From Annotated Clinical Narratives to Ontology: Structuring Brazilian Portuguese Clinical Data

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Abstract

Clinical NLP for Brazilian Portuguese remains limited by the lack of semantically structured resources that support interoperability and downstream health applications. Although existing corpora provide annotated clinical narratives, their flat annotation schemes restrict semantic expressiveness and alignment with standardized terminologies. In this work, we present a lightweight domain ontology that models clinical entities, contextual qualifiers, and semantic relations in Brazilian Portuguese texts. The ontology is derived from the original corpus annotations and conceptually aligned with standards to enhance interoperability while preserving corpus-specific semantics. This work establishes foundational infrastructure for Portuguese clinical NLP, supporting tasks such as entity normalization, semantic search, and ontology-guided annotation.

1 Introduction

Clinical narratives are a core component of electronic health records (EHRs), encoding diagnoses, symptoms, procedures, and clinical reasoning in free-text form. Converting this unstructured content into structured, machine-interpretable representations remains a central objective of clinical Natural Language Processing (NLP), supporting information extraction, decision support, and interoperability. In Brazilian Portuguese (PT-BR), however, progress is constrained by the scarcity of publicly available annotated EHR datasets, largely due to privacy concerns and the strict requirements of Brazil's data protection law (da Silva and Pazin-Filho, 2025). Although relevant initiatives have emerged, such as the *SemClinBr* corpus with 1,000 annotated notes and over 65,000 entities (Oliveira et al., 2022), a negation-annotated corpus from three hospitals (Dalloux et al., 2021), and task-specific extraction efforts (Kugic et al., 2024), comprehensive resources remain limited, often requiring the development of ad hoc corpora (Sousa et al., 2023). Terminological coverage in PT-BR is also substantially lower than in English in repositories such as UMLS (Névéol et al., 2018), and domain-adapted NLP tools remain underdeveloped, particularly for tasks such as negation scope detection and abbreviation disambiguation (de Souza et al., 2019; da Silva and Pazin-Filho, 2025).

Recent approaches have combined large language models (LLMs) with vector-based retrieval to generate RDF triples aligned with standards such as SNOMED CT[1] , fostering semantic interoperability (Manda, 2025). However, these efforts are typically disease-centered or terminology-driven and rarely focus on ontology construction grounded in annotated clinical corpora. To address this gap, we present ongoing work that transforms the *SemClinBr* corpus into a lightweight domain ontology, adopting a corpus-driven methodology in which classes, relations, and design patterns are derived directly from the annotation schema and empirical linguistic evidence rather than imposed independently of the data.

This paper is organized as follows: Section 2 discusses related ontology work; Section 3 presents the methodology and corpus used; Section 4 reports the results; and Section 5 concludes with final remarks and future work proposals.

2 Related Work

Prior ontology-driven initiatives in Brazilian clinical and biomedical domains, revealing a landscape that is both domain-specific and methodologically heterogeneous. Early efforts such as Santana et al. ((Santana et al., 2011), (Santana et al., 2012)) focused on representing complex biological and epidemiological processes, particularly in neglected tropical diseases and mortality surveillance, emphasizing formal expressiveness through description logics and competency-question validation. Subse-

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[1] https://www.snomed.org/

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quent works expanded toward applied public health scenarios, notably (Pellison et al., 2020), which leveraged Semantic Web standards to support interoperability across Brazilian tuberculosis information systems.

Other initiatives targeted specialized domains,including mental health decision support (Yamada et al., 2020) and nursing record standardization via ICNP[2] alignment (Yamada et al., 2020)), highlighting ontology alignment and logical consistency as evaluation strategies. More recently, (Bouscarrat et al., 2020)) addressed multilingual disease interoperability using Wikidata[3] and translation-based alignment metrics.

Recent advances in Brazilian Portuguese clinical NLP include (Dutra et al., 2023)'s frame-semantic model for detecting gender-based violence in hospital records and (Da Rocha et al., 2022)'s neural NER system, which extracts clinical entities. Our work complements these approaches by developing an ontology that serves as a bridge and intermediate representation, enabling interoperability with international standards which is a key challenge identified in studies.

