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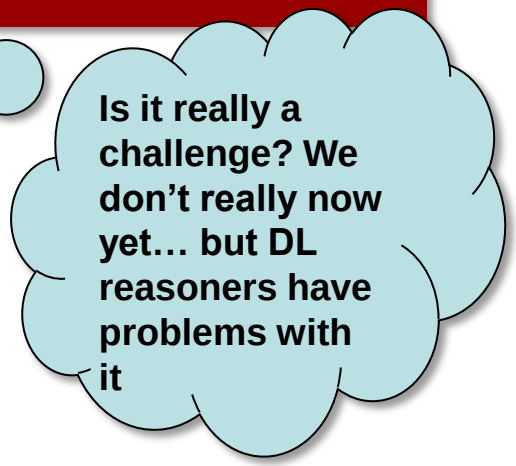
Bio_KB_101: A Challenge for TPTP First-Order Reasoners (?)

Vinay K. Chaudhri
Michael A. Wessel
Stijn Heymans



SRI International

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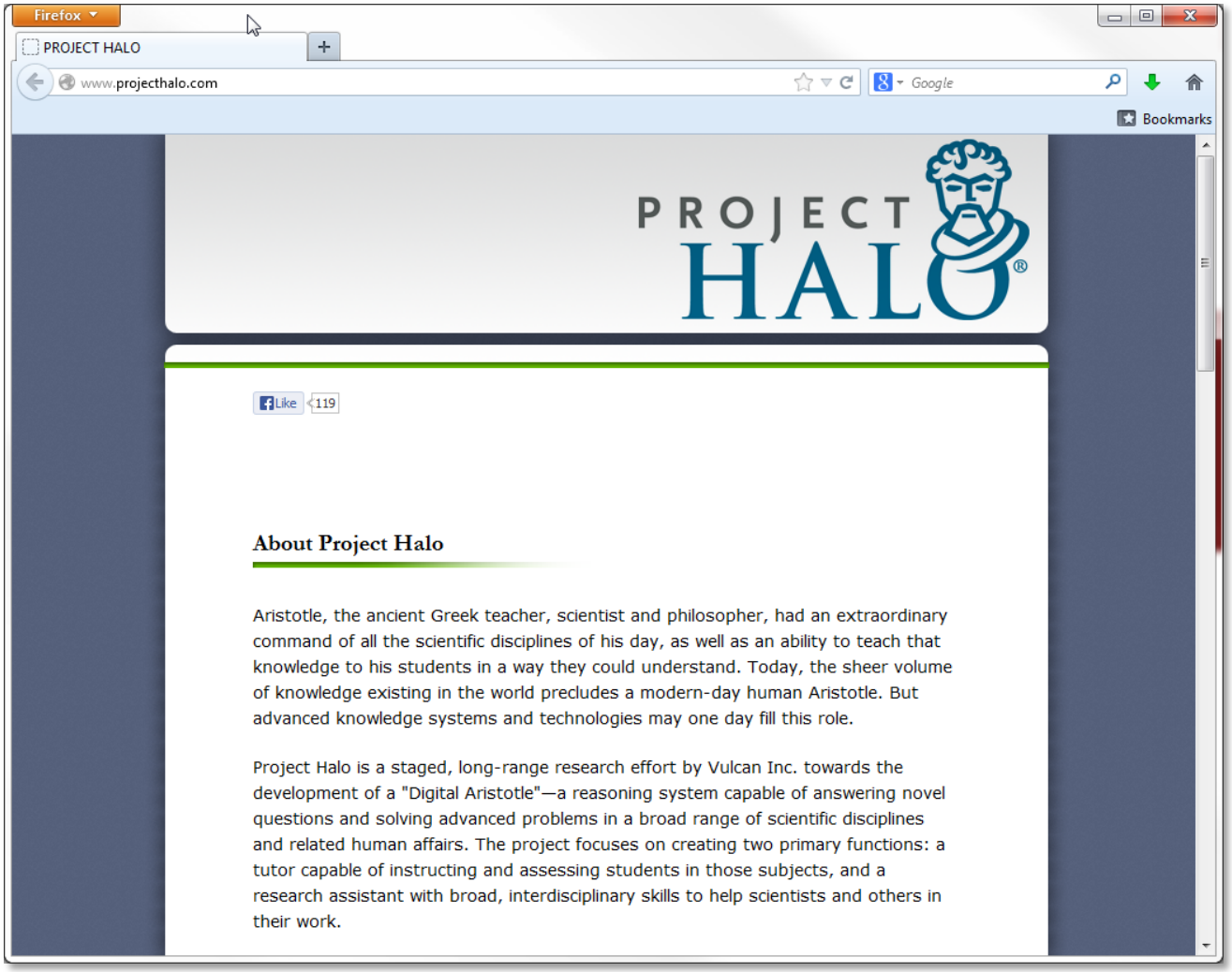
Acknowledgment

- This work has been funded by Paul Allens' Vulcan Inc.
  http://www.vulcan.com
  http://www.projecthalo.com



