METPO: A Pragmatic Ontology for Microbial Ecophysiological Traits

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How can we design experiments to make better use of microbes for our environment and economy?

We will need to characterize their ecophysiological traits:

Environmental preferences and metabolic capabilities that define where and how microbes grow:

- Temperature preference (psychrophilic ≤15°C, **mesophilic** 20-45°C, thermophilic ≥45°C)
- Oxygen requirements (aerobic, anaerobic)
- pH tolerance, salinity tolerance, metabolic pathways

The challenge: Trait data is abundant but semantically inconsistent across major datasets, limiting its use in machine learning.

The Microbial Ecophysiological Trait and Phenotype Ontology (METPO) provides standardization.

Data Source 1: Madin et al. (flat table)

condensed_traits_NCBI.csv

taxon	tax_id	optimum_tmp	temp_pref
Acetobacter fabarum	483199	28	mesophilic

Format: Flat CSV table

Taxon: `taxon` (name) + `tax_id` (NCBI taxonomy ID)

Temperature: Numeric (`optimum_tmp`) + qualitative (`temp_pref`)

Data Source 2: BactoTraits (3-header CSV)

BactoTraits_databaseV2_Jun2022.csv

		temp_Optimum		
		Celsius degree		
Bacdive_ID	Full_name	TO_27_to_30	TO_30_to_34	TO_>40
19	Acetobacter oeni Silva et al. 2006	**1**	0	0

Format: Semicolon-delimited CSV with 3 header rows (category, units, column names)

Taxon: `Bacdive_ID` + `Full_name` columns

Temperature: Weighted values across temperature ranges (sum to 1.0)

Data Source 3: BacDive (nested JSON)

BacDive API

```json
{
  "General": {
    "BacDive-ID": 100,
    "keywords": ["anaerobe", "mesophilic"],
    "NCBI tax id": [{"NCBI tax id": 33025, "Matching level": "species"}]
  },
  "Name and taxonomic classification": {
    "species": "Phascolarctobacterium faecium"
  },
  "Culture and growth conditions": {
    "culture temp": {
      "temperature": "37"
    }
  }
}
```

Format: Nested JSON (some paths are deeply nested)

Source: BacDive REST API

Cannot query "all mesophiles" across datasets without semantic normalization

Each dataset uses different:

- File formats (JSON, CSV)
- Column naming conventions
- Value representations (qualitative vs. quantitative)
- Taxon identifiers

Integration into KG-Microbe: 328K nodes, 1.86M edges from **observation-based** phenotypes (not genome predictions)

Solution: We need an ontology to provide semantic interoperability.

The Gap in the Ontology Landscape

We evaluated existing ontologies for microbial trait coverage:

Ontology	Last Updated
MPO (Microbial Phenotype Ontology)	2014
MicrO (Microbiology Ontology)	2018
MCO (Microbial Conditions Ontology)	2019
OMP (Ontology of Microbial Phenotypes)	2024
PATO (Phenotype and Trait Ontology)	Active

Key findings:

- No single ontology provides comprehensive coverage for BacDive, BactoTraits, and Madin datasets
- Many domain-specific ontologies lack active maintenance

The Gap: Technical Issues with Existing Ontologies

Technical issues limit their use:

- MicrO has 7,130 validation errors and 60 unsatisfiable classes when imported
- MPO embeddings are close to METPO but definitions are just label repetitions

