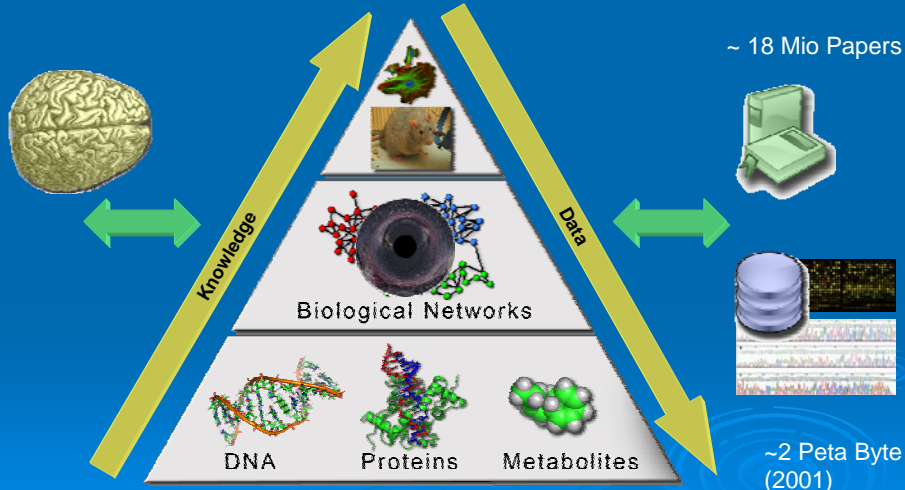
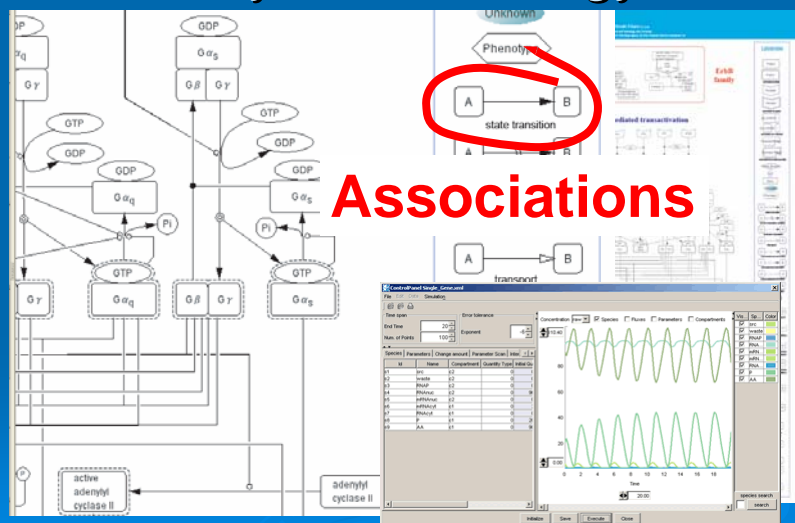


Understanding Complex Biological Systems



Systems Biology

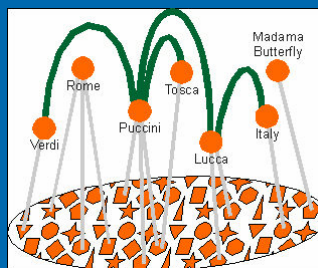


Questions

- Describing bidirectional associations ?
- Describing and merging different knowledge domains ?
- Ontologies for semantic structuring ?
- Semantic structures from free text ?
- Knowledge representation from distributed resources ?

=> Topic Maps

The Simple Reason



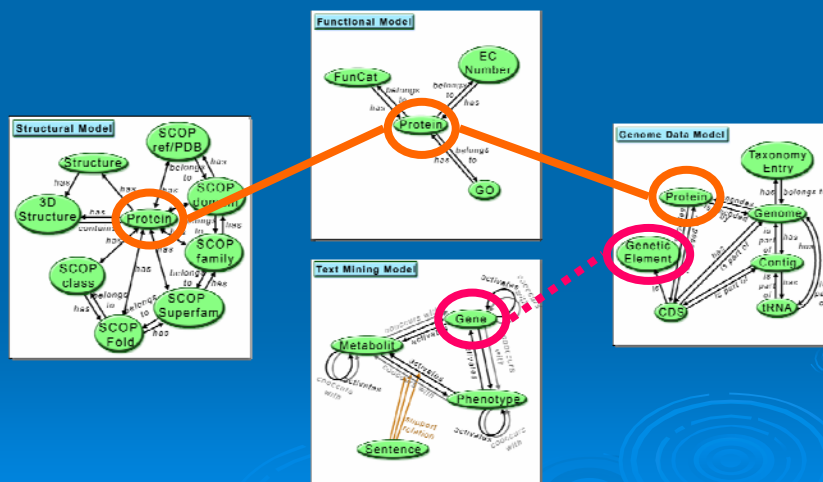
Bidirectional Association to Understand Extended Functional Context

