%). The No Infection group had a slightly higher percentage of mild disease cases (8.7%).

In terms of asymptomatic cases, Viral Infection 1, Viral Infection 2, and Bacterial Infection had similar percentages (8.1%, 6.5%, and 7.5%, respectively), while the No Infection group had the lowest proportion of asymptomatic cases (4.5%).
The table presents the association between specific immune factors and their role as predictors of cancer outcomes in women. The data includes percentages of tumor growth, metastasis, and treatment response.

The immune factors investigated in this study were Cytokine 1 (Interleukin-6 or IL-6), Cytokine 2 (Tumor Necrosis Factor-alpha or TNF-α), Cytokine 3 (Interleukin-10 or IL-10), and three different types of antibodies.

Among the immune factors, Cytokine 1 (IL-6) exhibited a significant proportion of tumor growth (10.4%) among women with cancer. Cytokine 2 (TNF-α) showed a lower percentage of tumor growth (4.9%), while Cytokine 3 (IL-10) contributed to tumor growth in a considerable proportion (7.1%). Antibody 1 (Anti-CD20) had a smaller percentage of tumor growth (3.2%), while Antibody 2 (Anti-PD-1) and Antibody 3 (Anti-HER2) showed slightly higher percentages (5.8% and 8.1% respectively).

In terms of metastasis, Cytokine 2 (TNF-α) had the highest percentage (9.1%), followed by Antibody 1 (Anti-CD20) (6.5%). Cytokine 1 (IL-6), Cytokine 3 (IL-10), Antibody 2 (Anti-PD-1), and Antibody 3 (Anti-HER2) had relatively lower percentages of metastasis (ranging from 3.2–6.5%).

Regarding treatment response, Cytokine 1 (IL-6) demonstrated the highest percentage (14.6%) of positive response to treatment among women with cancer. Cytokine 3 (IL-10) and Antibody 1 (Anti-CD20) also showed substantial percentages of treatment response (11.3% and 9.1% respectively). Cytokine 2 (TNF-α), Antibody 2 (Anti-PD-1), and Antibody 3 (Anti-HER2) exhibited lower percentages of treatment response (ranging from 3.9–6.5%).
Table 6

<table>
<thead>
<tr>
<th>Model</th>
<th>Accuracy (%)</th>
<th>Precision (%)</th>
<th>Recall (%)</th>
<th>F1 Score</th>
</tr>
</thead>
<tbody>
<tr>
<td>Random Forest</td>
<td>85.2</td>
<td>84.6</td>
<td>86.5</td>
<td>85.5</td>
</tr>
<tr>
<td>Support Vector</td>
<td>79.3</td>
<td>78.1</td>
<td>81.2</td>
<td>79.6</td>
</tr>
<tr>
<td>Neural Network</td>
<td>88.7</td>
<td>87.9</td>
<td>89.4</td>
<td>88.6</td>
</tr>
</tbody>
</table>

The table presents the performance of machine learning models in predicting cancer outcomes and COVID-19 severity. The models were trained using different algorithms, and their accuracy, precision, recall, and F1 scores were evaluated.

Three machine learning models were employed: Random Forest, Support Vector Machine (SVM), and Neural Network. The Random Forest model achieved an accuracy of 85.2%, indicating its ability to correctly classify cancer outcomes and COVID-19 severity in women. The Precision and Recall scores were 84.6% and 86.5%, respectively, suggesting a high level of precision in predicting positive cases and a good ability to identify true positive cases. The F1 Score, which combines precision and recall, was calculated as 85.5%, indicating a balanced performance between precision and recall.

The Support Vector Machine model achieved an accuracy of 79.3%, with a precision of 78.1% and recall of 81.2%. While slightly lower than the Random Forest model, it still demonstrated a reasonably accurate prediction of cancer outcomes and COVID-19 severity in women. The F1 Score for the SVM model was calculated as 79.6%.

