



SNOMED CT

Content Improvement Project

Elaboration phase

Project ID: artf6773

Topic: Microorganisms: defining characteristics
(aerobic/anaerobic, Gram positivity, morphology, etc)

Date 20121016

Version 1.1

Amendment History

Version	Date	Editor	Comments
0.1	20120312	James T. Case	First draft for comments
0.5	20120416	James T. Case	Changes made following review by Jeff Wilcke
0.55	20120810	James T. Case	Added the attribute Has GranularPart to relate antigens to organisms.
1.0	20121009	James T. Case	Revision of initial design to reflect result of testing of the model. Results of initial evaluation using the IHTSDO Workbench.
1.1	20121016	James T. Case	Revision based on review comments and input from BFO article on functions, roles and dispositions. First model iteration created.

Review Timetable

Review date	Responsible owner	Comments
20120406	Jeff Wilcke/Organism and Infectious Disease Project	Comments and questions included in the review were added to the document.
20121010	Suzanne Santamaria, Jeff Wilcke	Additional clarification and alignment with BFO with regards to Function, Role and Disposition needed.

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1 Glossary

1.1 Domain Terms

Taxon	Biology: A taxonomic category or group, such as a phylum, order, family, genus, or species
Motility (bacterial)	Self-propelled motion (as opposed to movement by environmental causes, e.g. Brownian). May be accomplished via flagella, axial filament, gliding, etc.)
Morphology	In the context of bacterial organisms, the shape of the individual bacterial cell
Property	A characteristic attribute possessed by all members of a class. (American Heritage Dictionary). In SNOMED CT it “specifies the kind of property being measured (e.g. concentration).” This is a tautologic definition and does not clarify the distinction from a quality. It originates from the harmonization process with the LOINC standard and thus carries the semantics implied by the LOINC definition.
Quality	An inherent or distinguishing characteristic; a property. (American Heritage Dictionary)
Serotype	A group of closely related microorganisms distinguished by the expression of a characteristic set of antigens. (American heritage dictionary). According to Bergey’s Manual of Determinative Bacteriology “Such ranks have no official standing in nomenclature, but often have great practical usefulness. (Bergey, Vol 2 p30)
Serogroup	Subgroups of a specific microorganism taxa differing only by their composition in terms of antigens. (Wiktionary). According to Bergey’s Manual of Determinative Bacteriology “Such ranks have no official standing in nomenclature, but often have great practical usefulness. (Bergey, Vol 2 p30)
Biovar	A group of bacterial strains distinguishable from other strains of the same species on the basis of their physiological characteristics. According to Bergey’s Manual of Determinative Bacteriology “Such ranks have no official standing in nomenclature, but often have great practical usefulness. (Bergey, Vol 2 p30)
Microorganism Complex	A group of genetically related microorganisms belonging to the same taxonomic class. This moniker is usually used when standard laboratory techniques are not able to distinguish among the related species. E.g. <i>Mycobacterium avium</i> complex
Strain	A subset of a bacterial species differing from other bacteria of the same species by some minor but identifiable difference usually descending from a single organism or pure culture isolate. According to Bergey’s Manual of Determinative Bacteriology “Such ranks have no official standing in nomenclature, but often have great practical usefulness. (Bergey, Vol 2 p30)
Serovar	Serological variant – used synonymously with serotype – According to Bergey’s Manual of Determinative Bacteriology “Such ranks have no official standing in nomenclature, but often have great practical usefulness. (Bergey, Vol 2 p30)
Organism class	A subpopulation of organisms with identical characteristics.
Phenotype	The observable characteristics of an organism, as determined by both genetic makeup and environmental influences.

