AURA

Automatic Strengthening of Graph-Structured Knowledge Bases

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PROJECT HALO

Acknowledgment

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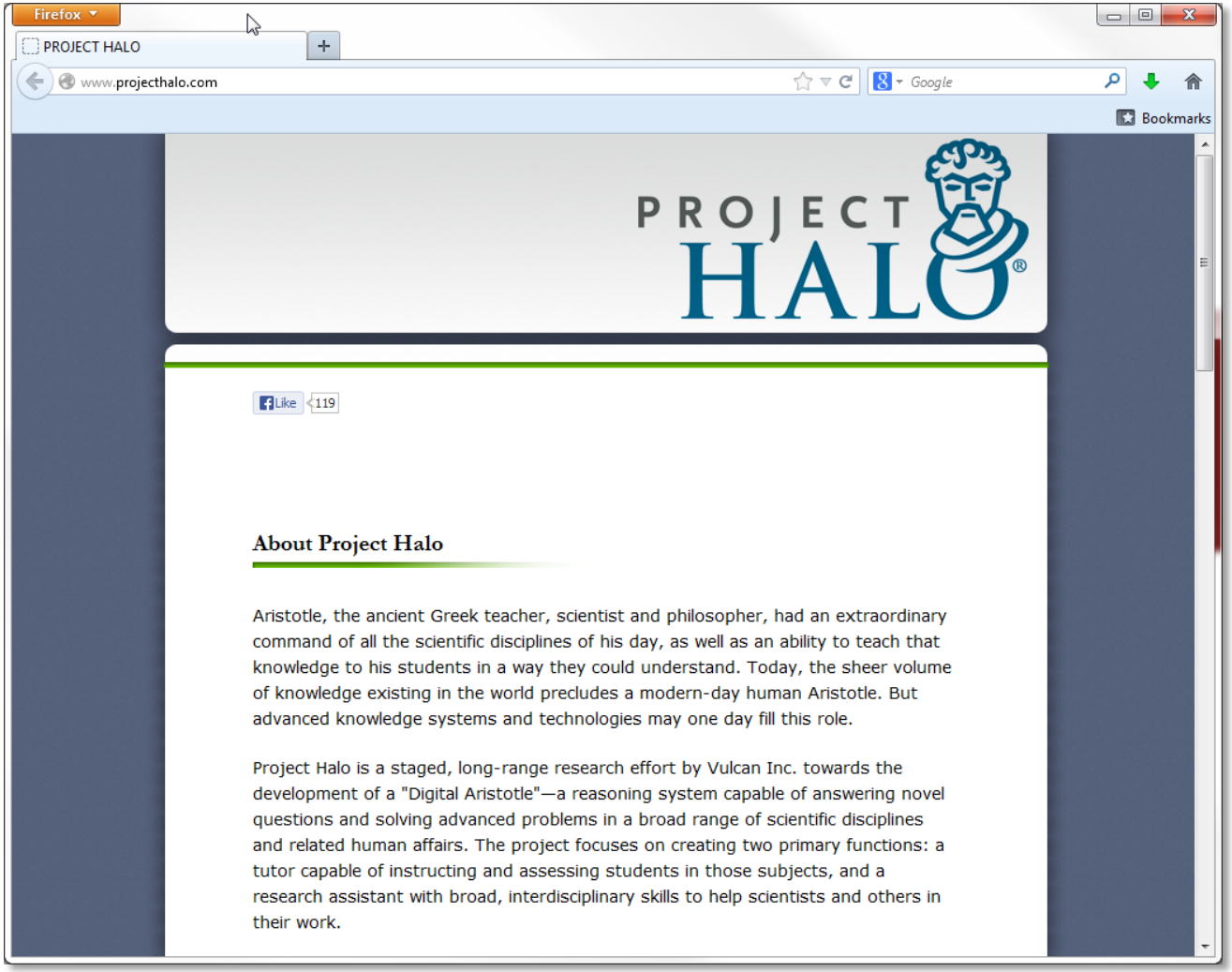
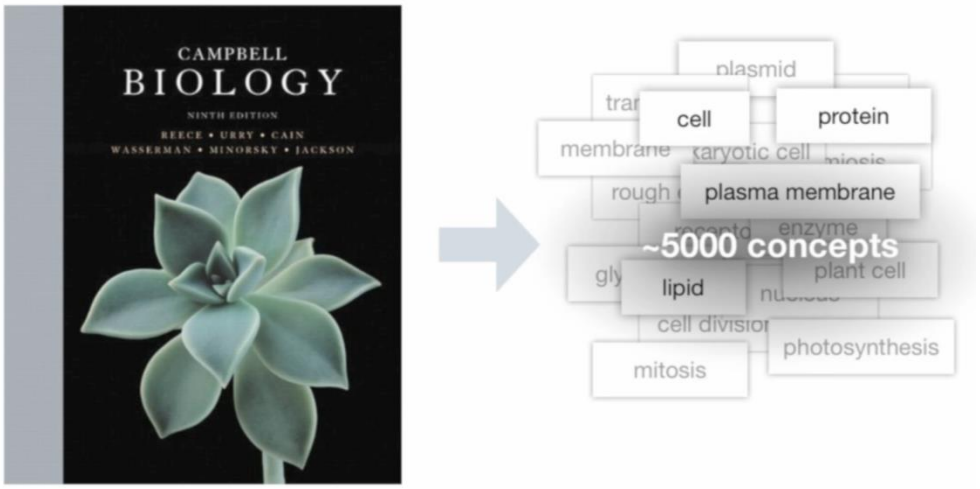
  http://www.vulcan.com
  http://www.projecthalo.com



