METPO: A Pragmatic Ontology for Microbial Ecophysiological Traits

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The Data Integration Challenge

Microbial trait data is abundant, but it's semantically inconsistent:

BacDive (nested JSON)

```
{
  "culture_temp": {
    "temperature":
      "mesophilic"
  }
}
```

BactoTraits (multi-header CSV)

```
Trait_class | Trait_name | Unit
Temperature | Class      |
            | mesophile  |
```

Madin et al. (flat table)

```
taxon,temp_pref
12345,mesophilic
```

Problem: Cannot query "all psychrophiles" across datasets without semantic normalization.

Solution: We need an ontology.

The Gap in the Ontology Landscape

We evaluated existing ontologies for microbial trait coverage:

Ontology	Last Updated	Status	Domain
MPO	2014	Unmaintained	Microbial Phenotypes
MicrO	2018	Unmaintained	Microbiology
MCO	2019	Unmaintained	Microbial Conditions
OMP	2024	Active	Microbe Phenotypes
PATO	Active	Active	Quality Attributes

Key findings:

- No single ontology provides comprehensive coverage for BacDive, BactoTraits, and Madin datasets
- Many domain-specific ontologies lack active maintenance
- Integration of multiple ontologies introduces significant complexity

Introducing METPO

Microbial Ecophysiological Trait and Phenotype Ontology

Design philosophy: Application-driven development

- **Focused:** 255 classes covering BacDive, BactoTraits, and Madin datasets
- **Lightweight:** Purpose-built for KG-Microbe knowledge graph
- **Modern:** ODK, ROBOT, OAK tooling
- **Maintained:** Active development for DOE CMM project

Core principle: Build ontologies that serve real applications, driven by actual data integration needs.

METPO's Modern & Pragmatic Design

1. Captures Real-World Variations

METPO synonyms handle messy data:

```
METPO:1000644 a owl:Class ;
  rdfs:label "heterotrophic" ;
  oboInOwl:hasRelatedSynonym
    "TT_heterotroph" ;         # BactoTraits
  oboInOwl:hasRelatedSynonym
    "aerobic_heterotrophy" ;  # Madin
  oboInOwl:hasRelatedSynonym
    "heterotroph" .           # Common variant
```

Enables semantic normalization across all three data sources.

2. LLM-Assisted Curation

Semantic search pipeline:

- OLS + BioPortal + Names4Life embeddings
- ~3,000 SSSOM mappings (exactMatch, closeMatch, etc.)

Modern development:

- ODK build system + ROBOT validation
- Spreadsheet-based curation
- CI/CD automation

ICBO 2025 Theme: AI-enabled ontology development

METPO in Production: KG-Microbe Statistics

Real-world usage across three major datasets:

Dataset	Records	METPO Edges	Coverage	METPO Terms Used
BactoTraits	19,456 strains	87,688	100%	91
Madin et al.	172,324 taxa	45,851	39.7%	36
BacDive	196,169 nodes	120,266	7.3%	61
Combined	1.86M edges	253,805	13.6%	**152 unique**

Source: Direct analysis of KG-Microbe transformed data (TSV files)

METPO in Action: Powering KG-Microbe

Before: Heterogeneous Data

```
// BacDive
{"culture_temp": "mesophilic"}

// BactoTraits
[blank][mesophile][blank]

// Madin
temperature_preference: mesophilic
```

Three formats, three field names, slight variations in values.

Cannot query across datasets.