3 Material and Methods

3.1 Corpus Ingestion

The initial phase involves acquiring and decompressing the SemClinBr files to access the source XML documents. From each document, four essential data points are extracted: (1) Document ID ("doc_id"): Derived by stripping the extension from the filename to create a unique identifier; (2) Main Text ("main_text"): The complete clinical narrative extracted from the <TEXT> tag; (3) Annotations: Clinical entities (including semantic tags inspired by UMLS[4] semantic groups, character spans, and abbreviations) extracted from the <TAGS> block and stored as dictionaries containing their ID, type, and text position; and (4) Relations: Dependencies between annotations (e.g., associated_with, negation_of) parsed from the <RELATIONS> block, linking annotation pairs to their specific relationship type.

3.2 Ontology Construction

The ontological schema defines a foundational framework of 14 high-level abstract classes via the `owl:Class` construct. These classes, such as `ClinicalEpisode`, `BodyStructure`, `Substance`, and `ClinicalFinding`, provide the structural backbone for the corpus data. Relationships between these classes are formalized through `owl:ObjectProperty` declarations, utilizing `rdfs:domain` and `rdfs:range` constraints to ensure semantic integrity. For example, the `hasFinding` property maps a `ClinicalEpisode` to a `Finding`, thereby enforcing domain-specific logic and ensuring that clinical observations are correctly contextualized within specific patient encounters.

A critical feature of this design is the explicit modeling of semantic associations and negations. The `associated_with` property serves as a general-purpose link between related entities when specific sub-properties are not defined. Furthermore, to support accurate clinical reasoning, the ontology implements a negation mechanism via a dedicated `negation_of` property. For instance, the absence of a clinical sign is represented by linking the individual representing that sign to a negation individual (e.g., `Concept_sem`, signifying "without"), ensuring the system distinguishes between the presence and absence of clinical findings.

3.3 Ontology Population

The ontology was automatically populated from the annotated SemClinBr corpus using a structured instantiation pipeline implemented in Python with Owlready2 and executed in Google Colab to ensure reproducibility.

Each unique annotated span was instantiated as an `owl:NamedIndividual` following the naming convention `Concept_[Portuguese_term]`, preserving traceability to the source text. Individuals were explicitly typed using `rdf:type`. The population workflow comprised four stages: (1) ontology loading, (2) URI sanitization, (3) individual instantiation, and (4) semantic relation assertion.

Tags were assigned to the most specific ontology class through a prefix-based mapping derived from SemClinBr tags. When no direct mapping was available, the system defaulted to the superclass *Finding*, ensuring complete coverage without interrupting execution. Each clinical document (`doc_id`) was instantiated as an individual of class *ClinicalEpisode*. Sanitized identifiers were preserved via the `hasID` data property.

Episode individuals were linked to concept instances through semantically appropriate object

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[2] https://www.icn.ch/icnp-browser

[3] https://www.wikidata.org/wiki/Wikidata:Main$_{Page}$

[4] https://www.nlm.nih.gov/research/umls/index.html

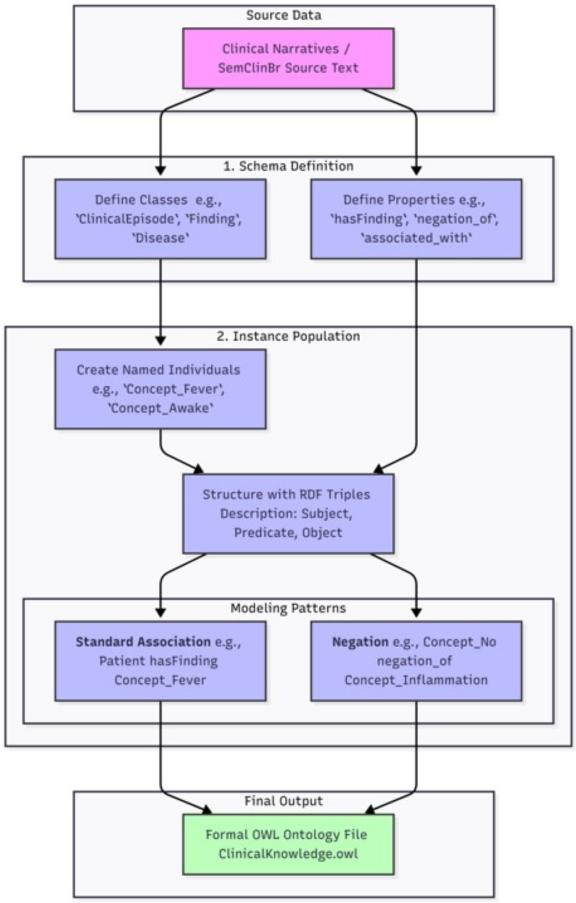

Figure 1: Overview of the corpus-driven workflow for ontology population and semantic relation assertion.

properties , such as `hasFinding`, `hasDisease`, and `hasMedication`. Two categories of relations were asserted. Episode-to-concept relations connect clinical episodes to findings, diseases, procedures, and other entities. Concept-to-concept relations encode semantic interactions such as `associated_with`, and `negation_of`.

