

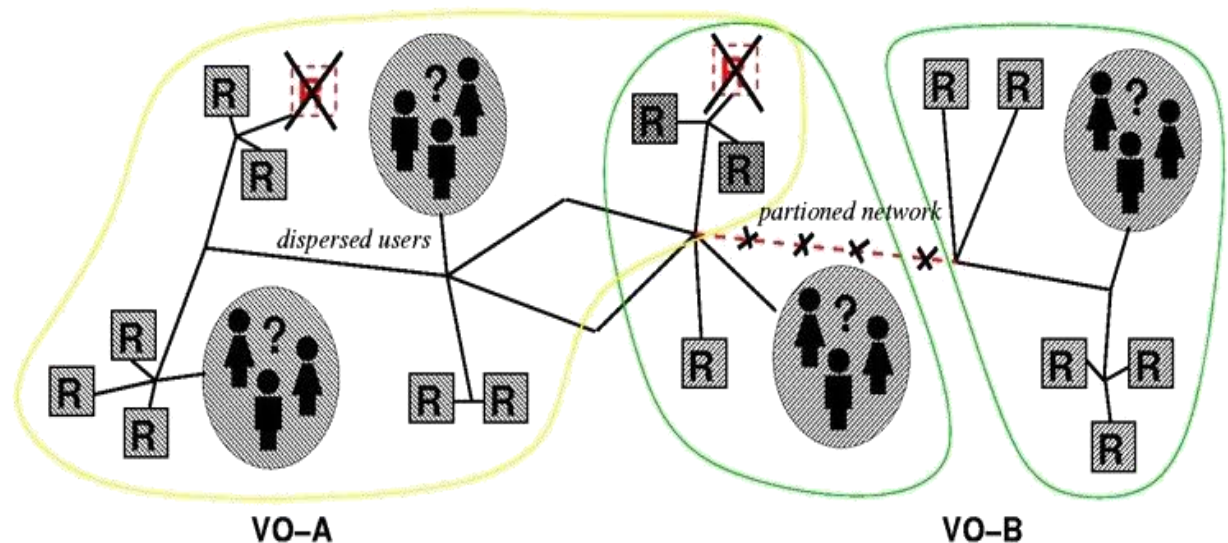


SEMANTIC GRID

Pham Thi Bich Lien
Nguyen Van Nhat
Nguyen Duy Thien

What is Grid?

- flexible, secure, coordinated resource sharing among dynamic collections of individuals, institutions, and resources
 - **virtual organizations.**



Why we need Semantic Grid?

- **Problem:** enabling scientists to generate, analyse, share and discuss their insights, experiments and results in a more **effective manner**.
- there is a high degree of **easy-to-use** and seamless automation and in which there are flexible collaborations and computations on a global scale.

Why we need Semantic Grid?

- **Example:** To illustrate, consider if a machine's operating system is described as "SunOS" or "Linux." To query for a machine that is "Unix" compatible, a user either has to:
 1. Explicitly incorporate the Unix compatibility concept into the request requirements by requesting a disjunction of all Unix-variant operating systems, e.g., (OpSys="SunOS" || OpSys="Linux")

Why we need Semantic Grid?

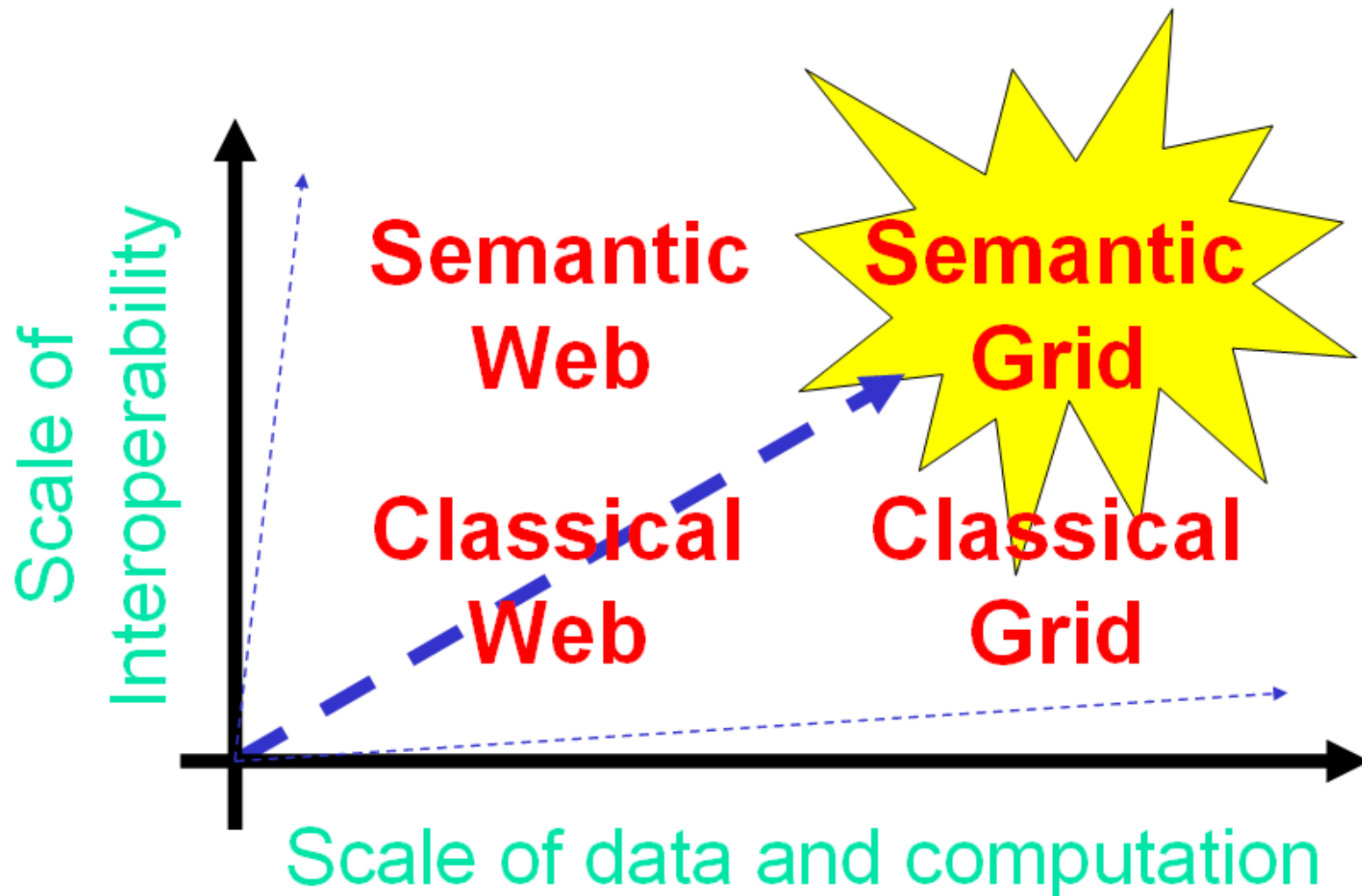
2. Wait for all interesting resources to advertise their operating system as Unix as well as either Linux or SunOS, e.g., (OpSys="SunOS," "Unix"), and then express a match as set-membership of the desired Unix value in the OpSys value set, e.g., hasMember(OpSys, "Unix").
- **Apply Semantics...**
 - Knowledge base: "SunOS and Linux are types of Unix operating system"
 - Request: "Need the Unix compatibility OS"

Why we need Semantic Grid?

Grid → “It is a truth universally acknowledged,
that an application in possession of
good middleware, must be in want of
meaningful metadata.”
↑
Semantic

-- prof. C. Goble

What is Semantic Grid?



What is Semantic Grid?



- An extension of the current **Grid** in which information and services are given **well-defined and explicitly represented meaning**, so that it can be **shared and used** by **humans and machines**, better enabling them to work in cooperation

What is Semantic Grid?



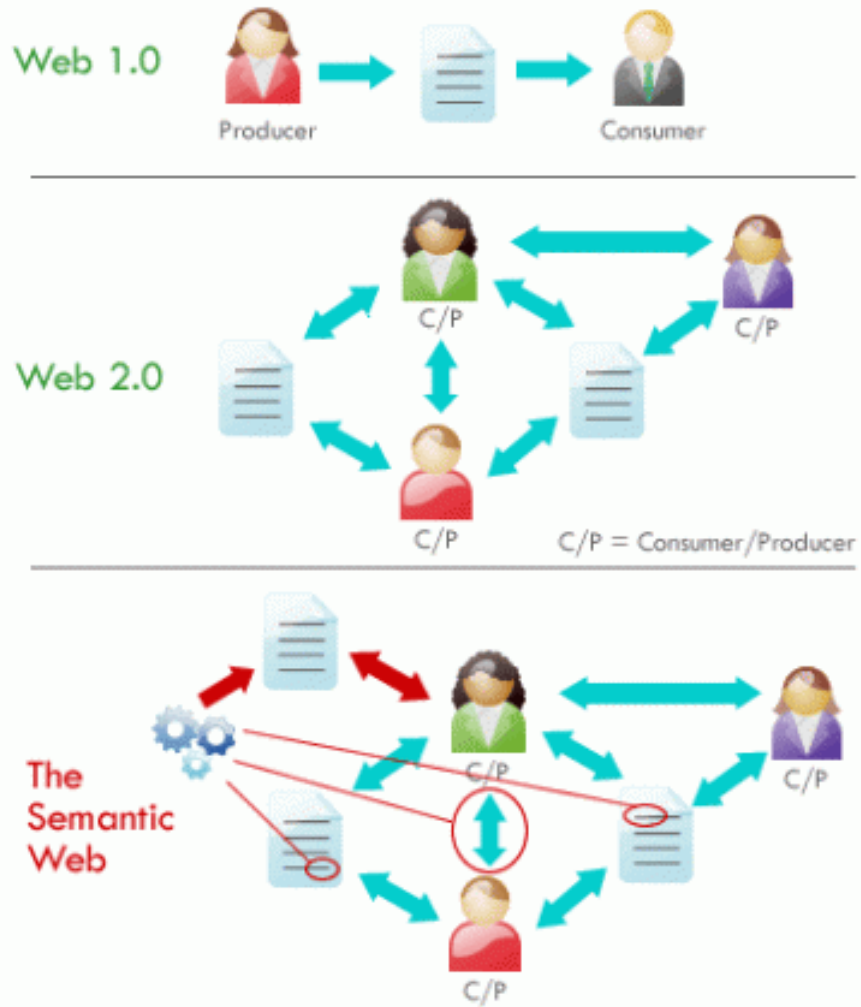
- An extension of the Grid
- Rich metadata is exposed and handled explicitly, shared, and managed via Grid protocols

What is Semantic Grid?



- The Semantic Grid uses metadata to describe information in the Grid.
- Turning information into something more than just a collection of data means understanding the context, format, and significance of the data.
- Therefore:
 - Understand information
 - Discovery and reuse

Semantic Web



Semantic Web

- “...to create a universal medium for the exchange of data. It is envisaged to smoothly interconnect personal information management, enterprise application integration, and the global sharing of commercial, scientific and cultural data.
- Facilities to put **machine-understandable data** on the Web are quickly becoming a high priority for many organizations, individuals and communities.

Semantic Web

- The Web can reach its full potential only if it becomes a place where data can be shared and processed by automated tools as well as by people.
- For the Web to scale, tomorrow's programs must be able to share and process data even when these programs have been designed totally independently.”

Semantic Web

- Current Web (WWW)
 - Is a huge library of interlinked documents that are transferred by computers and presented to people
 - Anyone can contribute to it
 - Quality of information or even the persistence of documents cannot be generally guaranteed
 - Contains a lot of information and knowledge, but machines usually serve only to deliver and present the content of documents describing the knowledge
 - People have to connect all the sources of relevant information and interpret them themselves

Machine can Process the content

But

Machine can't Understand content

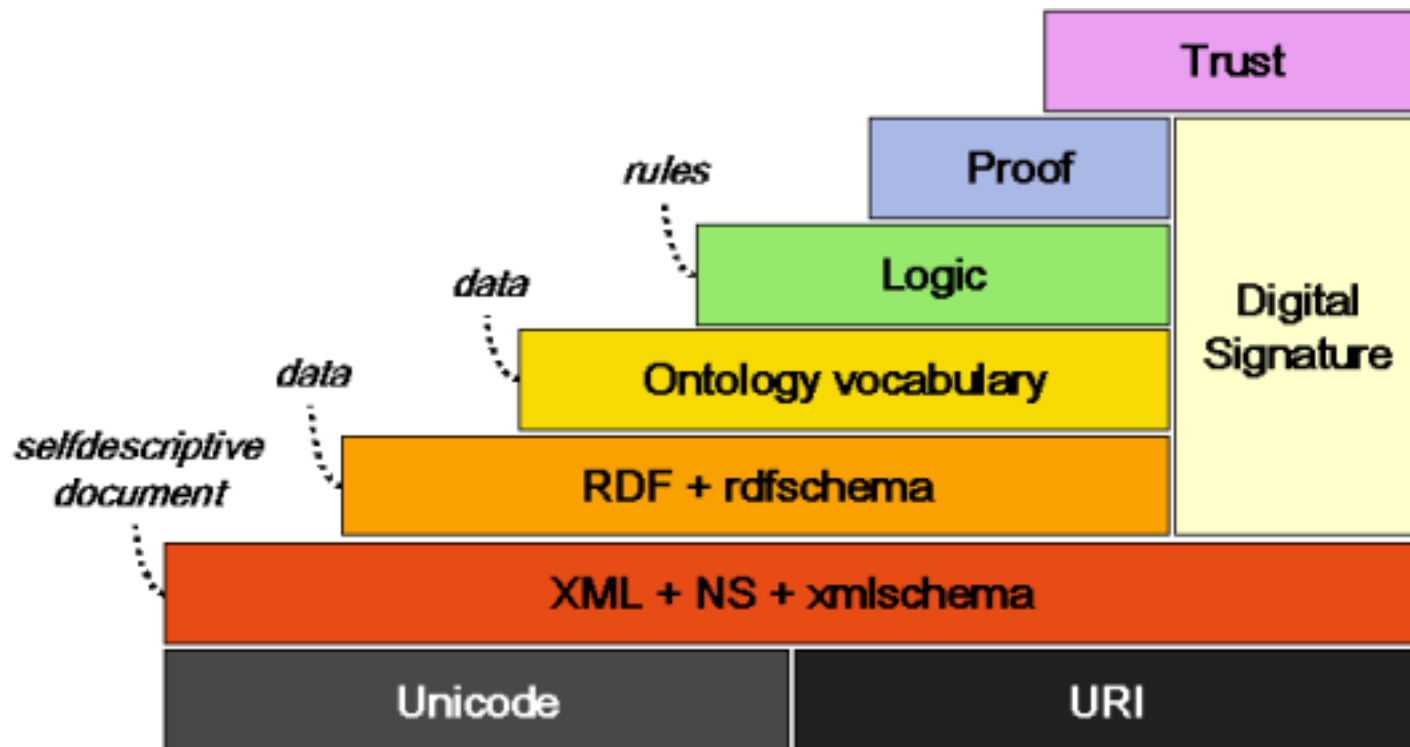
Semantic Web

- Definition

The **Semantic Web** is an extension of the current web in which the semantics of information and services on the web is defined, making it possible for the web to understand and satisfy the requests of people and machines to use the web content.