The screenshot shows the MIPs website interface. On the left is an 'Ontology viewer' with a tree structure showing categories like '01 METABOLISM' and '02 ENERGY', with '02.04 glyoxylate cycle' selected. The main content area displays 'Protein ao090009000219' with the following characteristics:

- Description:** isocitrate lyase
- Molecular Weight:** 60026.2650200003
- Sequence:** MGFLFEDDKKYLDDVQAVKAWWTDSDRWHTPEYPSNVSQKQWKLESFNFKVASFYI
- Length:** 538
- Organism:** Aspergillus oryzae

Below this, a table lists 'Protein ao090009000219' with columns for 'has function', 'is encoded within genome', and 'is encoded by CDS'. The table shows various EC numbers (e.g., 01.05.01.01) and their corresponding organisms (e.g., Aspergillus oryzae, Myces hansenii).

Merging Knowledge from Different Domains

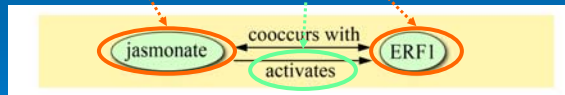


Associated Knowledge in Free Text

Free text

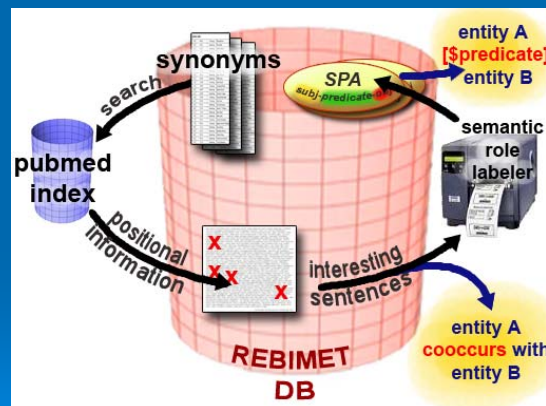
... of pathogen response genes that prevent disease progression.
 The expression of ERF1 can be activated rapidly by ethylene
 of jasmonate and can be activated synergistically by both hormones.
 In addition, both signalling ...

Topic Map

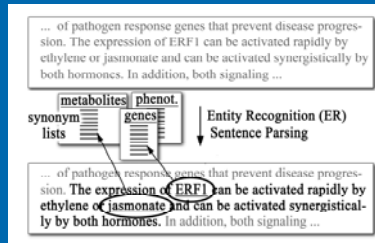


REBIMET

➤ Relation Extraction from Biomedical Texts



Entity Recognition



- Identification of relevant biological entities:
 - Based on synonym lists created from terms in taxonomies, gene names,
- Realized with Apaches Lucene

Information Extraction with Semantic Role Labeling and Cooccurrence

The expression of ERF1 can be activated rapidly by ethylene and jasmonate and can be activated synergistically by both hormones.

1. Semantic Role Labeling:

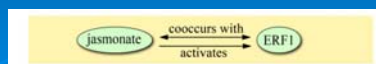


- 1.1 PAS structure for verb a)
- 1.2 PAS structure for verb b)

[arg1 The expression of ERF1] [argm-mod can] be [target activated] [argm-mmr rapidly] [arg0 by ethylene and jasmonate] and can be activated synergistically by both hormones

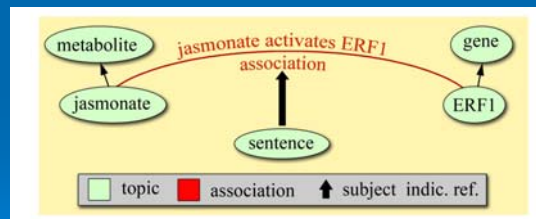
[arg1 The expression of ERF1] can be activated rapidly by ethylene and jasmonate and [argm-mod can] be [target activated] [argm-imp synergistically] [arg0 by both hormones]

2. Information Extraction:



Simplified TM Representation

- Generation of Topic Map fragments
- Connection to evidence in text by reification