2 Introduction

2.1 Purpose

The originally stated purpose of this project was to consider enhancements the Concept Model to allow representation of defining characteristics of “organisms”, e.g. Anaerobic Gram negative coccobacillus (organism) and Anaerobic Gram positive coccobacillus (organism). The characteristics of interest to be defined are solely the characteristics of microorganisms of the Kingdoms Archaea and Bacteria. Revisions to the concept model for other types of microorganisms as well as the Eukaryota will require separate analyses and is currently underway as part of the Organism and Infectious Disease project. Since the characteristics that are of importance in the classification of the other Kingdoms of organisms differ from single celled microorganisms, they are deemed out of scope for this project.

To determine which of the existing bacteria concepts should be assigned as subtypes is an additional, substantial task that remains to be undertaken. The expectations are that these concepts could ultimately be fully defined through roles and subsume subtypes which are also modeled. The project also aims to update the taxonomic assignment according to current references.

SNOMED CT projects transition from Inception Phase → Elaboration Phase → Construction Phase → Transition Phase. This document describes the Elaboration Phase.

It follows on from an Inception Phase report, which describes the detail of the problem to be addressed and its scope boundaries

The purpose of the Elaboration Phase document(s) is to document one (or more) possible technical solutions that have been developed and tested, and to recommend and provide a detailed specification of a preferred solution to be taken forward to the construction phase.

2.2 Audience and stakeholder domain

The audience for this document includes all standards terminology leaders, implementers and users but is especially targeted at those stakeholders from public health, clinical laboratory and infectious disease domains, including epidemiologists and public and private agencies involved in population health and disease surveillance.

A further significant audience is the community of SNOMED authors that may be requested to implement the recommended specification.

2.2.1 Input from stakeholders

Specific requests for the improved organization and comprehensiveness of organism concepts include:

- requests stemming from the Reportable Condition Mapping Table project, a US-wide effort to standardize the terminology surrounding reportable conditions,
- Improved representation of Salmonella serotypes (from CDC)

- Improved representation of E. coli serotypes and serogroups (from CDC)
- Improved coverage of generic organism findings (from Canada Health Infoway)

3 Solution Development

3.1 Initial Design

3.1.1 Outline of initial design

The initial design is based on the following general principles:

1. Concepts in the microorganism hierarchy should reflect the material existence of various subpopulations of an organism class that bear “identical” characteristics or qualities; i.e. in practice, we never deal with the entire population (i.e. the universe of organisms existing that fit in this classification).
2. The FSN of organisms reflects/implies the subpopulation nature of organisms as used in healthcare. For example:
 - a. *Escherichia coli* (organism)
 - b. The proposed definition associated with this hierarchy is “The implied meaning of each concept in the organism hierarchy is that it represents a real organism class that exists in nature and any subpopulation (including a single organism) of all organisms belonging to that class.”
 - c. For Linnaean taxonomic classes or organisms, the concept FSN uses the proper form for the taxonomic rank without the taxon rank name (e.g. Genus, Species, etc.)
 - i. *Escherichia coli*
 - ii. *Salmonella*
 - iii. *Corynebacteriaceae*
3. Every attempt will be made to represent the recognized Linnaean hierarchy for the organisms; however, concepts in the organism hierarchy will not be restricted to formal Linnaean taxonomy.
 - a. Defining characteristics will be attached to both the Linnaean and non-Linnaean subpopulation concepts to allow for autoclassification. For example:
 - i. *Enterobacteriaceae* BEARER OF Gram negative staining quality (qualifier value)
 - ii. Gram negative bacteria BEARER OF Gram negative staining quality (qualifier value)
 - b. Non-Linnaean categories will have no stated children.
 - c. Non-Linnaean categories will be based on phenotypic characteristics of clinical importance/interest.
4. The initial effort of the project will be concerned with assigning appropriate defining characteristics to non-Linnaean classes of bacterial organisms. These assignments will be done within the hierarchy to ensure that the classifier assigns all of the appropriate children rather than making stated IS-A parent assignments as is currently implemented.
 - a. Concepts in this category do not represent biological taxa *per se*, which are names for categories or groups with similar characteristics; i.e. organisms have an associated taxonomic quality, but are not the taxa themselves.
5. A review of the current non-Linnaean classes of bacterial organisms will inform the creation of a “Bacterial quality (qualifier value)” hierarchy that will be used to provide the defining values for the “BEARER OF” attribute.

