

Ontology COKB for Knowledge Representation and Reasoning in Designing Biological Taxonomy

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Abstract. Ontology plays a crucial role in the field of Artificial Intelligence (AI), particularly in the design and implementation of knowledge-based systems and intelligent reasoning agents. Knowledge representation and reasoning (KRR) are essential for building intelligent systems in biology and related scientific fields. Traditional classification models often struggle to represent complex biological relationships or support automated reasoning. This paper introduces an ontology-based approach using the Computational Object Knowledge Base (COKB) model to enhance biological classification systems. The COKB ontology combines structured taxonomic hierarchies with computational reasoning through six components: concepts, hierarchical and non-hierarchical relations, operators, functions, and rules. It also includes some example types of facts and automated deduction methods that simulate expert-level classification. This approach can be applied in biodiversity monitoring, education, and intelligent tools that explain classification decisions in a human-readable way. The work demonstrates how COKB can be adapted to the biological domain while keeping its strengths in logic-based knowledge modeling and practical applications.

Keywords: knowledge representation, biological ontology, taxonomy, COKB model, intelligent systems

1. Introduction

Biological taxonomy systems require precise knowledge representation to handle the complex relationships between millions of species. While traditional systems like Linnaean classification provide basic hierarchical structures, they lack formal mechanisms for automated reasoning and exception handling. The development of intelligent taxonomic systems demands ontologies that integrate:

1. Structured concept hierarchies
2. Multiple relationship types
3. Computational reasoning capabilities
4. Human-interpretable proof generation

The COKB model addresses these requirements through an integration of ontology engineering and object-oriented modeling. Previous applications in geometry problem-solving demonstrated COKB's effectiveness in educational domains. This paper adapts the framework to biological taxonomy by:

- Defining 12 specialized fact types for taxonomic knowledge
- Developing a specification language for biological concepts
- Implementing deduction algorithms for classification tasks
- Evaluating performance on standard biodiversity datasets

Key taxonomic challenges include:

- Polymorphic characteristics (e.g., fungi reproduction modes)
- Evolutionary exceptions (e.g., prokaryotic eukaryotes)
- Dynamic classification updates

The system produces solutions that mirror expert reasoning processes while maintaining computational efficiency (average 1.2s response time). Educational applications demonstrate how the framework generates step-by-step classification proofs that assist both students and researchers. It also details the COKB model's adaptation for biological taxonomy, while presenting the reasoning algorithms. Applications in biodiversity monitoring and comparative analysis with traditional methods are discussed later. Limitations and future research directions are outlined in the last section.

2. Definitions of Ontology in Artificial Intelligence

The term "ontology" often sparks debate in the context of artificial intelligence. Historically rooted in philosophy, it deals with the nature of existence. However, it is frequently misunderstood or confused with epistemology, which focuses on knowledge and the process of knowing. Here, ontology in artificial intelligence has evolved through various formal definitions from leading researchers:

2.1. Core Definitions

1. **Gruber (1993):** An Ontology is a formal specification of a shared agents conceptualization of a domain of interest "*An explicit specification of a conceptualization*"
 - Focuses on shared understanding between humans and machines
 - Emphasizes formal declaration of concepts and relationships
2. **John F. Sowa:** The subject ontology is the study of categories of things that exist or may exist in some domain. The product of such a study, called an ontology, is a catalog of the types of things that are assumed to exist in a domain of interest D from the perspective of a person who uses

a language L for the purpose of talking about D “A catalog of types assumed to exist in a domain from the perspective of a language user”

- Highlights categorical organization
 - Stresses domain-specific interpretation frameworks
3. **Stojanovic (2004):** For AI researchers, an ontology describes a formal, shared conceptualization of a particular domain of interest. Thus, ontologies provide a way of capturing a shared understanding of a domain that can be used both by humans and systems to aid in information exchange and integration “Formal, shared conceptualization of a domain enabling information exchange”
- Prioritizes interoperability
 - Supports machine-readable knowledge structures

2.2. Core COKB of Biological Taxonomy

2.2.1. Historical Perspective: Linnaean Taxonomy

The Linnaean system, developed by Carl Linnaeus in the 18th century, is the foundational framework for biological classification. It organizes living organisms into a hierarchical structure based on shared physical characteristics:

- **Kingdom**
- **Phylum**
- **Class**
- **Order**
- **Family**
- **Genus**
- **Species**

Example: Human Classification

- Kingdom: Animalia
- Phylum: Chordata
- Class: Mammalia
- Order: Primates
- Family: Hominidae
- Genus: Homo
- Species: Homo sapiens

While the Linnaean taxonomy provides a clear, structured approach, it is primarily descriptive and lacks formal mechanisms for automated reasoning or handling exceptions. Modern ontologies, such as COKB, build upon and extend these principles by introducing computational logic and richer relationship types.

2.2.2. Six Components (adapted from COKB model)

Concepts (C): Taxonomic ranks (Kingdom→Species) Hierarchy (H): IS-A relationships (Mammalia IS-A Chordata) Relations (R): Non-hierarchical links (symbiosis, parasitism) Operators (Ops): Taxonomic actions (merge_taxa,

split_species) Functions (Funcs): Computations (genetic_distance(), trait_similarity()) Rules (Rules): Deductive logic (IF unicellular THEN likely Protista)

2.2.3. Key Innovations for Biology

- 12 Fact Types
 - Object-Centric: Taxonomic ranks, traits, values (Kinds 1–3)
 - Relational: Evolutionary dependencies, ecological interactions (Kinds 4–6)
 - Functional: Genomic calculations, statistical models (Kinds 7–9)
 - Rule-Based: Classification logic, exceptions (Kinds 10–12)
- Computational Networks
 - Bio-Nets: Extend CO-Nets with:
 - Nodes = Taxa (Species, Genera)
 - Edges = Evolutionary/ecological relationships
 - Matrices = Trait-state mappings (e.g., presence/absence)
- Reasoning Algorithms
 - Forward Chaining: From traits → taxonomic placement
 - Constraint Propagation: Resolves conflicts in polyphyletic groups
 - Exception Handling: Manages atypical cases (e.g., Thermoplasma in Archaea)

2.2.4. Example Use Case

Problem: Classify an organism with:

- Eukaryotic cells
- Chitinous cell walls
- Absorptive nutrition

COKB Solution:

- Match eukaryotic → Exclude Bacteria
- chitinous_walls → Likely Fungi
- absorptive → Confirm Fungi

2.3. Foundational Model

Structural Components:

```
COKB_Model = {  
    'Concepts': 'Classes of computational objects',  
    'Hierarchy': 'IS-A relationships (taxonomic)',  
    'Relations': 'Non-hierarchical associations',  
    'Operators': 'Domain-specific operations',  
    'Functions': 'Computational methods',  
    'Rules': 'If-then deductive structures'  
}
```

3. Application of Ontology on Biological Taxonomy

3.1. Formal Definition

Com-Object $O := (\text{Attrs}, F, \text{Facts}, \text{Rules})$ where:

- $\text{Attrs}(O)$: Set of attributes
- F : Computational relations (equations)
- Facts : Object properties/events
- Rules : Deductive mechanisms

Knowledge Classification:

- Object-Type Facts (12 categories)
- Kind 1-3: Object identification
- Kind 4-6: Relational statements
- Kind 7-12: Functional dependencies

3.2. Object Type Facts

Kind 1: Taxonomic Rank Declaration

- **Structure:** `[organism, taxonomic_rank]`
- **Example:** `("Panthera leo", "species")`

Kind 2: Attribute Determination

- **Structure:** `[taxon, attribute]`
- **Example:** `{"taxon": "Fungi", "attribute": "cell_wall"}`

Kind 3: Value Assignment

- **Structure:** `[taxon.attribute = value]`
- **Example:** `"Homo_sapiens.chromosome_count = 46"`

3.3. Relational Facts

Kind 4: Taxonomic Equality

- **Structure:** `[taxon_A \equiv taxon_B]`
- **Example:** `"Canis lupus \equiv Gray Wolf"`

Kind 5: Phylogenetic Dependency

- **Structure:** `[trait_X requires trait_Y]`

- **Example:** "vertebral_column requires notochord"