--- Tim Berners-Lee

Semantic Web



Semantic Web

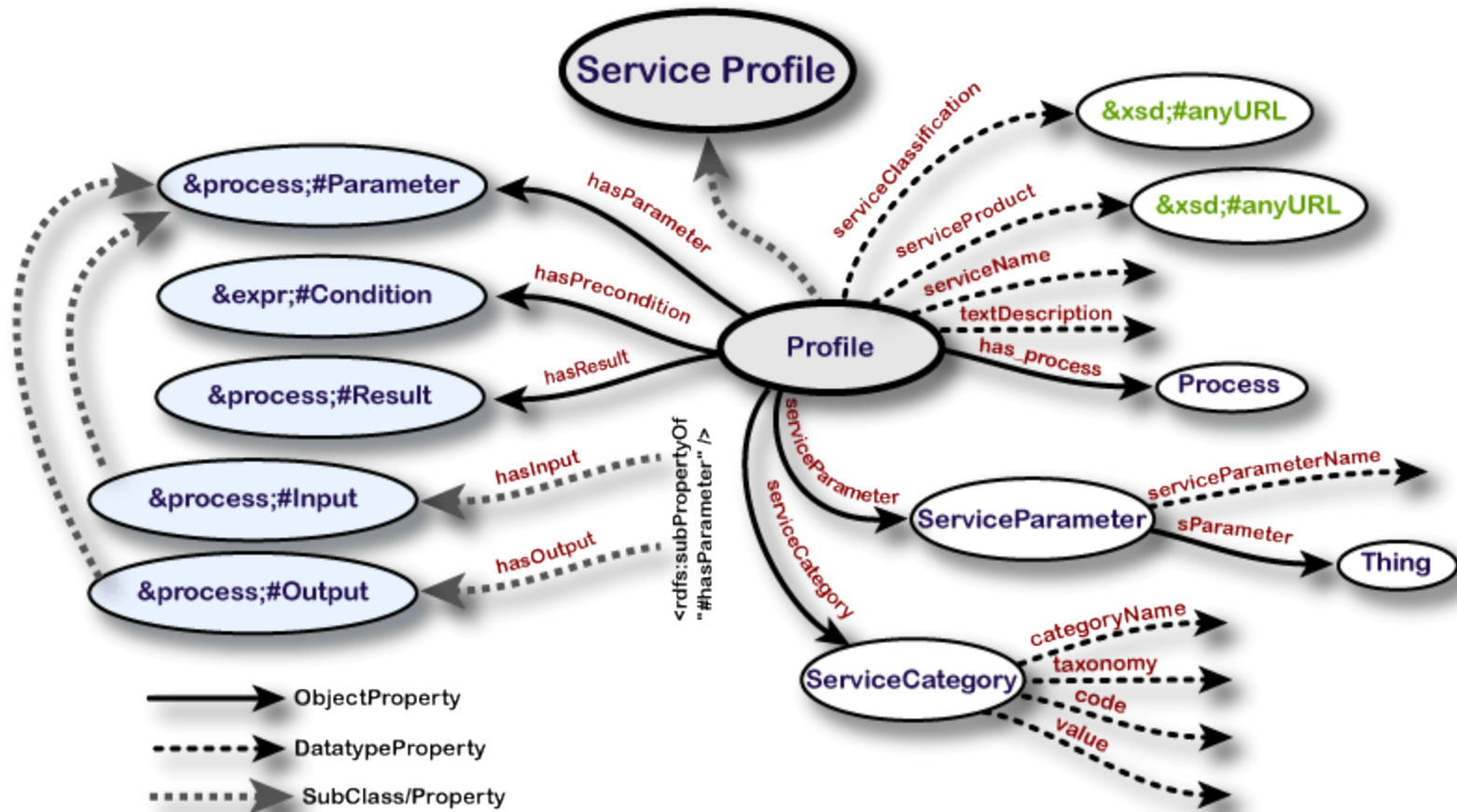


- **Ontology** is a formal representation of the knowledge by a set of concepts within a domain and the relationships between those concepts. It is used to reason about the properties of that domain, and may be used to describe the domain.
- Implement by XML, XML Namespace, XML Schema, RDF, RDF Schema và OWL

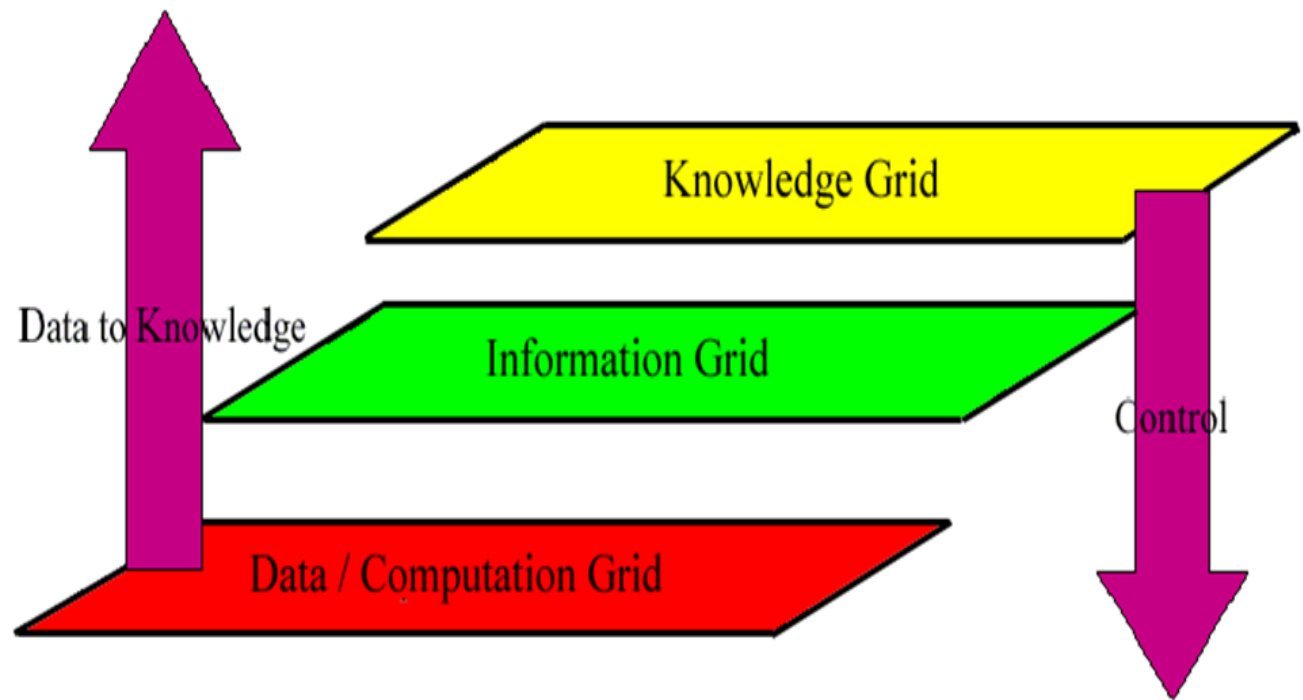
Semantic Web



- **Ontology example**



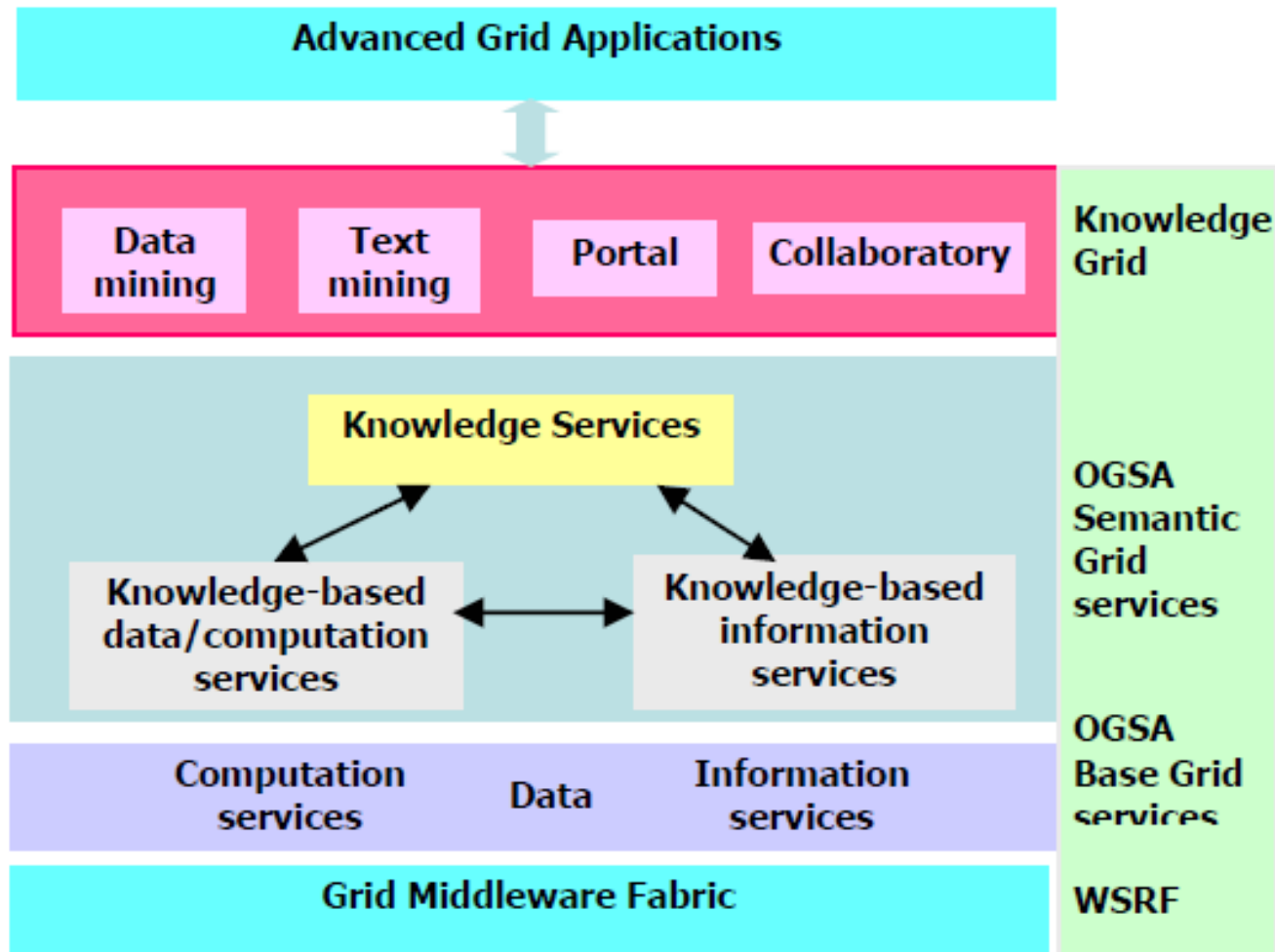
Semantic Grid Requirement



Semantic Grid Requirement

- *Resource description, discovery and use.*
- *Process description and enactment.*
- *Autonomic behaviour.*
- *Security and trust.*
- *Annotation.*
- *Information Integration.*
- *Synchronous information streams and fusion.*
- *Context-aware decision support.*
- *Communities.*
- *Smart environments.*

Semantic Grid Architecture



S-OGSA



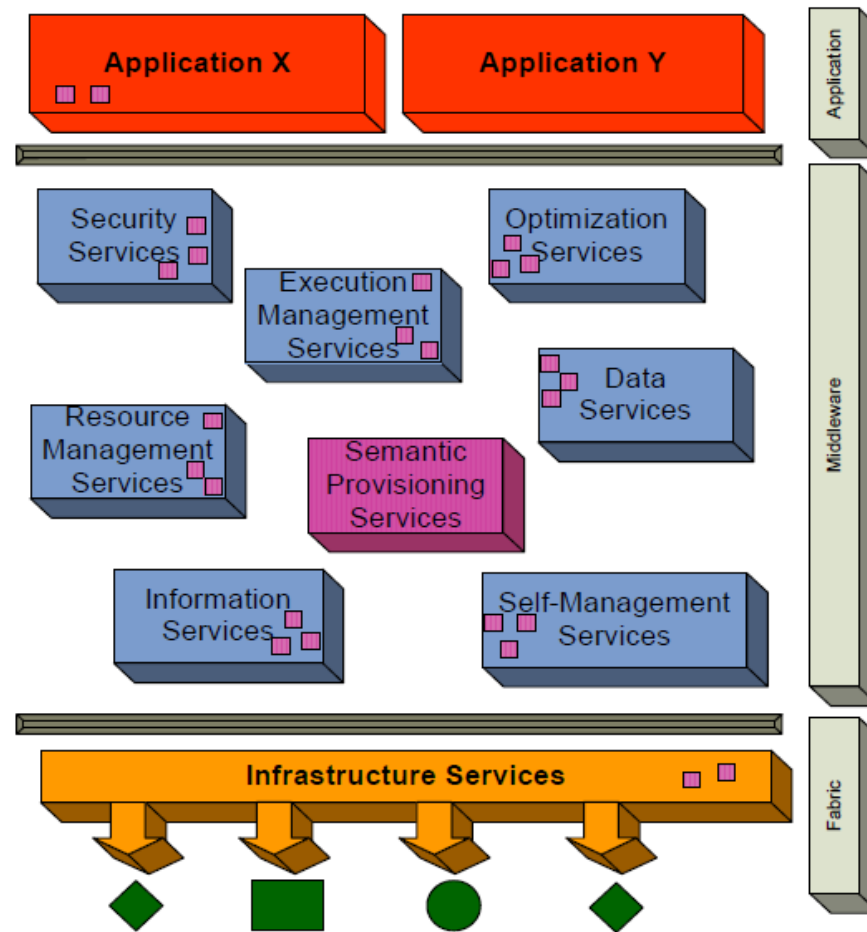
- A Grid usually consist of several different services by OGSA:
 - VO management service
 - Resource discovery and Management service
 - Job Management service
 - Security service
 - Data Management service
- The S-OGSA should (will) provide the metadata + semantic services to those services.

S-OGSA



- The Solution:
 - Attached the semantic to Grid entities.
 - Binding them together by semantic binding service.
 - Normal grid services can be “semantic” by the semantic binding service.

S-OGSA



DESIGN PRINCIPLES FOR A REFERENCE SEMANTIC GRID ARCHITECTURE



- **Parsimony** of architecture elements.
- **Extensibility** of the framework.
- **Uniformity** of the mechanisms.
 - Similar to the Grid resources they are associated with, knowledge and metadata should exhibit manageability aspects.
 - S-OGSA must encapsulate both stateless and stateful Grid services, as OGSA does.
 - Knowledge services in S-OGSA are OGSA-observant Grid services.

DESIGN PRINCIPLES FOR A REFERENCE SEMANTIC GRID ARCHITECTURE



- **Diversity** of semantic capabilities
 - Ignorant of the associated semantics of another entity.
 - Aware that another entity has explicit associated semantics but incapable of processing it.
 - Aware that another entity has explicit associated semantics and capable of processing it, partially or completely.
- **Heterogeneity** of semantic representation.