Background: The Digital Aristotle, Project Halo, and AI^2

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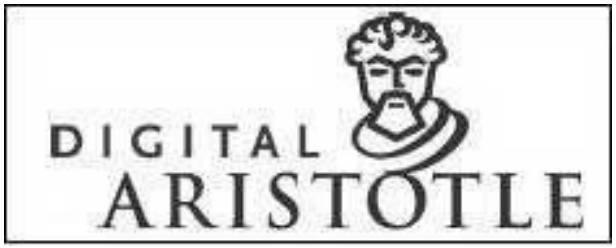

Digital Aristotle – a tutoring and reasoning sstem capable of teaching, answering novel questions and solving advanced problems in a broad range of scientific disciplines

Project Halo – Vulcan's phased, long-range past research effort to build the Digital Aristotle, with 3 areas of concentration:

- *AURA / Inquire:* A question-answering **biology** text (SRI)
- *SMW*: Low-cost knowledge from the public
- *SILK*: **S**emantic **I**nferencing on **L**arge **K**nowledge - a new semantic web rule language

Currently, Vulcan is in the process of defining its future direction for AI research (AI^2). SRI is looking at marketing opportunities for the developed technology.

AI^2 – Sponsors conferences, prizes, competitions, and the construction of large public knowledge bases

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Winner of the 2012 AAAI Video Award

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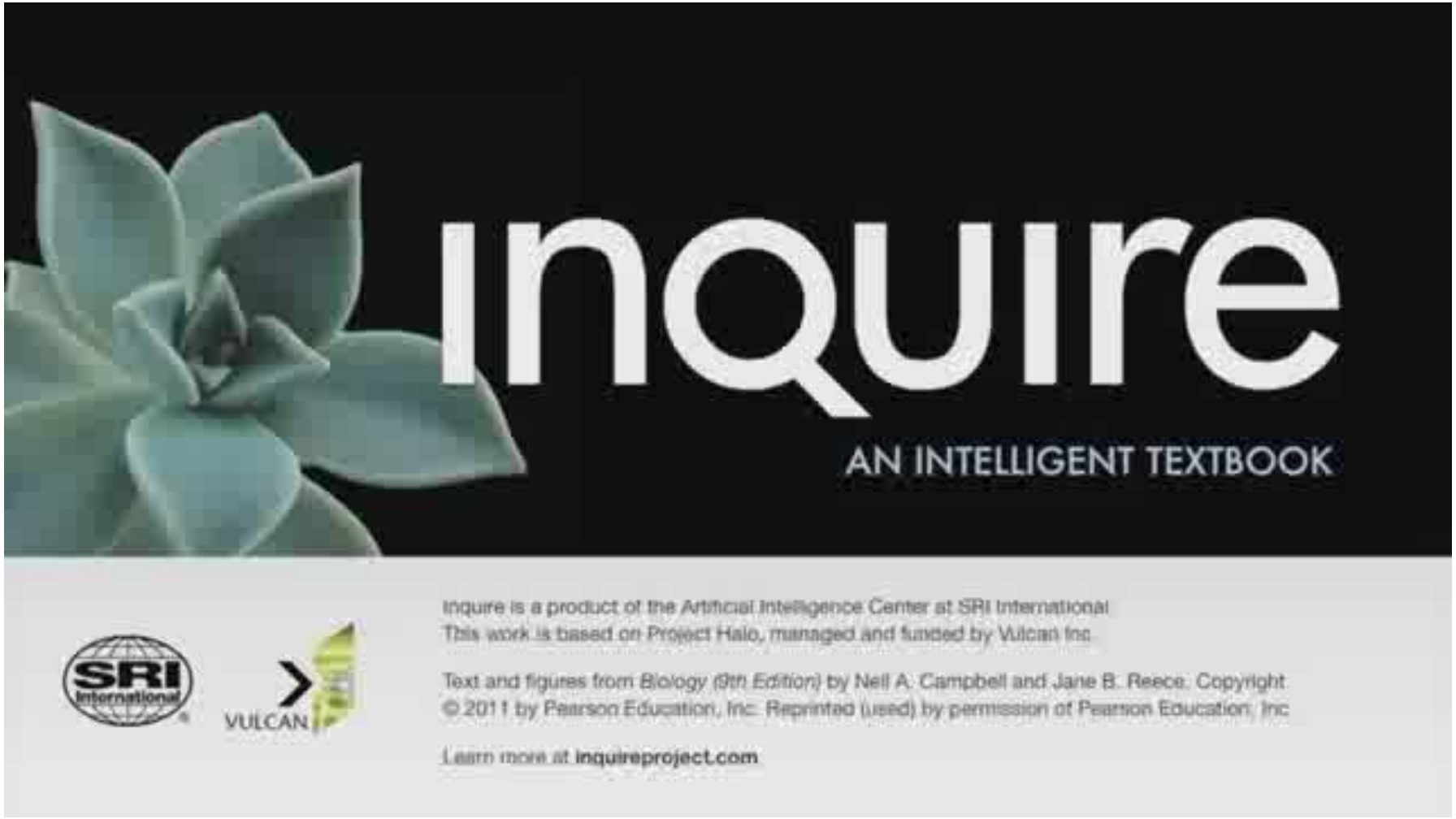

