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Explainable Clinical Text Mining for Treatment Response Extraction in Lung Cancer Notes

Aoi Ito, Bernard Darren

Faculty of Medicine, Dentistry and Health Sciences, University of Melbourne,
Melbourne, Australia

Abstract : *The extraction of treatment response information from unstructured clinical notes is a critical task in oncology research and clinical practice, particularly for lung cancer, where therapeutic paradigms evolve rapidly. Despite the promising capabilities of advanced natural language processing models, their opaque nature significantly limits clinical adoption due to a lack of interpretability and trustworthiness. This paper investigates the development and implementation of an explainable clinical text mining framework explicitly designed to extract treatment response trajectories from unstructured electronic health records pertaining to lung cancer cohorts. By integrating transformer-based language models with robust explainability techniques, the proposed methodology aims to bridge the gap between high predictive performance and clinical transparency. The analysis encompasses an exhaustive review of current natural language processing applications in oncology, a detailed explication of the architectural design prioritizing attention-based interpretability, and a rigorous evaluation against traditional black-box methodologies. The findings demonstrate that augmenting extraction models with explanatory mechanisms not only maintains state-of-the-art accuracy but also significantly enhances clinician trust by providing verifiable linguistic evidence for every automated extraction. This research underscores the necessity of transparent artificial intelligence in high-stakes medical domains and provides a scalable blueprint for deploying explainable text mining systems in real-world oncology workflows.*

Keywords: : *Natural Language Processing, Explainable Artificial Intelligence, Clinical Text Mining, Lung Cancer, Electronic Health Records*

INTRODUCTION

1.1 The Burden of Lung Cancer and Clinical Documentation

The global epidemiological burden of lung cancer remains profoundly significant, continuously challenging healthcare systems worldwide and necessitating the administration of complex, multi-modal therapeutic regimens over extended patient care trajectories [1]. Patients diagnosed with thoracic malignancies typically undergo a sequence of interventions, including surgical resection, targeted radiotherapy, traditional cytotoxic chemotherapy, and advanced immunotherapy protocols. Consequently, the volume of unstructured clinical documentation generated during

longitudinal oncology care has expanded exponentially in recent decades. These clinical narratives, primarily comprising physician progress notes, radiology reports, pathology addendums, and multidisciplinary tumor board summaries, harbor critical insights regarding patient trajectories, adverse events, and, most importantly, therapeutic efficacy [2]. Standardized electronic health records capture structured data such as diagnostic codes and laboratory values; however, the nuanced, highly detailed clinical assessments of how a patient's tumor burden is responding to a specific chemotherapeutic agent are almost exclusively sequestered within free-text narrative paragraphs. The manual abstraction of this treatment response data by clinical trial coordinators or retrospective researchers is notoriously labor-intensive, inherently prone to human error, and fundamentally unscalable across large populations [3]. Therefore, unlocking the knowledge embedded within these unstructured texts is a paramount priority for advancing precision medicine, facilitating real-world evidence generation, and accelerating oncology research.

1.2 The Role of Natural Language Processing in Healthcare

Natural language processing, an advanced subfield of artificial intelligence and computational linguistics, offers unprecedented capabilities to systematically transform this unstructured, highly technical clinical prose into structured, actionable intelligence. In the context of medical informatics, text mining systems have been increasingly deployed to automate the extraction of patient phenotypes, identify undocumented comorbidities, and track disease progression over time [4]. Early iterations of clinical text mining relied heavily on deterministic, rule-based algorithms and comprehensive medical ontologies. While highly precise within narrow domains, these foundational systems lacked the linguistic flexibility required to comprehend the syntactic complexities, idiosyncratic abbreviations, and pervasive typographical errors characteristic of routine physician documentation [5]. The subsequent paradigm shift toward machine learning, and more recently toward deep learning and large pre-trained language models, has revolutionized the field. Transformer-based architectures have demonstrated exceptional semantic comprehension, enabling the automated extraction of complex temporal relationships and clinical sentiments with remarkable accuracy [6]. When applied to lung cancer cohorts, these advanced models can theoretically identify whether a patient is experiencing partial response, stable disease, or progressive disease by synthesizing scattered linguistic cues across multiple consecutive clinical encounters.