6. Following the full definition of non_Linnaean classes, assignment of defining criteria to the Linnaean taxa according to the gold standard references will be made.
7. During the assignment of defining criteria the project will correct errors (i.e. correct IS-A parents and taxon names) based on current taxonomic assignments from gold standard sources.
 - a. During this phase, removal of taxon hierarchy names from organism FSNs will be completed.
8. Create new substances reflecting the bacterial antigens used in the identification of bacterial subtypes under the existing concept 116634000 - Bacterial antigen (substance).
 - a. E.g. Bacterial antigen
 - i. Bacterial somatic antigen
 - ii. Bacterial flagellar antigen
 - b. Based on the specificity of bacterial antigens, it may be necessary to create organism specific substances, regardless of the taxonomic relatedness of the organisms (e.g. *Salmonella*, *Escherichia* and *Klebsiella*)

New proposed attribute values to support the organism concept model (Table 1.)

Attribute name	Attribute description	Allowable value(s)
Bt:Bearer-of	From Biotop: “inheresIn (inverse: bearerOf) relates a quality, role, function, disposition, or information object with the physical entity it depends on.” Attribute used to assign differentia associated with organism qualities (e.g. shape, motility, staining, etc	Microorganism quality (qualifier value) >>concept ID
Bt:Has Proper Physical Part	From Biotop: “hasProperPhysicalPart (inverse: properPhysicalPartOf) obtains between physical objects. The distinction between parthood and locatedness is complex and does not obey strict criteria. This relation is irreflexive, i.e. a physical object cannot have itself as a physical proper part.” Attribute used to represent component parts of an organism of clinical interest (e.g. antigens, nucleic acid type, viral envelope, etc.).	TBD e.g. 41792001 – Flagellum, bacterial
Bt:Has Granular Part	From Biotop: “hasGranularPart (inverse: granularPartOf) relate	For this project: >>116633006 – Microbial

	Pluralities with their constituents. The constituents are of the same sort.” Attribute used to represent antigens based on the definition from Biotop, which implies that the loss of a single antigen grain does not affect the plurality of antigen parts.	antigen
SCT:Towards	An attribute derived from the proposed Observable Entity concept model to allow for a role group where the potential values for BEARER OF exist as concepts in other hierarchies (e.g. substance)	>>105590001 – Substance Others TBD

3.1.2 Significant design or implementation decisions / compromises

This design eliminates the need to differentiate as separate (or as currently structured, subordinate) hierarchies, i.e. Linnaean and Non-Linnaean organisms. Most non-Linnaean bacterial concepts will be defined as children of Superkingdom Bacteria with classification based on the defining characteristics and with no stated children. The remaining concepts will be placed under a fully modeled parent that most closely conveys the needed attribution. Correct assignment of defining attributes to the Linnaean organisms will allow autoclassification under the appropriate non-Linnaean categories.

Similar to the usage of organism concepts in the past, “Organism” concepts carry the implied context of “known present” when used as result values. This eliminates the need to create parallel findings values; however it does not address the need for complex organism-related types of findings (e.g. Plasmodium vivax OR Plasmodium falciparum), or to state the specific absence of an organism or findings about organisms that are not inherent qualities.

Currently, some of the structure of the non-Linnaean hierarchy is based on the chapter titles of Bergey’s manual of systematic bacteriology (e.g. Subclass endospore forming cocci). These will be retired where inappropriate for clinical use. There are a number of “catch-all” categories in the current microorganism list that will be individually evaluated and removed where deemed inappropriate for realistic useful categorization of bacteria.