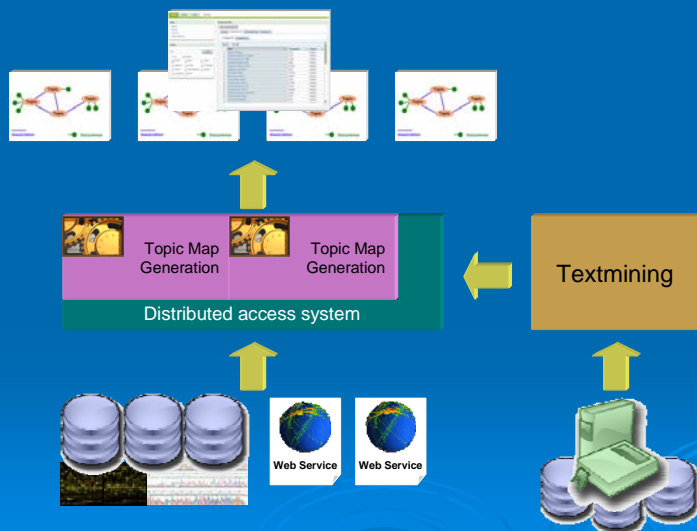


How To Generate the Topic Maps ?

Generation of TM fragments

- Problems with generation of one large TM
 - Very large data collections (storage problems)
 - Distributed
 - Update problems

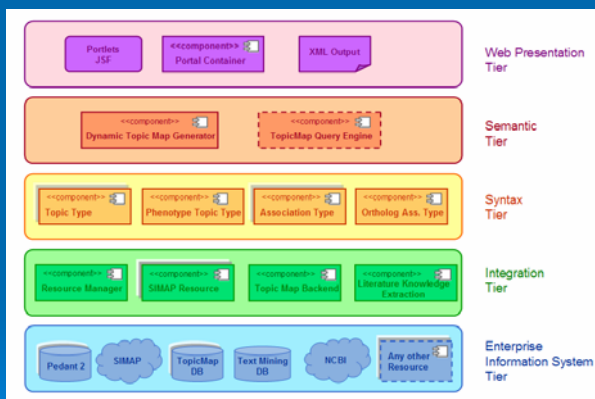
Large Scale Integration and Knowledge Representation



GeKnowME

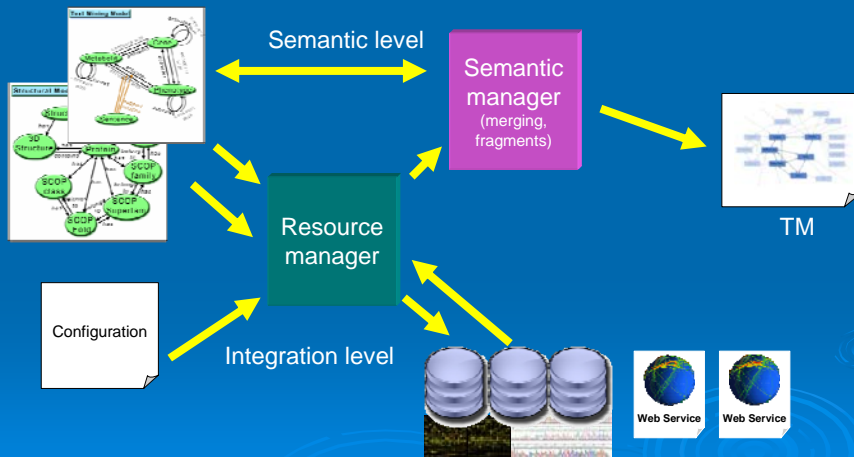
(Generic Knowledge Modeling Environment)

- Extension of our n-Tier J2EE based component and service oriented architecture (EJBs and Web Services)
- Simply by adding some syntactic components ..
- .. and one semantic Tier



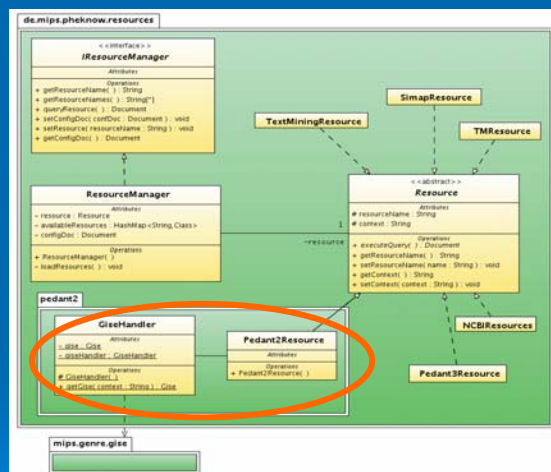
Concept:

- Independent semantic layer on top of arbitrary data sources



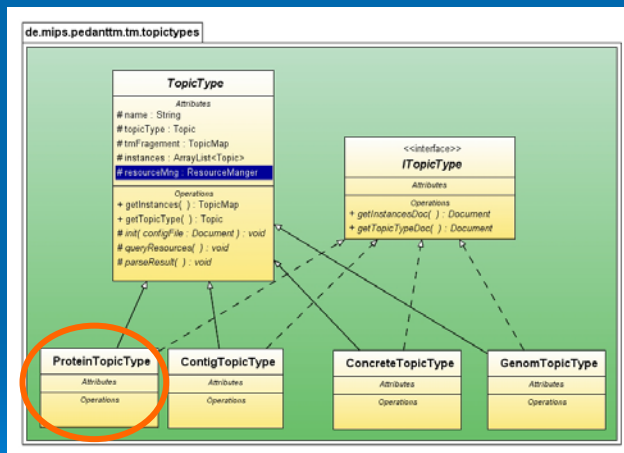
Integration Tier

- Resource:
 - Aware of mapping between topic / association types and methods from data source
- Handler:
 - Proxy
 - Manages connections
 - Execute query methods



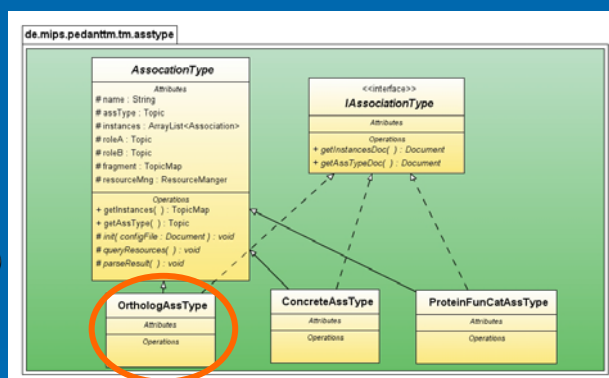
Syntax Tier – Topic Types

- Converts resource specific format into TM fragments
- May access multiple resources (handled by Resource Manager)



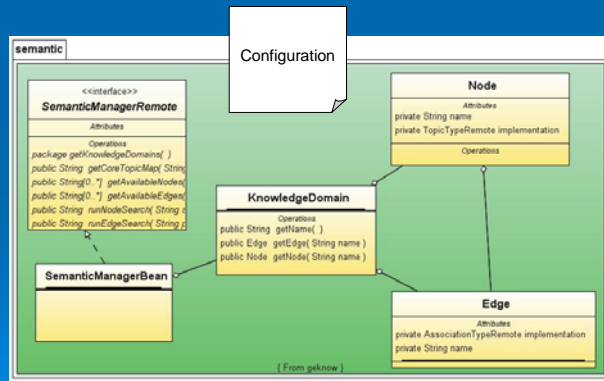
Syntax Tier – Association Types

- Converts resource specific format into TM fragments
- May access multiple resources (handled by Resource Manager)



Semantic Tier

- Responsible for
 - fragment generation
 - Merging
- No programming required (only configuration)



GeKnowME: Integration of PEDANT, SIMAP, NCBI data, NCBI PubMed

- PEDANT 3 ~ 600 GB
 - contains 450 genomes each stored in a single MySQL database
 - no possibilities for simultaneous cross genome comparison
- SIMAP ~ 540 GB compressed
 - contains over 7 Mio. unique protein sequences and their similarities
- NCBI
 - Taxonomy information (some thousands)
- Textmining from PubMed
 - 16 Mio. abstracts, 65 Mio Hits, 15 Mio. Sentences, 13 Mio. PAS structures
- Integration of these data on the fly
- Semantic linking of PEDANT databases with SIMAP and NCBI Taxonomy
- No redundant data

Screenshot Portal

- PSI based merging of textmining model with genome model

The screenshot displays a search result for a mutation in the XNPATR-X gene. The main content area shows a table with the following data:

Name	Type	Description	Organism
PID: 15508018	2005	Mutation in the 5' alternatively spliced region of the XNPATR-X gene causes Chudley-Lowry syndrome.	

Below the table, there is a detailed abstract for the article "Mutation in the 5' alternatively spliced region of the XNPATR-X gene causes Chudley-Lowry syndrome." The abstract includes the following text:

Abdel F.F., Cardoso C., Linsel AM., Lavery BB., Depireux D., Hachimi MS., Taha HA., Strommen BJ., Costas B., Chudley AE., Schwartz CE.,
SCell Research Institute, Greenwood Genetic Center, SC 29644, USA.

