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# **RESEARCH ARTICLE**



# Empowering healthcare with NLP-driven deep learning unveiling biomedical materials through text mining

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# Abstract

This study presents a comprehensive approach to automated biomedical materials discovery in healthcare applications by integrating text mining and deep learning techniques. The research methodology encompasses two main components: exploration of key research questions through graphical representation and evaluation of model performance using precision, recall, and F1-score metrics. The identification of pertinent research questions is visualized using bar charts, offering insights into the distribution of studies across domains such as data harmonization, heterogeneity, industrial textual data, and sequential data performance. The precision comparison chart highlights the strengths and weaknesses of different models, with model 1 demonstrating notable precision. The recall comparison chart emphasizes model 2's outstanding performance in capturing relevant information, while the f1-score comparison chart showcases the balanced metrics of model 2 and 4. These visual analyses contribute to a nuanced understanding of the research landscape and guide the development of the proposed NLP-ML pipeline. The study's findings underscore the significance of addressing data harmonization challenges and extracting insights from industrial textual data in advancing biomedical materials discovery. Overall, this research amalgamates exploratory data analysis and quantitative model evaluation to contribute to the evolving field of text mining and deep learning applications in biomedical material discovery for healthcare applications.

Keywords: Biomedical materials discovery, Text mining, Deep learning, Precision-recall trade-offs, Data harmonization, NLP-ML pipeline.

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# Introduction

The exponential growth of biomedical literature in recent years has propelled the scientific community into a daunting era characterized by an overwhelming influx of textual data (Alan Pounds, J., et al., 2006). The field of healthcare research is particularly inundated with a vast and diverse array of information, making manual literature review and knowledge extraction an increasingly arduous task (Janowski, A. 2023). In response to this challenge, researchers have turned to advanced computational techniques, leveraging the synergies of text mining (TM) and deep learning (DL), to facilitate automated discovery and extraction of valuable insights from the burgeoning biomedical literature. A comprehensive literature survey reveals a substantial body of work addressing the application of text mining and deep learning in the biomedical domain (Zhang, W., et al., 2023). Previous studies have explored the use of natural language processing (NLP) techniques to extract relevant information from biomedical texts, ranging from research articles and clinical notes to patents and electronic health records (EHRs). For instance, (Razack, H. I. A., et al., 2021) employed NLP methods for named entity recognition (NER) to identify biomedical entities such as genes, proteins, and diseases, thereby enabling automated

information extraction from vast biomedical corpora. The integration of machine learning (ML) algorithms, particularly deep learning models, has emerged as a pivotal approach to enhance the automated discovery process. Deep learning architectures, such as recurrent neural networks (RNNs) and transformer models, have demonstrated remarkable capabilities in capturing intricate relationships and patterns within biomedical texts. In a seminal work by Malik, N., & Bilal, M. (2023), a deep learning model was employed for information extraction from biomedical literature, achieving state-of-the-art results in tasks such as relation extraction and event extraction.

The significance of data harmonization in the context of biomedical text mining cannot be overstated. As highlighted by Silvestri, S., et al., (2023). The heterogeneity in data sources, formats, and terminology poses a significant challenge to effective information extraction. Efforts in data harmonization, such as the development of standardized biomedical ontologies and the establishment of interoperable data formats, play a crucial role in ensuring the robustness and generalizability of text mining and deep learning pipelines. Industrial textual data, including information from pharmaceutical patents, clinical trials, and biomedical reports, constitutes a valuable yet complex source for automated discovery in healthcare applications. Extensive studies, such as the work by (Petit-Jean, T., et al., 2023), have delved into the challenges and opportunities posed by industrial textual data, emphasizing the need for tailored text mining and deep learning approaches to extract actionable insights from these heterogeneous and domain-specific documents.

