valuesets

A LinkML-based Framework for Standardized Enumerations with Semantic Grounding

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The Problem: Data Standardization is Hard

Every project reinvents the wheel with inconsistent representations:

```
# Different datasets, same concept
vital_status = "alive"      # Dataset A
vital_status = "LIVING"     # Dataset B
vital_status = 1            # Dataset C
vital_status = "A"          # Dataset D
```

Result: Thousands of incompatible representations blocking data integration

The Semantic Chasm

Despite massive infrastructure investment:

- **NLM VSAC**: 1,520+ clinical value sets
- **NCI Thesaurus**: 192,000 cancer concepts
- **NIH CDEs**: 142,000+ common data elements
- **HL7 FHIR**: Healthcare terminology standards

Yet: Scientific software still uses ad-hoc enumerations

Why? Complexity gap between terminology services and everyday programming

The Gap: What Exists vs What Developers Need

Existing Systems Provide	Developers Actually Need
Runtime services	Compile-time artifacts
Comprehensive coverage	Common values quickly
Authentication & servers	Zero dependencies
Healthcare-focused	Cross-domain support
Complex APIs	Native enums with IDE support

valuesets: Bridging the Gap

Core Idea: Compile semantically-grounded value sets into type-safe native code

A collection of common, standardized enumerations that:

- Link every value to ontology terms
- Provide Python-first convenience with multi-language support
- Built on LinkML standards
- Have zero runtime dependencies

"Stealth Semantics" in Action

```python
from valuesets.enums.core import VitalStatusEnum

status = VitalStatusEnum.ALIVE
print(status.value)               # "ALIVE"
print(status.get_meaning())       # "NCIT:C37987"
print(status.get_description())  # "Living or alive"

# Semantic interoperability across systems
if status1.get_meaning() == status2.get_meaning():
    process_compatible_records()
```

Simple interface, semantic power when needed

Rich Metadata & Ontology Mappings

```python
from valuesets.enums.bio.structural_biology import StructuralBiologyTechnique

technique = StructuralBiologyTechnique.CRYO_EM
print(technique.get_description())
# "Cryo-electron microscopy"

print(technique.get_meaning())
# "CHMO:0002413" (Chemical Methods Ontology)

print(technique.get_annotations())
# {'resolution_range': '2-30 Å typical', ...}
```

