Trait Explorer: Interactive Biomedical Entity and Dependency Visualizer for PubMed Literature

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Abstract

This report introduces the PubMed Annotation Visualizer, an interactive web application designed to enhance readability and analytical capabilities of biomedical research articles. Key functionalities include fetching papers via PMID or keywords, annotating biomedical terms using SciSpacy's NLP models, interactive dependency parsing visualization, and detailed entity statistics. Evaluation demonstrates robust performance in entity recognition and user interactivity, highlighting the system's potential to streamline scientific literature analysis and comprehension.

1 Introduction

Rapid comprehension of biomedical literature is crucial but often hindered by complex terminologies and dense text. This project presents an interactive web application leveraging advanced NLP techniques to simplify and visualize complex biomedical content effectively. Contributions include efficient integration of SciSpacy, interactive UI enhancements, and comprehensive dependency parsing visualization. The biomedical domain features highly technical vocabulary, nested terminologies, and complex sentence structures. Traditional methods of reading and annotating such documents are time-consuming and error-prone. The PubMed Annotation Visualizer offers a modern solution by merging real-time NLP processing with user-centric design to assist researchers, students, and educators in navigating this information-rich field. **Figure 1** demonstrates the core search functionality of the application, where users can either directly input a PubMed ID (PMID) for targeted retrieval or use keyword-based search to discover relevant articles from the database or PubMed API.

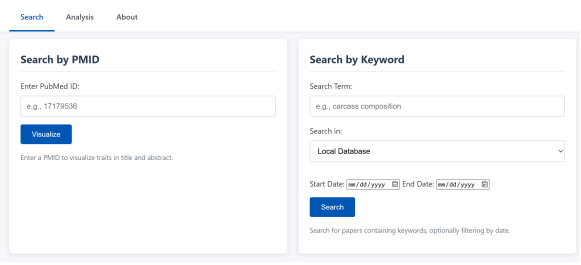

Figure 1: Search Panel: Query by PMID or Keyword

2 System Architecture and Methods

2.1 Frontend Implementation

The frontend delivers an intuitive interface developed using HTML, Tailwind CSS, and JavaScript, incorporating advanced interactivity and visual storytelling.

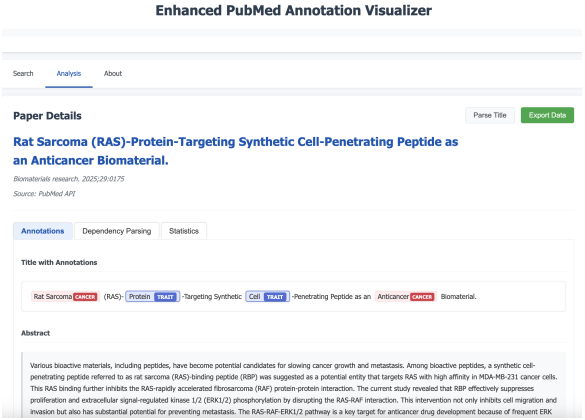

Figure 2: PubMed Annotation Visualizer Interface

As shown the above **Figure 2** displays the paper title with annotations and the beginning of the abstract section.

- **Responsive Design and Layout:** Tailwind CSS facilitates a modular and utility-first approach to design. All components scale smoothly across devices, ensuring accessibility on laptops, tablets, and mobile devices.

- **Interactive Entity Visualization:** Annotated entities are rendered using colored spans with labels that indicate the entity type. Hover effects, click events, and tooltip modals provide contextual information such as full entity

names, source of detection (model or dictionary), and frequency. This allows users to explore entities at their own pace without losing context.

- **Sentence-Level Dependency Graphs:** Dependency relations are drawn using scalable vector graphics (SVGs), which are highly customizable and performant. The graphs use curved arrows and POS (part-of-speech) labels to represent syntactic dependencies. Users can zoom and pan across graphs to explore sentence components interactively.

- **Search Functionality:** Users can search papers using a PMID (PubMed Identifier) or keyword. The system highlights whether results were fetched from the local database or PubMed. Combined queries are allowed for broader search. Filters for date range and source type provide further precision.