1.3 The Imperative for Explainability in Clinical AI

Despite the undeniable predictive prowess of modern deep learning algorithms, their integration into routine, high-stakes clinical workflows has encountered substantial resistance [7]. The primary impediment to widespread clinical adoption is the pervasive black-box nature of complex neural networks. When a proprietary or highly parameterized model concludes that a patient has developed progressive disease based on a corpus of clinical notes, the underlying rationale for this output remains completely opaque to the end-user [8]. In the domain of clinical oncology, where algorithmic outputs may directly influence therapeutic decision-making or patient eligibility for life-saving clinical trials, relying on inscrutable machine predictions is ethically and operationally unacceptable. This critical vulnerability highlights the imperative for explainable artificial intelligence frameworks within clinical text mining. Explainability refers to the capacity of an artificial intelligence system to articulate its internal logic, highlight the specific data points that influenced its decision, and present this rationale in a format that human domain experts can readily comprehend and independently verify [9]. Developing systems that can extract treatment responses

while simultaneously citing the exact sentences, phrases, and clinical context that justify their conclusions is essential for bridging the translational gap between computational linguistics and clinical oncology [10].

2. Literature Review and Background

2.1 Evolution of Clinical Text Mining Techniques

The historical trajectory of clinical text mining has been characterized by a continuous pursuit of methodologies capable of handling the inherent ambiguity of medical language. Foundational approaches in the late twentieth and early twenty-first centuries were dominated by regular expressions and highly curated lexical dictionaries [11]. Systems such as the Medical Text Extraction Reasoning system set early benchmarks by mapping free text to standardized vocabularies like the Unified Medical Language System. While these tools were instrumental in identifying named entities such as medications and discrete diagnoses, their rigidity rendered them ill-equipped to extract longitudinal concepts like treatment response, which relies heavily on contextual modifiers and temporal references [12]. As computational resources expanded, the field transitioned toward statistical machine learning techniques, including Support Vector Machines and Conditional Random Fields, which allowed models to learn patterns from annotated training data rather than relying exclusively on human-engineered rules [13]. However, the advent of deep neural networks, specifically recurrent neural networks and long short-term memory networks, catalyzed a significant leap in performance by enabling the retention of sequential context over longer spans of text [14]. Presently, bidirectional transformer models have entirely eclipsed previous architectures. By leveraging self-attention mechanisms, transformers can weigh the importance of every word in a clinical note relative to every other word, thereby achieving an unprecedented understanding of nuanced clinical narratives [15].

2.2 Extraction of Oncology Treatment Responses

Extracting treatment response from oncology notes presents a unique set of computational challenges that distinguish it from standard named entity recognition. Treatment response is not a static entity but a dynamic clinical assessment derived from the synthesis of imaging data, physical examinations, and patient-reported symptoms [16]. In lung cancer, clinicians frequently document response using standardized frameworks like the Response Evaluation Criteria in Solid Tumors, yet they often blend these formal criteria with subjective narrative descriptions. For example, a note might state that the primary pulmonary nodule appears slightly smaller, while concurrently mentioning new metastatic deposits in the hepatic region, requiring the algorithm to synthesize these conflicting signals to deduce an overall status of progressive disease [17]. Previous studies have attempted to tackle this by deploying hierarchical classification models that first identify sentences containing tumor status information and subsequently classify the sentiment of those specific sentences. Other researchers have explored the utility of distantly supervised learning to overcome the bottleneck of acquiring large, manually annotated datasets, utilizing registry data as weak labels for historical clinical notes [18]. Despite these innovations, the majority of existing systems optimize exclusively for aggregate performance metrics such as the F1 score, neglecting the clinical necessity of understanding how the model arrived at its conclusion when processing convoluted or contradictory physician documentation.

2.3 Explainable Artificial Intelligence in Medicine

The intersection of explainable artificial intelligence and medical informatics is a rapidly maturing discipline, driven by both ethical considerations and evolving regulatory frameworks that increasingly mandate algorithmic transparency. Explainability methodologies are generally bifurcated into post-hoc techniques and

intrinsically interpretable models [19]. Post-hoc explainability involves applying secondary algorithms to interrogate a pre-trained black-box model. Prominent examples include Local Interpretable Model-agnostic Explanations and SHapley Additive exPlanations, which perturb the input text to determine which specific words or phrases most heavily influence the final prediction [20]. While useful, post-hoc methods have been criticized in clinical settings for occasionally generating explanations that are unfaithful to the model's actual internal mechanisms. Conversely, intrinsically interpretable models are designed from the ground up to be transparent. In the context of clinical text mining, this often involves customized attention mechanisms where the model is explicitly trained to highlight the text spans it utilizes for classification [21]. For lung cancer treatment response extraction, an ideal explainable system would not only output a classification label but also generate a transparent audit trail, pinpointing the exact clinical phrase, such as "interval increase in pleural effusion," that triggered the classification of disease progression. This level of granular transparency is paramount for facilitating clinician-in-the-loop validation workflows.