The Chudley-Lowry syndrome (CHLS, OMIM 309490) is an X-linked recessive condition characterized by moderate to severe mental retardation, short stature, mild obesity, hypogonadism, and distinctive facial features characterized by depressed nasal bridge, anteverted nares, inverted-V-shaped upper lip, and macrostomia. The original Chudley-Lowry family consists of three affected males in two generations. Linkage analysis had localized the gene to

Related Links:

- Splicing mutation in the ATRX gene (doi:10.1093/hmg/ddi044)
- ATRX mutation causes impaired nuclear location (J Hum Genet. 2005)
- Determination of the genomic structure of the XN (Genomics. 1997)
- Intravital diagnosis of ATRX syndrome in a fly (Hum Hered. 2002)
- A novel splicing mutation of the ATRX gene in ATRX (Hum Hered. 2003)

See all Related Articles...

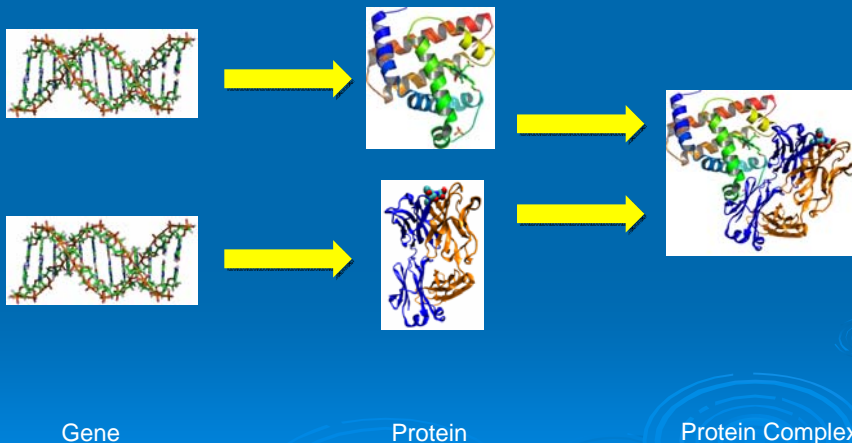
Proudly we went to
the bench biologists
and
successfully ...

... we failed

Why ?

- If you can't transport within 5 seconds your message you're gone (independent of the quality of the content)
- In our specific case the context will not be clear by providing just text with hyperlinks

Crash Course Biochemistry



Context From Web Based Graphical Interface

The screenshot displays a web-based graphical interface for searching and visualizing disease relationships. The search form at the top includes fields for 'Find' (set to 'Disease'), 'By' (set to 'Description'), 'To' (set to 'Choose one...'), and 'Which is' (set to 'ataxia'). The search results on the left list several diseases, with 'ATAxia-TELAnGIECTASIA; AT' selected. Below the results, there is a section for 'NCBI URL' and 'is described in' with a list of genes: ATN, NBR, RPA2, and RPA3. The main area on the right shows a topic map diagram with nodes representing diseases and their relationships. The nodes are: 'BLOOM SYNDROME; BLM' at the top, 'ERAF-T complex' in the middle, and 'ATAxia-TELAnGIECTASIA; AT' and 'FANCONI ANEMIA; FA' at the bottom. Arrows indicate relationships between these nodes.

Conclusion

- Can we explain the complexity of life ?
 -
- However:
 - TMs help us to model and associate information ...
 - ... in a way we WANT and NEED
 - We can utilize existing and open technologies to work with them
 - Topic Maps are suited to represent even some 100 millions of topics / associations
- Topic Maps will help us to understand at least the next level of complexity

A Final One: Do it for the user, not the technology

year	sentence
1998	Wine was the main source of alcohol, representing 67% of total alcohol intake in both genders.
1993	In Italy, wine was an important source of several nutrients, including iron and riboflavin.
1995	Multiple regression analyses were run where systolic and diastolic blood pressures were considered as separate dependent variables with the following independent variables: age, body mass index, physical activity, alcohol and coffee consumption, smoking, educational level; considered as continuous or categorical variables. eighty-eight per cent of all patients showed a moderate-low alcohol intake (1-50 g/day); wine was the preferred beverage.
2006	AIMS: Wine is the product of complex interactions between yeasts and bacteria in grape must.
1980	Although wine is the most popular beverage for all the women examined, it is significantly more often mentioned by women over 35 years, followed by aperitifs, beer and hard liquors.
1986	Chronic alcoholic gastritis is a very important social problem in the Health District of Arezzo, which covers an area where wine is an integral part of the diet.

Acknowledgements

- Filka Nenova
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Martin Münsterkötter
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Annotation Group
- Funding
Impuls- und
Vernetzungsfonds der
Helmholtz-Gemeinschaft
Deutscher
Forschungszentren e.V.