DESIGN PRINCIPLES FOR A REFERENCE SEMANTIC GRID ARCHITECTURE

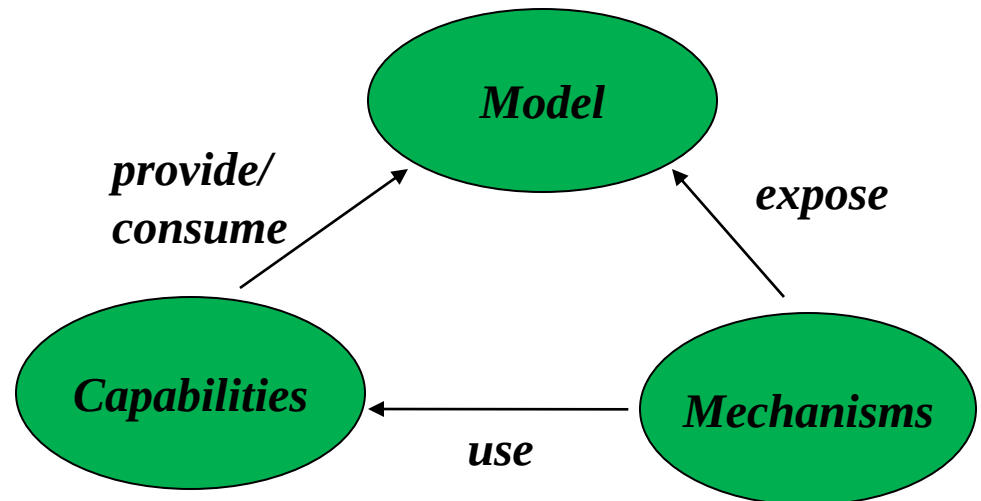


- **Enlightenment** of services
 - S-OGSA should have minimal impact on adding explicit semantics to current Grid entity interfaces or on Grid services that are ignorant of Semantic Grid entities;
 - Grid entities should not break if they can consume and process Grid resources but cannot consume and process their associated semantics (that is, if they are aware of the semantics but incapable of processing it);
 - If a Grid entity understands only part of the knowledge it consumes it should be able to use it as a best effort;
 - During their lifetime, Grid entities can incrementally acquire, lose and reacquire explicit semantics;

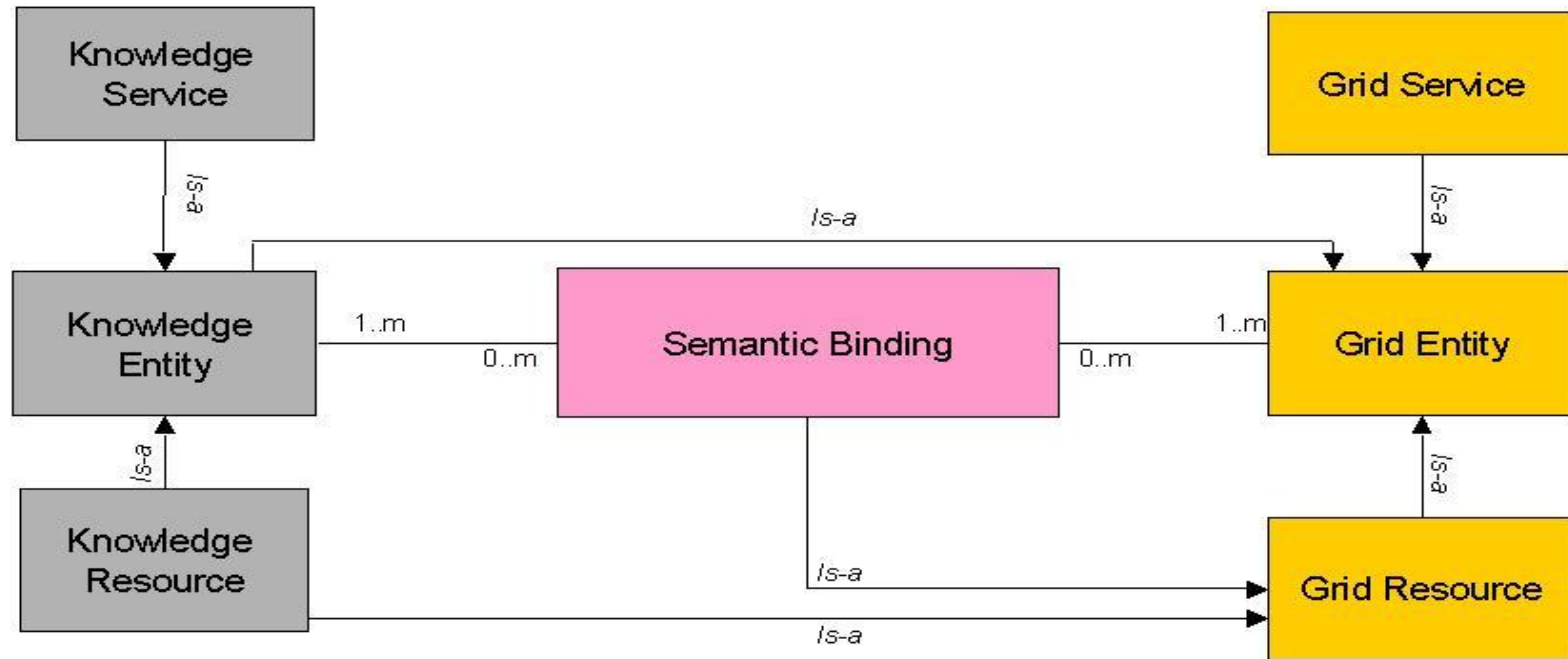
S-OGSA



- Defined by
 - Model
 - New entities
 - Capabilites
 - New functionalities
 - Mechanisms
 - How it is delivered

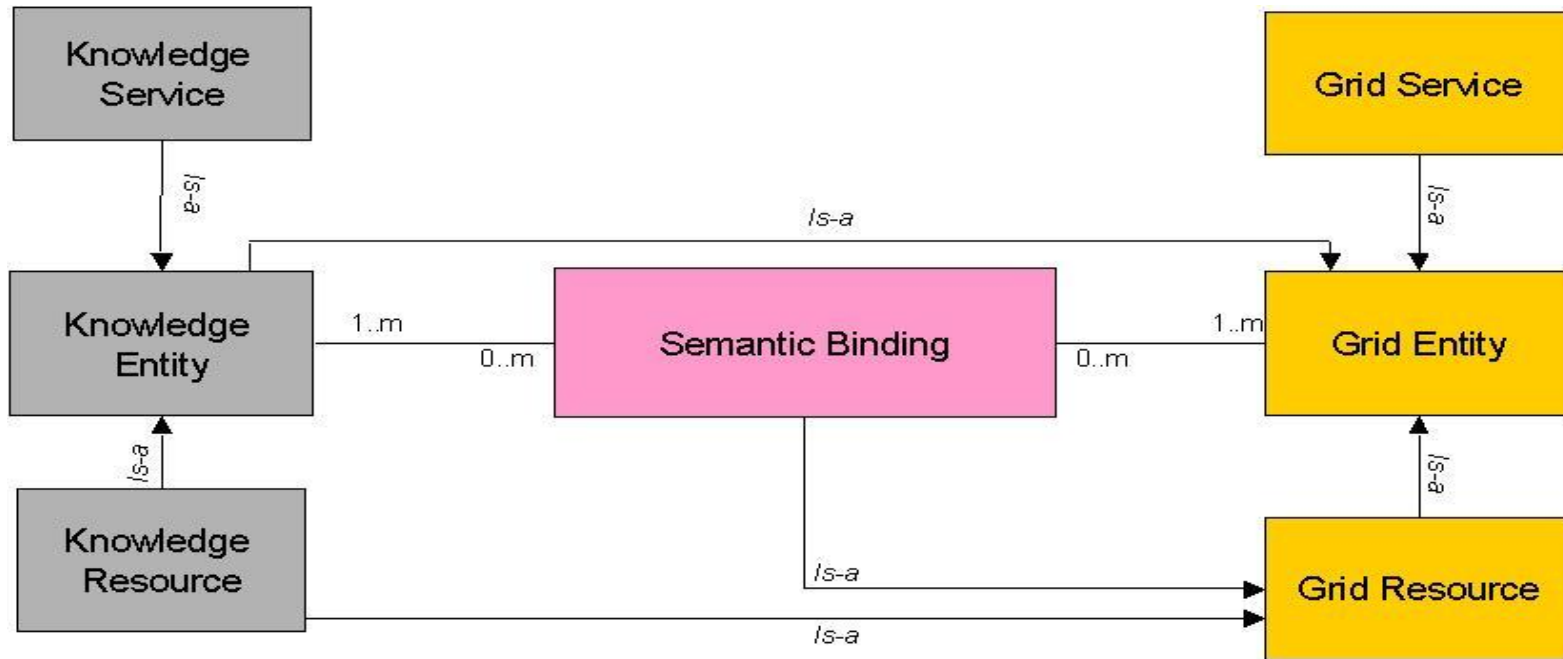


S-OGSA MODEL



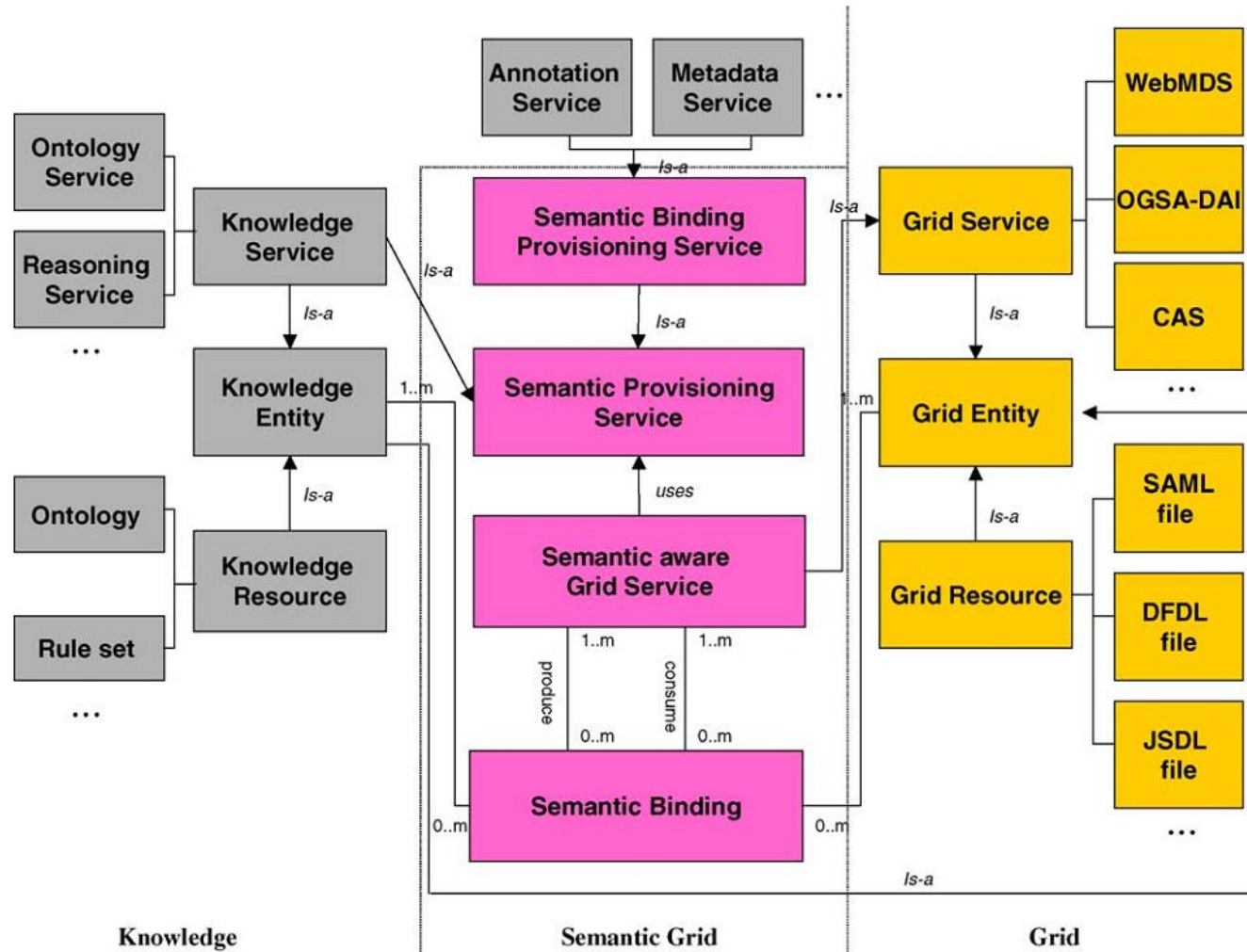
Entities in S-OGSA and their relationships.

S-OGSA MODEL



- **Grid Entities:** Grid resources and services
- **Knowledge Entities:** represent/operate with some form of knowledge (e.g ontologies, rules, knowledge bases ...)
- **Semantic Bindings:** entities associate of a Grid Entity with one or more Knowledge Entities

S-OGSA CAPABILITIES



S-OGSA CAPABILITIES



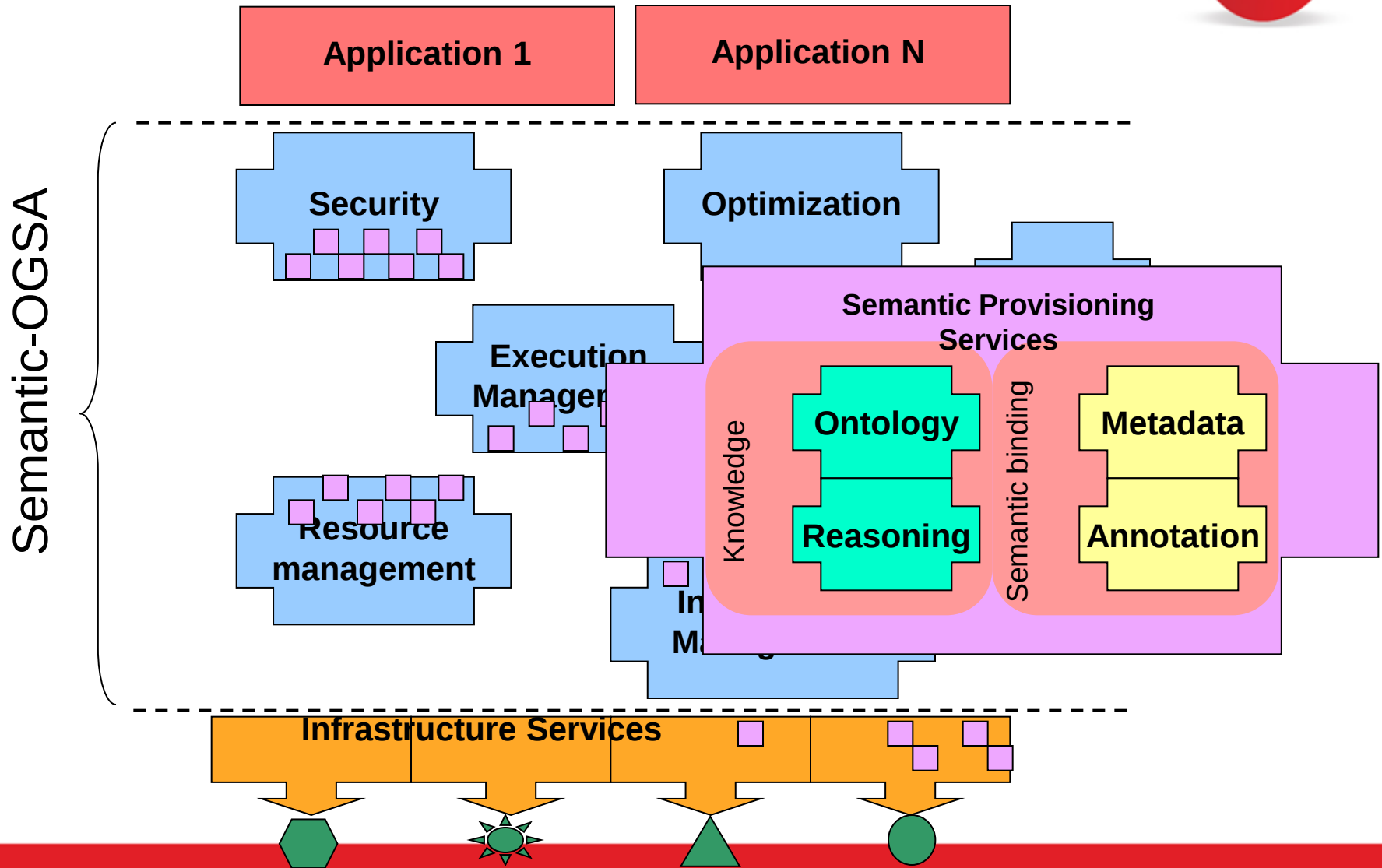
- **Semantic Provisioning Services – SPS**
 - provisioning and management of explicit semantics and its association with Grid entities
 - creation, storage, update, removal and access of different forms of knowledge and metadata
 - **Knowledge provisioning services**
 - ontology services , reasoning services .
- **Semantic binding provisioning services**
 - metadata services, annotation services .

