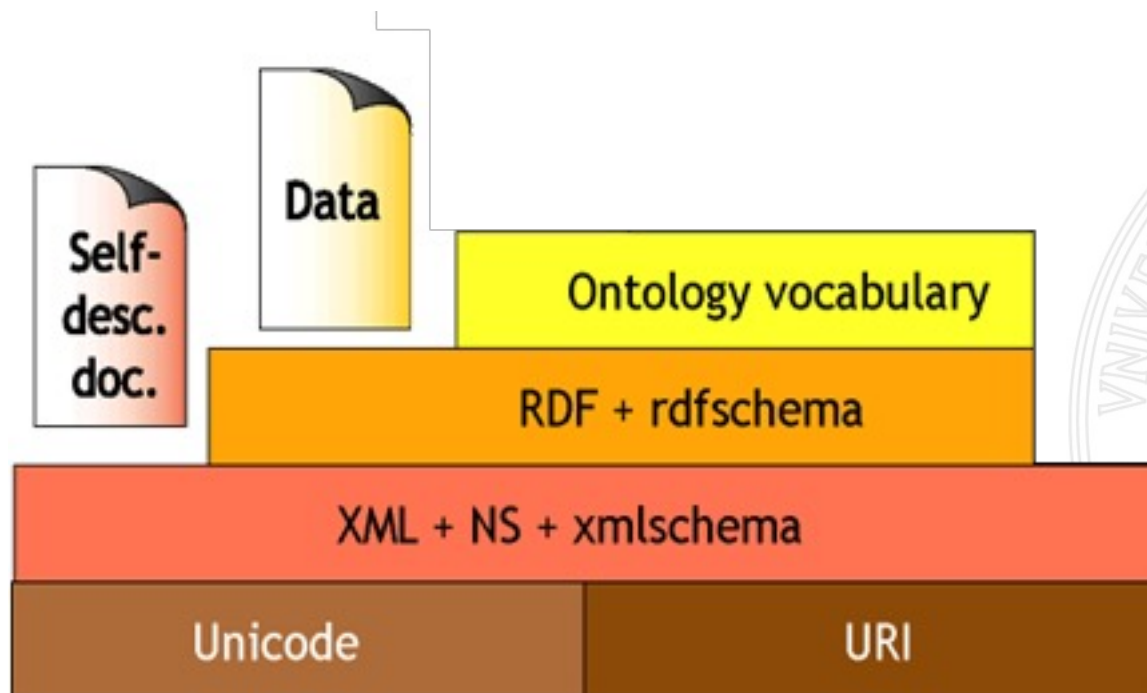


Introduction to bio-ontologies



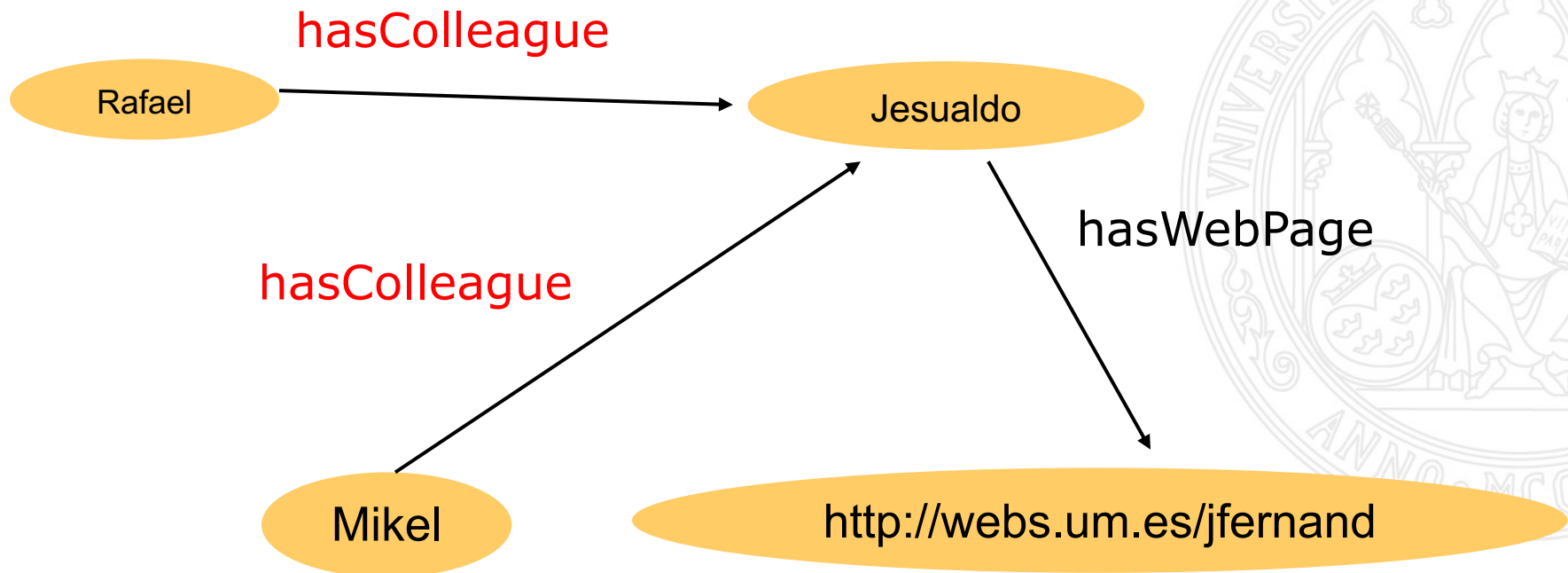
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(Part of) the Semantic Web Stack



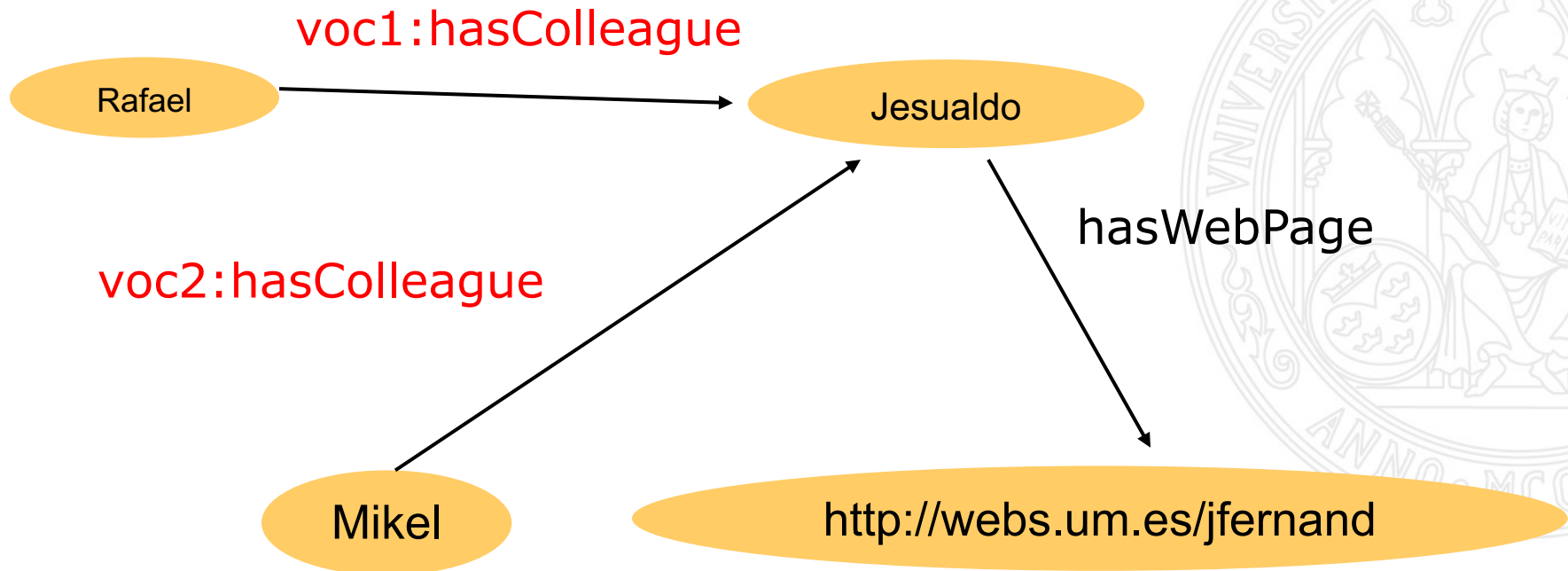
What if...

