

# OBOL

Open Bio-Ontology Language

GO Meeting  
Stanford  
Jan 2004

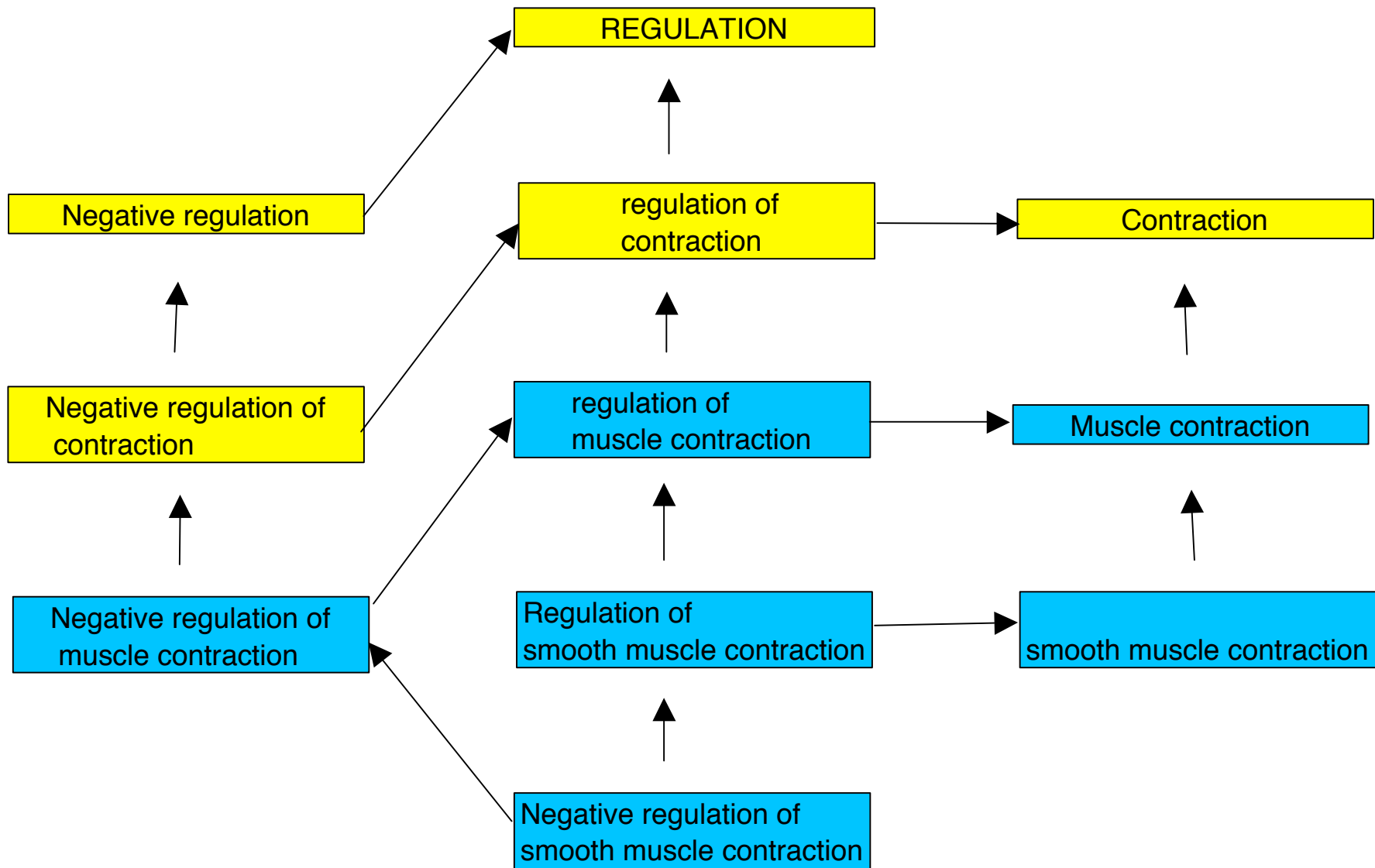
# Outline

- \_ Curation and annotation issues that OBOL addresses
- \_ *Grammatical* composition and decomposition
- \_ Making logical class definitions via slots
- \_ Rules for logical inference
- \_ DAG-Edit Plugin
- \_ Results so far
- \_ How it will work

# How OBOL will help

- \_ Slot-based annotations (eg interleukin-18 binding)
- \_ Cross-products and composite terms
  - decomposing existing terms
  - new composite terms
- \_ Consistency Checking
- \_ New term creation
- \_ Research (DLs, text-mining)