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The Underlying Knowledge Base

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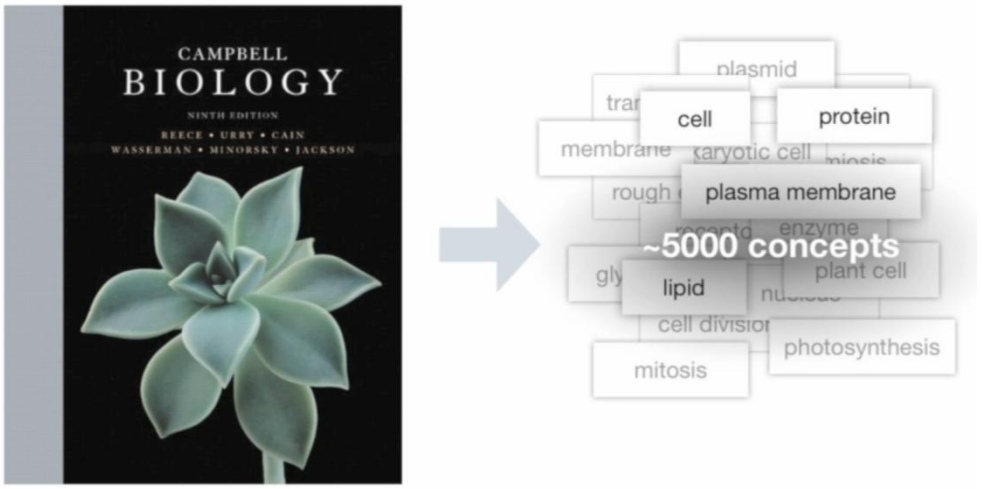

- A team of **biologists** is using graphical editors to curate the KB from the textbook, using a **sophisticated knowledge authoring process** (see below) http://dl.acm.org/citation.cfm?id=1999714

- The KB is a valuable asset: it contains 11.5 man years of biologists, and estimated 5 (2 Univ. Texas + 3 SRI) years for the upper ontology (CLib)

- Vulcan and SRI are giving this asset free of charge to the research community (subject to a research license agreement): http://www.ai.sri.com/halo/halobook2010/exported-kb/biokb.html

- The KB has non-trivial graph structure (unlike some medical ontologies)

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AURA Graphical Knowledge Editor

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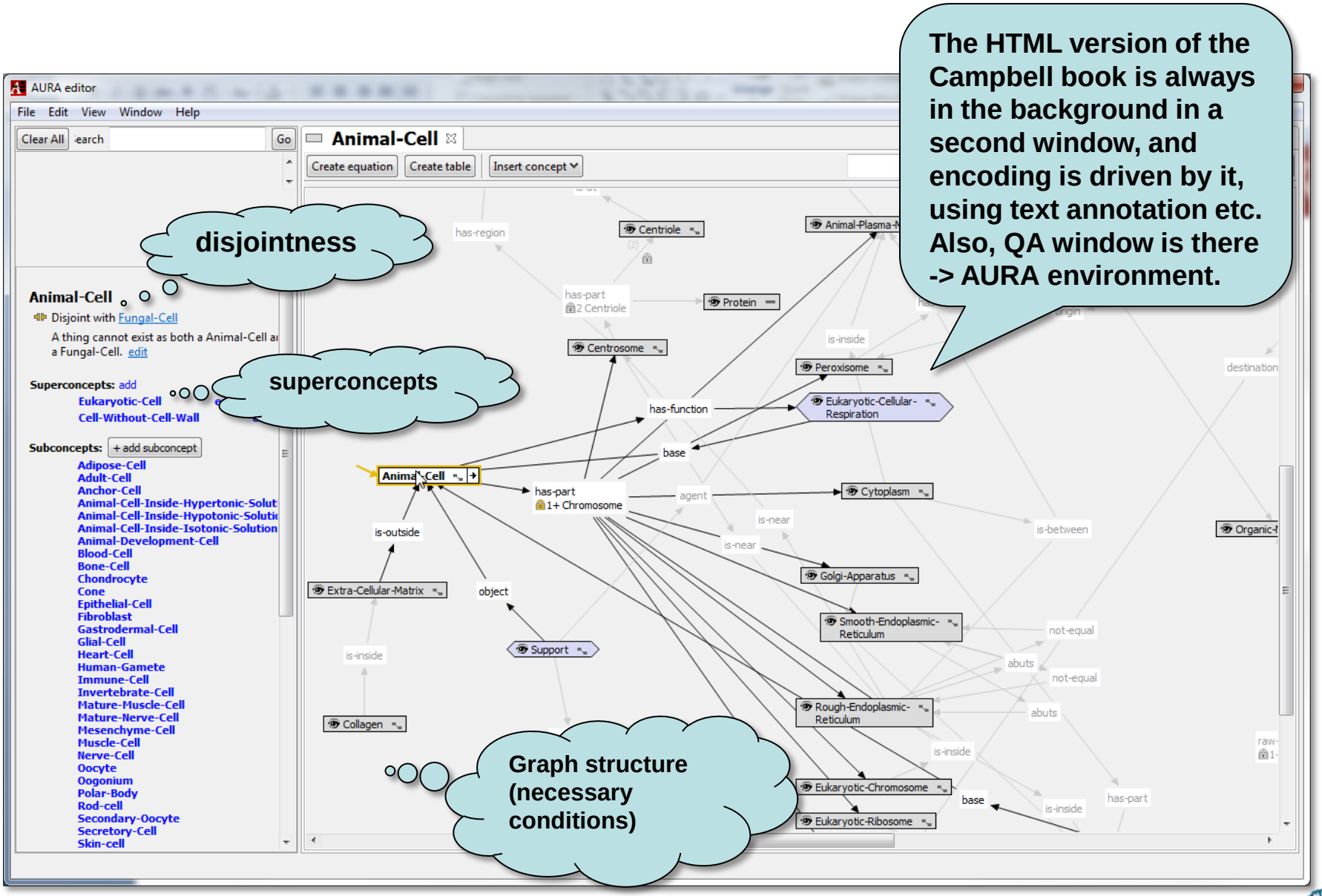