Inherently ambiguous classes of bacterial organisms (i.e. X-like organisms) will be initially listed as immediate children of the highest level of Linnaean taxonomy compatible with the knowledge of the organism type.

Organisms associated with a species specific pathogenesis (e.g. Enteropathogenic Escherichia coli (pathogenic in humans/primates, not in other animal types) will be modeled as subtypes of the

appropriate taxon. (Enteropathogenic E. coli serotype O157:H7 (organism) IS-A E. coli serotype O157:H7 (organism)).

Absence findings for organisms still need to be modeled as situations.

3.1.3 Evaluation of Design

3.1.3.1 Exceptions and Problems

There are specific use cases which are not well addressed by this model, due to the limits of the existing description logic, which does not support disjunction or negation. There is still a question about the proper assignment of the existing “X species” concepts. In the minds of many of the terminologists that have considered this problem, “X species” is synonymous with “Genus X”; however, in the view of many users, there is a difference between an organism that has been identified as a member of a particular Genus and an organism that has not or cannot be identified below the level of Genus. This has resulted in the creation of “X species unspecified (finding)” concepts in some extensions to SNOMED to accommodate this perception. This project does not directly address this issue and it is still an open issue.

Additional specific exceptions that are only partially addressed:

- Concepts with disjunction (e.g. Plasmodium vivax AND/OR Plasmodium falciparum)
- Partially unclassified organisms (e.g. Campylobacter-like species)
- Organisms that do not have a listing in the “Prokaryotic names with standing in the nomenclature”. e.g. 243267009 – CDC Corynebacterium group (organism)

There are currently few existing concepts to represent the various properties of organisms needed to define the values for the BEARER OF attribute (i.e. gram positive, motile, etc.). Of the existing concepts, they are variously spread throughout the terminology and would need to be reorganized to provide a consistent representation.

3.1.3.2 Design Strengths

The strength of the design is that it removes the perceived constraints of having to adhere to a strict phenotypic (Linnaean) hierarchy that does not support classifications of clinical interest. It allows the representation of both named organisms and broad categories of organisms allowing organism classes that are currently not supported by a Linnaean structure to be properly represented in a true subsumption hierarchy. The other advantage is the definition of the organisms and the named organism class level allows for proper classification under the clinically relevant subhierarchies (i.e. staining, motility, shape, etc) to be performed by the classifier instead of having to state these relationships explicitly, reducing the ongoing maintenance burden.

This design allows for subtypes of organisms not currently supported by Linnaean taxonomy to be represented as a continuation to it through the further specification of physical characteristics (e.g. antigen structures) as subtypes of species.

At the same time, the design emphasizes the need for a hierarchical representation based on current classifications representing phenotypic characteristics. The assignments of these hierarchical

relationships have their source in well referenced scientific data and the derived classifications are based on these identified characteristics.

3.1.3.3 Design Weakness

There are at least three potential options for representing the defining characteristics of organisms. These include:

1. Create a content model attribute for each type of defining quality (e.g. Organism morphology (attribute), Organism staining property (attribute), etc.). The number and type of attributes needed to represent characteristics of different Kingdoms and classes of organisms would result in a large number of new concept model attributes.
 - a. E.g. Organism concept (organism):Organism atmospheric requirement (attribute) = Atmospheric requirement quality (qualifier value)
 - i. Escherichia coli (organism):Organism atmospheric quality (attribute) = Facultative anaerobic (qualifier value);Cell wall stain quality (attribute) = Gram negative (qualifier value)
2. Create paired concept model attributes that would represent the quality/characteristic type and the value for that characteristic, E.g.:
 - a. BEARER OF (attribute): Cell wall stain quality (property)
 - b. VALUE (attribute): Gram positive (quality value)
3. Create a set of concept values that fully specify the value needed for the BEARER OF attribute, e.g.:
 - a. BEARER OF (attribute) = Gram positive cell wall (quality value)

While it is the opinion of the authors that the most straightforward approach for representing characteristics/qualities of organisms is limited to a single general attribute “BEARER-OF” it was apparent in initial testing that alone it is not robust enough to model the details of some aspects of organism function, nor would it take into account the existence of existing SNOMED CT content that could be used. It also would require a significant effort to enhance the current quality value hierarchy with all of the necessary concepts to represent the large variety of quality values needed to populate the target concept for this relationship. Thus the inclusion of a few additional attributes was necessary. It is still unclear without substantial testing of the model against known content whether additional attributes may be needed as the scope of the organism project expands to other organism types such as viruses, fungi and parasites.