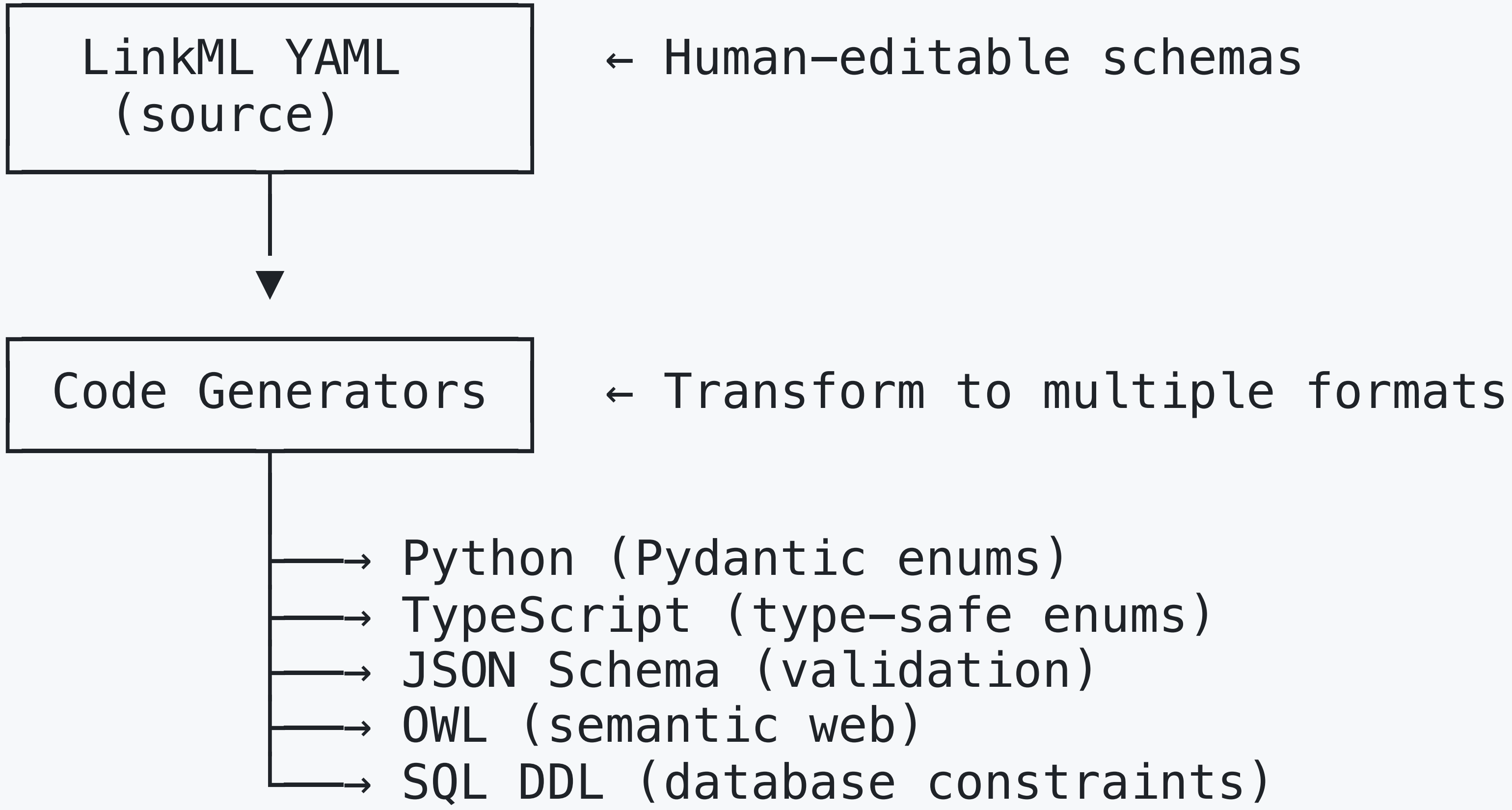
Cross-Domain Coverage

322 enumerations across 22 domains:

- **Biology** (127): Taxonomy, cell biology, structural techniques
- **Physical Sciences** (48): Chemical elements, materials, structures
- **Data Science** (43): Statistical tests, ML models, quality metrics
- **Healthcare** (29): Clinical findings, vital status, demographics
- **Computing** (23): File formats, languages, maturity levels
- **Geographic & Temporal** (31): Countries, time zones, spatial relations

78% have ontology mappings → 8,743 semantic links

Architecture: Build-Time not Runtime



LinkML YAML (source) ← Human-editable schemas

Code Generators ← Transform to multiple formats

- → Python (Pydantic enums)
- → TypeScript (type-safe enums)
- → JSON Schema (validation)
- → OWL (semantic web)
- → SQL DDL (database constraints)

Progressive Semantic Enhancement

Three levels of usage:

1. **~90% of use cases:** Simple type-safe enumerations

   ```
   status = VitalStatusEnum.ALIVE  # Just works
   ```

2. **~9% of use cases:** Access metadata for UIs/docs

   ```
   label = status.get_description()
   ```

3. **~1% of use cases:** Full semantic integration

   ```
   ontology_term = status.get_meaning()  # "NCIT:C37987"
   ```

Comparison with Established Systems

System	Scope	Access	Size	Advantage
VSAC	Clinical QM	API (auth)	Service	Cross-domain, no auth
NCIt	Cancer	500MB OWL	Service	Lightweight, simple
FHIR	Healthcare	Term. server	Service	Compile-time, no server
valuesets	Cross-domain	Native packages	<50MB	Developer-friendly

valuesets **complements** not replaces - provides practical bridge

Design Principles

1. **Semantic Grounding:** Every value links to ontologies
2. **Developer Ergonomics:** Native enums, full IDE support
3. **Modular Organization:** Import only what you need
4. **Extensibility:** Add new enums without breaking changes
5. **Multi-format:** JSON Schema, OWL, SQL, native code
6. **FAIR Compliance:** Persistent IDs, metadata, open access