S-OGSA CAPABILITIES

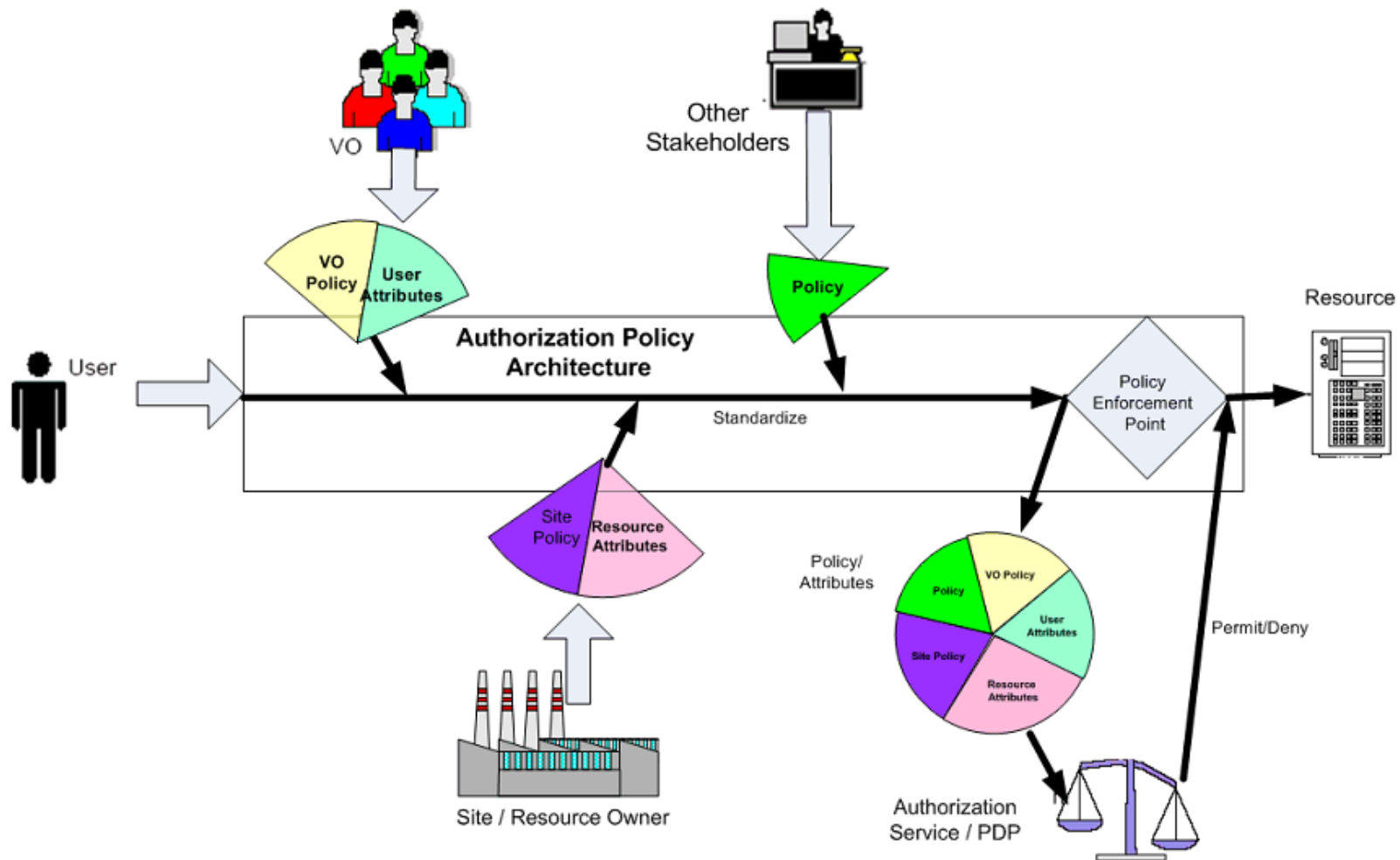


- **Semantically Aware Grid Services**
 - Be able to consume Semantics Bindings and being able to take actions based on knowledge and metadata
 - Sample Actions :
 - Metadata aware authorization of a given identity by a VO Manager service
 - Execution of a search request over entries in a semantic resource catalogue
 - Incorporation of a new concept in to an ontology hosted by an ontology service

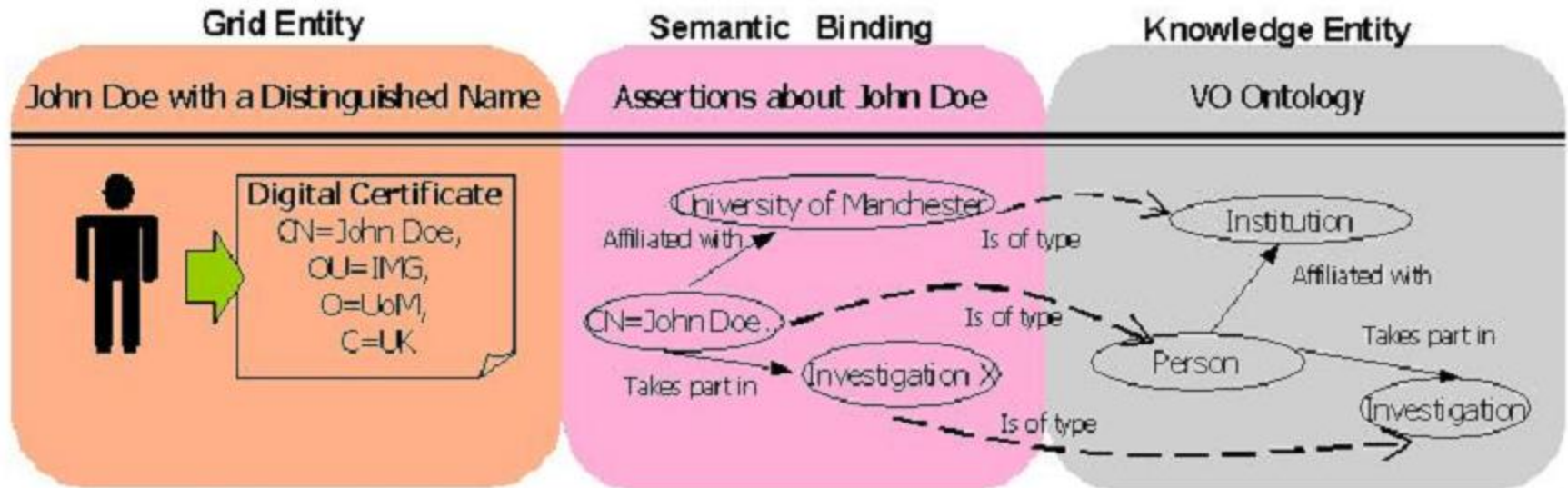
OGSA TO S-OGSA



EXAMPLE: S-OGSA MODEL AND CAPABILITIES



EXAMPLE: S-OGSA MODEL AND CAPABILITIES

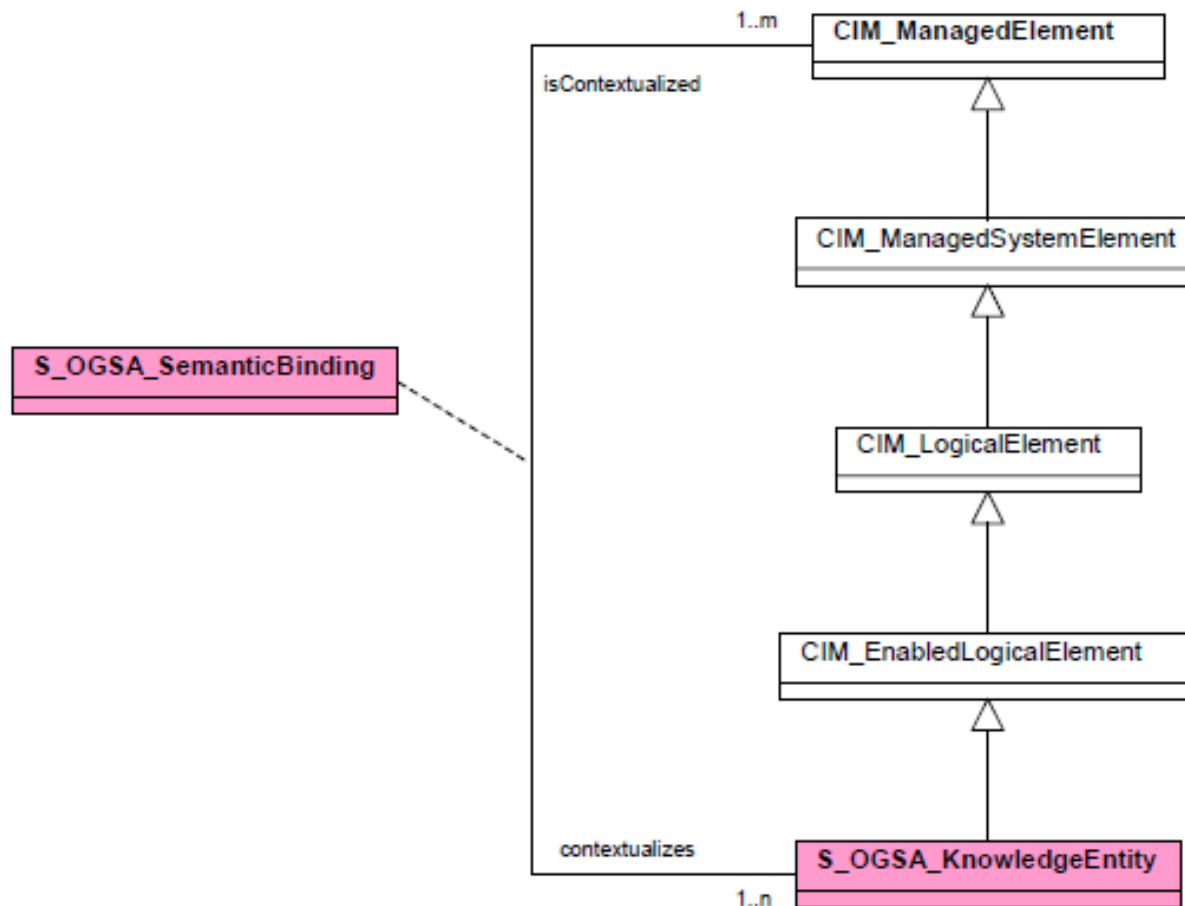


S-OGSA MECHANISMS



- Treating Knowledge Entities and Semantic Bindings as Grid Resources
 - Common Information Model (CIM) Resource Model
 - Grid Entities : class CIM-ManagedElement in the CIM Model.
 - Knowledge Entities : class S-OGSA-KnowledgeEntity
 - S-OGSA-SemanticBinding:Semantic Binding, the association between a Grid Entity (CIM-ManagedElement) and a Knowledge Entity (S-OGSA-KnowledgeEntity)

S-OGSA MECHANISMS

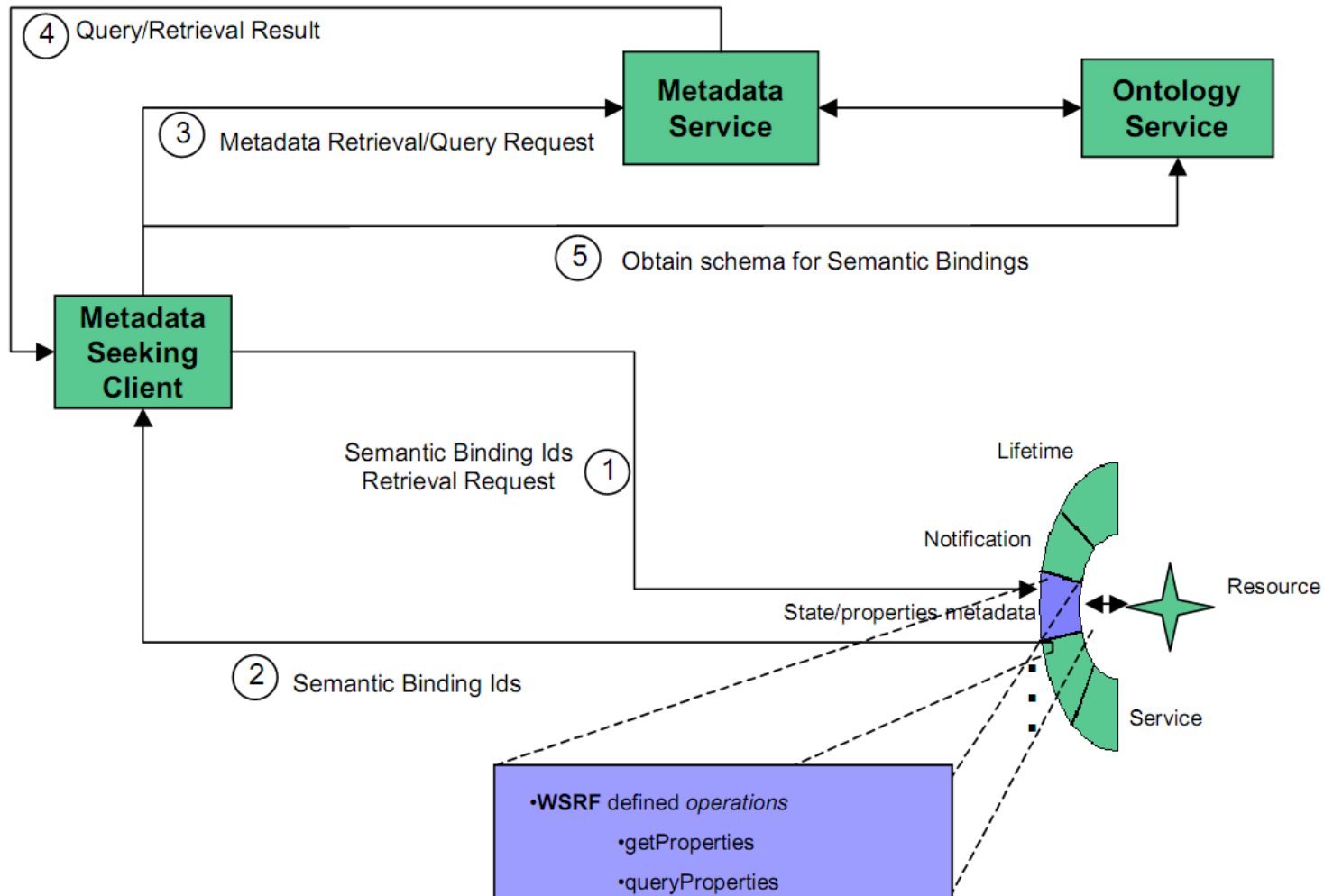


S-OGSA MECHANISMS



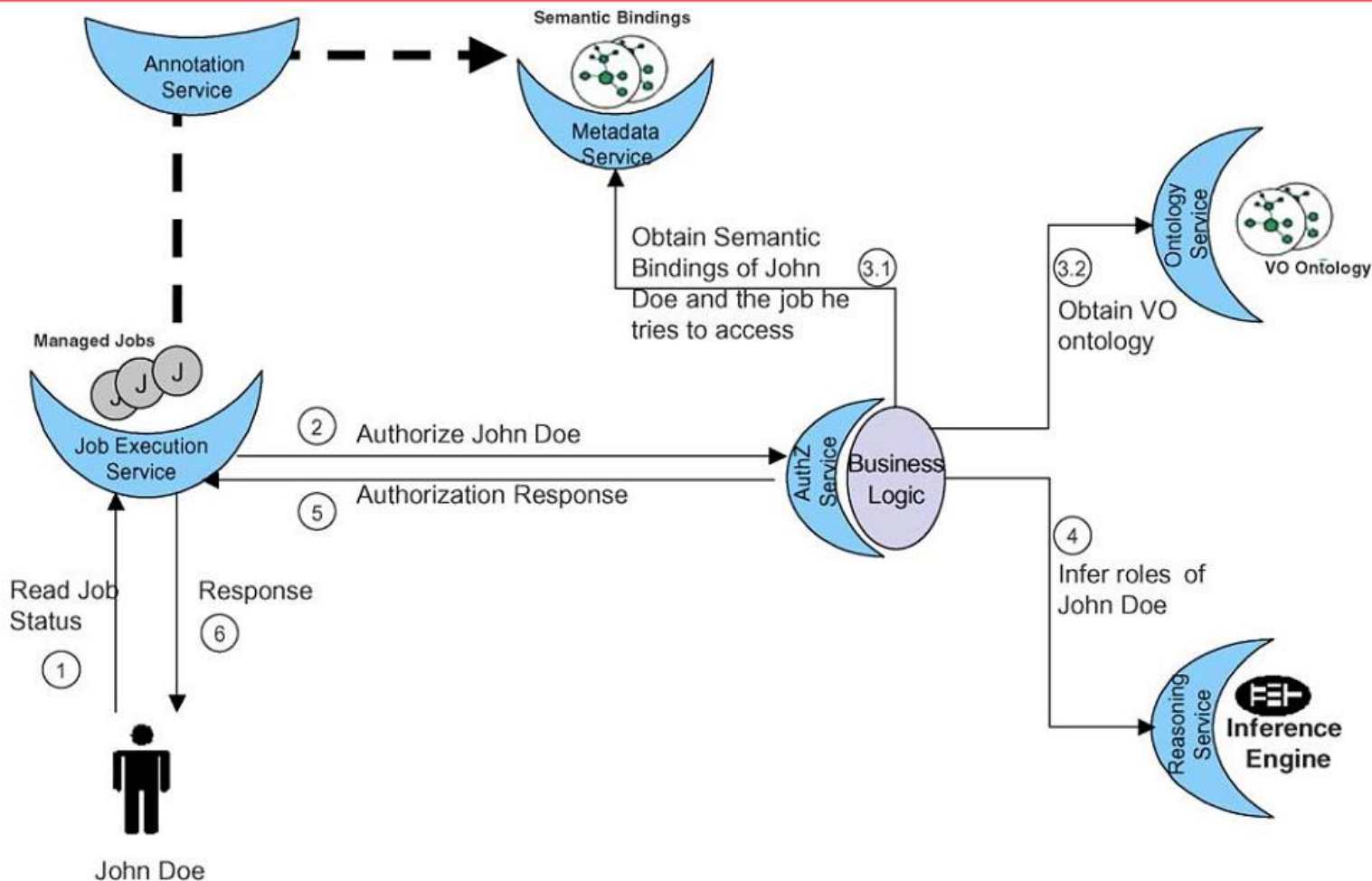
- S-Stateful Services: Delivery of Semantic Bindings by Grid Services.
 - Virtualise Grid resources
 - Set of mapping
 - Delivery mechanism rather than a descriptive framework

