**Semantic Graph Network Overview**

**The semantic graph network models concepts (CUIs) as nodes and their relationships, including attributes and characteristics, as edges connecting these nodes. The resulting structure embodies a rich interconnectivity where various data points interact, enabling intricate queries and in-depth analyses.**

**Key Components**

1. **Nodes:**
   * **Concepts (CUIs): Unique identifiers for each concept in the UMLS database, which represent diseases, procedures, and other health-related entities.**
   * **Atoms: Basic units of meaning that connect to concepts and provide additional descriptive power.**
2. **Edges:**
   * **Relationships: Semantic relationships that define how concepts connect with each other, including:**
     + **is-a: Hierarchical relationships depicting broader to narrower concept relationships (e.g., “Diabetes” is a type of “Disease”).**
     + **part-of: Specifies that a concept is a part of a broader concep.**
     + **related-to: Represents a general connection between concepts without specifying a hierarchical context.**
3. **Attributes: Additional characteristics associated with each node, such as:**
   * **Atoms: Including original, cleaned forms, cleaning type, grams, length, and semantic type.**
   * **Semantic Types: Designations that classify concepts into categories (e.g., diseases, procedures).**

**Network Visualization**

**The overall graph network can be visualized and represented as follows:**

**Task 1: Atom Extraction Based on ICD Code and CUIs**

**Process Overview**:

1. Input user-defined ICD code(s) or a list of CUIs.
2. Traverse the graph to filter relevant nodes (CUIs) and aggregate connected atoms.
3. Output atom characteristics linked to each selected CUI.

**Task 2: Semantic Relevancy Check Using MRSTY**

**Process Overview**:

1. Accept keywords and source CUIs related to these keywords.
2. Query the graph network to evaluate atom relevance against provided semantic types.
3. Return a structured response indicating relevant CUIs and corresponding atoms.

**Task 3: Atom Cleaning, Grams, and Length Calculation**

**Process Overview**:

1. For each retrieved atom, invoke user-defined cleaning functions.
2. Measure grams and length of cleaned atoms.
3. Consolidate results into a structured format linking atom characteristics back to their CUIs.

**Optimization Strategies**

* **Graph-Based Processing**: By maintaining a persistent graph representation in memory, the need for repetitive data loading is minimized. Operations performed across tasks leverage this graph, enhancing performance.
* **Modular Task Execution**: Each task function can access the shared graph structure, making it modular, allowing for specific enhancements or alterations without compromising overall functionality.

**Conclusion**

This conceptual framework illustrates a comprehensive approach to representing and processing UMLS data through a semantic relationship type network. By establishing nodes and edges that reflect the distinctions and connections among concepts and their attributes, we pave the way for intricate analyses grounded in real-world medical terminologies. Such a structure fosters optimal performance in querying and data manipulation, ultimately enriching our understanding of complex medical semantics.