

# Machine learning with biomedical ontologies

*Presented by Sarah Alghamdi, Azza Althagafi, Robert Hoehndorf, Maxat Kulmanov, Sumyyah Toonsi, Fernando Zhapa-Camacho*

# Learning Outcomes

- Introduce Ontologies and the description logic
- Discuss unsupervised machine learning methods that can “embed” from one structure to another
- Introduce different methods that use ontologies in machine learning models
- Introduce mOWL, a software library for machine learning with ontologies
- Incorporate mOWL in Biomedical data analysis using different approaches

# Preliminaries: What are Ontologies?

- “An ontology is a **logical theory** designed in order to capture the **intended models** corresponding to a certain conceptualization and to **exclude the unintended ones**” ... [Guarino 2009](#)



GENEONTOLOGY



upheno  
ontology



OOLS

Pheno→e



.ü

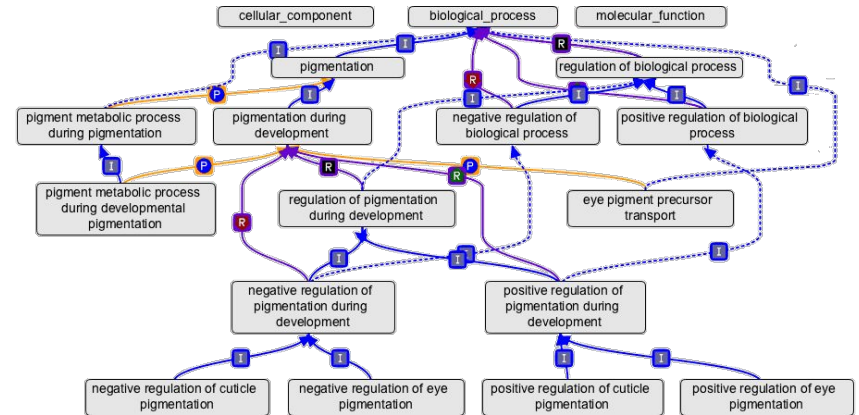
uberon



human  
phenotype  
ontology

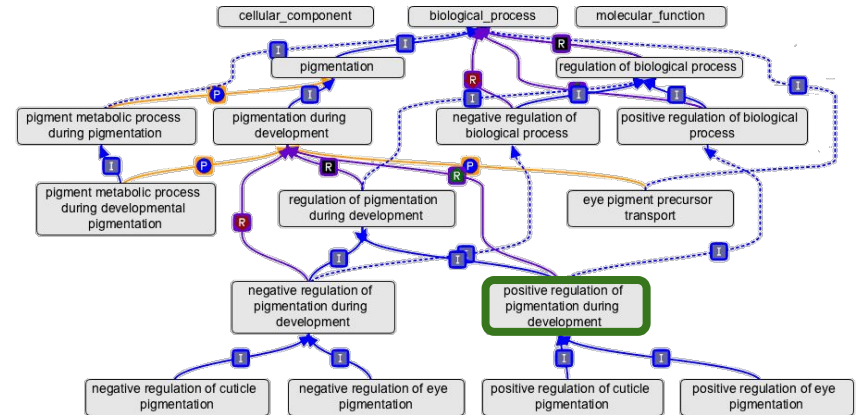
# Preliminaries: What are Ontologies?

- “An ontology is a **logical theory** designed in order to capture the **intended models** corresponding to a certain conceptualization and to **exclude the unintended ones**” ... [Guarino 2009](#)



# Preliminaries: What are Ontologies?

- “An ontology is a **logical theory** designed in order to capture the **intended models** corresponding to a certain conceptualization and to **exclude the unintended ones**” ... [Guarino 2009](#)



# Preliminaries: What are Ontologies?

- “An ontology is a **logical theory** designed in order to capture the **intended models** corresponding to a certain conceptualization and to **exclude the unintended ones**” ... [Guarino 2009](#)



GENE ONTOLOGY

*positiveregulationofdevelopmentalpigmentation*  $\equiv$  *biologicalprocess*  $\sqcap$   $\exists$ *positivelyregulates.developmentalpigmentation*

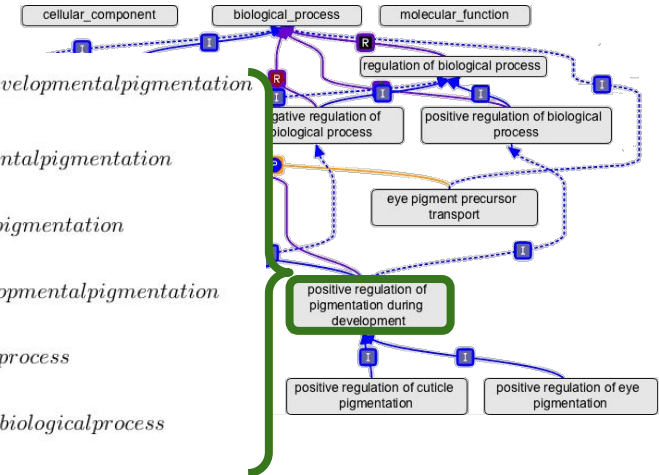
*positiveregulationofdevelopmentalpigmentation*  $\sqsubseteq$   $\exists$ *positivelyregulates.developmentalpigmentation*