The Biology KB of the AURA Project



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

- The KB is used as the basis of a smart question answering text book called **Inquire Biology** – questions are answered by AURA using forms of deductive reasoning

- The KB has non-trivial graph structure and is big (5662 concepts)

- 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)

Graphical Modeling in AURA

S1 Every *Cell* has part a *Ribosome* and a *Chromosome*.

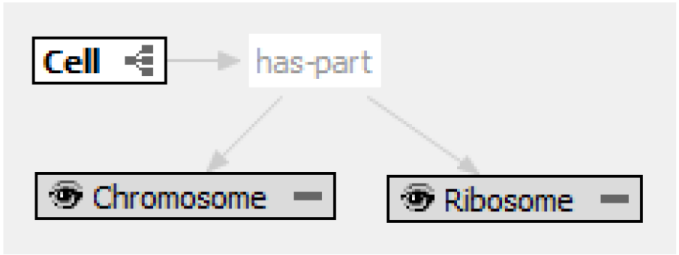
S2 Every *EukaryoticCell* is a *Cell*.

S3 Every *EukaryoticCell* has part a *EukaryoticRibosome*, a *EukaryoticChromosome*, a *Nucleus*, such that the *EukaryoticChromosome* is inside the *Nucleus*.

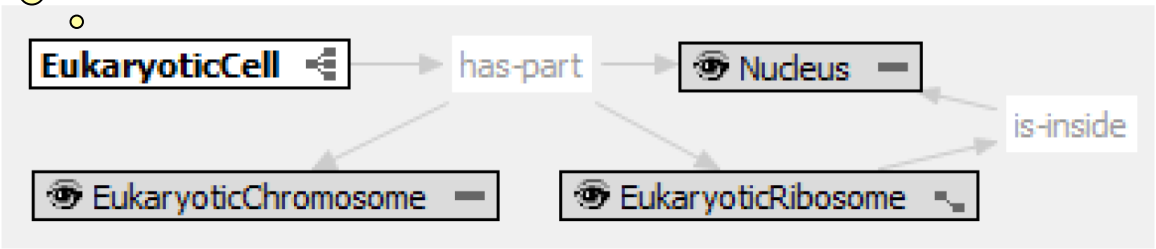
S4 Every *EukaryoticRibosome* is a *Ribosome*.

S5 Every *EukaryoticChromosome* is a *Chromosome*.

is-a edge implicit



Same Ribosome that S1 is referring to? "Co-Reference Resolution"



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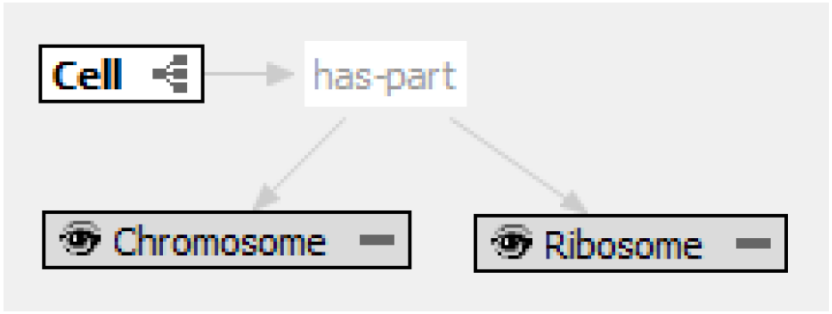
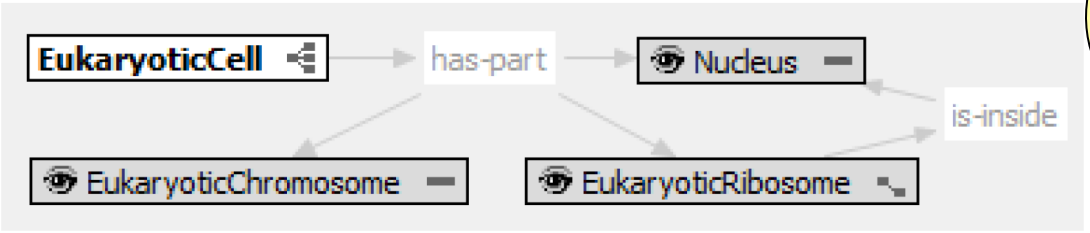
“Underspecified” KBs

AURA





Q: Ambiguity - is that the Ribosome inherited from Cell super class?

