

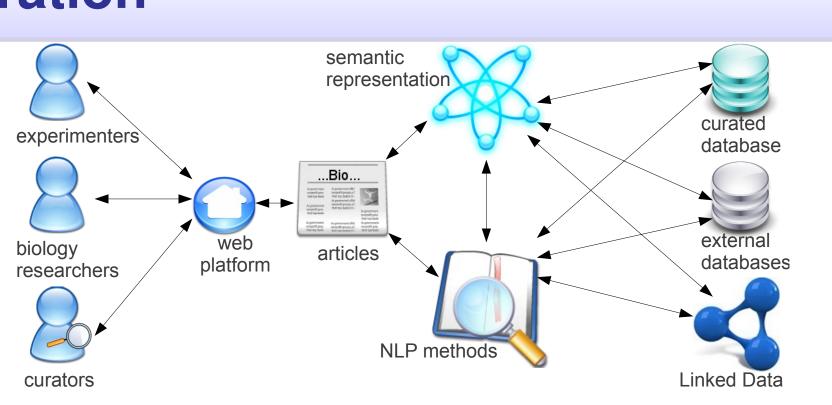
Empowering web portal users with personalized text mining services



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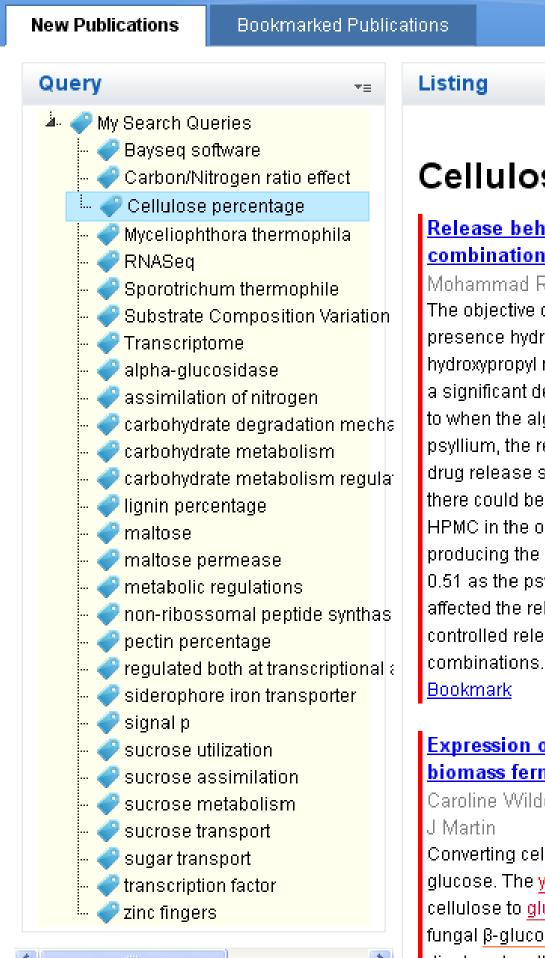
Literature Mining and Curation

- Reading, interpreting, curating bio-literature
- Labor-intensive, error-prone and expensive task
 - ⇒ Natural Language Processing (NLP) techniques: √extract knowledge from papers
 - ⇒ Semantic techniques:
 - ✓ connect information from various sources



Web Platform

Personalized view and results of semantic analysis



Cellulose percentage

Release behaviour of propranolol HCl from hydrophilic matrix tablets containing psyllium powder in combination with hydrophilic polymers. - 2011-11-29

Mohammad R Siahi-Shadbad, Kofi Asare-Addo, Kakali Azizian, Davoud Hassanzadeh, Ali Nokhodchi. The objective of this study was to investigate the release behaviour of propranolol hydrochloride from psyllium matrices in the presence hydrophilic polymers. The dissolution test was carried out at pH 1.2 and pH 6.8. Binary mixtures of psyllium and hydroxypropyl methylcellulose (HPMC) used showed that an increase in the percentage of HPMC in the binary mixtures caused a significant decrease in the release rate of propranolol. Psyllium-alginate matrices produced lower drug release as compared to when the alginate was the matrix former alone. When sodium carboxy methyl cellulose (NaCMC) was incorporated into the psyllium, the results showed that matrices containing the ratio of psyllium-NaCMC in the 1:1 ratio are able to slow down the drug release significantly as compared to matrices made from only psyllium or NaCMC as retardant agent suggesting that there could be a synergistic effect between psyllium and NaCMC. The double-layered tablets showed that the psyllium and HPMC in the outer shell of an inner formulation of psyllium alone had the greatest effect of protecting the inner core and thus producing the lowest drug release (DE = 38%, MDT = 93 min). A significant decrease in the value of n in Q = kt(n) from 0.70 to 0.51 as the psyllium content was increased from 50 to 150 mg suggests that the presence of psyllium in HPMC matrices affected the release mechanism. Psyllium powder had the ability in the combination with other hydrophilic polymers to produce controlled release profiles. Care and consideration should as such be taken when formulating hydrophilic matrices in different

<u>Bookmark</u>

Expression of a library of fungal β-glucosidases in Saccharomyces cerevisiae for the development of a biomass fermenting strain. - 2012-01-05

Caroline Wilde, Nicholas D Gold, Nancy Bawa, José Humberto M Tambor, Lina Mougharbel, Reginald Storms, Vincent J J Martin