Reality check: Mean structural coherence = 8.2%

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

Introducing METPO

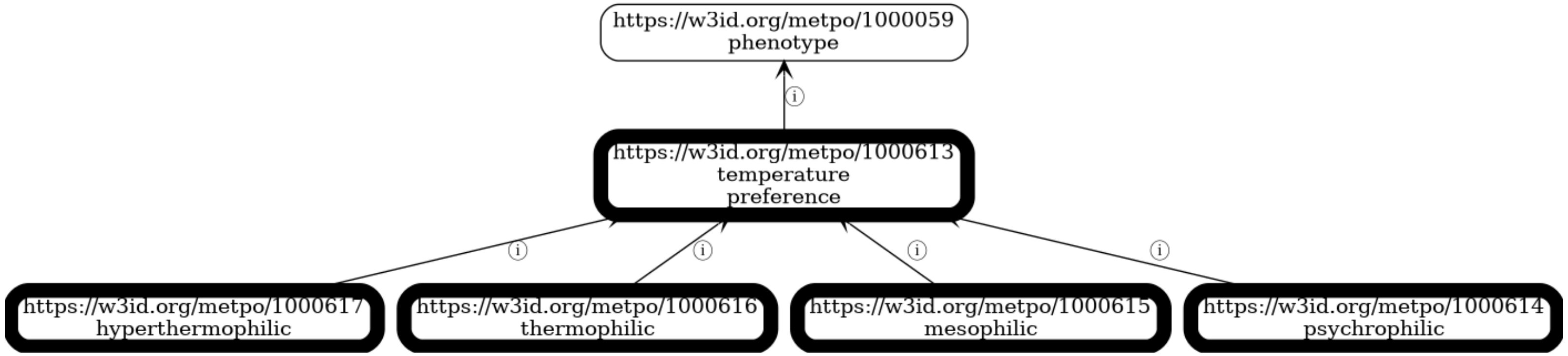
Microbial Ecophysiological Trait and Phenotype Ontology

Design philosophy: Application-driven development

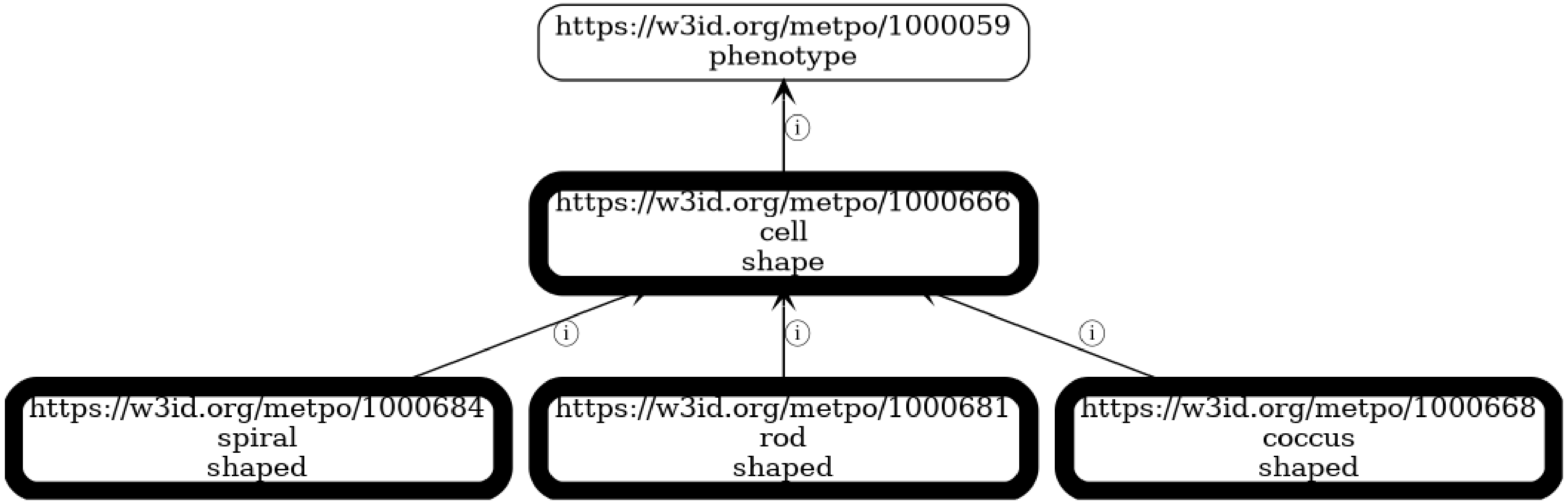
- **Focused:** 255 classes covering BacDive, BactoTraits, and Madin datasets
- **Lightweight:** Purpose-built for KG-Microbe knowledge graph
- **Modern:** ODK and ROBOT tooling
- **Maintained:** Active development for DOE CMM project and CultureBot