A primary weakness that is not specifically addressed is the perceived need by users for inherently ambiguous organism concepts or idiosyncratic classifications (e.g. CDC groups). These will be noted as identified and added as subsequent sub-projects for this ongoing very large project. Thus, while there will be a number of exceptional cases encountered during this project, the vast majority of existing issues surrounding the proper classification of organisms will be addresses in this first iteration.

3.1.3.4 Design Risks

Description of risk	Importance	Mitigation plan
The design may result in a perceived change in the semantics of Organisms that were at once based on a strict	High	Clear assignment of taxon quality FSNs and documentation of the semantics of taxon level and organism name must be

Linnaean representation and a set of clinical and phenotypic characteristics. Where users are used to seeing organism with an associated taxon prefix (i.e. Genus, Family). These would be relegated to a quality value, which might cause confusion.		created to enable users to understand the proper use of the concepts.
The distinction between what is an organism and what is a finding about an organism may be blurred.	High	Clear instruction in the user guide as to what is represented by the organism hierarchy as opposed to what you can say about an organism. Clear examples of organism vs. finding about an organism must be provided.
There is a future potential classification issue when dealing with phenotypic classification and genomic classification. At present, genomic classification of organisms is only substantially represented in the viruses, but is increasingly being used in other classes of organisms. The discrepancy between phenotype and genotype in bacteria will need to be addressed.	Moderate	Engage SMEs to begin a design that will support future expansion of organism model to address these discrepancies.
It is not yet clear how to define or restrict what characteristics will be assigned to Non-Linnaean classes	Moderate	Not important in the initial stages of the project, but will become more important as the need to represent very granular differences between organisms are requested (i.e. genomic differences).

3.2 Iteration One

3.2.1 Outline of revised design

Redesign the Solution Identify objectives of iteration, and the major changes to previous design

Communicate the revised design

In the original design, all of the qualities needed to define the values for organisms were located under a single quality hierarchy. Review of the top level ontologies has indicated that it is more appropriate to better organize these qualifiers in regards to their temporal and environmental contingencies. Thus, in order to align this model with other top level ontologies (specifically BFO), the differentiation between qualities and realizable entities that inhere in organisms should be made for the concepts used to define the characteristics of bacterial organisms. Two levels of qualifier values may be created:

Organism quality (qualifier value)

 Microorganism quality (qualifier value)

 Bacterial quality (qualifier value)

 Bacterial form

Bacterial atmosphere requirement
etc...

Organism realizable entity (qualifier value)

Microorganism realizable entity (qualifier value)

Bacterial realizable entity (qualifier value)

Bacterial function (qualifier value)

Catalase activity

Bacterial disposition (qualifier value)

Disposition to form endospore

Bacterial role (disposition)

Enteropathogenic

3.2.2 Significant design or implementation changes

While this does not significantly change the way in which organisms will classify, it makes clear those characteristics of bacterial that are persistent throughout the existence of an organism and those that exist only when the proper conditions leading to a realization of those characteristics exist. For example; the gram staining characteristic of an organism cell wall “quality” since it is always present, whereas the “disposition” to produce an endospore only exists under the proper nutritional and environmental conditions and many bacteria capable of producing spores do not ever do so in their lifetime.

