REWERSE
reasoning on the web

A2-D4

Bioinformatics Demonstrators

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Abstract

This deliverable presents demostrators, which build upon the use cases specified in A2-D3 and which showcase bioinformatics applications using rules, reasoning and the web.

- GoProteins allows users to browse the GeneOntology and retrieve protein structure data from the web. It uses ontologies, deduction rules, reaction rules, databases and XML.
- Sambo integrates bio-ontologies such as the GeneOntology and Mesh. It deploys novel algorithms for concept mapping.
- BioRevise reasons over metabolic networks using techniques from belief revision.
- EarthFeed reads RSS feeds on the web, extracts locations and maps them onto a map of the world. The demonstrator uses XML and reactivity.
- GoPubMed allows users to explore PubMed search results with the GeneOntology.

The demonstrators can be shown at the annual review meeting.

Keyword List

Demonstrators, bioinformatics, pathways, PubMed, ontologies

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Bioinformatics Demonstrators

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20 Feb 2006

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Contents

1 Introduction

The deliverable A2-D4 sets out to deliver the following contents:

> *Demonstrators*
>
> *With the requirement defined simple demonstrators will be produced. The demonstrators are mock-ups of future prototypes. They will demonstrate the main functionality of the specified applications and thus serve as a basis for the viability of the applications. Four applications will be pursued with the demonstrators:*
>
> - *Rule-based information integration and dissemination*
>   - *Application: rule-based integration for structured data, e.g. protein interactions*
>   - *Application: rule-based information dissemination for unstructured data, e.g. HIV information portal*
> - *Rule-based querying for bioinformatics databases and tools*
>   - *Application: rules, constraints, and ontologies to query structured data, e.g. constraints in sequence comparison*
>   - *Application: rule and ontology-based search for unstructured data, e.g. biomedical literature*

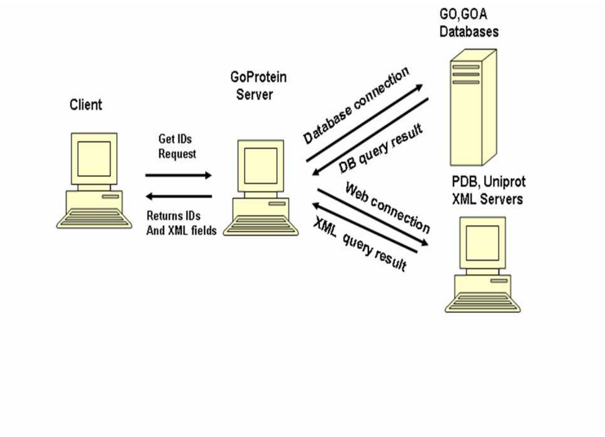
Here, we give a brief overview over the following demonstrators, which cover the applications sketched above.

- GoProteins allows users to browse the GeneOntology and retrieve protein structure data from the web. It uses ontologies, deduction rules, reaction rules, databases and XML.
- Sambo integrates bio-ontologies such as the GeneOntology and Mesh. It deploys novel algorithms for concept mapping.
- BioRevise reasons over metabolic networks using techniques from belief revision.
- EarthFeed reads RSS feeds on the web, extracts locations and maps them onto a map of the world. The demonstrator uses XML and reactivity.
- GoPubMed uses the GeneOntology to search the biomedical literature.

For GoProteins and Sambo the appendix contains details.

2 GoProtein

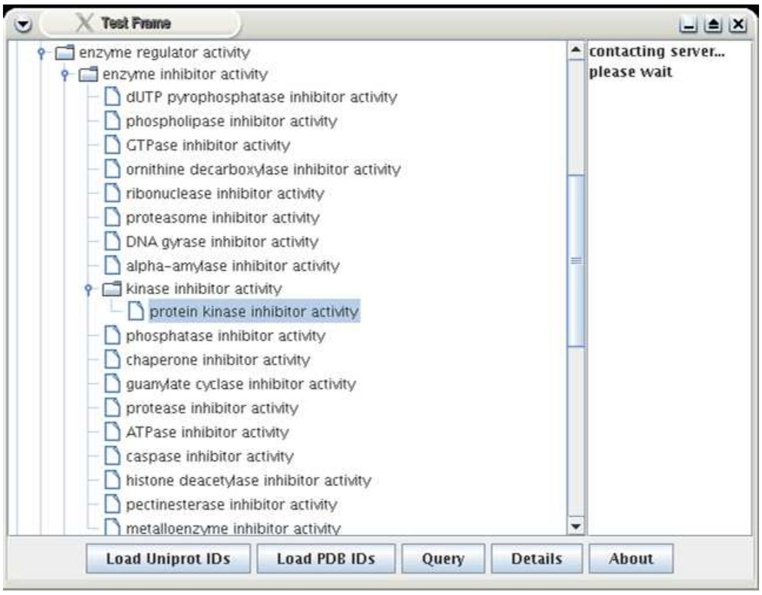
- **Name of the system:** GoProtein
- **Brief description:** The GoProtein tool browses the Gene Ontology (GO) and uses the Gene Ontology Annotation database(GOA) to retrieve relevant IDs for a selected term from the Protein Database Bank(PDB) and Uniprot protein databases. To retrieve more information from PDB and Uniprot, GoProtein connects to their respective URL, parses their XML entries and retrieves preselected fields. GoProtein implements the following workflow:



The user uses the client machine to issue a request to the server. The server then connects to the GO and GOA databases and process the query and returns the results to be displayed to the user. The user can request more information about the term by sending a query to PDB and Uniprot respective URLs and retrieve the query results.