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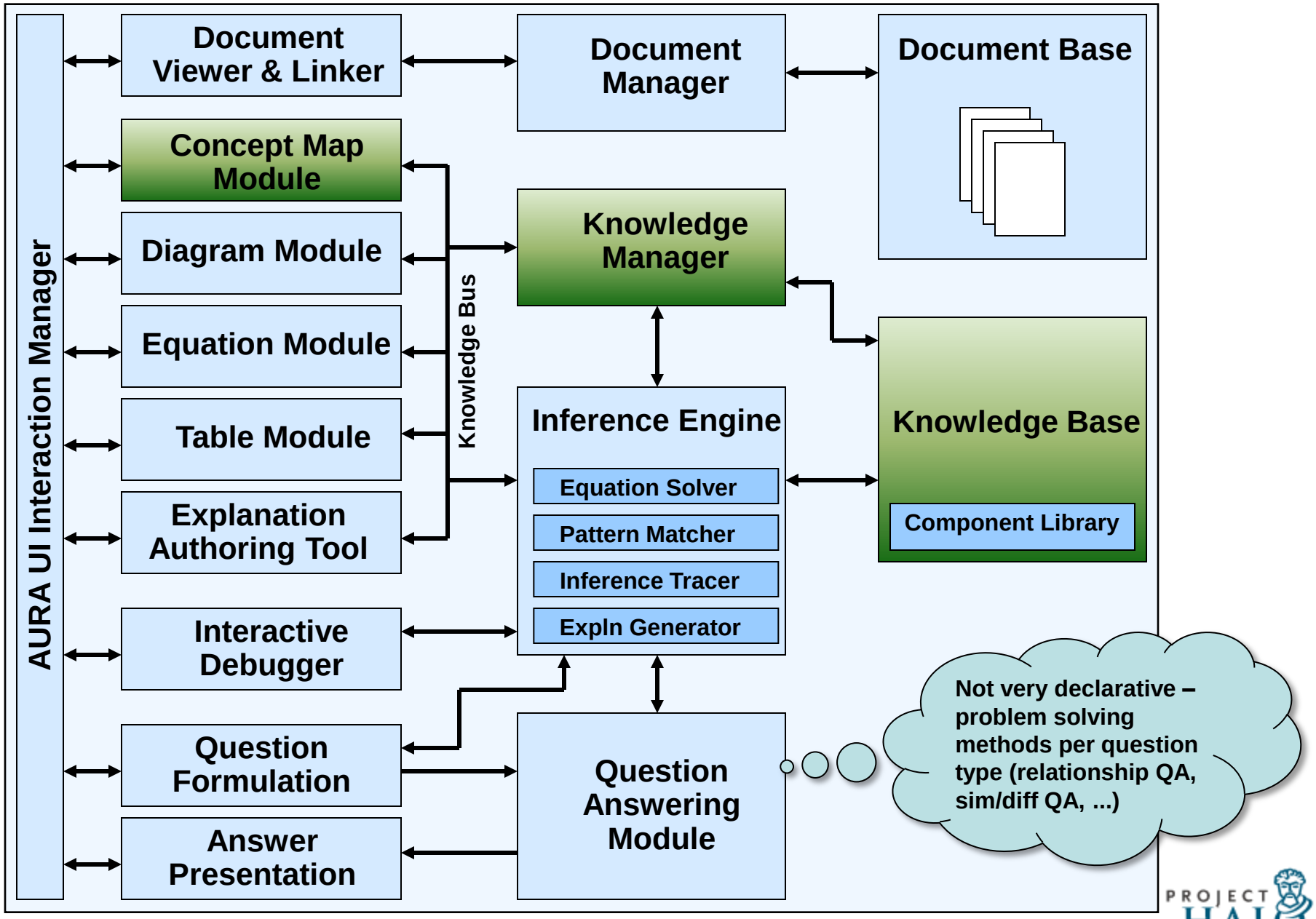
AURA Architecture