I think that RDF is OK but that there is too much freedom in the definition and use of properties



What if...

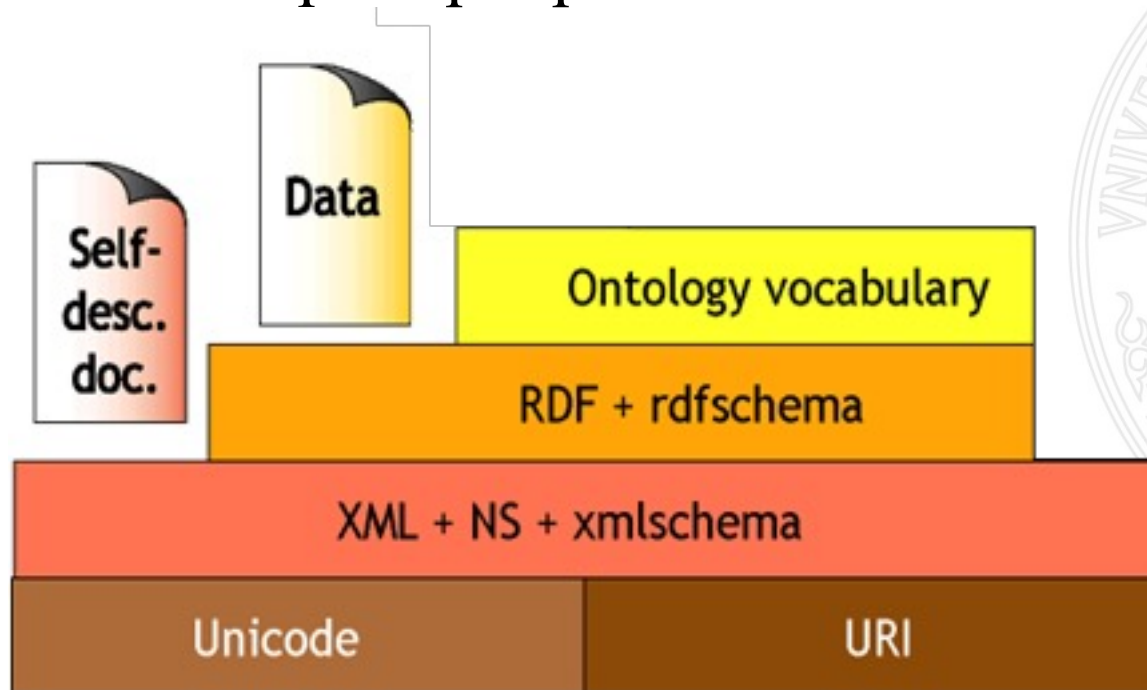
I think that RDF is OK but that there is too much freedom in the definition and use of properties



The Semantic Web Stack

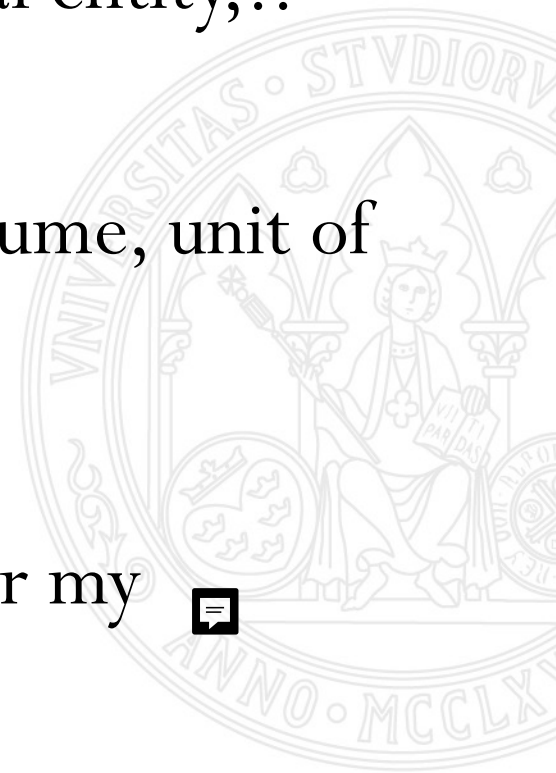
- **Ontology: Formal representation of the domain knowledge:**

concepts+properties+restrictions

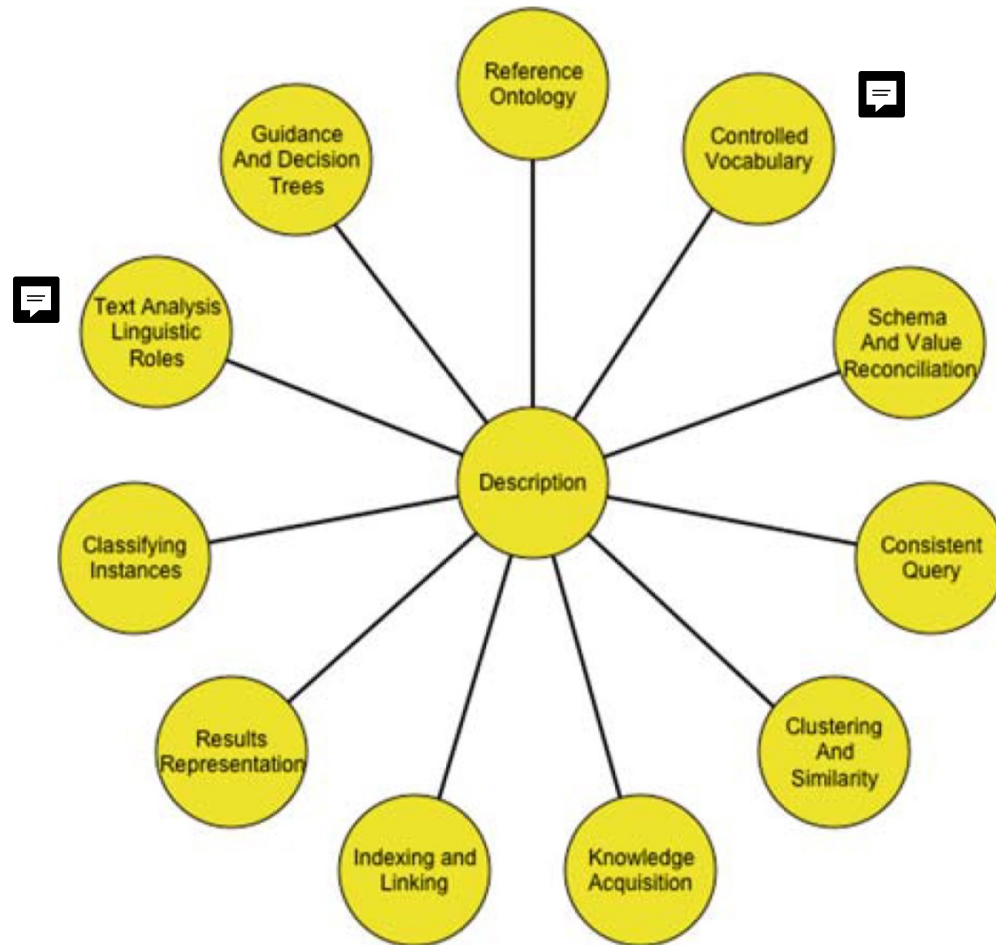


Types of ontologies

- Top-level ontologies: “domain-independent”
knowledge: Processes, objects, physical entity,...
- Domain ontologies: gene, protein, volume, unit of
measurement
- Application ontologies: “my genes” (for my
particular application)