Furthermore, the application of text mining and deep learning in handling sequential biomedical data showcases a promising avenue for advancing healthcare research. Performance evaluation in the context of sequential data is a critical aspect that demands meticulous attention. Recent studies, including the work by (Zitu, M. M. 2023) have explored the performance nuances of deep learning models when applied to sequential biomedical data, shedding light on the intricacies of model effectiveness and areas for improvement. In the convergence of text mining and deep learning holds immense potential for revolutionizing the automated discovery of biomedical materials in healthcare applications. This paper seeks to contribute to the existing body of knowledge by presenting a comprehensive NLP-ML pipeline designed to navigate the challenges posed by heterogeneous, sequential, and industrial textual data. By synthesizing insights from previous literature, we aim to position our work within the broader landscape of biomedical informatics, offering a novel and effective solution to the contemporary challenges in healthcare research and development. Despite the notable advancements in text mining and deep learning for

biomedical applications, a critical research gap persists in the effective handling of heterogeneous and domain-specific industrial textual data. Current literature, as evidenced by (Krauze, A., & Camphausen, K. 2022) emphasizes the need for tailored approaches in extracting meaningful insights from complex documents such as pharmaceutical patents and clinical reports. Our proposed NLP-ML pipeline aims to address this gap by providing a specialized solution for the automated discovery of biomedical materials in the intricate landscape of industrial textual data (Garcia, E. V. 2023).

### **Research Methodology**

The research methodology adopted in this study builds upon the integration of text mining and deep learning techniques for the automated discovery of biomedical materials in healthcare applications. The methodology encompasses two key components: (1) The exploration of research questions related to the domain, as exemplified by the graphical representation using bar charts, line charts, and scatter plots; and (2) The evaluation of the performance of different models through the visualization of precision, recall, and F1-score (Pacheco, J. A., et al., 2023). Identifying and exploring pertinent research questions constitute a fundamental aspect of our methodology. We employed bar charts to depict the distribution of studies across key research questions, namely heterogeneity, data harmonization, industrial textual data, and sequential data performance. Through this visual representation, we aimed to provide a comprehensive overview of the landscape of existing literature and pinpoint potential research gaps, aligning with the objectives outlined in the introduction (Srivani, M., et al., 2020).

Furthermore, our research methodology involves the evaluation of model performance in addressing the identified research questions. We employed line charts to illustrate the precision-recall trade-offs for different models, emphasizing the nuanced performance metrics associated with each. The precision comparison, visualized through bar charts, facilitates a detailed examination of modelspecific strengths and weaknesses (Saini, S., & Saxena, N. 2023). Concurrently, the scatter plots depicting F1-score comparisons offer insights into the holistic performance of each model, considering both precision and recall. The methodology underscores the significance of numerical evaluation in assessing the efficacy of the proposed NLP-ML pipeline. By utilizing precision, recall, and F1-score as performance metrics, inspired by established practices in the literature (Hawkins, N. T., et al., 2022); (Cohen, J., et al., 2020), we aim to provide a quantitative framework for the assessment of our methodology's robustness. The choice of these metrics aligns with the intricate nature of biomedical materials discovery, where precision is critical for minimizing false positives, recall ensures comprehensive information retrieval, and F1-score balances these competing objectives. In our research methodology amalgamates exploratory data analysis through graphical representation and quantitative model evaluation to comprehensively address the research questions posed in our study. The integration of these two components forms a cohesive approach that aims to contribute significantly to the burgeoning field of text mining and deep learning applications in biomedical material discovery for healthcare applications (Santos, H. D. P. D. (2021); (Yadav, S., *et al.*, 2020).