A: Maybe – there are models in which this is the case, and models in which this is not the case.

=> “underspecified KB”

S1 $\forall x : Cell(x) \Rightarrow \exists x_1, x_2 : hasPart(x, x_1), Ribosome(x_1), hasPart(x, x_2), Chromosome(x_2)$

S23 $\forall x : EukaryoticCell(x) \Rightarrow \exists x_3, x_4, x_5 : Cell(x), hasPart(x, x_3), Euk.Ribosome(x_3), hasPart(x, x_4), Euk.Chromosome(x_4), hasPart(x, x_5), Nucleus(x_5), inside(x_4, x_5)$

S4 $\forall x : Euk.Ribosome(x) \Rightarrow Ribosome(x)$

S5 $\forall x : Euk.Chromosome(x) \Rightarrow Chromosome(x)$

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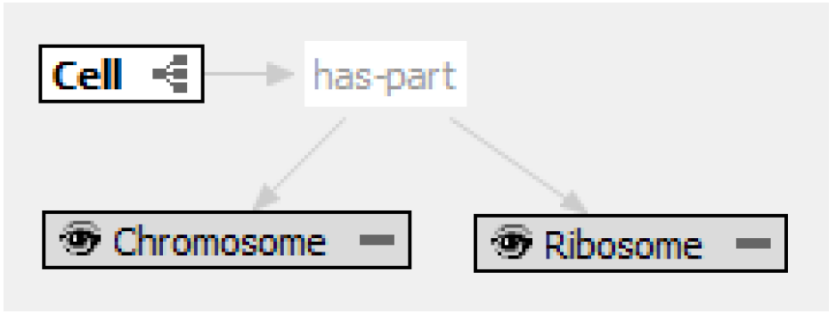
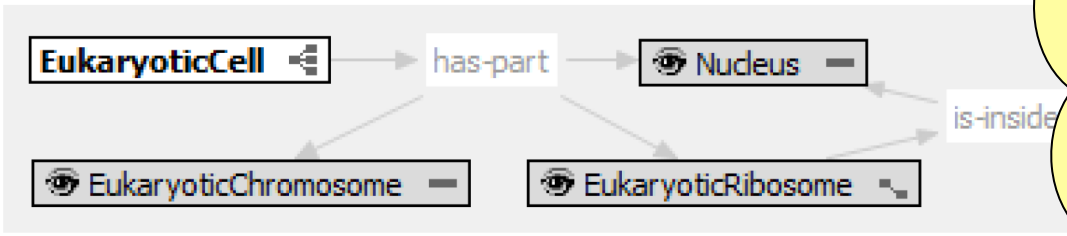
Strengthened KBs





Q: Ambiguity - is that the Ribosome inherited from Cell super class?

A: yes! Due to "Skolem function inheritance" and equality, this holds in ALL models of the KB -> answer is entailed
=> "strengthened KB"

S1 ' $\forall x : Cell(x) \Rightarrow$
$hasPart(x, f_1(x)), Ribosome(f_1(x)),$
$hasPart(x, f_2(x)), Chromosome(f_2(x)),$

S23' $\forall x : EukaryoticCell(x) \Rightarrow Cell(x),$
$hasPart(x, f_3(x)), Euk.Ribosome(f_3(x)),$
$hasPart(x, f_4(x)), Euk.Chromosome(f_4(x)),$
$hasPart(x, f_5(x)), Nucleus(f_5(x)),$
$inside(f_4(x), f_5(x))),$
$f_3(x) = f_1(x), f_4(x) = f_2(x)$

Why do we care for strengthened KBs?

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- **More entailments** (stronger KB / more deductive power)
- **Reduction of modeling effort** - suppose we extended Cell as follows:

In a Cell, every Ribosome is inside (a) Cytosol

S1b $\forall x : Cell(x) \Rightarrow \exists x_1, x_2, x_6 :$
$hasPart(x, x_1), Ribosome(x_1),$
$hasPart(x, x_2), Chromosome(x_2),$
$inside(x_1, x_6), Cytosol(x_6)$

underspecified

S1b' $\forall x : Cell(x) \Rightarrow$
$hasPart(x, f_1(x)), Ribosome(f_1(x)),$
$hasPart(x, f_2(x)), Chromosome(f_2(x)),$
$inside(f_1(x), f_0(x)), Cytosol(f_0(x))$

strengthened

only with **S1b'** can we deduce that this also holds for ***the*** EukaryoticRibosome in EukaryoticCell

