

Building a Unified Knowledge Graph for Nutrition with Mental Health Using Cross-Ontology Semantics

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Abstract—Biomedical knowledge integration across nutrition, mental health, and general health domains remains fragmented due to information silos in disparate ontologies. This paper presents a methodology for constructing a unified knowledge graph through cross-ontology semantic matching using BioBERT embeddings. The approach integrates concepts from multiple ontologies. The methodology employs enhanced Named Entity Recognition with BioBERT fine-tuned on BioCreative V Chemical-Disease Relation (BC5CDR) corpus, followed by entity normalization through hybrid matching combining exact string matching and semantic similarity calculation. Relation extraction utilizes dependency tree patterns validated by BioBERT-based classification models. The constructed knowledge graph comprises 666,343 unique concepts, establishing semantic bridge links between equivalent concepts across different ontologies. Experimental evaluation achieved F1-score of 0.94 for Named Entity Recognition with precision and recall values of 0.97 and 0.91 respectively. The framework supports eight relationship types enabling representation of complex biomedical interactions. The unified knowledge graph facilitates cross-domain knowledge exploration with potential applications in nutritional psychiatry research and clinical decision support systems.

Keywords—BioBERT, biomedical, cross-ontology integration, knowledge graph, semantic matching.

I. INTRODUCTION

Nutrition significantly influences mental health, as multiple research indicate that dietary choices and specific nutrient consumption might impact emotions and the likelihood of psychiatric problems. Therefore, a comprehensive framework is essential to fully comprehend this relationship [1, 2]. Nonetheless, biomedical understanding of the connection between nutrition and mental health remains disjointed across multiple ontologies,

a condition that directly hinders cross-domain data integration and comprehensive analysis [3].

The Knowledge Graph (KG) is a versatile knowledge representation framework that integrates diverse heterogeneous information sources, rendering it more adaptable than traditional rigid ontologies. This graph structure enables the mapping of multidirectional influences among nutrition, biochemistry, and mental health, which is essential in the biomedical domain [2]. While KG has advanced in specific biomedical domains, cross-ontology integration remains constrained, as current methodologies typically normalize entities to a singular ontology without accounting for the semantic equivalence of concepts, thus obstructing the identification of implicit relationships and the creation of cohesive knowledge representations [4].

The solutions offered by leading research in the field of nutrition and mental health focus on the development of a KG capable of integrating heterogeneous data from various sources to map the relationships between food, biochemistry, gut microbiota, and mental disorders [1, 5]. This approach involves the extraction of entities and relations from biomedical literature, the development of KG-based question-answering systems to enhance knowledge accessibility, and the integration of data on food, gut microbiota, and mental disorders to support knowledge-based dietary recommendations and practical applications in the field of mental health [6, 7]. Additionally, nutritional interventions are also recognized as important preventive and therapeutic strategies in mental health, making the integration of cross-disciplinary knowledge highly necessary [4]. However, all these solutions still have limitations, such as incomplete data coverage, potential data quality issues, and not fully exploring the causal relationships or in-depth mechanisms between nutrition and mental health. Therefore, further development is still needed to expand coverage, improve validation, and integrate clinical data and environmental factors to generate more comprehensive and applicable insights.

Challenges in establishing semantic connections between ontologies via cross-ontology semantic matching frequently arise from conventional entity normalization techniques that treat each ontology as distinct knowledge, without considering the underlying semantic similarity between concepts. This oversight leads to missed opportunities for cross-domain associations, such as those between nutrition in Food Ontology (FOODON) and therapeutic implications in disease ontologies. The proposed methodology uses BioBERT embeddings to comprehend and evaluate semantic similarity, therefore aligning cross-ontology concepts and constructing a more cohesive semantic framework [7]. This approach enables the integration of cross-domain knowledge and practical applications, such as nutrition recommendations for mental health and the identification of drug-nutrition interactions.

II. LITERATURE REVIEW

A. Knowledge Graph

Knowledge Graph (KG) is one of the widely used approaches to represent and manage complex knowledge in various fields, including biomedicine, due to its ability to integrate large and diverse data. However, KG also has limitations, such as incomplete coverage, data quality issues, and has not yet specifically explored the deep relationships

between certain domains, such as nutrition and mental health [8].