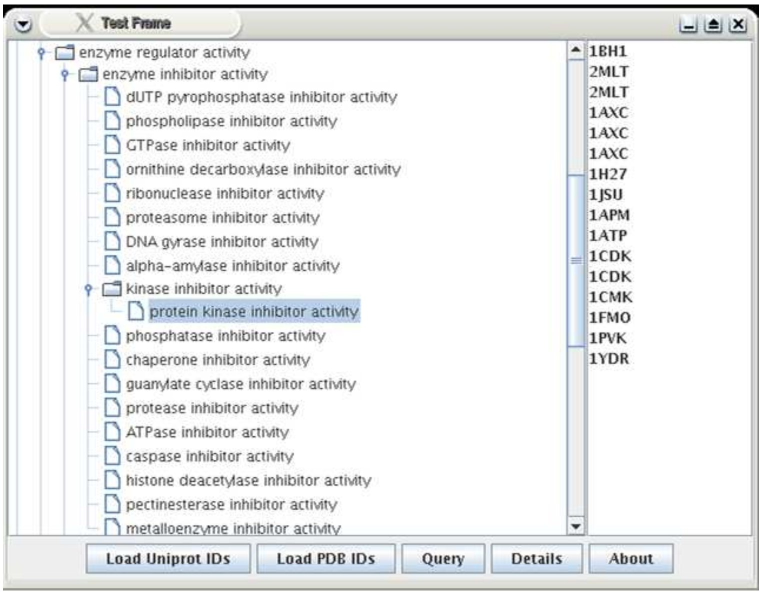
- **Requirements:** GoProtein is written in Prova. It requires online internet access to PDB and MySQL access to the GO and GOA databases.
- **Example:** The following screenshots summarise how to show all the PDB entries associated with the GO term 'protein kinase inhibitor activity'.

1. Select a term and wait for connection to database


Test Frame
enzyme regulator activity
enzyme inhibitor activity
dUTP pyrophosphatase inhibitor activity
phospholipase inhibitor activity
GTPase inhibitor activity
ornithine decarboxylase inhibitor activity
ribonuclease inhibitor activity
proteasome inhibitor activity
DNA gyrase inhibitor activity
alpha-amylase inhibitor activity
kinase inhibitor activity
protein kinase inhibitor activity
phosphatase inhibitor activity
chaperone inhibitor activity
guanylate cyclase inhibitor activity
protease inhibitor activity
ATPase inhibitor activity
caspase inhibitor activity
histone deacetylase inhibitor activity
pectinesterase inhibitor activity
metalloenzyme inhibitor activity
Load Uniprot IDs
Load PDB IDs
Query
Details
About

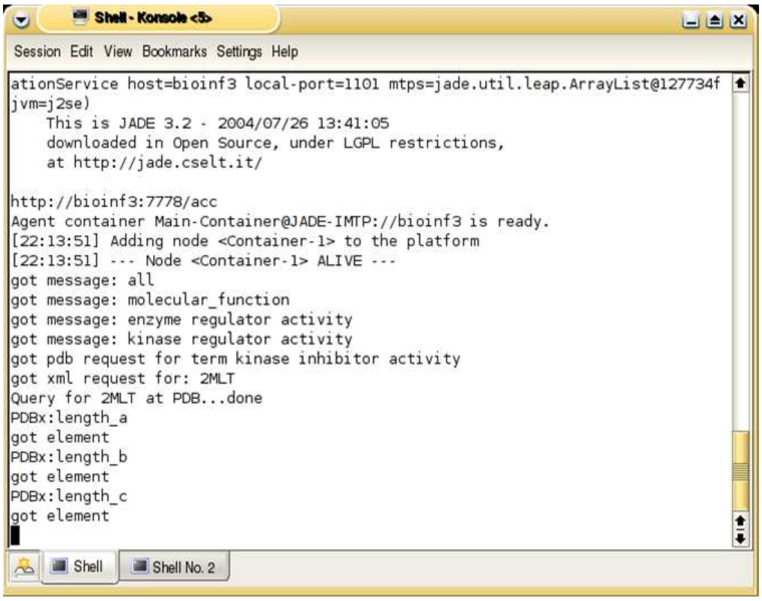
```
contacting server...
please wait
```

2. Retrieval of associated PDB IDs for the selected term


Test Frame
enzyme regulator activity
enzyme inhibitor activity
dUTP pyrophosphatase inhibitor activity
phospholipase inhibitor activity
GTPase inhibitor activity
ornithine decarboxylase inhibitor activity
ribonuclease inhibitor activity
proteasome inhibitor activity
DNA gyrase inhibitor activity
alpha-amylase inhibitor activity
kinase inhibitor activity
protein kinase inhibitor activity
phosphatase inhibitor activity
chaperone inhibitor activity
guanylate cyclase inhibitor activity
protease inhibitor activity
ATPase inhibitor activity
caspase inhibitor activity
histone deacetylase inhibitor activity
pectinesterase inhibitor activity
metalloenzyme inhibitor activity
Load Uniprot IDs
Load PDB IDs
Query
Details
About

```
1BH1
2MLT
2MLT
1AXC
1AXC
1AXC
1H27
1JSU
1APM
1ATP
1CDK
1CDK
1CMK
1FMO
1PVK
1YDR
```