*positiveregulationofdevelopmentalpigmentation*  $\sqsubseteq$   $\exists$ *regulates.developmentalpigmentation*

*positiveregulationofdevelopmentalpigmentation*  $\sqsubseteq$  *biologicalprocess*  $\sqcap$   $\exists$ *regulates.developmentalpigmentation*

*positiveregulationofdevelopmentalpigmentation*  $\sqsubseteq$   $\exists$ *regulates.biologicalprocess*

*positiveregulationofdevelopmentalpigmentation*  $\sqsubseteq$  *biologicalprocess*  $\sqcap$   $\exists$ *regulates.biologicalprocess*



# Preliminaries: What are Ontologies?

- “An ontology is a **logical theory** designed in order to capture the **intended models** corresponding to a certain conceptualization and to **exclude the unintended ones**” ... [Guarino 2009](#)
- Classes and relations
- Standard identifiers
- Axioms and formal definitions
- Metadata:
  - Labels, Synonyms
  - database cross references
  - ....

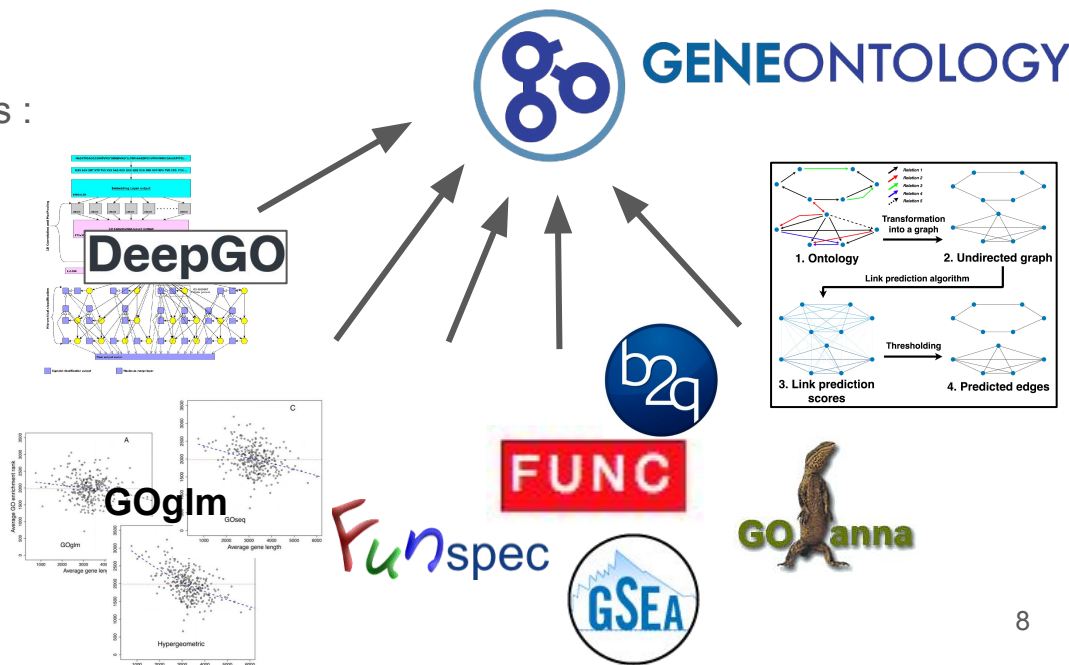
GO - Gene Ontology	
<div>Overview Browse DLQuery SPARQL Download</div>	
Annotation	Value
label	positive regulation of developmental pigmentation
definition	Any process that increases the frequency, rate or extent of the developmental process that results in the deposition of coloring matter in an organism.
class	<a href="http://purl.obolibrary.org/obo/GO_0048087">http://purl.obolibrary.org/obo/GO_0048087</a>
ontology	GO
Equivalent	<a href="#">biological regulation</a> and ( <a href="#">positively regulates</a> <a href="#">some</a> <a href="#">developmental pigmentation</a> )
SubClassOf	<a href="#">positively regulates</a> <a href="#">some</a> <a href="#">developmental pigmentation</a> , <a href="#">positive regulation of biological process</a> , <a href="#">regulation of developmental pigmentation</a>
has_obo_namespace	biological_process
synonyms	upregulation of developmental pigmentation, up regulation of developmental pigmentation, stimulation of developmental pigmentation, activation of developmental pigmentation, up-regulation of developmental pigmentation
id	GO:0048087



