Integrating text-mining efforts for pathway curation requires output standards.

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Introduction

Pathway Curation

Pathway Loom demo

Text mining

Text mining standard

How to expose text-mining results?

- Nifty website?

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- Sentences with "gold nuggets"?

How to expose text-mining results?

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- Sentences with "gold nuggets"?
- Precision/Recall

How to expose text-mining results?

- Nifty website?
- Sentences with "gold nuggets"?
- Precision/Recall
- SOAP
- REST
- csv/tsv
- Unix pipes (ie: cat textfile — makelist.sh — sort — uniq -c)

Finding novel pathway parts on a pathway (1)

OMICS A Journal of Integrative Biology
Volume 13, Number 5, 2009

DOI: 10.1089/omi.2009.0029

Original Article

Pathway Enrichment Based on Text Mining and Its Validation on Carotenoid and Vitamin A Metabolism

Andra Waagmeester,[1,2,3] Piotr Pezik,[1] Susan Coort,[3] Franck Tourniaire,[4] Chris Evelo,[3] and Dietrich Rebholz-Schuhmann[1]

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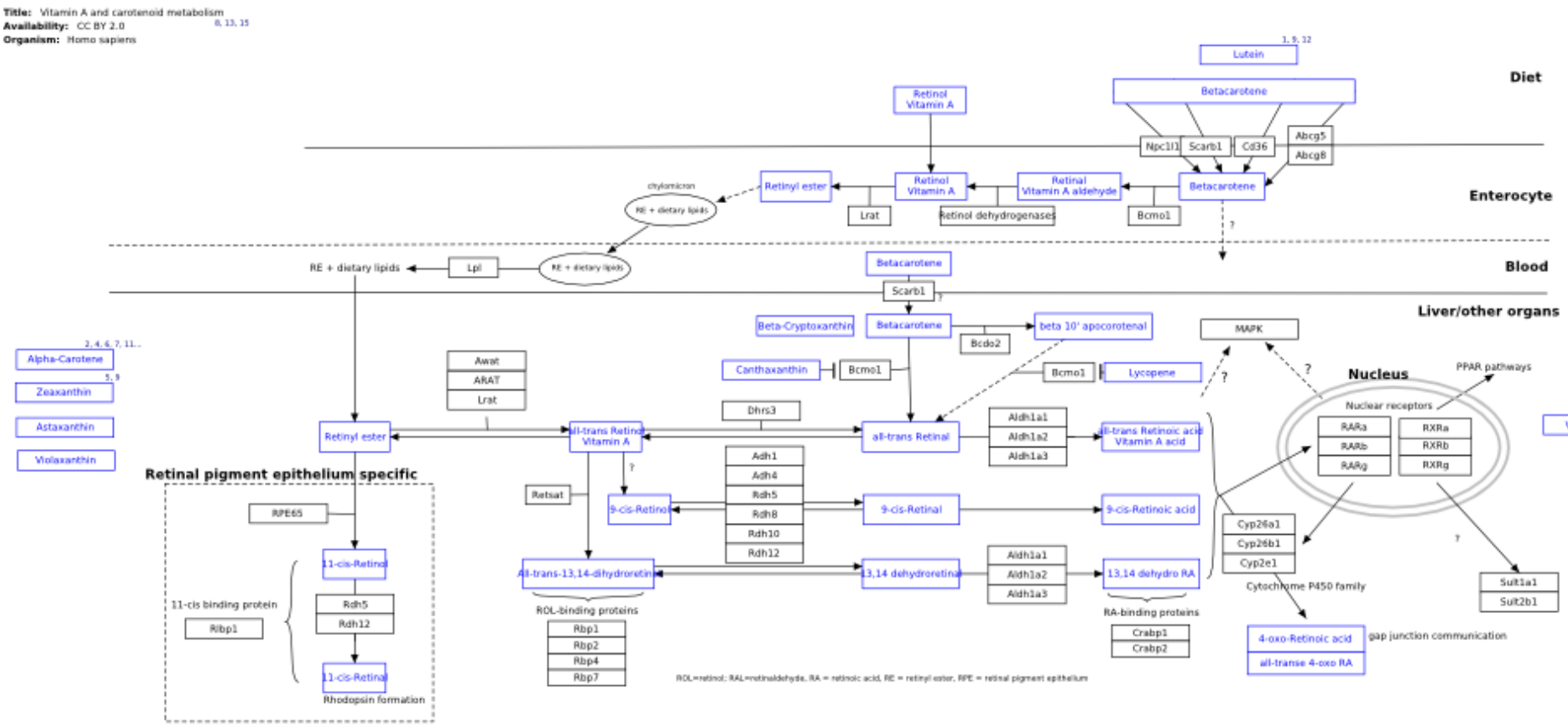
Finding novel pathway parts on a pathway (2)



