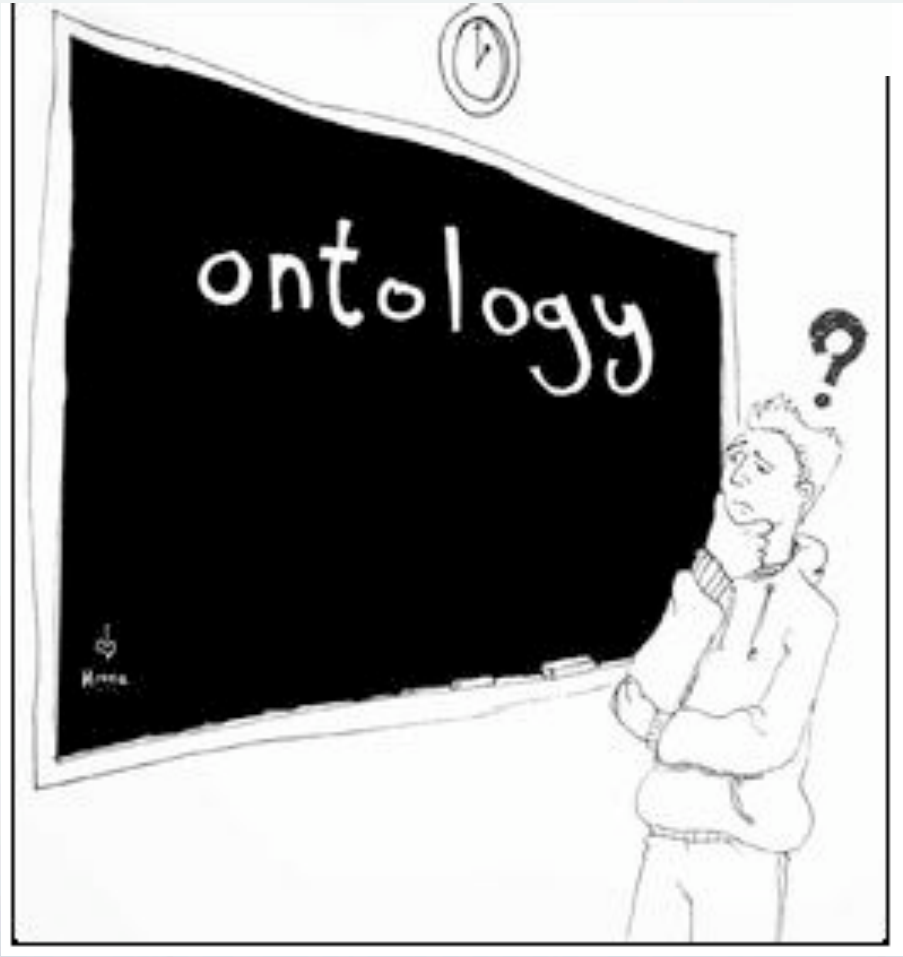
Anna Maria Masci
Background

Immunology wet lab experience for more than 15 years

- Working in Biomedical ontology since 2008
- Working with Gene Ontology, Cell Ontology, Protein Ontology, Infectious Disease Ontology,

Ontology for Biomedical Investigators

Since 2008


ontology
?

Ontology as a branch of philosophy is the science of what is, of the kinds and structures of the objects, properties and relations in every area of reality.

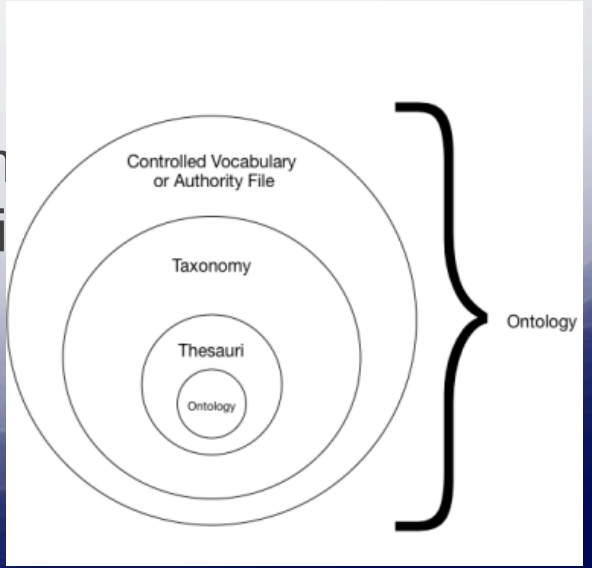
From *onto-logos*, the science of being.

Confusion with the word ontology

Controlled Vocabulary:
Is a restricted list of words used for labeling, indexing or categorizing

Taxonomy:
Is a classification system. The taxonomy in a controlled vocabulary indicates a hierarchical structure based on an IsA relationship

Ontology:
Is a controlled vocabulary with a taxonon
complex than complex than just IsA relati

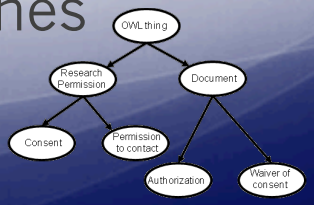


ONTOLOGY

List of terms in a specific domain that have different type of relationships in addition to IsA relation and have textual and logical definitions.

What is an ontology (in Computer Science)

- Provides a schema for organizing data
- Data annotation (e.g. NLP) and reusability
- Underlying concept for semantic web (World Wide Web Consortium Web 3C)
- Allows semantic reasoning by computer systems (Computable)
- Results in improved web searchers (e.g. Google, Microsoft, Facebook)
- In biomedical research used for: classification of data, representation of standards, enhanced searches



Ontology Key Points

- Ontology provides unique identifiers for classes and relations that represent a phenomena within a specific domain.
- Ontology provides labels for classes and relations.
- Ontology provides metadata associated with classes and relations that allow human users to understand their meaning and contribute to consistent use in annotation and other applications.
- Ontology provides axioms and formal definitions that enable computational access to some aspects of the meaning of the classes and relations.
- Combining the four main features of ontology facilitates semantic integration of heterogeneous multimodal data within and across domains and enable novel data mining methods that span traditional boundaries between domains and data types.

Biomedical Ontology

Scientific ontologies have special features
Every term must be such that the developers of the ontology believe it to refer to some entity on the basis of the best current scientific evidence
(Important role of instances that we can observe in the laboratory)

A methodology for building and testing ontologies

applied thus far in the biomedical domain on:

- FMA
- FuGO
- GO + other OBO Ontologies
- HL7-RIM
- ICF (International Classification of Functioning, Disability and Health)
- ISO Terminology Standards
- NCI Thesaurus
- SNOMED
- UMLS Semantic Network

Upper Level ontologies are ontologies that consist of very general terms common across all domains. Application ontologies are ontologies that consist of very specific term in a particular domain

Formal ontologies

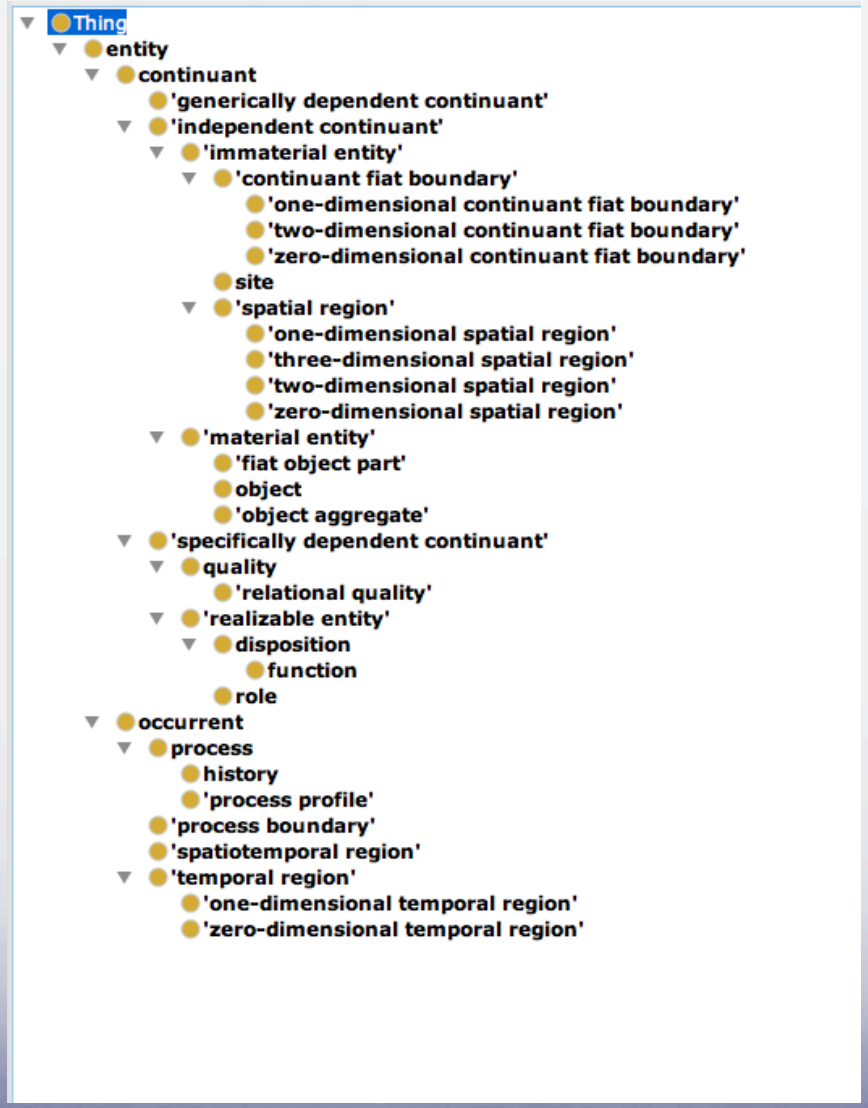
Upper ontology
BFO – Basic Formal Ontology
BORO – Business Objects Reference Ontology
CIDOC Conceptual Reference Model
Cyc (Cyc is not just an upper ontology, it also contains many mid-level and specialized ontologies as well)
UMBEL – Upper Mapping and Binding Exchange Layer, a subset of OpenCyc
DOLCE – Descriptive Ontology for Linguistic and Cognitive Engineering
GFO – General Formal Ontology
SUMO – Suggested Upper Merged Ontology

Upper Level ontologies are ontologies that consist of very general terms common across all domains. Application ontologies are ontologies that consist of very specific term in a particular domain

BFO
BASIC FORMAL ONTOLOGY

The Basic Formal Ontology is a small, upper level ontology that is designed for use in supporting information retrieval, analysis and integration in scientific and other domains. BFO is a genuine upper ontology. Thus it does not contain physical, chemical, biological or other terms which would properly fall within the coverage domains of the special sciences. BFO is used by more than 250 ontology-driven endeavors throughout the world. http://ifomis.uni-saarland.de/bfo/

BFO STRUCTURE



National Cancer Institute Thesaurus

Summary Classes Properties Notes Mappings Widgets

Jump To:

- Objective
- Observer
- Occupation or Discipline
  - Behavioral Sciences
    - Psychology
  - Biological Sciences
    - Anatomical Sciences
    - Biochemistry
    - Biology
    - Biophysics
    - **Histology**
    - Immunology
    - Neurosciences
    - Pharmacology
    - Physiology
    - Psychobiology
  - Complementary and Alternative Medicine
    - Alternative Medical System
    - Chinese Meridian Theory
    - Lifestyle and Disease Prevention
    - Mind-Body System
    - Orthomolecular Medicine
  - Health Sciences
    - Allied Health Sciences
    - Clinical Sciences
    - Dentistry
    - Environmental Health Sciences
    - Nursing
    - Nutritional Science
  - Medical Science
    - Cancer Science
    - Immunooncology
    - Medicine
  - Occupation
    - Allied Health Profession
    - Medical Occupation

Details | Visualization | Notes (0) | Class Mappings (27)

Preferred Name	Histology
Synonyms	Microanatomy
Definitions	The study of the structure of the cells and their arrangement to constitute tissues and, finally, the association among these to form organs. In pathology, the microscopic process of identifying normal and abnormal morphologic characteristics in tissues, by employing various cytochemical and immunocytochemical stains.
ID	http://ncicb.nci.nih.gov/xml/owl/EVS/Thesaurus.owl#C16681
ALT_DEFINITION	The study of tissues and cells under a microscope.
code	C16681
Contributing_Source	FDA
DEFINITION	The study of the structure of the cells and their arrangement to constitute tissues and, finally, the association among these to form organs. In pathology, the microscopic process of identifying normal and abnormal morphologic characteristics in tissues, by employing various cytochemical and immunocytochemical stains.
FULL_SYN	Microanatomy
label	Histology
Legacy_Concept_Name	Histology
Preferred_Name	Histology
prefixIRI	C16681
Semantic_Type	Biomedical Occupation or Discipline
UMLS_CUI	C0019638
subClassOf	Biological Sciences

Ontology for Biomedical Investigations

Summary Classes Properties Notes Mappings Widgets

Jump To:

- planned process
  - animal feeding
  - assay
    - 3D structure determination assay
    - activated partial thromboplastin time (aPTT) assay
    - age measurement assay
    - amplification of intermethylated sites (AIMS) assay
    - analyte assay
    - array based nucleic acid structure mapping assay
    - assay detecting IFN-gamma production
    - assay for transposase-accessible chromatin using se
    - bacterial one-hybrid
    - Bernoulli trial
    - binding assay
    - comet assay
    - copy number variation profiling
    - cytochalasin-induced inhibition of actin polymerizatic
    - cytometry assay
    - detection of molecular label
    - DNA replication timing by array assay
    - DNA sequence feature detection
    - DNA sequence variation detection
    - efficacy of epitope intervention experiment
    - electrophoretic mobility shift assay
    - epigenetic modification assay
    - extracellular electrophysiology recording
    - far-Western blot
    - fluorescence detection assay
    - gene dosage assay
    - gene knock-down assay
    - glucose tolerance test
    - handedness assay
    - hematology
    - **histology**
    - hydrogen/deuterium exchange assay
    - imaging assay
    - immune epitope assay
    - immune response assay
    - in container assay
    - in live cell assay
    - in live organism assay
    - in situ hybridization
    - in vivo intervention experiment
    - infectious agent detection assay
    - intra cellular electrophysiology reco

Details | Visualization | Notes (0) | Class Mappings (33)

Preferred Name	histology
Synonyms	histopathology
Definitions	the visual examination of cells or tissue (or images of them) with an assessment regarding a quality of the cells or tissue. Parts are: staining, imaging, judgement
ID	http://purl.obolibrary.org/obo/OBI_0600020
achieves_planned_objective	assay objective
alternative term	histopathology
curator note	need to incorporate partsn---\nThis is a very vague term, it should be in the same place as transcriptomics, proteomics metaboloimcs. It is the 'study' of tissues, not the process of studying tissues\n PRS:20090901: addition of alternative term = histopathology
definition source	OBI branch derived
editor preferred label	histology
example of usage	the counting of the number of cells with fluorescent label at their surface to determine the percentage of the population which was activated
has curation status	http://purl.obolibrary.org/obo/IAO_0000125
has part	staining imaging assay collecting specimen from organism histological sample preparation
label	histology
prefixIRI	OBI:0600020
prefLabel	histology
term editor	PERSON:Compiled by Helen Parkinson for Transcriptomics thanks to Adam Witney
textual definition	the visual examination of cells or tissue (or images of them) with an assessment regarding a quality of the cells or tissue. Parts are: staining, imaging, judgement
subClassOf	assay

Superclasses & Asserted Axioms

- assay
- has part some imaging assay
- has part some histological sample preparation
- has part some staining
- has part some collecting specimen from organism
- has_specified_output some (information content entity and (is about some (cell or organ section)))
- achieves_planned_objective some assay objective

Ontologies that use the Class

NCI thesaurus

Version: 17.06d (Release date: 2017-06-26)

Specimen (Code C19157)

Terms & Properties

Preferred Name: Specimen

Definition: A part of a thing, or of several things, taken to demonstrate or to determine the character of the whole, e.g. a substance, or portion of material obtained for use in testing, examination, or study; particularly, a preparation of tissue or bodily fluid taken for examination or diagnosis.