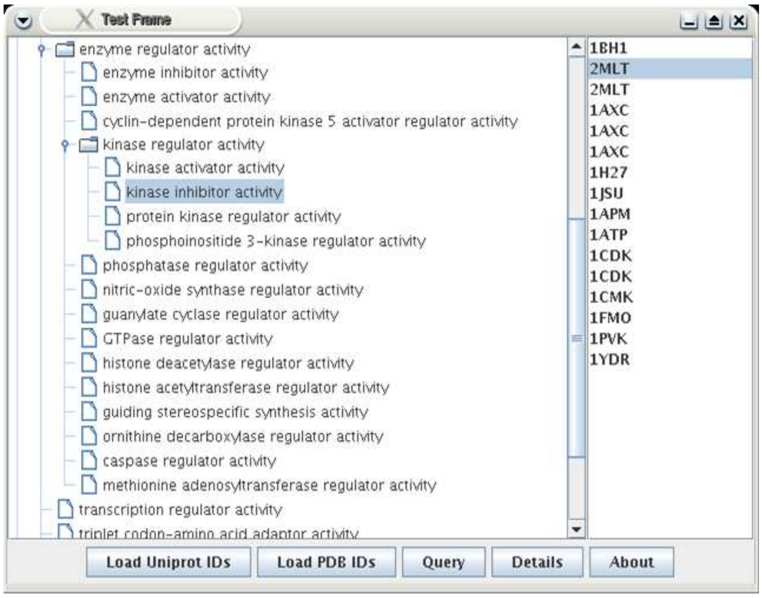
3. Message exchange between the two agents



```
ationService host=bioinf3 local-port=1101 mtps=jade.util.leap.ArrayList@127734f
jvm=j2se)
    This is JADE 3.2 - 2004/07/26 13:41:05
    downloaded in Open Source, under LGPL restrictions,
    at http://jade.cselt.it/

http://bioinf3:7778/acc
Agent container Main-Container@JADE-IMTP://bioinf3 is ready.
[22:13:51] Adding node <Container-1> to the platform
[22:13:51] --- Node <Container-1> ALIVE ---
got message: all
got message: molecular_function
got message: enzyme regulator activity
got message: kinase regulator activity
got pdb request for term kinase inhibitor activity
got xml request for: 2MLT
Query for 2MLT at PDB...done
PDBx:length_a
got element
PDBx:length_b
got element
PDBx:length_c
got element
```

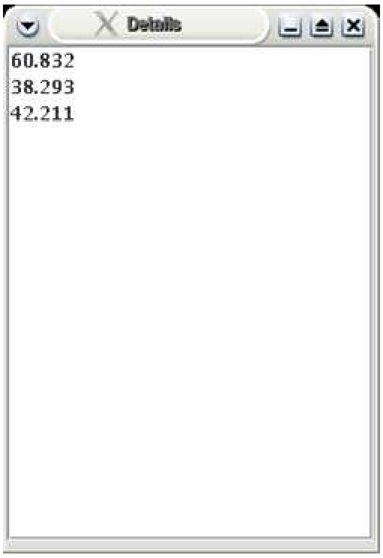
4. Connecting to the web and processing XML pages to retrieve additional information about the term



```
enzyme regulator activity
    enzyme inhibitor activity
    enzyme activator activity
    cyclin-dependent protein kinase 5 activator regulator activity
    kinase regulator activity
        kinase activator activity
        kinase inhibitor activity
        protein kinase regulator activity
        phosphoinositide 3-kinase regulator activity
    phosphatase regulator activity
    nitric-oxide synthase regulator activity
    guanylate cyclase regulator activity
    GTPase regulator activity
    histone deacetylase regulator activity
    histone acetyltransferase regulator activity
    guiding stereospecific synthesis activity
    ornithine decarboxylase regulator activity
    caspase regulator activity
    methionine adenosyltransferase regulator activity
transcription regulator activity
triplet codon-amino acid adaptor activity
```

```
1BH1
2MLT
2MLT
1AXC
1AXC
1AXC
1H27
1JSU
1APM
1ATP
1CDK
1CDK
1CMK
1FMO
1PVK
1YDR
```

5. Display of additional pages (sequence length)



60.832
38.293
42.211

- **Brief description how rules and other technologies are used:**

  GoProtein is written in Prova, which integrates Java with deduction and reaction rules. GoProteins uses these rules as follows:

  - Reaction rules specify the behaviour of the client, which displays the GUI, and the server agent, which handles database access and external access to the PDB server. The reaction rules include messaging in the agent communication language JADE.
  - Deduction rules are used by the client agent to traverse the ontology.
  - Database access is used by the server agent to access the GO database server.
  - XML documents, which provide details of the protein structures, are processed with rules on the server side.
  - The GUI is written entirely in Java, which is accessible from the Prova rule framework.