Post-population validation included: (i) verification of individual counts, (ii) enumeration of object and data properties, (iii) logical consistency checking using the HermiT reasoner (Horrocks et al., 2012) in Protégé (Musen, 2015), and SPARQL[5] queries.

Figure 1 summarizes the transformation pipeline from annotated narratives to the final OWL[6] ontology (`ClinicalKnowledge.owl`).

Table 1: Top 10 Annotation Types Frequency

Type	Freq.
Finding	4304
Sign or Symptom	3537
Quantitative Concept	3447
Health Care Activity	2155
Therapeutic or Preventive Procedure	1805
Lab or Test Result	1518
Negation	1514
Disease or Syndrome	1345
Temporal Concept	1230
Abbreviation	1171

Table 2: Frequency of Relation Types

Relation	Freq.
associated_with	9852
negation_of	1606

4 Results and Discussion

4.1 Corpus Analysis

Table1 shows that the corpus is dominated by descriptive clinical entities, particularly *Finding* and *Sign or Symptom*, followed by measurement- and procedure-related categories (e.g., *Quantitative Concept*, *Therapeutic or Preventive Procedure*). Linguistic types such as *Negation* and *Abbreviation* further emphasize contextual and polarity modeling. As shown in Table 2, `associated_with` is the predominant relation, indicating dense semantic connectivity, while `negation_of` encodes clinically relevant polarity.

Although inspired by UMLS semantic groups, the hierarchy lacks explicit description-logic constraints and formal alignment with SNOMED CT. Several classes participate in polyhierarchical structures, and linguistic constructs (e.g., *Negation*, *Abbreviation*, *Temporal Concept*) are modeled alongside biomedical entities. This mixing of abstraction levels introduces semantic overlap and weakens subsumption clarity. Such structural characteristics limit automated reasoning and logical consistency. To support ontology construction and semantic interoperability, SemClinBr requires reorganization toward a higher-level hierarchy more closely aligned with SNOMED CT.

4.2 Ontology Analysis

Table 3 summarizes the global ontology metrics. The ontology was implemented using Protegé (Musen, 2015) and comprises 57 classes, 17,663 individuals, 23 object properties, and 7 data prop-

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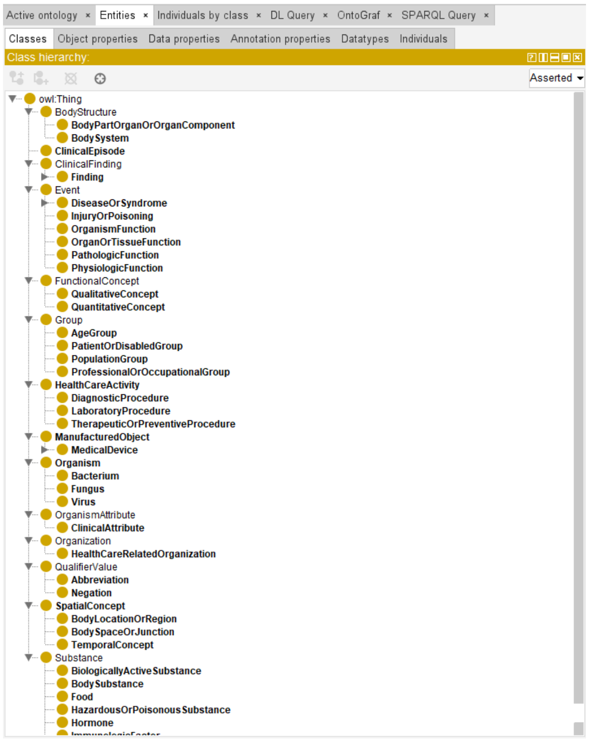
[5] https://www.w3.org/TR/sparql11-query/
[6] https://en.wikipedia.org/wiki/Owl