Label: Specimen

NCI Thesaurus Code: C19157 (Search for linked caDSR metadata) (search value sets)

NCI Metathesaurus Link: C0370003 (see NCI Metathesaurus info)

Synonyms & Abbreviations: (see Synonym Details)

Research Specimen
Sample
Specimen

External Source Codes:

UMLS CUI	C0370003

Other Properties:

Name	Value (qualifiers indented underneath)
code	C19157
Legacy_Concept_Name	Specimen
Semantic_Type	Physical Object

Additional Concept Data:

Defined Fully by Roles: No

URL: https://nciterms.nci.nih.gov/ncitbrowser/ConceptReport.jsp?dictionary=NCI_Thesaurus&code=C19157

Ontology for Biobanking

Keywords: Search terms

Class: specimen

Term IRI: http://purl.obolibrary.org/obo/OBI_0100051

Definition: A material entity that has the specimen role.

Annotations

- **editor note:** Note: definition is in specimen creation objective which is defined as an objective to obtain and store a material entity for potential use as an input during an investigation.
- **definition editor:** Philippe Rocca-Serra, James Malone
- **definition source:** GROUP: OBI Biomaterial Branch
- **example of usage:** Biobanking of blood taken and stored in a freezer for potential future investigations stores specimen.
- **has curation status:** ready for release

Equivalents

- material entity and (has role some specimen role)

Class Hierarchy

Thing
+ entity
+ continuant
+ independent continuant
+ material entity
- fiat object
+ object aggregate
+ object
+ molecular entity
+ cell
- material information bearer
+ collection packet
- medication material
+ processed material
+ population
+ organization
+ material sample
+ manufacturer
- molecular-labeled material
+ collection of specimens
- target of material addition
- disorder
- post-office box
- street
- aggregate of organizations
more...
- specimen
+ material sample
+ processed specimen
+ specimen with known storage state
+ specimen from organism
- microdissected specimen
- specimen meeting specification
- normal specimen

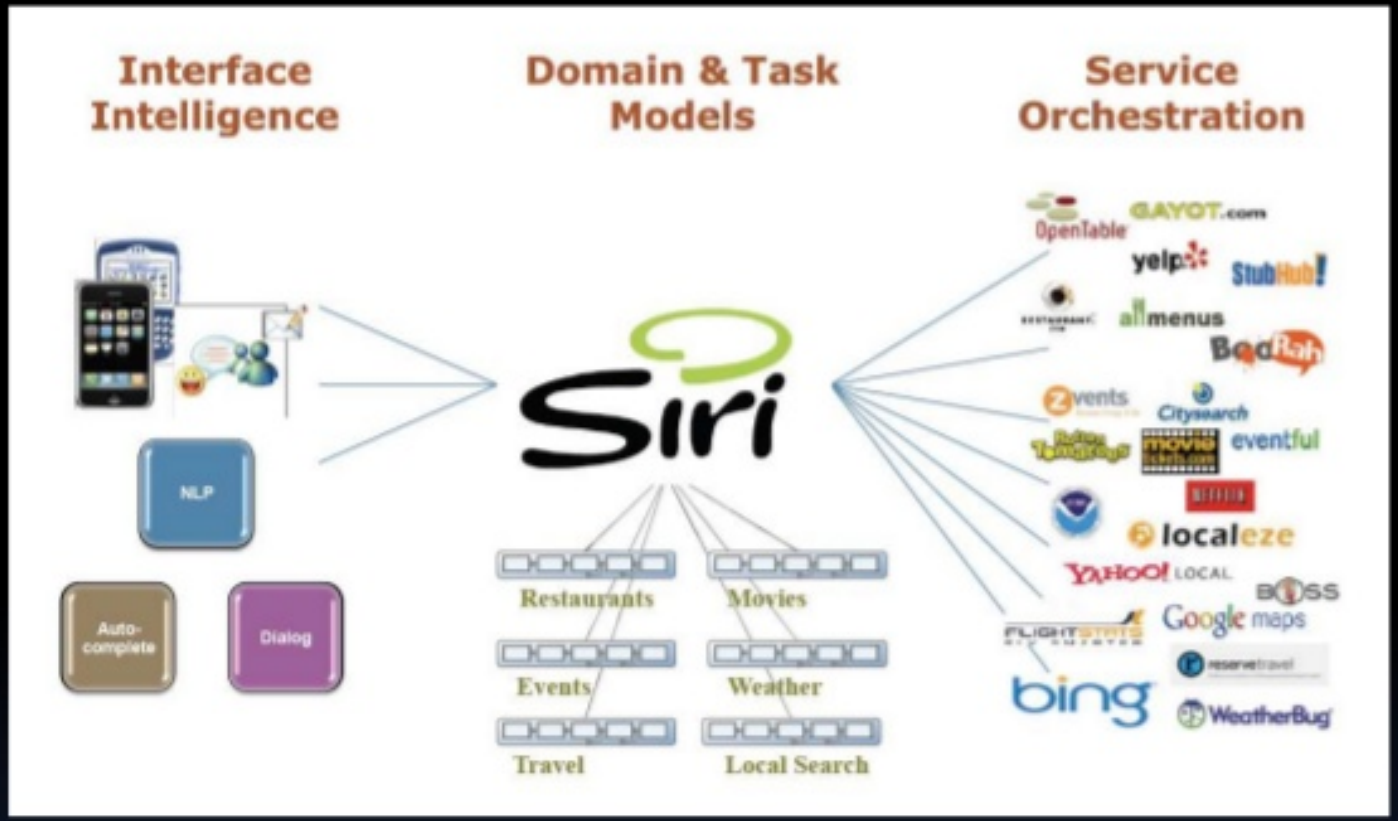
Superclasses & Asserted Axioms

- material entity

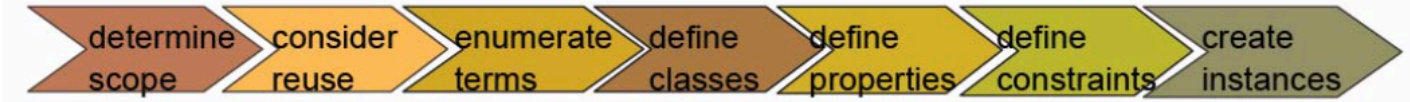
Examples of BFO-based ontology frameworks in other areas

UNEP Ontology Framework	United Nations Environment Programme
CIA Ontology Framework	Central Intelligence Agency
USGS National Map	United States Geological Survey
Joint Doctrine Ontologies	US Air Force Research Labs
Common Core Ontologies (CCO)	US Army / I2WD and ARL, IARPA, JIDO, ONR, AFRL
TRIP Ontologies	Federal Highway Administration (FHWA) Transportation Research Informatics Platform (TRIP)

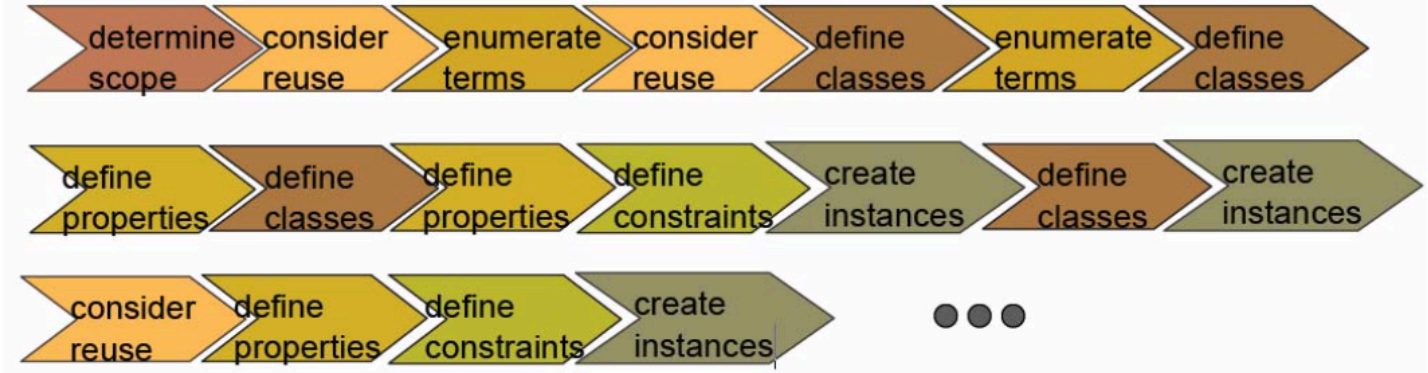
Overview of Siri Technology



Ontology Development Process



In reality - an iterative process:



Ontology Repositories for Life Sciences

- Ontobee
  http://www.ontobee.org/

- Bioportal project
  http://bioportal.bioontology.org/

- Ontology Look up service
  http://www.ebi.ac.uk/ols/index

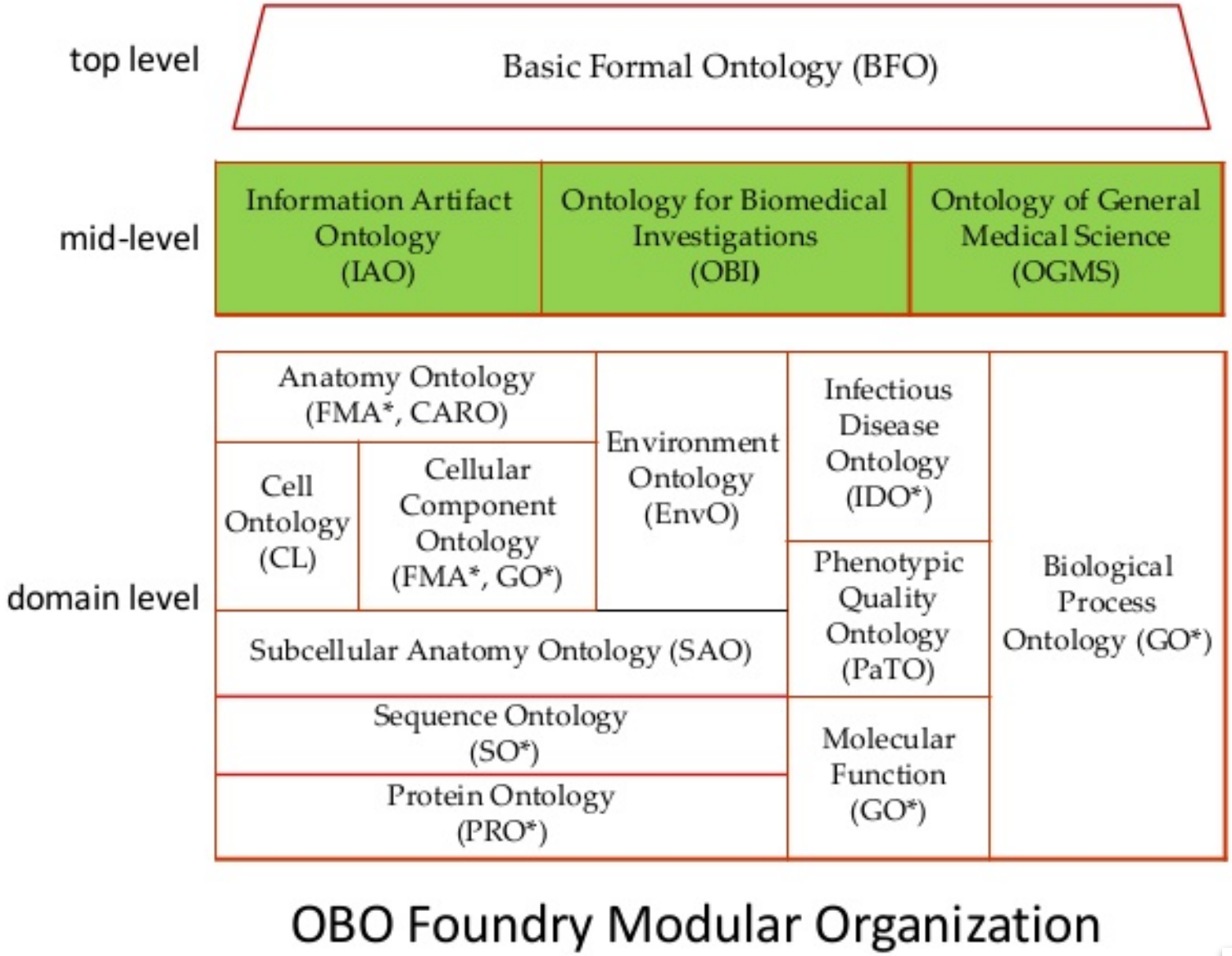
Best practices for developing ontologies @ OBO foundry:
http://www.obofoundry.org/

The OBO Foundry : a step-by-step, principles-based approach

- Developers commit in advance to collaborating with developers of ontologies in adjacent domains and
- To working to ensure that, for each domain, there is community convergence on a single ontology

OBO FOUNDRY PRINCIPLES

- COMMON GOVERNANCE
- COMMON TRAINING
- ROBUST VERSIONING
- COMMON ARCHITECTURE



OBO Foundry Modular Organization

Ontologies adopting the BFO structure

BFO Basic Formal Ontology

Home GitHub Guidebook Publications FOL Users

Users

Below you find an alphabetic list of ontologies and institutions/groups using *BFO*. If you want to be added, just contact us!