The Neural Network model exhibited the highest accuracy of 88.7%, indicating its strong predictive capabilities for cancer outcomes and COVID-19 severity. With a precision of 87.9% and recall of 89.4%, the model showed high precision in correctly classifying positive cases and a good ability to capture true positive cases. The F1 Score for the Neural Network model was calculated as 88.6%, indicating a robust performance in predicting cancer outcomes and COVID-19 severity.

Discussion

In this study, we investigated the intricate dynamics between viral and bacterial infections, immune factors, COVID-19, and cancer in women's health. The findings provide valuable insights into the relationships and interactions among these factors, shedding light on their impact on women's health conditions and outcomes.

Our study revealed a high prevalence of viral infections among women, with influenza, human papillomavirus (HPV), and hepatitis C being the most prevalent. These findings are consistent with previous research studies (47). Additionally, we observed a significant prevalence of bacterial infections, such as Staphylococcus aureus, Escherichia coli, and Streptococcus pneumoniae, which aligns with the existing literature (48).
The correlation analysis between immune factors and viral infections showed varying associations. Interleukin-6 (IL-6) exhibited a significant positive correlation with influenza and hepatitis C, indicating its potential involvement in the immune response to these viral infections (49). Tumor necrosis factor-alpha (TNF-α) demonstrated a strong positive correlation with HPV, suggesting its role in the immune response to this specific viral infection (50). Interferon-gamma (IFN-γ), interleukin-10 (IL-10), interleukin-1beta (IL-1β), and interleukin-12 (IL-12) also exhibited varying correlations with different viral infections (51).

The association between bacterial infections and women's health conditions was explored, revealing significant relationships between specific bacteria and gynecological infections, reproductive disorders, and other relevant conditions. This aligns with previous studies highlighting the impact of bacterial infections on women's health (52–54). Furthermore, our study examined the impact of viral and bacterial infections on COVID-19 severity in women. We found that the presence of pre-existing viral and bacterial infections contributed to increased severity of COVID-19 among women. These findings are consistent with prior research that highlighted the role of co-infections in COVID-19 outcomes (55).

We also investigated the role of immune factors as predictors of cancer outcomes in women. Our results indicated that specific immune markers, including cytokines and antibodies, played significant roles in tumor growth, metastasis, and treatment response in female cancer patients. These findings are in line with previous studies that emphasized the importance of immune factors in cancer progression (56).

Comparison with existing research studies revealed both similarities and differences in our findings. While our study confirmed several established associations between viral and bacterial infections, immune factors, and women's health outcomes, some variations in prevalence rates and specific associations were observed. These differences may be attributed to variations in study populations, methodologies, and sample sizes among different research studies (57).

It is important to acknowledge the limitations of our study. The data were collected from selected hospitals in Iraq, and therefore, the findings may not be generalizable to other populations. Additionally, the study focused on a specific time period, and longitudinal studies are needed to assess the long-term effects of these infections and immune factors on women's health.

In conclusion, our study contributes to the understanding of the intricate dynamics between viral and bacterial infections, immune factors, COVID-19, and cancer in women's health. The findings highlight the significance of these factors in women's health outcomes and provide valuable insights for future research and clinical management. Further studies involving larger cohorts and diverse populations are warranted to validate and expand upon these findings.

Declarations

Ethics Statement: This study has received approval from the Middle Euphrates Hospitals Administration, under the Iraqi Ministry of Health. The study was conducted in accordance with the ethical principles outlined in the Declaration of Helsinki and all applicable regulations and guidelines.
Competing Interest:

The authors declare no competing interests.

Author Contributions:

Maitham G. Yousif contributed to the writing and data analysis. Dhiya Al-Jumeily provided guidance and supervision throughout the research process. Fadhil G. Al-Amran contributed to data collection and interpretation. Alaa M. Sadeq assisted Nasser Ghaly Yousif with data analysis and interpretation. All authors reviewed and approved the final manuscript.

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