B. BioBERT

In recent years, Transformer-based language representation models like Bidirectional Encoder Representations from Transformers (BERT) have driven significant advancements in biomedical text mining, but general models often perform sub-optimally on biomedical texts due to differences in word distribution and domain-specific terminology. In response to this challenge, researchers developed BioBERT by pre-training it on large biomedical corpora such as PubMed to enhance its suitability for biomedical tasks. BioBERT has been used for extracting relationships between biomedical entities, drug interaction extraction, and processing breast cancer pathology reports. In various studies, BioBERT shows superior performance compared to general BERT and traditional methods in biomedical natural language processing tasks such as named entity recognition, relation extraction, and question answering. For example, in drug interaction extraction, the BioBERT model with an attention mechanism achieved high F-scores on the benchmark corpus [7]. Pathology reports on breast cancer, BioBERT also shows higher accuracy compared to conventional methods.

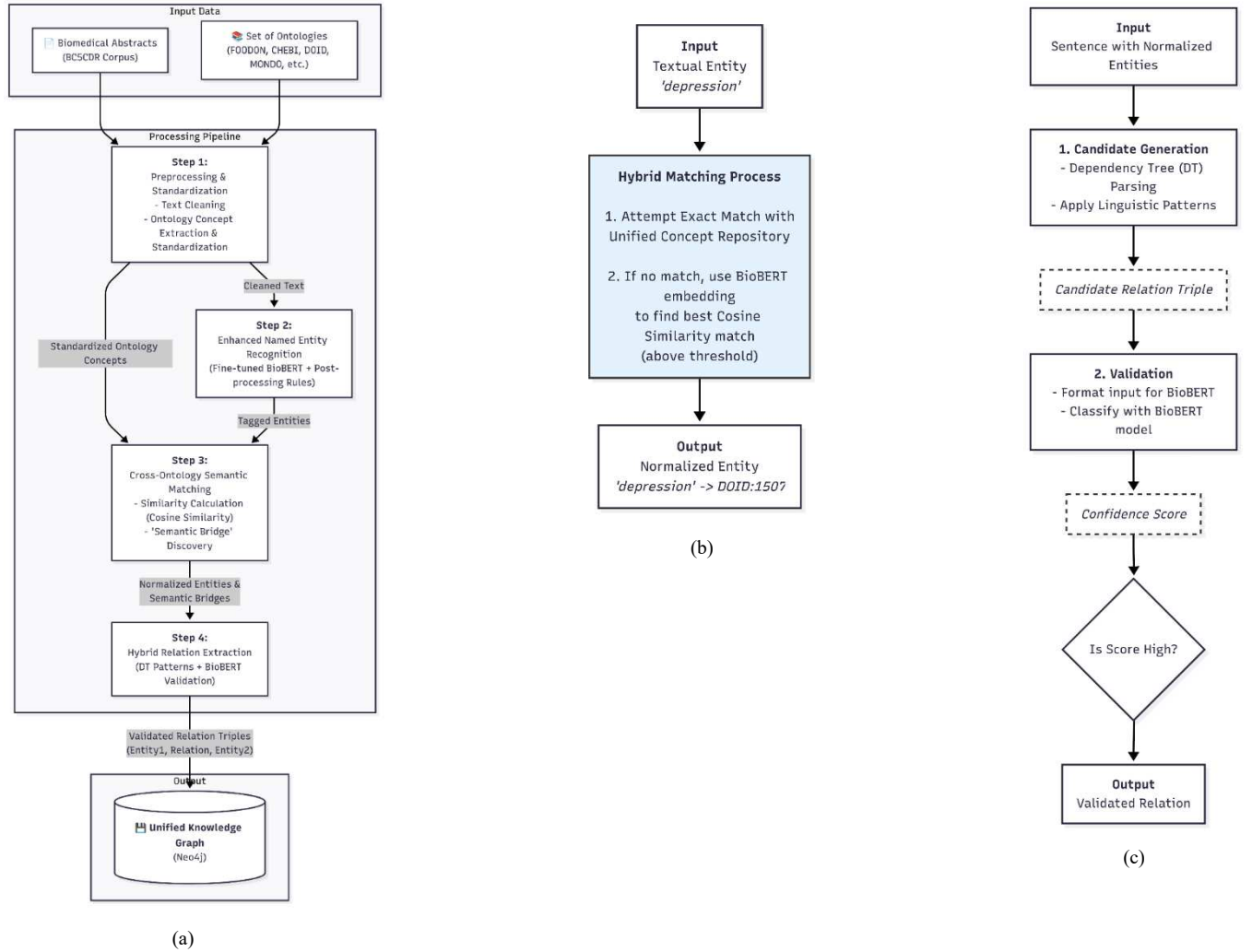


Fig. 1. System Architecture and Workflow. This image summarizes the three main phases of the proposed system: (a) Framework of Proposed Method, (b) Normalized Entity, and (c) Hybrid Relation Extraction

C. Named Entity Recognition (NER)

Named Entity Recognition (NER) is the task of identifying and classifying named entities into predefined categories, such as disease names, chemical compounds, genes, or foods. In the biomedical context, the accuracy of NER is of paramount importance [9]. Early approaches relied on lexicons and linguistic regulations, but these were deficient in their ability to process variations in terminology and the emergence of novel entities. The advent of language models founded on the Transformer architecture, most notably BERT, has precipitated a paradigm shift in the domain of NER, a field that has benefited from the models profound contextual understanding [10]. For specific domains such as biomedicine, the BioBERT model was developed by pre-training on a large-scale biomedical corpus (i.e., PubMed abstracts and PMC full-text articles) [7].

D. Relation Extraction (RE)