- **Brief summary of benefits:**

  - Distributed application using XML, databases, reaction rules with messaging, and deduction rules for ontologies;
  - Easy browsing of the Gene ontology tree;
  - Instant access to informations from databases and web resources about protein annotation;
  - Resilience to change (databases and web sites change often);
  - Use of open source technologies;
  - Location transparency (local, remote, mirrors);

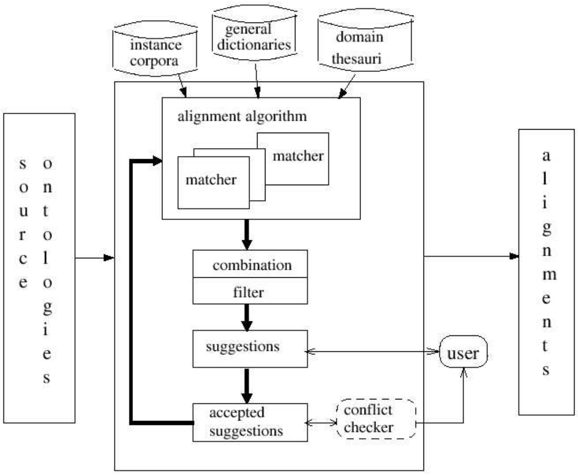


Figure 1: A general alignment strategy.

3 Sambo

- **Name of the system:** Sambo
- **Brief description:**

  SAMBO is an ontology alignment and merging tool.

  Figure 1 shows a general strategy for aligning two ontologies. An alignment algorithm receives as input two source ontologies. The algorithm can include several matchers. The matchers can implement strategies based on

  – linguistic matching (e.g. string matching),

  – structure-based strategies (e.g. similarity of children and parents),

  – constraint-based approaches (e.g. inferring similarity from similar ranges of concepts),

  – instance-based strategies (e.g. inferring similarity of GeneOntology terms from similarity of annotated proteins),

  – strategies that use auxiliary information (e.g. domain knowledge from additional databases),

  – or a combination of these.

  The matchers calculate similarities between the terms from the different source ontologies. Alignment suggestions are then determined by combining and filtering the results generated by one or more matchers. The pairs of terms with a similarity value above a certain threshold are retained as alignment suggestions. By using different matchers and combining them and filtering the results in different ways we obtain different alignment strategies. The suggestions are then presented to the user who accepts or rejects them.

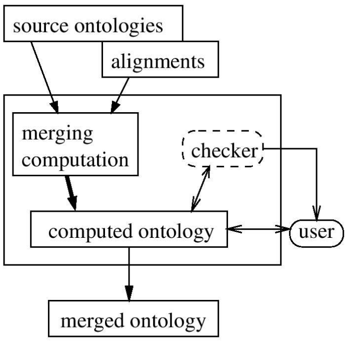


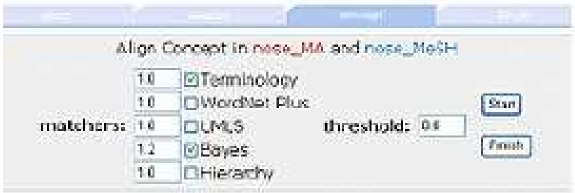
Figure 2: A general merging algorithm.

The acceptance and rejection of a suggestion may influence further suggestions. Further, a conflict checker is used to avoid conflicts introduced by the alignment relationships. The output of the alignment algorithm is a set of alignment relationships between terms from the source ontologies.

Figure 2 shows a simple merging algorithm. A new ontology is computed from the source ontologies and their identified alignment. The checker is used to avoid conflicts as well as to detect unsatisfiable concepts and, if so desired by the user, to remove redundancy.

- **Requirements:** Sambo is implemented in Java and deployed in Tomcat.
- **Example:** The following screenshots summarise a session in Sambo.

1. Choosing different matchers and assigning weights

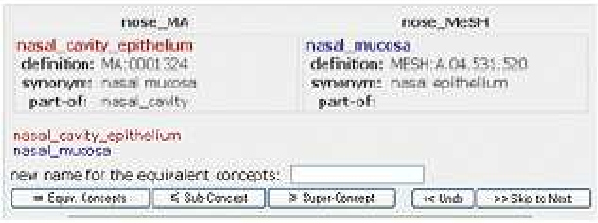


Align Concept in nose_MA and nose_MeSH

matchers:
1.0 ☑ Terminology
1.0 □ WordNet Plus
1.0 □ UMLS
1.2 ☑ Bayes
1.0 □ Hierarchy

threshold: 0.6

2. Alignment suggestion including definition/identifier, synonyms, relations

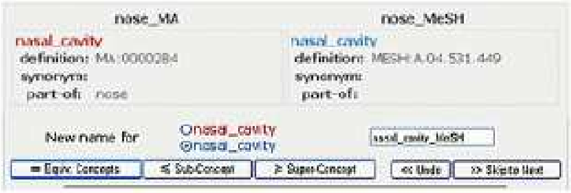


nose_MA	nose_MeSH
nasal_cavity_epithelium	nasal_mucosa
definition: MA:0001324	definition: MESH:A.04.531.520
synonym: nasal mucosa	synonym: nasa epithelium
part-of: nasal_cavity	part-of:

nasal_cavity_epithelium
nasal_mucosa

new name for the equivalent concepts:

3. Rejecting a suggestion



nose_MA

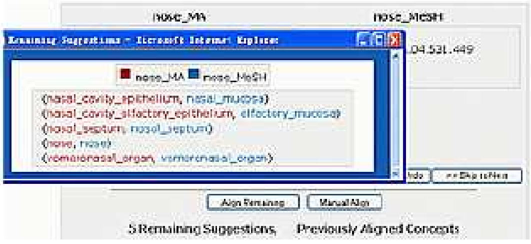
nasal_cavity
definition: MA:0000284
synonym:
part-of: nose

nose_MeSH

nasal_cavity
definition: MESH:A.04.531.449
synonym:
part-of:

New name for ○nasal_cavity ◉nasal_cavity ssal_cavity_MeSH

4. Overview over remaining alignments



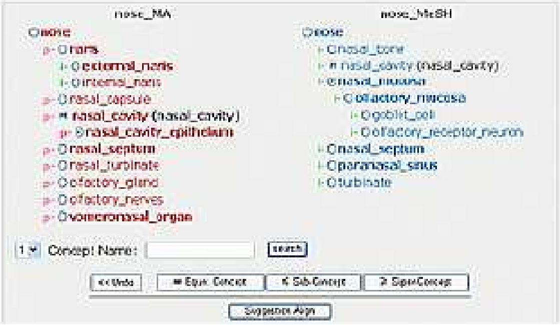
Remaining Suggestions - Microsoft Internet Explorer

🟥 nose_MA 🟦 nose_MeSH

(nasal_cavity_epithelium, nasal_mucosa)
(nasal_cavity_olfactory_epithelium, olfactory_mucosa)
(nasal_septum, nasal_septum)
(nose, nose)
(vomeronasal_organ, vomeronasal_organ)

5 Remaining Suggestions, Previously Aligned Concepts

5. Manual alignment



nose_MA

```
○nose
  ○naris
    ○external_naris
    ○internal_naris
  ○nasal_capsule
  = nasal_cavity (nasal_cavity)
    ○nasal_cavity_epithelium
  ○nasal_septum
  ○nasal_turbinate
  ○olfactory_gland
  ○olfactory_nerves
  ○vomeronasal_organ
```

nose_MeSH

```
○nose
  ○nasal_bone
  = nasal_cavity (nasal_cavity)
  ○nasal_mucosa
    ○olfactory_mucosa
      ○goblet_cell
      ○olfactory_receptor_neuron
  ○nasal_septum
  ○paranasal_sinus
  ○turbinate
```

- **Brief description how rules and other technologies are used:**

  OWL is used to represent ontologies

- **Brief summary of benefits:**

  Sambo allows users to integrate ontologies, this is a key functionality in bioinformatics as there are many ontologies, which partially overlap. For specific applications, users typically need a domain specific ontologies, which integrates parts of existing ontologies such GeneOntology, Mesh, UMLS, SnoMed, etc. Thus, Sambo is very important for an ontology-based information integration tasks.

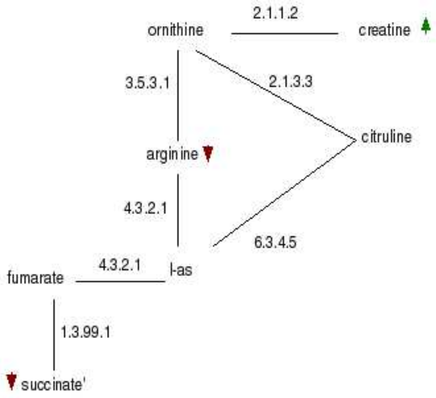


Figure 3: An example of a metabolic sub-network involving metabolites affected by hydrazine.

4 BioRevise

- **Name of the system:** BioRevise
- **Brief description of the system:** The BioRevise system is built on *REVISE* a non-monotonic reasoning system that revises extended logic programms. It is based on logic programming with explicit negation and integrity constraints and provides two-valued revision assumptions to remove contradictions from the knowledge base. This Belief revision system is used to model inhibition of reactions in metabolic and biosynthesis pathways to explain the alternation on the concentration levels of metabolites after being exposed to external factors like toxins. The system will process the data related to the *Pathways* which are extracted from the *KEGG* pathways database.
- **Requirements:** Swiprolog installation and REVISE.
- **Example:** Identifying the effect of toxin in metabolic networks.

  BioRevise can predict inhibitory effects of hydrazine on metabolic networks to assess the potential harmful side effects of a drug. Information on up/down changes in metabolite concentrations after hydrazine treatment is obtained from NMR spectra. This information is combined with KEGG metabolic diagrams, which contain information on the chemical reactions and associated enzymes (see Fig. 3).

  The example is implemented as follows:

  - Observables

    The observations of the concentration level of the metabolites after the use of Hydrazine.

    ```
    concentration('succinate',down).
    concentration('creatine',up).
    ```

  - Background knowledge.

The background knowledge describes the reactions taking place between the metabolites and the enzyme involved in the metabolic networks as explained in the KEGG database.

```
reaction(['succinate'], '1.3.99.1',  ['fumarate']).
reaction(['fumarate','arginine'], '4.3.2.1', ['l-as']).
reaction(['l-as'], '6.3.4.5', ['citruline']).
reaction(['ornithine'], '2.1.3.3', ['citruline']).
reaction(['arginine'], '3.5.3.1', ['ornithine']).
reaction(['ornithine'], '2.1.1.2', ['creatine']).
```

- Abducible Predicate.

  ```
  revisable(inhibited(_) ).
  ```

  The abducible indicates that the predicates truth-value can be changed in order to remove contradictions.