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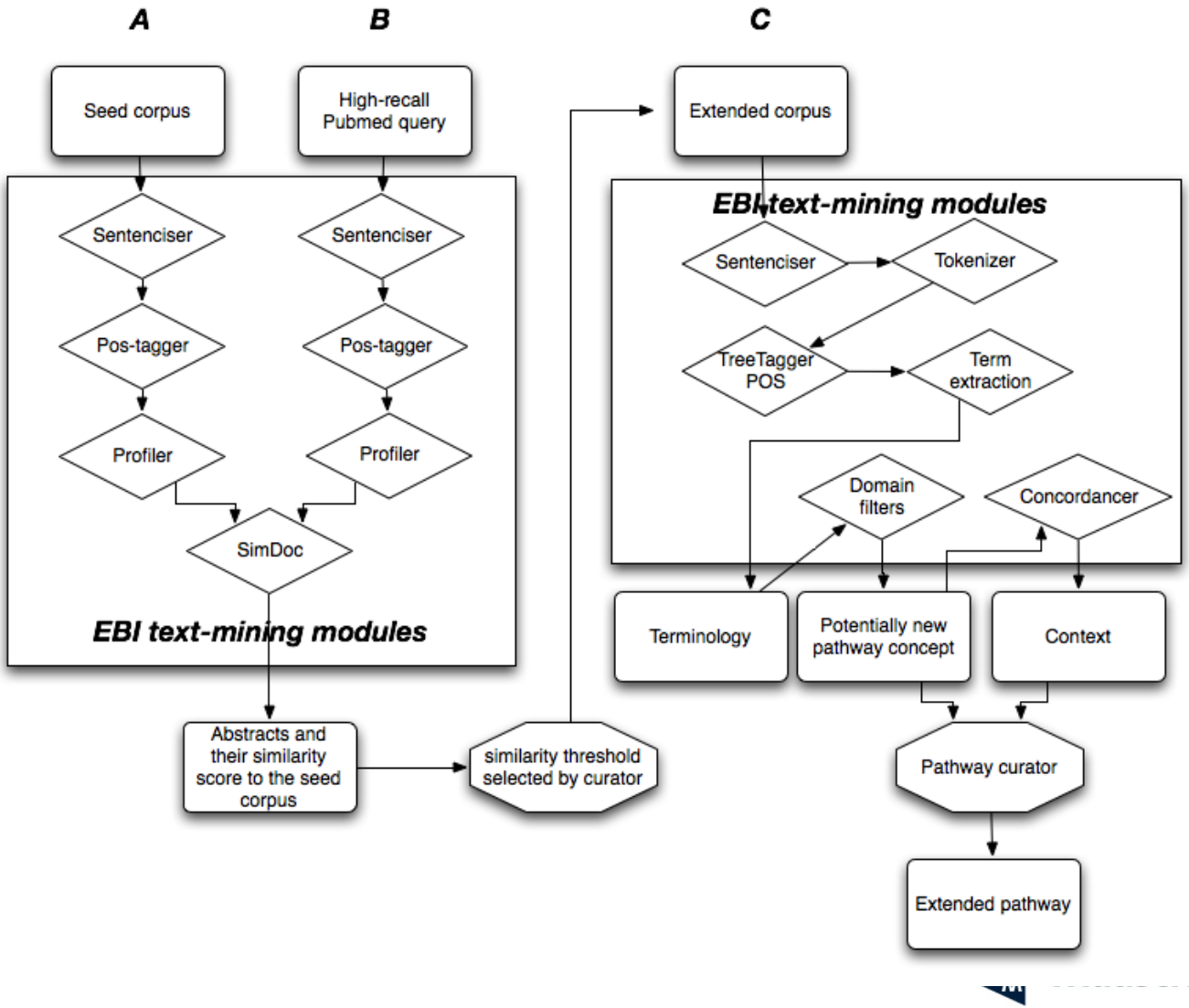
Finding novel pathway parts on a carotenoid pathways (3)