- owl:Thing
  - BodyStructure
    - BodyPartOrganOrOrganComponent
    - BodySystem
  - ClinicalEpisode
  - ClinicalFinding
    - Finding
  - Event
    - DiseaseOrSyndrome
    - InjuryOrPoisoning
    - OrganismFunction
    - OrganOrTissueFunction
    - PathologicFunction
    - PhysiologicFunction
  - FunctionalConcept
    - QualitativeConcept
    - QuantitativeConcept
  - Group
    - AgeGroup
    - PatientOrDisabledGroup
    - PopulationGroup
    - ProfessionalOrOccupationalGroup
  - HealthCareActivity
    - DiagnosticProcedure
    - LaboratoryProcedure
    - TherapeuticOrPreventiveProcedure
  - ManufacturedObject
    - MedicalDevice
  - Organism
    - Bacterium
    - Fungus
    - Virus
  - OrganismAttribute
    - ClinicalAttribute
  - Organization
    - HealthCareRelatedOrganization
  - QualifierValue
    - Abbreviation
    - Negation
  - SpatialConcept
    - BodyLocationOrRegion
    - BodySpaceOrJunction
    - TemporalConcept
  - Substance
    - BiologicallyActiveSubstance
    - BodySubstance
    - Food
    - HazardousOrPoisonousSubstance
    - Hormone

Figure 2: Protegé Ontology Class Hierarchy.

Table 3: Global Ontology Statistics

Metric	Value
Axiom	87,634
Class Count	57
Individual Count	17,663
Object Property Count	23
Data Property Count	7
Hierarchy Maximum Depth	6
Clinical Episodes	1,000

erties. The class hierarchy reaches a maximum depth of 6 levels, indicating moderate taxonomic complexity.

All individuals were typed, following two dominant naming patterns: *Concept_* and *ClinicalEpisode_*. The most populated semantic categories are *Abbreviation*, *Finding*, and *SignOrSymptom*, followed by *LaboratoryOrTestResult* and *QuantitativeConcept*. The ontology encodes 1,000 clinical episodes with an average of 16 connections per episode.

The presence of *ClinicalAttribute* and *Negation* as classes in Figure 2 stems from the SemClinBr annotation schema, which treats these as primary semantic tags. Our current lightweight ontology prioritizes a high-fidelity mapping of the corpus's entity types and relation types. We acknowledge that in formal ontology engineering, these should be refactored into properties.

Duplicate instances were detected due to case variation, accent normalization, token segmentation, and word-order permutation (e.g., "paciente", "PACIENTE", "Paciente"; "hemodinamicamente estável" vs. "estável hemodinamicamente"; "sistema fechado de aspiração" vs. "sistema de aspiração fechado"). These surface variations represent semantically equivalent entities and artificially inflate instance counts suggesting the need for lexical normalization and canonicalization strategies.

4.3 Consistence and Validation

Reasoning over the ontology confirmed logical consistency, with no detected contradictions, and enabled the inference of additional implicit relations. SPARQL queries executed over the inferred ontology revealed a coherent and densely connected structural backbone, consistent with the rich and narrative-driven nature of clinical records.

The most frequent and structurally dominant relation is associated_with, which appears in thousands of triples, reflecting the broad associative nature of clinical documentation where findings, procedures, substances, and other concepts are frequently co-occurring or contextually linked within the same episode. In contrast, semantically more precise and critical relations such as negation_of appear in a smaller but highly meaningful subset (e.g., 27 results in the negation-focused query), highlighting negation patterns that are essential for accurate clinical interpretation and modeling refinement.

Other targeted relations (*hasFinding*, *hasDisease*, etc.) show consistent and expected usage patterns, with results typically ranging from dozens to hundreds of triples depending on the specificity of the query. These patterns confirm that the ontology captures the multifaceted and relational character of real-world clinical knowledge, while also exposing opportunities for further refinement, particularly in strengthening negation modeling and reducing overly generic associated_with links where more precise semantics (e.g., causes, treats, located_in) could be introduced.

Screenshots from Protegé queries (Figures 3 to 5) are provided in the Appendix section for reference.