After: Unified Knowledge Graph (KGX)

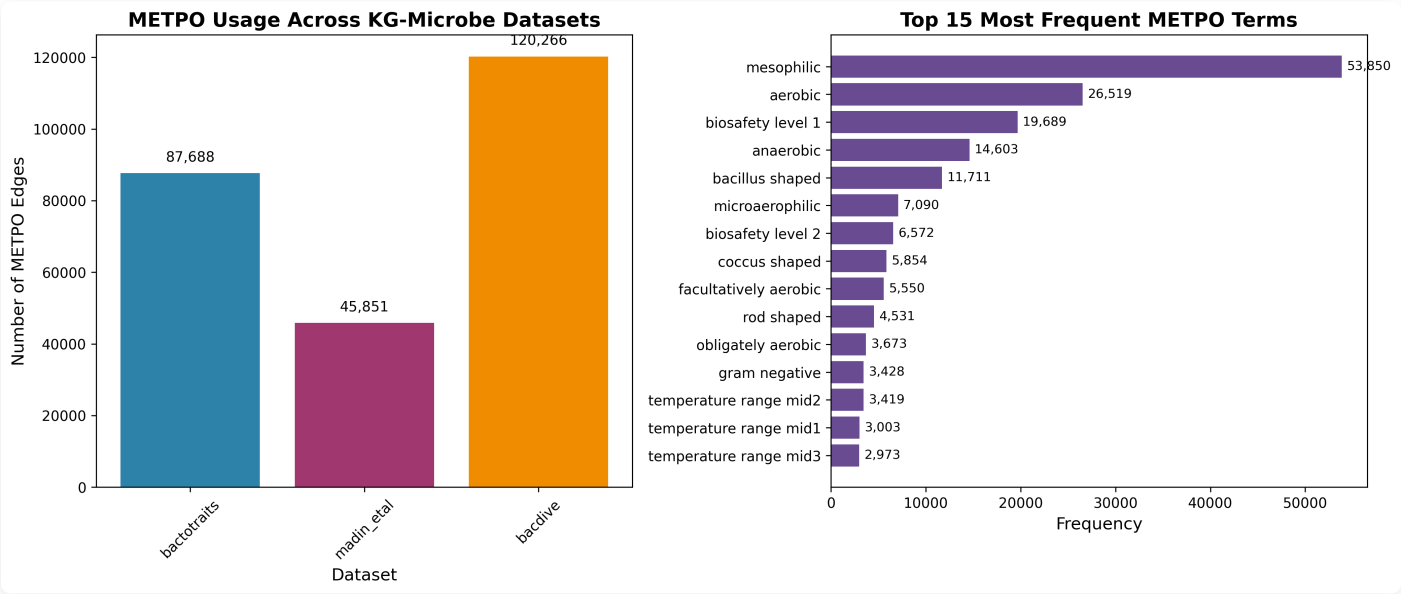
```
subject            predicate               object
NCBITaxon:100   biolink:has_phenotype  METPO:1000615
NCBITaxon:200   biolink:has_phenotype  METPO:1000615
NCBITaxon:300   biolink:has_phenotype  METPO:1000615
```

All variations normalized to single METPO CURIE.

Now queryable with SPARQL:

```
SELECT ?taxon WHERE {
  ?taxon biolink:has_phenotype METPO:1000615
}
```

KG-Microbe: METPO as Semantic Backbone



Production knowledge graph for growth media prediction:

- **253,805 METPO edges** across 1.86M total edges
- **152 unique METPO terms** normalize traits from three heterogeneous datasets
- **Biolink model compliance** enables standard graph queries
- **Application:** CMM project - predicting organisms for REE biorecovery

Real Data Example: KG-Microbe Triples

From transformed data (BacDive → KGX):

```
# Nodes
METPO:1000615  biolink:PhenotypicQuality  mesophilic
METPO:1000602  biolink:PhenotypicQuality  aerobic
METPO:1000614  biolink:PhenotypicQuality  psychrophilic
METPO:1000644  biolink:PhenotypicQuality  heterotrophic

# Edges
NCBITaxon:100  biolink:has_phenotype  METPO:1000615  RO:0002200  bacdive:17384
NCBITaxon:100  biolink:has_phenotype  METPO:1000602  RO:0002200  bacdive:17385
NCBITaxon:200  biolink:has_phenotype  METPO:1000614  RO:0002200  bacdive:23451
```

This is production data - METPO CURIEs in use, enabling ML predictions.