Ontologies

- ACGT Master Ontology (ACGT MO): represent the domain of cancer research and management in a computationally tractable manner
- Algorithm-Implementation-Execution Ontology Design Pattern
- Animals in Context Ontology (ACO)
- Autism-DSM-ADI-R Ontology (ADAR)
- Alzheimer Disease Ontology (ADO)
- Adverse Event Reporting Ontology (AERO)
- AFO Foundational Ontology
- Actionable Intelligence Retrieval System (AIRS)
- Apollo Structured Vocabulary (Apollo-SV)
- Bacterial Clinical Infectious Diseases Ontology (BCIDO)
- Behavior Perspective Model (BPM)
- Bank Ontology
- Battle Management Ontology (BMO)
- Beta Cell Genomics Application Ontology (BCGO)
- BioAssay Ontology
- Bioinformatics Web Service Ontology (OBIWS) (see also here)
- Biological Collections Ontology (BCO)
- Biomedical Ethics Ontology
- Biomedical Grid Terminology (BiomedGT, retired): open, collaboratively developed terminology for translational research
- Biomimetic Ontology
- BioTop: A Biomedical Top-Domain Ontology
- BIRNLex: controlled terminology for annotation of BIRN data sources
- Blood Ontology (BLO)
- Body Fluids Ontology (BFLO)
- Bone Dysplasia Ontology (BDO) (see also here)
- Cancer Cell Ontology (OncoCL)
- Cancer Chemoprevention Ontology (CanCo)
- Cardiovascular Disease Ontology (CVDO) (Winner of FOIS 2014 Ontology Competition)
- Cell Behavior Ontology (CBO)
- Cell Culture Ontology (CCONT)
- Cell Cycle Ontology: application ontology for the representation and integrated analysis of the cell cycle process
- Cell Expression, Localization, Development and Anatomy Ontology (CELDA)
- Cell Line Ontology (CLO)
- Cell Ontology: designed as a structured controlled vocabulary for cell types
- Cellular Microscopy Phenotype Ontology (CMPO)
- Chemical Analysis Ontology (CAO)
- Chemical Entities of Biological Interest (ChEBI): freely available dictionary of molecular entities focused on .small. chemical compounds
- Chemical Information Ontology (CHEMINF)
- Chemical Methods Ontology (CHMO)
- CHRONIOUS Ontology Suite
- Cigarette Smoke Exposure Ontology (CSEO)
- Clusters of Orthologous Groups (COG) Analysis Ontology (CAO)
- Cognition-Guided Surgery (CGS) Ontology
- Cognitive Paradigm Ontology (COGPO)
- Common Anatomy Reference Ontology (CARO): anatomical structures in all organisms
- Common Core Ontologies (CCO)
- Communication Standards Ontology (CSO)
- Comparative Data Analysis Ontology (CDAO)
- Computational Neuroscience Ontology (CNO)
- Computer Aided Engineering Modeling Language Ontology (CAEMLOnto)
- Computer-Based Patient Record Ontology (CPRO)
- Conceptual Model Ontology (CMO)
- Core Data Integration Model (CDIM)
- Coriell Cell Line Ontology
- CPR Ontology for the Institute of Medicine's (IOM) Computer-Based Patient Record Ontology
- Diabetes mellitus Diagnosis Ontology (DDO)
- Document Act Ontology (D-Acts)
- Drug Interaction Ontology (DIO): ontology-driven inferences of possible drug-drug interactions
- Drug Ontology (DrOn)
- Drug-drug Interaction Evidence Ontology (DIDEO)
- Drug-drug Interaction Ontology (DINTO)
- Dynamic Earth Sciences Ontologies: Process and Event Ontologies
- Eagle-I Research Resource Ontology (ERO)
- Economics Ontology (EcO)
- Electrocardiography Ontology (ECG)
- Email ontology
- Emotion Ontology (EMO): an ontology to describe affective phenomena
- ENanoMapper (ENM)
- Environment Ontology: an ontology that supports the annotation of the environment of any organism or biological sample
- Epidemiology Ontology (EPO)
- Epilepsy and Seizure Ontology (EPSO)
- Event-Based Functional Behavior Ontology (EFBO)
- Evolution Ontology (EO)
- Experimental Factor Ontology (EFO)
- (EXperimental ACTions) Biomedical Protocol Ontology (EXACT2)
- Exposé: An Ontology for Data Mining Experiments (see also here)
- Flybase Drosophila Anatomy Ontology (DAO)
- Fission Yeast Phenotype Ontology (FYPO)
- Flower-Visiting Domain Ontology (FV), Known Flower-Visiting Group Domain Ontology (KFG), Flower-Visiting Behavior Application Ontology (FVB) and Observation-Date Application Ontology (OBD)
- Food Ontology (FoodOn)
- Foundational Model of Anatomy (FMA): structure of the mammalian and in particular the human body (Further reading)
- Gastrointestinal Endoscopy Ontology (GIEO)
- Gene Regulation Ontology (GRO)
- General Information Model (GIM)
- Genomic Epidemiology Ontology (GenEpiO)
- Genomic Feature and Variation Ontology (GFVO)
- Gestalt: Federated Access to Cyber Observables for Detection of Targeted Attack
- Health Data Ontology Trunk (HDOT)
- Hemocomponents and Hemoderivatives Ontology (HEMONTO)
- Host Pathogen Interactions Ontology (HPO)
- Human Experience Realist Ontology (HERO)
- Human Interaction Network Ontology (HINO)
- Human Physiology Simulation Ontology (HuPSON) (see also here)
- Infectious Disease Ontology
- Information Artifact Ontology (IAO)
- Informed Consent Ontology (ICO)
- Interaction Network Ontology (INO)
- Interdisciplinary Prostate Ontology Project (IPOP)
- International Center for Food Ontology, Operability, Data and Semantics (IC-FOODS)
  - uc_Eating: An ontology for the characterization of eating, drinking and otherwise consuming foods
  - uc_FoodDrugInteractionOntology: An ontology for the characterization of interactions between foods and drugs
  - uc_Milk: An ontology for the characterization of mammalian milks
  - uc_Processing: An ontology for the characterization of processing methods and the products they engender
  - uc_Sense: An ontology for the characterization of sensory perception, qualities, and attributes
- Intracranial aneurysm (ICA) Ontology
- Knowledge Base Of Biomedicine (KaBOB)
- Lipid Ontology
- Major histocompatibility complex (MHC) Restriction Ontology (MRO)
- Malaria Ontology (IDOMAL)
- Materials Ontology (MatOnto)
- Mental Disease Ontology
- Mental Functioning Ontology
- Microbiology Ontology (MicrO)
- Minimum Information Model for Patient Safety (MIMPS)
- miRNAO: An Ontology Unfolding the Domain of microRNAs
- Middle Layer Ontology for Clinical Care (MLOCC)
- Military Ontology (see publication)
- Military Scenario Ontology (MSO)
- MIRO and IRbase: IT Tools for the Epidemiological Monitoring of Insecticide Resistance in Mosquito Disease Vectors
- Model for Clinical Information (MCI)
- Mouse Pathology Ontology (MPATH)
- Name Reaction Ontology (RXNO)
- Nanoparticle Ontology (NPO): Ontology for Cancer Nanotechnology Research
- Neomark Oral Cancer Ontology (NEOMARK4)
- NeuroPsychological Testing Ontology (NPT)
- Neuroscience Information Framework (see also here)
  - Neuroscience Information Framework Cell Ontology (NIFCELL)
  - Neuroscience Information Framework Dysfunction Ontology (NIFDYS)
  - Neuroscience Information Framework Standard Ontology (NIFSTD): a collection of OWL modules covering distinct domains of biomedical reality
- Neural Electromagnetic Ontologies (NEMO): Ontology-based Tools for Representation and Integration of Event-related Brain Potentials
- Neuroscience Information Framework (NIF) Cell Ontology
- Neuroscience Information Framework (NIF) Subcellular Ontology (NIFSUBCELL)
- New Upper Level Ontology
- Next Generation Sequencing Ontology (NGSONTO)
- Non-Coding RNA Ontology (NCRO)
- NMR-Instrument Component of Metabolomics Investigations Ontology
- Ocular Disease Ontology (ODO)
- OncoCL-KB: a Knowledgebase for Integration of Clinical and Molecular Cancer Data
- OntoAlign++: a Combined Strategy for Improving Ontologies Alignment
- OntoForInfoScience: a Detailed Methodology for Construction of Ontologies and its Application in the Blood Domain
- Ontologized Minimum Information About Biobank data Sharing (OMIABIS)
- Ontology for Adverse Events (OAE)
- Ontology for Autism Spectrum Disorder
- Ontology for Biobanking (OBIB)
- Ontology for Biomedical Investigations (OBI): design, protocol, instrumentation, and analysis applied in biomedical investigations
- Ontology for Dengue Fever (IDODEN)
- Ontology for Drug Discovery Investigations (DDI)
- Ontology for Energy Investigations (OEI)
- Ontology for Functionally Graded Materials (OFGM)
- Ontology for General Medical Science (OGMS)
- Ontology for Genes and Genomes (OGG)
- Ontology for Genes and Genomes - Mouse (OGG-MM)
- Ontology for Genetic Disease Investigations (OGDI)
- Ontology for Genetic Interval (OGI)
- Ontology for Genetic Susceptibility Factor (OGSF)
- Ontology for Guiding Appropriate Antibiotic Prescribing
- Ontology for Laparoscopic Surgeries (LapOntoSPM)
- Ontology for Microbial Phenotypes (OMP)
- Ontology for MicroRNA Target Prediction (OMIT) (here)
- Ontology for Newborn Screening and Translational Research (ONSTR)
- Ontology for Next Generation Sequencing Experiments (NGS Ontology)
- Ontology for Pain and Related Disability, Mental Health and Quality of Life (OPMQoL)
- Ontology for Periodontitis (PERIO)
- Ontology of Clinical Research (OCRe)
- Ontology of Biobanking Administration (OMIABIS)
- Ontology for Parasite LifeCycle (OPL): Reference ontology for parasite life cycle stages
- Ontology for Rehabilitation (Traumatic Brain Injury)
- Ontology of Biological and Clinical Statistics (OBCS)
- Ontology of Data Mining (OntoDM)
- Ontology of Datatypes (OntoDT) (see also here)
- Ontology of Experimental Variables and Values (OOEVV)
- Ontology of Medically Related Social Entities (OMRSE)
- Ontology of Social Participation (OPS)
- Ontology of Vaccine Adverse Events (OVAE)
- Ontology-Based Data Access (OBDA)
- Ontology-Based eXtensible Data Model (OBX)
- Ontology-Driven Information System (ODIS)/Ontology-Driven Scenario Generator (ODSG)
- Oral Health and Disease Ontology (OHD)
- Parasite Experiment Ontology (PEO)
- Patient Safetry Categorial Structure (PS-CAST)
- Petrochemical Ontology
- Phenotypic Quality Ontology (PaTO): qualities of biomedical entities
- Plant Experimental Assay Ontology (PEAO)
- Plant Ontology (PO)
- Population and Community Ontology (PCO)
- Population Health Record (PopHR)
- Porifera Ontology (PORO)
- Pre-Eclampsia Ontology (PEO)
- Proper Name Ontology (PNO)
- Protein-Ligand Interaction Ontology (PLIO)
- Proteomics data and process provenance ontology (ProPreO): bioinformatics for glycan expression, integrated technology resource for biomedical glycomics
- Protein Ontology (PRO): protein types and modifications classified on the basis of evolutionary relationships
- Quality of Service (QoS) Ontology
- RNA Ontology (RnaO): RNA features, interactions and motifs
- Role Ontology (ROLEO)
- Saliva Ontology (SALO)
- Schistosomiasis Process Ontology (IDOSCHISTO)
- Scientific Evidence and Provenance Information Ontology (SEPIO)
- Semantic Electronic Health Record (SEHR) Model from Linked2Safety (see also here and here)
- Senselab Ontology with applications to NeuronDB and BrainPharm
- Sequence Ontology (SO): features and properties of nucleic sequences
- Semanticscience Integrated Ontology (SIO)
- Situation Awareness Ontology (SAO)
- Skin Physiology Ontology (SPO)
- Sleep Domain Ontology (SDO) (see also here)
- SMART Protocols: SeMAntic RepresenTation for Experimental Protocols
- Software Ontology (SWO)
- Spatiotemporal Ontology for the Administrative Units of Switzerland (SONADUS)
- Special Nuclear Materials Detection Ontology (SNM-DO)
- Statistics Ontology (STATO)
- Subcellular Anatomy Ontology (SAO) of NCMIR
- Suggested Ontology for Pharmacogenomics (SO-Pharm)
- Surface Water Ontology (SWO)
- Taxonomy for rehabilitation of knee conditions (TRAK)
- Time Event Ontology (TEO)
- Translational Medicine Ontology (TMO)
- Tumour-Node-Metastasis Ontology (TNM-O)
- (Microbial) Typing Ontology (TypOn)
- United Nations SDG (Sustainable Development Goals) Ontology Framework
- Universal Core Semantic Layer
- Vaccination Informed Consent Ontology (VICO)
- Vaccine Ontology (VO)
- Vital Sign Ontology (VSO)
- Xenopus Anatomy Ontology (XAO)
- YAMATO (Yet Another More Advanced Top-Level Ontology)
- yOWL: ontology-driven knowledge base for yeast biologists
- Zebrafish Anatomical Ontology (ZAO): anatomical structures in D. rerio

Institutions, Groups and Projects

- Air Force Research Laboratory, Rome, New York
- Applied Physics Laboratory (APL), Johns Hopkins University
- AstraZeneca - Clinical Information Science (see also here)
- Berkeley Bioinformatics Open-Source Projects (BBOP)
- Biomedical Knowledge Engineering Lab at Seoul National University (SNU BiKE)
- Brain Operation Database (BODB)
- CTSAconnect
- Darwin Core (DwC) (see also)
- L3 Data Tactics Corporation (see also)
- DOQS: Data-Oriented Quality Solutions
- DSpace at NTNUA
- Dumontier Lab
- eagle-i Consortium: a biomedical research resource discovery network
- Elsevier Smart Content Strategy
- eNanoMapper
- EuPathDB
- Extensible Neuroimaging Archive Toolkit (XNAT)
- Good Ontology Design (GoodOD)
- HIGHFLEET
- Influenza Research Database (IRD)
- INRIA Lorraine Research Unit
- Kobe University, Graduate School of Medicine, Department of Sociomedical Informatics
- Language and Computing
  Bought by Nuance
- Medical University Graz - Institute of Medical Informatics, Statistics and Documentation
- National Center for Multi-Source Information Fusion
- Ontology Research Group at the New York State Center of Excellence in Bioinformatics & Life Sciences
  - Ontology, Logic and Technology Unit
  - Qualitative Spatiotemporal Reasoning Unit
  - Referent Tracking Unit
- OntoCAT
- OntoCOG
- OntoMaton
- openEHR
- Open Access Journals Integrated service System Project (GoOA)
- Open PHACTS
- Praxis: EMR research on interoperability and query of clinical records
- REMINE
- Saitama University - Faculty of Liberal Arts (see also here)
- Science Commons - Neurocommons
- Securboration
- Skeletome
- SMART Protocols
- U.S. Geological Survey (USGS) - Center of Excellence for Geospatial Information Science (CEGIS)
- University Hospital Erlangen - Radiology
- University of Arkansas, Biomedical Informatics, Medical Center, Little Rock
- University of Augsburg - Computer Science - Software Methodologies for Distributed Systems
- University of South Alabama - School of Computing - South Biomedical Informatics (SBI) Research Group (see also here)
- University of Texas Southwestern Medical Center (see also here)
- University of Washington - Structural Informatics Group (SIG)
- Virus Pathogen Resource (VIPR)
- VIVO: An interdisciplinary national network enabling collaboration and discovery between scientists across all disciplines
  (see also here)

OWL: W3C Web Ontology Language

Key features of OWL is automatic reasoning (aka classification) with a reasoner using Description Logic (DL) which can perform several tasks including:

Subsumption, automatically organizes classes in an ontology into a hierarchy of sub/super-classes

Consistency, highlight inconsistent statements e.g. a given compound can't be organic and inorganic at the same time because these are disjoint