# Introduction

## - Examples of ontologies application in biomedical domain:

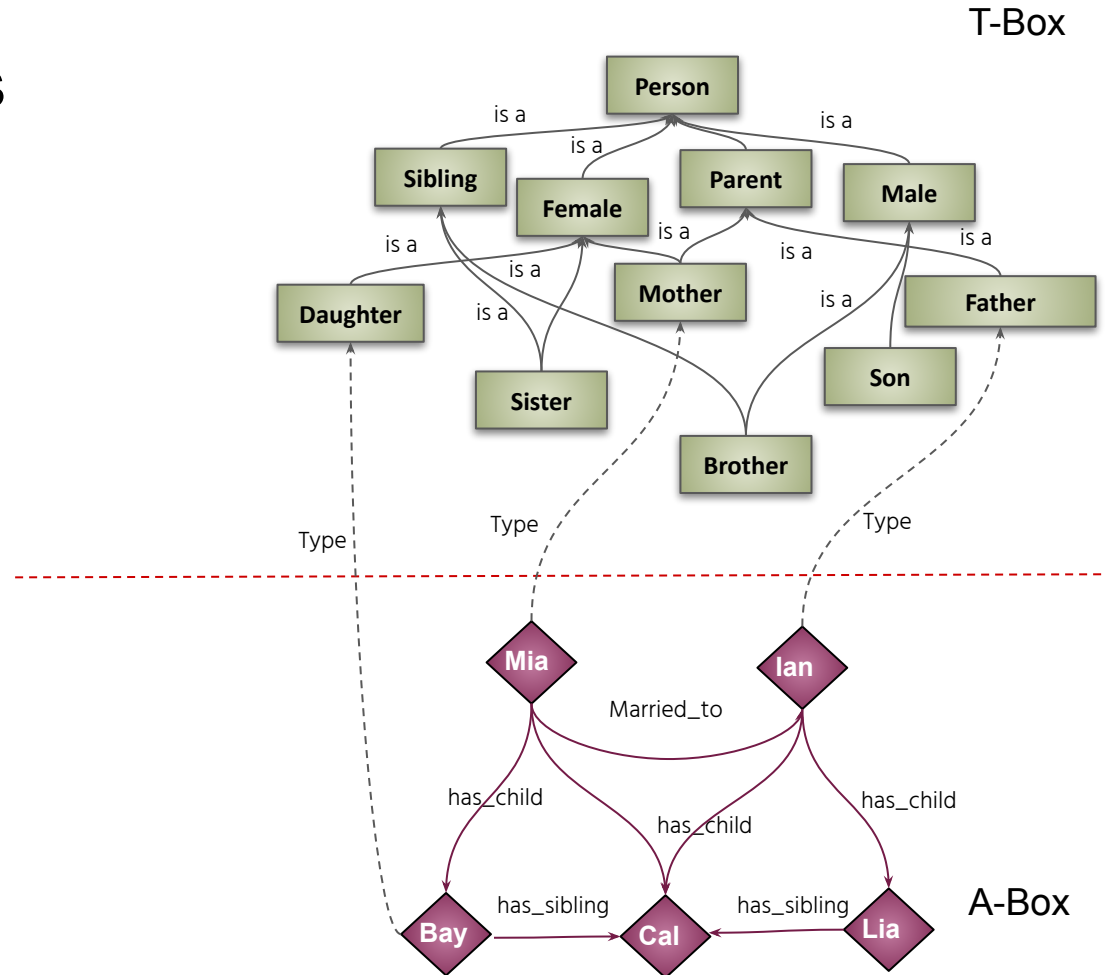
- Annotation and data integration
- Ontologies as vocabularies
- Statistical and predictive data analysis :
  - Enrichment analysis
  - Semantic similarity
- Regression analysis
- Relation prediction
- Classification
  - Supervised
  - Unsupervised





# Preliminaries: ontologies

- Ontology consist of :  
 $O=\{C,R,I,F\}$
- T-Box
  - Set of terminological
- A-Box
  - Set of assertions