After the entities are identified, the next step is Relation Extraction (RE), which involves finding semantic relationships between pairs of entities. Commonly used RE methods include rule-based approaches, such as syntactic patterns from Dependency Tree (DT), which offer high precision and good pattern readability but often have low recall due to dependence on specific sentence structures and a significant need for manual engineering [1, 7]. Both rule-based methods and machine learning are evaluated using standard metrics such as precision, recall, and F1-score to assess the accuracy and coverage of the results.

E. Cross ontology

Cross ontology is an approach that integrates multiple ontologies to enable cross-domain data exchange, interoperability, and analysis. In the extant literature, ontology integration is frequently examined within the paradigm of amalgamating deductive reasoning from ontologies with inductive reasoning from machine learning. This integration fosters the development of artificial intelligence systems that are characterized by enhanced

flexibility and adaptability. This approach can be categorized into several types, such as learning-enhanced ontologies, semantic data mining, and learning and reasoning systems. Each of these categories utilizes a combination of machine learning techniques and ontologies to enhance data processing and understanding [11].

III. METHODOLOGY

This session delineates a research approach for constructing a KG that integrates the domains of nutrition, mental health, and general health through cross-ontology semantic matching to align concepts, with each study phase elucidated for clarity and replicability.

A. Framework

The suggested methodology is a systematic approach that purifies and standardizes biomedical texts and ontologies, employing BioBERT for entity recognition and semantic mapping, utilizing hybrid approaches for relationship extraction, and constructing an integrated knowledge graph in Neo4j. The entire workflow of this is in Fig. 1a.

TABLE I. Ontology Dataset

Ontology Name	Abbreviation	Number of Concepts (Classes)
Food Ontology	FOODON	36,114
Chemical Entities of Biological Interes	CHEBI	173,566
Human Disease Ontology	DOID	9,451
MFO Mental Disease Ontology	MFOMD	25,679
Symptom Ontology	SYMP	1,118
Mondo Disease ontology	MONDO	215
Synonym List	THERASaurus	222,950
Foundational Model of Anatomy	FMA	104,717
Disorders Cluster	APADISORDERS	822
Autism Spectrum Disorder Phenotype Ontology	ASDPTDO	36,114