- More entailed ("inherited") information – *hasPart(x, y1)* atom in **S23** is entailed from **{ S1b', S2 }**, but not from **{ S1b, S2 }**
- **Reduces KB size,** as entailed atoms are redundant
- **Provenance** ("from where is an atom inherited") is important for the modelers (Biologists in our case)

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This Work…

… presents an algorithm to construct a strengthened KB from an underspecified KB (**GSKB strengthening algorithm**)

S1 $\forall x : Cell(x) \Rightarrow \exists x_1, x_2 :$
$hasPart(x, x_1), Ribosome(x_1),$
$hasPart(x, x_2), Chromosome(x_2)$

S23 $\forall x : EukaryoticCell(x) \Rightarrow \exists x_3, x_4, x_5 : Cell(x),$
$hasPart(x, x_3), Euk.Ribosome(x_3),$
$hasPart(x, x_4), Euk.Chromosome(x_4),$
$hasPart(x, x_5), Nucleus(x_5), inside(x_4, x_5)$

S4 $\forall x : Euk.Ribosome(x) \Rightarrow Ribosome(x)$

S5 $\forall x : Euk.Chromosome(x) \Rightarrow Chromosome(x)$

S1b' $\forall x : Cell(x) \Rightarrow$
$hasPart(x, f_1(x)), Ribosome(f_1(x)),$
$hasPart(x, f_2(x)), Chromosome(f_2(x)),$
$inside(f_1(x), f_0(x)), Cytosol(f_0(x))$

S23' $\forall x : EukaryoticCell(x) \Rightarrow Cell(x),$
$hasPart(x, f_3(x)), Euk.Ribosome(f_3(x)),$
$hasPart(x, f_4(x)), Euk.Chromosome(f_4(x)),$
$hasPart(x, f_5(x)), Nucleus(f_5(x)),$
$inside(f_4(x), f_5(x))),$
$f_3(x) = f_1(x), f_4(x) = f_2(x)$

S4 $\forall x : Euk.Ribosome(x) \Rightarrow Ribosome(x)$

S5 $\forall x : Euk.Chromosome(x) \Rightarrow Chromosome(x)$

Note that this algorithm is not purely deductive by nature – it requires unsound reasoning namely hypothesization of equality atoms, NOT only Skolemization!

There may be more than one strengthened KB for a given underspecified KB.

Also note that the is-a relations and hence the taxonomy are given here. This is NOT a subsumption checking / classification problem!

Description Logics don't help for a variety of reasons (graph structures, unsound / hypothetical reasoning required, etc.)

The GSKB Strengthening Algorithm

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Input: KB $\sum$ must be "admissible"
(no cycles -> finite model property)

Output: strengthened KB $\sum'$

1. **Skolemize KB $\sum$ -> KB $\sum_S$**
2. **Construct minimal Herbrand model of $\sum_S$: $(\Delta_{\mathcal{H}}, \cdot^{\mathcal{I}_{\mathcal{H}}})$**
3. **Use $(\Delta_{\mathcal{H}}, \cdot^{\mathcal{I}_{\mathcal{H}}})$ to construct a so-called preferred model of $\sum$: $(\Delta_{\mathcal{A}}, \cdot^{\mathcal{I}_{\mathcal{A}}})$**

   This step is non-deterministic, and it requires guessing of equalities. $\Delta_{\mathcal{A}} = \Delta_{\mathcal{H}} \backslash =$ is the quotient set of the Herbrand universe under those "guessed" equalities (=).
4. **Use $(\Delta_{\mathcal{A}}, \cdot^{\mathcal{I}_{\mathcal{A}}})$ and $\sum_S$ to construct $\sum'$**

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Preferred Models – Intuition

AURA

S1 $\forall x : Cell(x) \Rightarrow \exists x_1, x_2 :$
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$hasPart(x, x_2), Chromosome(x_2)$

S23 $\forall x : EukaryoticCell(x) \Rightarrow \exists x_3, x_4, x_5 : Cell(x),$
$hasPart(x, x_3), Euk.Ribosome(x_3),$
$hasPart(x, x_4), Euk.Chromosome(x_4),$
$hasPart(x, x_5), Nucleus(x_5), inside(x_4, x_5)$

S4 $\forall x : Euk.Ribosome(x) \Rightarrow Ribosome(x)$

S5 $\forall x : Euk.Chromosome(x) \Rightarrow Chromosome(x)$

1. **In a preferred model, the concept models have the form of non-overlapping connected graphs, one node per variable**

2. **For every concept, there is at least one unique model which instantiates only this concept and its superconcepts, no other concepts - e.g., there is a model of Cell which is NOT also a model of EukaryoticCell**