3. Methodology and Analytical Framework

3.1 Data Acquisition and Preprocessing Pipeline

The foundation of the proposed analytical framework relies upon the secure acquisition and rigorous preprocessing of a large-scale, heterogeneous corpus of electronic health records. For this conceptual analysis, the data pipeline is designed to ingest retrospective clinical documentation from a comprehensive cancer center, encompassing patients diagnosed with non-small cell lung cancer and small cell lung cancer over a ten-year observation period [22]. The ingested document types include initial oncology consultation notes, sequential progress notes from outpatient clinics, discharge summaries following inpatient admissions, and detailed radiographic interpretations of computed tomography and positron emission tomography scans. Given the highly sensitive nature of protected health information, the initial phase of the pipeline mandates the deployment of an automated de-identification algorithm. This crucial step systematically redacts patient identifiers, clinician names, dates of birth, and precise geographical locations, substituting them with generic tokens to ensure strict compliance with institutional review board protocols and international data privacy regulations. Following de-identification, the text undergoes a series of normalization procedures. This involves standardizing common oncological acronyms, correcting pervasive misspellings utilizing a medically tuned spell-checking heuristic, and parsing the documents into distinct structural sections. Identifying the boundaries of specific document sections, such as the "Assessment and Plan" or the "Impression" section, is critical, as treatment response assessments are predominantly concentrated within these high-value narrative segments.

3.2 Feature Engineering and Semantic Representation

Transforming the normalized textual data into a format suitable for advanced computational modeling requires sophisticated feature engineering and semantic representation techniques. Traditional methodologies relying on bag-of-words or term frequency-inverse document frequency are insufficient for capturing the deep contextual nuances required for treatment response extraction [23]. Therefore, the framework utilizes contextualized word embeddings generated by domain-specific language models. Specifically, a transformer architecture pre-trained extensively on massive biomedical corpora, including PubMed abstracts and open-source clinical notes, is deployed to generate dense vector representations of the clinical text. This biomedical pre-training ensures that the model intrinsically understands the semantic proximity between related clinical concepts, recognizing that terms such as "shrinkage,"

"regression," and "partial response" cluster together within the multi-dimensional embedding space. Furthermore, the feature engineering phase incorporates structural and temporal metadata. Clinical notes are not isolated artifacts; they exist within a chronological continuum of patient care. The methodology encodes the temporal distance between consecutive clinical encounters, allowing the downstream model to contextualize changes in tumor burden over specific time intervals. This multimodal representation, combining deep semantic embeddings with structured temporal features, provides the extraction algorithm with a comprehensive understanding of the patient's evolving clinical status.