3.2.3 Evaluation of Revised Design

TBD

3.2.3.1 Exceptions and Problems

3.2.3.2 Design Strengths

3.2.3.3 Design Weakness

3.2.3.4 Design Risks

Description of risk	Importance	Mitigation plan

4 Recommendation

4.1.1 Detailed design final specification

Design the Solution Identify major design elements and how they collaborate to realize the scenario
 Communicate the design

1. Review the current hierarchy under the concept 115166000 – Kingdom prokaryote. Identify all concepts that are non-Linnaean.
 - a. Assign all non-Linnaean bacterial concepts as immediate children under the concept [409822003] – Superkingdom Bacteria (organism) Retire the categorical concept [41146007] – Bacteria (organism) See example Fig 1.

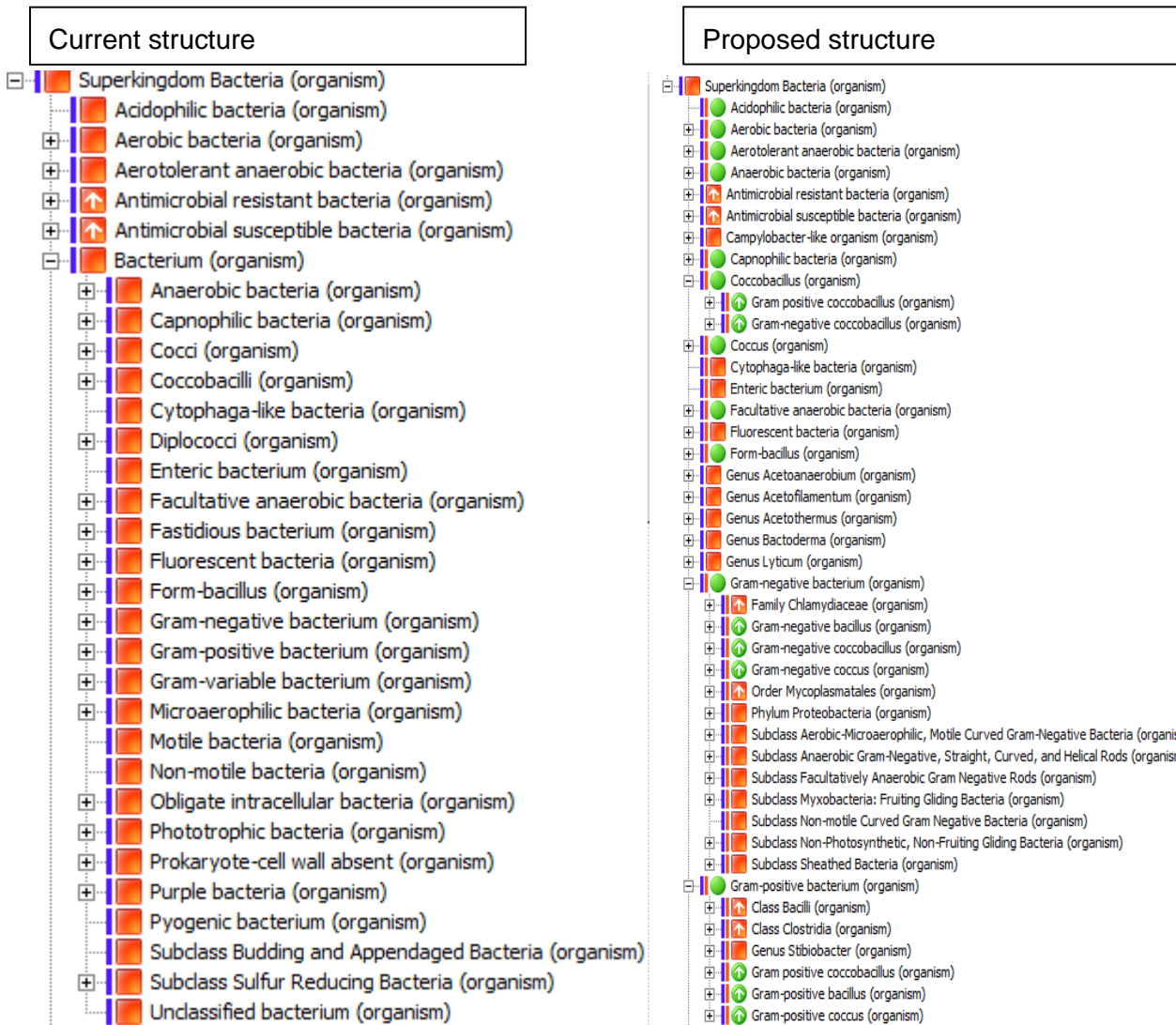


Figure 1. Reorganization of non-Linnaean categories of bacteria

1. Create 4 new concept model attributes (some adopted from Biotop ontology):
 - a. BEARER OF – definition (Biotop): "inheresIn (inverse: bearerOf) relates a quality, role, function, disposition, or information object with the physical entity it depends on.
 - i. This attribute is used to relate organism characteristics.

- b. HAS PROPER PHYSICAL PART – definition (Biotop): definition hasProperPhysicalPart (inverse: properPhysicalPartOf) obtains between physical objects. The distinction between parthood and locatedness is complex and does not obey strict criteria. This relation is irreflexive, i.e. a physical object cannot have itself as a physical proper part.
 - i. This attribute is used to relate physical components (e.g. nucleic acid subtype)
 - c. HAS GRANULAR PART – Definition (biotop): hasGranularPart (inverse: granularPartOf) relate Pluralities with their constituents. The constituents are of the same sort. Attribute used to represent antigens based on the definition from Biotop, which implies that the loss of a single antigen grain does not affect the plurality of the entity.
 - d. TOWARD - An attribute derived from the proposed Observable Entity concept model to allow for a role group where the potential values for BEARER OF exist as concepts in other hierarchies (e.g. substance)