## **Results And Discussion**

#### **Research Questions vs. Number of Studies**

The graphical representation in Figure 1 of our research questions against the number of studies, as illustrated in the bar chart (Research Questions vs. Number of Studies), provides a visually insightful depiction of the distribution of existing literature across key domains. Notably, the research question pertaining to data harmonization emerges as a focal point, with 25 studies addressing this critical aspect. The prominence of data harmonization underscores its significance in the realm of biomedical materials discovery, emphasizing the scholarly attention dedicated to the challenges and opportunities associated with harmonizing heterogeneous data sources. Heterogeneity follows closely, with 14 studies reflecting a substantial body of work directed toward understanding and addressing the complexities arising from diverse biomedical data. The prevalence of studies in this area accentuates the acknowledged challenges of managing heterogeneous datasets within the biomedical context. In contrast, Industrial textual data and sequential data performance research questions exhibit 23 and 8 studies, respectively. The focus on industrial textual data highlights the growing importance of extracting insights from domain-specific documents such as pharmaceutical patents and clinical reports. Meanwhile, the relatively fewer studies on sequential data performance signify a nascent but evolving area within the broader landscape of biomedical materials discovery. The limited number of studies in this domain suggests a potential research gap, necessitating further exploration and emphasis on the challenges posed by sequential data in healthcare applications (Nunes, C. V. D. S. 2020).

The graphical representation not only provides a snapshot of the current state of literature but also serves as a foundation for discussion and potential avenues for future research. The distribution of studies across research questions offers valuable insights into the collective focus of the research community, thereby guiding our interpretation of the existing landscape and informing the development of our NLP-ML pipeline. Overall, this visual analysis facilitates a nuanced understanding of the research ecosystem surrounding biomedical materials discovery, laying the groundwork for a more targeted and informed discussion within the broader context of our paper.



Figure 1: Research questions vs. number of studies



Figure 2: Research questions vs. number of studies

The graphical representation in Figure 2 of our research questions against the number of studies, as illustrated in the bar chart (Research Questions vs. Number of Studies), reveals compelling insights into the distribution and emphasis of existing literature across distinct domains in the biomedical materials discovery landscape. Notably, the research question about data harmonization emerges as a predominant focus, with 40 studies dedicated to addressing the challenges and nuances associated with harmonizing heterogeneous biomedical data. The heightened attention to data harmonization underscores its critical role in the evolution of biomedical informatics, emphasizing the scholarly commitment to developing strategies that bridge the gap between disparate data sources. Heterogeneity closely follows, with 20 studies dedicated to unraveling the complexities associated with diverse biomedical datasets. This distribution affirms the sustained scholarly interest in addressing the intricacies of data heterogeneity, reflecting the ongoing challenges inherent in managing and extracting meaningful insights from diverse sources within the biomedical domain (Hoang, K. L. (2023).

Conversely, industrial textual data and sequential data performance research questions exhibit 60 and 10 studies, respectively. The substantial number of studies on industrial textual data suggests a heightened awareness of the need to extract actionable insights from domain-specific documents, such as pharmaceutical patents and clinical reports. The emphasis on sequential data performance, with a relatively smaller but still notable number of studies, indicates a recognition of the evolving nature of biomedical materials discovery, particularly in the context of sequential data applications in healthcare. The graphical representation not only provides a quantitative snapshot of the current state of literature but also serves as a foundation for a robust discussion on the trends, priorities, and potential gaps within the field. The weighted distribution of studies across research questions directs our interpretation of the existing landscape, guiding the development of our NLP-ML pipeline. Overall, this visual analysis facilitates a nuanced understanding of the research ecosystem surrounding biomedical materials discovery, informing a targeted and insightful discussion within the broader context of our paper.

The graphical representation in Figure 3 of our research questions against the number of studies, exemplified in the bar chart (Research Questions vs. Number of Studies), illuminates the distribution and scholarly focus within the biomedical materials discovery domain. Notably, the research question of data harmonization emerges as a central theme, with a significant 30 studies dedicated to understanding and mitigating the challenges posed by heterogeneous biomedical data. This concentration reflects the acknowledged importance of harmonizing disparate data sources, as highlighted by various scholars (Johnson et al., 2020), underscoring the ongoing efforts to establish standardized practices for effective data harmonization in biomedical research. Following closely is the research question of industrial textual data, with 50 studies dedicated to exploring the intricacies of extracting valuable insights



Heterogeneity and Sequential Data Performance, with 15 and 25 studies, respectively, represent nuanced but significant areas within the biomedical materials discovery landscape. The moderate distribution of studies across these research questions suggests an acknowledgment of the persistent challenges associated with managing diverse biomedical datasets and the evolving nature of sequential data applications in healthcare. This graphical representation serves as a quantitative summary of existing literature and a foundation for a comprehensive discussion on the current state and potential future directions within the field. The weighted distribution of studies across research questions directs the interpretation of trends and gaps, guiding the development of our proposed NLP-ML pipeline. In conclusion, this visual analysis contributes to a nuanced understanding of the research landscape, emphasizing the critical importance of addressing data harmonization challenges and extracting insights from industrial textual data in advancing biomedical materials discovery.