Applications of ontologies in bioinformatics

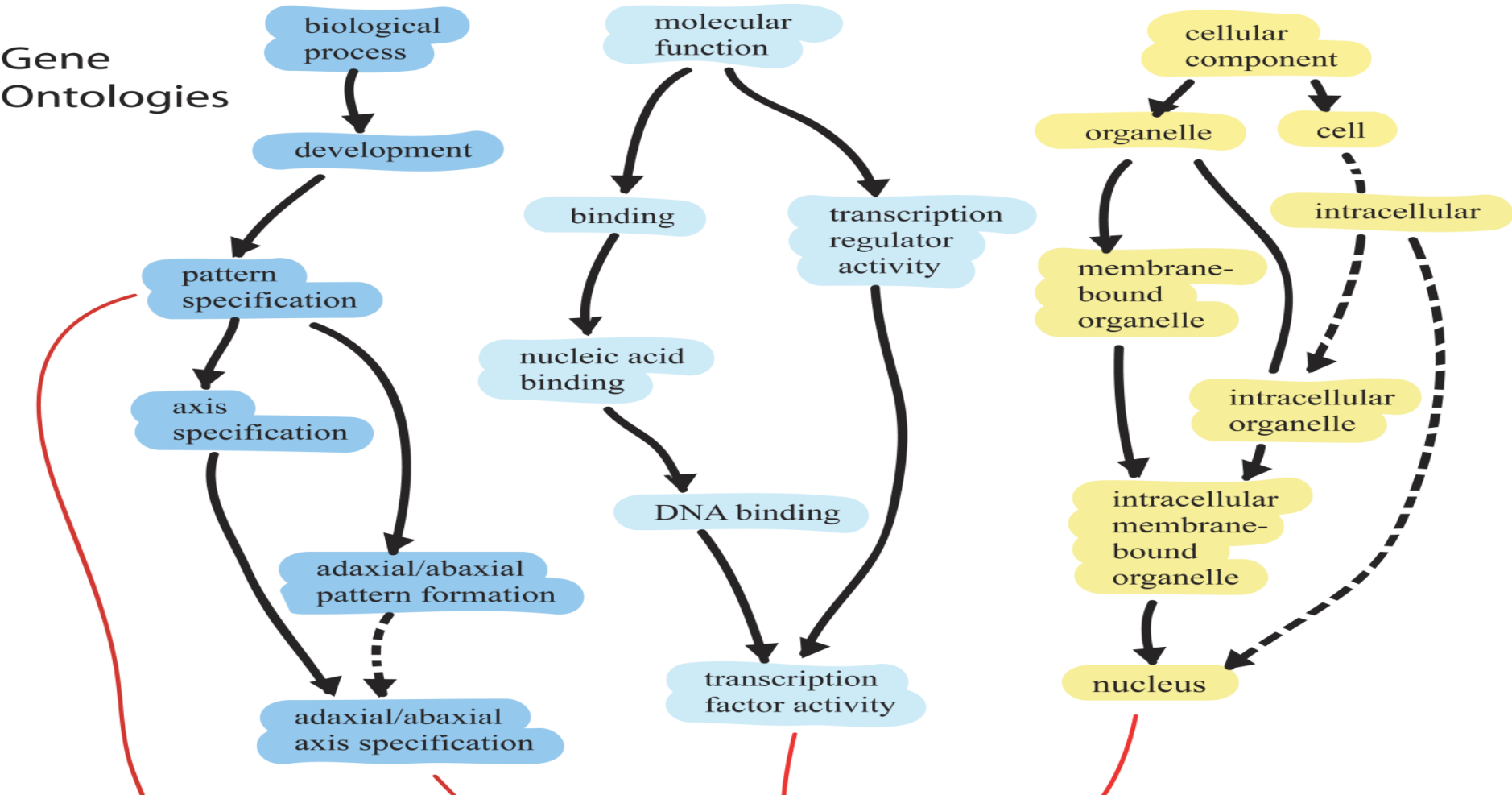


Stevens, Robert,
and Phillip Lord.
"Application of
ontologies in
bioinformatics."
*Handbook on
ontologies*.
Springer, Berlin,
Heidelberg, 2009.
735-756.

Fig. 1. A classification scheme for the uses of ontology and ontology-like artefacts within biology

The Gene Ontology

(<https://www.geneontology.org>)



The Sequence Ontology

(<http://www.sequenceontology.org>)

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- + sequence_attribute
- + sequence_collection
- sequence_feature
 - + junction
 - region
 - + biological_region
 - + biomaterial_region
 - experimental_feature
 - assembly
 - + fragment_assembly
 - sequence_assembly
 - + contig
 - expressed_sequence_as
 - + golden_path
 - + partial_genomic_sequer
 - + tiling_path
 - virtual_sequence
- + assembly_component
- + consensus_region
- + conserved_region
- + experimentally_defined_bindi
- high identity region

Term Only



as

OBO Format



Export

sequence_assembly (CURRENT_SVN)

SO

Accession:

SO:0000353 (SOWiki)

Definition:

A sequence of nucleotides that has been algorithmically derived from an alignment of two or more different sequences.

Synonyms:

sequence assembly

DB Xrefs:

SO: ma

Parent:

assembly (SO:0001248)

Children:

partial_genomic_sequence_assembly (SO:0001876)

expressed_sequence_assembly (SO:0001428)

gap (SO:0000730)

contig (SO:0000149)

tiling_path (SO:0000472)

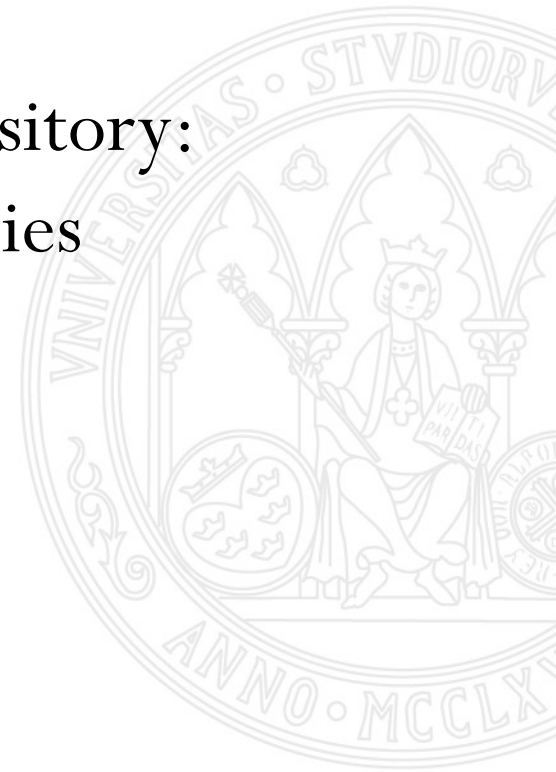
virtual_sequence (SO:0000499)

golden_path (SO:0000688)

In the image below graph nodes link to the appropriate terms. Clicking the image background will toggle the image between large and small formats.