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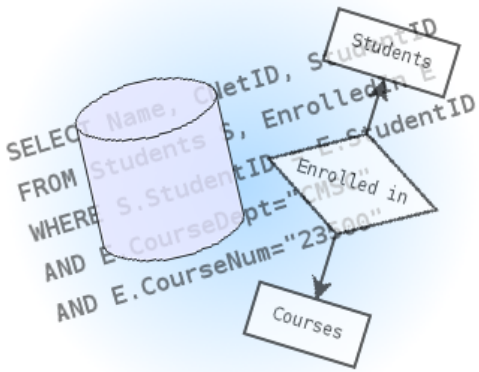
Finding novel pathway parts on a carotenoid pathways (4)

We were able to retrieve 13 novel pathway parts from Pubmed abstracts:

- Vitamin D3
- ADH3
- alpha-carotene
- astaxantin
- beta-cryptoxanthin
- Canthaxanthin
- lutein
- lycopene
- zeaxanthin
- PEPCK
- cryptoxanthin
- triglyceride
- lipase

Pathway curation

Knowledge is hidden in:



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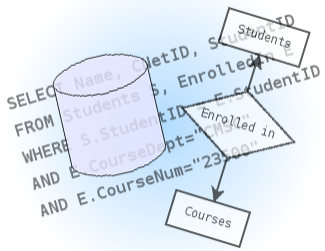
Computers

× Can't listen



√ Can Query

× Can't read

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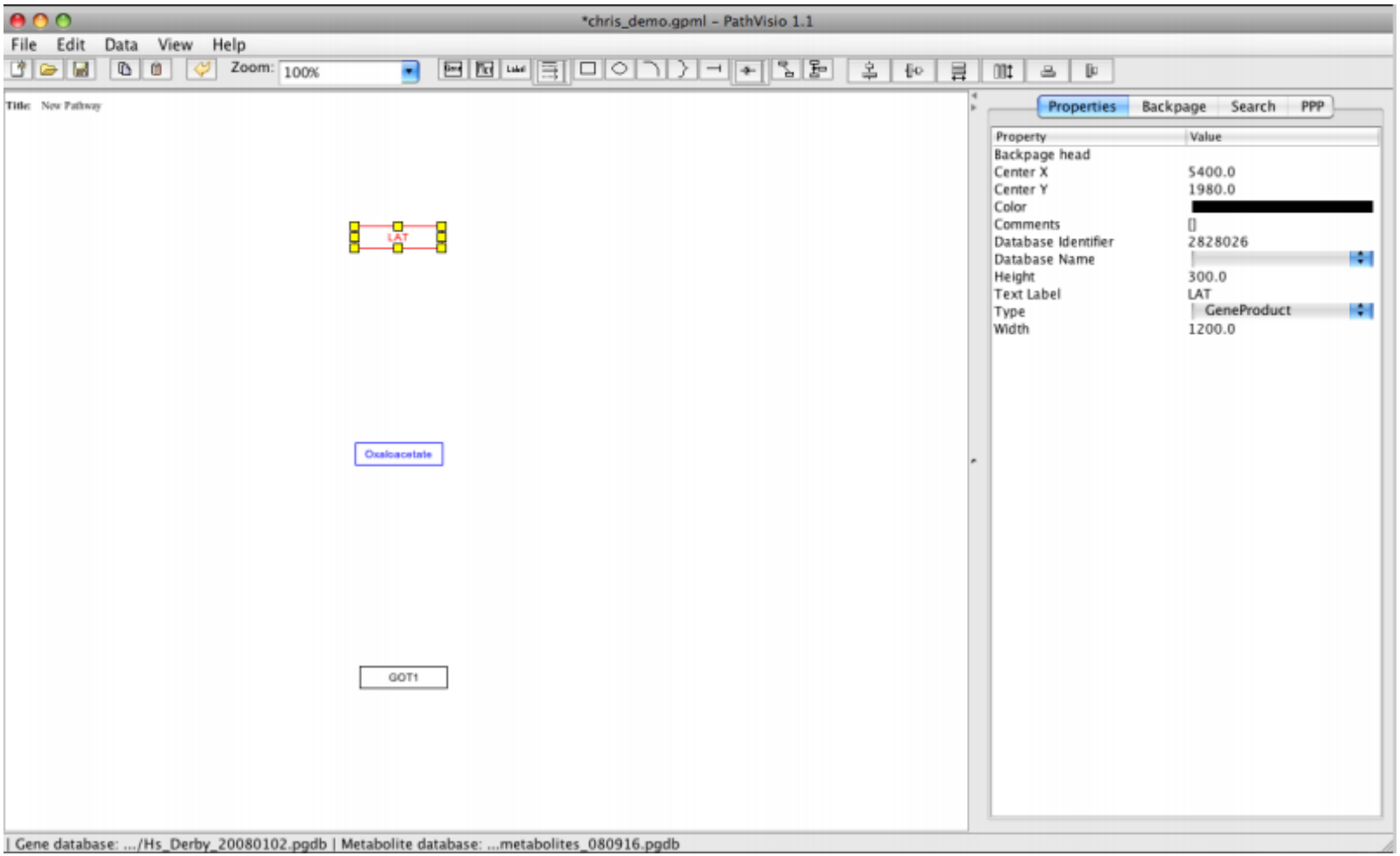
Pathway Loom demo (1)