S-OGSA MECHANISMS



Retrieving and Querying Semantic Bindings of Resources

S-OGSA MECHANISMS

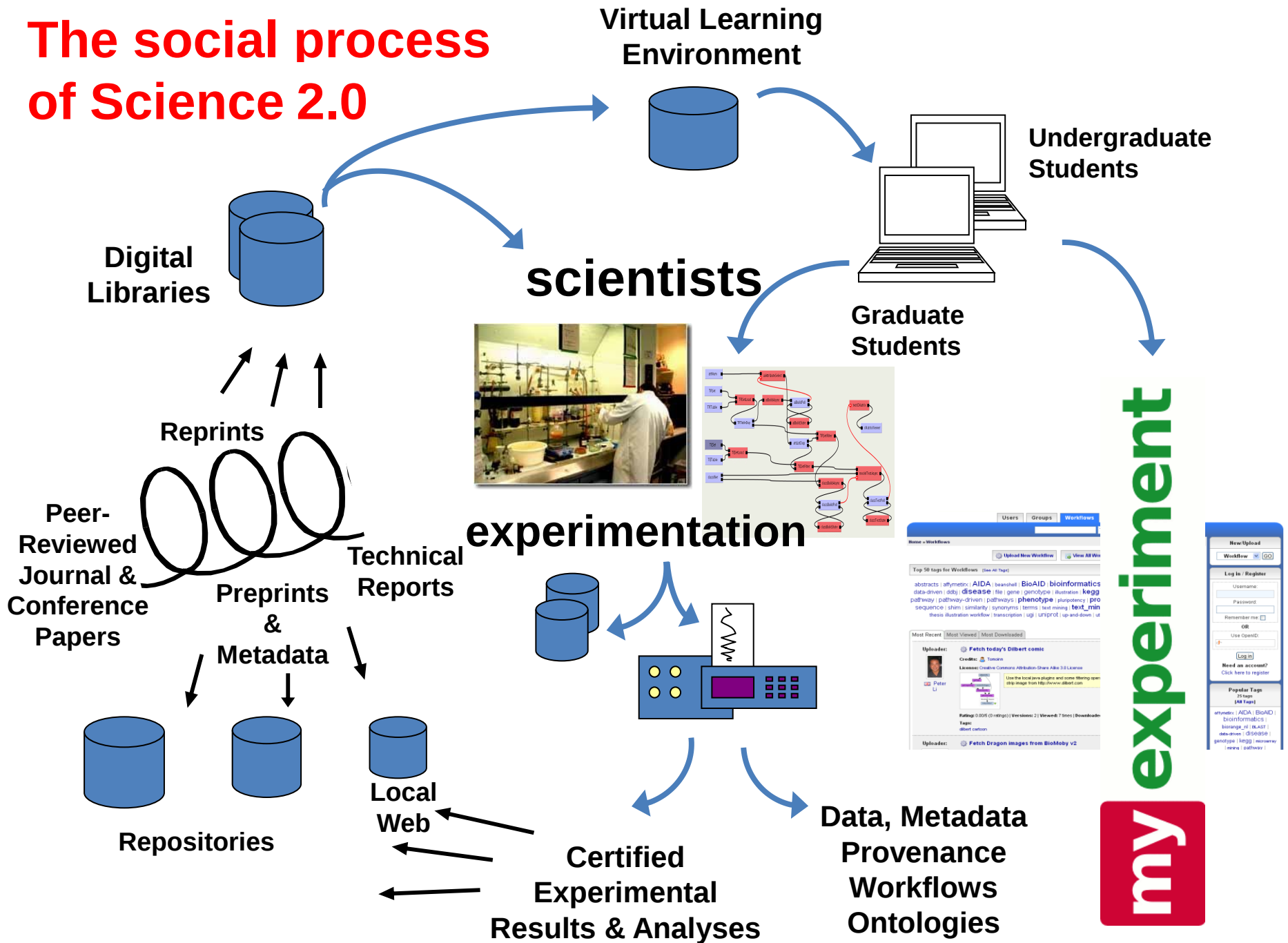


A semantic aware authorization service consuming an input that could in relation with S-OGSA Semantic Provisioning Services.

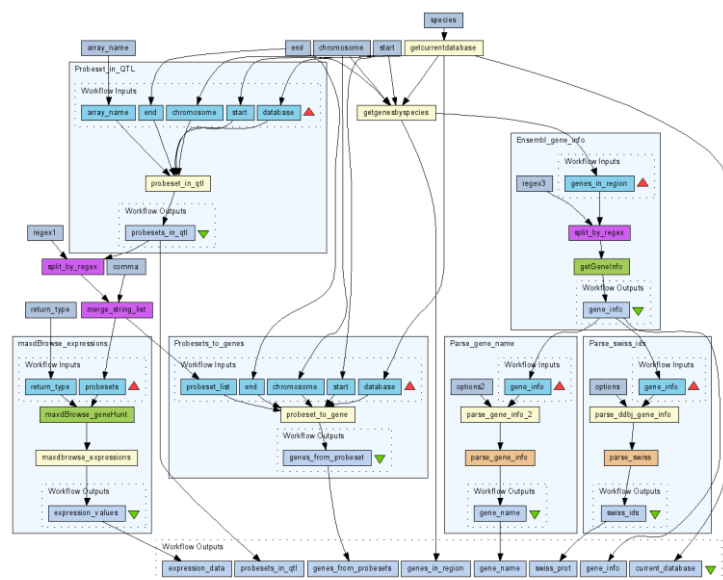


- What is it?
- How it is built?
- Towards the e-Laboratory

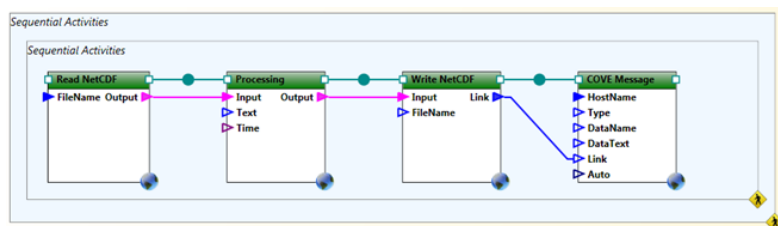
The social process of Science 2.0



Sharing pieces of process



<http://www.mygrid.org.uk/tools/taverna/>



<http://www.microsoft.com/mscorp/tc/trident.msp>

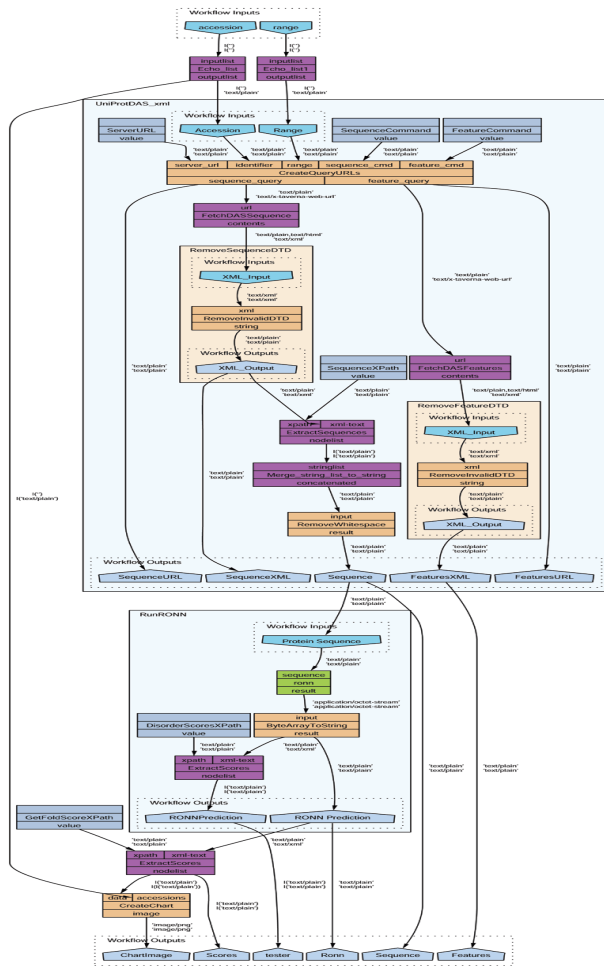
Monitor the formation of an aromatic imine by HMR and CMR in CDC13

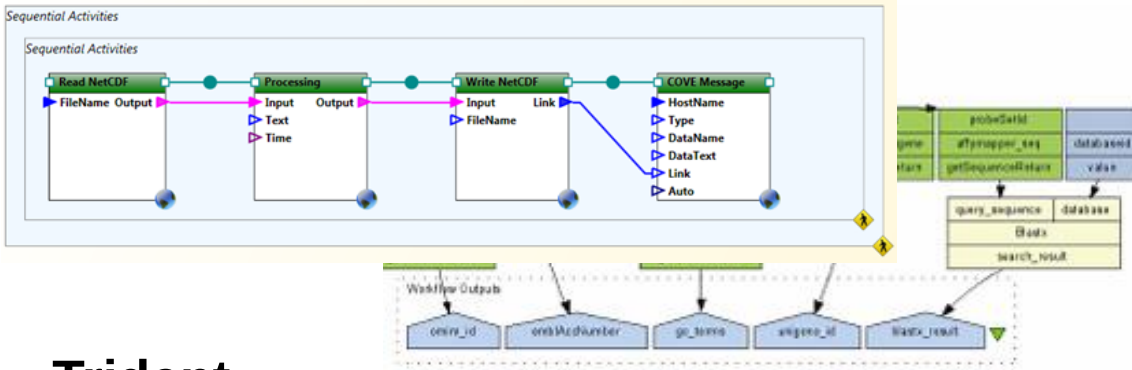
1. Make up separate 1 mL of 1M solutions of piperonal and 5-methylfurfurylamine in CDC13.
2. Take HMRs and CMRs of the aldehyde and amine. Use 5 sec relaxation time and acquire for about 15 mins for the CMR. This should be good enough based on [James' results](#) at 1M in methanol.
3. Combine the two solutions into a 1 dram vial and shake vigorously then transfer to an NMR tube.
4. Take HMR at 5, 10 and 20 minutes after mixing.
5. Take CMR at 25 min after mixing.
6. Take HMR at 40 min after mixing.
7. Take CMR at 45 min after mixing.
8. Take HMR at 80 mins after mixing.
9. Take CMR at 85 mins after mixing.
10. Continue to take NMRs after interval doubling until no more change is observed.

<http://usefulchem.wikispaces.com/page/code/EXPLAN001>

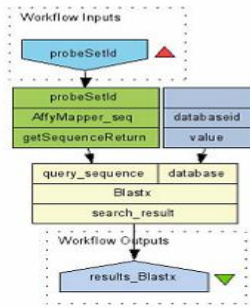
E. Science laboris

- Workflows are the new rock and roll
- Machinery for **coordinating** the execution of (scientific) services and **linking** together (scientific) resources
- The era of Service Oriented Applications
- Repetitive and mundane boring stuff made easier

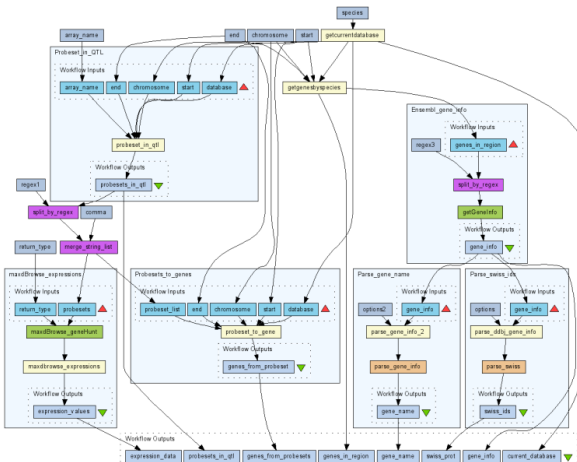




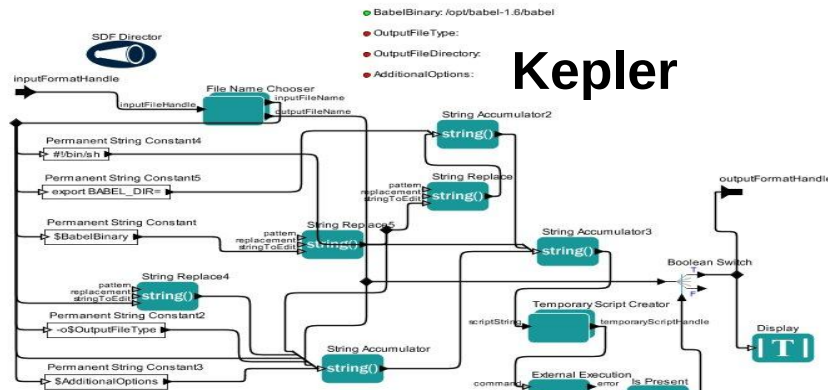
Trident



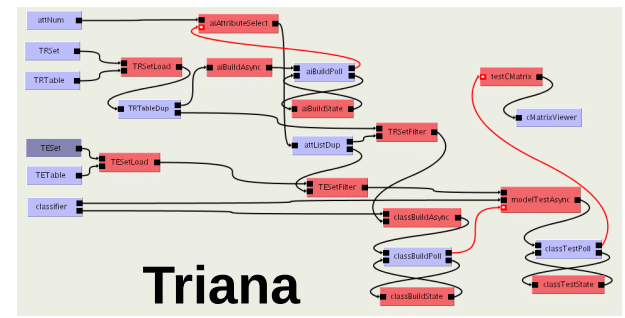
Taverna



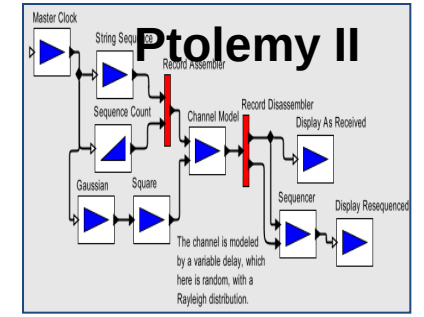
Kepler



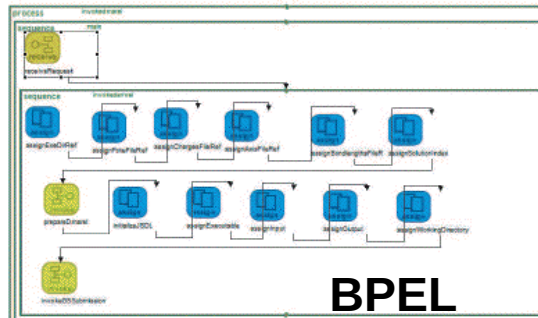
Triana



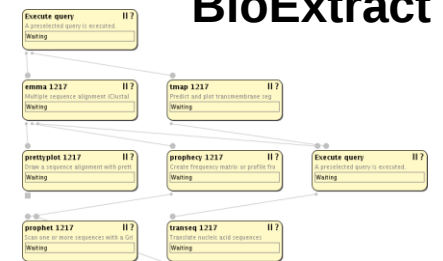
Ptolemy II



BPEL

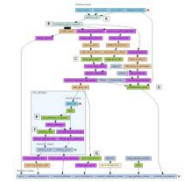


BioExtract



Reuse, Recycling, Repurposing

- Paul writes workflows for identifying biological pathways implicated in resistance to Trypanosomiasis in cattle
- Paul meets Jo. Jo is investigating Whipworm in mouse.
- Jo reuses one of Paul's workflow **without change**.
- Jo identifies the biological pathways involved in sex dependence in the mouse model, believed to be involved in the ability of mice to expel the parasite.
- Previously a manual **two year study** by Jo had failed to do this.