METPO's Object Property Model

1. Phenotype Assertions

```
metpo:2000102 a owl:ObjectProperty ;
  rdfs:label "has phenotype" ;
  rdfs:domain metpo:1000525 ;  # microbe
  rdfs:range metpo:1000059 .   # phenotype

# Usage example:
NCBITaxon:562 metpo:2000102 metpo:1000602 .
# E. coli has_phenotype aerobic
```

2. Process Capabilities

```
metpo:2000103 a owl:ObjectProperty ;
  rdfs:label "capable of" ;
  rdfs:domain metpo:1000525 ;  # microbe
  rdfs:range metpo:1000630 .   # process

# B. subtilis capable_of sporulation
```

3. Chemical Interactions (20+ subproperties)

```
metpo:2000001 a owl:ObjectProperty ;
  rdfs:label "organism interacts with chemical" ;
  rdfs:domain metpo:1000525 ;  # microbe
  rdfs:range metpo:1000526 .   # chemical

# Subproperties include:
# ferments, uses_as_carbon_source, degrades,
# uses_as_electron_acceptor, oxidizes, reduces
# ... 14 more

# Example:
NCBITaxon:562 metpo:2000011 CHEBI:17234 .
# E. coli ferments glucose
```

Future Work: Literature-Based Discovery

Expanding METPO through OntoGPT experiments:

Input: PubMed abstract

```
Methylovirgula ligni gen. nov., sp. nov.,
an obligately acidophilic, facultatively
methylotrophic bacterium...

Two strains of Gram-negative, aerobic,
non-pigmented, non-motile, rod-shaped
bacteria were isolated...
```

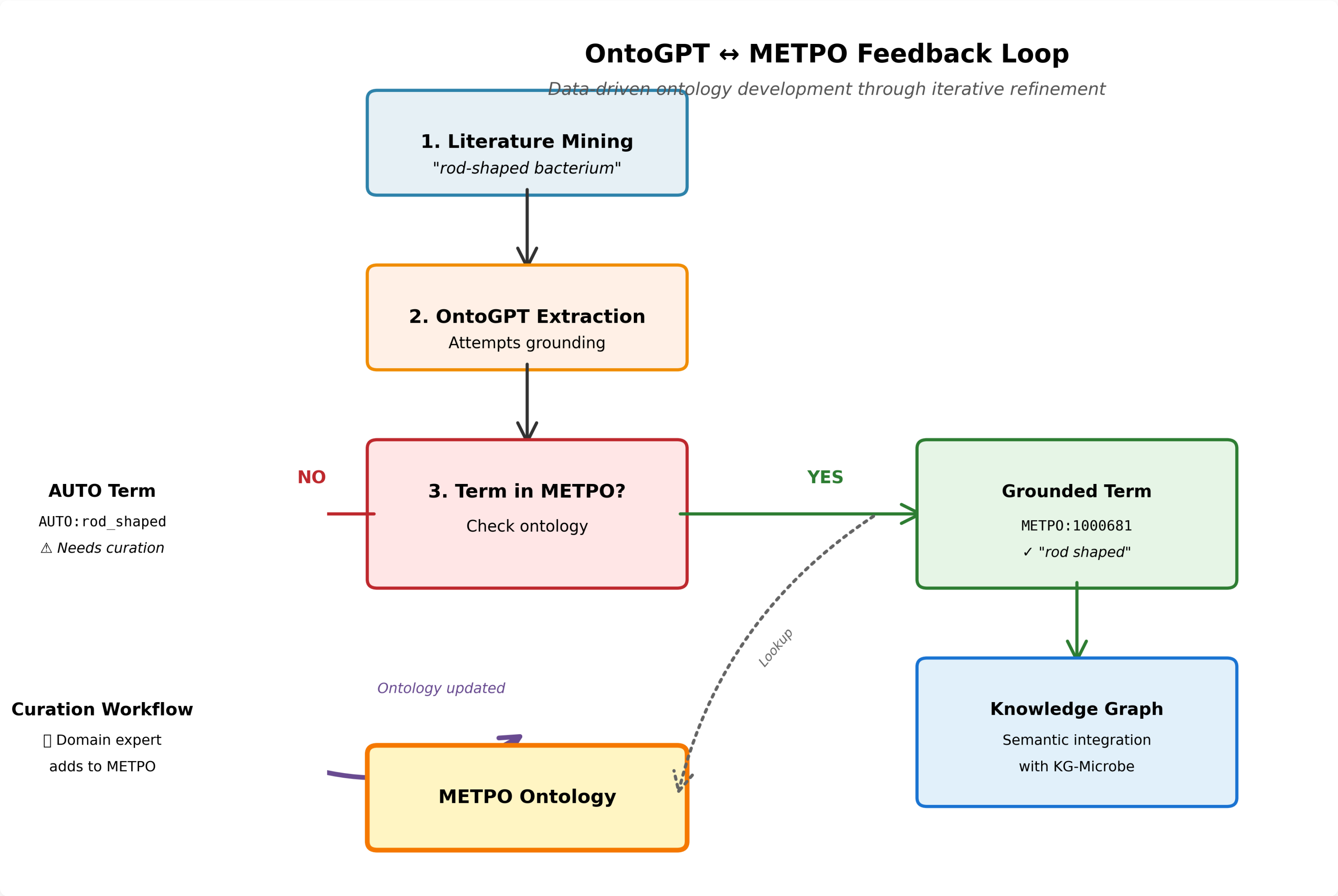
Output: RDF triples (Turtle)

```
AUTO:BW863
  has_phenotype METPO:1000143 . # ✅ Gram-negative
AUTO:BW863
  has_phenotype METPO:1000602 . # ✅ aerobic
AUTO:BW863
  has_phenotype AUTO:rod-shaped . # ❌ gap!
AUTO:BW863
  has_phenotype METPO:1000181 . # ✅ mesophilic
```