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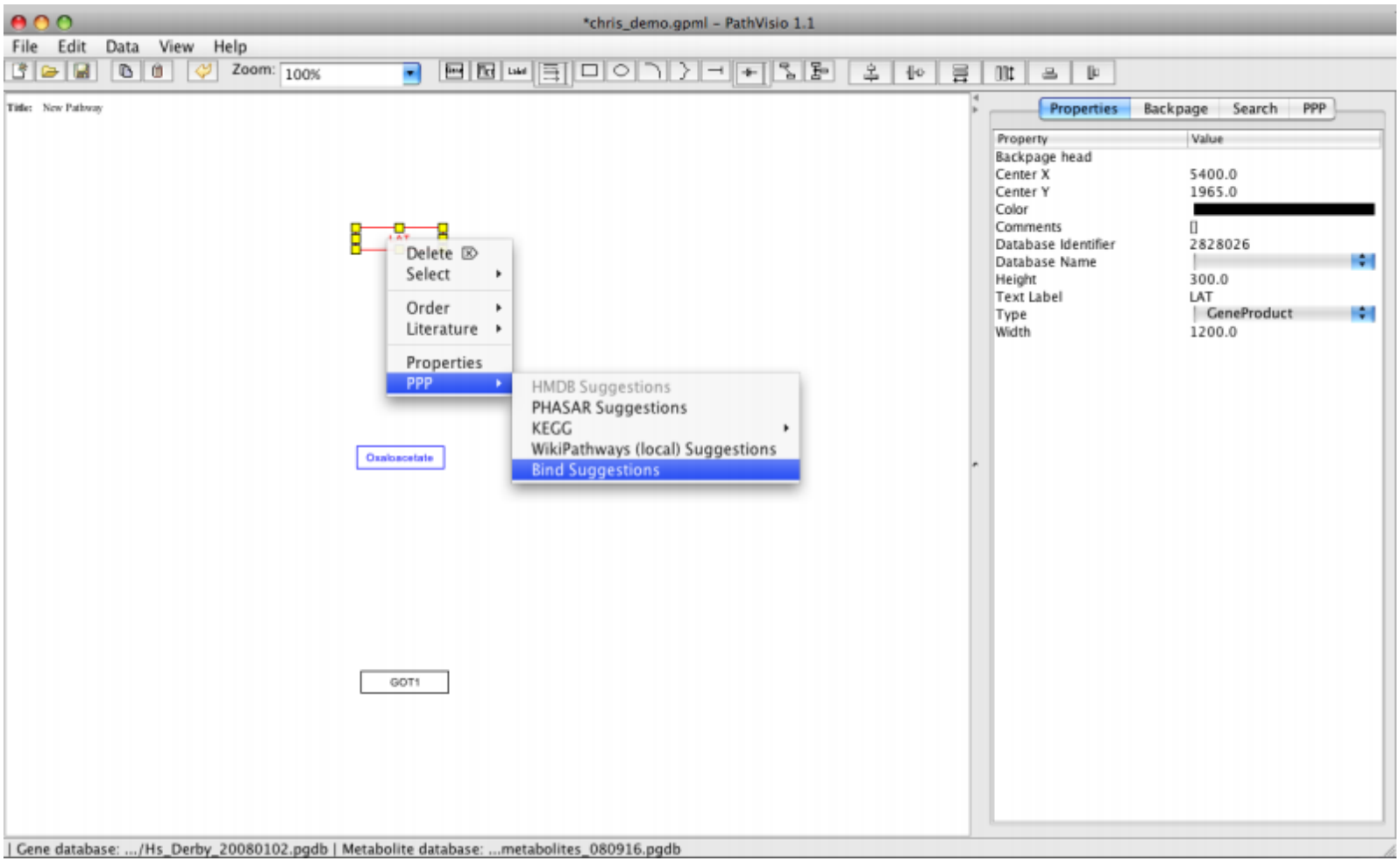
Pathway Loom demo (2)