Knowledge Authoring Process

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1) Determining Relevance and Pre-Planning

Pre-planning	Determining relevance of sentences Status labeling per sentence: relevant, irrelevant

2) Reaching Consensus

Universal Truth authoring, Concept chosen	QA check

3) Encoding Planning

Group common UTs, Identify KR/KE issues, Identify already encoded, Write how to encode	Planning, QA check Status Labeling: Encoding Complete, KR Issue (closed)

4) Encoding

Encode, File KR JIRA issues	QA check Status Labeling: Encoding Complete, KE Issue (closed)

5) Key Term Review

KR evaluated by modeling expert and SME, Encoder makes changes	KR evaluated by modeling expert and SME QA check

6) Question-Based Testing

Use Minimal Test Suite, File reasoning JIRA issues, Encoder fills KB gaps	QA check with screenshots of 'Passing' comparison and relationship questions

Knowledge Authoring Process

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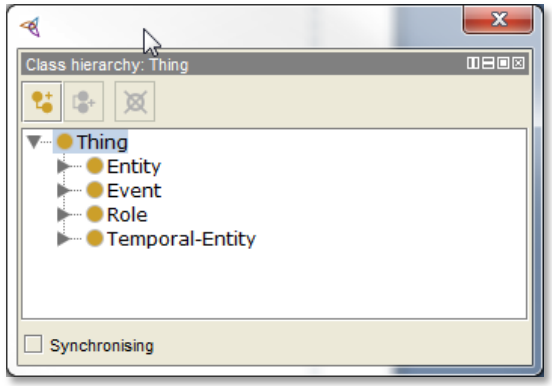
Expressive Means Used in AURA



- Classes (concepts) in a class hierarchy
  - multiple inheritance
  - top classes below Thing:
    Entity (Cell), Event (Diffusion), Role (Nutrient)
  - disjointness
  - necessary and sufficient conditions (“triggers”)
    GRAPH STRUCTURED DESCRIPTIONS (NOT TREES)
  - (tables, equations, descriptions / annotations, …)
- Relations and attributes (properties)
  - domain, range and (inverse) functionality
  - transitivity
  - converse
  - hierarchy
  - composition and qualified composition
  - qualified number restrictions (a là OWL2) in classes
- Upper Ontology Clib: arbitrary “First-Order Axioms” in KM
- Biologists can only model CMaps, superclasses, disjointness axioms, but cannot change CLib, nor define new relations

Illustration of Bio Concept and Clib Axiom in KM

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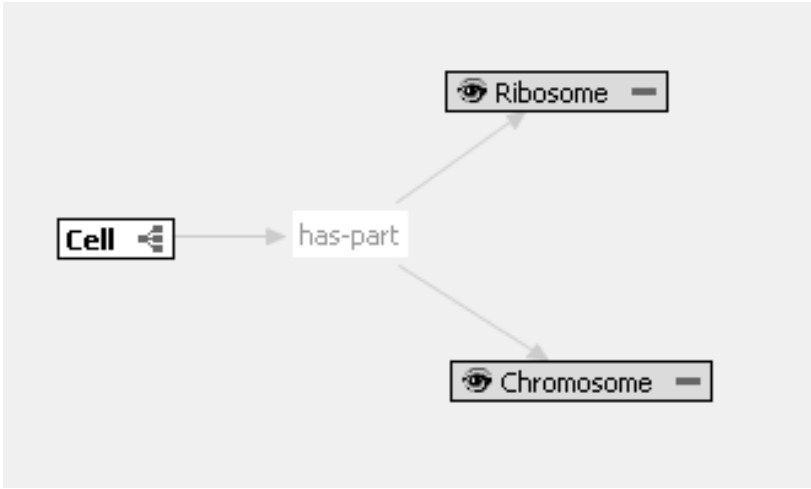
```
(_Cell1172 has
  (has-part (_Ribosome1180
             _Chromosome1179))
  (instance-of (Cell))
  (prototype-participants (_Ribosome1180
                           _Chromosome1179
                           _Cell1172))
  (prototype-participant-of (_Cell1172))
  (prototype-of (Cell))
  (prototype-scope (Cell)))

(_Ribosome1180 has
  (instance-of (Ribosome))
  (is-part-of (_Cell1172))
  (prototype-participant-of (_Cell1172)))

(_Chromosome1179 has
  (instance-of (Chromosome))
  (is-part-of (_Cell1172))
  (node-coordinate ((:pair 165 660)))
  (prototype-participant-of (_Cell1172)))
```

KM Prototype



KM First-Order Axiom

```
(Move has
       (superclasses    (Action)))

(every Move has
       (object ((a Spatial-Entity)
                (excluded-values
                       (the origin of Self)
                       (the destination of Self)
                       (the away-from of Self)
                       (the toward of Self)
                       (the path of Self)
                       (the site of Self)))))
```