3. **In those concept models, the extensions of (possibly singleton) conjunctions are minimized – i.e., there is no admissible model which has a smaller extension for that conjunction. This forces us to identify successors "inherited from superclasses" with "locally specialized" versions**

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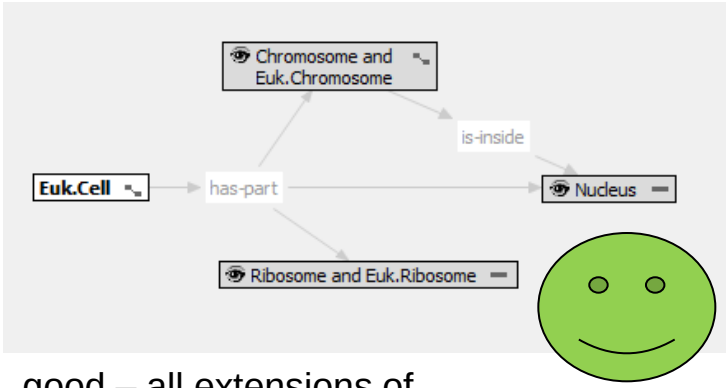
Models and Preferred Models

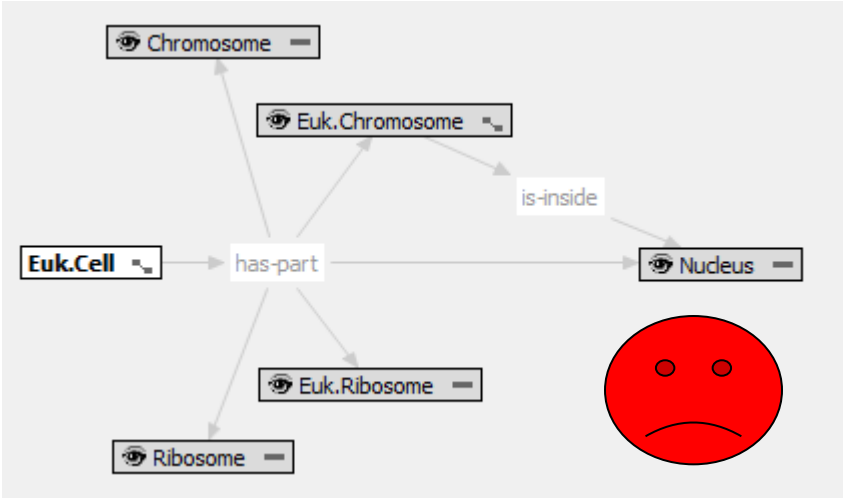
AURA

1



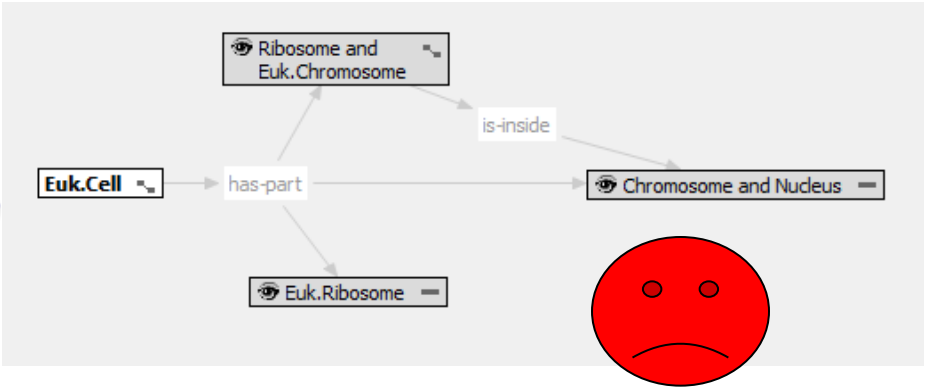
good – all extensions of (singleton) conjunctions minimal!
This is a preferred model !

2



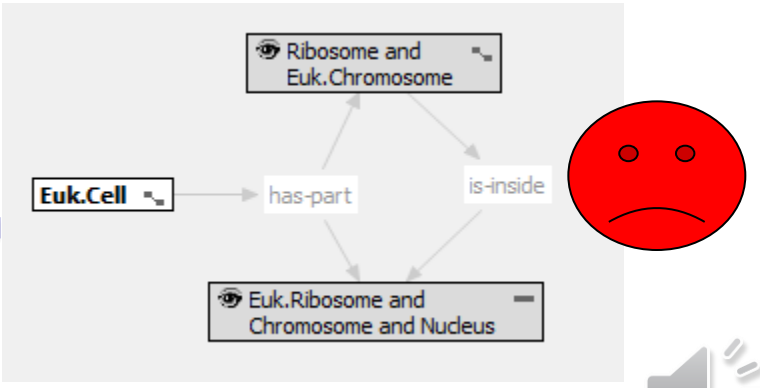
… too many Ribosomes and Chromsomes…

3



… non-empty extension of conjunction **Ribosome /\ Euk.Chromosome** (there are smaller models in which this conjunction is empty!)