# Preliminaries: ontologies

- Description Logic (DL) is used to formally and explicitly represent ontologies

Name	DL syntax	Semantics
Top concept	$\top$	$\Delta^{\mathcal{I}}$
Bottom concept	$\perp$	$\emptyset$
Concept	$C$	$C^{\mathcal{I}} \subseteq \Delta^{\mathcal{I}}$
Concept disjunction	$C_1 \sqcup C_2$	$C_1^{\mathcal{I}} \cup C_2^{\mathcal{I}}$
Concept conjunction	$C_1 \sqcap C_2$	$C_1^{\mathcal{I}} \cap C_2^{\mathcal{I}}$
Concept negation	$\neg C$	$\Delta^{\mathcal{I}} \setminus C^{\mathcal{I}}$
Universal restriction	$\forall R.C$	$\{x \in \Delta^{\mathcal{I}} \mid \forall y \in \Delta^{\mathcal{I}} ((x, y) \in R^{\mathcal{I}} \wedge y \in C^{\mathcal{I}})\}$
Existential restriction	$\exists R.C$	$\{x \in \Delta^{\mathcal{I}} \mid \exists y \in \Delta^{\mathcal{I}} ((x, y) \in R^{\mathcal{I}} \rightarrow y \in C^{\mathcal{I}})\}$
Subclass of	$C_1 \sqsubseteq C_2$	$C_1^{\mathcal{I}} \subseteq C_2^{\mathcal{I}}$
Subproperty of	$R_1 \sqsubseteq R_2$	$R_1^{\mathcal{I}} \subseteq R_2^{\mathcal{I}}$
Equivalent class	$C_1 \equiv C_2$	$C_1^{\mathcal{I}} = C_2^{\mathcal{I}}$
Equivalent property	$R_1 \equiv R_2$	$R_1^{\mathcal{I}} = R_2^{\mathcal{I}}$

## Concepts , Roles

*Person*  $\sqsubseteq \top$

*Female*  $\sqcap$  *Male*  $\sqsubseteq \perp$

*Female*  $\sqcup$  *Male*  $\sqsubseteq \top$

*Female*  $\equiv \neg$  *Male*

*Parent*  $\equiv \exists$  *has\_child*. *Person*

*Son*  $\sqsubseteq$  *Male*  $\sqcap \exists$  *child\_of*. *Person*

*Mother*  $\sqsubseteq$  *Female*  $\sqcap$  *Parent*

*Sibling*  $\sqsubseteq \exists$  *has\_sibling*. *Person*

*has\_brother*  $\sqsubseteq$  *has\_sibling*

# Preliminaries: ontologies

- Description Logic (DL) is used to formally and explicitly represent ontologies

DL Syntax	Manchester Syntax
$C \sqcap D$	C and D
$C \sqcup D$	C or D
$\neg C$	not C
$\exists R.C$	R some C
$\forall R.C$	R only C
$(\geq nR.C)$	R min n C
$(\leq nR.C)$	R max n C
$(= nR.C)$	R exactly n C
$\{a\} \sqcup \{b\} \sqcup \dots$	{a b ...}

## Classes , Relations

*Person*  $\sqsubseteq \top$

*Female*  $\sqcap$  *Male*  $\sqsubseteq \perp$

*Female*  $\sqcup$  *Male*  $\sqsubseteq \top$

*Female*  $\equiv \neg$  *Male*

*Parent*  $\equiv \exists$  *has\_child*. *Person*

*Son*  $\sqsubseteq$  *Male*  $\sqcap \exists$  *child\_of*. *Person*

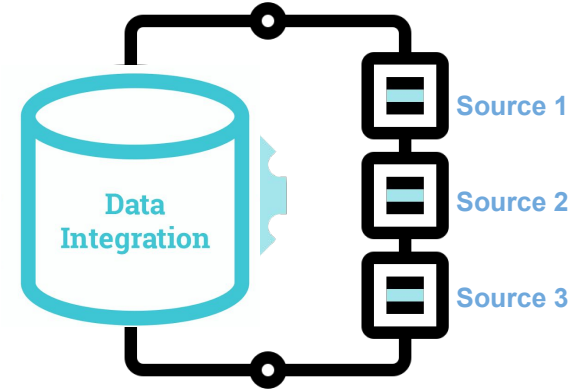
*Mother*  $\sqsubseteq$  *Female*  $\sqcap$  *Parent*

*Sibling*  $\sqsubseteq \exists$  *has\_sibling*. *Person*

*has\_brother*  $\sqsubseteq$  *has\_sibling*

# How Ontologies are used in Databases

- Annotations and data integration
  - Ontologies play a crucial role in facilitating data integration across databases due to their usage of standard identifiers for classes and relations



# How Ontologies are used in Databases

- Annotations and data integration
  - Ontologies play a crucial role in facilitating data integration across databases due to their usage of standard identifiers for classes and relations

# How Ontologies are used in Databases

- Annotations and data integration

## GAF fields

The annotation flat file format is comprised of 17 tab-delimited fields.