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

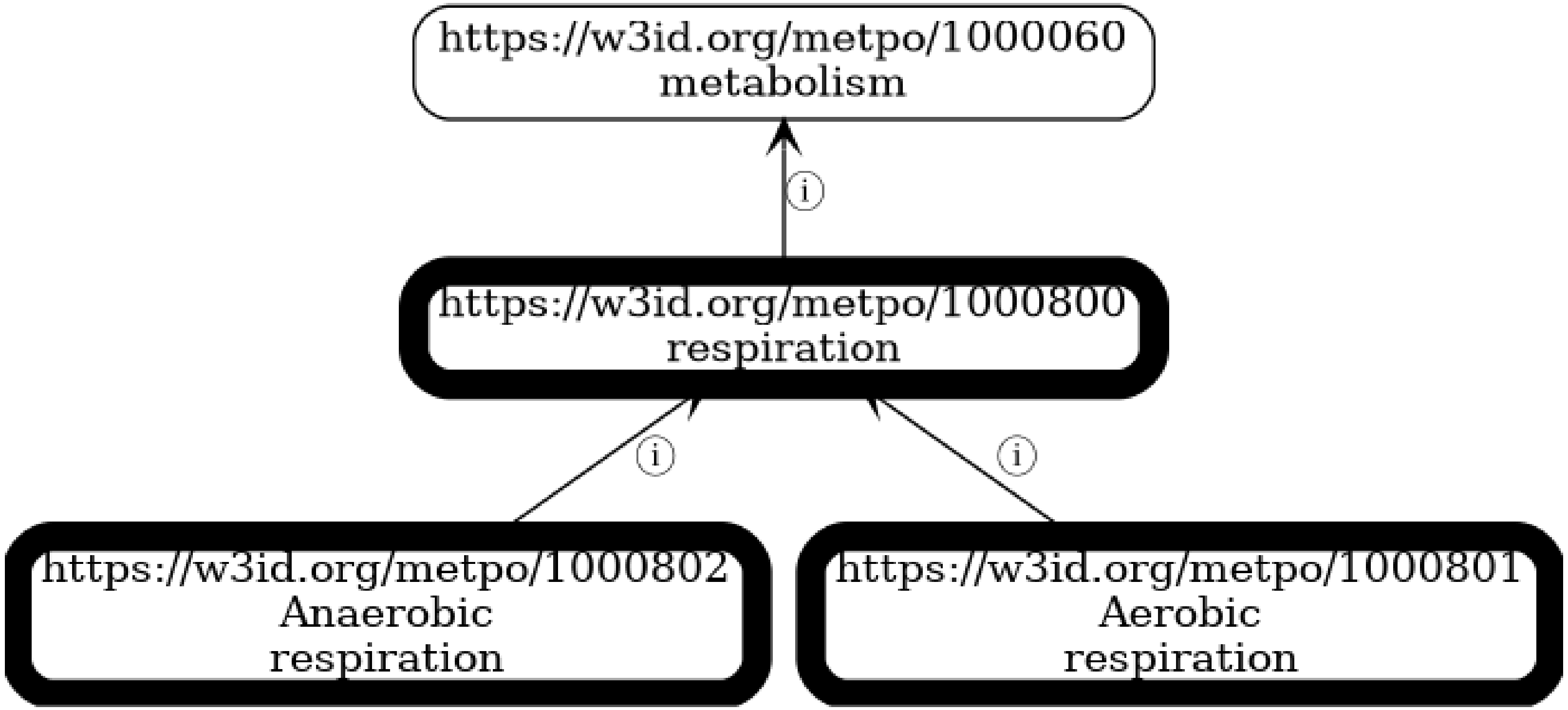
METPO's Phenotype Hierarchies: Temperature Preference


