Notes on talks

Lars Vogt

Link to talk:
https://www.researchgate.net/publication/331652272_Semantic_Instance_Anatomies_Phenotype_descriptions_and_their_accompanying_metadata_as_instance-based_semantic_graphs_that_are_organized_into_several_named_graphs

Phenotype data are based on observations of particulars (as instances of kinds)
Data that is a product of an observation process
Metadata is important (about the observation)
Always involves descriptive and diagnostic components
Moph-D-Base - repository for specimen data, images, phylogenetic matrices
Semantic Programming - going fully semantic: not only the data but the specification of the application itself is provided in form of semantic graphs stored in a store, source code contained in a source code ontology, a Java-based middleware interprets the specification in the source code ontology and produces the application on the fly, ontology for semantic programming provides resources for describing/specifying an application and the middleware understands these descriptions/specifications. Semantic Programming separates the steering logic of an application from its interpretation logic
SOCCOMAS - FAIR Web CMS based on Semantic Programming

Provides FAIR data, integrates RDF with HTML, is a one-stop single-layer development framework, provides pre-defined generic functions such as user admin, login, session management, Entry life cycle, provenance tracking, change-log tracking, etc.

Used soccomas to build a module for morphological data - MorphBase.

- Will allow for adding metadata
- Free text description
- Semantic annotations
- All data as RDF in tuple store
- Can write a “paper” that is stored as a named graph
- All parts of the phenotype stored as named graphs (weight, part, etc)
- Get a “semantic instance anatomy” (SIA) A-box graph
    - Organized along a partonomy
    - Links to ontology classes
- Individual observation (as a named graph) is the smallest unit of description
- Define data views by referencing named graph classes
- Facilitates alignment and comparison of different SIAs
- Application provides templates for descriptions
- Metadata is also a graph - highly structured.

- Can assign metadata to individual input fields (e.g., which specimen, preparation method, who, when)
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Brian Stucky

- Link to talk: https://drive.google.com/open?id=1NIWJXGOkDXYa6hRQwuQTaTG6C9xFqQnO
- Plant Phenology Ontology - PPO
- Standardized vocab and semantic framework for plant pheno data
- Record information about plant life cycle events
- Existing data collection networks throughout the world, but largely non-interoperable
- PPO provides ontological framework for automatic integration of these different sources
- How PPO models a phenological observation
- Phenophase name and phenophase ID - a developmental stage of the plant or population
- Phenophase status - 1 of 0, in phase or not
- Intensity value -- how many of structure that corresponds to structure
- [cjm comment: looks like OBO needs to do a better job of defining standardized measurement design patterns]
- Instance of a trait that is a quality of a plant that was input of an observing process
- Store count values as data properties.
- Depending on value of count, determines if the trait instance (e.g. instance of flower presence) is also an instance of flowers present or flowers absent.
- Aligns with existing OBO ontologies
- Flexible regarding how observation happens (e.g., human or machine)
- Relatively low graph overhead - don't usually need to instantiate observing process
- No required ontological commitment to phenological stages - researcher decides this
- May or may not comply with canonical OBI/PATO model? [Does that even exist?]
- Wades into the ontology absence quagmire

Matt Yoder

- Link to talk: https://docs.google.com/presentation/d/19KROI2EZrPNxpi-cA9SapnFm9ccAIxaLvpSN4mzazdk/edit?usp=sharing
- TaxonWorks - http://taxonworks.org and https://github.com/SpeciesFileGroup/taxonworks
- Provide a comprehensive web-based workbench for biological taxonomists
- Provide an environment that supports development

- Taxonomists have not traditionally used the terms phenotype, trait, or quality that often. The use of “character” is more recent. Their use has emerged as we want to quantify work.
- TW knowledge model is an ontology-based, graph-aware relational database
- Observation model -- observation linked to entity and descriptor, entity has_rich context
- Entity at the OTU level, collection level
- Descriptors start out as free text, but could become fully semantic
- Dynamic views available
- Can add images on any annotation
- Trying to mimic workflows taxonomists are familiar with
- Interfaces can bias semantics and encourage their use
- E.g., using graphical interface for annotations
- Semantic similarity approaches

Jim Balhoff

Link to talk:

- Phenoscape
- Models of trait evolution
- Mission to make evolutionary phenotypes computable
- Less specimen focus, more on species or taxa
- Link to data on evo-devo in MODs
- Approaches to recombine trait data across studies
- Built of work from ZFIN, apply to other fish
- EQ model of phenotypes
- Data comes in as phylogenetic matrices with text for characters and states
- Ontology terms allow unification of diverse words from text descriptions
- Mostly modeling in the T-box. Instance data for the matrix that it came from
- Onto-trace - automatic generation of presence/absence character matrix
- Infer P or A from all aggregated characters, even if indirect. E.g., if no forelimb bud, can’t have a forelimb or forelimb bone. E.g., if humerus is rod-shaped, humerus must be present.
- Phylogenetic comparative methods. Lots of good models for molecular data, but not morphological. Want to use ontology to determine, e.g., if characters are not independent. Building structured Markov models
- RPhenoscape API - services for incorporating ontology-based knowledge into computational tools

Marie Angelique LaPorte

Link to slides:
https://www.dropbox.com/s/5lpw058gc23xrw3/oops_march2019_laporte.pptx?dl=0
Internet connection not stable enough for the talk

Discussion

Links in a taxonomy as a local element, and you can get bizarre problems when they are subclassed into an ontology. Are there any processes for avoiding that?

- Jim: OBO Foundry ontology has loose or tight coordination that can help with that, e.g., by reuse.
- Chris - use of disjoint axioms, taxon constraints, lots of curation work

What kind of reasoning systems are people using?

- Protege with reasoners in there
- OWL Reasoners
- PPO uses hermit to build pre-reasoned version of the ontology, but use ELK to reason over instance data. Do some axiom manipulations compatible with what ELK can do.
- Matt - have nomenclature ontology which is the largest part - copy validations into code base, so that they can respond in real time.
- Export pre-reasoned data to an index or DB for fast query
- All solutions seem to involve some ad hoc processes - but this makes the systems harder to develop, run, and maintain

Maybe having more ODPs can help with first issue raised

(From a project that is trying to define semantic primitives). Would a broad-based foundational ontology be of any use in this system?

Do people differentiate between phenotypes, traits, and characters?

Phenotype - the actual flower color is red
  Traits - characteristic - like flower color

Model organisms vs. Intra-taxon differences

- Describing the trait can happen the same way, but what you store has to be different

Observing processes -> can you predict the observation

What is a character, what is a character state (decades old debate in phylogenetics)?

Upheno (https://github.com/obophenotype/upheno) -> a set of design patterns/templates, mailing list and design patterns, has YAML representation (nice!) -> compiles down to OWL; there are non controversial design patterns for (some) morphology

- For example, if we all agreed on how we model absence, we could be compatible. Some ODPs are non-controversial, but some are harder
- POTATO meeting at biocuration meeting in April

Absences -

- Subtle distinctions
- If you say absence of lower teeth is a subclass of tooth absence, then tooth absence does not mean all teeth are absent

People who are interested in collaborating on the paper (who were not speakers or organizers):

- Gary Berg Cross
- Bertram Luedescher
- Deborah McGuinness
- Robert Warren

Other systems

- FungDB

Relevant Papers

- https://bdj.pensoft.net/article/33303/