Results (10 PubMed abstracts):

- Phenotype: 32.5% to METPO (25/77)
- Chemical: 100% to ChEBI (47/47)
- Taxonomy: 100% to NCBITaxon (22/22)
- 52 AUTO terms → coverage gaps

Data-Driven Ontology Development



OntoGPT ↔ METPO Feedback Loop

Data-driven ontology development through iterative refinement

1. Literature Mining
"rod-shaped bacterium"

2. OntoGPT Extraction
Attempts grounding

3. Term in METPO?
Check ontology

AUTO Term
`AUTO:rod_shaped`
⚠ *Needs curation*

Grounded Term
`METPO:1000681`
✓ *"rod shaped"*

Knowledge Graph
Semantic integration
with KG-Microbe

Curation Workflow
▯ Domain expert
adds to METPO

METPO Ontology

Failed groundings drive iterative expansion:

OntoGPT Grounding: Data-Driven Expansion

Structured data integration (Phase 1): Production-ready

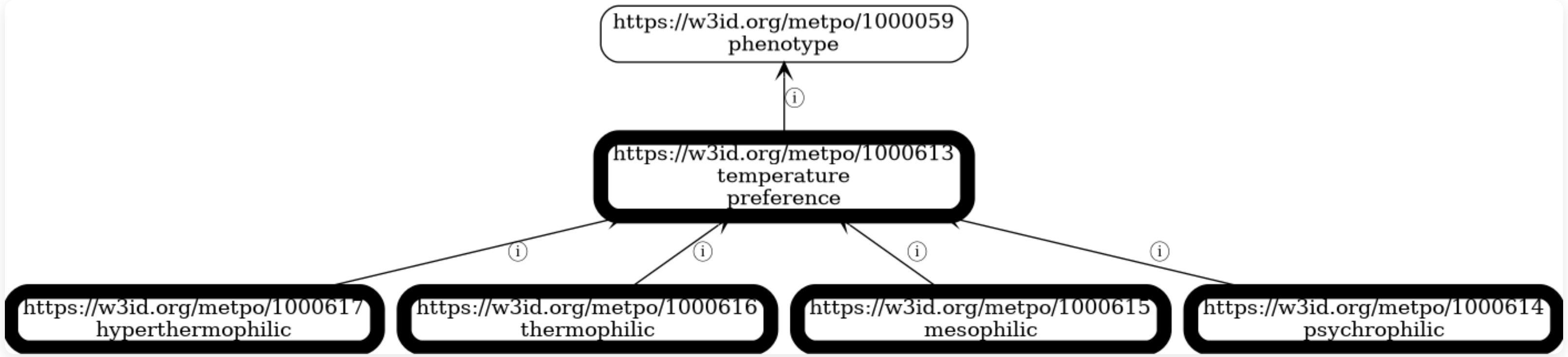
- 253,805 METPO edges in KG-Microbe
- Three major datasets fully integrated
- METPO provides semantic normalization layer