- “Facebook for Scientists”
...but different to Facebook!
- A repository of research methods
- A community social network
- A Virtual Research Environment
- Open source (BSD) Ruby on Rails application with HTML, REST and SPARQL interfaces
- Project started March 2007
- Closed beta since July 2007
- Open beta November 2007

myExperiment currently has 1712 registered users, 141 groups, 584 Taverna workflows plus 81 others, and 51 packs

Go to www.myexperiment.org to access publicly available content or create an account

Keep up to date

Get the latest news about what your online community is doing and what's happening with your Research Objects.

Form Friends & Groups

Explore and manage the social network. You have fine control over the privacy and sharing of your Research Objects.

Find Workflows

See the latest and most popular workflows: discover, view, download, run, tag and rate. Upload your workflows.

Build Packs

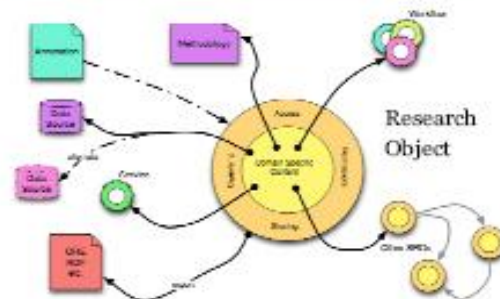
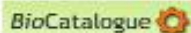
Share collections of items as individual packs — like all the digital items in an experiment. Include external items too.

Content types

We provide special support for workflow systems including Taverna and Trident, as well as experiment plans, providing a foundation for the e-Laboratory.

Curating process

Workflows capture pieces of research process which are curated by their authors, experts and the community. These curation models are also used in the BioCatalogue service registry.



All about the Research Object

See and manage all the essential extrinsic information and 'social metadata' — licence, tags, sharing, ratings.

Credits and attributions are an essential feature to support flow of rights and reputation.

All about me

Easy navigation using a dashboard of all the things relating to me and my social network.

JISC EPSRC



myexperiment

myExperiment Features

- User Profiles
- Groups
- Friends
- Sharing
- Tags
- Workflows
- Developer interface
- Credits and Attributions
- Fine control over privacy
- Packs
- Federation
- Enactment



Version 1 (of 1)

Version created on: 08/05/08 @ 15:25:29 by: Saeedeh | [Revision comments](#)

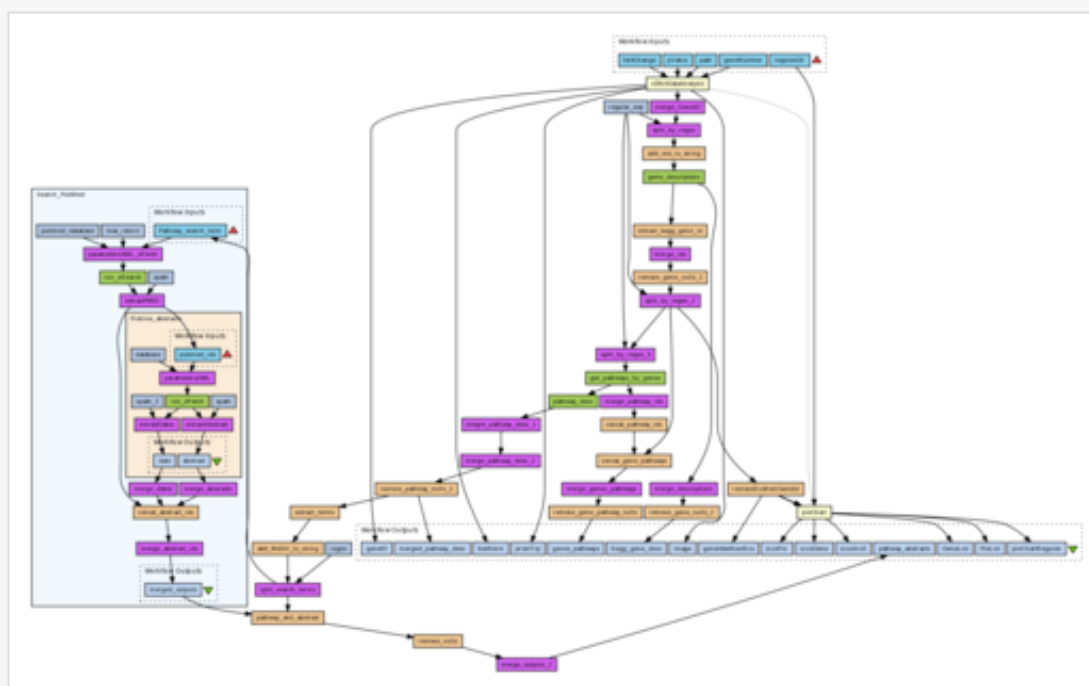
Last edited on: 12/05/08 @ 09:01:37 by: Saeedeh

Title: Escherichia coli : From cDNA Microarray Raw Data to Pathways and Published Abstracts

Type: Taverna 1

Preview

(Click on the image to get the full size)



[Download Scalable Diagram \(SVG\)](#)

Taverna 1 workflow

Original Uploader



Saeedeh

License

All versions of this Workflow are licensed under the **Creative Commons Attribution-Share Alike 3.0 License**.

Credits (2)

(People/Groups)



Saeedeh



Paul Fisher

Attributions (1)

(Workflows/Files)



HUMAN Microarray CEL file to candidate pathways

Tags (5)

☐ Original Uploader tags

[e.coli](#) | [kegg](#) | [Kegg Pathways](#)
| [pathways](#) | [pubmed](#)

Control over sharing

Upload Workflow

Workflow File:

Tags

Credit and Attribution

Defaults: you are the only person who gets credit; no attributions.

Sharing

Defaults: anyone can view, but only Friends can download; no one is allow

License/Rights

Default: people are allowed to build on this Workflow, but must give author(s) credit and give attribution to this Workflow. They must also share under the same conditions. ([Creative Commons Attribution-Share Alike 3.0 License](#))

Share with my Groups:

☐ UsefulChem	View and Download only
☐ Taverna 2 beta tester programme	View and Download only
☐ Social Scientific Land	View and Download only
☐ Mark's Project	View and Download only
☐ GNU	View and Download only
☐ myExperiment	View and Download only
☐ Music workflows	View and Download only

The most important aspect of myExperiment
Designed by scientists

For Developers

- All the myExperiment services are accessible through simple RESTful programming interfaces
 - use your existing environment and augment it with myExperiment functionality
 - build entirely new interfaces and functionality mashups
- The Ruby on Rails codebase is open source (BSD) so you can run your own myExperiment – perhaps for your own lab or to develop new functionality
- Go to wiki.myexperiment.org for information about our Developer Community

Google Gadgets

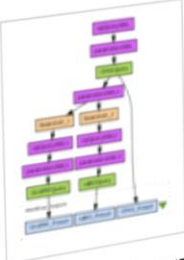
myExperiment Workflow Gadget

myexperiment

Search myExperiment..

Latest Workflows

 [Using CQL to query proteins data](#)



Wei Tan
Tags: [protein](#), [cabig](#), [cagrid](#), [cal](#), [grid service](#), [globus](#), [cancer res](#)

Created: 05 December 2008 22:03:03

myExperiment Tag Cloud

myexperiment

A B C D E F G H I J K L M N O P Q R S T

All (593 / 593)

[abstracts](#) [access grid](#) [accurate mass](#) [aceta](#)
[affmetrix](#) [affymetrix](#) [affymetrix](#) [africa](#) [afi](#)
[aging](#) [agricola](#) [agricultural](#) [biotechnology](#) [AIDA](#) [a](#)
[amber beta](#) [analysis](#) [and join](#) [and split](#) [animal](#) [biot](#)
[annotated services](#) [annotation](#) [append](#) [appen](#)
[aromaticity detection](#) [art2a](#) [astrogr](#)
[astronomy](#) [astrophysics](#) [atmosph](#)
[typing](#) [atomtyping](#) [augustus](#) [automatic fu](#)

myExperiment Workflow Search

myexperiment

10 results found for "cdk".

- GROUP
[cdk-taverna plugin](#)
- GROUP
[CDK-Taverna](#)
- GROUP
[Cheminformatics](#)
- WORKFLOW
[Insert Molecules into Database](#)

Bringing myExperiment
to the iGoogle user

Taverna Plugin

The screenshot displays the Taverna Workbench v1.7.1.0 interface. The main window is divided into two panes. The left pane, titled 'Design', shows a search results page for the tag 'emboss'. It lists 70 tags found, including 'AIDA', 'benchmarks', 'BioAID', 'bioinformatics', 'BLAST', 'example', 'FASTA', 'genotype', 'go', 'pattern', 'disease', 'ebi', 'emboss', 'kegg', 'microarray', 'multiple', 'sequence', 'terms', 'interpro', 'iteration', 'ncbi', 'ncbi_blast', 'nucleotide', 'alignment', 'mygrid', 'nticonworkflows', 'pdo', 'phenotype', 'phylogenetic', 'tree', 'protein', 'protein', 'sequence', 'similarity', 'taverna', 'text', 'annotation', 'protein', 'structure', 'pubmed', 'r', 'scaffold', 'sequence', 'alignment', 'structure', 'transmembrane', 'search', 'shim', 'similarity', 'smith-waterman', 'social', 'sciences', 'transmembrane', 'mining', 'text_mining', 'text_mining_network', 'transmembrane', 'prediction', 'tree', 'uniprot', 'upi', 'user_interaction', 'utility', 'VL-e'. Below the tag list, there are two workflow cards. The first card is titled 'BiomartAndEMBOSSAnalysis (version 2)' by Alan Williams, with a description: 'Using Biomart and EMBOSS soaplab services. This workflow retrieves a number of sequences from 3 species: mouse, human, rat, align them, and returns a plot of the alignment result. Corresponding sequence ids are also returned.' The second card is titled 'A workflow version of the EMBOSS tutorial (version 1)' by Alan Williams, with a description: 'Designed to show the use of EMBOSS based Soaplab services from Taverna. this workflow has no inputs as all initial values are specified as string constants. A sequence set is fetched using the seqret tool, then simultaneously scanned for predicted transmembrane regions and subjected to a multiple alignment using emma. This alignment is then plotted to a set of PNG images and also used to build a profile using the prophet and prophet tools.' The right pane, titled 'Workflow Preview', shows a workflow entry titled 'Link_protein_to_OMIM_disease (version 1)' by Marco Roos. The workflow diagram shows a sequence of steps: 'keyword' (input) leads to 'search', which leads to 'split_OMIM_region', which leads to 'filter_disease_region', which leads to 'Extract_diseases_from_OMIM', which leads to 'label_OMIM_disease', which leads to 'Parse_list', which leads to 'Remove_duplicate_strings', which leads to 'Workflow Outputs' (output). Below the diagram, there is a 'Tags' section with the tags 'BioAID', 'AIDA', 'bioinformatics', 'demo', and a 'Credits' section with the credit 'Marco Roos, AD'.

Taverna Workbench v1.7.1.0

File Tools Workflows Advanced

Design Results myExperiment (beta) Tags Browser

Example Workflows Latest Workflows Search Workflows All tags Refresh

70 tags found

affymetrix AIDA alignment beanshell benchmarks BioAID bioassist_ni bioinformatics biomoby biorange_ni BLAST clustal clustalw data-driven dbfetch ddtj demo design

pattern disease ebi emboss example FASTA genotype go terms interpro interproscan iteration kegg microarray multiple sequence alignment mygrid nticonworkflows ncbi ncbi_blast nucleotide

sequence pathway pathway-driven pathways pdo phenotype phylogenetic tree protein protein sequence similarity

annotation protein structure pubmed r scaffold sequence alignment structure taverna text

search shim similarity smith-waterman social sciences transmembrane

mining text_mining text_mining_network transmembrane

prediction tree uniprot upi user_interaction utility VL-e

7 workflows found for tag 'emboss'

BiomartAndEMBOSSAnalysis (version 2)
Uploader: Alan Williams
Using Biomart and EMBOSS soaplab services. This workflow retrieves a number of sequences from 3 species: mouse, human, rat, align them, and returns a plot of the alignment result. Corresponding sequence ids are also returned.

A workflow version of the EMBOSS tutorial (version 1)
Uploader: Alan Williams
Designed to show the use of EMBOSS based Soaplab services from Taverna. this workflow has no inputs as all initial values are specified as string constants. A sequence set is fetched using the seqret tool, then simultaneously scanned for predicted transmembrane regions and subjected to a multiple alignment using emma. This alignment is then plotted to a set of PNG images and also used to build a profile using the prophet and prophet tools.

Workflow Preview

Workflow information found. Last fetched: Mon Jul 14 11:08:59 BST 2008

Workflow Entry: **Link_protein_to_OMIM_disease (version 1)**
Uploader: Marco Roos
Created at: Mon Dec 10 22:13:35 GMT 2007
License: Creative Commons Attribution-Share Alike 3.0 License

Workflow Inputs

keyword

search

split_OMIM_region

filter_disease_region

Extract_diseases_from_OMIM

label_OMIM_disease

Parse_list

Remove_duplicate_strings

Workflow Outputs

OMIM_disease_label

No description

Tags

BioAID AIDA bioassist_ni demo

Credits

Marco Roos, AD

Bringing myExperiment to the Taverna user



[Home](#) | [Search](#) | [Upload workflows](#) | [My Workflows](#) | [My Friends 's Workflows](#) | [Invite](#) | [Feedback](#) [User Guide](#)

 MyExperiment

 marco roos All Search

[Advanced Search](#)

Search result for keyword: marco roos

workflows(28) **users(1)** groups(10)

Page 1



Name: [Marco Roos](#)
Joined: 21/Jul/2007 @ 02:43:23
Email: roos@science.uva.nl
Website: <http://home.medewerker.uva.nl/m.roos1>

Facebook



- What is it?
- How it is built?
- Towards the e-Laboratory

Servers and Repositories
(Wikis, Dspace, S3, etc.)

YouTube, Facebook, etc.
(social networks, videos, etc.)

myExperiment
(workflows, projects, Web Services, etc.)

Google Scholar
Live Academic Search

The Web Cloud

Discover, access, share,
browse, annotate...