B. Data Preparation and Pre-processing

The quality of the constructed knowledge graph is greatly influenced by the source data used, so the first stage of this methodology is data preparation, which employs two main categories: an unstructured text corpus from the BC5CDR PubTator dataset consisting of 1,500 PubMed abstracts (chosen for their relevance to the health domain and the availability of established annotations) and semi-structured biomedical ontologies from various domains to expand semantic coverage, including FOODON (food), CHEBI (chemistry), DOID and MONDO (diseases), SYMP (symptoms), MFOMD (mental disorders), and THESAURUS for broader biomedical terminology. An overview of the scale of the ontology resources used is presented in TABLE I. These two types of data are processed through a parallel pre-processing pipeline: textual data is normalised (removal of non-standard characters, lowercase) and tokenised using the BioBERT tokeniser, while ontologies are extracted for concept information, labels, definitions, and synonyms to produce a unified representation that simplifies the subsequent cross-ontology semantic mapping process.

C. Enhanced Named Entity Recognition (NER)

The Named Entity Recognition (NER) stage of this study employs the BioBERT model, which has been fine-tuned on the BC5CDR corpus. The selection of this model was predicated on its demonstrated proficiency in processing biomedical text, a proficiency attributable to its pre-training on pertinent literature. To refine the identification results, a post-processing mechanism employing dependency tree-based rules was applied to correct the entity spans generated by BioBERT. The result of this stage is text with identified entities and their type labels, which is then prepared for the normalization process.

D. Cross Ontology Semantic Matching and Entity Normalization

After identifying entities with NER, entity normalization connects these entities to standard concepts from organized knowledge sources using a mixed method. The system first tries to find exact matches between the entity text and the names or synonyms of concepts in the ontology. If it can't find exact matches, it uses BioBERT embeddings to create vector representations for matching based on meaning similarity using cosine similarity. The system attempts exact string matching between entity text and concept names/synonyms across all ontology. When exact matches

fail, BioBERT embeddings generate vector representations for semantic similarity-based matching using cosine similarity [12]. Concepts with similarity scores exceeding the 0.95 threshold are designated as matches, with the process performed across combined concepts from multiple ontologies rather than single sources [1]. The 0.95 threshold was chosen based on empirical evaluation to optimally balance precision and recall minimizing false positives while ensuring that only highly similar concepts are linked. Lower thresholds introduced more noise, while higher thresholds risked missing valid matches. When entities show strong similarity to concepts from different ontologies, "semantic bridge" links are created to suggest that they might be equivalent across those ontologies [13]. The entire workflow of this in Fig. 1b.

E. Hybrid Relation Extraction

Following the normalization of the entities, the subsequent step is relation extraction, which aims to identify semantic relationships between entity pairs within a sentence. The present study employs a hybrid approach that integrates linguistic patterns with neural validation models. The process commences with DT analysis to comprehend the grammatical structure of the sentence. This analysis is subsequently employed by a series of linguistic patterns to identify candidate relations. To validate these candidates, a BioBERT-based relation classification model is employed. Each relation candidate, along with its sentence context, is fed into the BioBERT classifier to obtain a confidence score. The acceptance of a relation is contingent upon its successful identification by the DT pattern, followed by validation with a high confidence score from the BioBERT model. The entire workflow of this in Fig. 1c.

F. Construction and Enrichment of Knowledge Graph

The final phase involves KG construction using validated relation triples as input. Neo4j graph database stores the KG, where each normalized entity becomes a node and each validated relation becomes an edge. the resulting KG structure integrates three types of information: (1) relations extracted from text, (2) existing relations from external sources, and (3) semantic equivalence links between ontologies. The performance of the relation extraction task is also evaluated using confidence score, where this evaluation is specifically designed to measure the increase in precision resulting from the addition of the BioBERT semantic filter.

IV. RESULT AND DISCUSSION

A. Evaluation of Named Entity Recognition (NER)

We evaluated the core component of our hybrid NER system, a fine-tuned BioBERT model on the official BC5CDR test set, focusing on Chemical and Disease entities. Performance was benchmarked against the widely used scispaCy baseline, with results summarized in Table II.

