Introduction to ontologies and GO term analysis



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Metadata

• Data about data.

 Annotation is the process of linking metadata to data.

 Modern databases store and query metadata to facilitate more complicated queries.

Tons of data are available

 High throughput methods yield large amount of data, often annotated in several different but related ways:

 Annotations related to tissue and developmental stage where a gene is expressed.

Geographical distribution of alleles. Resistance to drugs. Ability to transmit a disease.

The modern tower of Babel (I) Currently data produced by a research project are stored in a homemade database specifically designed to serve the purpose of the project.

Innovative Vector Control Consortium - IVCC The WHO/Gates Foundation Vector Biology and Control Project -VBC

African Network on Vector Research – ANVR

Malaria Atlas

. The modern tower of Babel (II)

- Not a single format / standard to describe the same datatypes.
 - Genbank vs EMBL
 - Generic Feature Format GFF version 2 vs version 3
 - GVF (Genome Variation Format) vs VCF (Variant Call Format)
 - OBO vs OWL



Biological data separated in "silos"

- Lab / pathological data.
- Data related to medical records.
 - Clinical data.
 - Patient history
 - Imaging data
- Gene expression datasets (microarrays, RNAseq).
- Proteomics data (mass spectrometry).
- Genomic Variation data.



• We need to link all these databases and to make them interoperable.

 Need to develop IT tools and decision support systems to take advantage and retrieve data from all those sources.

Ontology

• Branch of philosophy focusing to everything that exists.

(IT) Ontology is a typical network of knowledge representation.

• In biomedical domain , ontologies are ways to represent and organize meta-data.



Basic elements of an ontology

- Terms unambiguously defined.
 - Synonyms.

 Connections with the other terms of the ontology via logically defined relations.



Reference and application ontologies Reference ontologies describe a scientific domain and provide the basis for the

 Application ontologies which aim to serve the needs of a specific scientific community.

Scientific vs operational ontologies

	Upper level ontologies	Domain specific ontologies
Scientific ontologies	BFO , Dolce , SUMO	GO, FMA, IDO
Operational ontologies	FOAF	Amazon.com, Library of Congress

The tower of Babel revisited

- There are many ways to create an ontology but the number of available ontologies is not solving the "data isolation" problem by itself.
- If every community or group creates an ontology using a different jargon interoperability is not promoted.
 - Drug database based on brand names only.
 - Metabolic resistance vs Detoxification process
- Scientific ontologies have to be linked together.

Ways to link ontologies together

- Use common reference ontologies while developing application ontologies for related fields.
 - Disease ontology (DO)

Infectious disease ontology (IDO) Malaria ontology (IDOMAL) Dengue Fever ontology (IDODEN)

- Reference ontologies contain generic terms which remain more or less the same, while application ontologies are more flexible to cover the needs as our knowledge is increased.
 - Neither DO or IDO have changed when a fifth serotype of Dengue virus had discovered and added to IDODEN.

Ways to link ontologies (II)

• Common use of relations in all ontologies related to a specific domain.

 OBO Foundry is an international consortium of ontology developers for the biomedical domain has issued a set of rules to facilitate ontology interoperability.

OBO Foundry rules

 Every term has to be related with another term via an <u>is a</u> relation. (<u>is a</u> completeness).

• Every term has only one *is_a* parent.

 There is a predefined set of relations that has to be used in all biomedical ontologies.

Relations available for use in OBO Foundry							
is_a	has_agent						
part_of	instance_of						
integral_part_of	realizes						
proper_part_of	inheres_in						
located_in	bearer_of						
contained_in	has_quality						
adjacent_to	has_function						
transformation_of	has_role						
derives_from	has_disposition						
preceded_by	has_participant						

Ontological realism

- Describe the scientific domain according to our best knowledge at the present time.
- Add terms and relations in order to describe what is true in reality and not some simplified computerbased model.
- An ontology is the product of collaboration between specialist from several different fields.

Basic elements of an ontology

- Terms unambiguously defined.
- Synonyms.