Ontology repository

- Database of ontologies
- Different types of ontologies in a repository:
domain, top-level, application ontologies
- Domain-specific repositories
- Quality control/assurance



Biomedical ontologies: Bioportal

<http://bioportal.bioontology.org>

Statistics

Ontologies

1,086

Classes

14,646,888

#	name	# visits
1	Medical Dictionary for Regulatory Activities Terminology (MedDRA) (MEDDRA)	23,031
2	SNOMED CT (SNOMEDCT)	10,222
3	RxNORM (RXNORM)	7,780
4	National Drug Data File (NDDF)	3,785
5	Foundational Model of Anatomy (FMA)	2,369
6	Read Codes, Clinical Terms Version 3 (CTV3) (RCD)	1,977
7	National Cancer Institute Thesaurus (NCIT)	1,766
8	Medical Subject Headings (MESH)	1,376
9	National Drug File - Reference Terminology (NDFRT)	1,348
10	Logical Observation Identifier Names and Codes (LOINC)	1,026
11	EDAM - Bioscientific data analysis ontology (EDAM)	982

Bioportal: Ontologies

Category

- ☐ All Organisms (31)
- ☐ Anatomy (71)
- ☐ Animal Development (16)
- ☐ Animal Gross Anatomy ...
- ☐ Arabidopsis (3)
- ☐ Biological Process (54)

Group

- ☐ BIBLIO (10)
- ☐ BIS (3)
- ☐ CGIAR (1)
- ☐ CTSA (6)
- ☐ OBO_Foundry (11)
- ☐ PSI (4)

Format

- ☐ OBO (100)
- ☐ OWL (638)
- ☐ SKOS (26)
- ☐ UMLS (31)



Bioportal: Ontologies

Medical Dictionary for Regulatory Activities Terminology (MedDRA) (MEDDRA)

notes
1**projects**
10**classes**
74,056

MedDRA is an international medical terminology with an emphasis on use for data entry, retrieval, analysis, and display

Uploaded: 9/25/20

SNOMED CT (SNOMEDCT)

notes
3**projects**
23**classes**
359,263

SNOMED Clinical Terms

Uploaded: 9/25/20

RxNORM (RXNORM)

projects
7**classes**
109,013

RxNorm Vocabulary

Uploaded: 9/25/20

Information about the ontology

Gene Expression Ontology

Last uploaded: December 16, 2015



Summary [Classes](#) [Properties](#) [Notes](#) [Mappings](#) [Widgets](#)

Details

Acronym	GEXO
Visibility	Public
Description	An application ontology for the domain of gene expression. The ontology integrates fragments of GO and MI with data from GOA, IntAct, UniProt, NCBI, and orthology relations using ontological properties from RO and ISO.
Status	Beta
Format	OWL
Contact	Vladimir Mironov, vladimir.n.mironov@gmail.com
Categories	Biological Process

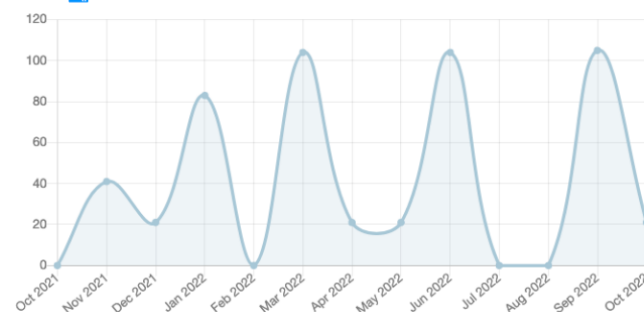
Metrics ?

Classes	166,254
Individuals	157,102
Properties	12
Maximum depth	21
Maximum number of children	50,996
Average number of children	49
Classes with a single child	968
Classes with more than 25 children	150
Classes with no definition	0

Submissions

Version	Released	Uploaded	Downloads
2015 (Parsed, Indexed, Metrics, Annotator)	12/16/2015	12/16/2015	OWL CSV RDF/XML
2015 (Archived)	09/08/2012	03/06/2015	OBO

Visits ↓



Projects using GEXO +

No projects using GEXO

Views of GEXO +

No views of GEXO available

Accessing the ontology

Gene Expression Ontology

Last uploaded: December 16, 2015



Summary Classes Properties Notes Mappings Widgets

Jump to:

- entity
 - abstract entity
 - physical entity
 - material entity
 - processual entity
 - process
 - biological process
 - gene expression
 - gene expression process
 - CAAX-box protein modification
 - CAAX-box protein processing
 - cap snatching
 - cis assembly of pre-catalytic spliceosome
 - cleavage involved in rRNA processing
 - DNA-templated transcription, elongation
 - DNA-templated transcription, initiation
 - DNA-templated transcription, termination
 - DNA-templated transcriptional open complex for
 - DNA-templated transcriptional preinitiation complex
 - DNA-templated transcriptional start site selection
 - dosage compensation complex assembly
 - formation of cytoplasmic translation initiation complex
 - formation of quadruple SLU4U5U6 snRNP
 - formation of translation initiation ternary complex
 - formation of translation preinitiation complex
 - generation of catalytic spliceosome for first tran
 - generation of catalytic spliceosome for second tran
 - maintenance of chromatin silencing
 - maintenance of transcriptional fidelity during DN
 - maintenance of translational fidelity
 - mRNA branch site recognition
 - mRNA export from nucleus
 - mRNA splice site selection

Details Visualization Notes (0) Class Mappings (18)

Preferred Name	positive regulation of histone gene expression
Synonyms	up-regulation of histone gene expression upregulation of histone gene expression positive regulation of expression of histone-encoding gene
Definitions	Any process that increases the frequency, rate or extent of expression of a histone-encoding gene. Gene expression is the process in which a gene's coding sequence is converted into a mature gene product or products (proteins or RNA). This includes the production of an RNA transcript as well as any processing to produce a mature RNA product or an mRNA (for protein-coding genes) and the translation of that mRNA into protein.
ID	http://purl.obolibrary.org/obo/GO_0036207
altLabel	up-regulation of histone gene expression upregulation of histone gene expression positive regulation of expression of histone-encoding gene
definition	Any process that increases the frequency, rate or extent of expression of a histone-encoding gene. Gene expression is the process in which a gene's coding sequence is converted into a mature gene product or products (proteins or RNA). This includes the production of an RNA transcript as well as any processing to produce a mature RNA product or an mRNA (for protein-coding genes) and the translation of that mRNA into protein.
hasOBONamespace	biological_process
id	GO:0036207
notation	GO:0036207
prefLabel	positive regulation of histone gene expression
subClassOf	regulation of histone gene expression positive regulation of gene expression

Term mappings

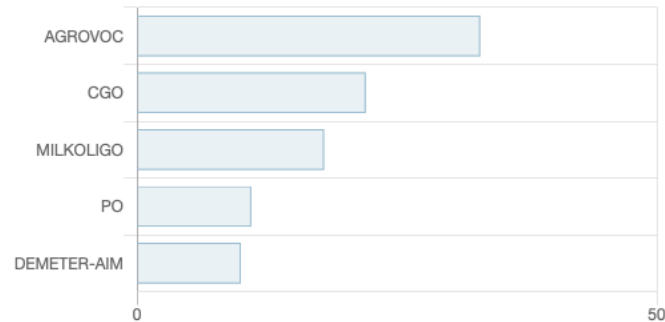
Summary	Classes	Properties	Notes	Mappings	Widgets
ONTOLOGY					MAPPINGS
A formal representation of the knowledge within the domain of Isotopes for Food Science					4
AdaLab ontology					119
AdaLab-meta ontology					2
Adherence and Integrated Care					4
Adherence and Integrated Care in Spanish					3
Adverse Childhood Experiences Ontology					5
Adverse Event Reporting Ontology					10
AGRONomy Ontology					28
Allotrope Merged Ontology Suite					19
Alzheimer Disease Map Ontology					687

GENE EXPRESSION ONTOLOGY	ADALAB-META ONTOLOGY	SOURCE
entity	Entity	LOOM
association	Association	LOOM

- These mappings do not mean equivalency

- It uses the BioPortal infrastructure for agriculture

Ontology Visits (October 2023)