Querying, answering questions about an ontology (e.g. query languages like SPARQL and SPARQ-DL)

```
<!-- http://purl.obolibrary.org/obo/RO_0002201 -->

<owl:ObjectProperty rdf:about="http://purl.obolibrary.org/obo/RO_0002201">
    <rdfs:subPropertyOf rdf:resource="http://www.w3.org/2002/07/owl#topObjectProperty"/>
    <rdf:type rdf:resource="http://www.w3.org/2002/07/owl#FunctionalProperty"/>
    <obo:IAO_0000114 rdf:resource="http://purl.obolibrary.org/obo/IAO_0000125"/>
    <obo:IAO_0000115>inverse of has phenotype</obo:IAO_0000115>
    <obo:IAO_0000117 xml:lang="en">Chris Mungall</obo:IAO_0000117>
    <oboInOwl:inSubset rdf:resource="http://purl.obolibrary.org/obo/RO_0002259"/>
    <oboInOwl:inSubset rdf:resource="http://purl.obolibrary.org/obo/ro/subsets#ro-eco"/>
    <rdfs:label xml:lang="en">phenotype of</rdfs:label>
</owl:ObjectProperty>



<!-- http://purl.obolibrary.org/obo/RO_0002202 -->

<owl:ObjectProperty rdf:about="http://purl.obolibrary.org/obo/RO_0002202">
    <rdfs:subPropertyOf rdf:resource="http://purl.obolibrary.org/obo/RO_0002258"/>
    <owl:inverseOf rdf:resource="http://purl.obolibrary.org/obo/RO_0002203"/>
    <rdf:type rdf:resource="http://www.w3.org/2002/07/owl#TransitiveProperty"/>
    <rdfs:domain rdf:resource="http://purl.obolibrary.org/obo/BFO_0000004"/>
    <rdfs:range rdf:resource="http://purl.obolibrary.org/obo/BFO_0000004"/>
    <obo:IAO_0000114 rdf:resource="http://purl.obolibrary.org/obo/IAO_0000125"/>
    <obo:IAO_0000115>x develops from y if and only if either (a) x directly develops from y or (b) there exists some z such that x directly develops from z and z
evelops from y</obo:IAO_0000115>
    <obo:IAO_0000117 xml:lang="en">Chris Mungall</obo:IAO_0000117>
    <obo:IAO_0000117 xml:lang="en">David Osumi-Sutherland</obo:IAO_0000117>
    <obo:IAO_0000117>Melissa Haendel</obo:IAO_0000117>
    <obo:IAO_0000117 xml:lang="en">Terry Meehan</obo:IAO_0000117>
    <rdfs:comment>This is the transitive form of the develops from relation</rdfs:comment>
    <rdfs:label xml:lang="en">develops from</rdfs:label>
</owl:ObjectProperty>



<!-- http://purl.obolibrary.org/obo/RO_0002203 -->

<owl:ObjectProperty rdf:about="http://purl.obolibrary.org/obo/RO_0002203">
    <rdfs:subPropertyOf rdf:resource="http://purl.obolibrary.org/obo/RO_0002286"/>
    <rdfs:subPropertyOf rdf:resource="http://purl.obolibrary.org/obo/RO_0002387"/>
    <rdfs:subPropertyOf rdf:resource="http://purl.obolibrary.org/obo/RO_0002388"/>
    <rdf:type rdf:resource="http://www.w3.org/2002/07/owl#TransitiveProperty"/>
    <obo:IAO_0000114 rdf:resource="http://purl.obolibrary.org/obo/IAO_0000125"/>
    <obo:IAO_0000115>inverse of develops from</obo:IAO_0000115>
    <obo:IAO_0000117 xml:lang="en">Chris Mungall</obo:IAO_0000117>
    <obo:IAO_0000117 xml:lang="en">David Osumi-Sutherland</obo:IAO_0000117>
    <obo:IAO_0000117 xml:lang="en">Terry Meehan</obo:IAO_0000117>
    <oboInOwl:inSubset rdf:resource="http://purl.obolibrary.org/obo/RO_0002259"/>
    <rdfs:label xml:lang="en">develops into</rdfs:label>
```

Same word can have different meanings

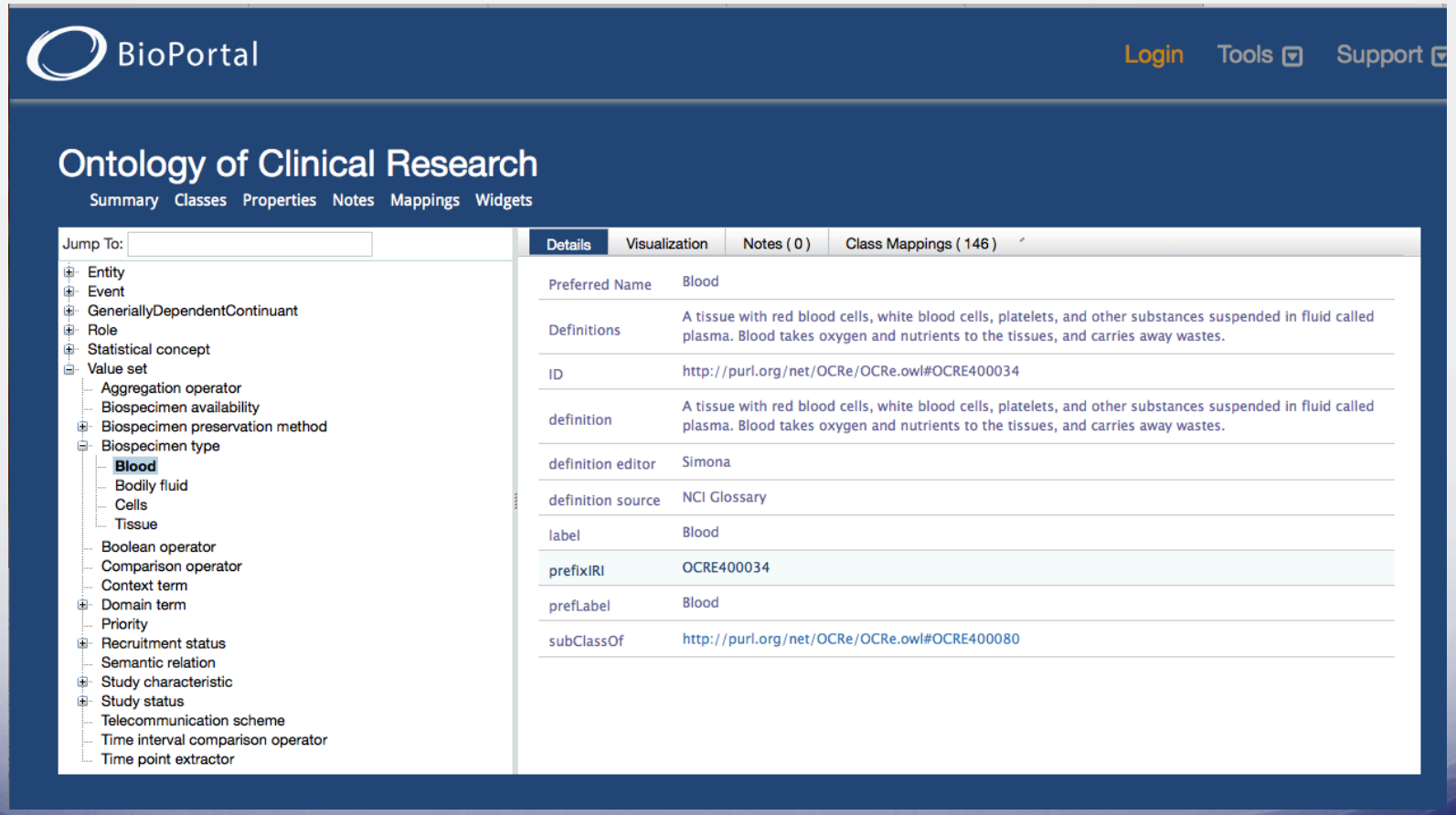
Same meaning can be express using different words

What is Blood?

Tissue

Fluid

What is wrong here?



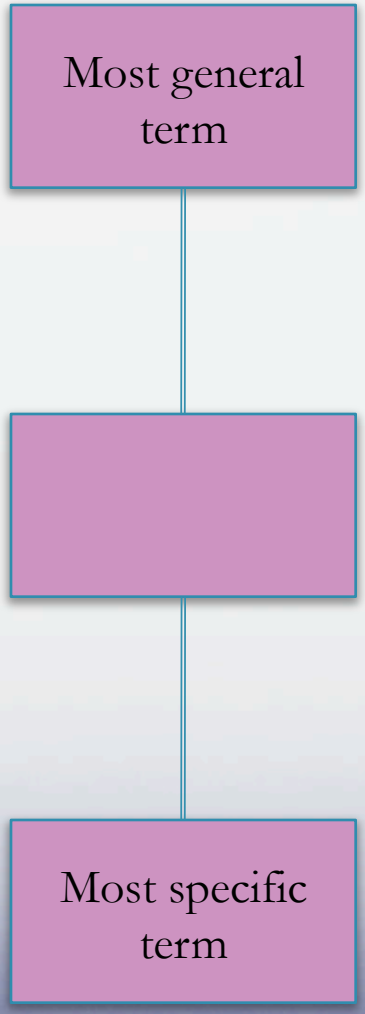
https://bioportal.bioontology.org/search?utf8=✓&query=blood&button=

Controlled vocabularies

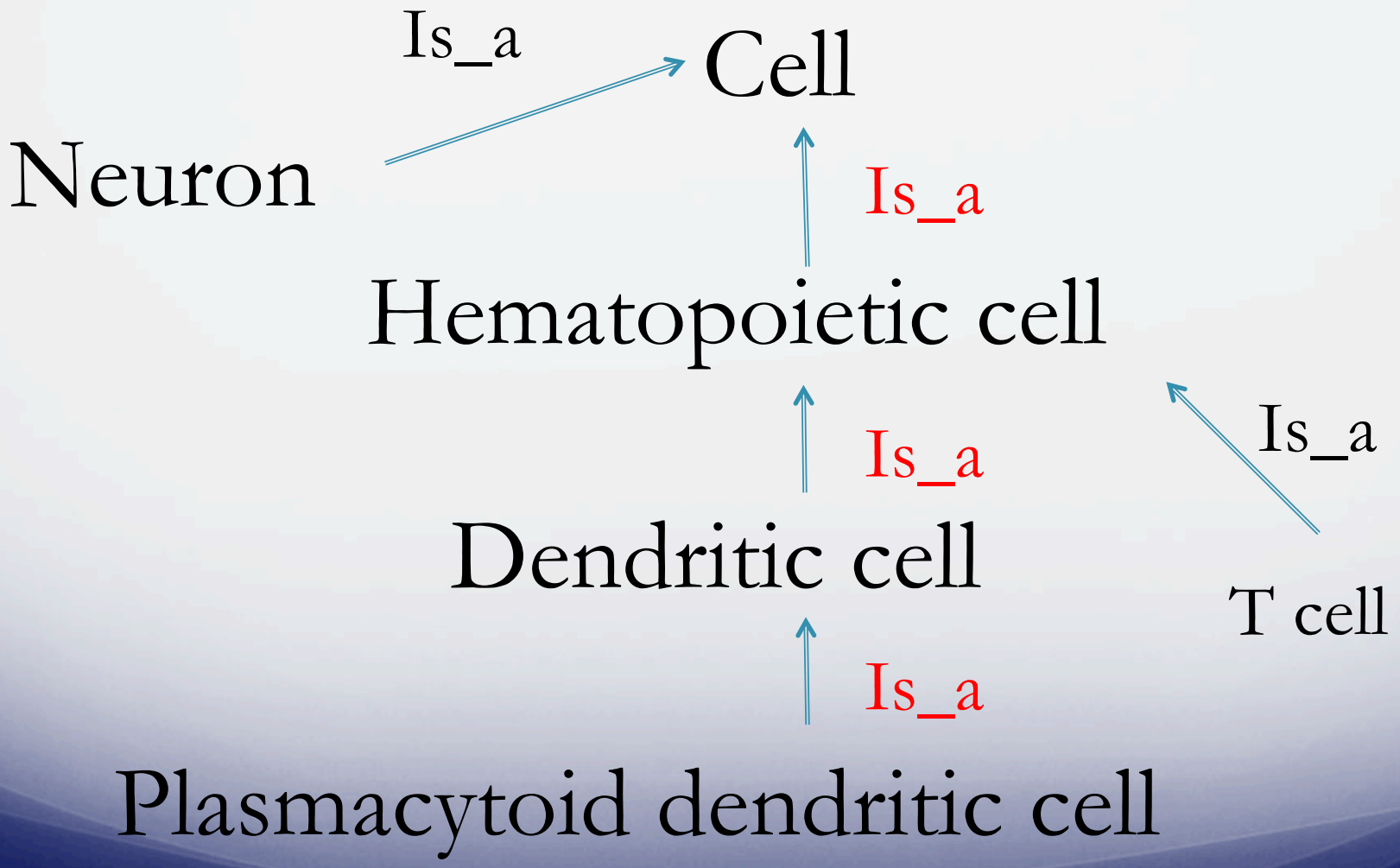
- Particular concept is assign to a single term

What does it mean that Ontology has relationships?

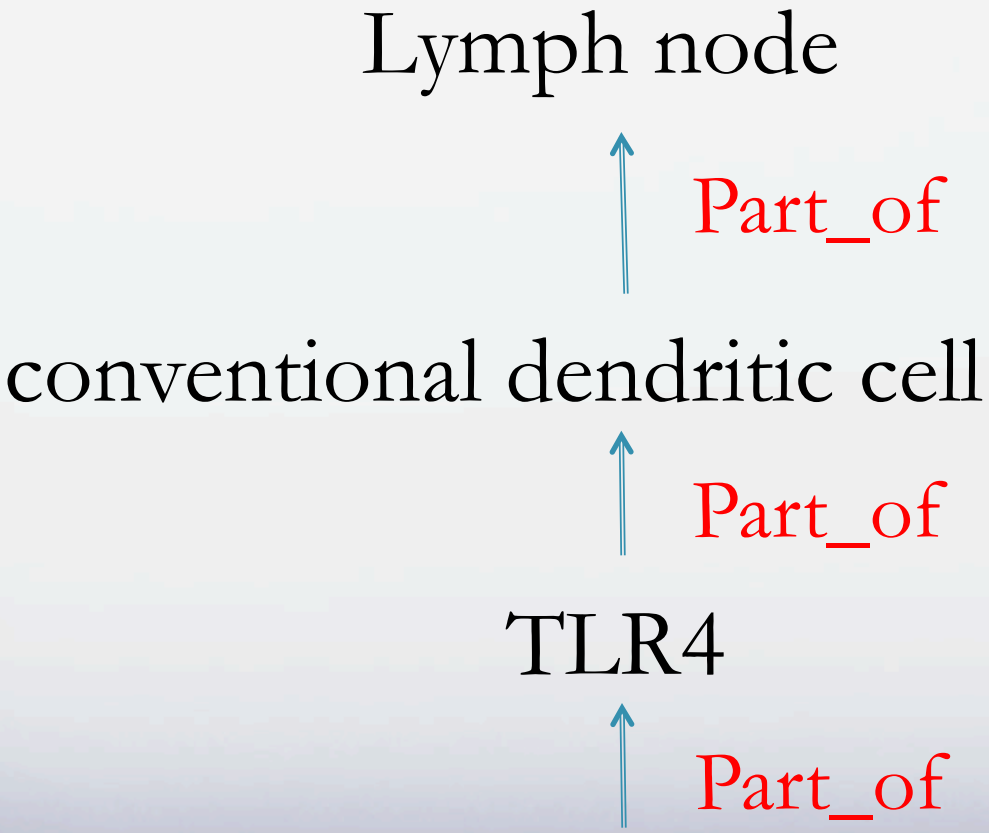
Hierarchy



Example


Is_a
Cell
Neuron
Is_a
Hematopoietic cell
Is_a
Is_a
Dendritic cell
T cell
Is_a
Plasmacytoid dendritic cell