LinkML: The Foundation

```yaml
enums:
  VitalStatusEnum:
    description: Status indicating whether individual is alive or deceased
    permissible_values:
      ALIVE:
        description: Living or alive
        meaning: NCIT:C37987
      DECEASED:
        description: Dead or deceased
        meaning: NCIT:C28554
      UNKNOWN:
        description: Vital status is not known
        meaning: NCIT:C17998
```

Human-readable → Machine-processable → Multiple outputs

Integration Patterns

Four primary adoption strategies:

1. **Direct Adoption:** Greenfield projects
2. **Mapping Layer:** Legacy system translation
3. **Hybrid Approach:** Dev/test vs. production
4. **Semantic Bridge:** Ontology integration

All paths support incremental adoption

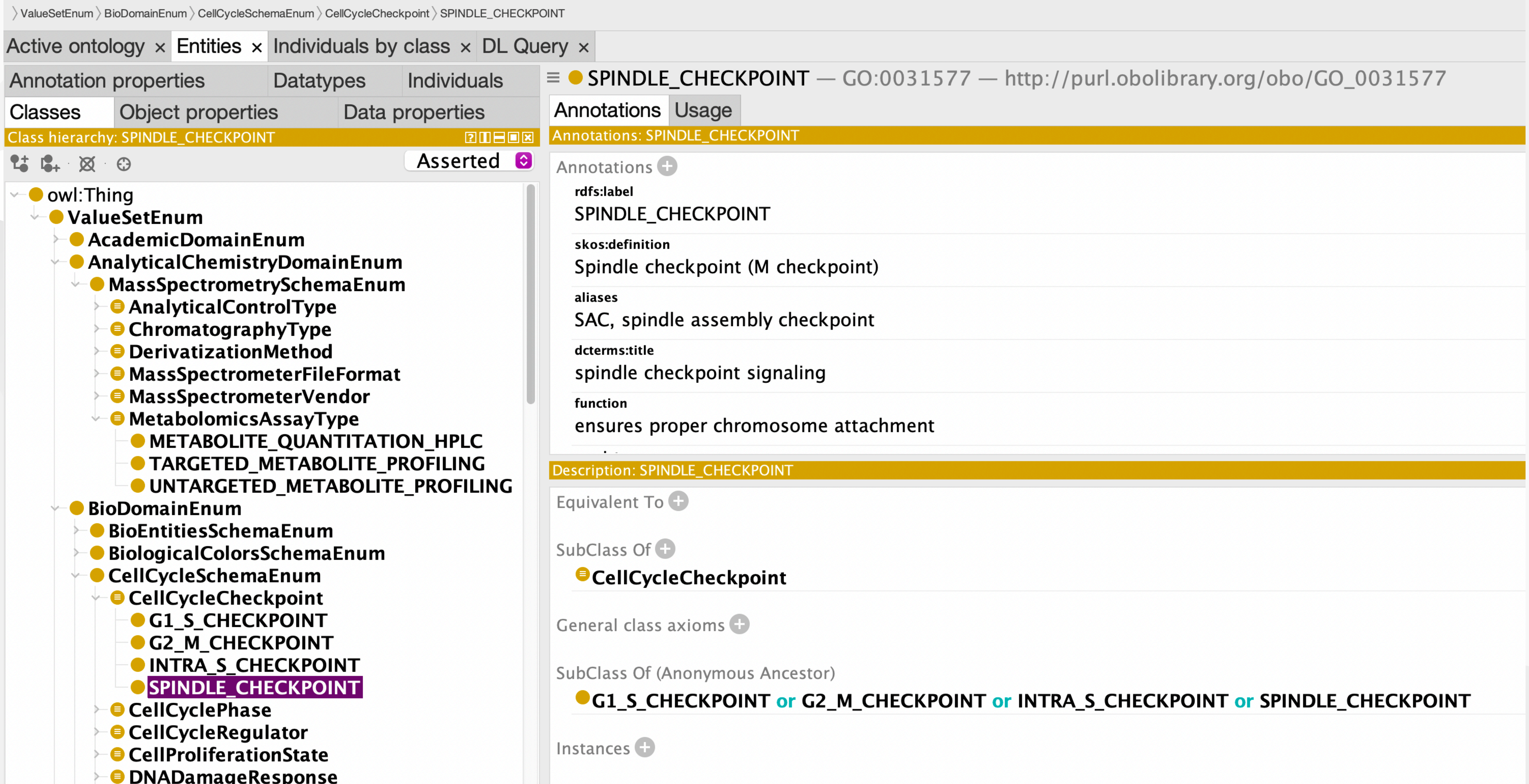
FAIR Data Principles

valuesets is FAIR-compliant:

- **Findable:** w3id.org permalinks, rich metadata
- **Accessible:** Open source, multiple formats
- **Interoperable:** LinkML, OWL, JSON-LD, FHIR
- **Reusable:** Clear licensing, documented provenance

Published as OWL ontology: https://w3id.org/valuesets/valuesets.owl.ttl

OWL Rendering in Protege



〉ValueSetEnum 〉BioDomainEnum 〉CellCycleSchemaEnum 〉CellCycleCheckpoint 〉SPINDLE_CHECKPOINT

Class hierarchy: SPINDLE_CHECKPOINT

- owl:Thing
  - ValueSetEnum
    - AcademicDomainEnum
    - AnalyticalChemistryDomainEnum
      - MassSpectrometrySchemaEnum
        - AnalyticalControlType
        - ChromatographyType
        - DerivatizationMethod
        - MassSpectrometerFileFormat
        - MassSpectrometerVendor
        - MetabolomicsAssayType
          - METABOLITE_QUANTITATION_HPLC
          - TARGETED_METABOLITE_PROFILING
          - UNTARGETED_METABOLITE_PROFILING