2. Evaluate the current Linnaean structure with the recommended sources (PNST) and realign as necessary. Since the current structure is significantly out of date, this will require substantial review.
 3. Using the gold standard reference for bacterial classification (Bergey’s Manual of Systematic Bacteriology, 2nd ed.) Assign appropriate BEARER-OF values at the appropriate level in the hierarchy.
 4. Create a new concept “Organism quality (quality value) to locate the organism specific qualities needed as values for defining relationships. Create necessary quality values to support the defining relationships.
 5. Create a new concept Organism realizable entity (qualifier value) to locate the various concepts needed to support functions, roles and dispositions that inhere in bacteria.
 6. For organism subtypes identified by their antigens, assign the appropriate “Microbial antigen (substance)” using the HAS GRANULAR PART relationship.
 - a. Create new antigen substances as needed under 116633006 - Microbial antigen (substance).
 7. For each non-Linnaean category of bacteria, assign the appropriate BEARER-OF values from the “Organism quality” and “Organism realizable entity hierarchies.

4.1.2 Iteration plan

5 Quality program criteria

5.1 Quality metrics

5.1.1 Quality metric 1

Component	Characteristic and Description		Metric	Target	Result
Logic definitions of concepts in organism	Char:	sufficiently defined	<ul style="list-style-type: none"> - Proportion sufficiently defined - Numerator: count of those defined. - Denominator: count of all concepts under 115166000 – Kingdom Prokaryote 	95%	
	Descr:	Concept logic definitions should be “defined” not “primitive”			

5.1.2 Quality metric 2

Component	Characteristic and Description		Metric	Target	Result
Fully specified names in <domain>	Char:	Adherence to terming guidelines	<ul style="list-style-type: none"> - Proportion meeting guidelines, based on manual review 	100%	
	Descr:	The fully specified name should adhere to terming guidelines listed in the editorial guide, sections <list sections>			

5.2 Use case scenarios

Create Test Cases: Review the requirements to be tested as set out in the Inception Phase document. **Identify and outline relevant Test Cases.** Identify test data needs. Share and evaluate the Test Cases