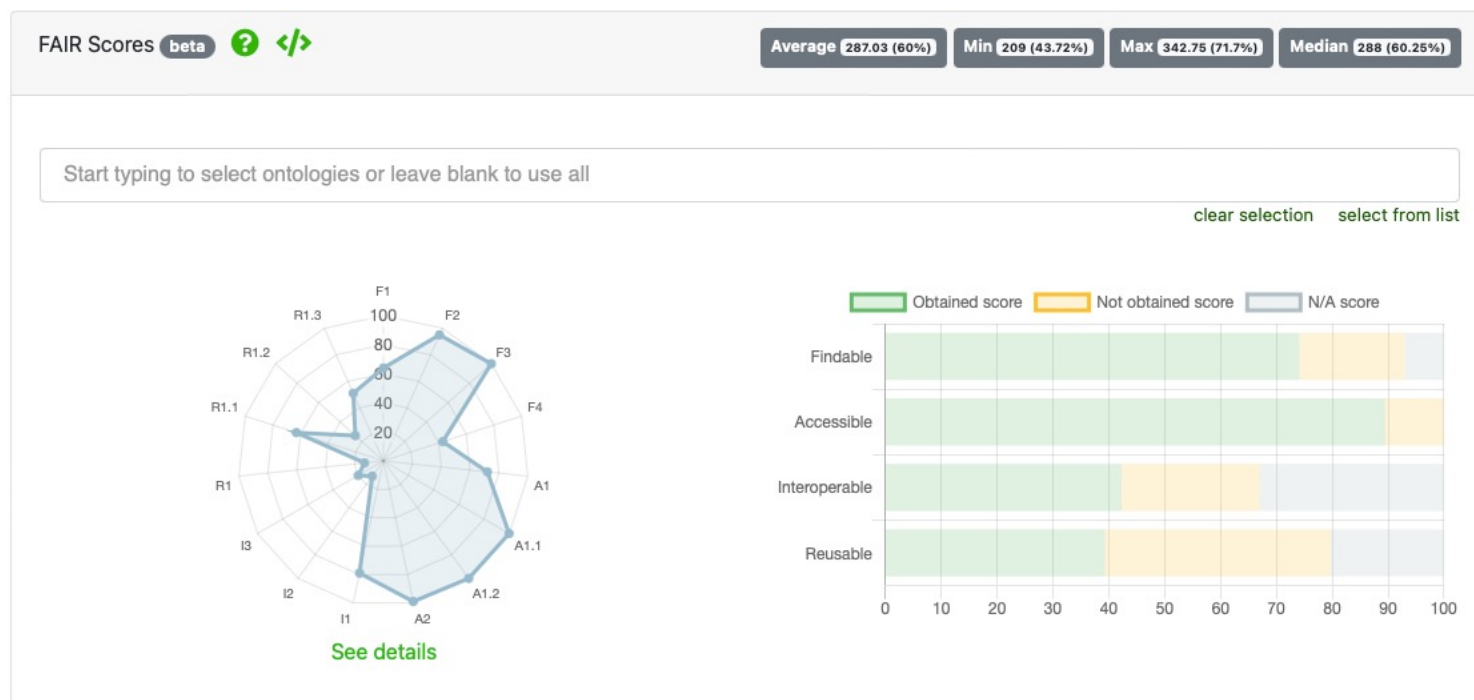


[More](#)

AgroPortal Statistics

Ontologies	158
Classes	688,240
Individuals	2,987,613
Projects	59
Users	390

- It uses the BioPortal infrastructure for agriculture



Category

- ☐ Agricultural Resear... (23)
- ☐ Animal Science an... (10)
- ☐ Biodiversity and Ec... (17)
- ☐ Breeding and Gene... (1)
- ☐ Farms and Farming... (7)
- ☐ Fisheries and Aqua... (2)
- ☐ Food Security (2)
- ☐ Food and Human ... (6)

Group

- ☐ AGBIODATA (18)
- ☐ AGROLD (5)
- ☐ CROP (37)
- ☐ INRAE (30)
- ☐ OBO-FOUNDRY (23)
- ☐ RICE (24)
- ☐ SEMANDIV (11)
- ☐ WHEAT (19)

Format

- ☐ OBO (12)
- ☐ OWL (100)
- ☐ SKOS (11)
- ☐ UMLS (2)

Ontology Content

- ☐ Notes (3)
- ☐ Reviews (2)
- ☐ Projects (110)
- ☐ Summary Only (0)

Is of Type

- ☐ Application Ontology (44)
- ☐ Core Ontology (2)
- ☐ Domain Ontology (53)
- ☐ Task Ontology (0)
- ☐ Upper Level Ontol... (6)
- ☐ Vocabulary (3)

Natural Language

- ☐ German (2)
- ☐ English (115)
- ☐ French (15)
- ☐ Italian (2)
- ☐ Portuguese (3)
- ☐ Spanish (4)

Formality Levels

- ☐ Classification sche... (2)
- ☐ Dictionary (0)
- ☐ Gazetteer (0)
- ☐ Glossary (0)
- ☐ List (0)
- ☐ Name authority list (0)
- ☐ Ontology (99)
- ☐ Semantic network (1)

OBO Foundry repository

<http://www.obofoundry.org/>

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The Open Biological and Biomedical Ontology (OBO) Foundry

Community development of interoperable ontologies for the biological sciences

Learn about OBO best practices and community resources

- [More about the OBO Foundry](#)
- [OBO Foundry principles](#)
- [OBO tutorial](#)
- [Ontology browsers, tutorials, and tools](#)



























Participate

- [Join the OBO mailing list](#)
- [OBO Foundry Operations and Working Groups](#)
- [Submit bug reports or suggestions for improvement via GitHub](#)
- [Submit your ontology to be considered for inclusion in the OBO Foundry](#)

OBO Library: find, use, and contribute to community ontologies

The table below lists current OBO ontologies (in alphabetical order, but with the ontologies that have been manually reviewed by the OBO Foundry listed first, and obsolete ontologies listed last).

Download table as: [[YAML](#) | [JSON-LD](#) | [RDF/Turtle](#)]

bfo	Basic Formal Ontology 	The upper level ontology upon which OBO Foundry ontologies are built. Detail	      
chebi	Chemical Entities of Biological Interest 	A structured classification of molecular entities of biological interest focusing on 'small' chemical compounds. Detail	       
doid	Human Disease Ontology 	An ontology for describing the classification of human diseases organized by etiology. Detail	       

OBO Foundry repository

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Gene Ontology

An ontology for describing the function of genes and gene products

 Follow @news4go 2,064 followe

OntoBee AberOWL OLS AmiGO

The goal of the Gene Ontology (GO) project is to provide a uniform way to describe the functions of gene products from organisms across all kingdoms of life and thereby enable analysis of genomic data

Products

go.owl	GO (OWL edition)	The main ontology in OWL. This is self contained and does not have connections to other OBO ontologies [page]
go.obo	GO (OBO Format edition)	Equivalent to go.owl, in obo format [page]
go.json	GO (JSON edition)	Equivalent to go.owl, in obograph json format [page]
go/extensions/go-plus.owl	GO-Plus	The main ontology plus axioms connecting to select external ontologies, with subsets of those ontologies [page]
go/go-base.owl	GO Base Module	The main ontology plus axioms connecting to select external ontologies, excluding the external ontologies themselves [page]
go/extensions/go-plus.json	GO-Plus	As go-plus.owl, in obographs json format [page]
go/go-basic.obo	GO-Basic, Filtered, for use with legacy tools	Basic version of the GO, filtered such that the graph is guaranteed to be acyclic and annotations can be propagated up the graph. The relations included are is a, part of, regulates, negatively regulates and positively regulates. This version excludes relationships that cross the

ID Space	go
PURL	http://purl.obolibrary.org/obo/go.owl
License	CC BY 4.0
Review Date	2010
Review Document	n/a
Homepage	http://geneontology.org/
Contact	Suzi Aleksander
Trackers	https://github.com/geneontology/geneontology/issues/
Domain	biology
Taxon	All life
Dependencies	uberon cl ncbitaxon ro go/extensions/go-bridge-to-nifstd.owl

View Edit PURL

Generated by: [_layouts/ontology_detail.html](#)

See [metadata guide](#)

Edit the metadata for this page: [go.md](#) (GitHub will help you create a fork and pull request.)