4



… even this is a model, but similar problems: non-empty conjunctions without necessity

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Constructing a Preferred Model

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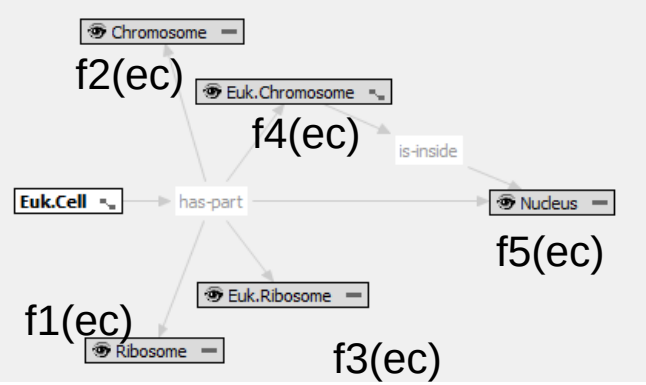
- **Start with the Herbrand model – this will satisfy conditions 1 and 2 of the admissible model**



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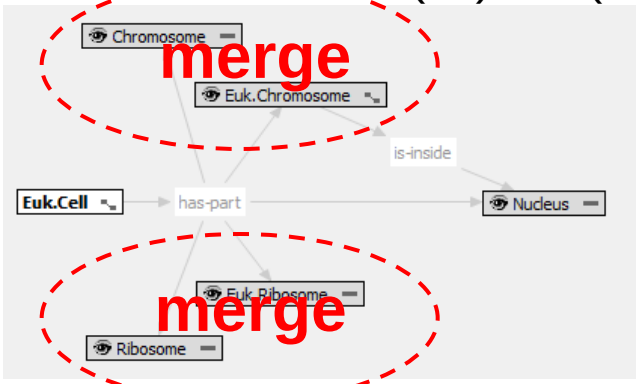
$hasPart(x, f_5(x)), Nucleus(f_5(x)),$
$inside(f_4(x), f_5(x))),$

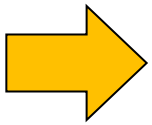
- **Identify and merge compatible successors using a non-deterministic merge rule, apply it exhaustively, and record in equality relation "="**

f2(ec) = f4(ec)

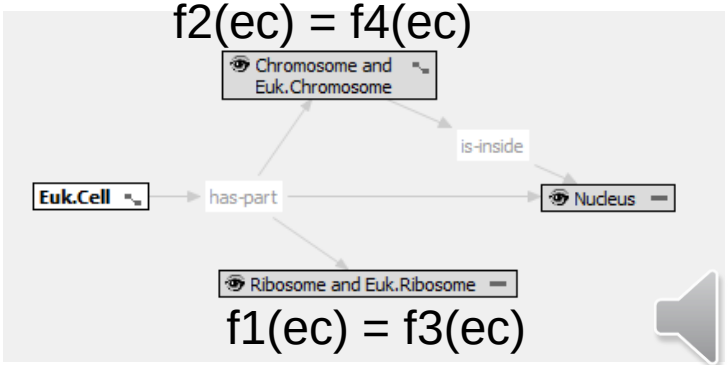


f1(ec) = f3(ec)

$\Delta_{\mathcal{H}}$



f2(ec) = f4(ec)



f1(ec) = f3(ec)

$\Delta_{\mathcal{A}} = \Delta_{\mathcal{H}} \setminus =$

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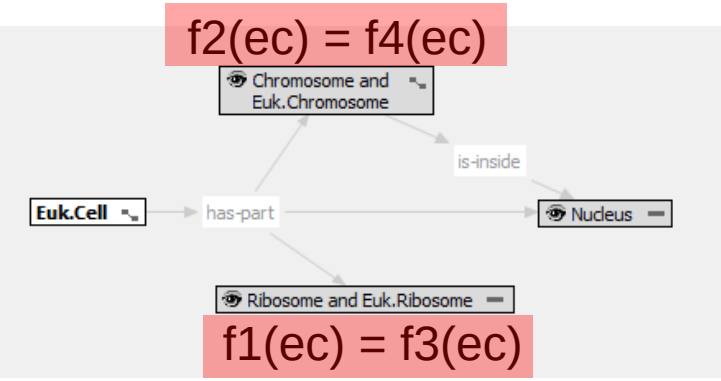
Constructing a Strengthened KB

- **For construction of the preferred model, the merge rule has been applied exhaustively**
  - **this has maximized the congruence / equality relation "="**

- **Now we simply add the equalities in "=" as equality atoms to the skolemized KB**



$$\Delta_{\mathcal{A}} = \Delta_{\mathcal{H}} \setminus =$$

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- $\sum'$ **is a strengthened KB and has preferred models**