Column	Content	Required?	Cardinality	Example
1	<a href="#">DB</a>	required	1	UniProtKB
2	<a href="#">DB Object ID</a>	required	1	P12345
3	<a href="#">DB Object Symbol</a>	required	1	PHO3
4	<a href="#">Qualifier</a>	required	1 or 2	NOTInvolved_in
5	<a href="#">GO ID</a>	required	1	GO:0003993
6	<a href="#">DB:Reference (IDB:Reference)</a>	required	1 or greater	PMID:2676709
7	<a href="#">Evidence Code</a>	required	1	IMP
8	<a href="#">With (or) From</a>	optional	0 or greater	GO:0000346
9	<a href="#">Aspect</a>	required	1	F
10	<a href="#">DB Object Name</a>	optional	0 or 1	Toll-like receptor 4
11	<a href="#">DB Object Synonym (ISynonym)</a>	optional	0 or greater	hTollTollbooth
12	<a href="#">DB Object Type</a>	required	1	protein
13	<a href="#">Taxon(Itaxon)</a>	required	1 or 2	taxon:9606
14	<a href="#">Date</a>	required	1	20090118
15	<a href="#">Assigned By</a>	required	1	SGD
16	<a href="#">Annotation Extension</a>	optional	0 or greater	part_of(CL:0000576)
17	<a href="#">Gene Product Form ID</a>	optional	0 or 1	UniProtKB:P12345-2

# How Ontologies are used in Databases

## ● Annotations and data integration

1.	UniProtKB	1.	MGI
2.	A0A024RBG1	2.	MGI:1913300
3.	NUDT4B	3.	0610009B22Rik
4.	enables	4.	enables
5.	GO:0003723	5.	GO:0001222
6.	GO_REF:0000043	6.	MGI:MGI:4834177 GO_REF:0000096
7.	IEA	7.	ISO
8.	UniProtKB-KW:KW-0694	8.	UniProtKB:P0DI82
9.	F	9.	F
10.	Diphosphoinositol polyphosphate phosphohydrolase	10.	RIKEN cDNA 0610009B22 gene
11.	NUDT4B	11.	protein_coding_gene
12.	NUDT4B	12.	taxon:10090
13.	Protein	13.	20210709
14.	taxon:9606      20221109	14.	MGI
15.	UniProt	15.	
16.		16.	
17.		17.	

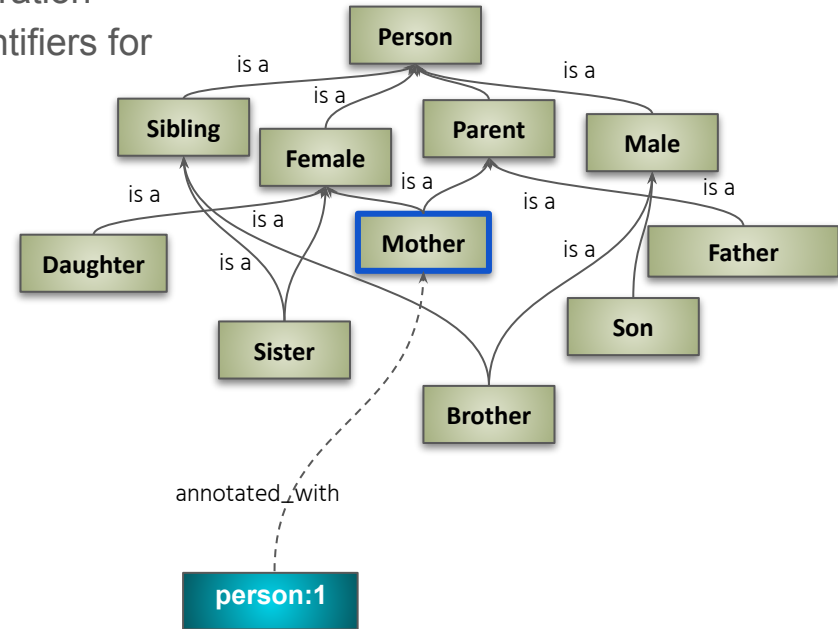
## GAF fields

The annotation flat file format is comprised of 17 tab-delimited fields.

Column	Content	Required?	Cardinality	Example
1	<a href="#">DB</a>	required	1	UniProtKB
2	<a href="#">DB Object ID</a>	required	1	P12345
3	<a href="#">DB Object Symbol</a>	required	1	PHO3
4	<a href="#">Qualifier</a>	required	1 or 2	NOTInvolved_in
5	<a href="#">GO ID</a>	required	1	GO:0003993
6	<a href="#">DB:Reference (IDB:Reference)</a>	required	1 or greater	PMID:2676709
7	<a href="#">Evidence Code</a>	required	1	IMP
8	<a href="#">With (or) From</a>	optional	0 or greater	GO:0000346
9	<a href="#">Aspect</a>	required	1	F
10	<a href="#">DB Object Name</a>	optional	0 or 1	Toll-like receptor 4
11	<a href="#">DB Object Synonym (ISynonym)</a>	optional	0 or greater	hToll      Tollbooth
12	<a href="#">DB Object Type</a>	required	1	protein
13	<a href="#">Taxon(ITaxon)</a>	required	1 or 2	taxon:9606
14	<a href="#">Date</a>	required	1	20090118
15	<a href="#">Assigned By</a>	required	1	SGD
16	<a href="#">Annotation Extension</a>	optional	0 or greater	part_of(CL:0000576)
17	<a href="#">Gene Product Form ID</a>	optional	0 or 1	UniProtKB:P12345-2