Ontobee visualization

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Gene Ontology

Keywords: Search terms

Ontology: GO

- IRI: <http://purl.obolibrary.org/obo/go.owl>
- OBO Foundry: Foundry
- Download: <http://purl.obolibrary.org/obo/go.owl>
- Home: <http://geneontology.org/>
- Documentation: [Gene Ontology documentation](#)
- Contact: suzia@stanford.edu
- Description: An ontology for describing the function of genes and gene products

Annotations

- description: The Gene Ontology (GO) provides a framework and set of concepts for describing the functions of gene products from all organisms.
- title: Gene Ontology
- versionIRI: <http://purl.obolibrary.org/obo/go/releases/2020-10-09/go.owl>
- default-namespace: gene_ontology
- has_obo_format_version: 1.2
- license: <http://creativecommons.org/licenses/by/4.0/>

Number of Terms (including imported terms) ([Detailed Statistics](#))

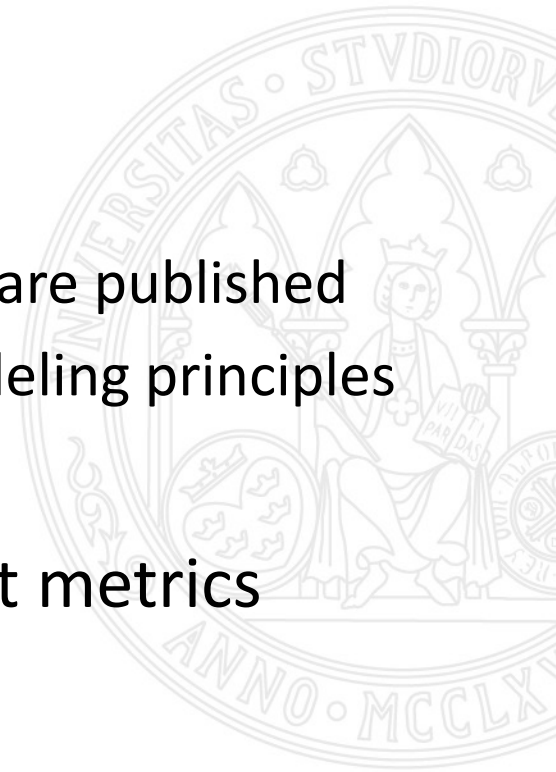
- [Class](#) (50422)
- [ObjectProperty](#) (9)
- [AnnotationProperty](#) (50)

Number of SPARQL queries:8

Check http://www.ontobee.org/ontology/GO?iri=http%3A%2F%2Fpurl.obolibrary.org%2Fobo%2FGO_0042995

Quality control in repositories

- BioPortal, AgroPortal:
 - Users can freely upload their ontologies
- OBO Foundry:
 - The consortium decides which ontologies are published
 - Ontologies are expected to adhere to modeling principles
- In general, not much information about metrics



OBO Foundry principles

<http://www.obofoundry.org/principles/fp-000-summary.html>

- Overview
- Open (principle 1)
- Common Format (principle 2)
- URI/Identifier Space (principle 3)
- Versioning (principle 4)
- Scope (principle 5)
- Textual Definitions (principle 6)
- Relations (principle 7)
- Documentation (principle 8)
- Documented Plurality of Users (principle 9)
- Commitment To Collaboration (principle 10)
- Locus of Authority (principle 11)
- Naming Conventions (principle 12)
- Maintenance (principle 16)



Ontology building

- Classes (Concepts): gene, protein (sets of individuals that share some properties)
- Individuals (Instances)
- Properties
 - Object properties (relations between instances of classes): regulates
 - Datatype properties (attributes, associations between instances of classes and data types): length
 - Annotations: label, synonym
- Axioms (restrictions, asserted conditions): gene codified in 1 organism

Ontology building

- **Terminological Knowledge (T-BOX)**
 - Axioms that describe the structure of the domain (conceptual schema, class level)
- **Knowledge about individuals (A-BOX)**
 - Axioms describing data, facts (instance level)
HappyFather(John)
hasChild(John, Mary)

Web Ontology Language Requirements

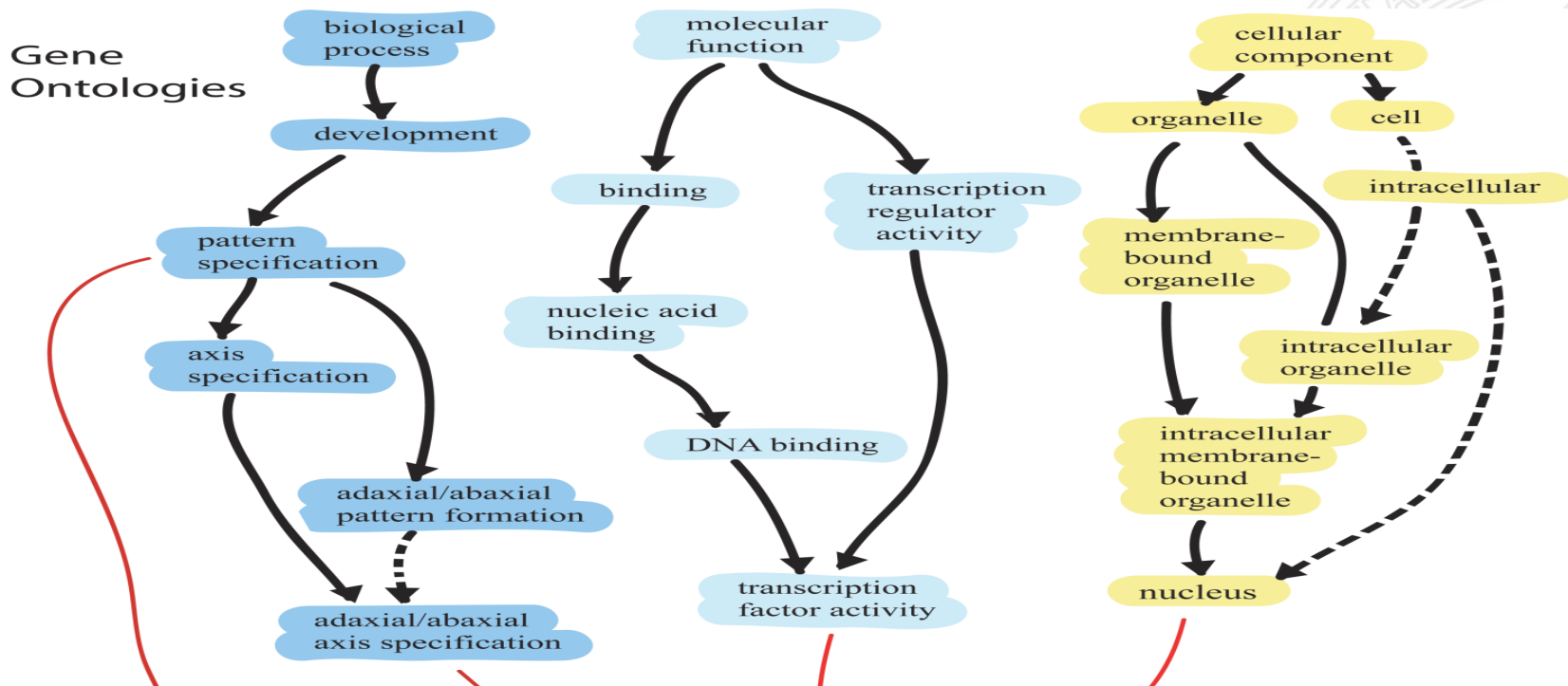
Desirable features identified for Web Ontology Language:

- Extends existing Web standards
 - Such as XML, RDF, RDFS
- Easy to understand and use
 - Should be based on familiar Knowledge Representation idioms
- Formally specified
- Of “adequate” expressive power
- **Possible to provide automated reasoning support**



Taxonomy (IS A, subClassOf)

- Hierarchical relation to define types of classes, from the most general to the most specific ones. These rules apply:
 - Rule “is-a”: Every subclass is an instance of the superclass
 - It is transitive (C is-a B and B is-a A then C is-a A)