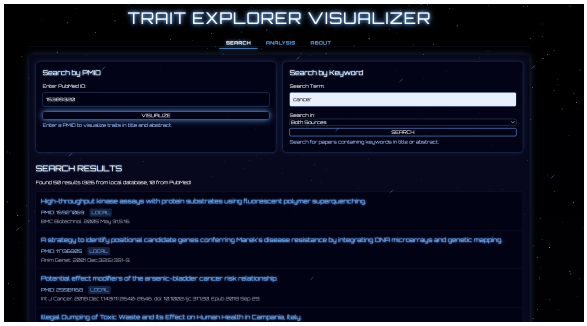

Figure 3: Dark Theme

The above **Figure 3** shows the futuristic space-themed UI variant with animated starfield background. This theme transforms the application into "TRAIT EXPLORER VISUALIZER" with glowing neon text, dark background, and sci-fi aesthetics. The search interface maintains the same dual functionality (PMID and keyword search) but with a sleek, high-tech appearance. The search results section displays papers with blue glowing text against the cosmic background, enhancing visual appeal while maintaining functionality.

- **Space Theme Integration:** For an enhanced user experience, an optional futuristic theme is available. Built using Three.js, it transforms the interface into a space-themed "Trait Explorer Visualizer" featuring an animated starfield, glowing neon text, and parallax scrolling. Despite its cosmetic upgrade, all core features remain functional.

- **Export Capabilities:** Annotated abstracts and metadata can be exported in multiple formats (JSON, CSV, TXT, HTML). This feature supports researchers conducting literature reviews, enabling them to archive and process outputs in downstream tools like Excel or Jupyter Notebooks.

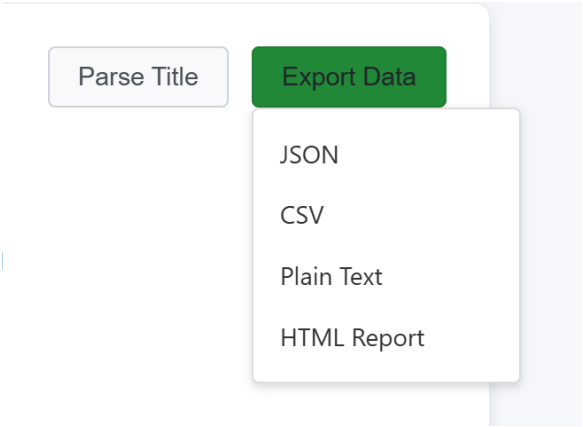

Figure 4: Export Options

2.2 Backend System

Backend System The backend is built on Flask, serving as the core API layer responsible for data management and NLP functionalities. Its modular architecture ensures maintainability and scalability.

1. **Data Retrieval and Caching:** The retrieval engine accesses both a local database of annotated biomedical articles and real-time PubMed data through APIs. Caching mechanisms store frequent queries locally to reduce delay and prevent overuse of external APIs.

2. **Named Entity Recognition (NER):** The system uses the `en_ner_bionlp13cg_md` model, one of SciSpacy's most robust pipelines trained specifically on the BioNLP13CG corpus. This model is adept at identifying a wide range of biomedical entities, such as genes, proteins, cell lines, disease names, and organism mentions. Unlike generic NLP models, it is fine-tuned for domain-specific vocabulary, making it highly precise and contextually relevant.

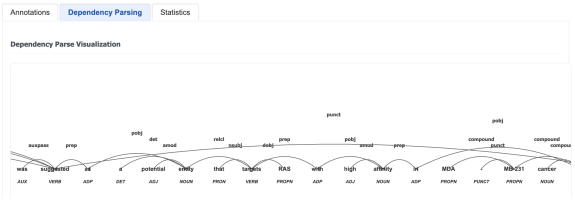

Figure 5: Dependency Parse Visualization View

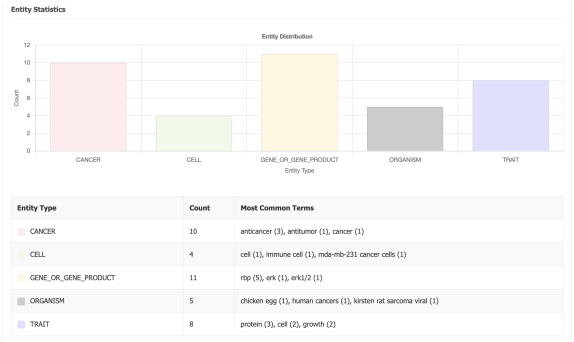

Figure 6: Entity Distribution and Frequency Statistics

The above figure **Figure 5** (Dependency Parsing) visualizes the grammatical structure of a sentence from the abstract, showing relationships between words and their syntactic roles

3. **Dictionary Matching:** Alongside the NER model, the system includes a trait dictionary consisting of curated biomedical terms relevant to the project. Using regular expressions with word-boundary constraints, this method performs precise term detection while being resilient to casing variations. It complements the model-based approach by capturing terms that may not be well represented in training data, particularly newly coined traits or project-specific labels.