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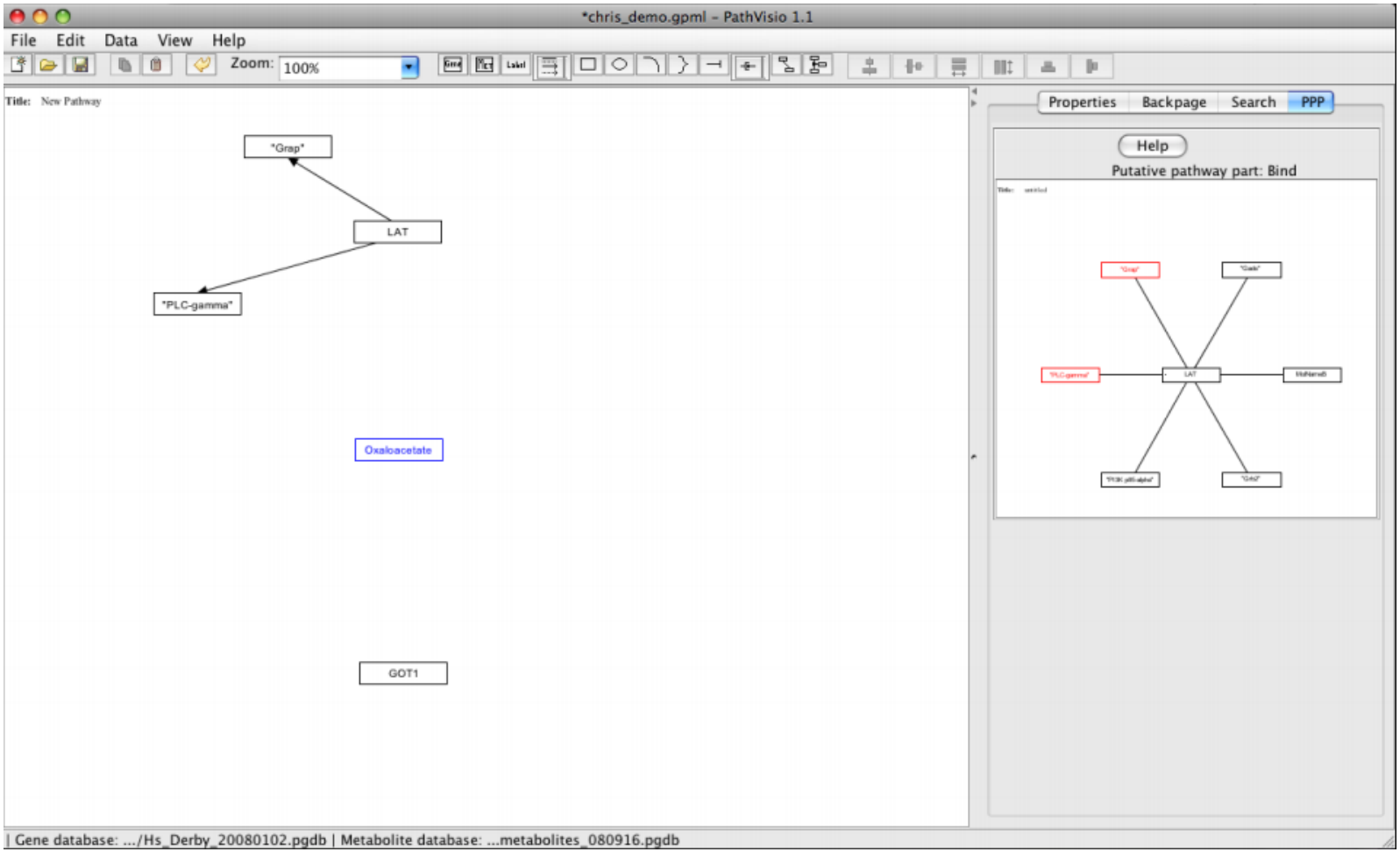
Pathway Loom demo (3)