 Connections with the other terms of the ontology via logically defined relations.

Some definitions

• Entity: Everything that exists: An object, a process, a function, space, text, computer software.

• Universal entities versus instances.

• Human beings versus specific individuals.

• An ontology focuses on universals where as a database focuses on instances.



In a scientific ontology

• Every term represents both universal entities and their instances.

• Every term represents only one universal entity.

• Therefore we can define ontology as a representation of universals.

A photograph is a representation of an instance



We can't photograph a universal but we can create it's representation



H	Periodic Table of the Elements									2 He							
3 Li	Be	alkali metals				 poor metals nonmetals noble gases 			В	C	N	08	۶	¹⁰ Ne			
11 Na	12 Mg	-	transi	tion m	etals		na 🛛	re ear	th met	als		AI	si	15 P	S ¹⁶	17 Cl	18 Ar
19 K	Ca	SC SC	Ti Ti	V ²³	Cr ²⁴	25 Mn	²⁶ Fe	27 Co	28 Ni	Cu Cu	Zn Zn	31 Ga	32 Ge	33 As	³⁴ Se	35 Br	³⁶ Kr
87 Rb	³⁸ Sr	39 Ƴ	40 Zr	41 Nb	42 Mo	43 TC	44 Ru	45 Rh	46 Pd	47 Ag	48 Cd	49 In	⁵⁰ Sn	51 Sb	Te	53 	Xe
Cs	Ba	57 La	Hf	Ta	74 W	Re Re	76 Os	r Ir	Pt	79 Au	Hg	81 Ti	⁸² Pb	83 Bi	⁸⁴ Po	At 85	86 Rn
87 Fr	⁸⁸ Ra	AC	¹⁰⁴ Unq	Unp	Unh	107 Uns	108 Uno	Une	Unn								

Ce	Pr	Nd	Pm	62 Sm	Eu	Gd ⁶⁴	Tb ⁶⁵	66 Dy	67 Ho	Er	Tm	Yb	⁷¹ Lu
Th ⁹⁰	91 Pa	92 U	93 Np	94 Pu	Am	96 Cm	97 Bk	Cf	99 Es	100 Fm	101 Md	102 No	103 Lr









Linguistic problems

• Sometimes the same word/term is used for a universal entity and a subset of instances generating confusion.

• Ebola virus can cause death.

• Ebola virus is transmitted uncontrollably in west Africa.

Scientific ontology

• An artifact to represent universals and the relations that relate them

Gene Ontology (GO)

• A structured representation of the qualities / properties of genes available to all interested to the universal biological reality.

GO is not an ontology, but 3 independent ontologies together

cellular component

molecular function

biological process

No connections between the 3 main components of GO

cellular component

molecular function

biological process







cellular component

biological process

molecular function cellular biological process organism-level biological process











GO curation

• GO curators develop the ontology and also provide annotations on behalf of the model organism databases.

Evidence codes

GO Evidence Code Decision Tree



GO usage

- The Gene Ontology (GO) provides core biological knowledge representation for modern biologists, whether computationally or experimentally based.
- GO annotations provide largely species-neutral, comprehensive statements about what gene products do.
- The general user of GO resources often misses fundamental distinctions about GO structures, GO annotations, and what can and can not be extrapolated from GO resources.

Know the Source of the GO Annotations You Use

• The GO site has the most comprehensive and current sets of annotations.

 Annotations are also contained within external tools and applications, although these may not be updated often.

Understand the Scope of GO Annotations

 The GO annotation stream focuses on the capture of the knowledge about the functional activities of specific proteins, the larger biological process (such as photosynthesis) as part of which these specific functions collectively act, and the cellular locality where all this occurs.

Consider Differences in Evidence Codes

 There are 21 evidence codes currently in use to document how data are obtained, and GO may adopt an evidence code classification in the near future.
 Some evidence codes indicate different classes of experiments such as "inferred by direct assay." Some indicate different approaches to prediction from comparative analysis such as "inferred from sequence orthology."