5 Conclusion and Future Work

In summary, the SemClinBr-derived ontology provides a valuable intermediate representation that bridges clinical NLP annotations and formal ontology engineering. Although lightweight, the ontology is well-structured, as demonstrated by

SPARQL queries that reveal its capacity to model complex clinical relations and support disambiguation. For example, the explicit use of properties such as negation_of allows the system to distinguish between the presence and absence of clinical findings, while the associated_with relation captures contextual links between entities. These features, combined with the ontology's ability to represent and query semantic relations, facilitate more precise clinical interpretation and reduce ambiguity in narrative data.

Although this work establishes a foundational infrastructure for Brazilian Portuguese clinical NLP, we recognize that the research is currently in an initial stage. Our future roadmap includes the implementation of lexical normalization and canonicalization strategies to handle surface variations (e.g., case and accentuation) that currently inflate instance counts. Furthermore, upcoming developments will focus on the explicit modeling of disease–symptom relations and full alignment with global standards, such as ICD[7] and SNOMED CT, to ensure semantic interoperability across diverse healthcare applications.

To transition this resource from a valuable intermediate representation into a formal domain ontology, future work will focus on concept consolidation and lexical normalization to resolve the current overlap between domain and linguistic layers. These efforts will include the implementation of stronger logical axiomatization such as disjointness domain/range constraints, and the explicit modeling of disease–symptom relations. Ultimately, alignment with standards will ensure that the ontology provides a rigorous framework for clinical reasoning and automated inference for Brazilian Portuguese healthcare data.

6 Acknowledgments

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[7] https://icd.who.int/en/

[8] https://github.com/HAILab-PUCPR

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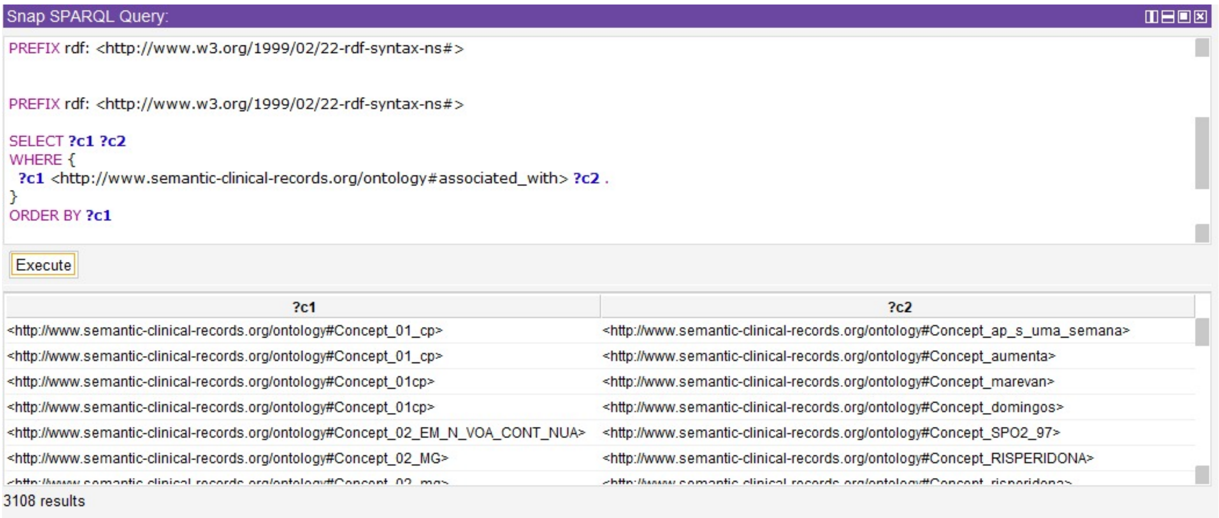
A Appendix