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

METPO's Phenotype Hierarchies: Cell Shape


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

METPO's Phenotype Hierarchies: Respiration


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

Synonym provenance tracking using annotated axioms

Direct synonym assertion (no provenance):

```
metpo:1000644 oboInOwl:hasRelatedSynonym "aerobic_heterotrophy" .
metpo:1000644 oboInOwl:hasRelatedSynonym "heterotroph" .
```

Annotated axioms (with provenance):

```
[] a owl:Axiom ;
  owl:annotatedSource metpo:1000644 ;
  owl:annotatedProperty oboInOwl:hasRelatedSynonym ;
  owl:annotatedTarget "aerobic_heterotrophy" ;
  IAO:0000119 <https://github.com/jmadin/bacteria_archaea_traits> .

[] a owl:Axiom ;
  owl:annotatedSource metpo:1000644 ;
  owl:annotatedProperty oboInOwl:hasRelatedSynonym ;
  owl:annotatedTarget "heterotroph" ;
  IAO:0000119 <https://bacdive.dsmz.de/> .
```

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
```

METPO in Production: Powering KG-Microbe

Before: Heterogeneous Data

```
// BacDive (nested JSON)
Culture and growth conditions.culture temp.temperature: "37"

// BactoTraits (boolean columns)
TO_27_to_30: 1

// Madin (qualitative term)
temp_pref: "mesophilic"
```

Three formats, three schemas, different representations.

Cannot query across datasets.

After: Unified Knowledge Graph (KGX)