    - BioDomainEnum
      - BioEntitiesSchemaEnum
      - BiologicalColorsSchemaEnum
      - CellCycleSchemaEnum
        - CellCycleCheckpoint
          - G1_S_CHECKPOINT
          - G2_M_CHECKPOINT
          - INTRA_S_CHECKPOINT
          - SPINDLE_CHECKPOINT
        - CellCyclePhase
        - CellCycleRegulator
        - CellProliferationState
        - DNADamageResponse

SPINDLE_CHECKPOINT — GO:0031577 — http://purl.obolibrary.org/obo/GO_0031577

Annotations: SPINDLE_CHECKPOINT

Annotations

rdfs:label
SPINDLE_CHECKPOINT

skos:definition
Spindle checkpoint (M checkpoint)

aliases
SAC, spindle assembly checkpoint

dcterms:title
spindle checkpoint signaling

function
ensures proper chromosome attachment

Description: SPINDLE_CHECKPOINT

Equivalent To

SubClass Of
CellCycleCheckpoint

General class axioms

SubClass Of (Anonymous Ancestor)
G1_S_CHECKPOINT or G2_M_CHECKPOINT or INTRA_S_CHECKPOINT or SPINDLE_CHECKPOINT

Instances

Quality Assurance

Automated validation on every commit:

Validation Type	Coverage	Purpose
Syntax	100% schemas	LinkML compliance
Semantic	All mappings	Ontology term verification
Cross-reference	All namespaces	External reference resolution
Completeness	All enums	Missing descriptions/mappings
Consistency	All values	Duplicate detection

Dynamic Enums (Coming Soon)

Current: Static values with ontology mappings

Future: Runtime expansion from ontologies

```
CellTypeEnum:
  reachable_from:
    source_ontology: obo:cl
    source_nodes:
      - CL:0000540  # neuron
    relationship_types:
      - rdfs:subClassOf
```

Hybrid: static core + dynamic expansion for comprehensive coverage

Future Directions

Coverage Expansion:

- Social sciences, engineering, humanities

Technical Enhancements:

- Web-based validation APIs
- AI-assisted mapping tools
- Enhanced dynamic enum support

Governance:

- Domain-specific editorial committees
- Formal deprecation policies
- Maturity level indicators

Sustainability Through Simplicity

Technical Sustainability:

- Zero runtime dependencies
- No infrastructure costs
- Works offline, on laptops

Social Sustainability:

- Low barrier to contribution (edit YAML)
- Community-driven development
- Clear exit strategies

Economic Sustainability:

- No hosting/licensing costs

By the Numbers

Metric	Count
Enumerations	322
Permissible Values	7,512
Ontology Namespaces	117
Semantic Mappings	8,743
Domain Modules	22
Schemas	68
Ontology Mapping Coverage	78%

Quick Start

```
# Install
pip install valuesets

# Use immediately
from valuesets.enums.bio.taxonomy import CommonOrganismTaxaEnum
from valuesets.enums.core import VitalStatusEnum

human = CommonOrganismTaxaEnum.HUMAN
print(human.get_meaning())  # "NCBITaxon:9606"

status = VitalStatusEnum.ALIVE
print(status.get_meaning())  # "NCIT:C37987"
```

5-minute experience: Value within 5 minutes of discovery

Contributing

We welcome contributions from:

- **Domain Experts:** Add value sets for your field
- **Developers:** Improve tooling, fix issues
- **Users:** Report missing enums, share use cases

Process:

1. Edit YAML schema files
2. Add ontology mappings (use OLS)
3. Include descriptions and examples
4. Submit pull request

See: `CONTRIBUTING.md`

Development Commands

```
# Using just command runner
just --list          # Show all commands
just test            # Run tests
just doctest         # Run doctests
just validate        # Validate schemas
just site            # Build documentation
```

All managed through modern development workflows

Resources

- **Docs:** https://linkml.io/valuesets/
- **Repository:** https://github.com/linkml/common-value-sets
- **PyPI:** https://pypi.org/project/valuesets/
- **OWL Ontology:** https://w3id.org/valuesets/valuesets.owl.ttl
- **LinkML:** https://linkml.io/

Key Insight

> "The problem is not missing standards but mismatched abstractions"

valuesets bridges the gap:

- Terminology services → Terminology artifacts
- Runtime flexibility → Compile-time guarantees
- Institutional deployment → Developer laptops

Making semantic standards accessible to everyday programming

valuesets

Making Data Standardization Simple, Semantic, and Scalable

Try it today:

```
pip install valuesets
```

Questions?

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Appendix: Example Domains

Biological Sciences:

- Taxonomy (NCBI), Cell types (CL), Cell cycle (GO)
- Gene Ontology evidence codes
- Structural biology techniques (CHMO)
- Model organisms

Data Science:

- Statistical tests (STATO)
- ML model types, dataset splits
- Data quality indicators

Clinical/Healthcare:

- Vital status (NCIT), blood types (SNOMED)

Appendix: Semantic Web Integration

```
from valuesets.enums.bio.cell_cycle import CellCyclePhase

# Generate SPARQL query
phase = CellCyclePhase.S_PHASE
go_term = phase.get_meaning()  # "GO:0000084"

sparql = f"""
SELECT ?gene ?function
WHERE {{
    ?gene cellCyclePhase <{go_term}> .
    ?gene hasFunction ?function .
}}
"""
```

Seamless integration with knowledge graphs

Appendix: Multi-Language Support

Current:

- Python (Pydantic enums)
- TypeScript (type-safe)
- JSON Schema
- OWL/RDF

Planned:

- Java
- R
- Julia
- Rust

LinkML generates idiomatic code for each language

Credits & Acknowledgments

Contributors:

- **Christopher J. Mungall** - Lawrence Berkeley National Laboratory
- **Justin Reese** - Lawrence Berkeley National Laboratory

Built with:

- **LinkML** - Linked Data Modeling Language
- **linkml-project-copier** - Project template
- **OBO Foundry** - Biological ontologies
- **OLS/BioPortal** - Ontology lookup services

Open source • MIT License • Community-driven