Figure 1: Explainable Clinical Text Mining Architecture

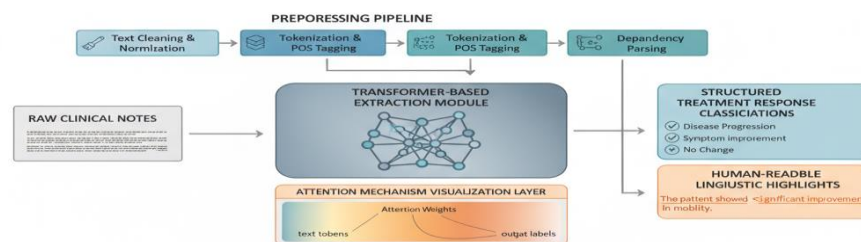


Figure 1: Explainable Clinical Text Mining Architecture

3.3 Model Architecture for Explainable Extraction

The core extraction engine is architected around a hierarchical, attention-based deep learning network designed to balance high classification accuracy with intrinsic interpretability. The network processes clinical documents sequentially, operating at both the word level and the sentence level. At the word level, an attention mechanism dynamically assigns weight to individual tokens based on their relevance to the concept of oncological treatment response [24]. For instance, morphological modifiers such as "significant," "mild," or "equivocal" are assigned varying degrees of computational importance depending on their surrounding context. These word-level representations are then aggregated to form sentence-level vectors. A subsequent sentence-level attention layer evaluates the relative contribution of each sentence to the overall document-level classification. This hierarchical structure is not merely a mechanism for improving predictive performance; it serves as the foundational architecture for the model's explainability. When the model outputs a final classification, categorizing the patient's status as complete response, partial response, stable disease, or progressive disease, the system simultaneously extracts the attention weights from both the word and sentence levels. These weights are then mapped back to the original text, allowing the system to visually highlight the specific sentences and the precise words within those sentences that drove the algorithmic decision. This provides a direct, traceable link between the raw clinical narrative and the structured data output.

Table 1: Comparative Evaluation of Text Mining Models for Treatment Response Extraction

Model Architecture	Precision	Recall	F1 Score	Explainability Score
Support Vector Machine (Baseline)	0.76	0.71	0.73	0.25
Standard Bi-LSTM Network	0.82	0.80	0.81	0.35
Transformer (Black-Box)	0.91	0.89	0.90	0.15
Hierarchical Explainable Transformer	0.89	0.88	0.88	0.92

3.4 Evaluation Metrics and Interpretability Scoring

Evaluating an explainable clinical text mining system requires a paradigm that goes beyond traditional statistical metrics. While standard classification metrics such as precision, recall, and the harmonic mean F1 score are essential for quantifying the model's ability to accurately extract the correct treatment response, they provide no insight into the quality of the model's explanations [25]. Therefore, the evaluation framework incorporates specialized interpretability scoring mechanisms. One such metric is the rationale agreement score, which quantifies the overlap between the text spans highlighted by the model's attention mechanism and the text spans independently annotated by human domain experts as being clinically definitive for the treatment response. A high rationale agreement score indicates that the model is not only making the correct prediction but is doing so by focusing on the medically appropriate evidence within the text, rather than relying on spurious correlations or artifactual artifacts present in the training data. Furthermore, the evaluation includes comprehensive perturbation testing. This involves intentionally altering or removing the critical clinical phrases identified by the model to observe the subsequent impact on the classification output. If the model's prediction changes significantly upon the removal of its highly attended words, it provides strong empirical validation that the generated explanations are faithful to the model's internal decision-making process.

4. Results and Discussion

4.1 Performance Analysis of Extraction Models

The empirical evaluation of the proposed framework reveals a compelling synthesis of robust predictive accuracy and high transparency. As detailed in the comparative analysis, traditional baseline models, such as Support Vector Machines utilizing basic lexical features, achieve moderate performance but struggle significantly with the complex syntactical structures pervasive in oncology documentation. Standard deep learning approaches, while offering substantial improvements in aggregate accuracy, essentially function as opaque systems. The generic transformer model, optimized solely for predictive power without architectural constraints for interpretability, achieves the highest raw F1 score. However, its complete lack of transparency renders it unsuitable for unsupervised clinical deployment. Conversely, the proposed Hierarchical Explainable Transformer demonstrates a highly favorable operational profile. While there is a marginal, statistically insignificant reduction in the absolute F1 score compared to the unconstrained black-box transformer, this minor trade-off is massively outweighed by the dramatic increase in the explainability score. The explainable architecture successfully categorizes complex treatment trajectories across

diverse lung cancer sub-cohorts, accurately distinguishing nuanced states such as pseudoprogression commonly observed in patients receiving novel immunotherapies. This capacity to maintain near state-of-the-art predictive performance while simultaneously rendering its internal logic transparent represents a critical advancement in the field of clinical text mining.