```
 subject            predicate               object
NCBITaxon:227942  biolink:has_phenotype  METPO:1000615
NCBITaxon:438751  biolink:has_phenotype  METPO:1000615
NCBITaxon:552064  biolink:has_phenotype  METPO:1000615
```

All variations normalized to single METPO CURIE.

Now queryable with SPARQL (for example):

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

KG-Microbe Statistics

Real-world usage across three major datasets:

Dataset	Source Records	Total KG Edges	METPO Object Edges	METPO Utilization so far*	METPO Terms
BactoTraits	19,455 strains	87,688	87,688	100%	91
Madin et al.	172,324 taxa	115,399	45,851	39.7%	36
BacDive	196,169 strains	1,656,667	120,266	7.3%	61
Combined	—	1,859,754	253,805	13.6%	**152 unique**

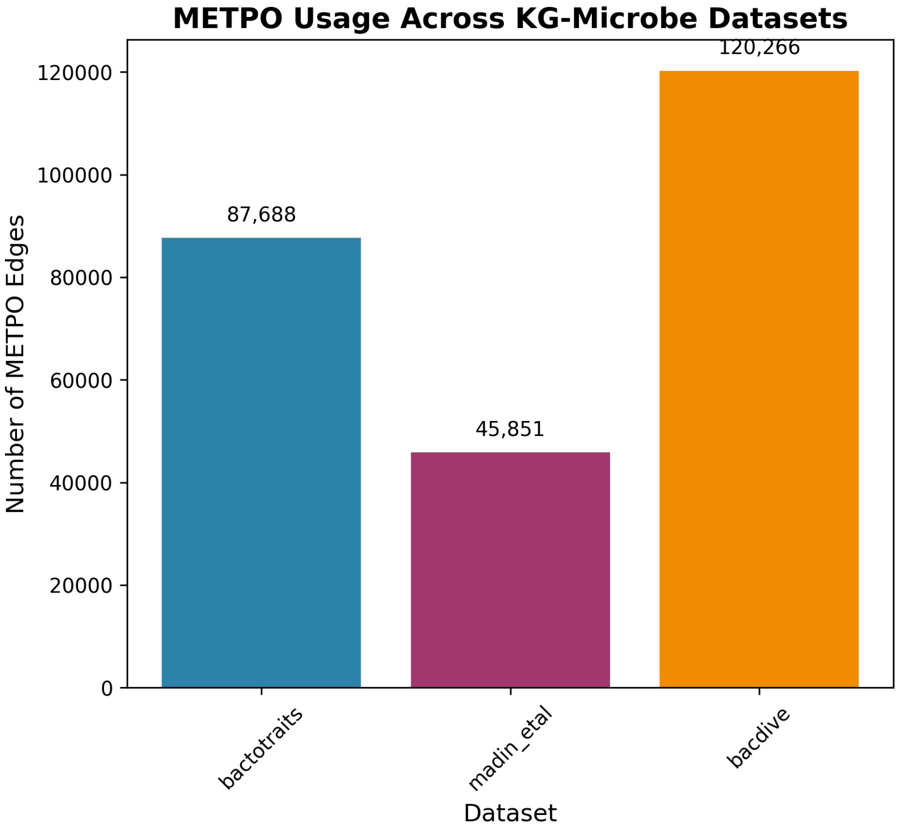
Object prefix distribution (top 3 by edge count):

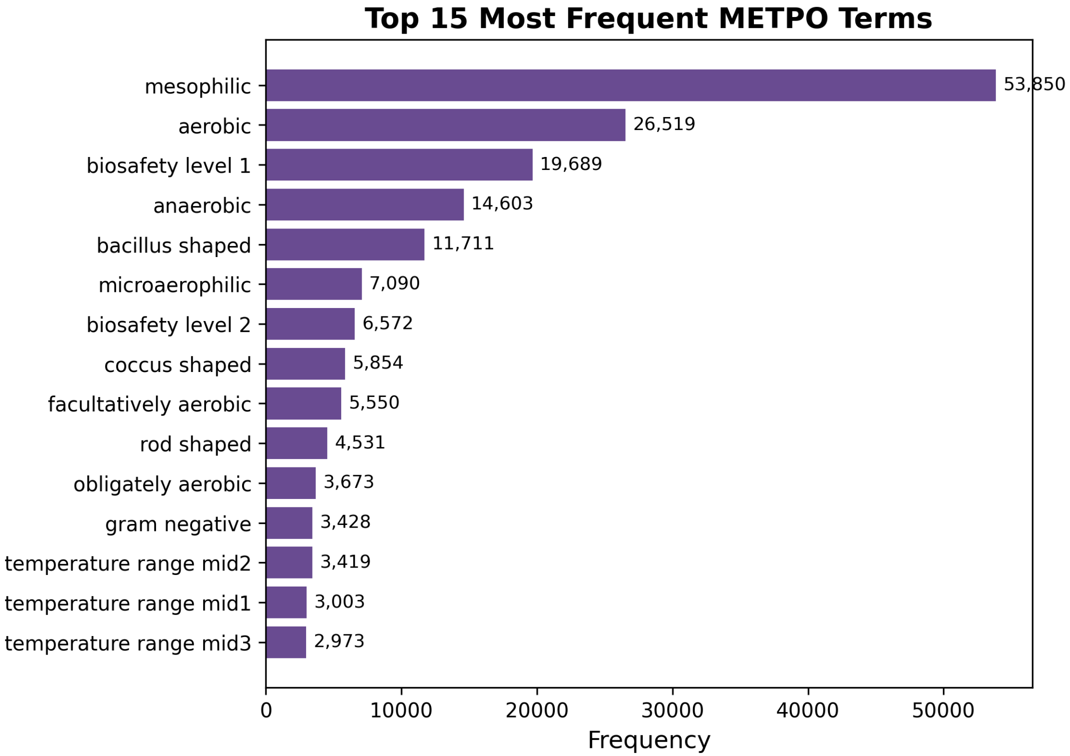
- **Madin**: METPO (45,851), CHEBI (37,173), NCBITaxon (26,649)
- **BacDive**: NCBITaxon (678,379), CHEBI (428,815), EC (186,014), *then* METPO (120,266)

METPO Utilization so far* = % of edges using METPO terms in object position (semantic grounding)

*Utilization is ETL-dependent: reflects what was extracted, not full METPO potential

KG-Microbe: METPO as Semantic Backbone





152 unique METPO terms normalize traits across all three datasets

KG-Microbe: Key for Medium Prediction

Top 3 METPO Objects:

- **aerobic** (26,611 edges)
- **anaerobic** (14,637 edges)
- **mesophilic** (53,850 edges)

Impact:

- **37% of all METPO edges**
- Directly determine growth medium requirements (oxygen atmosphere and temperature ranges)
- Carry high weight in CultureBot's machine learning models

KG-Microbe Applications: CultureBot & DOE CMM-REE

KG-Microbe → METPO dependency chain

CultureBot (LBNL LDRD FY24-FY25, NCE through Dec 2025)

- AI-driven prediction of microbial growth conditions
- **Depends on:** KG-Microbe as feature backbone for graph learning
- **Needs METPO for:** Consistent phenotype encoding across training data
- **Result:** Explainable predictions for lab automation

Joachimiak + Deutschbauer (EGSB)
github.com/culturebotai

DOE CMM-REE Project

- Rare Earth Element biorecovery research
- **Depends on:** KG-Microbe for microbial trait integration
- **Needs METPO for:** Standardized phenotype vocabulary
- **Result:** Data-driven microbe selection

Both projects validate METPO's design:

- Real production dependencies (not demos)
- Drive active maintenance & curation
- Prove value of application-driven ontology development

OntoGPT Grounding: Literature-Driven Expansion

Structured data integration (Phase 1): Near completion

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

Literature mining (Phase 2): Less mature

- 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

Literature-Based Discovery with OntoGPT

Expanding METPO through OntoGPT experiments:

Input: PubMed abstract

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

Two strains (BW863T and BW865) of
Gram-negative, aerobic, non-pigmented,
non-motile, rod-shaped bacteria were
isolated...
```