5.2.1 Scenario One

5.2.1.1 Expected Setting

5.2.1.2 Data capture requirement

5.2.1.3 Data retrieval requirement

5.2.2 Scenario Two

5.2.2.1 Expected Setting

5.2.2.2 Data capture requirement

5.2.2.3 Data retrieval requirement

5.2.3 Scenario ...

5.3 Test cases

6 Updated Project Resource Estimates

Estimate project size; Forecast project velocity and duration

Evaluate risks; Establish costs and articulate value; Plan deployment; Outline project lifecycle

6.1 Scope of construction phase

6.1.1 Skills required

Extensive knowledge of the organism domains (i.e. bacteriology, virology, mycology) will be essential to the creation of the non-Linnaean categories.

6.1.2 Preventing recurrence of problem

Prevention will be implemented through a formal style guide for the representation of organisms of each domain.

6.1.3 Division of project into stages

Due to the overall size of the project and limited resources available, it is recommended that individual domains be addressed sequentially and that needed modifications to the underlying model that arise during construction be retrospectively applied to the domains as recognized.

6.2 Projection of remaining overall project resource requirements

6.2.1 Expected project resource requirement category

This project is extremely large and should most likely be addressed by subprojects that involve either a top-down approach or a focus on high value subhierarchies (such as pathologic bacterial types, i.e. Salmonella, E. coli). The focus of this elaboration has been on the bacterial microorganisms due to the wide variety of representations currently needed to support public health reporting.

6.2.2 Expected project impact and benefit

The projected impact is VERY HIGH – significant improvement to a large set of high priority use cases.

The benefit would be a robust representation of organisms allowing for multiple comprehensive clinically relevant representations inferred from the defining characteristics. This would eliminate the sporadic representation that current exists due to stated IS-A relationships.

6.2.3 Indicative resource estimates for construction, transition and maintenance:

The project resource requirement is classed as HUGE – more than 3 person years

Construction and transition phase: 10,000-12,000 microorganism concepts to be authored or reauthored. Creation of up to 100-200 new concepts to support the quality values for bacteria alone.

Maintenance phase: 500-1000 new 'frequent usage' concept requests in 1st 3 years, based on current submission rates for microorganisms.

7 Appendix

7.1 Bacteria differentia (non-exhaustive)

- Morphology
 - Stain retention
 - Gram stain retention
 - Gram negative
 - Gram positive
 - Gram variable
 - Acid Fast
 - Shape
 - Cocci
 - Diplococcus
 - Chaining
 - Bacilli
 - Coccobacillus
 - Pleomorphic
 - Curved
 - Spiral
 - Spore-formation
 - Terminal
 - Central
 - Subterminal
 - Flagella
 - Monotrichous
 - Polar
 - Lophotrichous
 - Amphitrichous
 - Peritrichous\
 - Capsules
 - Encapsulated (smooth)
 - Non-encapsulated (rough)
- Biochemistry
 - Catalase
 - Coagulase
 - Oxidase
 - Urease
- Sugar fermentation
 - Lactose
 - Glucose
 - Maltose
- Aerophilicity
 - Aerobic
 - Anaerobic
 - Microaerophilic
 - Aerotolerant
 - Facultative anaerobic
- Hemolysis
 - Beta
 - Alpha
 - Gamma
- Motility
 - Motile
 - Non motile
- Temperature
 - Thermophilic
 - Mesophilic
 - Psychrophilic
- Growth requirements
 - X factor (hemin)
 - V factor (NAD/NADP)
 - Cysteine
 - Charcoal yeast agar with iron AND cysteine
- Antigens
 - Somatic
 - Flagellar
- Antimicrobial resistance
- Pathogenic activity
 - Enterotoxin production
 - Exotoxin production
 - Diarrheagenic
 - Pyogenic/Caseating