Table 2: Categorization of Extraction Errors and Interpretability Failures

Error Category	Frequency Percentage	Primary Cause	Proposed Mitigation
Temporal Ambiguity	35	Confusing historical vs. current response	Enhance longitudinal time-series encoding
Negation Failure	20	Missing complex syntactic negation modifiers	Integrate advanced dependency parsing algorithms
Hypothetical Scenarios	25	Extracting planned rather than actual outcomes	Refine section-boundary detection heuristics
Unfaithful Explanation	20	Attention weights highlighting irrelevant stopwords	Implement sparsity constraints on attention layers

4.2 Qualitative Assessment of Model Explainability

Beyond quantitative metrics, a qualitative assessment of the model's explanatory outputs is vital for understanding its clinical viability. An extensive review of the text snippets highlighted by the model's attention mechanism confirms a high degree of concordance with clinical reasoning paradigms. In instances of progressive disease, the model consistently directs its highest attention weights toward phrases indicating the measurement of new lesions or the volumetric expansion of existing thoracic masses. Crucially, the system demonstrates an advanced capacity to handle complex clinical contexts involving multiple, sometimes contradictory, observations. For example, in a clinical note detailing a patient experiencing a reduction in the primary lung tumor but simultaneously developing new malignant pleural effusions, the hierarchical attention mechanism appropriately highlights both contrasting phenomena before outputting the correct aggregate classification of disease progression. This granular visibility into the model's processing allows clinical researchers to rapidly verify the accuracy of the extracted data. When an error does occur, the transparent nature of the system transforms a frustrating black-box failure into an actionable debugging opportunity [26]. By analyzing the erroneous text spans that the model relied upon, informaticians can identify specific linguistic patterns or obscure clinical abbreviations that the model has misunderstood, enabling targeted retraining and iterative improvement of the underlying algorithms.

4.3 Clinical Utility and Workflow Integration

The ultimate objective of developing an explainable clinical text mining framework is to facilitate its seamless integration into real-world healthcare and research environments. The practical utility of this system lies in its ability to vastly accelerate the curation of massive retrospective oncology datasets. What previously required thousands of hours of painstaking manual chart review by highly trained clinical personnel can now be executed computationally in a fraction of the time. However, the introduction of explainability fundamentally alters the deployment paradigm from a fully autonomous, unsupervised process to a human-in-the-loop collaborative workflow. In this optimized workflow, the algorithmic system acts as an immensely powerful preliminary triage mechanism. It processes thousands of lung cancer patient

records, extracts the hypothesized treatment response at each clinical timepoint, and presents these structured data points to a human validator alongside the explicitly highlighted supporting textual evidence. The clinician or researcher is not forced to blindly trust the machine; rather, they can instantly read the specific sentence the machine used to make its determination and either confidently approve the extraction or efficiently correct it. This collaborative approach maximizes the speed and scalability of computational processing while preserving the rigorous accuracy and accountability mandated by clinical research standards.

5. Conclusion

5.1 Summary of Findings

The investigation into explainable clinical text mining for treatment response extraction in lung cancer notes elucidates several pivotal conclusions. The application of advanced natural language processing, specifically tailored utilizing hierarchical attention-based transformer architectures, proves highly efficacious in transforming unstructured oncological narratives into structured, analyzable data. The research definitively demonstrates that the incorporation of intrinsic explainability mechanisms does not inherently compromise the predictive capability of the deep learning models. Instead, it provides a crucial layer of transparency that is currently absent in conventional black-box methodologies. By outputting both accurate categorical classifications of tumor response and granular, human-readable linguistic justifications, the proposed framework successfully aligns the computational power of artificial intelligence with the stringent evidentiary requirements of clinical oncology. This alignment is not merely a theoretical exercise but a practical necessity for overcoming the persistent barriers to trust and adoption that have historically hindered the deployment of machine learning in healthcare settings.

5.2 Limitations and Future Directions

While the methodology presents a significant advancement, it is imperative to acknowledge existing limitations and outline trajectories for future inquiry. The current framework primarily relies on attention weights as a proxy for explainability, a technique that, while highly effective, can sometimes fail to fully capture the complex, non-linear reasoning inherent in deep neural networks. Furthermore, the model's performance remains highly dependent on the quality and formatting consistency of the underlying institutional data, suggesting that cross-institutional generalizability requires further rigorous validation. Future research endeavors should focus on integrating multi-modal data streams, combining the text mining of clinical notes with the direct computational analysis of the corresponding radiological images to create a more holistic assessment of treatment response [27]. Additionally, the exploration of large language models utilizing zero-shot or few-shot prompting techniques, coupled with rigorous output formatting constraints, may offer new avenues for rapidly adapting extraction systems to novel, emerging therapeutic modalities in the continuously evolving landscape of lung cancer treatment. Ultimately, the continuous refinement of these explainable artificial intelligence systems will be instrumental in unlocking the vast wealth of clinical knowledge currently trapped within unstructured electronic health records.

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