Our fine-tuned BioBERT model outperformed scispaCy, achieving a 0.14 higher F1-score (0.94 vs 0.80). The most significant gain was in recall, which increased from 0.77 (scispaCy) to 0.91 (BioBERT), while precision remained comparable (0.97 vs. 0.84). This substantial recall improvement is particularly valuable for knowledge graph construction, as it enables the extraction of a broader set of

TABLE II. NER Performance Comparison

Model	Precision	Recall	F1-Score
Baseline scispaCy	0.84	0.77	0.80
Proposed	0.97	0.91	0.94

relevant entities, potentially resulting in a more comprehensive knowledge network. These findings are consistent with recent studies showing BioBERT's superior F1-scores and recall over scispaCy on BC5CDR and other biomedical NER datasets.

For broader context, we also reference the GENA system, which inspired this work. However, direct numerical comparison is limited by differences in evaluation datasets: GENA was assessed on its own manually annotated data, reporting an F1-score of 0.84, precision: 0.93, recall: 0.78 [1]. Our model's F1-score of 0.94 is competitive, our precision 0.97 and recall 0.91 is notably higher, suggesting our approach is effective for comprehensive entity extraction. Nevertheless, differences in evaluation settings should be considered when interpreting these results.

B. Evaluation and Analysis of Cross-Ontology Results

The dense base graph was constructed from 666,343 unique concepts processed from 10 knowledge sources, resulting in 666,343 nodes and 5,384,554 edges, with the largest node distribution coming from THESAURUS (222,950 nodes) and CHEBI (221,729 nodes). The majority of the 5.3 million edges are RELATED_TO relations resulting from the semantic clustering process that connects concepts across different ontologies, with other types of relations including ASSOCIATED_WITH (general associative relationship), CAUSES (direct causal relationship), TREATS (therapeutic relationship), INHIBITS (inhibitory effect), STIMULATES (stimulatory effect), MODIFIES (condition change), and DIAGNOSES (connecting symptoms with medical conditions). Fig. 2 illustrates cross-ontology semantic integration through a hub-centered network structure that positions mental health concepts from the ASDPTO ontology (blue) as the central integrator connecting different biomedical domains, including chemical entities from THESAURUS (brown), diseases from MONDO (red), and medical symptoms from SYMP (light brown), with seizure and epilepsy emerging as the main hubs based on degree centrality. Edge thickness represents semantic similarity strength, indicating the robustness of conceptual relationships across traditional disciplinary boundaries. This integrated structure supports three application areas: multi-type data analysis, discovery of cross-domain therapy options for drug development and mental health nutrition, and clinical decision support through concept relationship visualization [9]. Two notable examples illustrate this integration: the nicotine-seizure association and self-referential loops in seizure disorders.

In the first example, the association "Nicotine → CAUSES → Seizures" visible in Fig. 2 is best interpreted as an indirect biochemical relationship. Nicotine inhibits CYP2A6, slowing nicotine metabolism and consequently increasing nicotine levels that may heighten seizure risk. Thus, this link reflects an indirect toxicological effect rather than a direct neuropharmacological action of nicotine itself [13]. Although nicotine itself is not classified as an