# How Ontologies are used in Databases

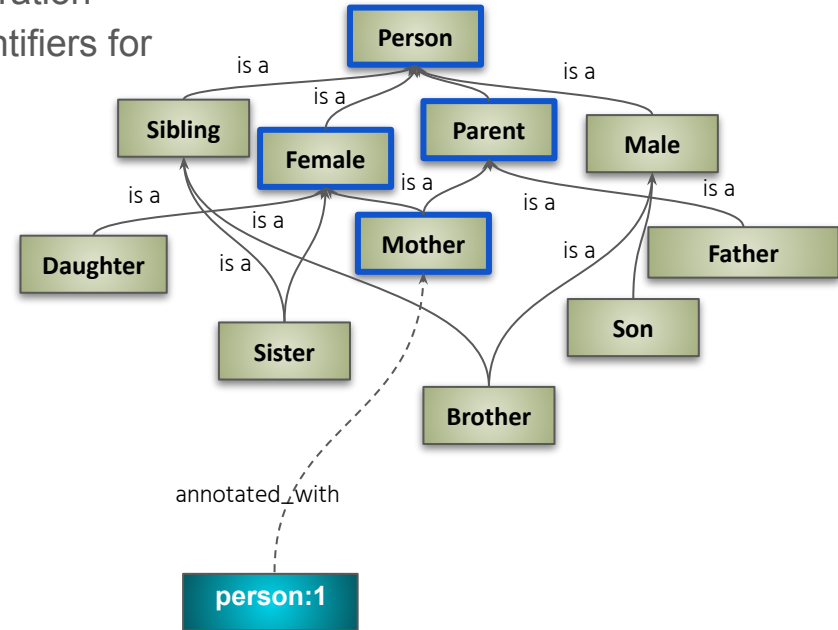
- Annotations and data integration
  - Ontologies play a crucial role in facilitating data integration across databases due to their usage of standard identifiers for classes and relations
- True path rule:
  - Annotation for a class is passed to its ancestors





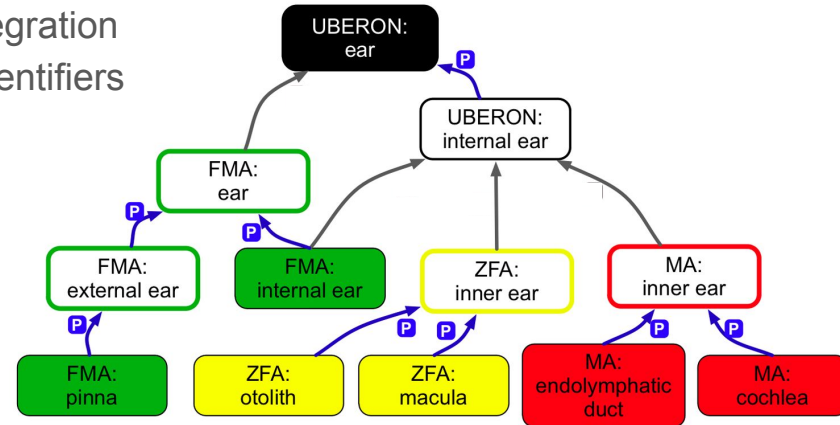
# How Ontologies are used in Databases

- Annotations and data integration
  - Ontologies play a crucial role in facilitating data integration across databases due to their usage of standard identifiers for classes and relations
- True path rule:
  - Annotation for a class is passed to its ancestors



# How Ontologies are used in Databases

- Annotations and data integration
  - Ontologies play a crucial role in facilitating data integration across databases due to their usage of standard identifiers for classes and relations
- True path rule:
  - Annotation for a class is passed to its ancestors