Output: RDF triples (Turtle)

```
# BW863 → AUTO:BW863 (extracted organism)
AUTO:BW863 strain_of NCBITaxon:569860 . # Methylovirgula ligni
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
```

OntoGPT Grounding Rates

10 PubMed abstracts:

- Phenotype: **41.0%** grounded to METPO (25/61)
- Chemical: **75.0%** grounded to ChEBI (33/44)
- Taxonomy: **93.3%** grounded to NCBITaxon (14/15)
- 36 AUTO phenotype terms → coverage gaps

Comparative Annotator Performance

10 ICBO abstracts, GPT-4o:

- **METPO**: 26 groundings (**9 unique terms**)
- **OMP**: 8 groundings (**2 unique terms**) — narrow coverage
- **PATO**: 8 groundings (**2 unique terms**) — too general
- **MicrO**: 10 groundings (**4 unique terms**)

Data-Driven Ontology Development

Failed groundings drive iterative expansion:

1. Literature mining identifies phenotype: "rod-shaped"
2. OntoGPT cannot ground → produces AUTO:rod-shaped
3. Triggers curation workflow
4. Domain expert adds term to METPO
5. Future extractions ground successfully

Interoperability: METPO is a Good Citizen

SSSOM Mappings: ~3,000 via embedding search (OLS + BioPortal + n4l_merged)

- Relaxed: 3,008 mappings (mostly broadMatch/relatedMatch)
- Optimized: 2,883 mappings (73 exactMatch)
- Method: `text-embedding-3-small`
- **Note:** Only 19.6% exact matches - embeddings alone insufficient for precise integration

Availability:

- BioPortal, GitHub (berkeleybop/metpo)

Formats: OWL/RDF

Compatible tools: OAK, ROBOT, Protégé

Sustainability & Governance

Users of METPO:

- **CultureBot LDRD:** ML models for predicting microbial growth conditions
- **DOE CMM-REE:** Rare earth element biorecovery research

Built for longevity:

- **Active funding:** DOE CMM project (FY26) + CultureBot LDRD (through 2025)
- **Low-barrier contributions:** Spreadsheet-based curation, LLM-assisted workflows
- **Modern build system:** ODK + ROBOT (standard OBO tooling, won't bitrot)
- **Open source:** GitHub repository, community contributions welcome

Conclusion

METPO demonstrates an application-driven approach:

- **Production validation:** 253,805 METPO edges in BacDive, BactoTraits, and Madin integration (KG-Microbe includes additional node and edge sources)
- **Sustainability:** Active funding, real dependencies, modern tooling
- **Institutional support:** Candidate for BER Data Lake House
- **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.com/berkeleybop/metpo
bioportal.bioontology.org/ontologies/METPO