Converting cellulosic biomass to ethanol involves the enzymatic hydrolysis of cellulose and the fermentation of the resulting glucose. The <mark>yeast</mark> Saccharomyces cerevisiae is naturally ethanologenic, but lacks the enzymes necessary to degrade cellulose to glucose. Towards the goal of engineering S. cerevisiae for hydrolysis of and ethanol production from cellulose, 35 fungal β-glucosidases (BGL) from the BGL1 and BGL5 families were screened for their ability to be functionally expressed and displayed on the cell surface. Activity assays revealed that the BGL families had different substrate specificities, with only the BGL1s displaying activity on their natural substrate, cellobiose. However, growth on cellobiose showed no correlation between the specific growth rates, the final cell titer, and the level of BGL1 activity that was expressed. One of the BGLs that expressed the highest levels of cellobiase activity, Aspergillus niger BGL1 (Anig-Bgl101), was then used for further studies directed at developing an efficient cellobiose-fermenting strain. Expressing Anig-Bgl101 from a plasmid yielded higher ethanol levels when secreted into the medium rather than anchored to the cell surface. In contrast, ethanol yields from anchored and secreted Anig-Bgl101 were comparable when integrated on the chromosome. Flow cytometry analysis revealed that chromosomal integration of Anig-Bgl101 resulted in a higher percentage of the cell population that displayed the enzyme but with overall lower expression levels.

with indexers, summarizers, entity extractors, etc. <u>cellobiase, BGL1, FPC, BGL</u> endoglucanase, cellulase, hydrolase, CMC)-stabilized. Aniq-Bql101, MCC, aq-SEC, <u>CPA, AF, α-amylase, RC009,</u>

Enzyme

Bql CMCase CMC.

<u>RC008, Ana, PA, K15M,</u>

<u>normal-phase AD, endo,</u>

<u>endo-β-mannanase</u>,

endothelial nitric oxide

synthase, reversed-phase,

topical SE CPU0123 SD.

Man, cellulases, CMC/Fe,

RC016, β-glucosidases,

<u>artery TS, RP eNOS,</u>

Glycoside Hydrolase

Substrate

▼ EnzymeStats

<u>BGL families, GH9,</u>

differential scanning

Saccharomyces cerevisiae

<u>hydrolase family</u>

<u>cellulase</u>

▼ Family

▼ Assay

<u>calorimetry</u>

▼ OrganismStats

Organism

▼ Gene

BGL1

TEM, API, Akt/eNOS, coronary

CPU0213 VP protein kinase

35

User-defined display of results (map, index, highlighting in the source text, etc.)

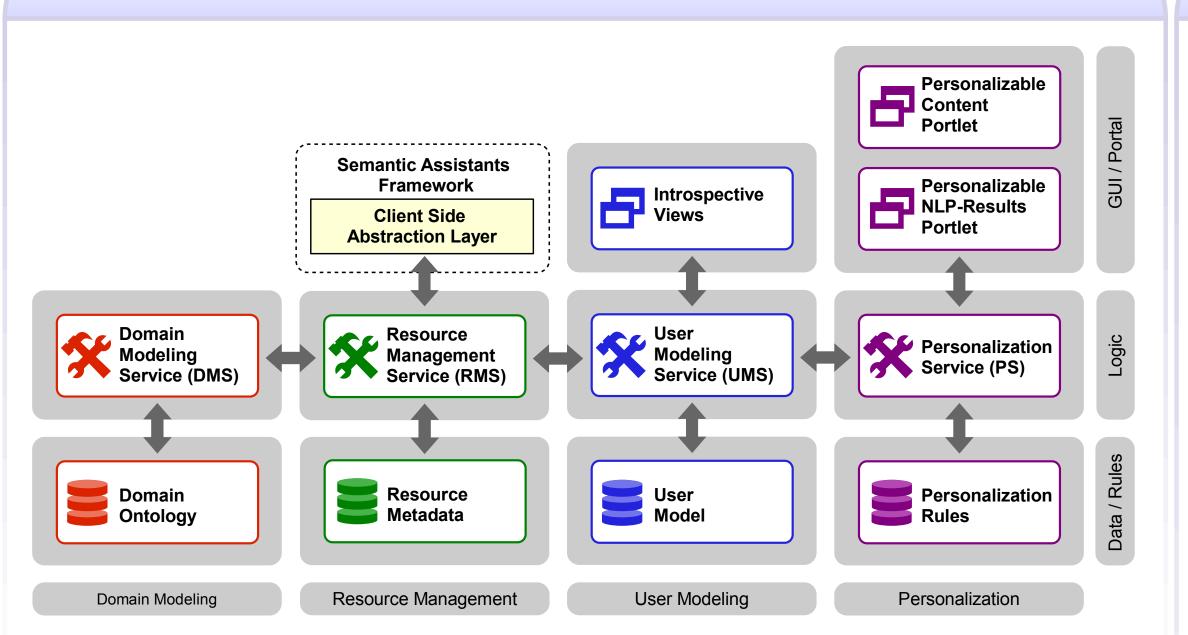
Content processing

named

Server: minion.cs.concordia.ca 💌 Assistants: Yahoo Search JavadocMiner Information Extractor ReportedSpeechFinder English Durm Indexer OrganismTagger ▼ mycoMINE A pipeline that provides information for lignocellulose research. Run Parameters No parameter applicable Run Assistant Results ■ Map Portlet ☐ Image Portlet ✓ Index Portlet ☑ Origin Portlet Display Results ► IR Information Extractor Person and Location Extractor

System Architecture

Remove Bookmark



Funding: Genome Canada, Génome Québec, NSERC, IBM Deutschland R&D Collaboration: J. Powlowski and all the participants of the user study GmbH.

at CSFG. Technical support: Andrei Wasylyk

GENOZYMES*

Acknowledgment

Follows Ben Shneiderman's information seeking mantra

Rich-interaction visualization of semantic user models

- Overview first, zoom and filter, then details-on-demand
- Intuitive mechanisms for editing user models
- Direct propagation of model changes on the content

IntrospectiveViews