Access through
any browser

People

Web Services

Projects

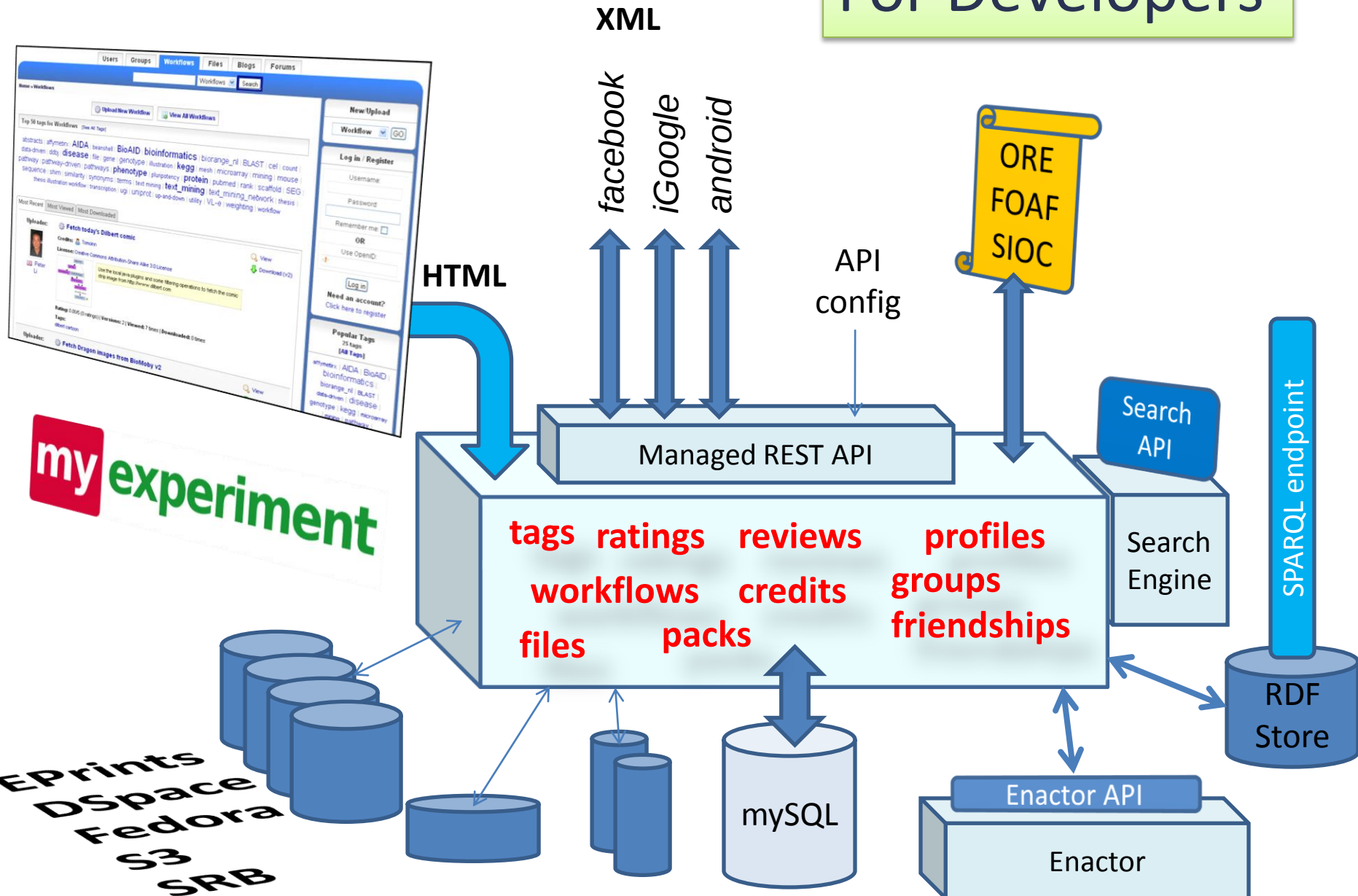
Workflows

Papers

Wikis

my experiment

For Developers



SPARQL endpoint

myExperiment SPARQL Endpoint

Querying

Query Type: SELECT

Results Format: SPARQL Results

Display Format: 

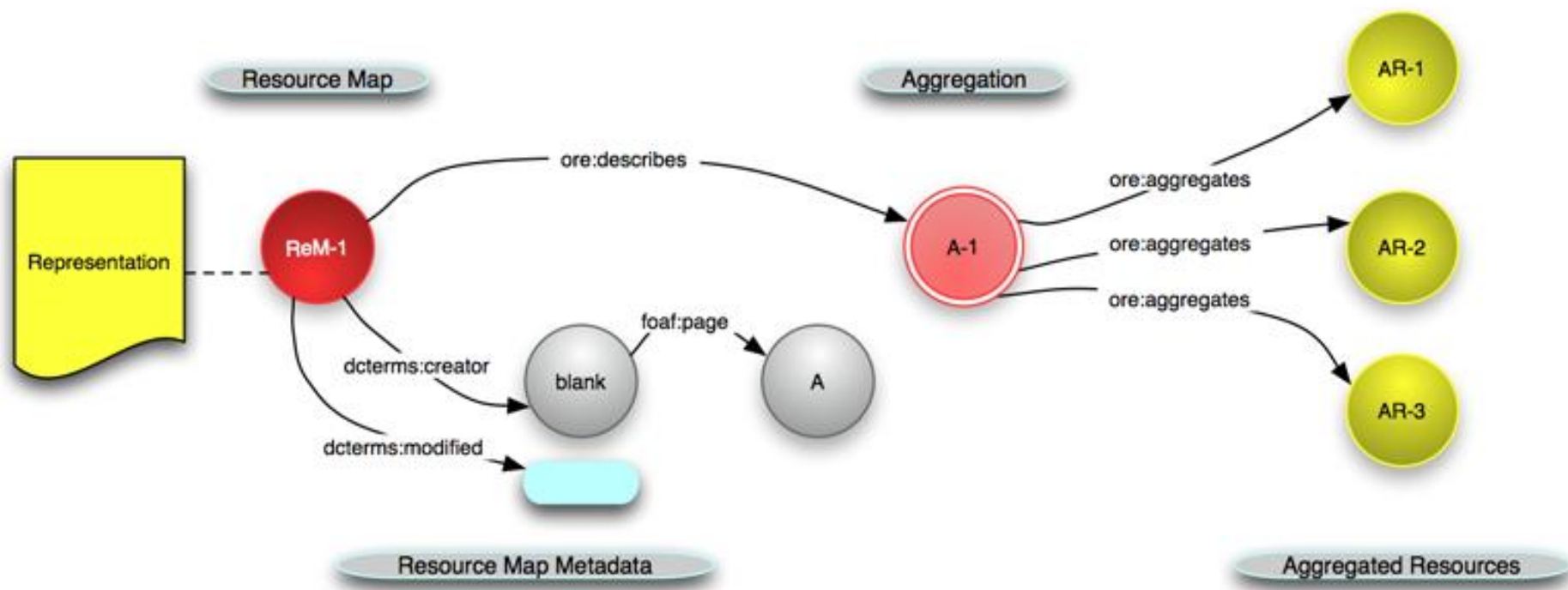
```
PREFIX rdf: <http://www.w3.org/1999/02/22-rdf-syntax-ns#>
PREFIX myexp: <http://rdf.myexperiment.org/ontology#>
PREFIX sioc: <http://rdfs.org/sioc/ns#>
select ?friend1 ?friend2 ?acceptedat where {?z rdf:type
<http://rdf.myexperiment.org/ontology#Friendship> . ?z myexp:has-requester
?x .
?x sioc:name ?friend1 . ?z myexp:has-accepter ?y . ?y sioc:name ?friend2 .
?z myexp:accepted-at ?acceptedat }
```

All accepted Friendships
including accepted-at time



Semantically-Interlinked
Online Communities

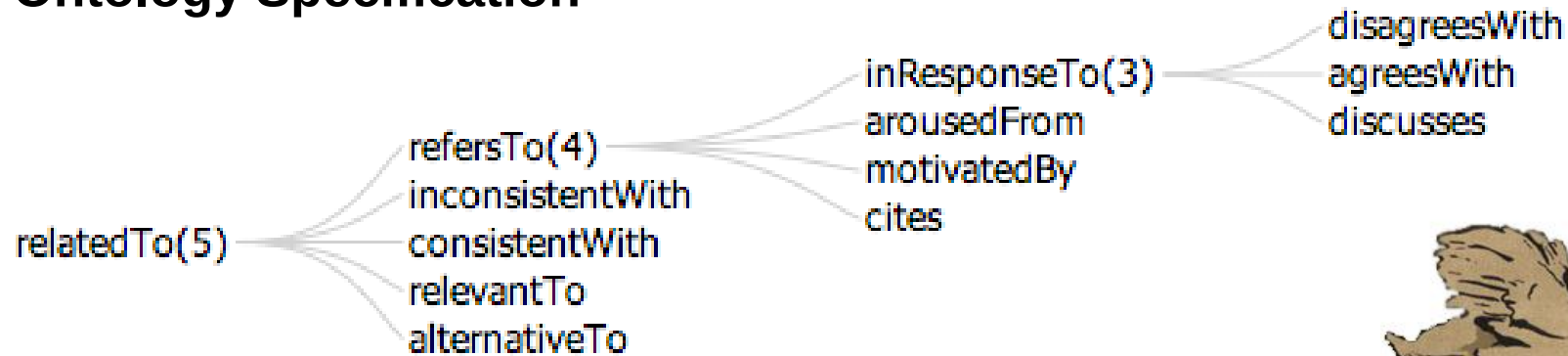
Exporting packs



Open Archives Initiative
Object Reuse and Exchange



Scientific Discourse Relationships Ontology Specification

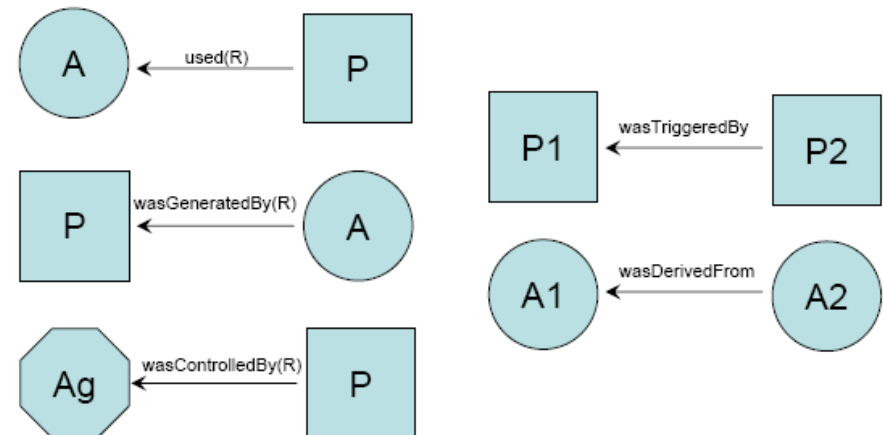


THE PROVENANCE OF ELECTRONIC DATA

It would include details of the processes that produced electronic data as far back as the beginning of time or at least the epoch of provenance awareness.

Provenance is well understood in the study of fine art where it refers to the documented history of some art object. Given that documented history, the object attains an authority that allows scholars to understand and appreciate its importance and context relative to other works. Art objects that lack a proven history may be viewed with skepticism by those who study them.

If the provenance of data produced by computer systems could be determined, then users would be able to understand how documents had been assembled, how simulation results were determined, and how financial analyses were carried out. Computer applications should thus

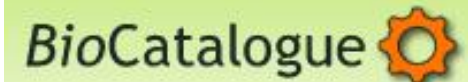
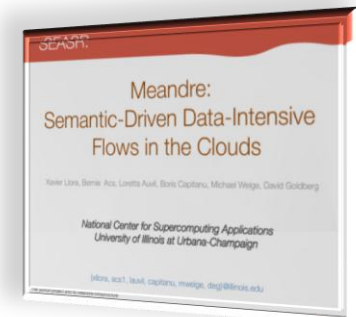


Open Provenance Model

Phase 2

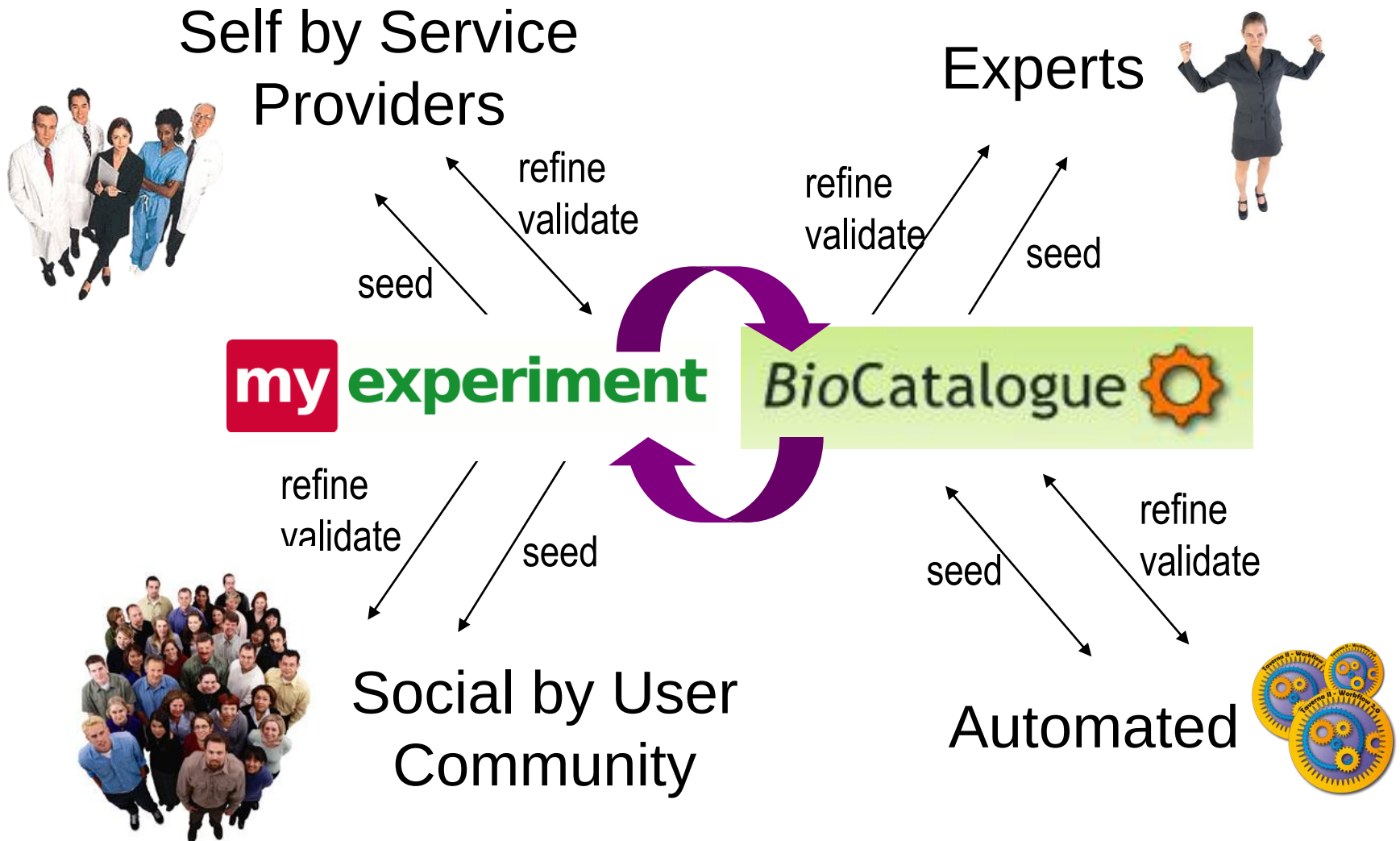
- Repository integration (institutional: EPrints, Fedora)
- Controlled vocabularies
- Relationships between items (in and between packs)
- Recommendations
- Improved search ranking and faceted browsing
- Indexing of packs
- New contribution types (Meandre, Kepler, e-books)
- Further blog / wiki integration
- Biocatalogue integration

Phase 2



Reuse and Symbiosis

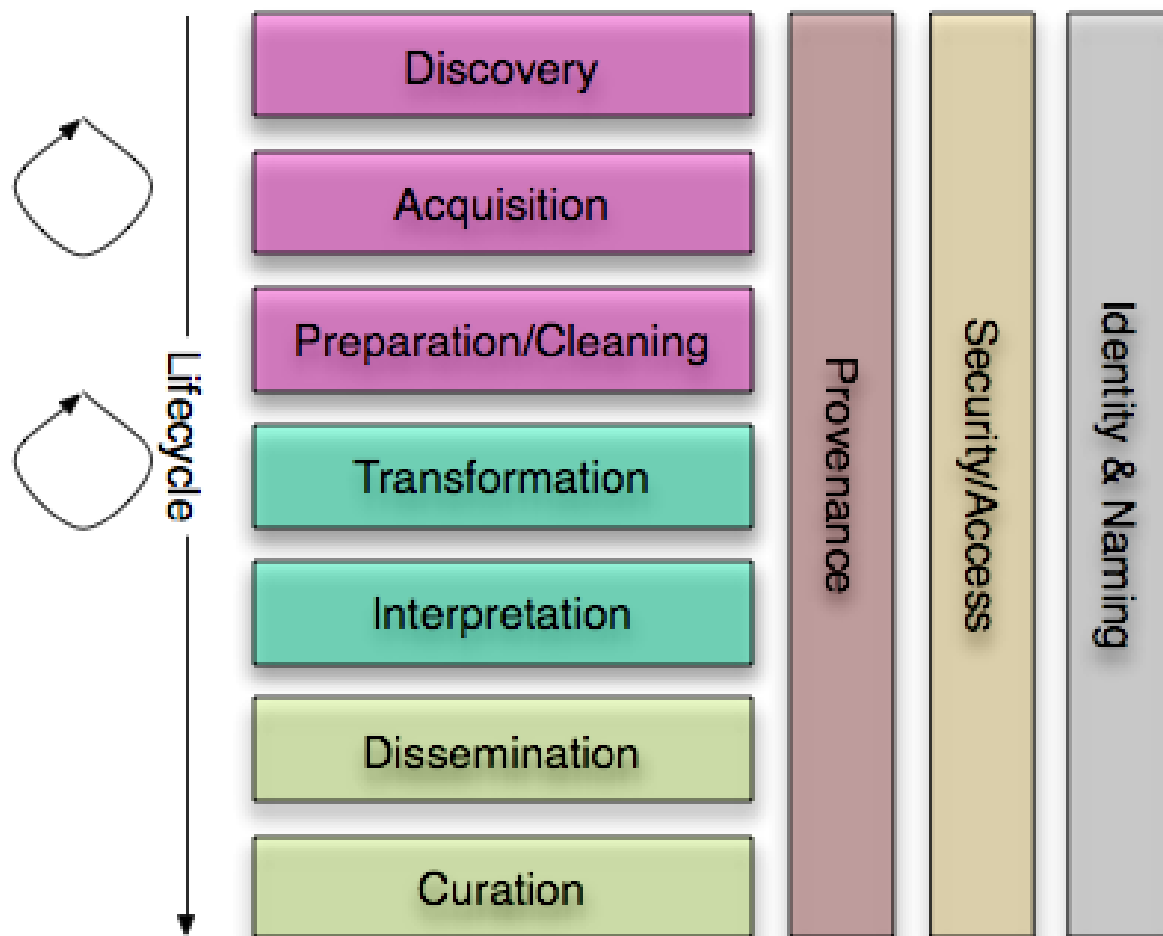
Content Capture and Curation





- What is it?
- How it is built?
- Towards the e-Laboratory

e-Laboratory Lifecycle



**Local projects
using Taverna
and/or
myExperiment**

SysMO

Ondex

Obesity eLab

Shared Genomics

NEMA

CombeChem

LifeGuide

IBBRE

What is an e-Laboratory?