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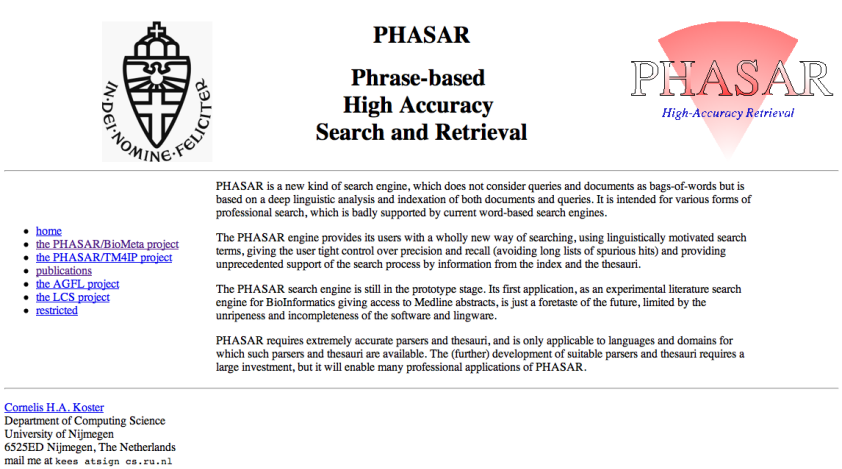
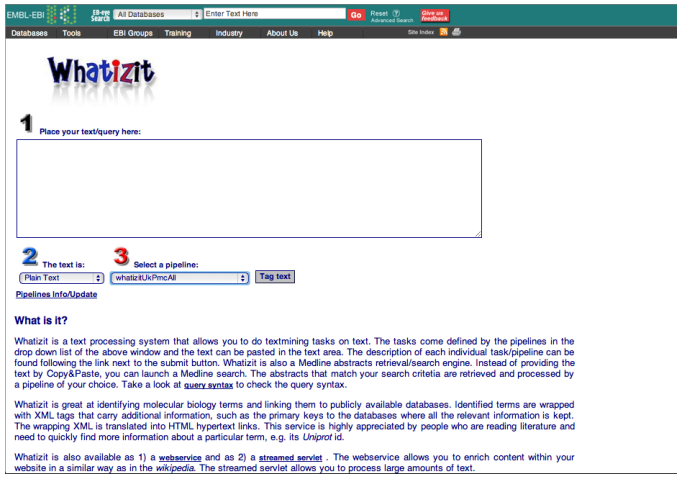


(g) PHASAR



(h) WHATIZIT (http://www.ebi.ac.uk/webservices/whatizit/info.jsf

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Andra Waagmeester 488 ●9 | log out | faq search

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Which are stable text mining solution for biologists.

4

I am working on integrating pathway relations into a pathway diagram. I have two text mining solutions that I use to find interactions. I am looking for new suggestions. The idea is that I provide a pathway entity (ie. gene/protein, metabolite) and all relations based on the literature are returned.

text-mining interaction pathway

2 edit | rollback | close | delete | flag

edited Mar 1 at 7:28
Lars Juhl Jensen ♦
4,441 ●4 ●15

asked Feb 26 at 21:08
Andra Waagmeester
488 ●9

Could you please tell us which are the two text mining solutions that you already have? – Lars Juhl Jensen ♦ Feb 27 at 7:57

I am using Whatizit: ebi.ac.uk/webservices/whatizit/info.jsf and Phasar: phasar.cs.ru.nl. The first works decently, the second has issues with performance and accessibility. – Andra Waagmeester Feb 27 at 9:41