Literature mining (Phase 2): Experimental validation

- 10 PubMed abstracts processed through OntoGPT
- Mixed grounding success identifies where METPO needs expansion
- 52 failed groundings → curation priorities for domain experts

Insight: Failed groundings are features, not bugs—they guide ontology development

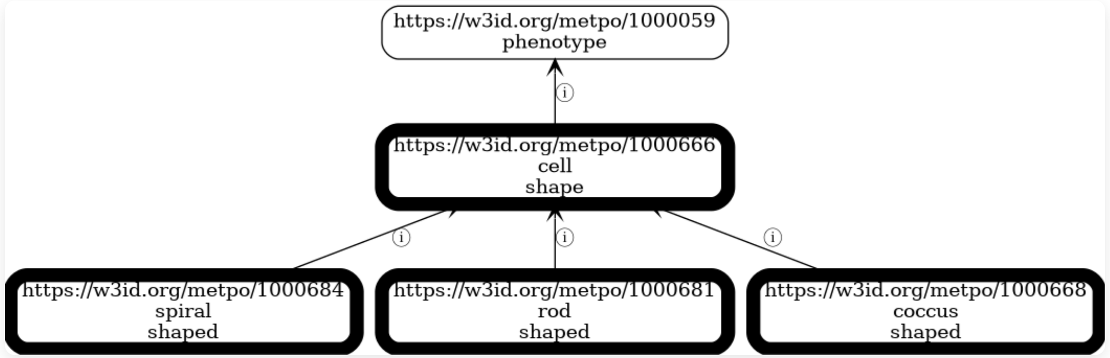
METPO's Phenotype Hierarchies


https://w3id.org/metpo/1000059
phenotype
i
https://w3id.org/metpo/1000613
temperature preference
i
i
i
i
https://w3id.org/metpo/1000617
hyperthermophilic
https://w3id.org/metpo/1000616
thermophilic
https://w3id.org/metpo/1000615
mesophilic
https://w3id.org/metpo/1000614
psychrophilic

Temperature preference phenotypes:

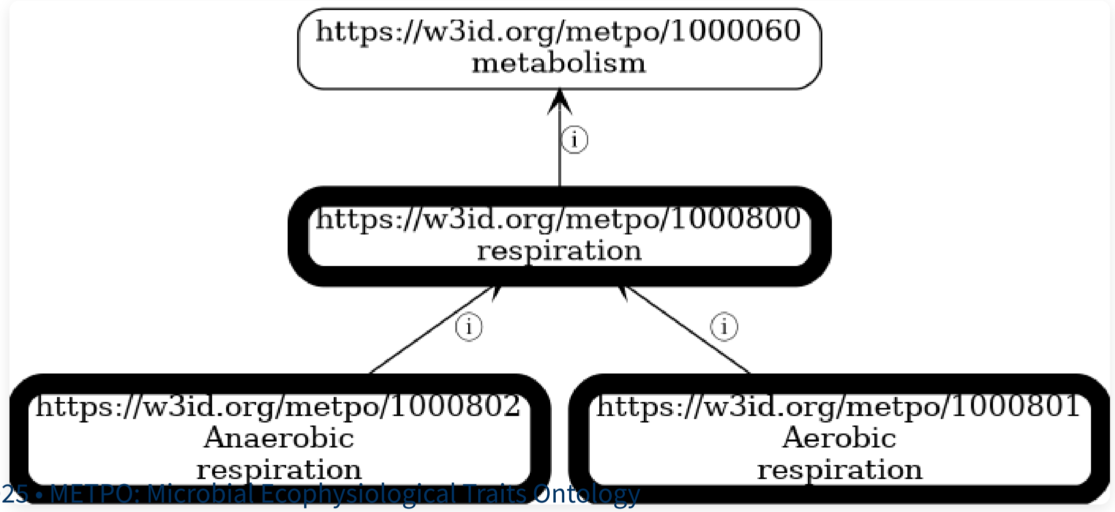
- **Psychrophilic** (≤15°C) - grows at low temperatures
- **Mesophilic** (20-45°C) - grows at intermediate temperatures
- **Thermophilic** (≥45°C) - grows at elevated temperatures
- **Hyperthermophilic** (≥80°C) - grows at very high temperatures