Probe Completeness of GO Annotations

• While the GO annotation corpus generally has excellent broad coverage of available knowledge about gene products via structurally based annotations from sources such as InterPro, the completeness of annotations derived from biomedical literature is uneven because there are not enough GO curators to keep them current on all fronts.

 The lack of a GO annotation does not mean that a gene product does not perform a particular function or act in a particular role.

Understand the Complexity of the GO Structure

 The GO structure, relations, and terminology are modified every day by GO ontology editors. New relations between terms are added as the GO refines the representation of biological knowledge.

• There is a need to know the version of the ontology which is being used by our analysis tool.

Choose Analysis Tools Carefully

• Hundreds of GO-focused applications and tools are available.

Term enrichment analysis, a common use of GO resources, is incorporated into many different applications and analysis tool sites. Different implementations/algorithms may give different results.

AmiGO 2

More information on quick search @



Term annotations

What are the direct and indirect annotations to term	? Go »		
What are the direct and indirect annotations for organism	(scientific name)	to term	? Go »
Gene product annotations			
What are all the annotations for gene product	Go »		
Gene products associated v	vith terms		
What are the gene products annotated to term	but not term	? Go »	
What are the gene products annotated to term	and term	? Go »	
Protein family			
What are the annotations associated with the protein fam	nily Go	»	

AmiGO 2





Gene IDs

Gene IDs

Species

H. sapiens

Ontology

biological process

Correction

Use Bonferroni correction

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Resource

PANTHER

Results viewer

AmiGO

Submit



Species

H. sapiens

H. sapiens

- M. musculus
- R. norvegicus
- G. gallus
- D. rerio
- D. melanogaster
- C. elegans
- D. discoideum
- S. pombe
- S. cerevisiae
- A. thaliana
- E. coli
- C. albicans

Ontology

biological process

biological process molecular function cellular component biological process (experimental only) molecular function (experimental only) cellular component (experimental only)

Gene product annotations

What are all the annotations for gene product Notc

What are the gene products annotated to term

What are the gene products annotated to term

Protein family

What are the annotations associated with the

Notch4 (MGI:MGI:107471/Mus musculus) Gene products associa Notch2 (MGI:MGI:97364/Mus musculus) Notch1 (MGI:MGI:97363/Mus musculus) NOTCH1 (UniProtKB:F1MSM3/Bos taurus) NOTCH2 (UniProtKB:F1MPE9/Bos taurus) NOTCH4 (UniProtKB:G3X812/Bos taurus) NOTCH3 (UniProtKB:E1BPT8/Bos taurus) Human Notch 3 (UniProtKB:Q14962/Homo sapiens) NOTCH2 (UniProtKB:F1P236/Gallus gallus) NOTCH1 (UniProtKB:F1NZ70/Gallus gallus)

Go »

Free	e-text filtering	
	Your search is pinned to these filte	rs
+	document_category: annotation	
	User filters	[
+	bioentity: UniProtKB:Q14962	1
•	Source	
•	Assigned by	
•	Ontology (aspect)	
•	Evidence type	
•	PANTHER family	
•	Qualifier	

Х

Х

Taxon

Direct annotation

Inferred annotation

anatomical structure morphogenesis	(1) + -
biological_process	(1) + -
cell part	(1) + -
cellular_component	(1) + -
developmental process	(1) + -
integral component of membrane	(1) + -
integral component of plasma membrane	(1) + -
membrane part	(1) + -
plasma membrane part	(1) + -

Found entities Х Total: 2; showing 1-2 Results count 10 v 0 ß 14 Evidence PANTHER Isoform Gene/product Qualifier Direct Annotation Gene/product Source Taxon Evidence Reference annotation extension with family name Human Notch 3 PMID:7698746 anatomical UniProtKB Homo TAS Notch 3 protein structure sapiens morphogenesis Human Notch 3 integral UniProtKB TAS PMID:7835890 Homo Notch 3 protein component of sapiens plasma membrane

http://geneontology.org/page/guidego-evidence-codes

Thank you!