OWL Class Constructors

- Build new classes from Class, property and individuals
- Union
- Intersection



OWL Class Constructors

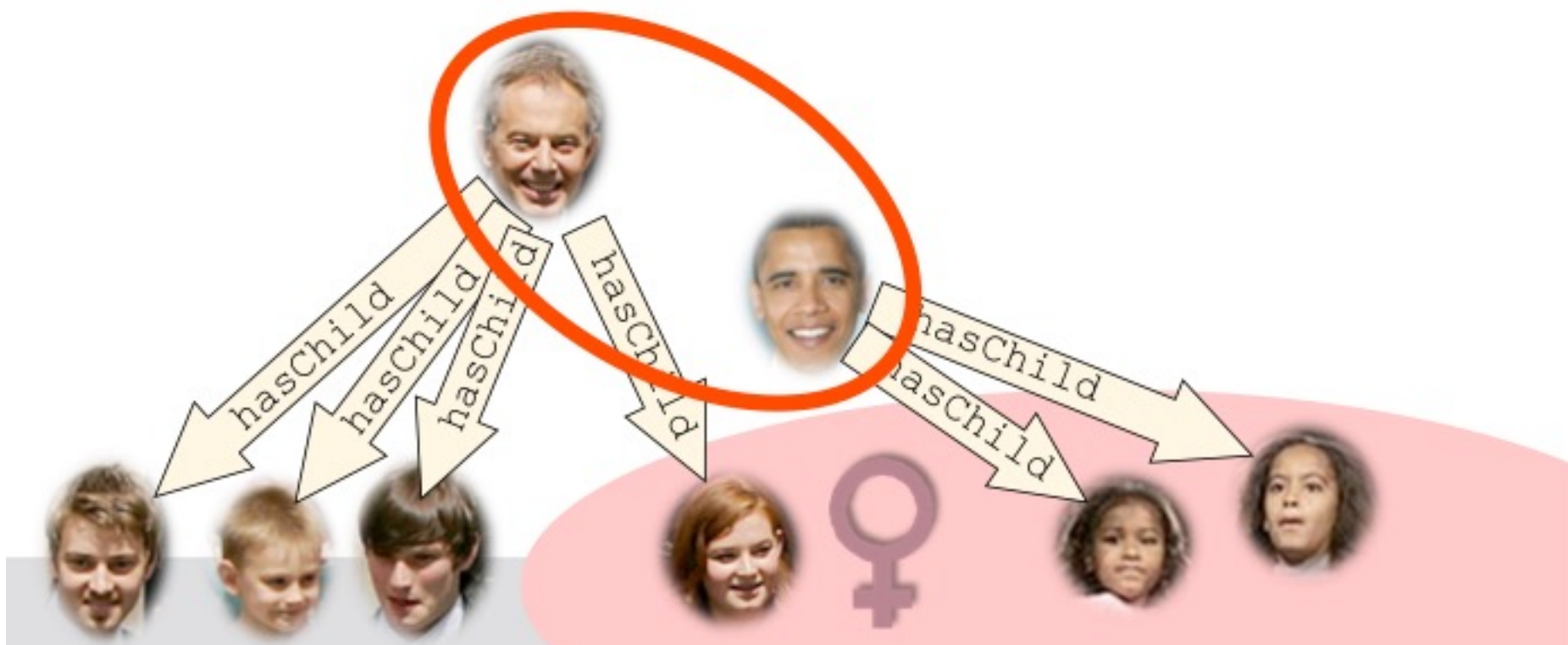
- Build new classes from Class, property and individuals
- Complement: not politician 
- Closed classes 



OWL Class Constructors

- build new classes from class, property and individual names
 - existential quantification: $\exists \text{hasChild.Female}$

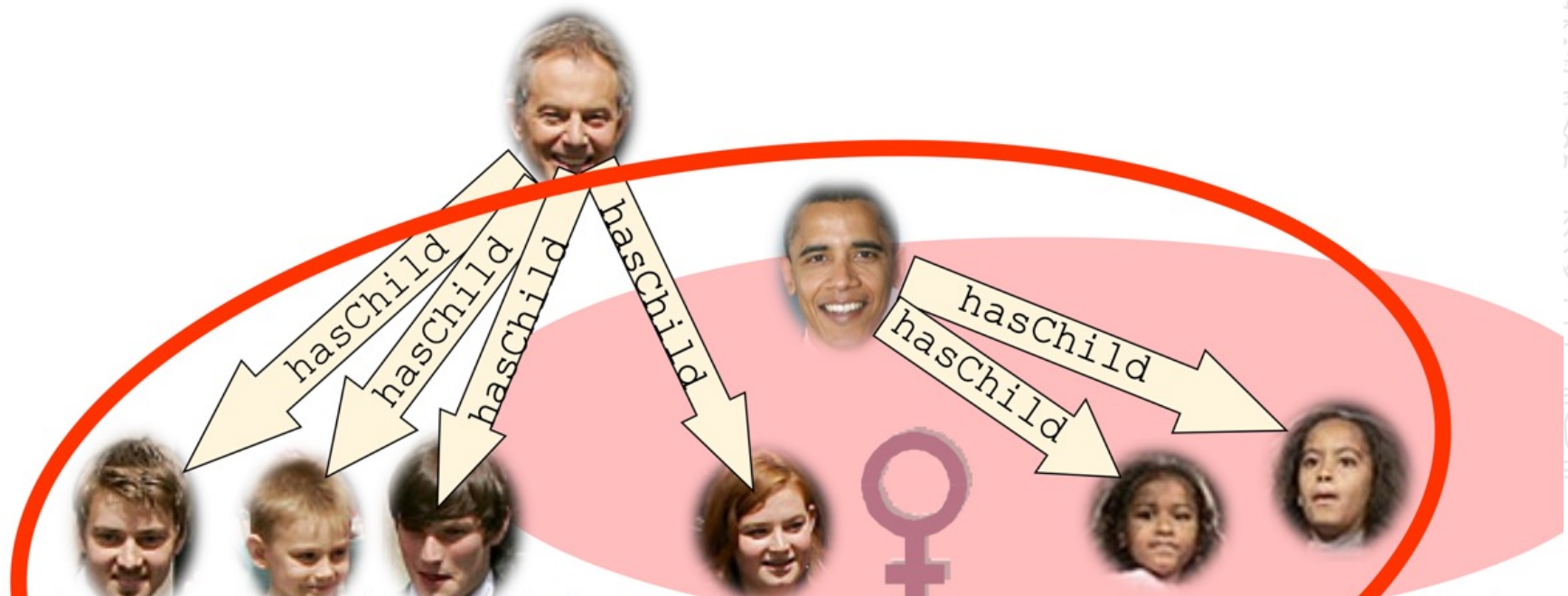
```
<owl:Restriction>  
  <owl:onProperty rdf:resource="hasChild"/>  
  <owl:someValuesFrom rdf:resource="Female"/>  
</owl:Restriction>
```



OWL Class Constructors

- build new classes from class, property and individual names
 - universal quantification: $\forall \text{hasChild.Female}$