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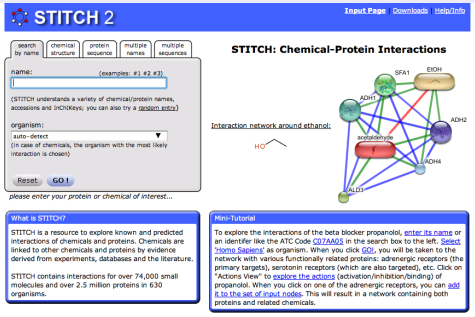
4 Answers

oldest newest votes

5

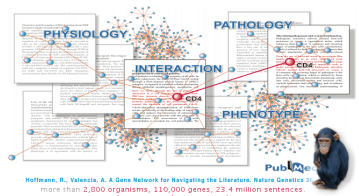
You might want to take a look at STITCH. It is a database that allows you to query with a gene/protein or a small molecule (e.g. a metabolite) and retrieve the interaction partners. A very large part of the evidence in STITCH comes from text mining, and if you really want to, you can turn off all the other evidence types to *exclusively* get the results obtained through text mining.

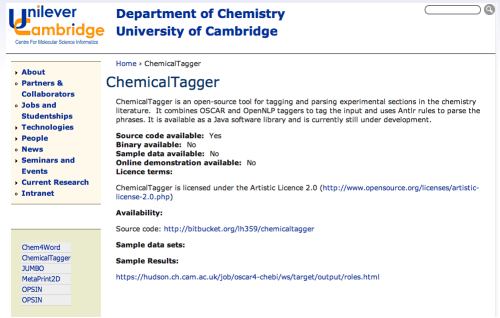
Nature Precedings : doi:10.1038/npre.2011.5850.1 : Posted 25 Mar