Example


Lymph node
Part_of
conventional dendritic cell
Part_of
TLR4
Part_of
TIR domain

part_of

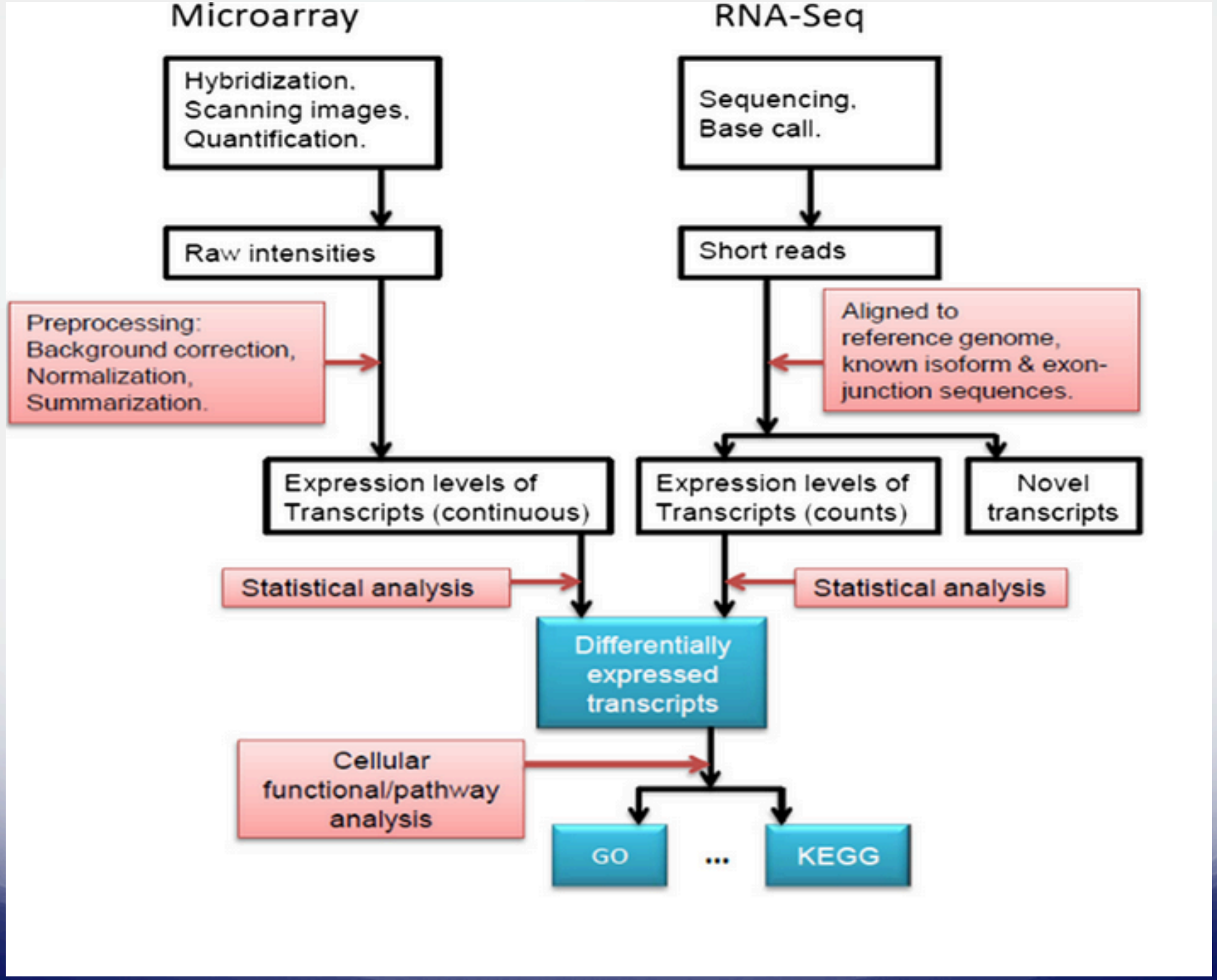
ID	OBO_REL:part_of
Name	part_of
Relation properties	[transitive] [reflexive] [anti-symmetric]
inverse_of	OBO_REL:has_part (instance level)
Definition	For continuants: C part_of C' if and only if: given any c that instantiates C at a time t, there is some c' such that c' instantiates C' at time t, and c *part_of* c' at t. For processes: P part_of P' if and only if: given any p that instantiates P at a time t, there is some p' such that p' instantiates P' at time t, and p *part_of* p' at t. (Here *part_of* is the instance-level part-relation.)
Comments	Parthood as a relation between instances: The primitive instance-level relation p part_of p1 is illustrated in assertions such as: this instance of rhodopsin mediated phototransduction part_of this instance of visual perception. This relation satisfies at least the following standard axioms of mereology: reflexivity (for all p, p part_of p); anti-symmetry (for all p, p1, if p part_of p1 and p1 part_of p then p and p1 are identical); and transitivity (for all p, p1, p2, if p part_of p1 and p1 part_of p2, then p part_of p2). Analogous axioms hold also for parthood as a relation between spatial regions. For parthood as a relation between continuants, these axioms need to be modified to take account of the incorporation of a temporal argument. Thus for example the axiom of transitivity for continuants will assert that if c part_of c1 at t and c1 part_of c2 at t, then also c part_of c2 at t. Parthood as a relation between classes: To define part_of as a relation between classes we again need to distinguish the two cases of continuants and processes, even though the explicit reference to instants of time now falls away. For continuants, we have C part_of C1 if and only if any instance of C at any time is an instance-level part of some instance of C1 at that time, as for example in: cell nucleus part_ of cell.

http://bioportal.bioontology.org/ontologies/OBOREL?p=properties

Which is the problem we are going to solve by using ontology

How to find your data?
How to reason with data when you find it?
How to understand the significance of the data you collected 3 years earlier?
How to integrate with other people's data?
Part of the solution must involve consensus based, standardized terminologies and coding schemes

How Ontology can help researcher


Microarray
RNA-Seq
Hybridization.
Scanning images.
Quantification.
Sequencing.
Base call.
Raw intensities
Short reads
Preprocessing:
Background correction,
Normalization,
Summarization.
Aligned to
reference genome,
known isoform & exon-
junction sequences.
Expression levels of
Transcripts (continuous)
Expression levels of
Transcripts (counts)
Novel
transcripts
Statistical analysis
Statistical analysis
Differentially
expressed
transcripts
Cellular
functional/pathway
analysis
GO
...
KEGG

Ontology annotation

How to create annotation

Manual curation

Computer inference

BMC Genomics. 2008 Feb 27;9:102. doi: 10.1186/1471-2164-9-102.

Protein abundance profiling of the Escherichia coli cytosol.

Ishihama Y[1], Schmidt T, Rappsilber J, Mann M, Hartl FU, Kerner MJ, Frishman D.

Author information

Abstract

BACKGROUND: Knowledge about the abundance of molecular components is an important prerequisite for building quantitative predictive models of cellular behavior. Proteins are central components of these models, since they carry out most of the fundamental processes in the cell. Thus far, protein concentrations have been difficult to measure on a large scale, but proteomic technologies have now advanced to a stage where this information becomes readily accessible.

RESULTS: Here, we describe an experimental scheme to maximize the coverage of proteins identified by mass spectrometry of a complex biological sample. Using a combination of LC-MS/MS approaches with protein and peptide fractionation steps we identified 1103 proteins from the cytosolic fraction of the Escherichia coli strain MC4100. A measure of abundance is presented for each of the identified proteins, based on the recently developed emPAI approach which takes into account the number of sequenced peptides per protein. The values of abundance are within a broad range and accurately reflect independently measured copy numbers per cell. As expected, the most abundant proteins were those involved in protein synthesis, most notably ribosomal proteins. Proteins involved in energy metabolism as well as those with binding function were also found in high copy number while proteins annotated with the terms metabolism, transcription, transport, and cellular organization were rare. The barrel-sandwich fold was found to be the structural fold with the highest abundance. Highly abundant proteins are predicted to be less prone to aggregation based on their length, pI values, and occurrence patterns of hydrophobic stretches. We also find that abundant proteins tend to be predominantly essential. Additionally we observe a significant correlation between protein and mRNA abundance in E. coli cells.

CONCLUSION: Abundance measurements for more than 1000 E. coli proteins presented in this work represent the most complete study of protein abundance in a bacterial cell so far. We show significant associations between the abundance of a protein and its properties and functions in the cell. In this way, we provide both data and novel insights into the role of protein concentration in this model organism.

PMID: 18304323 [PubMed - indexed for MEDLINE] PMCID: PMC2292177 Free PMC Article

Gene Product Associations

Free-text filtering X

Your search is pinned to these filters

+ document_category: annotation

+ bioentity: UniProtKB:P30850

No current user filters.

- Source
- Assigned by
- Ontology (aspect)
- Evidence type
- PANTHER family
- Qualifier
- Taxon
- Direct annotation
- Inferred annotation
- Annotation extension

Found entities

Total: 24; showing 1-10 **Results count** 10

Gene/product	Gene/product name	Qualifier	Direct annotation	Annotation extension	Assigned by	Taxon	Evidence	Evidence with	PANTHER family	Isoform	Reference	Date
rnb	ribonuclease II		rRNA processing		GO_CENTRAL	Escherichia coli K-12	IBA	PANTHER:PTN000599170	ribonuclease pthr23355	PR:000023787	GO_REF:0000033	20150212
rnb	ribonuclease II		exosome (RNase complex)		GO_CENTRAL	Escherichia coli K-12	IBA	PANTHER:PTN000599170	ribonuclease pthr23355	PR:000023787	GO_REF:0000033	20150212
rnb	ribonuclease II		3'-5'-exoribonuclease activity		GO_CENTRAL	Escherichia coli K-12	IBA	PANTHER:PTN000599170	ribonuclease pthr23355	PR:000023787	GO_REF:0000033	20150212
rnb	ribonuclease II		RNA phosphodiester bond hydrolysis, exonucleolytic		GO_CENTRAL	Escherichia coli K-12	IBA	PANTHER:PTN000599170	ribonuclease pthr23355	PR:000023787	GO_REF:0000033	20150212
rnb	ribonuclease II		cytosol		EcoCyc	Escherichia coli K-12	IDA		ribonuclease pthr23355	PR:000023787	PMID:18304323	20140602
rnb	ribonuclease II		protein binding		IntAct	Escherichia coli K-12	IPI	UniProtKB:P0A7W1	ribonuclease pthr23355	PR:000023787	PMID:24561554	20140512
rnb	ribonuclease II		protein binding		IntAct	Escherichia coli K-12	IPI	UniProtKB:P0A7W1	ribonuclease pthr23355	PR:000023787	PMID:15690043	20140512
rnb	ribonuclease II		hydrolase activity		UniProtKB	Escherichia coli K-12	IEA	SP_KW:KW-0378	ribonuclease pthr23355	PR:000023787	GO_REF:0000037	20150523
rnb	ribonuclease II		RNA catabolic process		InterPro	Escherichia coli K-12	IEA	InterPro:IPR011804	ribonuclease pthr23355	PR:000023787	GO_REF:0000002	20150523
rnb	ribonuclease II		exonuclease activity		UniProtKB	Escherichia coli K-12	IEA	SP_KW:KW-0269	ribonuclease pthr23355	PR:000023787	GO_REF:0000037	20150523

Evidence code

A simple controlled vocabulary used to record evidence that supports the association between the gene and the GO term

- Inferred from Experiment (EXP)
- Inferred from Direct Assay (IDA)
- Inferred from Physical Interaction (IPI)
- Inferred from Mutant Phenotype (IMP)
- Inferred from Genetic Interaction (IGI)
- Inferred from Expression Pattern (IEP)
- Inferred from Sequence or structural Similarity (ISS)
- Inferred from Sequence Orthology (ISO)
- Inferred from Sequence Alignment (ISA)
- Inferred from Sequence Model (ISM)
- Inferred from Genomic Context (IGC)
- Inferred from Biological aspect of Ancestor (IBA)
- Inferred from Biological aspect of Descendant (IBD)
- Inferred from Key Residues (IKR)
- Inferred from Rapid Divergence(IRD)
- Inferred from Reviewed Computational Analysis (RCA)
- Traceable Author Statement (TAS)
- Non-traceable Author Statement (NAS)
- Inferred by Curator (IC)
- No biological Data available (ND) evidence code

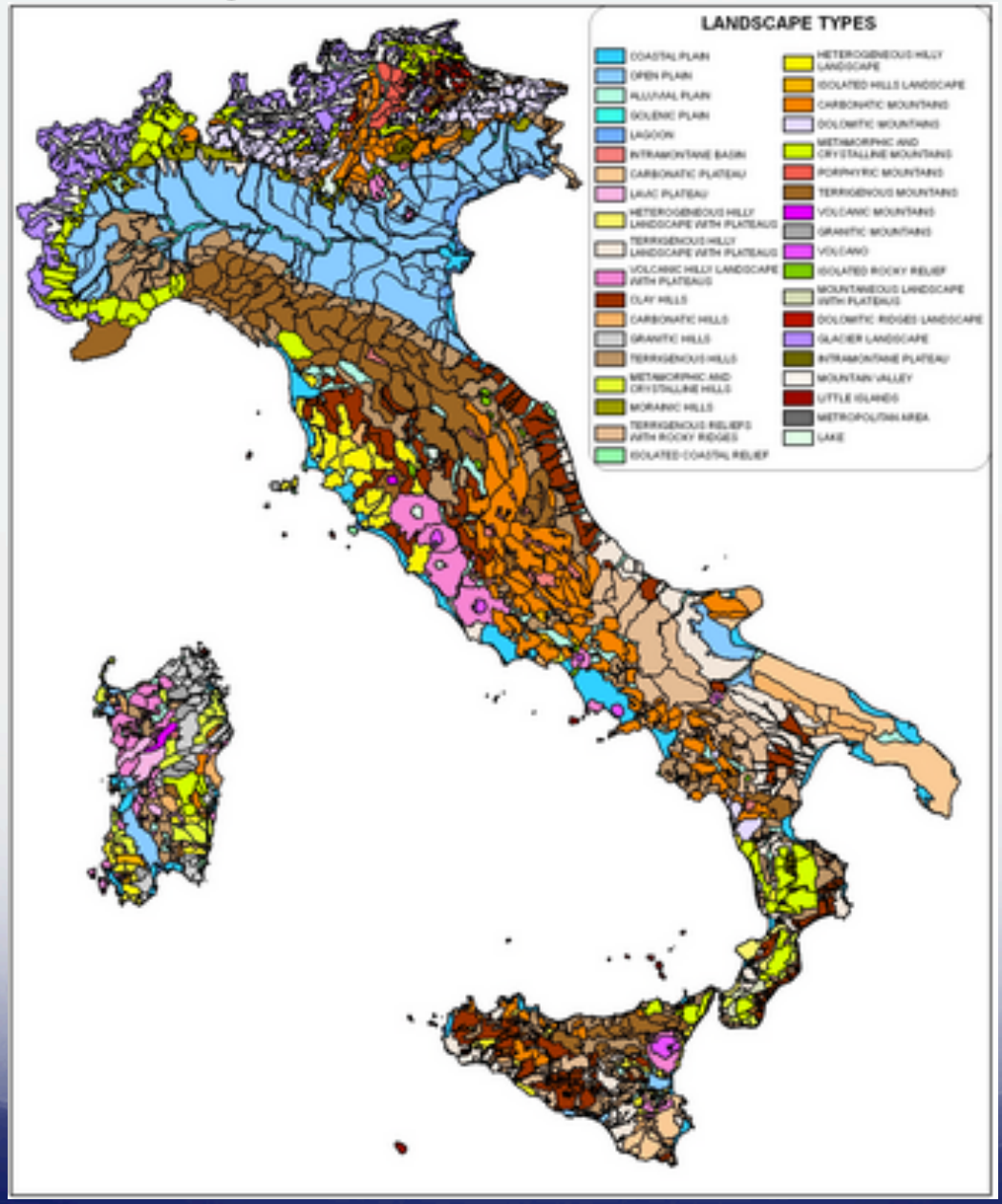
Automatically-Assigned evidence code is:

- Inferred from Electronic Annotation (IEA)