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From KM to FOPL to <name your logic>

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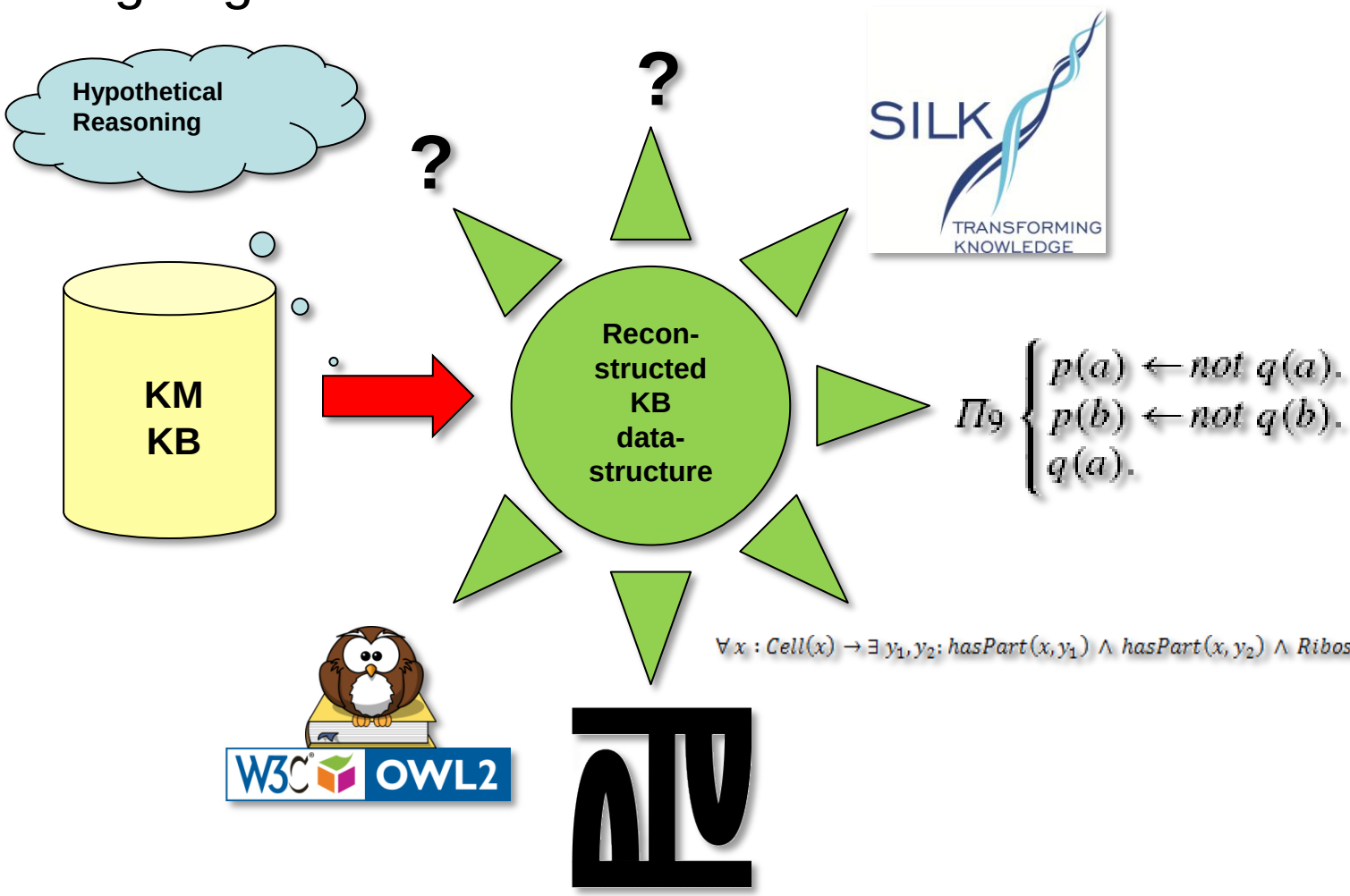
- The **logical reconstruction** of the KM KB turns out to be challenging, due to some unsound default reasoning going on there



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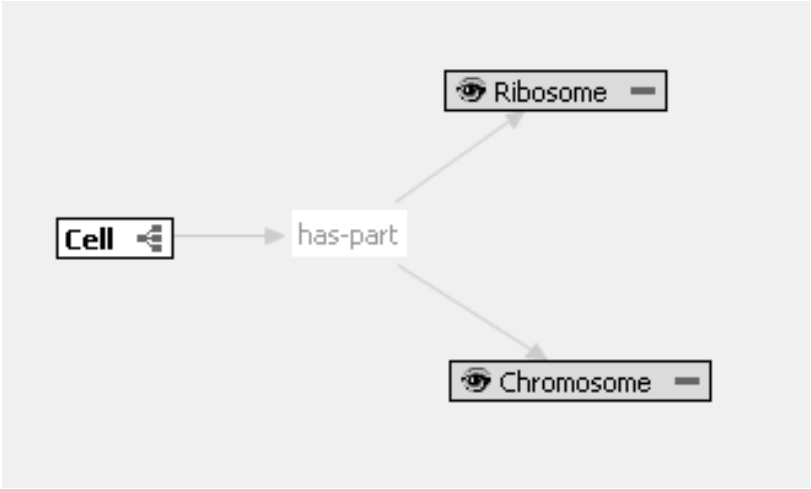
Reconstructed KB in FOPL