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PI: Marcin Joachimiak

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Data: BactoTraits, Madin et al., BacDive, Names for Life

Infrastructure: OBO Foundry, NCBO BioPortal, ODK/ROBOT/OAK, OntoGPT

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

Real Data Example: KG-Microbe Triples

From BacDive transformed data (`edges.tsv`):

subject	predicate	object	relation	primary_knowledge_source
NCBITaxon:100	biolink:has_phenotype	METPO:1001102	RO:0002200	bacdive:17384
NCBITaxon:100	biolink:has_phenotype	METPO:1000615	RO:0002200	bacdive:17391
NCBITaxon:100	biolink:has_phenotype	METPO:1000615	RO:0002200	bacdive:17384

KGX format combines:

- **Biolink predicates** (`biolink:has_phenotype`) - high-level semantic relations
- **RO relations** (`RO:0002200` = "has phenotype") - precise OBO semantics
- **Primary source** - Each triple traceable to BacDive strain ID

Technical Details: METPO Development

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

Build system: Ontology Development Kit (ODK)

Validation: ROBOT validation passed

Semantic search: OLS + BioPortal + n4l_merged embeddings, generates SSSOM mappings

Data infrastructure: All three datasets (BacDive, BactoTraits, Madin) staged in MongoDB alongside IJSEM metadata and text mining results from ePMC

AI Usage: Literature extraction (OntoGPT/GPT-4o), definition quality assessment (Claude 3.5). NOT used for: class design, final definitions, hierarchy (all human-curated)

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

Design Rationale (continued)

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)
- **24 retained** for mapping (20 from OLS, 4 from BioPortal only, plus n4l_merged)

Final set: 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

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

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
- Others: quality-centric, interaction-centric, or process-centric

Multiple Backend Registries for Semantic Search

METPO embedding search uses three complementary backends:

1. **OLS (Ontology Lookup Service)** - Primary OBO Foundry registry
2. **BioPortal** - Broader biomedical ontology collection (includes DSMZ ontologies)
3. **Semantic-SQL** - SQL-queryable ontology views

Semantic-SQL Quality Metric

Semantic-SQL as a quality metric:

- Some ontologies don't convert cleanly to semsql with standard methods
- Conversion failure indicates structural or metadata issues
- Used alongside OLS/BioPortal availability to assess ontology quality

METPO integration:

- Available in all three backends (OLS, BioPortal, semantic-sql)
- Queryable via SPARQL, REST APIs, and SQL
- Part of broader OBO ecosystem

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

Object Prefix Distribution: METPO Expansion Opportunities

Object prefix distribution by edge count:

Madin et al. (115,399 edges):

- METPO: 45,851 edges (39.7%)
- CHEBI: 37,173 (32.2%)
- NCBITaxon: 26,649 (23.1%)
- pathways: 4,463 (3.9%)
- GO: 1,262 (1.1%)
- carbon_substrates: 1

BactoTraits (87,688 edges):

- METPO: 87,688 edges (100%)

BacDive (1,656,667 edges):

- NCBITaxon: 678,379 edges (40.9%)
- CHEBI: 428,815 (25.9%)
- EC: 186,014 (11.2%)
- strain: 185,928 (11.2%)
- METPO: 120,266 (7.3%)
- medium: 52,995 (3.2%)
- pathogen: 3,411 (0.2%)
- salinity: 190
- pathways: 183
- assay: 455
- CAS-RN: 31

METPO Expansion Opportunities

Based on unique values in object position:

- **salinity:** 4 unique values (`extremely_halophilic` , `moderately_halophilic` , etc.) - could align to METPO halophilic classes
- **pathogen:** 3 unique values (`animal` , `human` , `plant`) - could align to existing pathogenicity ontologies or add to METPO
- **pathways:** 72-73 unique values (`denitrification` , `aromatic_compound_degradation` , etc.) - consider alignment to GO biological processes

~8,000 edges could increase METPO coverage with better ETL alignment