Experiments

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- We have a working KB strengthening algorithm which was applied to the AURA KB: it identified 82% of the 141,909 atoms as inherited and hypothesized 22,667 equality atoms. Runtime: 15 hours
- The algorithm works differently than described here, but the presented model-theoretic framework is a first step towards a logical formal reconstruction of the algorithm
- The native KR&R language of AURA is “Knowledge Machine” (KM)
  - the exploited KM representation does not support arbitrary equality atoms, hence this algorithm
- The actual implemented algorithm can handle additional expressive means, not yet addressed by the formal reconstruction (future work)
- The strengthened KB is also the basis for the AURA KB exports which are available for download!

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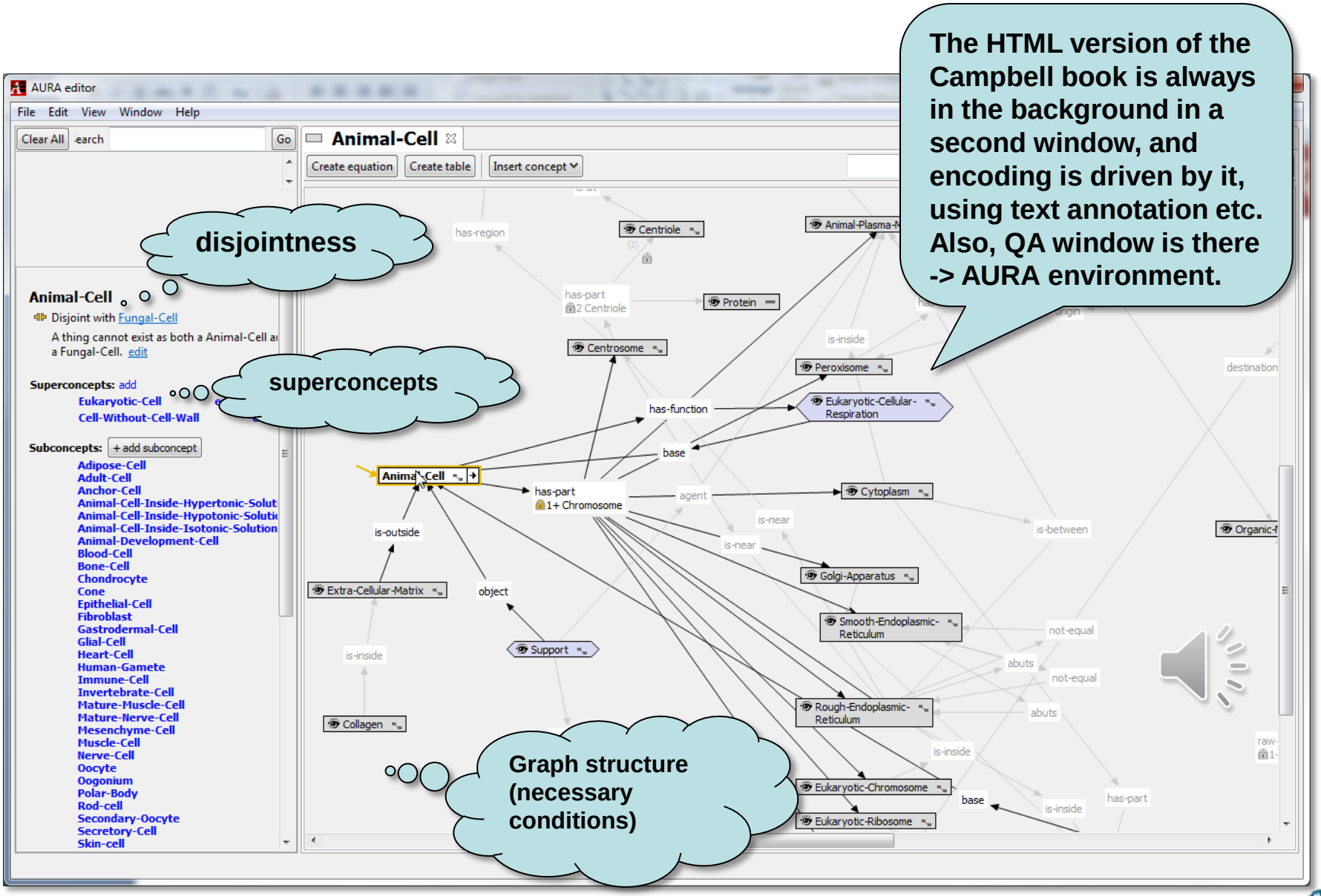
AURA Graphical Knowledge Editor

AURA



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AURA KB Stats (LATEST)