# A Typical Fiendishly Hard Lattice



# An Observation

- \_ GO Term “sentences” often follow consistent implicit rules
  - \_ Ogden et al
- \_ Hidden knowledge is embedded in the text strings
- \_ It should be possible to *decompose/parse* GO terms into **logical definitions** (and also to *compose/generate* new GO terms from new **logical definitions**)
- \_ We can do this with a **Grammar**

# Formal Grammars

- \_ A rule system for parsing (decomposing) and generating (composing) sequences of symbols (eg sentences, NA or AA sequences)
- \_ Invented by Chomsky in the 50s
- \_ Used all over computer science (e.g. Compilers)
- \_ Also in bioinformatics – eg RNA structure analysis

# Grammars

- \_ Terminal and non-terminal symbols
- \_ We write non-terminals in upper case by convention
- \_ Production Rules  $X \rightarrow Y, Z$ 
  - Specify means of making LHS by composing RHS
  - (or decomposing RHS into LHS)
  - Recursive

# A Simple English Language Grammar

- \_ Sentence --> NounPhrase, VerbPhrase
- \_ VerbPhrase --> Verb, NounPhrase
- \_ NounPhrase --> Det, Noun
- \_ Det --> a | the
- \_ Noun --> cat | mouse | house
- \_ Verb --> scares | hates | eats | kisses
- \_ Eg “the cat scares a mouse”