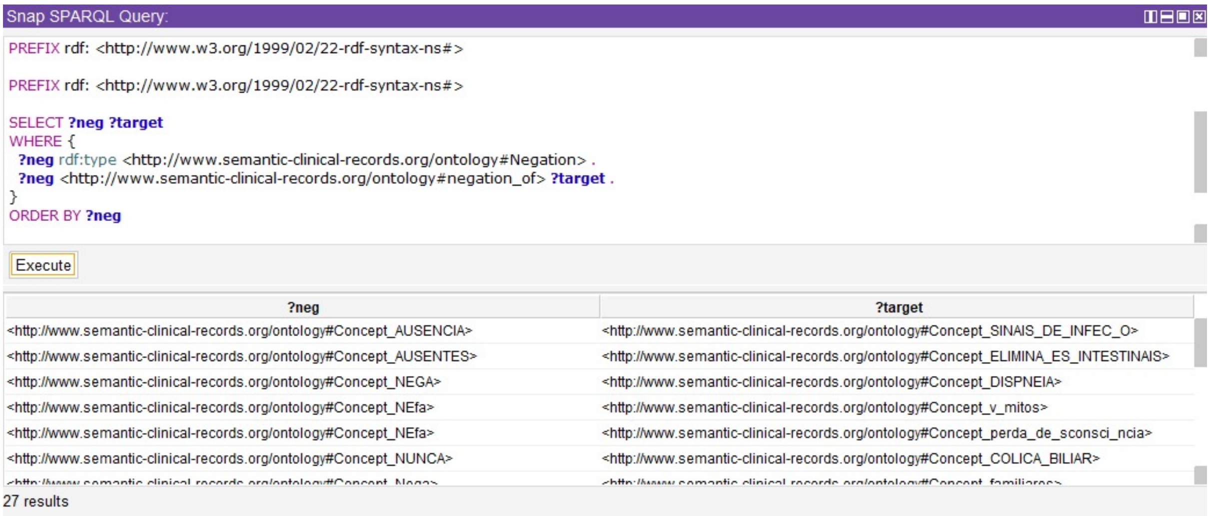


```
PREFIX rdf: <http://www.w3.org/1999/02/22-rdf-syntax-ns#>


PREFIX rdf: <http://www.w3.org/1999/02/22-rdf-syntax-ns#>

SELECT ?c1 ?c2
WHERE {
  ?c1 <http://www.semantic-clinical-records.org/ontology#associated_with> ?c2 .
}
ORDER BY ?c1
```

?c1	?c2
<http://www.semantic-clinical-records.org/ontology#Concept_01_cp>	<http://www.semantic-clinical-records.org/ontology#Concept_ap_s_uma_semana>
<http://www.semantic-clinical-records.org/ontology#Concept_01_cp>	<http://www.semantic-clinical-records.org/ontology#Concept_aumenta>
<http://www.semantic-clinical-records.org/ontology#Concept_01cp>	<http://www.semantic-clinical-records.org/ontology#Concept_marevan>
<http://www.semantic-clinical-records.org/ontology#Concept_01cp>	<http://www.semantic-clinical-records.org/ontology#Concept_domingos>
<http://www.semantic-clinical-records.org/ontology#Concept_02_EM_N_VOA_CONT_NUA>	<http://www.semantic-clinical-records.org/ontology#Concept_SPO2_97>
<http://www.semantic-clinical-records.org/ontology#Concept_02_MG>	<http://www.semantic-clinical-records.org/ontology#Concept_RISPERIDONA>
<http://www.semantic-clinical-records.org/ontology#Concept_02_mg>	<http://www.semantic-clinical-records.org/ontology#Concept_risperidona>

3108 results

Figure 3: SPARQL results: associated_with relations between clinical concepts (3,108 triples).