# Transforming GO annotations to ontology axioms

- Annotations to T-Box

The annotated entity **C** is added as a class to the ontology

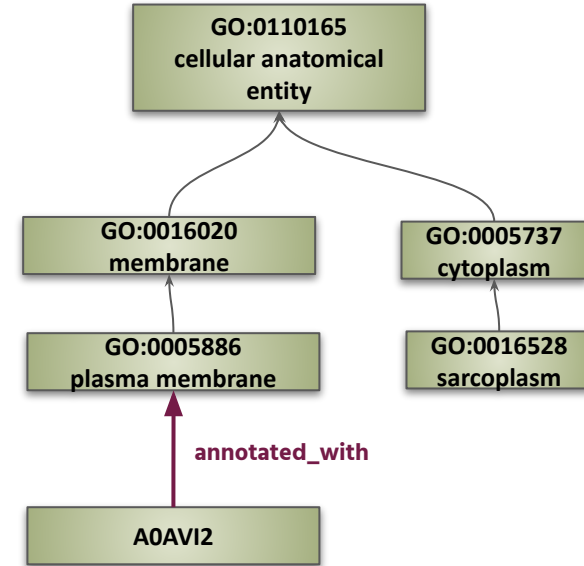
The annotation is added a relation  $R$  as follows

$$\mathbf{C} \sqsubseteq \exists R. \mathbf{D}$$

Example:

Annotating protein **A0AVI2** To Gene Ontology

- $\mathbf{A0AVI2} \sqsubseteq \exists \textit{annotated\_with}. \mathbf{Plasma\ membrane}$



# Transforming GO annotations to ontology axioms

- Annotations to T-Box

The annotated entity **C** is added as a class to the ontology

The annotation is added a relation  $R$  as follows

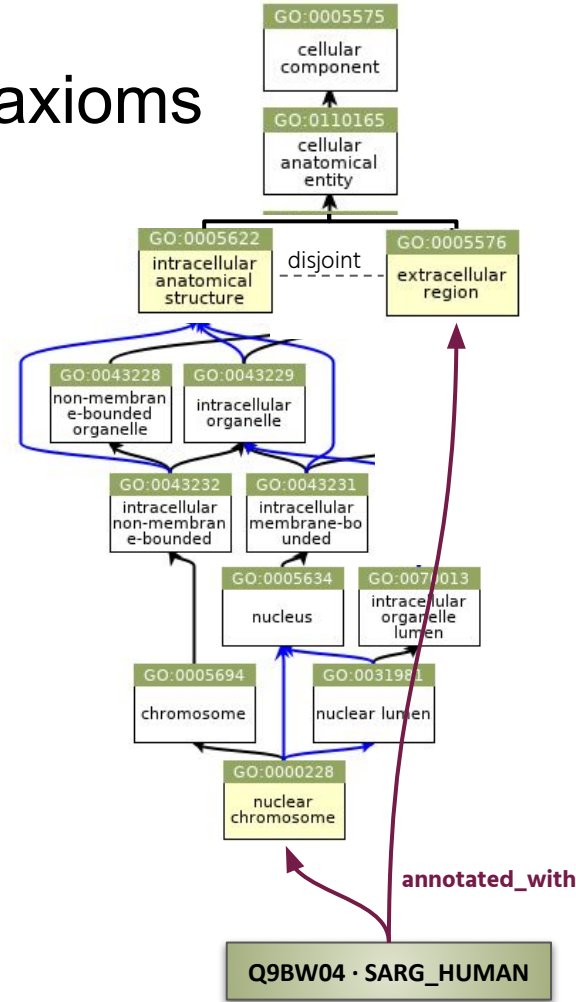
$$\mathbf{C} \sqsubseteq \exists R. \mathbf{D}$$

Example:

Annotating protein **A0AVI2** To Gene Ontology

- $\mathbf{A0AVI2} \sqsubseteq \exists \text{annotated\_with. Plasma membrane}$

Problem, when an entity is annotated to disjoint annotations.



# Transforming GO annotations to ontology axioms

- Annotations to T-Box

The annotated entity **C** is added as a class to the ontology

The annotation is added a relation  $R$  as follows

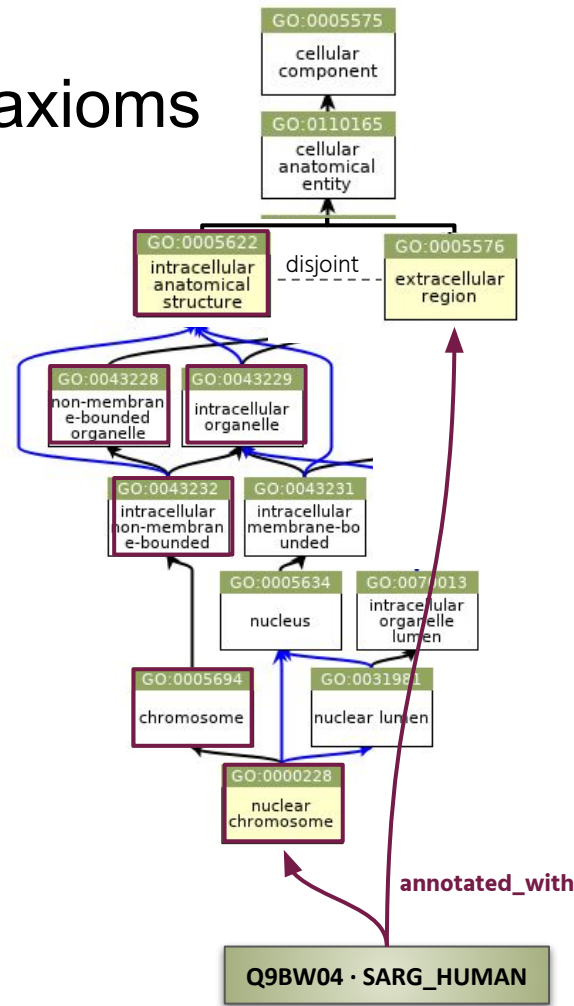
$$\mathbf{C} \sqsubseteq \exists R. \mathbf{D}$$