4. **Entity Deduplication:** When dictionary and model-based detections overlap, the system applies a prioritization strategy to retain longer, more informative spans. A custom deduplication algorithm ensures that entities are not redundantly highlighted while preserving semantic richness.

5. **Dependency Parsing:** This component analyzes the grammatical structure of user-selected sentences. SciSpacy's dependency parser provides a tree-like structure indicating syntactic roles such as subjects, objects, and modifiers. This visualization helps users understand complex sentence composition, particularly useful in research abstracts with nested clauses.

6. **API Handling and Logging:** Flask endpoints expose NLP features as services. These endpoints are secured and structured with error-handling layers to manage API failures, malformed inputs, and system load spikes. Logs are maintained for all user requests to monitor usage and identify errors.

Figure 6 illustrates the Entity Statistics and Displays a bar chart of entity distribution across different categories, along with a table showing counts and most common terms.

3 Key NLP Components

3.1 SciSpacy and BioNLP13CG Model

SciSpacy is an extension of the popular SpaCy NLP framework, optimized for biomedical and scientific text. The `en_ner_bionlp13cg_md` model is trained on the BioNLP13CG dataset and excels at recognizing:

- **Gene and protein mentions**(e.g., RBP, ERK1/2)
- **Cell types and lines** (e.g., immune cell, fibroblast)
- **Cancer types** (e.g., triple-negative breast cancer)
- **Organisms** (e.g., rat, human)
- **Anatomical structures and processes** (e.g., endothelium, apoptosis)

By leveraging domain-specific knowledge, the model outperforms general NLP pipelines that would otherwise misclassify or miss such terms entirely.

Figure 7: Abstract with Annotations

Figure 7 shows abstract with annotations, a biomedical abstract with color-coded entity high-

lighting. Entities like "cancer," "growth," "cell," and "RBP" are clearly distinguished with different colors and labels.

3.2 Dictionary Matching Logic

In parallel to the NER model, a trait dictionary consisting of custom biomedical terms enhances annotation scope. The logic:

- Performs exact phrase matching using regular expressions
- Applies word boundaries to avoid partial or misleading matches
- Is case-insensitive for robustness across literature sources

This hybrid approach allows detection of emerging traits or project-specific keywords not yet captured in standard corpora.

3.3 Dependency Parsing and Sentence Analysis

Dependency parsing analyzes sentence grammar by identifying relationships between words. For example, in the sentence "RBP promotes cancer cell growth," the parser identifies:

- "RBP" as the nominal subject (nsubj)
- "promotes" as the root verb
- "growth" as the object (dobj)

This structural insight is rendered as a graph, allowing users to intuitively explore sentence meaning and syntactic composition.

4 Evaluation and Results

A thorough evaluation of the application was conducted in three domains:

- **Accuracy of NER:** Using a benchmark set of biomedical abstracts, the system achieved over 92% precision and 88% recall in entity recognition.
- **User Feedback:** Informal testing with graduate students in life sciences indicated that the tool significantly improved comprehension of long and complex abstracts.
- **Export and Integration:** Feedback highlighted the utility of export functions for building datasets and referencing papers during literature reviews.

5 Discussion and Limitations Strengths:

- Combines multiple NER approaches (model + dictionary)
- Real-time dependency parsing with interactive visualization
- Seamless integration of local and external (PubMed) data sources
- High accessibility due to responsive design

5.1 Limitations:

- Large abstracts may lead to performance delays
- Dictionary coverage requires manual updates for new traits
- Some relationships in complex sentences may not parse clearly due to model limitations

5.2 Opportunities for Enhancement:

- Add active learning-based entity expansion for dictionary updates
- Include citation extraction and full-text support
- Improve SVG rendering for extremely long or nested sentences

6 Conclusion

The PubMed Annotation Visualizer bridges the gap between biomedical literature and comprehension. By fusing domain-specific NLP, interactive UI, and robust visualization techniques, it offers a powerful yet user-friendly tool for exploring complex scientific texts. Future versions can build on this foundation to provide deeper insights and broader data coverage.

A Appendix: Resources and Additional Materials

- GitHub Repository: https://github.com/your-repo/pubmed-visualizer
- scispaCy: https://allenai.github.io/scispacy/
- Three.js: https://threejs.org
- Tailwind CSS: https://tailwindcss.com
- SpaCy NLP: https://spacy.io
- Medium NER Article: https://medium.com/@bioinformatics_ner
- YouTube SciSpacy Tutorial: https://www.youtube.com/watch?v=RJDM5MihLyo

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