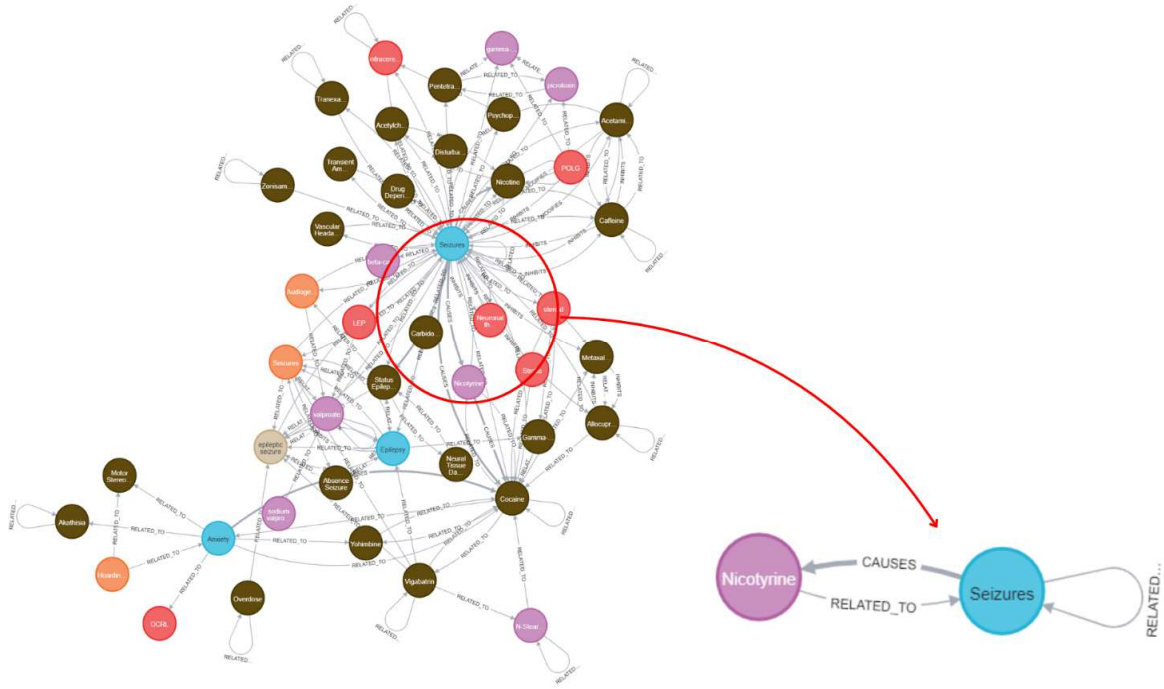


Fig. 2. Fragment of the Integrated Knowledge Graph Demonstrating Complex Cross-Domain Relationships.

addictive or neurotoxic substance, its close biochemical relationship with nicotine may indirectly influence neurological pathways related to anxiety, as reflected in the knowledge graph [14]. In the second example, the self-referencing loop $\text{Seizures} \rightarrow \text{RELATED_TO} \rightarrow \text{Seizures}$ illustrates the self-perpetuating nature of seizure disorders through kindling phenomenon and neuronal hyperexcitability, where one seizure episode lowers the threshold for subsequent seizures. These findings suggest that knowledge graphs can help identify complex relationship patterns between mental health conditions, where one condition can be both a risk factor and a consequence of another condition [16].

C. Case Study

The relationships identified in the knowledge graph between cocaine, methadone, and choreoathetosis are clinically validated and supported by literature, reflecting the model's capacity to capture real-world biomedical associations. Cocaine has been consistently reported to induce choreoathetoid movements due to its dopaminergic stimulation in the basal ganglia, while methadone, though less common, has also been associated with similar movement disorders, particularly during toxicity or withdrawal episodes. These evidence-based connections [17] confirm the accuracy of the graph's inferred relations such as INDUCE_TO , RELATED_TO , and RISK_FACTOR , thereby demonstrating its clinical relevance and potential for supporting hypothesis generation in pharmacological and neurological contexts.

D. Discussion

The proposed hybrid relation extraction (RE) component in this study identified 5,169 functional relations from the text corpus, with an average confidence score of 0.79. This result suggests that the extracted relations possess a relatively high degree of semantic validity, supported by contextual validation using BioBERT. In comparison, the

GENA model [1] reported relation extraction performance with a precision of 0.77, recall of 0.54, and F1-score of 0.63 on 43,367 relations derived from dependency tree and PASMED-based pattern extraction. While GENA emphasizes coverage and generalization through syntactic patterns, the approach in this study prioritizes semantic reliability by incorporating a BioBERT-based confidence filtering layer.

In terms of knowledge graph (KG) construction, this research integrated 666,343 concepts from multiple ontologies, with THESAURUS and CHEBI as the largest contributors. The enhancements to the GENA framework included the adoption of BioBERT for Named Entity Recognition (NER), which achieved an F1-score of 0.94, comparable to GENA's 0.84 [1]. The inclusion of broader ontology coverage (such as MONDO and THESAURUS) may contribute to a more comprehensive representation of biomedical concepts.