Kind 6: Ecological Relations

- **Structure:** [organism_A → interaction → organism_B]
- **Example:** "Ophiocordyceps → parasitizes → Ant"

3.4. Functional Facts

Kind 7: Function Declaration

- **Structure:**

```
def function_name(parameters):
    return computation
def genetic_distance(species1, species2):
    return nucleotide_divergence(species1, species2)
```

Kind 8: Function Valuation

Structure: [function(input) = output]

Example: "gc_content('Streptomyces') = 0.723"

Kind 9: Object-Function Binding

Structure: [object = function(parameters)]

Example: "Type_specimen = holotype('SH-2024-001')"

3.5. Complex Rule Facts

Kind 10: Function Relations

Structure: [f(X) = g(X) + constant]

Example: "metabolic_rate(X) = 2.3 * mass(X)^0.75"

Kind 11: Deductive Rules

- Structure IF [conditions] THEN [conclusion]
- Example IF has_feathers(X) AND has_beak(X) THEN clade(X, Aves)

Kind 12: Exceptional Cases

Structure: [Despite condition, conclusion]

Example: "Despite unicellularity, Choanoflagellata are Animalia"

3.5.1. Implementation Examples

JSON Representation (Kind 2):

```
{
  "fact_kind": 2,
  "taxon": "Plantae",
  "attribute": "photosynthetic"
}
```

3.5.2. Reasoning Workflow

Taxonomic Determination Algorithm

```
def classify_organism(characteristics):
    knowledge_base = load_COKB("taxonomy.cokb")

    # Forward chaining
    for rule in knowledge_base.rules:
        if rule.premises.match(characteristics):
            characteristics.update(rule.conclusions)

    # Hierarchy traversal
    current = find_leaf_node(characteristics)
    while current.parent:
        yield current
        current = current.parent

    return kingdom_level(current)
```

Input Characteristics:

- Eukaryotic cells
- Chitinous cell walls
- Absorptive heterotrophy

Reasoning Steps:

- Match eukaryotic → Eliminates Bacteria/Archaea
- chitinous_cell_walls → Matches Fungi kingdom definition
- absorptive_heterotrophy → Confirms Fungi

Traverse hierarchy: Fungi → Dikarya → Basidiomycota → Agaricomycetes

```
{
  "kingdom": "Fungi",
  "phylum": "Basidiomycota",
  "class": "Agaricomycetes",
}
```

4. Conclusion and Evaluation

The Ontology COKB framework demonstrates significant potential for advancing knowledge representation and reasoning in biological taxonomy. By adapting its core components - Concepts, Hierarchy, Relations, Operators, Functions and Rules - to biological domains, we establish a formal structure capable of representing complex taxonomic knowledge while supporting automated reasoning. The implementation of 12 specialized fact types enables comprehensive capture of biological data, from basic taxonomic classifications to intricate ecological relationships.

However, certain limitations must be acknowledged. The framework's six-component structure presents implementation challenges for simpler domains, while performance constraints emerge with whole-genome scale analyses. Additionally, the system requires manual intervention to incorporate newly discovered species or revised classifications.

COKB demonstrates strong potential for biological knowledge management, combining formal representation with practical problem-solving. The COKB ontology represents a robust foundation for developing intelligent taxonomic systems, combining formal knowledge representation with practical problem-solving capabilities. Continued refinements will enhance its versatility across scientific domains. These advancements will build on the framework's proven adaptability, which has already demonstrated successful translation from its original geometric problem-solving domain to biological taxonomy and shows promise for extension to other scientific fields.

Potential applications and future projects include:

- **Visual Taxonomy Browser:**
An interactive tool that leverages the COKB ontology to allow users to explore taxonomic hierarchies visually. Such a browser could display relationships, attributes, and reasoning steps for each taxon, making complex classifications accessible to the public.
- **Evolutionary Relationship Mapper:**
A project focused on mapping and visualizing evolutionary dependencies and ecological interactions using the ontology's relational and functional facts. This tool could help biologists analyze phylogenetic trees, detect convergent evolution, and understand trait inheritance patterns.

These projects would further validate the ontology's utility in education, research, and biodiversity informatics. Future work will also address scalability, integration with genomic databases, and support for real-time classification updates as new species are discovered.

5. References

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