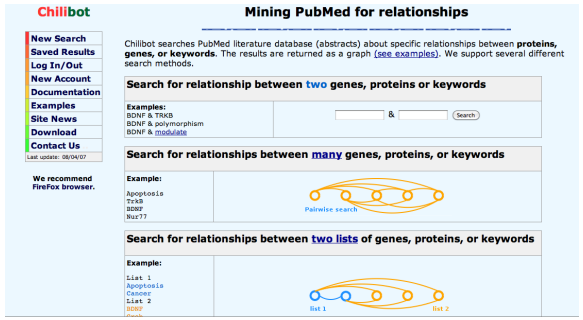
(i) STITCH

(j) iHOP

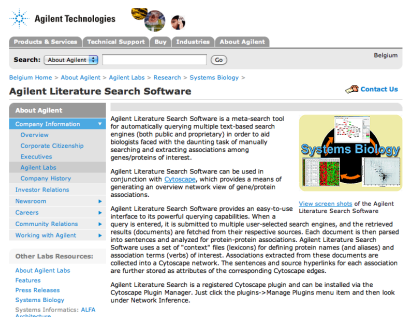




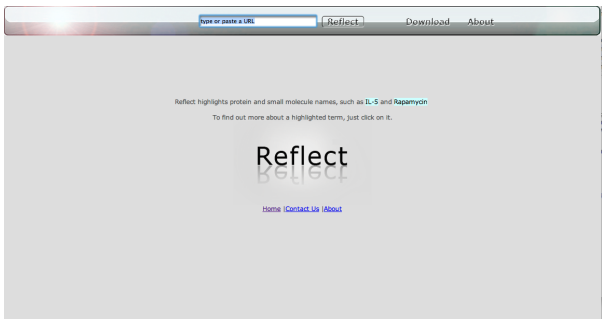
(k) CHEMICAL TAGGER



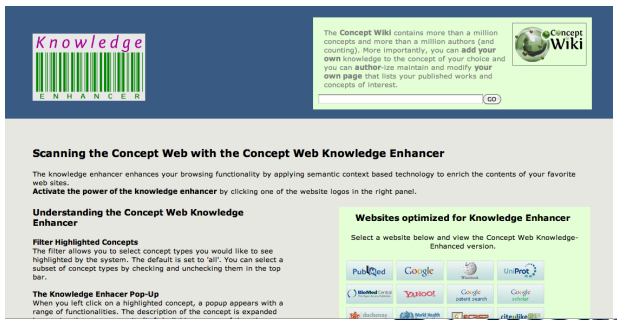
(l) CHILIBOT



(m) AGILENT



(n) REFLECT



(o) KNOWLEDGEENHANCER

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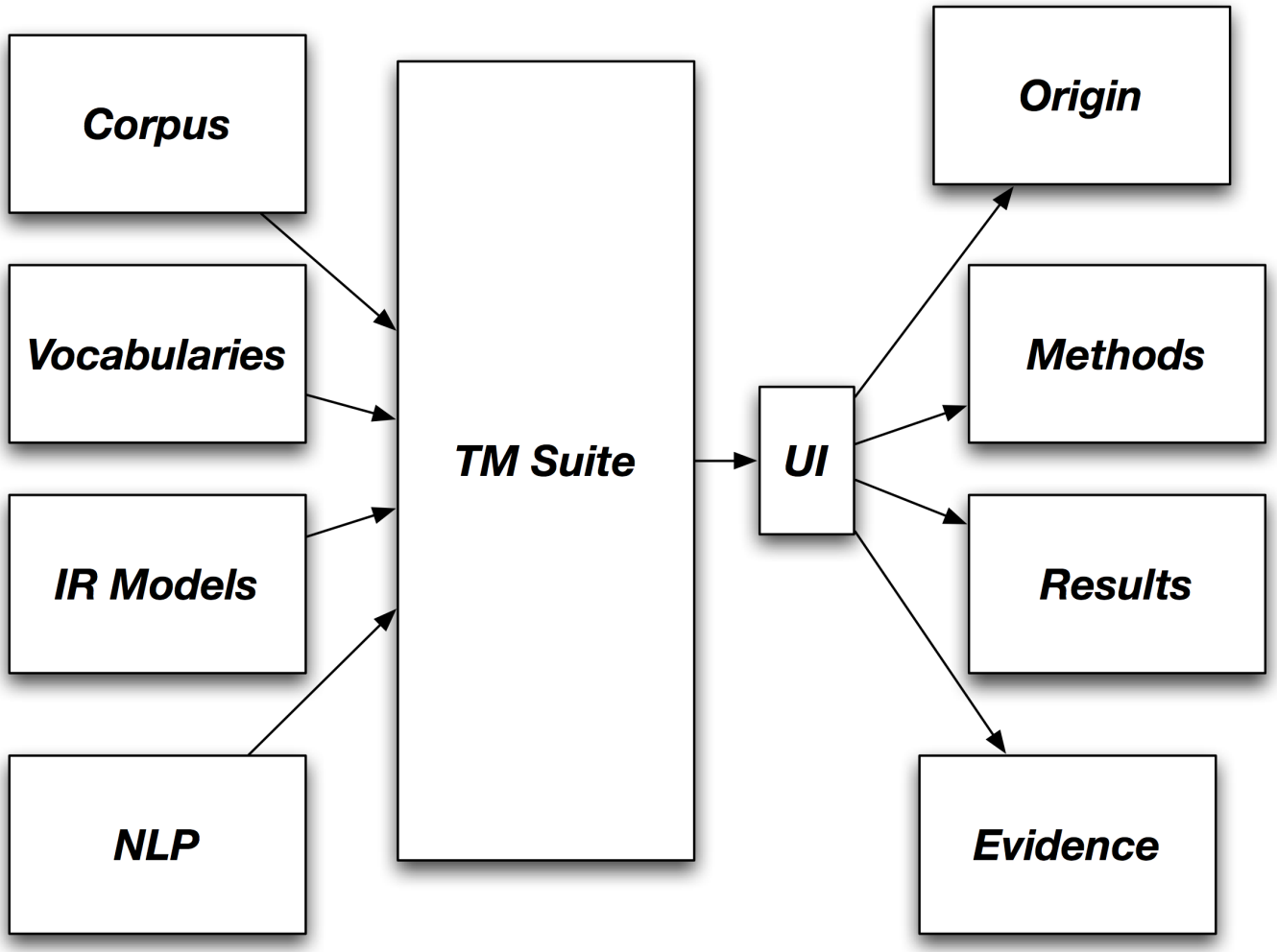
Text-mining standard for pathway curation



Origin

- Description
- Corpora
- Identifiers

Methods used

- Description
- Method name
- Vital statistics

Results

- Source
- Target
- Source Identifiers
- Target Identifiers

Evidence

- Relevant text parts

Awknowledgements

Maastricht University

- Chris Evelo
- Thomas Kelder
- Martina Kutmon
- Jahn Saito
- Martijn van Iersel

USC - SF

- Alexander Pico

BIOSTAR http://biostar.stackexchange.com

- Lars Juhl Jensen
- Casey Bergman
- Egon Willighagen
- Dominique Noel

nbic netherlands bioinformatics centre

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