Morphological and Process Phenotypes


https://w3id.org/metpo/1000059
phenotype
i
https://w3id.org/metpo/1000666
cell
shape
i
i
i
https://w3id.org/metpo/1000684
spiral
shaped
https://w3id.org/metpo/1000681
rod
shaped
https://w3id.org/metpo/1000668
coccus
shaped

Cell morphology phenotypes:

- Coccus shaped (spherical), Rod shaped (bacillus), Spiral shaped


https://w3id.org/metpo/1000060
metabolism
i
https://w3id.org/metpo/1000800
respiration
i
i
https://w3id.org/metpo/1000802
Anaerobic
respiration
https://w3id.org/metpo/1000801
Aerobic
respiration

Interoperability: METPO is a Good Citizen

SSSOM Mappings via embedding searches on METPO labels:

Generated ~3,000 mappings using semantic search (OLS + BioPortal + Names4Life):

- **Relaxed strategy:** 3,008 mappings (mostly broadMatch/relatedMatch)
- **Optimized strategy:** 2,883 mappings (only 73 exactMatch)

Method: Embedding-based semantic search using `text-embedding-3-small`

Reality check: Mean structural coherence = 8.2%

- Semantic matches exist, but hierarchical organization differs significantly
- Justifies purpose-built ontology over importing external structures

Availability:

- BioPortal: https://bioportal.bioontology.org/ontologies/METPO
- GitHub: https://github.com/berkeleybop/metpo
- Standard formats: OWL/RDF, works with OAK, ROBOT, Protégé

Sustainability & Governance

METPO supports CultureBot (LBNL LDRD):

- **Goal:** ML models to predict growth conditions for unculturable microbes
- **KG-Microbe's role:** Training data (253K+ phenotype assertions)
- **METPO's role:** Semantic normalization enabling predictions

How we ensure METPO won't be abandoned:

1. **Active funding:** DOE CMM project + CultureBot LDRD
2. **Production dependency:** ML pipeline requires standardized phenotypes
3. **Modern tooling:** ODK, ROBOT, OAK
4. **Accessible curation:** Spreadsheet-based, LLM-assisted

Governance: PI Marcin Joachimiak (LBNL), application-driven, GitHub contributions

ICBO 2025 Theme: Long-term sustainability

Conclusion

METPO demonstrates an application-driven approach:

✅ **Production validation:** 253,805 edges in 1.86M-edge knowledge graph
✅ **Sustainability:** Active funding, real dependencies, modern tooling
✅ **Transparency:** All claims traceable to primary sources
✅ **Interoperability:** ~3,000 SSSOM mappings (but low structural coherence: 8.2%)
✅ **AI-assisted:** LLM-powered curation workflows

Key insight: Purpose-built ontologies work when driven by real needs—even when existing ontologies have poor structural alignment

Thank You

Resources:

GitHub: github.com/berkeleybop/metpo • BioPortal: bioportal.bioontology.org/ontologies/METPO

KG-Microbe: github.com/Knowledge-Graph-Hub/kg-microbe

Contact: Mark Miller, LBNL • PI: Marcin Joachimiak

Acknowledgments:

CultureBot LDRD • DOE CMM Program • LBNL Biosciences • OntoGPT/OAK teams

Questions?