Example:

Annotating protein **A0AVI2** To Gene Ontology

- $\mathbf{A0AVI2} \sqsubseteq \exists \text{ annotated\_with. } \mathbf{Plasma\ membrane}$

Problem, when an entity is annotated to disjoint annotations.



# Transforming GO annotations to ontology axioms

- Annotations to T-Box

The annotated entity **C** is added as a class to the ontology

The annotation is added a relation *R* as follows

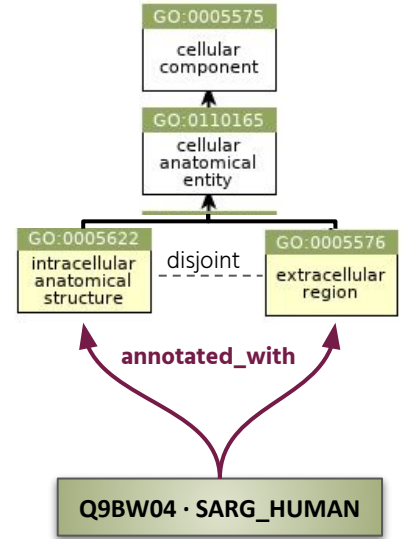
$$\mathbf{C} \sqsubseteq \exists R. \mathbf{D}$$

Example:

Annotating protein **A0AVI2** To Gene Ontology

- A0AVI2**  $\sqsubseteq \exists$  *annotated\_with*. **Plasma membrane**

Problem, when an entity is annotated to disjoint annotations.

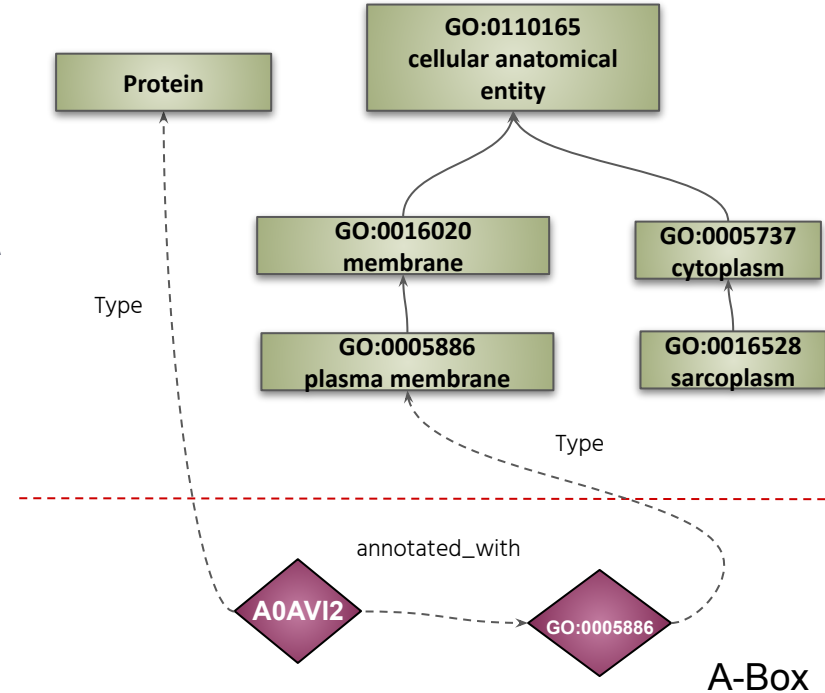


# Transforming GO annotations to ontology axioms

Example:

Annotating protein **A0AVI2** To Gene Ontology

- Annotations to T-Box
  - A0AVI2**  $\sqsubseteq \exists$  *annotated\_with*. **GO:0005886**
- Annotations to A-Box
  - Protein(**A0AVI2**)
  - annotated\_with*(**A0AVI2**, **GO:0005886**)



## Following this

- Ontologies and text mining → utilizing class labels and descriptions
- Graph based embedding → utilizing axioms and class labels and descriptions
- Syntactic embedding → utilizing axioms and class labels and descriptions
- Semantic embedding → utilizing axioms