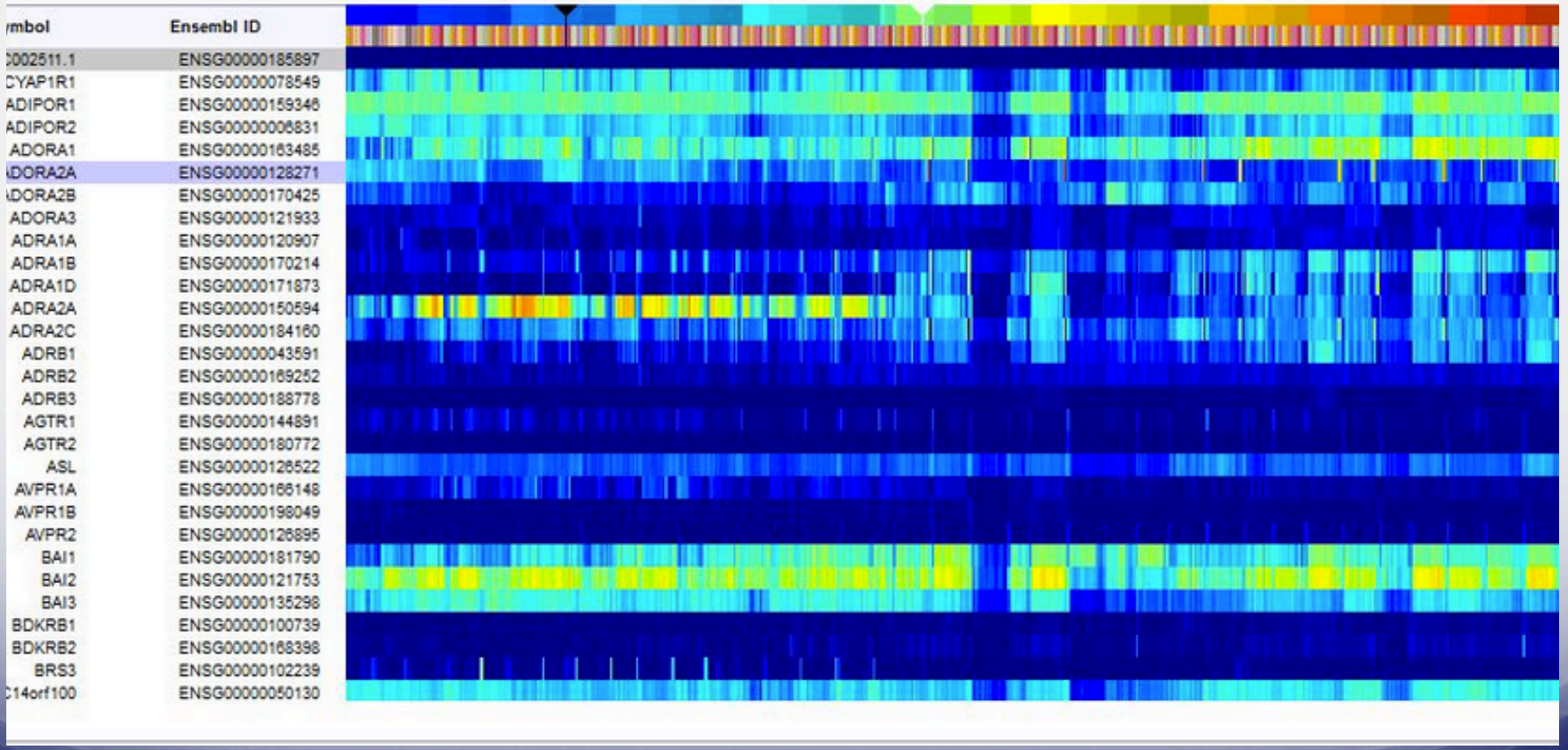
Why develop an Ontology?

- To share common understanding of the entities in a specific domain
- Among people
- Among software
- Among people and software

Legend for maps



Ontologies are legends for data

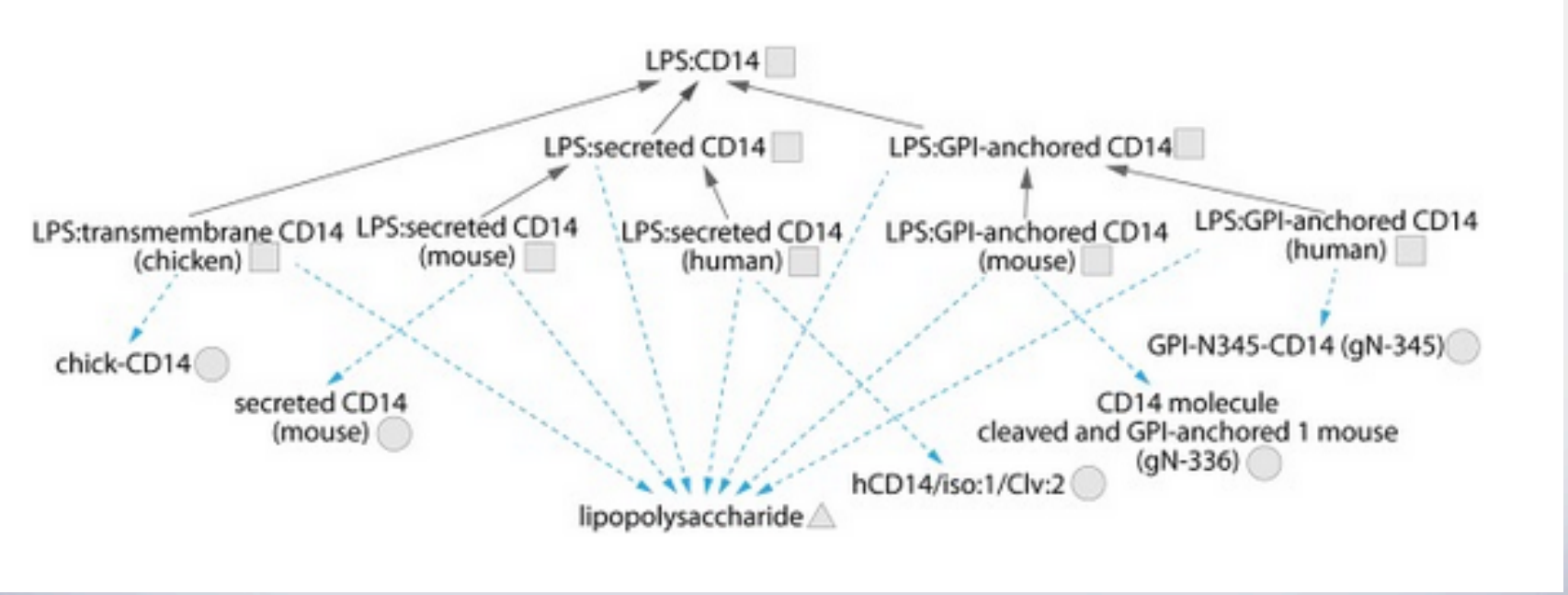


NCBO

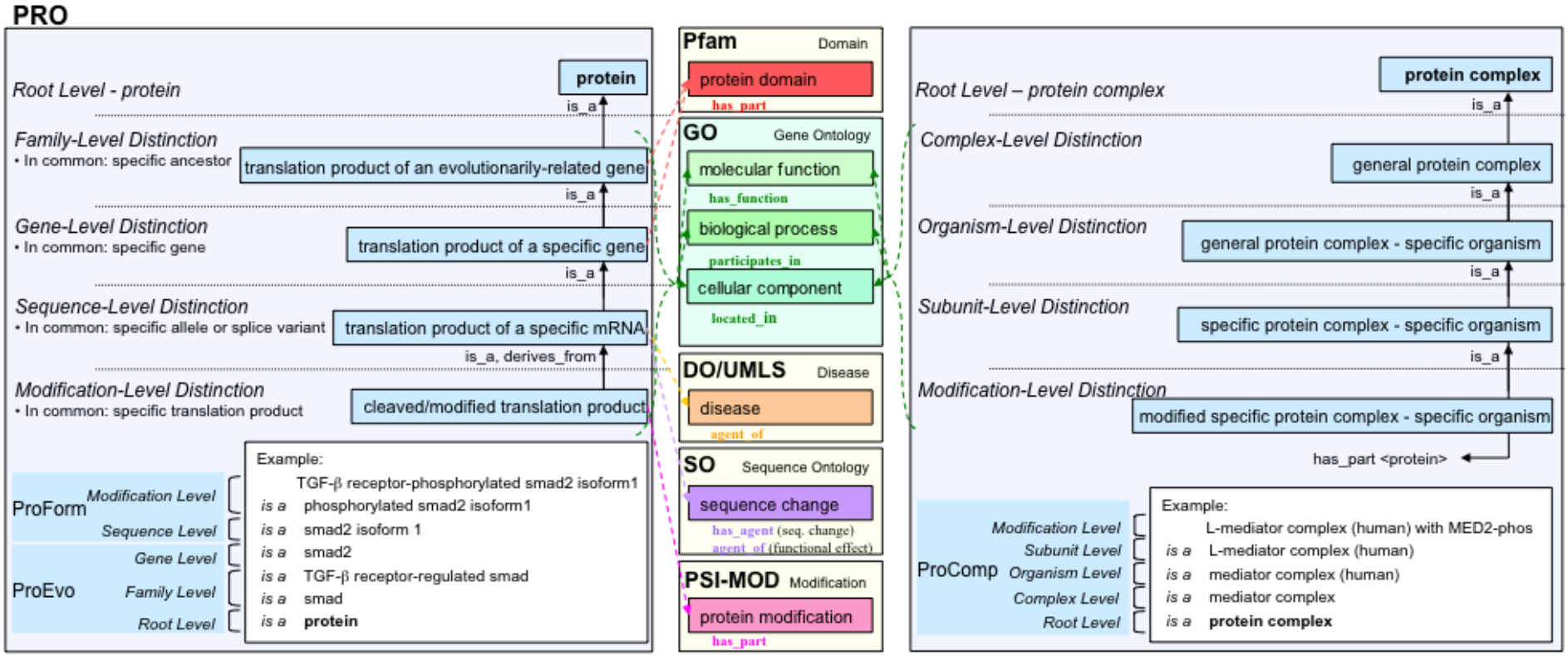
- Dissemination and Ontology Best Practices of the National Center for Biomedical Ontology

- http://bioontology.org

Ontologies are modular
Example: The Protein Ontology



Toll-Like Receptor Signaling in Vertebrates: Testing the Integration of Protein, Complex, and Pathway Data in the Protein Ontology Framework. Masci et al.2015

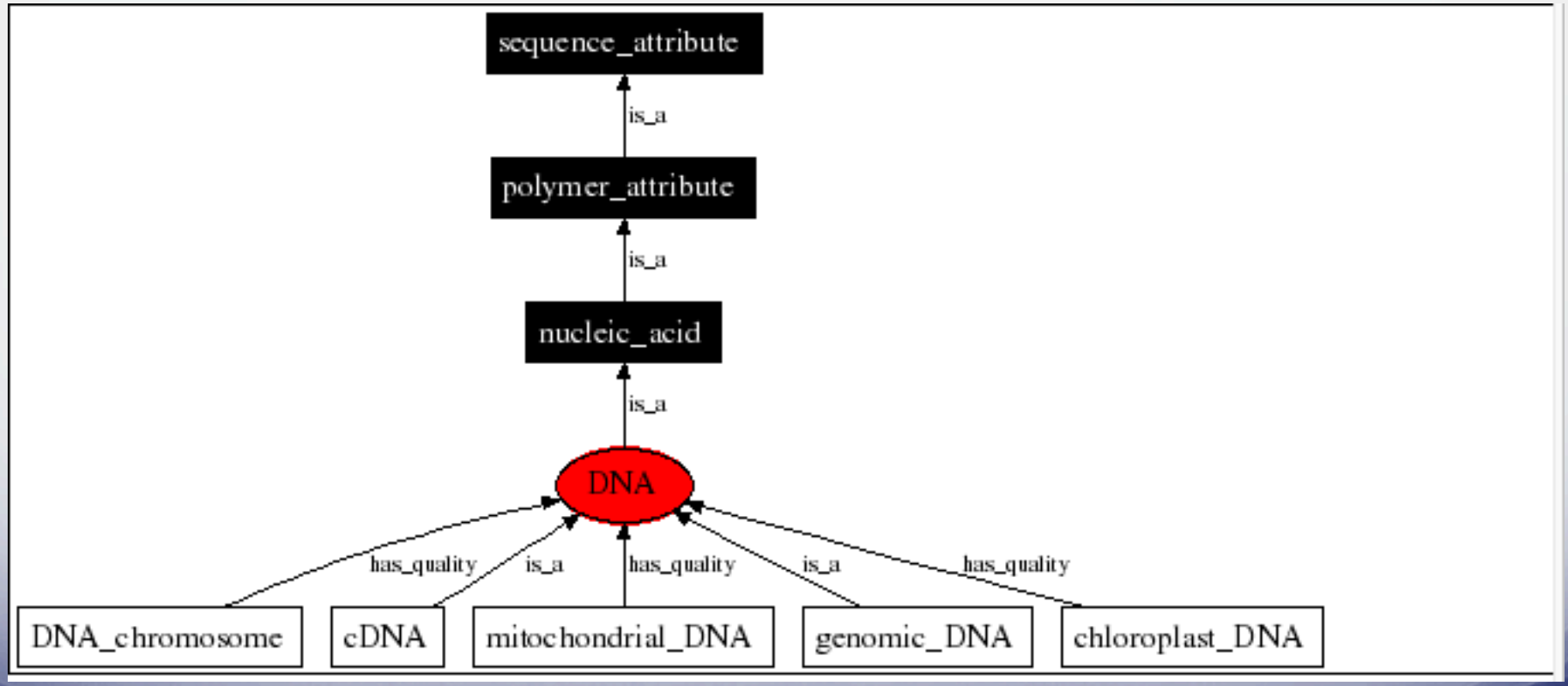


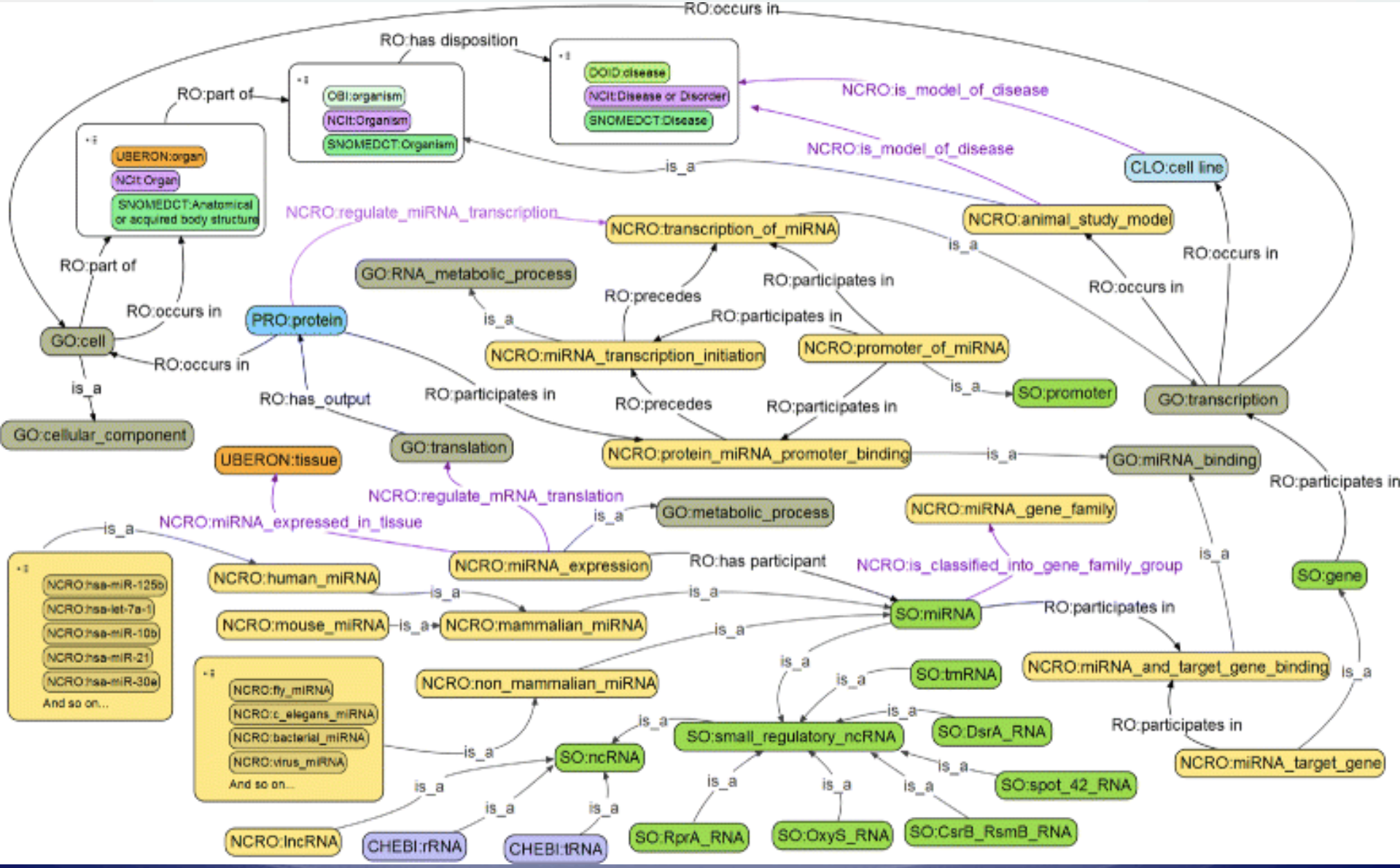
http://research.bioinformatics.udel.edu/pro/entry/PR%3A000001155/