- Program rules.

  The following rules describes the underlying mechanism of the effect of inhibition of a toxin by defining the observable concentration predicate.

  ```
  concentration(Sub,down) <-
         reaction(Sub,Enz,Prod), % X <--Enz-- Y
         inhibited(Enz),
          concentration(Prod,up).

  concentration(Sub,V) <-
          reaction(Sub,Enz,Prod), % X <--Enz-- Y
          not inhibited(Enz),
          concentration_all(Prod,V).

  concentration(Sub,up) <-
          reaction(Prod,Enz,Sub), % Y <--Enz-- X
          inhibited(Enz),
          concentration(Prod,down).
  ```

- Integrity constraints.

  ```
  <- concentration(M, up), concentration(M, down).
  ```

- Possible results for the above example

  ```
  ?- solution(A).

  A = [[inhibited('1.3.99.1')], []] ;
  ```

```
A = [[inhibited('2.1.1.2')], []] ;

A = [[inhibited('2.1.3.3'), inhibited('3.5.3.1')], []] ;

A = [[inhibited('3.5.3.1'), inhibited('4.3.2.1')], []] ;

A = [[inhibited('3.5.3.1'), inhibited('6.3.4.5')], []] ;

No
```

- **Brief description how rules and other technologies are used:**

  The whole system is modelled using Prolog rules: examples:-

  $reactionnode(Metabolite1, Enzyme, Metabolute2)$
  describe the topology of the network of the *metabolic pathways*. At the end we can get as a result, possible explanations for the change of the concentrations related to the observation, knowing which enzymes are affected and therefore which reactions are inhibited. This explanations are presented in predicates:

  $inhibited(Enzyme, Metabolite1, Metabolite2)$
  capturing the hypothesis that the reaction from $Metabolite1$ to $Metabolite2$ is inhibited by one toxin through an adverse effect on the enzyme, $Enzyme$, that normally catalyzes this reaction .

  We need to take into consideration the predicate:

  $reactionnode(Metabolites1, Enzymes, Metabolites2)$
  where $Metabolites1$, $Metabolites2$ and $Enzymes$ could be a list of metabolites and enzymes, respectively.

- **Brief summary of benefits:**;

  In the development of new drugs it is useful to know all metabolic reactions affected by the drug and which enzymes will be inhibited with the introduction of toxins in the system. Since the number of *metabolic pathways* is huge, this work contributes explanations about how observed changes in the concentration of metabolites can be explained by inhibited enzymes in *metabolic pathways*.

5 EarthFeed and BioChemFeed

- **Name of the system**: *EarthFeed* and *BioChemFeed*
- **Brief description of the system**:

  The EarthFeed engine is a RSS/ATOM News Feed visualization tool that displays news summaries in the context of their geographical localization. A high-resolution satellite image (210 mega-pixels) is used as background and provides a beautiful way to stay Earth-tunned. The system relies on the analysis of raw free text and its categorization against an ontological background knowledge. In EarthFeed, a straightforward ontology for continents, countries, cities, places of interest and institutions provides terms that are looked for and extracted from the title and summary of the news item. This simple geographical ontology admits an obvious and beautiful visualization, a high resolution satellite image of the earth itself. News are being fetched continously from a list of URLs. The systems automatically moves all around the world, displaying news items as they come.

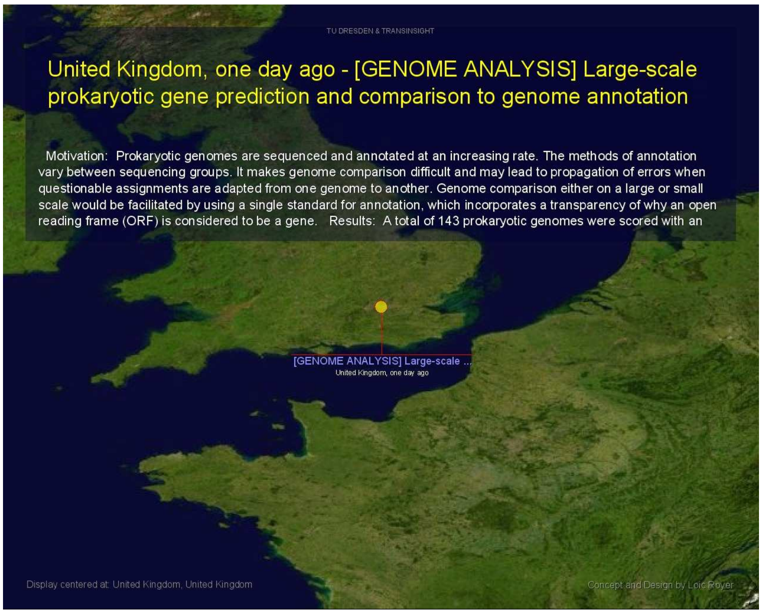
  Building on the abstract idea of *Semantic Visualization*, we designed BioChemFeed: replace the earth image with a digital scan of the Biochemical Pathways (the so-called Bohringer map) and the ontology by the enzymes mentioned in the map. News items mentioning enzymes can simply obtained through the new RSS facility offered by PubMed for a given search.
- **Requirements**:
  - Java Runtime Environment 1.5;
  - EarthFeed JAR file.
- **Brief description how rules and other technologies are used:**

  RSS and ATOM standards are supported by EarthFeed and BioChemFeed. The system is reactive and hence could deploy reaction rules.
- **Brief summary of benefits:**

  EarthFeed and BioChemFeed are experiments in semantic visualization, giving an example of how internet connectivity, ontological knowledge, and visualization can be combined together.