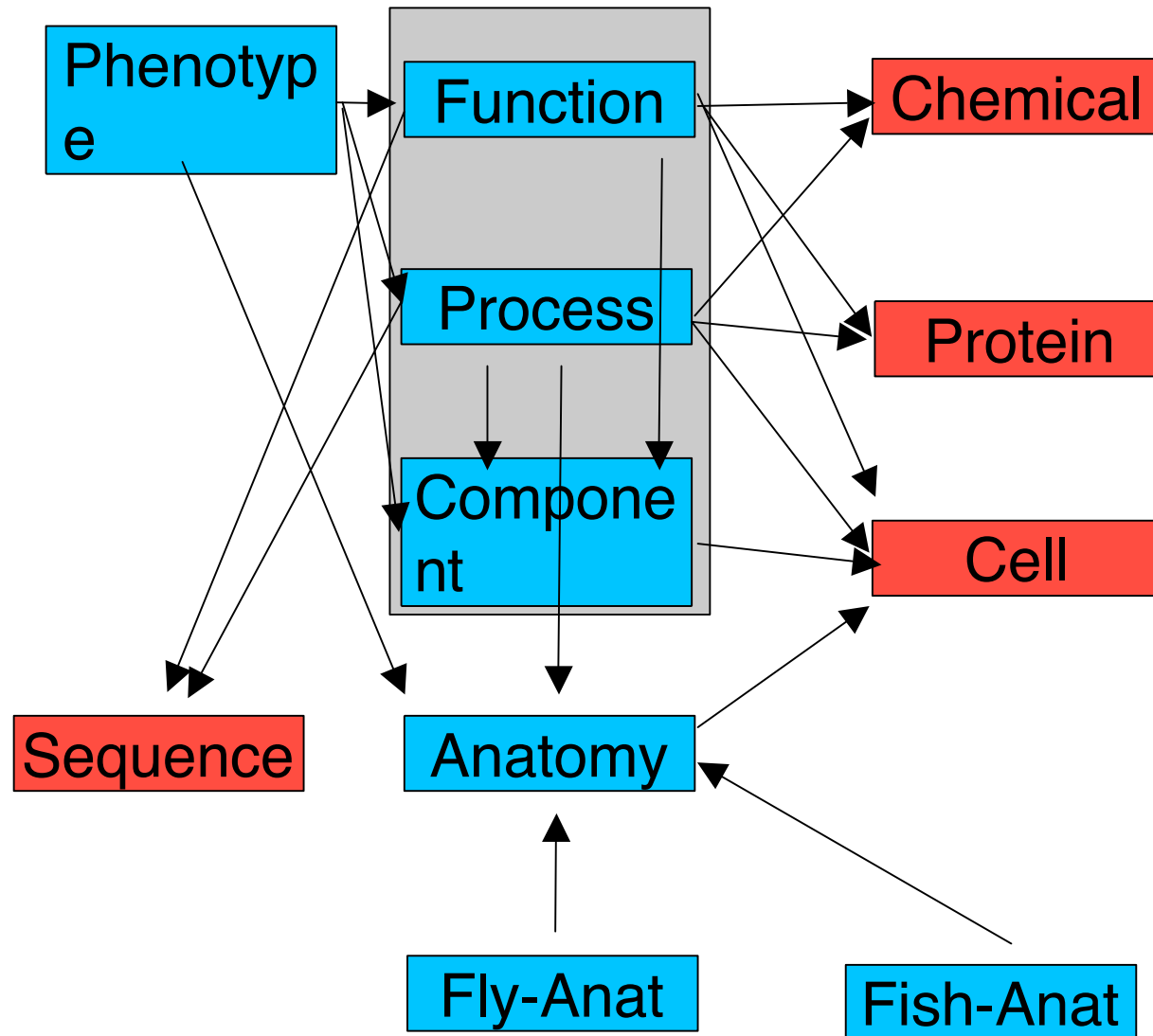
# A grammar for OBO terms

- \_ All(?) OBO terms are NOUN-PHRASES
- \_ A NOUN-PHRASE is (recursively) made from
  - a noun
  - an adjective followed by a NOUN-PHRASE
  - a NOUN-PHRASE preceeded by a NOUN-PHRASE acting as adj
  - a NOUN-PHRASE then preposition then NOUN-PHRASE
  - an (optional) NOUN-PHRASE then a relational adjective then a NOUN-PHRASE
- \_ Precedence rules
- \_ Implemented in Prolog (one page of code!)

# OBO WordLists

- \_ Partitioned by ontology
- \_ Types:
  - nouns
  - adjectives
  - prepositions
  - relational adjectives (*cytosolic*, *coated*)
- \_ Incomplete information
  - orphan nouns

# The OBO Universe (partial)



# An example

- \_ negative regulation of smooth muscle contraction

np = adj+np

- \_ negative regulation of smooth muscle contraction
- \_ (negative **regulation**) (smooth **muscle**)

np = np+np

- \_ negative regulation of smooth muscle contraction
- \_ (negative **regulation**) ((smooth **muscle**)  
**contraction**)
- \_ (**negative regulation**) (**smooth muscle**)

np = np+p+np

- \_ negative regulation of smooth muscle contraction
- \_ ((negative **regulation**) ((smooth **muscle**)  
**contraction**))
- \_ (negative **regulation**) ((smooth **muscle**)  
**contraction**)
- \_ (**negative regulation**) (**smooth muscle**)

# alternate parses

- \_ smooth muscle contraction
- \_ (smooth (muscle **contraction**)) <-- wrong!!
- \_ (muscle **contraction**)



# Making Logical Class Definitions from Parse Trees

- \_ Tokenize OBO/GO term strings
- \_ Make ParseTree using Prolog Grammar
- \_ Transform tree to class definition using slot definitions
- \_ *reversible*
- \_ *Classdefs can be represented in OBO format or OWL format*

# Making classes via slots

## \_ slot: regulates

- domain (subject): regulation
- range (object): biological\_process
- grammar-context: preposition(of)

## \_ slot: qualifier

- domain (subject): regulation
- range (object): **negative OR positive**
- grammar-context: adjective

# A Recursively Defined Class

- \_ Regulation (**biological\_process** class)
  - *type*: negative (**general** class)
  - *regulates*:
    - \_ Contraction (**biological\_process** class)
      - *affects\_cell*:
        - \_ Muscle (**cell** class)
        - *type*: smooth (**general** class)

# COPII-coated vesicle membrane

- \_ membrane (**cellular\_component** class)
  - *part\_of*
    - \_ vesicle (**cellular\_component** class)
      - *has\_part*
        - \_ coat (**cellular\_component** class)
        - \_ *made\_from*
          - \_ COPII (**complex** class)

# Reasoning over class definitions

- \_ Use inference over classdefs to
  - place new terms in the correct place in the DAG
  - check for missing relationships in the DAG
  - find inconsistencies within the DAG
  - other kinds of reasoning?
- \_ Method:
  - Inference rules implemented in Prolog