http://pir.georgetown.edu/cgi-bin/pro/browser_pro?ids=PR:000001155

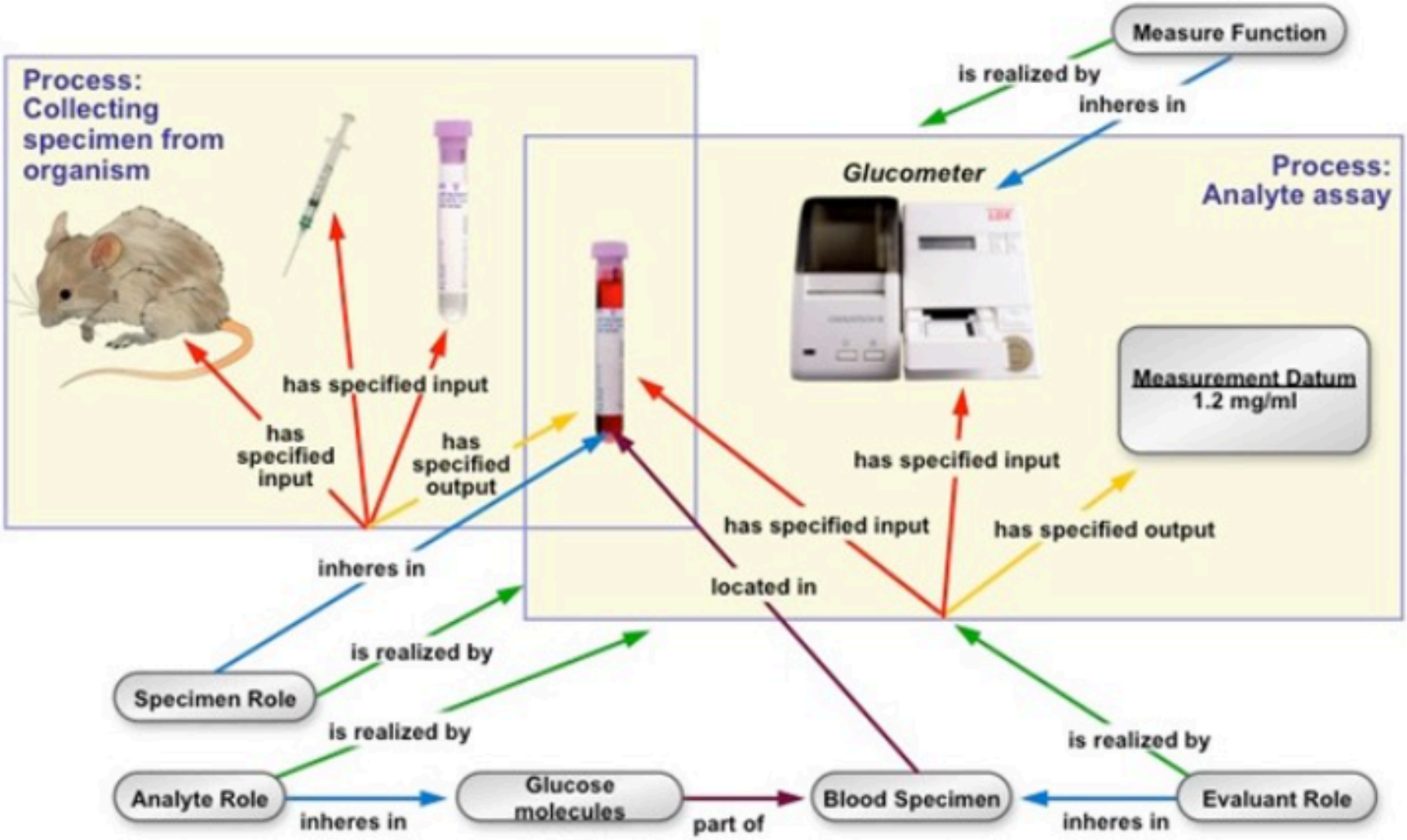
http://pir.georgetown.edu/cgi-bin/ipcSF?id=PIRSF800008

Sequence ontology

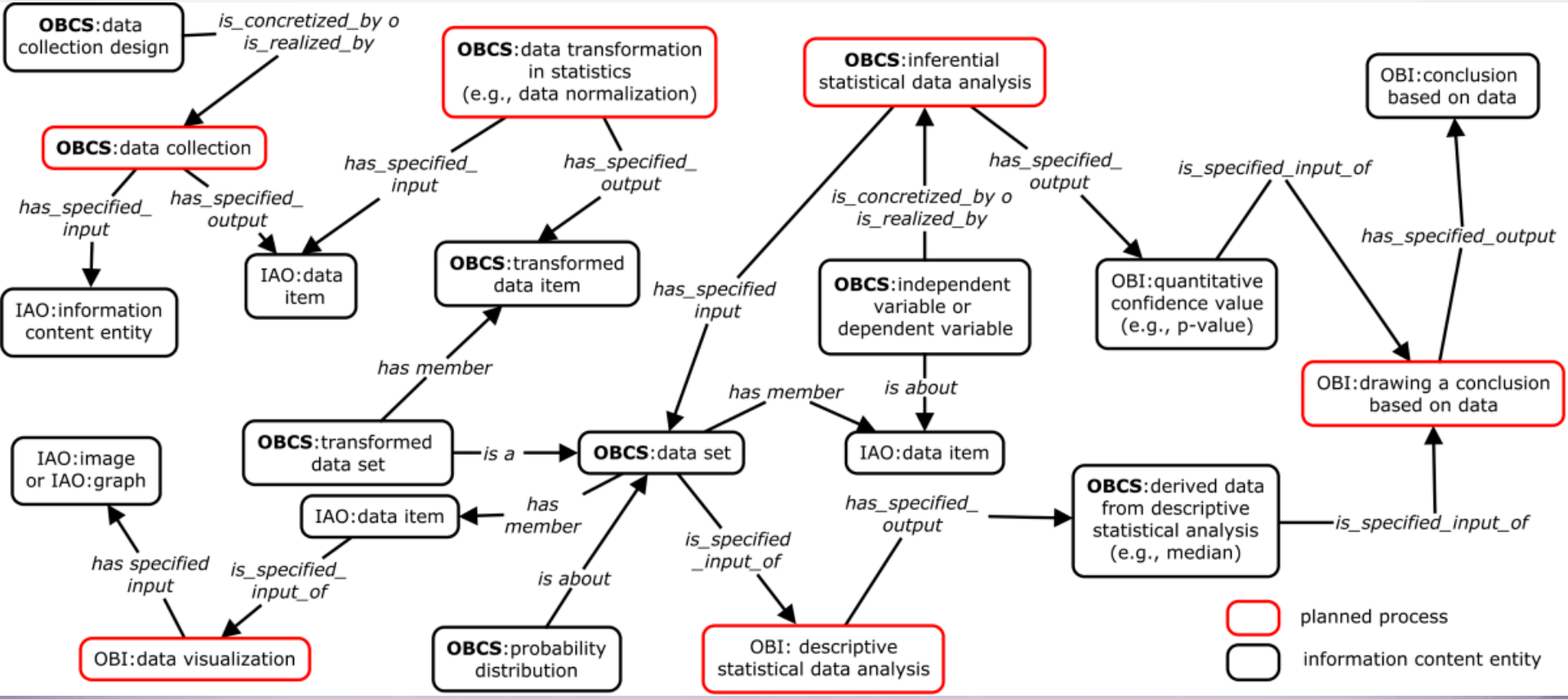



RO:occurs in
RO:has disposition
RO:part of
DOID:disease
NCIt:Disease or Disorder
SNOMEDCT:Disease
OBI:organism
NCIt:Organism
SNOMEDCT:Organism
UBERON:organ
NCIt:Organ
SNOMEDCT:Anatomical or acquired body structure
NCRO:is_model_of_disease
NCRO:is_model_of_disease
CLO:cell line
is_a
NCRO:animal_study_model
NCRO:regulate_miRNA_transcription
NCRO:transcription_of_miRNA
is_a
RO:occurs in
RO:occurs in
RO:part of
GO:RNA_metabolic_process
RO:precedes
RO:participates in
RO:occurs in
PRO:protein
RO:participates in
GO:cell
NCRO:miRNA_transcription_initiation
NCRO:promoter_of_miRNA
RO:occurs in
is_a
SO:promoter
GO:transcription
is_a
RO:has_output
RO:participates in
RO:precedes
RO:participates in
GO:cellular_component
GO:translation
NCRO:protein_miRNA_promoter_binding
is_a
GO:miRNA_binding
RO:participates in
UBERON:tissue
NCRO:regulate_mRNA_translation
is_a
GO:metabolic_process
NCRO:miRNA_gene_family
is_a
NCRO:miRNA_expressed_in_tissue
NCRO:miRNA_expression
RO:has participant
NCRO:is_classified_into_gene_family_group
is_a
SO:gene
NCRO:hsa-miR-125b
NCRO:hsa-let-7a-1
NCRO:hsa-miR-10b
NCRO:hsa-miR-21
NCRO:hsa-miR-30e
And so on...
NCRO:human_miRNA
is_a
is_a
SO:miRNA
RO:participates in
NCRO:mouse_miRNA
is_a
NCRO:mammalian_miRNA
is_a
NCRO:miRNA_and_target_gene_binding
is_a
NCRO:fly_miRNA
NCRO:c_elegans_miRNA
NCRO:bacterial_miRNA
NCRO:virus_miRNA
And so on...
NCRO:non_mammalian_miRNA
is_a
SO:tmRNA
is_a
is_a
SO:small_regulatory_ncRNA
SO:DsrA_RNA
is_a
RO:participates in
NCRO:miRNA_target_gene
SO:ncRNA
is_a
is_a
SO:spot_42_RNA
is_a
is_a
is_a
is_a
NCRO:lncRNA
CHEBI:rRNA
CHEBI:tRNA
SO:RprA_RNA
SO:OxyS_RNA
SO:CsrB_RsmB_RNA

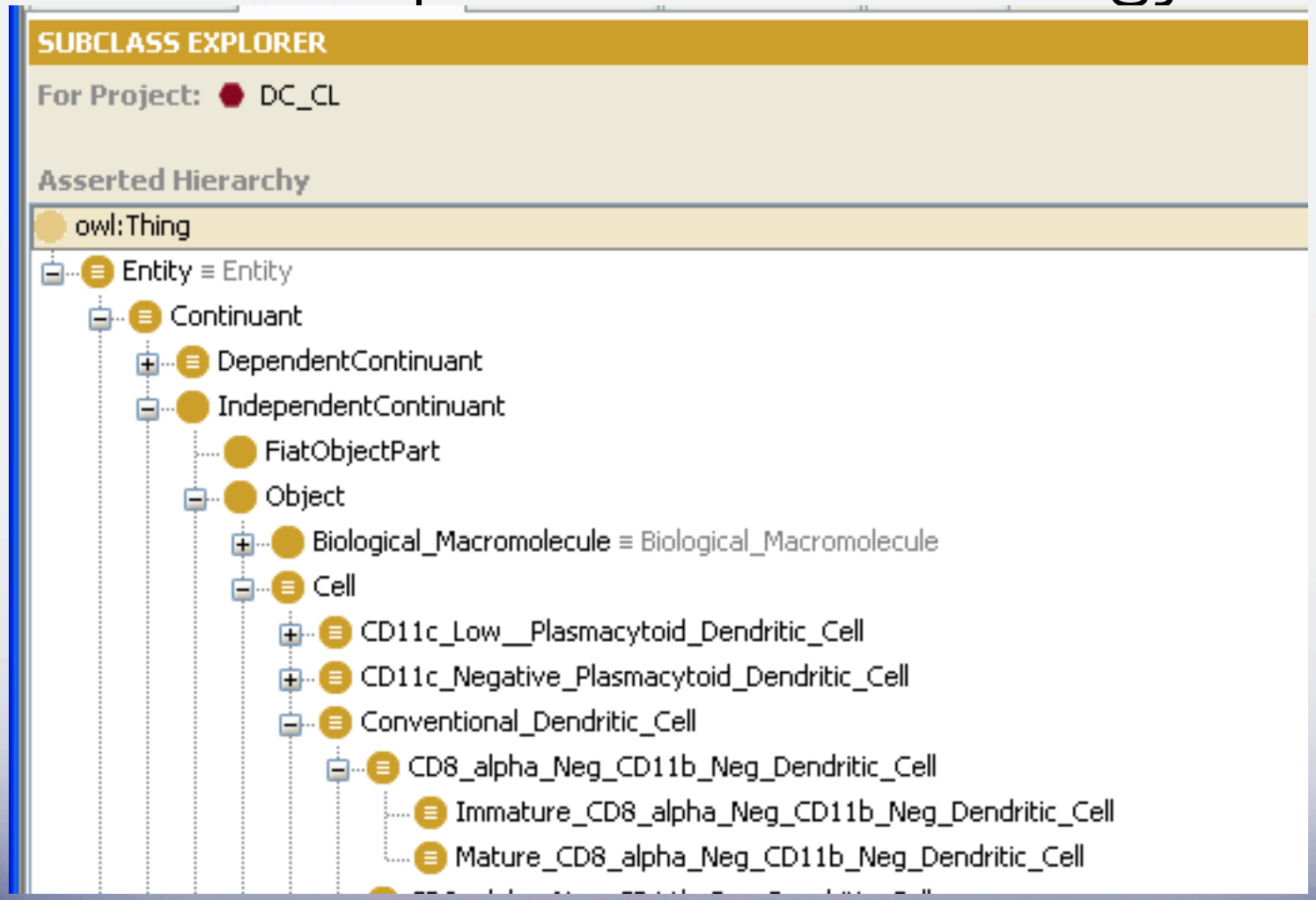
A strength of OBI is modeling the processes that connect biological source material to the data generated about it