AURA

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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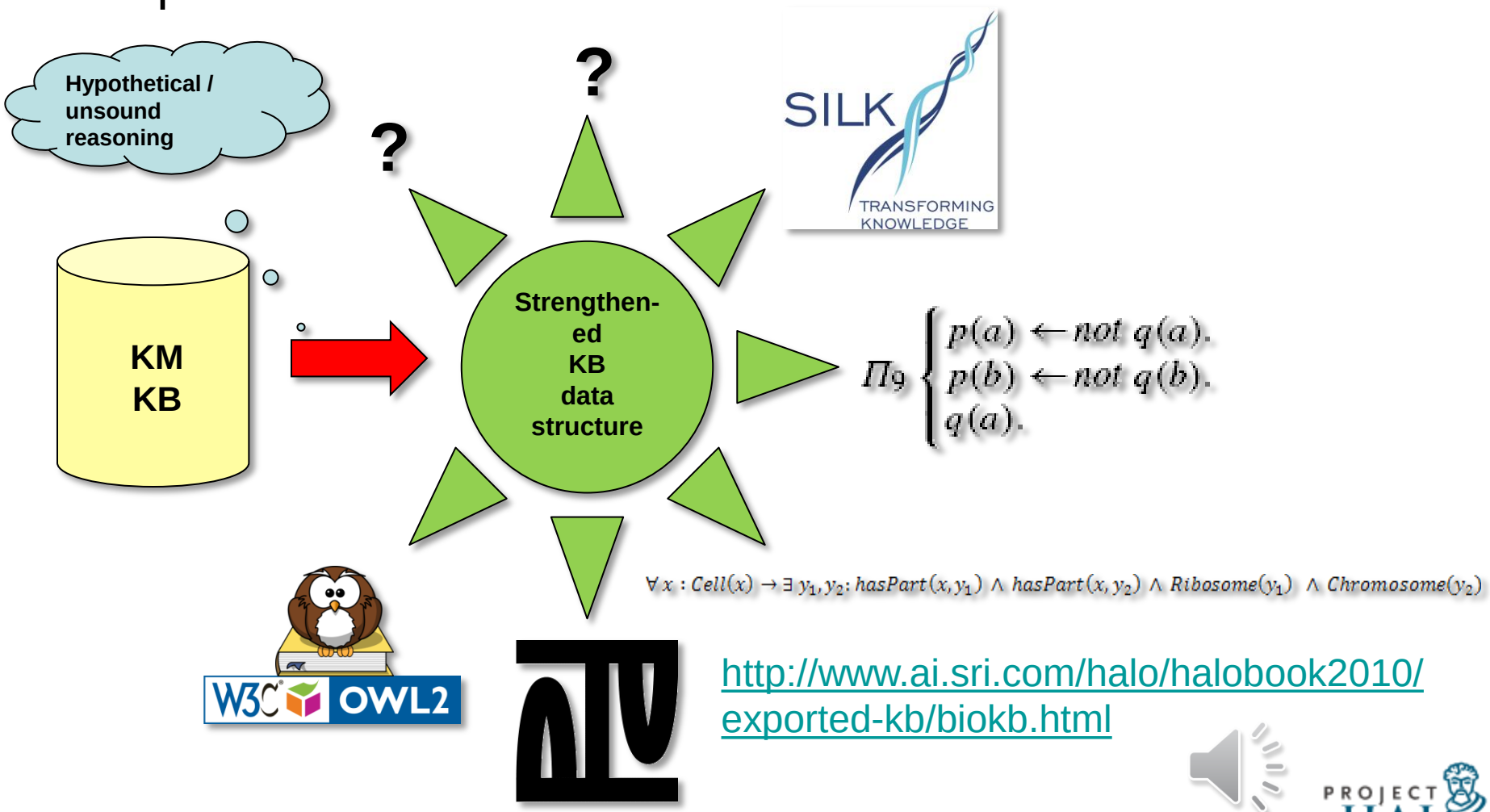
The Strengthened KB and AURA Exports

AURA

From the underlying KM representation, we are constructing the strengthened KB, which then gets exported into various standard formats



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

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Conclusion

AURA

- Strengthened GSKBs are important for a variety of reasons
  - to maximize entailed information / deductive power
  - to reduce KB size
  - to show correct provenance of atoms (inherited? local?) to KB authors
- Authoring strengthened KBs can be tedious or impossible (if the input is underspecified in the first place), hence an automatic strengthening algorithm is required
  - this is an unsound / hypothetical reasoning process which requires guessing of equalities
- We have presented first steps towards a formalization & logical reconstruction of an algorithm which solved an important application problem in the AURA project
  - our formalization is model-theoretic in nature and presents and exploits a novel class of preferred models
- As a by-product of these efforts, the AURA KB can now be exported into standard formats and KB_Bio_101 is available for download

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

Thank you!

AURA Team in 2011