# Inferring intermediate terms and ISAs

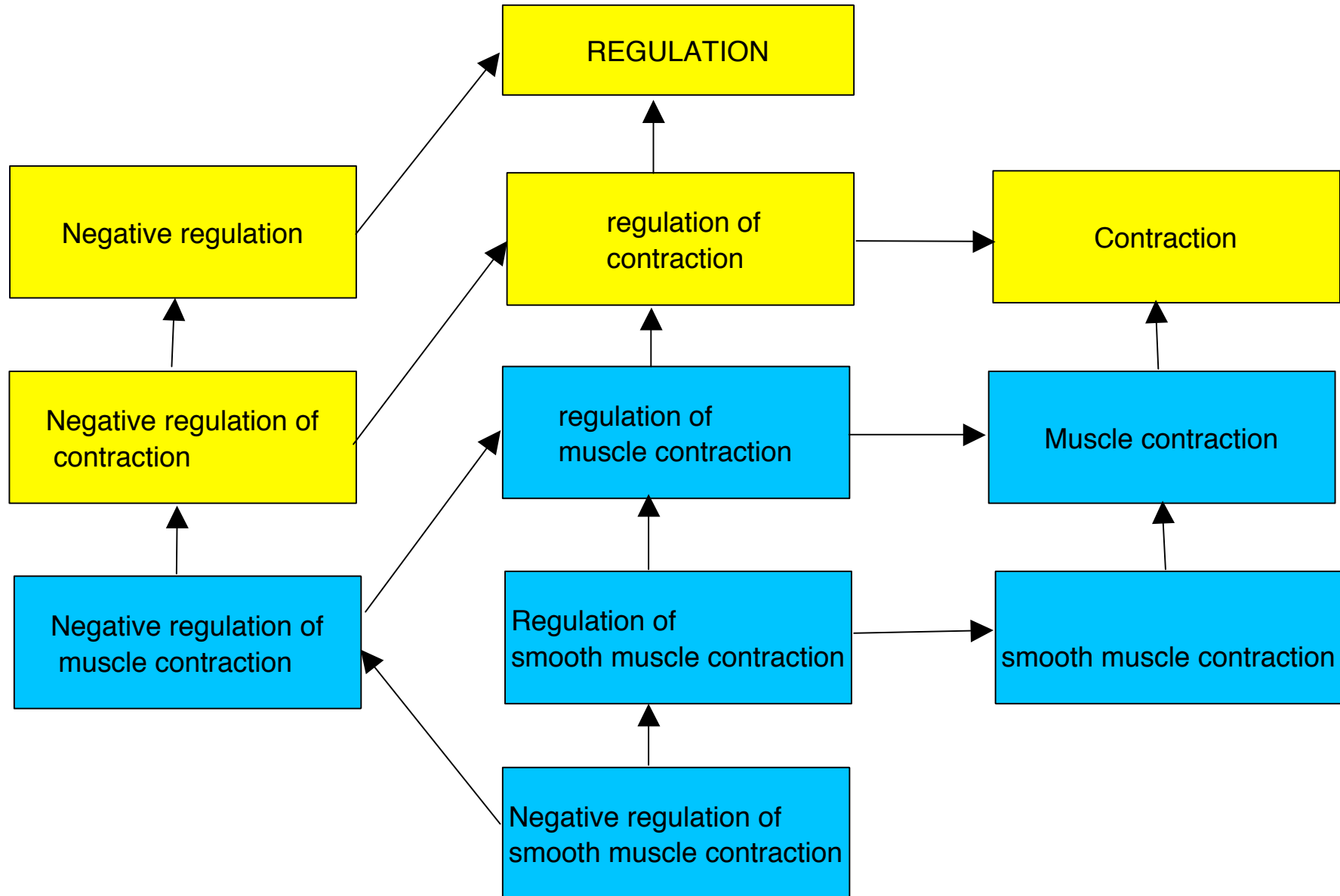
regulation(process\_regulated:R,qual:Q) isa  
regulation(process\_regulated:R',qual:Q)

$\Leftrightarrow$

R isa R'

IFF the stem-class is the same AND all the slot-values in the restriction-list are identical EXCEPT for one slot, where the slot-values are linked by an isa, then the classdefs are linked by an isa

# Inference of terms and rels



# Inference in Prolog is easy

- **% DATABASE OF FACTS**

- isa(carb\_binding, binding).

- isa(polysac\_binding,  
carb\_binding).

- isa(chitin\_binding,  
polysac\_binding)

- isa(cellulose\_binding,  
polysac\_binding).

- **% INFERENCE RULES**

- isaT(X,Y):- isa(X, Y).

- isaT(X,Y):-isa(X,Z),  
isaT(Z,Y).

- ?- isaT(chitin\_binding, binding).