- A **laboratory** is a facility that provides *controlled conditions* in which scientific research, experiments and measurements may be performed, offering a work space for researchers.
- An **e-Laboratory** is a set of integrated components that, used together, form a distributed and collaborative space for e-Science, enabling the planning and execution of *in silico* experiments -- processes that combine data with computational activities to yield experimental results

e-Labs

An e-Lab consists of:

1. a community
2. work objects
3. generic resources for building and transforming work objects

People



Data

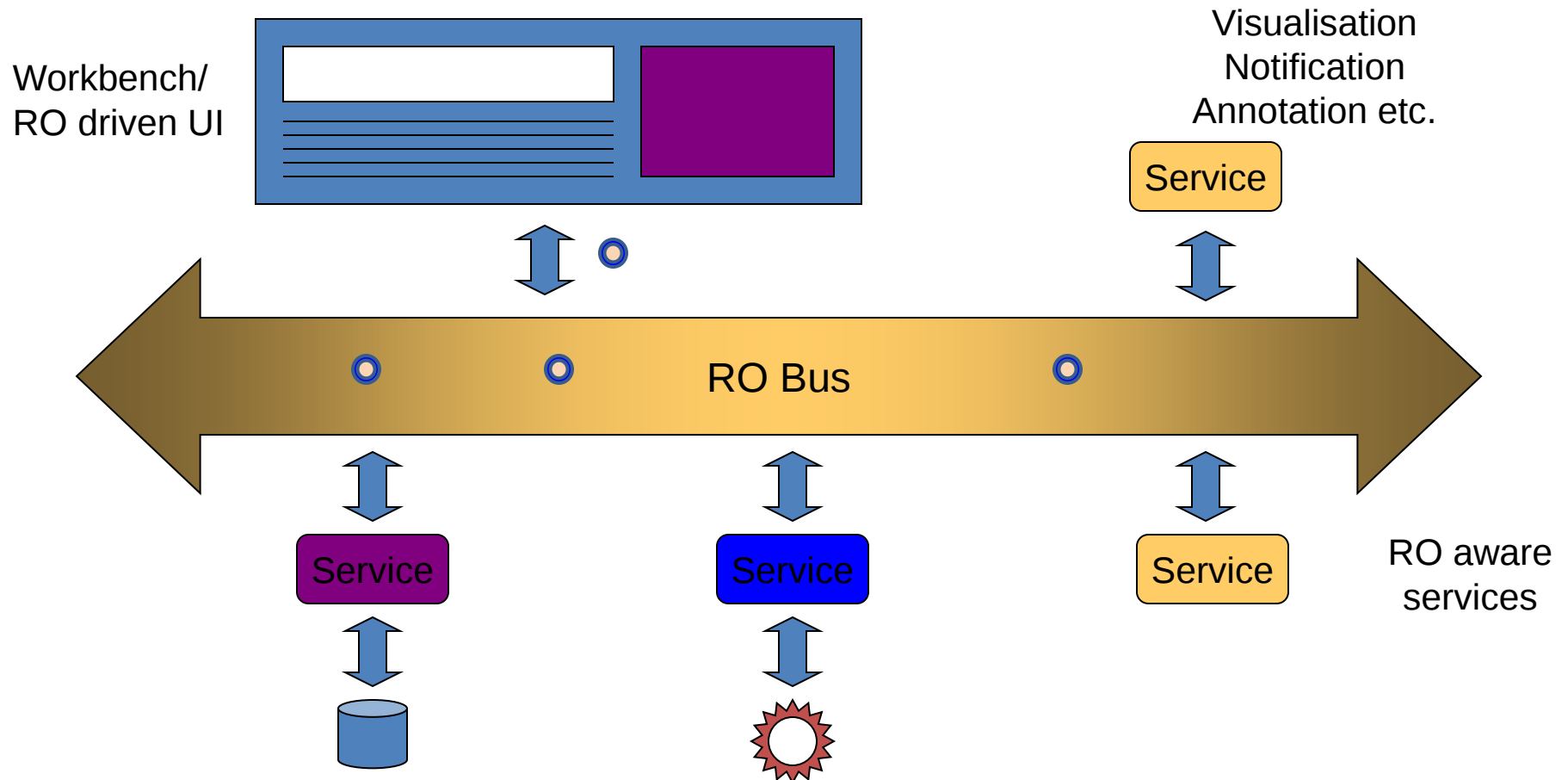


Methods

Sharing infrastructure *and* content across projects

e-Labs + Research Objects

- An e-Lab is built from a collection of **services**, consuming and producing **Research Objects**

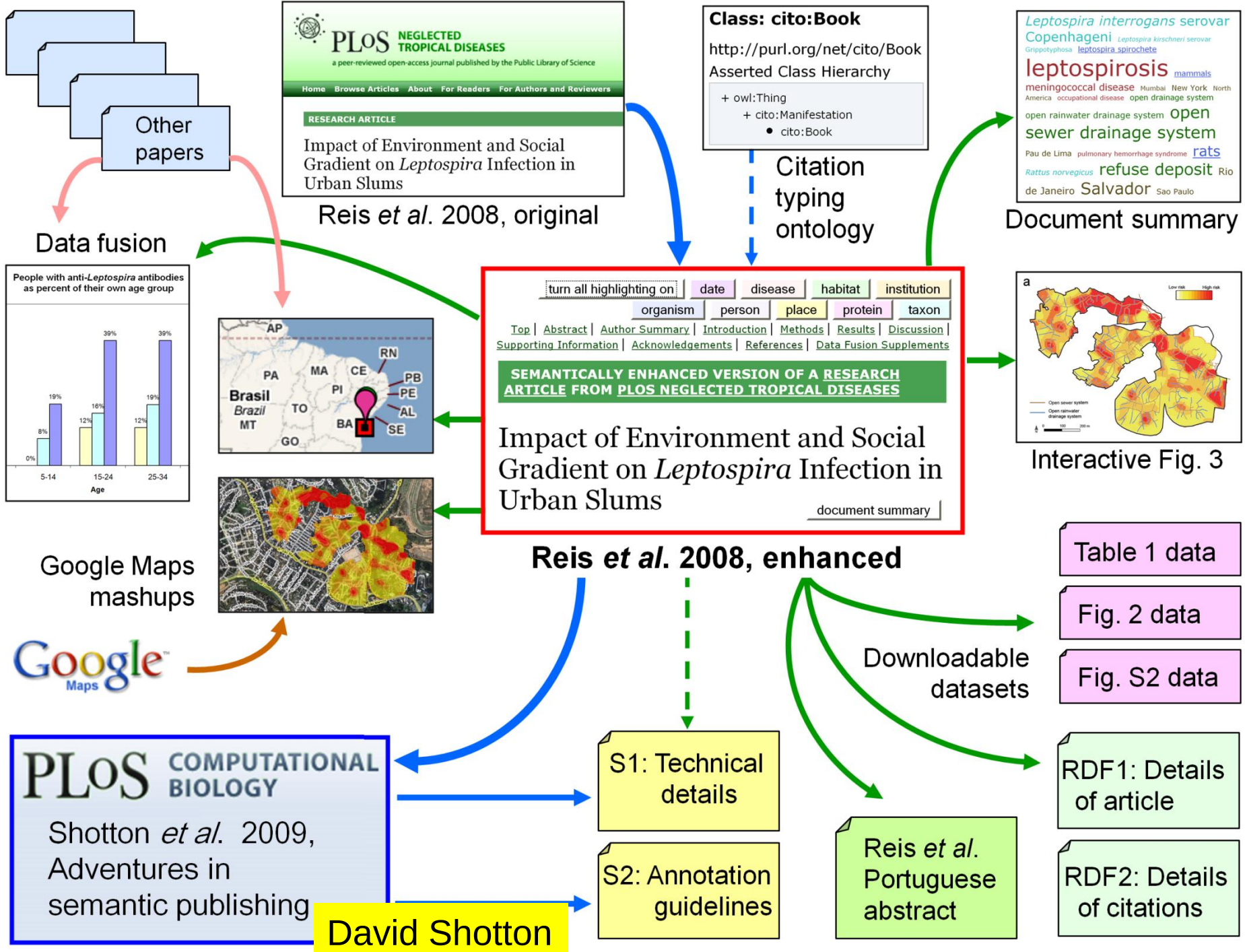


Assembling e-Laboratories

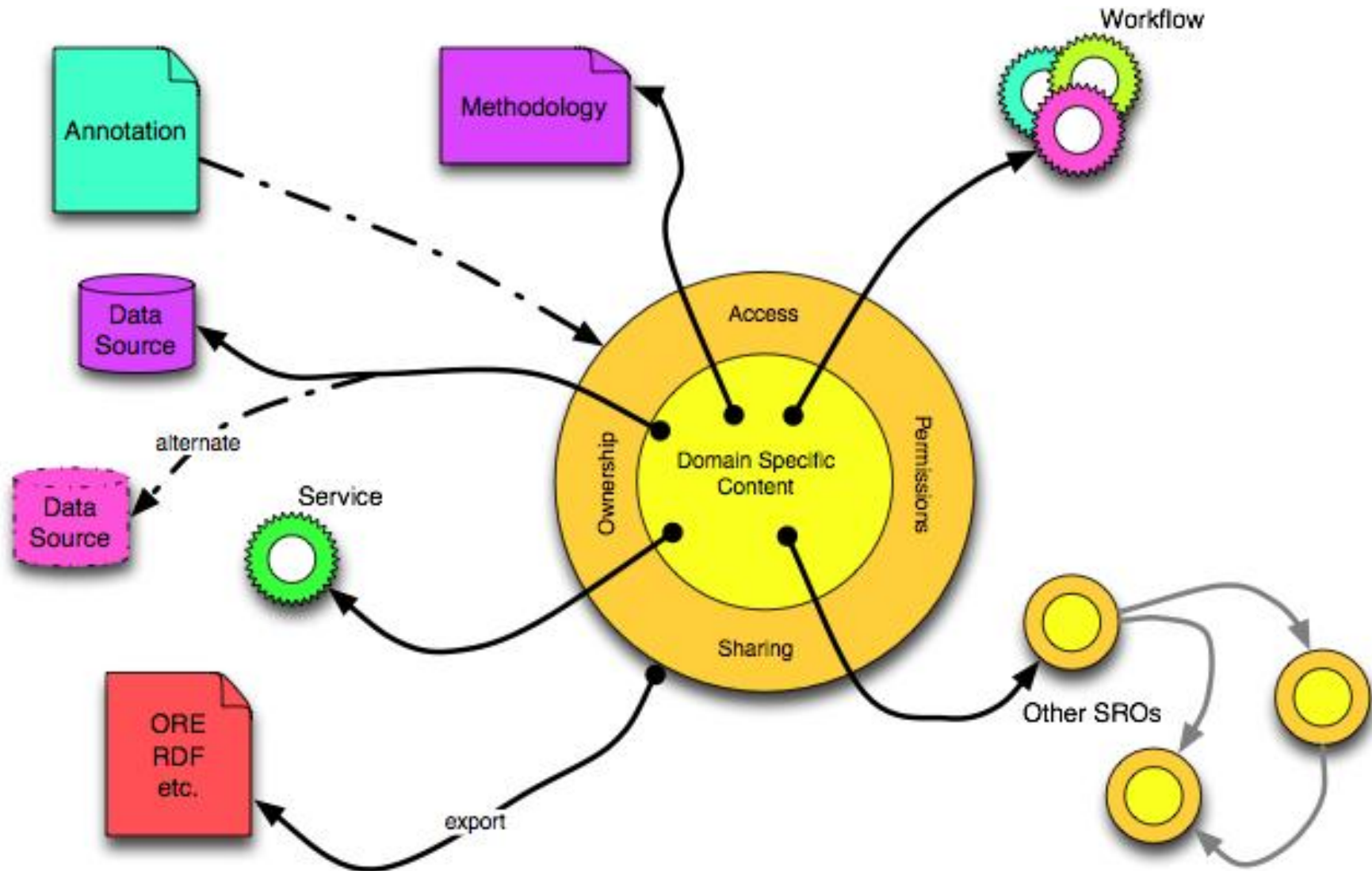
- An e-Lab is a set of components and resources
 - An open system, not a software monolith
 - Utility of components transcends their immediate application
- We envisage an ecosystem of cooperating e-Laboratories
- What are the e-Lab components and services?
- What are the Research Objects?

Example Core Services

Workflow Monitoring
Event Logging
Social Metadata
Annotation Service
Search, ranking
User Registration
Distributed Data Query
Job Execution
Naming and Identity
Anonimisation
Text Mining
Research Object
Management
Probity
Coreference Resolution



Anatomy of a Research Object



Characteristics of a Research Object

1. **Composite.** Contain typed interrelationships and dependencies between resources but are in turn labelled and identifiable as an individual resource.
2. **Distributed.** Structured collections of references to locally managed and externally located resources. Implications for reliability, consistency, mixed stewardship, versioning and identity resolution.
3. **Annotated.** Carry metadata concerning provenance profile, lifecycle profile, sharing profile (permissions, licensing, downloads, views), curation profile (tags, comments, ratings) and usage profile.
4. **Repeatable.** Capture information about the lifecycle of the investigation facilitating experiments to be *repeatable (without change)*, *reusable (with reconfiguration)*, *replayable and/or repurposable (as new components or templates)*.
5. **Interoperable.** Publishable and exchangeable units that facilitate interoperability; OAI-ORE standards increase interoperability and facilitate the consumption of Research Objects in between applications.

Thoughts

- myExperiment provides social infrastructure – it facilitates sharing and enables scientists to “collaborate in order to compete”
- myExperiment has growing community and growing content
- New content types: Meandre, Kepler, R, matlab, spreadsheets, ... SPARQL queries?
- We are targetting how we believe research will be conducted in the future, through the assembly of e-Laboratories which share Research Objects
- SPARQL endpoint is an effective alternative to the API – provides any service you want!
- Workflows for Semantic Web scripting?

References



- David De Roure, Nicholas R. Jennings and Nigel R. Shadbolt: The Semantic Grid: Past, Present and Future
- David De Roure, Nicholas R. Jennings and Nigel R. Shadbolt: The Semantic Grid: A Future e-Science Infrastructure
- Fran Berman, Anthony J. G. Hey, Geoffrey C. Fox: Grid Computing Making the Global Infrastructure a Reality
- Oscar Corcho*, Pinar Alper, Ioannis Kotsiopoulos, Paolo Missier, Sean Bechhofer, Carole Goble: An overview of S-OGSA: A Reference Semantic Grid Architecture, 2006
- <http://www.semanticgrid.org/vision.html>
- MIT - HCLS IG F2F - myExperiment



THANK YOU!