These methodological differences may support more robust and semantically meaningful analyses, as illustrated by the identification of "seizures" and "epilepsy" as central hub nodes, reflecting their clinical significance and interconnectedness. However, differences in evaluation metrics and system design between this approach and GENA should be considered when interpreting comparative results. Further benchmarking and application-specific validation are recommended to clarify the practical impact of these enhancements.

V. CONCLUSION

This study presents an approach for constructing a unified knowledge graph (KG) that integrates information from nutrition, mental health, and general health by aligning multiple ontologies with BioBERT embeddings. By addressing the fragmentation of biomedical information, the method enables more comprehensive data integration across previously isolated domains. Experimental evaluation demonstrated robust performance in named entity

recognition F1-score: 0.94, precision: 0.97, and recall: 0.91 and effective relation extraction, with the hybrid component identifying 5,169 functional relations at an average confidence score of 0.79. The resulting KG comprises 666,343 unique concepts and supports eight relationship types, providing a flexible foundation for representing complex biomedical interactions.

Despite these advances, several limitations remain. The evaluation was conducted on a subset of the BC5CDR corpus, and the use of a high semantic similarity threshold 0.95 may have excluded weaker but potentially relevant connections. Nevertheless, The knowledge graph developed in this study demonstrates strong potential for real-world applications, such as supporting clinical decision-making by enabling healthcare professionals to explore connections between nutritional factors and mental health, assisting researchers in uncovering novel links between nutrient deficiencies and neurological disorders, and powering health chatbots that can answer specific patient questions for example, “which nutrients are associated with reduced depressive symptoms?” or “are there interactions between certain vitamin supplements and antidepressant medications?” thus making the knowledge graph not only a tool for data integration but also a practical resource for research, healthcare services, and AI-driven applications. Future work should aim to expand coverage to additional biomedical domains, develop automated updating mechanisms, and implement advanced reasoning capabilities to further enhance the KG’s utility and adaptability. Additionally, incorporating manual evaluation or expert annotation such as sampling and reviewing extracted relations will be important for more robust and reliable assessment of knowledge graph accuracy.