- **Example:**

EarthFeed



TU DRESDEN & TRANSINSIGHT

United Kingdom, one day ago - [GENOME ANALYSIS] Large-scale prokaryotic gene prediction and comparison to genome annotation

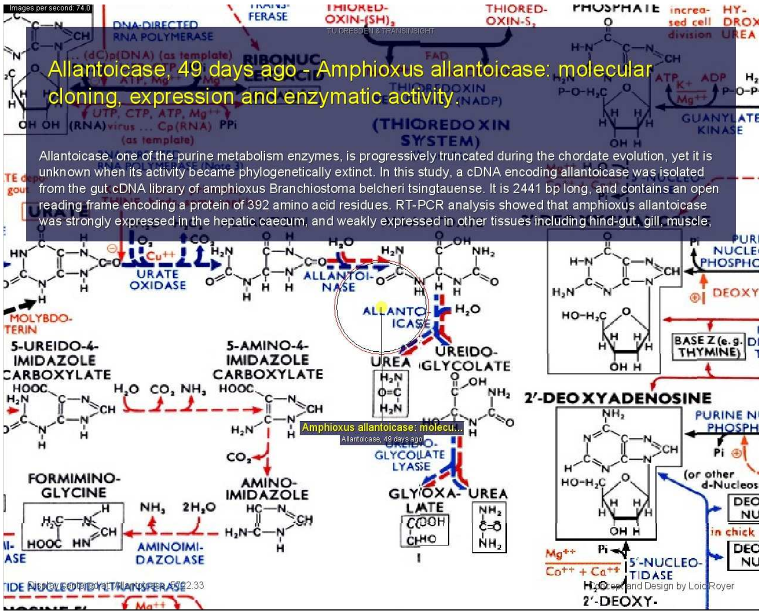
Motivation: Prokaryotic genomes are sequenced and annotated at an increasing rate. The methods of annotation vary between sequencing groups. It makes genome comparison difficult and may lead to propagation of errors when questionable assignments are adapted from one genome to another. Genome comparison either on a large or small scale would be facilitated by using a single standard for annotation, which incorporates a transparency of why an open reading frame (ORF) is considered to be a gene. Results: A total of 143 prokaryotic genomes were scored with an

[GENOME ANALYSIS] Large-scale ...
United Kingdom, one day ago

Display centered at: United Kingdom, United Kingdom

Concept and Design by Loic Royer

BioChemFeed



Images per second: 74.0

TU DRESDEN & TRANSINSIGHT

Allantoicase, 49 days ago - Amphioxus allantoicase: molecular cloning, expression and enzymatic activity.

Allantoicase, one of the purine metabolism enzymes, is progressively truncated during the chordate evolution, yet it is unknown when its activity became phylogenetically extinct. In this study, a cDNA encoding allantoicase was isolated from the gut cDNA library of amphioxus Branchiostoma belcheri tsingtauense. It is 2441 bp long, and contains an open reading frame encoding a protein of 392 amino acid residues. RT-PCR analysis showed that amphioxus allantoicase was strongly expressed in the hepatic caecum, and weakly expressed in other tissues including hind-gut, gill, muscle,

Display centered at: Allantoicase, 5722.33

Concept and Design by Loic Royer

6 GoPubMed

- **Name of the system**: GoPubMed
- **Brief description of the system:**

  GoPubMed is an alternative to classical literature search. GoPubMed submits keywords to PubMed, extracts GO-terms from the retrieved abstracts, and presents the induced ontology for browsing. The induced ontology is the minimal subset of GO, which comprises all GO terms found in the documents. The users actually queries PubMed.

- **Requirments:**

  GoPubMed is a freely available Web application. A DSL internet connection and a modern browser will do.

- **Example:**

  Example: Actin:

  Which term is most obviously related to actin? Many researchers will promptly reply myosin. In GoPubMed such obvious relationships can be identified by exploring the most frequently occurring GO terms. In the case of actin GoPubMed suggests that some 80 papers mention cellular components or any sub-terms, nearly 80 papers cell or sub-terms, some 70 intracellular, 67 cytoplasm, 57 cytoskeleton, 50 actin cytoskeleton and 9 myosin. Thus, in only 5 clicks the user can relate actin and myosin and even underpin this relationship through the statements of associated abstracts, such as PMID 15679101: Syntrophin was also able to inhibit actin-activated myosin ATPase activity.