- **YES**

- ?-isaT(X, polysac\_binding).

- **X=carb\_binding.**

- **X=chitin\_binding.**

- **X=cellulose\_binding.**

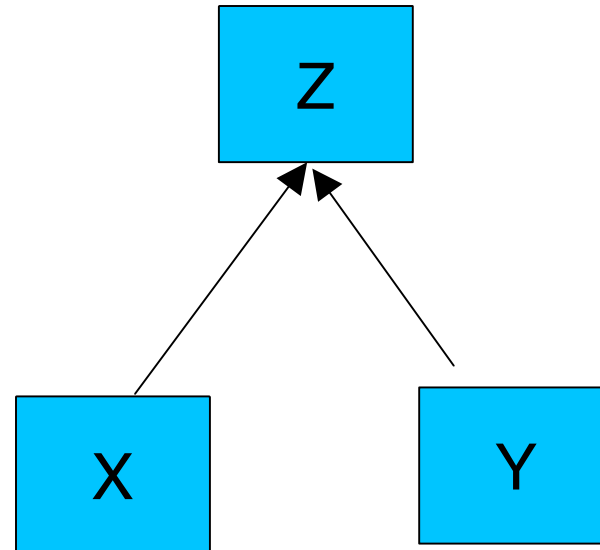
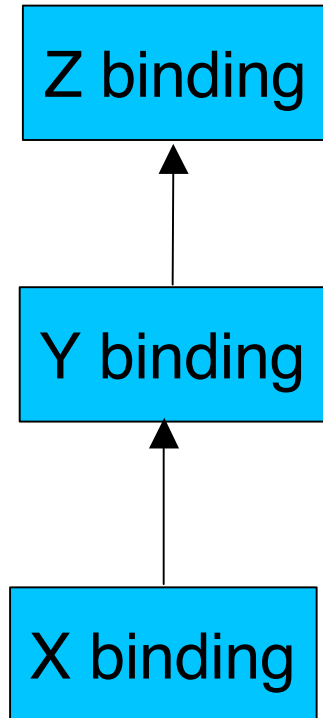
- ?-isaT(chitin\_binding,  
cellulose\_binding).

- **NO**

- **?-isaT(X, Y). % returns all  
paths**



# Detecting inconsistencies



# OBOL: Combining Grammars and Reasoning

- \_ Allows complex logical definitions to be maintained as linear text strings
- \_ Maintains facade of narrative approach, whilst implementing a combinatorial approach behind the scenes
- \_ Description Logic Reasoners can be used
  - Racer, FACT – OR use OBOL prolog rules
- \_ Speeds up term creation?
- \_ Flexibility for annotators

# Results so far

- \_ Main corpus of logical rules implemented
- \_ wordlists and slot definitions incomplete
- \_ Unique classdefs:
  - function: 2133
  - process: 3240
  - component: 430
- \_ Missing relationships (UNVALIDATED): 130
- \_ Existing relationships that can be inferred: ?

# Problems to address

- \_ Multiple parses
- \_ Difficulties with nascent biochemical ontology
- \_ No cross-species anatomy ontology (as yet)
- \_ No protein/complex ontology
- \_ Can we use OBOL to help build these other ontologies?

# Gradual Introduction of OBOL

- \_ now: periodic generation of **editlists**
- \_ **soon: DAG-Edit plugin**
- \_ **hopefully soon: anatomy and biochem  
onts**
- \_ **on request: autogeneration of  
crossproducts**
- \_ **?: maintenance of classdefs in OBO files**
- \_ **?: regular releases in OWL format**
- \_ **?: slot-based annotation**

# What next?

- \_ Grammar for Text-Definitions
- \_ Extend inference rules
  - e.g. Non-monotonic reasoning (cell HAS-PART nucleus EXCEPT erythroctye)
- \_ Getting it to work as a DAG-Edit plugin
- \_ Wait for, or help create good chemical, protein and “meta-anatomy” ontologies

# Conclusions

- \_ Decomposing GO terms is useful, and achievable
- \_ Reasoning over the resulting logical definitions is possible, and can help maintenance
- \_ Combination of grammar & reasoning is powerful – rigor + ease of use
- \_ A new way of thinking about GO/OBO?
- \_ Useful in all realms of complex biological data modeling

# Acknowledgements

- \_ Suzi
- \_ John
- \_ Brad
- \_ David & Joel
- \_ Michael
- \_ GO Curators
- \_ Chris Wroe
- \_ Robert Stevens