Measurement of Glucose concentration in blood

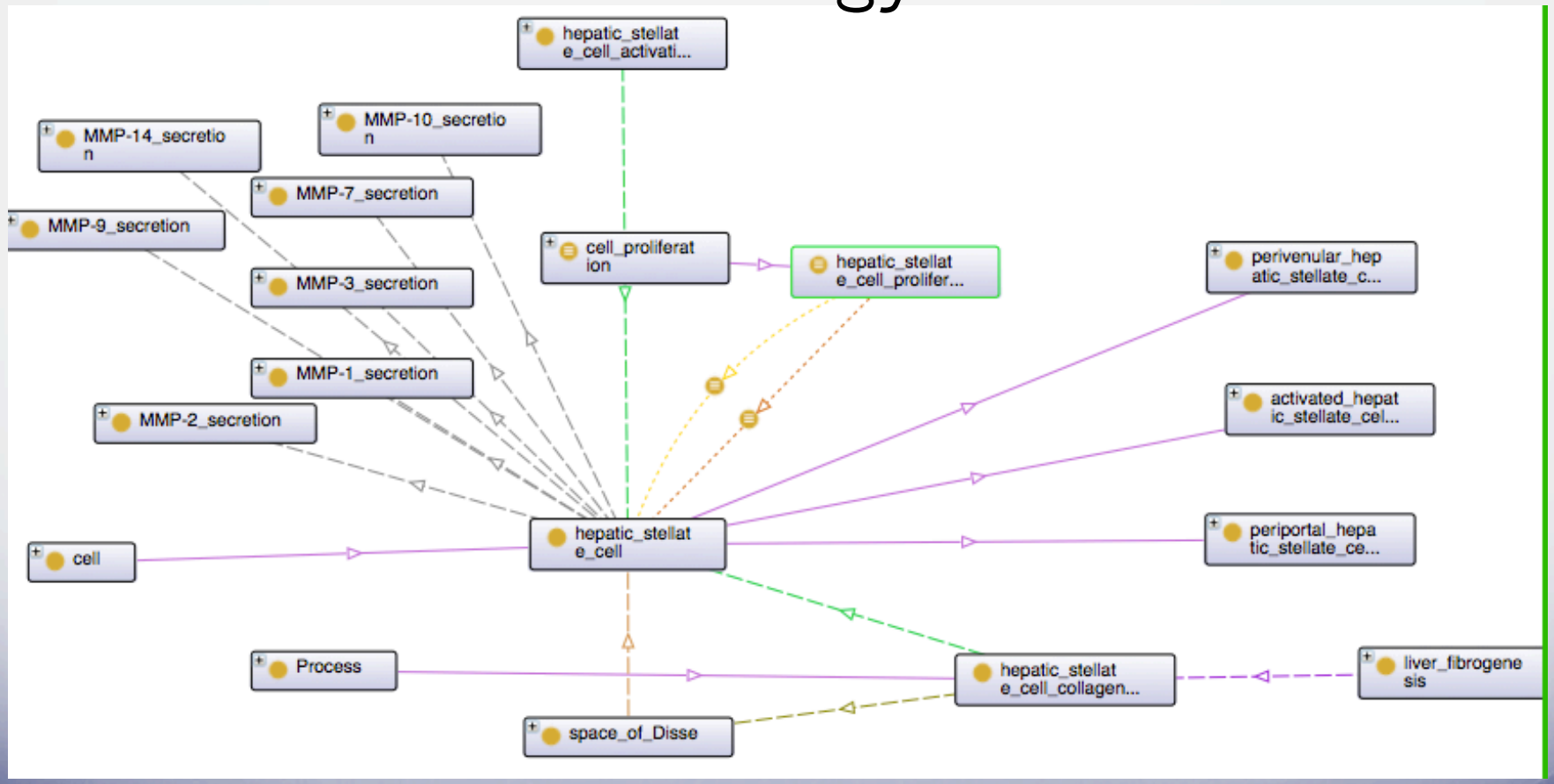

OBCS:data collection design
is_concretized_by o is_realized_by
OBCS:data collection
has_specified_ input
has_specified_ output
IAO:information content entity
IAO:data item
OBCS:data transformation in statistics (e.g., data normalization)
has_specified_ input
has_specified_ output
OBCS:transformed data item
has member
OBCS:transformed data set
is a
OBCS:data set
IAO:image or IAO:graph
has specified input
IAO:data item
has member
is_specified_ input_of
OBCS:probability distribution
is about
is_specified _input_of
OBI: descriptive statistical data analysis
has_specified input
OBCS:inferential statistical data analysis
is_concretized_by o is_realized_by
OBCS:independent variable or dependent variable
has member
is about
IAO:data item
has_specified_ output
OBCS:derived data from descriptive statistical analysis (e.g., median)
has_specified_ output
OBI:quantitative confidence value (e.g., p-value)
is_specified_input_of
OBI:conclusion based on data
has_specified_output
OBI:drawing a conclusion based on data
is_specified_input_of
OBI:data visualization
planned process
information content entity

Ontologies are Modular
Example: The Cell Ontology

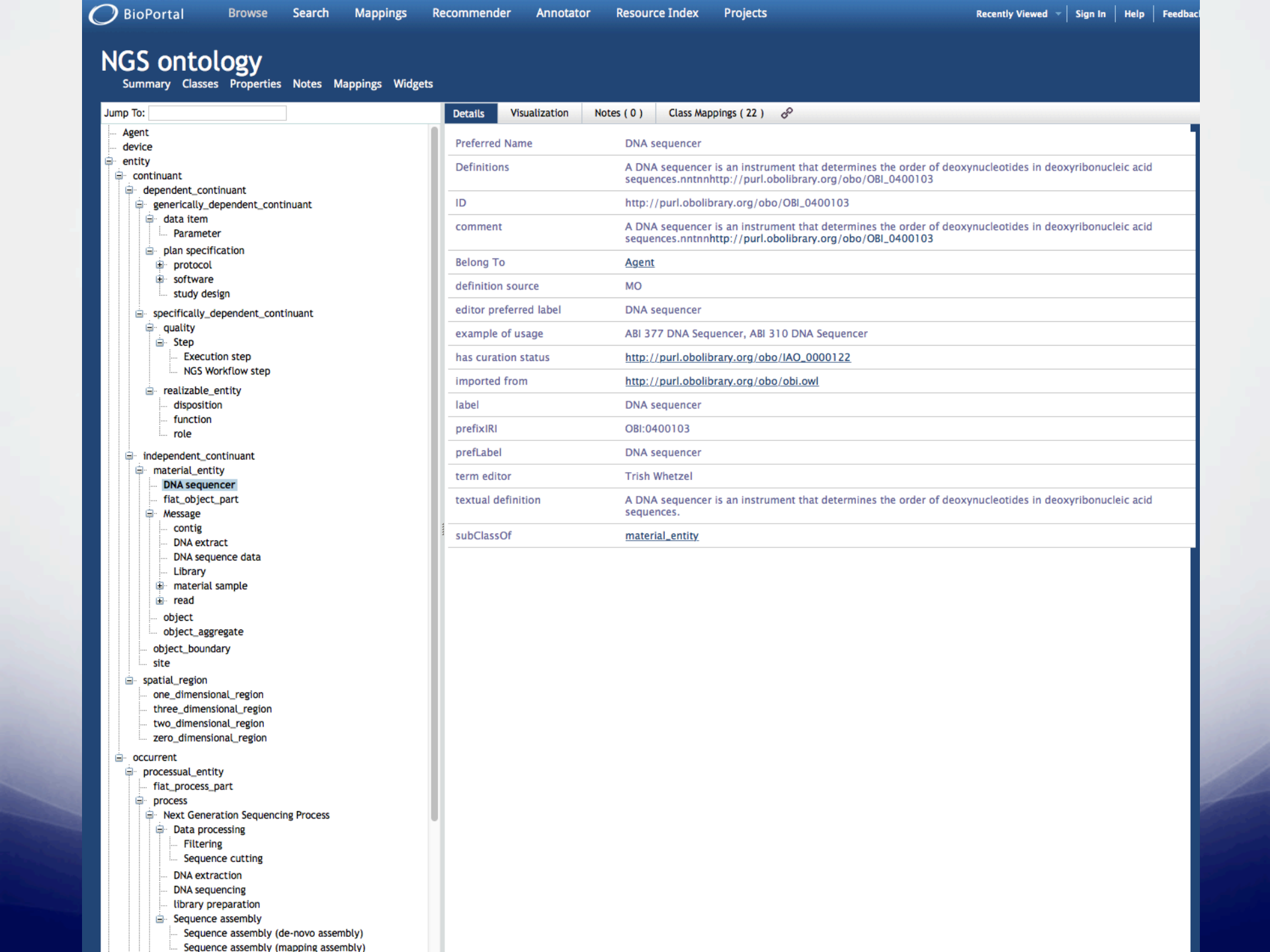


An improved ontological representation of dendritic cellsas a paradigm for all cell type. Masci et al. 2009

Ontologies are modular
Example: The Liver Immunology Ontology



Bridging Multiple Ontologies: Representation of the Liver Immune Response. Masci et al. 2011


BioPortal
Browse
Search
Mappings
Recommender
Annotator
Resource Index
Projects
Recently Viewed
Sign In
Help
Feedback
NGS ontology
Summary
Classes
Properties
Notes
Mappings
Widgets
Jump To:
Agent
device
entity
continuant
dependent_continuant
generically_dependent_continuant
data item
Parameter
plan specification
protocol
software
study design
specifically_dependent_continuant
quality
Step
Execution step
NGS Workflow step
realizable_entity
disposition
function
role
independent_continuant
material_entity
DNA sequencer
fiat_object_part
Message
contig
DNA extract
DNA sequence data
Library
material sample
read
object
object_aggregate
object_boundary
site
spatial_region
one_dimensional_region
three_dimensional_region
two_dimensional_region
zero_dimensional_region
occurrent
processual_entity
fiat_process_part
process
Next Generation Sequencing Process
Data processing
Filtering
Sequence cutting
DNA extraction
DNA sequencing
library preparation
Sequence assembly
Sequence assembly (de-novo assembly)
Sequence assembly (mapping assembly)
Details
Visualization
Notes (0)
Class Mappings (22)
Preferred Name
DNA sequencer
Definitions
A DNA sequencer is an instrument that determines the order of deoxynucleotides in deoxyribonucleic acid sequences.nntnnhttp://purl.obolibrary.org/obo/OBI_0400103
ID
http://purl.obolibrary.org/obo/OBI_0400103
comment
A DNA sequencer is an instrument that determines the order of deoxynucleotides in deoxyribonucleic acid sequences.nntnnhttp://purl.obolibrary.org/obo/OBI_0400103
Belong To
Agent
definition source
MO
editor preferred label
DNA sequencer
example of usage
ABI 377 DNA Sequencer, ABI 310 DNA Sequencer
has curation status
http://purl.obolibrary.org/obo/IAO_0000122
imported from
http://purl.obolibrary.org/obo/obi.owl
label
DNA sequencer
prefixIRI
OBI:0400103
prefLabel
DNA sequencer
term editor
Trish Whetzel
textual definition
A DNA sequencer is an instrument that determines the order of deoxynucleotides in deoxyribonucleic acid sequences.
subClassOf
material_entity

Example ontologies

Basic Formal Ontology (BFO)

http://ifomis.uni-saarland.de/bfo/

Common Anatomy Reference Ontology (CARO)

http://www.bioontology.org/wiki/index.php/CARO:Main_Page

Environment Ontology (EnvO)

http://environmentontology.org/

Foundational Model of Anatomy (FMA)

http://sig.biostr.washington.edu/projects/fm/

Gene Ontology (GO)

http://geneontology.org/

Protein Ontology (PRO)

http://pir.georgetown.edu/pro/

Cell Ontology (CL)

http://cellontology.org/

Infectious Disease Ontology (IDO)

http://infectiousdiseaseontology.org/page/Main_Page

Ontology for Biomedical Investigations (OBI)

http://obi-ontology.org/page/Main_Page

Phenotypic Quality Ontology (PATO)

http://wiki.obofoundry.org/wiki/index.php/PATO:Main_Page

Relation Ontology (RO)

Ontologies and terminologies

SNOMED

http://www.ihtsdo.org/snomed-ct

Unified Medical Language System

http://www.nlm.nih.gov/research/umls/

National Cancer Institute Thesaurus

https://ncit.nci.nih.gov/ncitbrowser/

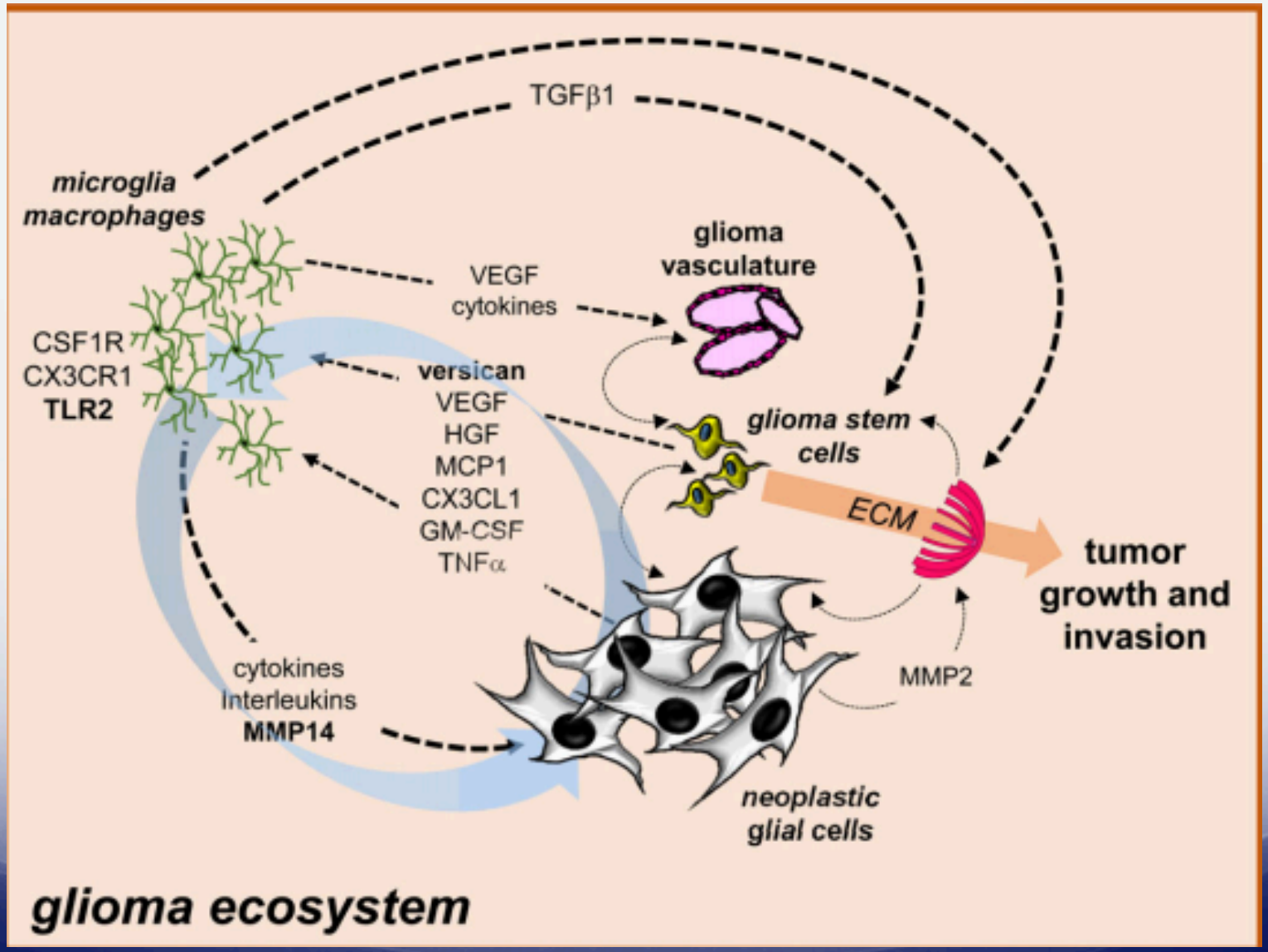
HL7 Reference Information Model

http://www.hl7.org/implement/standards/product_brief.cfm?product_id=78

International Classification of Diseaseas ICD

http://www.who.int/classifications/icd/en/

Can we reasoning on this?



GUTMANN DH., NEURO ONCOL 2015

- To enable reuse of data and information
- Avoid re-invention of the wheel
- Introduce standards to allow interoperability and automatic reasoning

Helping comunication between researchers

annamaria.masci@duke.edu