Backup Slides

CMM Project Context

Advanced Biorecovery of Critical Minerals through AI/ML-Guided Design

Goal: Recover Rare Earth Elements (Nd, Pr, Dy) from e-waste using engineered microbes

KG-CMREE extends KG-Microbe:

- Adds REE bioaccumulation phenotypes
- Lanthanophore biosynthetic pathways
- Spectroscopic measurements
- High-throughput screening results

METPO's role: Annotates microbial traits critical for REE recovery

- pH tolerance, temperature tolerance, metal tolerance, metabolic capabilities
- Enables AI models to predict which microbes can thrive in REE recovery conditions

Technical Details: METPO Development

Source of truth: ROBOT-compatible spreadsheets (Google Sheets)

Build system: Ontology Development Kit (ODK)

Validation: ROBOT (0 errors, 318 minor whitespace warnings)

Semantic search: OLS + BioPortal + Names4Life embeddings, generates SSSOM mappings

Statistics: 255 terms, 118 with definitions (46.3%), 158 mapped to 24 external ontologies

Design Rationale: Why Build METPO?

Coverage challenge:

- Existing ontologies lack comprehensive coverage for our three datasets
- Integration complexity increases non-linearly with number of source ontologies
- Unmaintained ontologies present long-term sustainability risks

Practical approach:

- Build focused ontology for immediate application needs
- Map to external ontologies for interoperability (~3,000 SSSOM mappings)
- Maintain lightweight hierarchy optimized for our use cases

Development efficiency:

- 255 terms covers core needs vs. integrating dozens of partial ontologies
- Spreadsheet-based curation accessible to domain experts
- ODK/ROBOT automation prevents technical debt

Comprehensive Ontology Survey: What We Evaluated

Systematic embedding-based testing:

- **39 ontologies tested** (778K total embeddings)
- **Top tested:** CHEBI (221K), upheno (192K), GO (84K), OBA (73K)
- **24 retained** (20 OLS + 4 BioPortal-only)
- **15 removed** (including CHEBI - worst ROI)

Final retained: upheno, go, oba, flopo, micro, pato, envo, ecocore, eupath, phipo, mco, eco, omp, ohmi, cmpo, biolink, apo, pco, geo, exo + d3o, meo, miso, n4l_merged

Result: 3,019 SSSOM mappings

See: PRIMARY_SOURCE_ONTOLOGY_ANALYSIS.md

Why Not Import? Minimum Import Set Analysis

Q: Based on high-quality matches, how many ontologies would we need to import?

Excellent matches (similarity ≥ 0.75):

- 182 matches across 21 ontologies
- Top 8 provide 91% coverage: micro (91), upheno (19), mpo (16), n4l_merged (14), oba (10), envo (4), biolink (4), flopo (3)

Answer: ~8 ontologies for 90% coverage

Why METPO uses mappings instead:

- **8 ontology imports:** Complex integration, licensing, hierarchy conflicts, maintenance burden
- **255 METPO classes + 3,019 mappings:** Structural independence, clean hierarchies, focused scope
- Both achieve interoperability, but METPO maintains consistency for KG-Microbe reasoning

Structural incompatibility: Different hierarchical philosophies make direct import challenging

- METPO: trait-centric organization for database annotation

Semantic-SQL Ontology Registry

INCATools semantic-sql provides standardized SQL views for 113+ ontologies

Registry: `semantic-sql/src/semsql/builder/registry/ontologies.yaml`

METPO integration:

- Available as `metpo.db`
- Queryable via SQL
- Part of broader OBO ecosystem

Ontology availability:

- **In OLS:** micro, upheno, oba, flopo, envo, biolink, go, pato
- **BioPortal-only:** d3o, meo, miso (DSMZ)
- **Not in registries:** n4l_merged (Names4Life)

More info: https://github.com/INCATools/semantic-sql