Every cell has a ribosome part and a chromosome part



$$\forall x : Cell(x) \rightarrow \exists y_1, y_2 : hasPart(x, y_1) \wedge hasPart(x, y_2) \wedge Ribosome(y_1) \wedge Chromosome(y_2)$$

- However, what we really need is this skolemized version, so that classes that refer to Cell can refer to its Ribosome and Chromosome by means of the Skolem functions:

$$\forall x : Cell(x) \rightarrow hasPart\left(x, f_{Cell}\#1(x)\right) \wedge hasPart\left(x, f_{Cell}\#2(x)\right) \wedge Ribosome\left(f_{Cell}\#1(x)\right) \wedge Chromosome\left(f_{Cell}\#2(x)\right)$$

Skolem Function Inheritance and Equality

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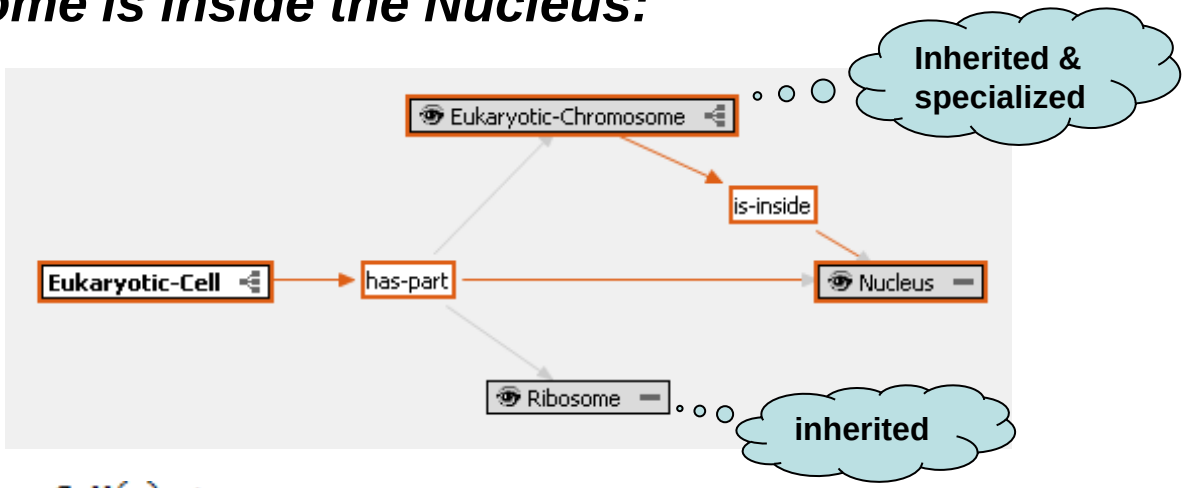
- ***Every Eukaryotic-Cell is a Cell***
- ***Every Eukaryotic-Cell has part a Eukaryotic-Chromosome, a Ribosome, and a Nucleus, such that the Eukaryotic-Chromosome is inside the Nucleus:***



$$\forall x : EukaryoticCell(x) \rightarrow Cell(x) \ \wedge$$
$$hasPart\left(x, f_{ECell}\#1(x)\right) \wedge hasPart\left(x, f_{ECell}\#2(x)\right) \wedge hasPart\left(x, f_{ECell}\#3(x)\right) \wedge$$
$$EukaryoticChromsome\left(f_{ECell}\#3(x)\right) \wedge Nucleus\left(f_{ECell}\#1(x)\right) \wedge Ribosome\left(f_{ECell}\#2(x)\right) \wedge$$
$$isInside\left(f_{ECell}\#3(x), f_{ECell}\#1(x)\right)$$
$$f_{ECell}\#3(x) = f_{Cell}\#2(x), \qquad f_{ECell}\#2(x) = f_{Cell}\#1(x)$$

Often, those equalities are NOT explicit in the KM KB,
but they need to be ***reconstructed*** by a special algorithm.

Also, the equalities can describe “node unifications”.