#### Precision Comparison for Different Models

The precision comparison for different models in Figure 4, illustrated in the bar chart (Precision Comparison for Different Models), offers a comprehensive view of the model-specific performance metrics within our NLP-ML pipeline. Model 1 stands out with a precision score of 0.9, reflecting its high accuracy in minimizing false positives during the automated discovery of biomedical materials. This superior precision aligns with the findings of several notable studies, emphasizing the effectiveness of advanced



Figure 3: Research questions vs. number of studies



Figure 4: Precision comparison for different models

deep-learning architectures in extracting precise information from biomedical texts. Model 2, with a precision score of 0.10, exhibits a lower precision compared to model 1. This discrepancy underscores the nuanced nature of model performance, with variations in precision metrics attributable to architectural differences and training data complexities. The comparison provides valuable insights into the tradeoffs inherent in different models, informing researchers and practitioners about the strengths and limitations of each approach. Model 3 and 4, with precision scores of 0.7 and 0.8, respectively, contribute to understanding the holistic performance spectrum within our NLP-ML pipeline. The moderate precision scores indicate a balance between minimizing false positives and maximizing true positives, offering a nuanced perspective on the models' overall efficacy. The visual representation of precision scores aids in the identification of model-specific strengths and informs decision-making processes in selecting the most appropriate model for specific biomedical materials discovery tasks (Satpute, R. S., & Agrawal, A. 2023).

The precision comparison chart serves as a vital tool for discussions surrounding the trade-offs between precision and recall, crucial considerations in biomedical informatics. The variation in precision scores among the different models prompts a deeper exploration into the factors influencing performance, such as the complexity of the biomedical text, the volume of data, and the architectural intricacies of each model. In the precision comparison chart enriches our understanding of the NLP-ML pipeline's performance, highlighting the intricacies of model-specific precision metrics. This visual analysis facilitates an informed discussion on the strengths and weaknesses of each model, providing a foundation for future refinements and optimizations within the context of automated biomedical materials discovery.

## **Recall Comparison for Different Models**

The recall comparison chart, depicted in the bar chart titled "Recall Comparison for Different Models," serves as a pivotal element in evaluating the performance of our NLP-ML pipeline for automated biomedical materials discovery (Figure 5). Model 2 emerges as a standout performer with a recall score of 0.950, indicating its capacity to comprehensively





capture relevant information from biomedical texts. This high recall aligns with the observations of previous research, showcasing the effectiveness of advanced deeplearning models in achieving comprehensive information retrieval. Model 4 closely follows, with a recall score of 0.875, demonstrating a robust ability to retrieve pertinent information from the biomedical literature. The comparison between model 2 and 4 reveals nuanced differences in recall metrics, shedding light on the trade-offs inherent in different model architectures and training approaches. These variations in recall underscore the importance of carefully considering model-specific strengths and limitations when selecting the most suitable approach for biomedical materials discovery. Model 3, with a recall score of 0.825, and model 1, with a recall score of 0.750, exhibit moderate recall performance. The visual representation of recall metrics provides a comprehensive view of the models' abilities to retrieve relevant information, facilitating a nuanced understanding of their comparative strengths and weaknesses. This nuanced performance evaluation is particularly crucial in the context of biomedical informatics, where the accurate retrieval of information is paramount for successful automated discovery (Bako, A. T. (2021).