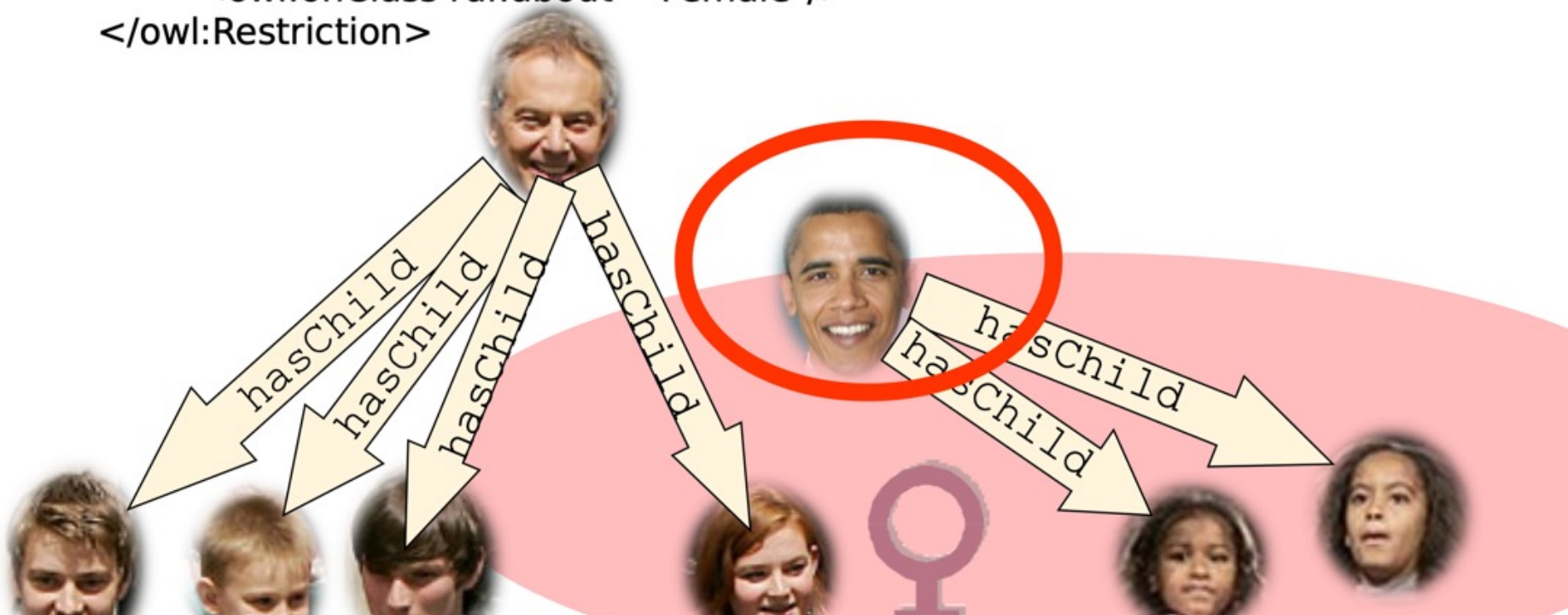
```
<owl:Restriction>  
  <owl:onProperty rdf:resource="hasChild"/>  
  <owl:allValuesFrom rdf:resource="Female"/>  
</owl:Restriction>
```



OWL Class Constructors

- build new classes from class, property and individual names
 - cardinality restriction: ≥ 2 hasChild.Female

```
<owl:Restriction>  
  <owl:minQualifiedCardinality rdf:datatype="&xsd;nonNegativeInteger">  
    2 </owl:minQualifiedCardinality>  
  <owl:onProperty rdf:about="hasChild"/>  
  <owl:onClass rdf:about="Female"/>  
</owl:Restriction>
```

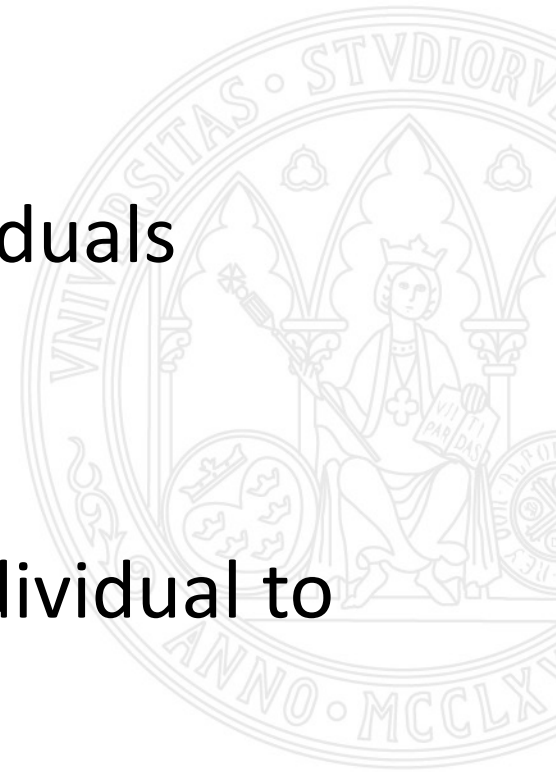


OWL Class Constructors

Constructor	DL Syntax	Example	Modal Syntax
intersectionOf	$C_1 \sqcap \dots \sqcap C_n$	Human \sqcap Male	$C_1 \wedge \dots \wedge C_n$
unionOf	$C_1 \sqcup \dots \sqcup C_n$	Doctor \sqcup Lawyer	$C_1 \vee \dots \vee C_n$
complementOf	$\neg C$	\neg Male	$\neg C$
oneOf	$\{x_1\} \sqcup \dots \sqcup \{x_n\}$	{john} \sqcup {mary}	$x_1 \vee \dots \vee x_n$
allValuesFrom	$\forall P.C$	\forall hasChild.Doctor	$[P]C$
someValuesFrom	$\exists P.C$	\exists hasChild.Lawyer	$\langle P \rangle C$
maxCardinality	$\leq nP$	≤ 1 hasChild	$[P]_{n+1}$
minCardinality	$\geq nP$	≥ 2 hasChild	$\langle P \rangle_n$

Special classes and properties

- Top class: class that contains all the individuals
 - owl:Thing
- Bottom class: empty class, no individuals
 - owl:Nothing
- Universal property: it links every individual to every individual
 - owl:topObjectProperty



Manchester OWL Syntax

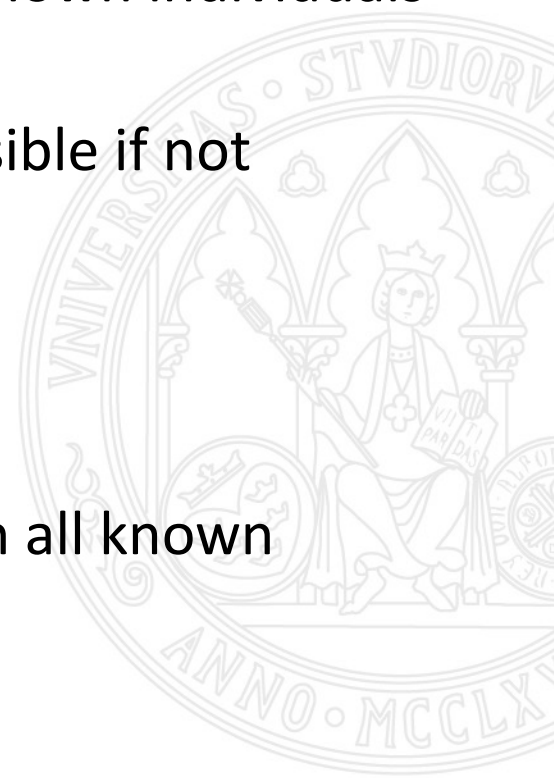
- Closer to DL and closed to natural language

OWL	DL Symbol	Manchester OWL Syntax Keyword	Example
someValuesFrom	\exists	some	hasChild some Man
allValuesFrom	\forall	only	hasSibling only Woman
hasValue	\ni	value	hasCountryOfOrigin value England
minCardinality	\geq	min	hasChild min 3
cardinality	$=$	exactly	hasChild exactly 3
maxCardinality	\leq	max	hasChild max 3

OWL	DL Symbol	Manchester OWL Syntax Keyword	Example
intersectionOf	\sqcap	and	Doctor and Female
unionOf	\sqcup	or	Man or Woman
complementOf	\neg	not	not Child

Open Vs Closed World Assumption

- Open World Assumption (OWA)
 - The knowledge base may not contain all known individuals and facts
 - The existence of further individuals is possible if not explicitly excluded
- Closed World Assumption (CWA)
 - The knowledge base is assumed to contain all known individuals and facts
- Which one do you think is used in OWL?



Open Vs Closed World Assumption

	Are all children of Bill male?	No idea, since we do not know all children of Bill.	If we assume that we know everything about Bill, then all of his children are male.
child(Bill,Bob)		DL answers	Prolog
Man(Bob)	$? \models \forall \text{child.Man(Bill)}$	don't know	yes
$\leq 1 \text{ child.T(Bill)}$	$? \models \forall \text{child.Man(Bill)}$	yes	Now we know everything about Bill's children.

Questions, comments...

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