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TPTP Export Illustration

```
fof(a11860,axiom,(
  ! [X, Y] :
    ( ( has_part(X, Y) )
     =>
      ( tangible_entity(Y) ) ))).

fof(a11861,axiom,(
  ! [X, Y] :
    ( ( has_part(X, Y) )
     =>
      ( tangible_entity(X) ) ))).

fof(a11862,axiom,(
  ( ( has_part(X, Y)
    & has_part(Z, Y) )
   =>
    ( X=Z ) ))).

fof(a11863,axiom,(
  ! [X, Y] :
    ( ( has_part(X, Y) )
     =>
      ( has_structure(X, Y)
        & related_to(X, Y)
        & has_part_or_unit(X, Y)
        & is_part_of(Y, X) ) ))).

fof(a12942,axiom,(
  ! [X, Y, Z] :
    ( ( has_part_or_unit(X, Y)
      & element(Y, Z)
      & tangible_entity(X)
      & aggregate(Y)
      & tangible_entity(Z) )
     =>
      ( has_part_star(X, Z) ) ))).
```

```
fof(a13502,axiom,(
  ! [X] :
    ( ( cell(X) )
     =>
      ( original_name(X, "Cell")
        & description(X, "The basic unit from which living organisms
are made, consisting of an aqueous solution of organic molecules
enclosed by a membrane.  All cells arise from existing cells, usually
by a process of division into two.  (Alberts:ECB:G-3).")
        & class2words(X, "cell")
        & living_entity(X)
        & ribosome(fn_cell_1(X))
        & chromosome(fn_cell_2(X))
        & has_part(X, fn_cell_2(X))
        & has_part(X, fn_cell_1(X)) ) ))).



fof(a13504,axiom,(
  ! [X] :
    ( ( eukaryotic_cell(X) )
     =>
      ( original_name(X, "Eukaryotic-Cell")
        & class2words(X, "eukaryotic cell")
        & class2words(X, "eukaryotic-cell")
        & cell(X)
        & nucleus(fn_eukaryotic_cell_1(X))
        & ribosome(fn_eukaryotic_cell_2(X))
        & eukaryotic_chromosome(fn_eukaryotic_cell_3(X))
        & has_part(X, fn_eukaryotic_cell_1(X))
        & is_inside(fn_eukaryotic_cell_3(X), fn_eukaryotic_cell_1(X))
        & has_part(X, fn_eukaryotic_cell_3(X))
        & has_part(X, fn_eukaryotic_cell_2(X))
        & fn_eukaryotic_cell_3(X)=fn_cell_2(X)
        & fn_eukaryotic_cell_2(X)=fn_cell_1(X) ) ))).
```

KB Stats

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Regarding Class Axioms:

# Classes	# Relations	# Constants	Avg. # Skolems / Class	Avg. # Atoms / Necessary Condition	Avg. # Atoms / Sufficient Condition
6430	455	634	24	64	4

# Constant Typings	# Taxonomical Axioms	# Disjointness Axioms	# Equality Assertions	# Qualified Number Restrictions
714	6993	18616	108755	936

Regarding Relation Axioms:

# DRAs	# RRAs	# RHAs	# QRHAs	# IRAs	# 12NAs / # N21As	# TRANS + # GTRANS
449	447	13	39	212	10 / 132	431

Regarding Other Aspects:

# Cyclical Classes	# Cycles	Avg. Cycle Length	# Skolem Functions
1008	8604	41	73815

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Why Might It Be Challenging?

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- KB contains
  - graph structured descriptions
  - sufficient conditions
  - plenty of cycles
  - qualified number restrictions
  - transitive relations
  - almost arbitrary composition axioms of the form
    $\forall x, y, z : R(x,y) \wedge S(y,z) \Rightarrow T(x,z)$

-> neither tree- nor finite model property,
reasoning with the full KB is likely to be undecidable
(KM doesn't really do logical reasoning with it)

- Subsets / fragments of it might be decidable (prefix classes)
- Description logic / OWL reasoners have problems even with small fragments of it
- It may contain yet undiscovered inconsistencies

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Why Did We Submit it to KINAR?

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- Among the translation we have, the FOPL translation is the most truthful / complete one (OWL etc. is lossy)
  - we want to apply FOPL reasoners
  - we want to be more declarative
  - we want to engage with the research community on first-order reasoning
  - we want to promote the KB, which is a valuable asset
- What are simple reasoning tasks we care about?
  - check consistency
    - we have successfully used Protégé 4.2 and Fact++ to debug simple inconsistencies resulting from interactions between disjointness, domain and range restrictions, and taxonomic axioms
  - find implicit subclasses
  - computation of (inferred) slot fillers and conjunctive query answering
- More complex reasoning tasks for QA
  - finding relationships
  - sim/diff (sim is similar to computation of a LCS in DLs)
  - …

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http://www.ai.sri.com/halo/halobook2010/exported-kb/biokb.html

Thank you!

AURA Team in 2011

Points for the Discussion

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- Which TPTP reasoners should we start with?
- The KB contains logical inconsistencies
  - para consistent reasoning?
- How can we define interesting reasoning problems more declaratively
  - e.g., relationship question answering
  - some require unsound reasoning
    (e.g., going to subclasses and looking up information there)
  - those unsound inferences are desired by the Biologists
- How can we leverage and promote the KB?
  - what other KB applications might be interesting besides reasoner benchmarks

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Backup Material – One More Video

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Optional – Simple Demo

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