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REFERENCES

- [1] L. D. Dang, U. T. P. Phan, and N. T. H. Nguyen, “GENA: A knowledge graph for nutrition and mental health,” *Journal of Biomedical Informatics*, vol. 145, no. July, p. 104460, 2023, doi: 10.1016/j.jbi.2023.104460.
- [2] R. A. H. Adan, E. M. van der Beek, J. K. Buitelaar, J. F. Cryan, J. Hebebrand, S. Higgs, H. Schellekens, and S. L. Dickson, “Nutritional psychiatry: Towards improving mental health by what you eat,” *European Neuropsychopharmacology*, vol. 29, no. 12, pp. 1321–1332, 2019, doi: 10.1016/j.euroneuro.2019.10.011.
- [3] M. C. Silva, P. Eugénio, D. Faria, and C. Pesquita, “Ontologies and Knowledge Graphs in Oncology Research,” *Cancers*, vol. 14, no. 8, pp. 1–27, 2022, doi: 10.3390/cancers14081906.
- [4] M. Grajek, K. Krupa-Kotara, A. Bialek-Dratwa, K. Sobczyk, M. Grot, O. Kowalski, and W. Staśkiewicz, “Nutrition and mental health: A review of current knowledge about the impact of diet on mental health,” *Frontiers in Nutrition*, vol. 9, no. August, 2022, doi: 10.3389/fnut.2022.943998.
- [5] C. Fu, Z. Huang, F. van Harmelen, T. He, and X. Jiang, “Food4healthKG: Knowledge graphs for food recommendations based on gut microbiota and mental health,” *Artificial Intelligence in Medicine*, vol. 145, no. August 2022, p. 102677, 2023, doi: 10.1016/j.artmed.2023.102677.
- [6] C. Fu, Z. Huang, F. van Harmelen, T. He, and X. Jiang, *Food Recommendation for Mental Health by Using Knowledge Graph Approach*, vol. 13705 LNCS. Springer Nature Switzerland, 2022. doi: 10.1007/978-3-031-20627-6_22.
- [7] J. Lee, W. Yoon, S. Kim, D. Kim, S. Kim, C. H. So, and J. Kang, “BioBERT: A pre-trained biomedical language representation model for biomedical text mining,” *Bioinformatics*, vol. 36, no. 4, pp. 1234–1240, 2020, doi: 10.1093/bioinformatics/btz682.
- [8] D. N. Nicholson and C. S. Greene, “Constructing knowledge graphs and their biomedical applications,” *Computational and Structural Biotechnology Journal*, vol. 18, pp. 1414–1428, 2020, doi: 10.1016/j.csbj.2020.05.017.
- [9] A. F. Septiyanto, Y. F. C. Cahyono, R. Sarno, F. Taufany, S. H. Larekeng, K. R. Sungkono, K. Syahrudin, E. G. Lestari, and Sholiq, “An Improved Method for Prioritizing Polymerase Chain Reaction (PCR) Primer Design in Sanger Sequencing,” *Proceeding - 6th International Conference on Information Technology, Information Systems and Electrical Engineering: Applying Data Sciences and Artificial Intelligence Technologies for Environmental Sustainability, ICITISEE 2022*, pp. 443–448, 2022, doi: 10.1109/ICITISEE57756.2022.10057821.
- [10] A. N. Sutranggono, R. Sarno, and I. Ghazali, “Multi-Class Multi-Level Classification of Mental Health Disorders Based on Textual Data from Social Media,” *Journal of Information and Communication Technology*, vol. 23, no. 1, pp. 77–104, 2024, doi: 10.32890/jict2024.23.1.4.
- [11] S. Ghidalia, O. L. Narsis, A. Bertaux, and C. Nicolle, “Combining Machine Learning and Ontology: A Systematic Literature Review,” 2024, [Online]. Available: <http://arxiv.org/abs/2401.07744>
- [12] D. L. Yonia, S. C. Hidayati, R. Sarno, and A. F. Septiyanto, “DNA Pattern Matching Algorithms within Sorghum bicolor Genome: A Comparative Study,” *Proceedings - International Conference on Informatics and Computational Sciences*, pp. 36–41, 2024, doi: 10.1109/ICICoS62600.2024.10636821.
- [13] F. P. Kurniyanto, R. Sarno, K. R. Sungkono, A. T. Haryono, A. F. Septiyanto, and Shaliq, “Enhancing Electronic Health Records Security with Semantic-Aware Hierarchical Encryption,” *2024 Beyond Technology Summit on Informatics International Conference, BTS-I2C 2024*, pp. 359–364, 2024, doi: 10.1109/BTS-I2C63534.2024.10941752.
- [14] Stålhandske, T., & Slanina, P. Nicotyrine inhibits in vivo metabolism of nicotine without increasing its toxicity. *Toxicology and applied pharmacology*. 1982; 65 3. [https://doi.org/10.1016/0041-008X\(82\)90382-9](https://doi.org/10.1016/0041-008X(82)90382-9)
- [15] F. Vorspan, W. Mehtelli, G. Dupuy, V. Bloch, and J. P. Lépine, “Anxiety and Substance Use Disorders: Co-occurrence and Clinical Issues,” *Current Psychiatry Reports*, vol. 17, no. 2, 2015, doi: 10.1007/s11920-014-0544-y.
- [16] Y. Yu, F. Han, and Q. Wang, “A Hippocampal-Entorhinal Cortex Neuronal Network for Dynamical Mechanisms of Epileptic Seizure,” *IEEE Transactions on Neural Systems and Rehabilitation Engineering*, vol. 31, pp. 1986–1996, 2023, doi: 10.1109/TNSRE.2023.3265581.
- [17] Daras, M., Koppel, B., & Atos-Radzion, E. Cocaine - induced choreoathetoid movements ('crack dancing'). *Neurology*. 1994; 44. <https://doi.org/10.1212/WNL.44.4.751>.