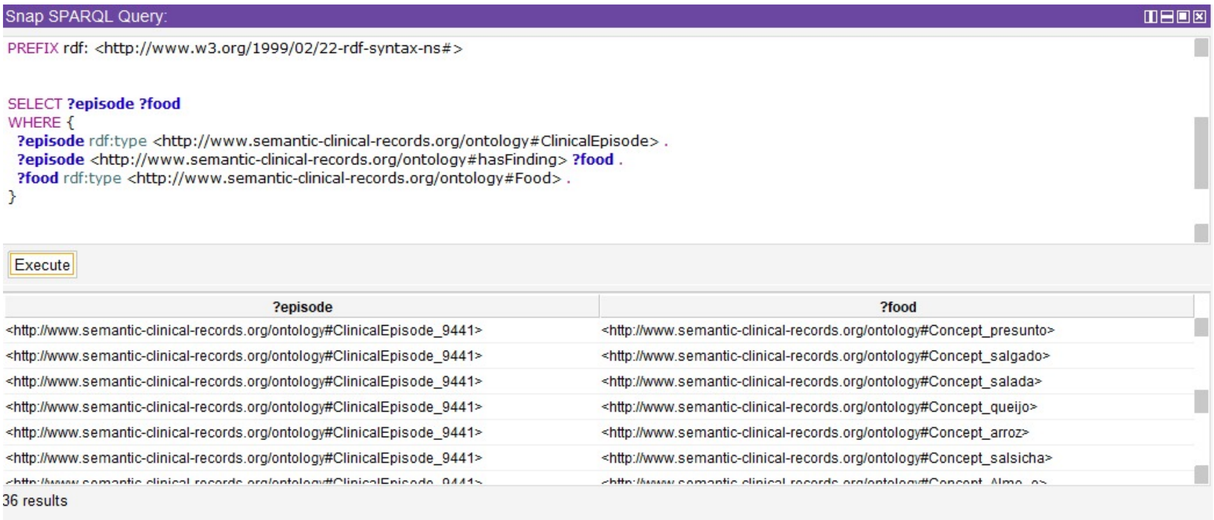


```
PREFIX rdf: <http://www.w3.org/1999/02/22-rdf-syntax-ns#>

PREFIX rdf: <http://www.w3.org/1999/02/22-rdf-syntax-ns#>

SELECT ?neg ?target
WHERE {
  ?neg rdf:type <http://www.semantic-clinical-records.org/ontology#Negation> .
  ?neg <http://www.semantic-clinical-records.org/ontology#negation_of> ?target .
}
ORDER BY ?neg
```

?neg	?target
<http://www.semantic-clinical-records.org/ontology#Concept_AUSENCIA>	<http://www.semantic-clinical-records.org/ontology#Concept_SINAIS_DE_INFEC_O>
<http://www.semantic-clinical-records.org/ontology#Concept_AUSENTES>	<http://www.semantic-clinical-records.org/ontology#Concept_ELIMINA_ES_INTESTINAIS>
<http://www.semantic-clinical-records.org/ontology#Concept_NEGA>	<http://www.semantic-clinical-records.org/ontology#Concept_DISPNEIA>
<http://www.semantic-clinical-records.org/ontology#Concept_NEfa>	<http://www.semantic-clinical-records.org/ontology#Concept_v_mitos>
<http://www.semantic-clinical-records.org/ontology#Concept_NEfa>	<http://www.semantic-clinical-records.org/ontology#Concept_perda_de_sconsci_ncia>
<http://www.semantic-clinical-records.org/ontology#Concept_NUNCA>	<http://www.semantic-clinical-records.org/ontology#Concept_COLICA_BILIAR>
<http://www.semantic-clinical-records.org/ontology#Concept_Nega>	<http://www.semantic-clinical-records.org/ontology#Concept_familiares>

27 results

Figure 4: SPARQL results: negation_of assertions (27 triples).



```
PREFIX rdf: <http://www.w3.org/1999/02/22-rdf-syntax-ns#>


SELECT ?episode ?food
WHERE {
  ?episode rdf:type <http://www.semantic-clinical-records.org/ontology#ClinicalEpisode> .
  ?episode <http://www.semantic-clinical-records.org/ontology#hasFinding> ?food .
  ?food rdf:type <http://www.semantic-clinical-records.org/ontology#Food> .
}
```

?episode	?food
<http://www.semantic-clinical-records.org/ontology#ClinicalEpisode_9441>	<http://www.semantic-clinical-records.org/ontology#Concept_presunto>
<http://www.semantic-clinical-records.org/ontology#ClinicalEpisode_9441>	<http://www.semantic-clinical-records.org/ontology#Concept_salgado>
<http://www.semantic-clinical-records.org/ontology#ClinicalEpisode_9441>	<http://www.semantic-clinical-records.org/ontology#Concept_salada>
<http://www.semantic-clinical-records.org/ontology#ClinicalEpisode_9441>	<http://www.semantic-clinical-records.org/ontology#Concept_queijo>
<http://www.semantic-clinical-records.org/ontology#ClinicalEpisode_9441>	<http://www.semantic-clinical-records.org/ontology#Concept_arroz>
<http://www.semantic-clinical-records.org/ontology#ClinicalEpisode_9441>	<http://www.semantic-clinical-records.org/ontology#Concept_salsicha>
<http://www.semantic-clinical-records.org/ontology#ClinicalEpisode_9441>	<http://www.semantic-clinical-records.org/ontology#Concept_Almo_o>

36 results

Figure 5: SPARQL results: 36 Clinical episodes associated with Food findings (hasFinding → Food).