  Example: Author profiles

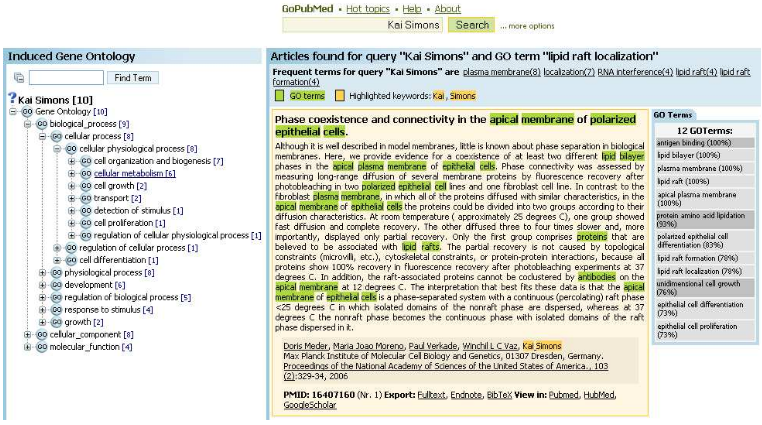
  GoPubMed is generally useful to gain an overview over a set of articles and to define a profile for these articles. This feature can be used to quickly get an insight into the topics a researcher is working on. Specifying e.g. the name and affiliation of a researcher as query to GoPubMed one will be able explore the researcher's interest and focus of research. In particular, the induced GeneOntology can serve as a profile representing that researcher. As an example, consider Kai Simons in Dresden. The PubMed query simons dresden returns some 20 articles. The induced ontology for these papers indicates that he is working on cell organisation and biogenesis (within the process ontology) and in particular on lipid raft formation, a term that is found in 13 papers.

- **Brief description how rules and other technologies are used:**

  GoPubMed handles ontologies in OWL and documents in PubMed XML. GoPubMed implements simple reasoning computing induced ontologies from given documents.

- **Brief summary of the benefits:**

  First, it gives an overview over literature abstracts by categorizing abstracts according to the Gene Ontology and thus allowing users to quickly navigate through the abstracts by category. Second, it automatically shows general ontology terms related to the original query, which often do not even appear directly in the abstract. Third, it enables users to verify its classification because GeneOntology terms are highlighted in the abstracts and as each term is labelled with an accuracy percentage. Fourth, exploring PubMed abstracts



Kai Simons [10]
- Gene Ontology [10]
  - biological_process [9]
    - cellular process [8]
      - cellular physiological process [8]
        - cell organization and biogenesis [7]
        - cellular metabolism [6]
        - cell growth [2]
        - transport [2]
        - detection of stimulus [1]
        - cell proliferation [1]
        - regulation of cellular physiological process [1]
      - regulation of cellular process [1]
      - cell differentiation [1]
    - physiological process [8]
    - development [6]
    - regulation of biological process [5]
    - response to stimulus [4]
    - growth [2]
  - cellular_component [8]
  - molecular_function [4]

Articles found for query "Kai Simons" and GO term "lipid raft localization"

Frequent terms for query "Kai Simons" are plasma membrane(8) localization(7) RNA interference(4) lipid raft(4) lipid raft formation(4)

🟩 GO terms 🟨 Highlighted keywords: Kai , Simons

Phase coexistence and connectivity in the apical membrane of polarized epithelial cells.

Although it is well described in model membranes, little is known about phase separation in biological membranes. Here, we provide evidence for a coexistence of at least two different lipid bilayer phases in the apical plasma membrane of epithelial cells. Phase connectivity was assessed by measuring long-range diffusion of several membrane proteins by fluorescence recovery after photobleaching in two polarized epithelial cell lines and one fibroblast cell line. In contrast to the fibroblast plasma membrane, in which all of the proteins diffused with similar characteristics, in the apical membrane of epithelial cells the proteins could be divided into two groups according to their diffusion characteristics. At room temperature (approximately 25 degrees C), one group showed fast diffusion and complete recovery. The other diffused three to four times slower and, more importantly, displayed only partial recovery. Only the first group comprises proteins that are believed to be associated with lipid rafts. The partial recovery is not caused by topological constraints (microvilli, etc.), cytoskeletal constraints, or protein-protein interactions, because all proteins show 100% recovery in fluorescence recovery after photobleaching experiments at 37 degrees C. In addition, the raft-associated proteins cannot be coclustered by antibodies on the apical membrane at 12 degrees C. The interpretation that best fits these data is that the apical membrane of epithelial cells is a phase-separated system with a continuous (percolating) raft phase <25 degrees C in which isolated domains of the nonraft phase are dispersed, whereas at 37 degrees C the nonraft phase becomes the continuous phase with isolated domains of the raft phase dispersed in it.

Doris Meder, Maria Joao Moreno, Paul Verkade, Winchil L C Vaz, Kai Simons
Max Planck Institute of Molecular Cell Biology and Genetics, 01307 Dresden, Germany.
Proceedings of the National Academy of Sciences of the United States of America., 103 (2):329-34, 2006

PMID: 16407160 (Nr. 1) **Export:** Fulltext, Endnote, BibTeX **View in:** Pubmed, HubMed, GoogleScholar

12 GOTerms:
- antigen binding (100%)
- lipid bilayer (100%)
- plasma membrane (100%)
- lipid raft (100%)
- apical plasma membrane (100%)
- protein amino acid lipidation (93%)
- polarized epithelial cell differentiation (83%)
- lipid raft formation (78%)
- lipid raft localization (78%)
- unidimensional cell growth (76%)
- epithelial cell differentiation (73%)
- epithelial cell proliferation (73%)

Figure 4: Screenshot of GoPubMed

with GoPubMed is useful as it shows definitions of GeneOntology terms without the need for further look up.