The recall comparison chart serves as a valuable tool for researchers and practitioners, offering insights into the recall trade-offs inherent in different models. The variations in recall metrics prompt a deeper exploration into the factors influencing performance, such as the nature of the biomedical text, the complexity of the data, and the architectural intricacies of each model. This visual analysis enhances our understanding of the NLP-ML pipeline's performance, guiding further refinements and optimizations in the pursuit of robust and comprehensive automated biomedical materials discovery. In the recall comparison chart provides a nuanced perspective on the recall performance of different models within our NLP-ML pipeline. This visual representation facilitates an informed discussion on the models' ability to retrieve relevant information, offering valuable insights for future advancements in automated biomedical materials discovery.

#### F1-Score Comparison for Different Models

The f1-score comparison chart in Figure 6, encapsulated in the "F1-Score Comparison for Different Models" bar chart, comprehensively evaluates our NLP-ML pipeline's performance in automated biomedical materials discovery. Model 2 emerges as a standout performer with an impressive F1-score of 0.92, showcasing its balanced precision and recall metrics. This high F1-score aligns with the findings of prior studies, underscoring the effectiveness of advanced deep-learning models in achieving a harmonized balance between precision and recall. Model 4 closely follows, boasting an F1-score of 0.88, indicating its capability to strike a robust equilibrium between minimizing false positives



Figure 6: F1-score comparison for different models

and maximizing true positives. The comparison between model 2 and 4 reveals nuanced differences in F1-score metrics, shedding light on the intricate trade-offs inherent in different model architectures and training approaches. These variations underscore the significance of considering modelspecific strengths and limitations when selecting an optimal approach for biomedical materials discovery. Model 3, with an F1-score of 0.80, and model 1, with an F1-score of 0.80, exhibit moderate F1-score performance. The visual representation of F1-score metrics provides a comprehensive view of the models' ability to balance precision and recall, offering insights into their comparative strengths and weaknesses. This nuanced evaluation is particularly pivotal in the biomedical informatics domain, where achieving a delicate balance between minimizing false positives and false negatives is essential for the success of automated discovery processes.

The F1-score comparison chart serves as a valuable tool for researchers and practitioners, enabling a deeper understanding of the trade-offs inherent in different models. The variations in F1-score metrics prompt an exploration into the factors influencing performance, such as the nature of the biomedical text, the complexity of the data, and the architectural intricacies of each model. This visual analysis enhances our understanding of the NLP-ML pipeline's overall performance, guiding further refinements and optimizations for robust and balanced automated biomedical materials discovery. In the F1-score comparison chart offers a nuanced perspective on the overall performance of different models within our NLP-ML pipeline. This visual representation facilitates an informed discussion on the models' ability to balance precision and recall, providing valuable insights for future advancements in automated biomedical materials discovery.

#### Conclusion

The graphical representation of research questions against the number of studies reveals distinct emphases within the biomedical materials discovery landscape. Notably, data harmonization and heterogeneity emerge as prominent focal points, reflecting the scholarly commitment to addressing challenges in managing diverse data sources.

The precision, recall, and F1-score comparison charts offer nuanced insights into the model-specific performance metrics within the NLP-ML pipeline. Model 2 stands out for its exceptional recall and F1-score, showcasing its effectiveness in comprehensive information retrieval and achieving a harmonized balance between precision and recall.

The distribution of studies across research questions and the performance metrics of different models contribute to a comprehensive understanding of the research landscape. These findings underscore the significance of addressing data harmonization challenges and extracting insights from industrial textual data for advancing biomedical materials discovery.

The variations in performance metrics among models highlight the trade-offs inherent in different architectures and training approaches. Model 1 demonstrates notable precision, while model 4 strikes a robust equilibrium between minimizing false positives and maximizing true positives, providing valuable insights for model selection in specific biomedical materials discovery tasks.

In this study amalgamates exploratory data analysis and quantitative model evaluation to contribute significantly to the evolving field of text mining and deep learning applications in biomedical material discovery for healthcare applications. The findings inform targeted discussions on trends, priorities, and potential gaps within the field, guiding the development of the proposed NLP-ML pipeline and offering valuable insights for future advancements in automated biomedical materials discovery.

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