



David De Roure (1145)



The social process of Science 2.0

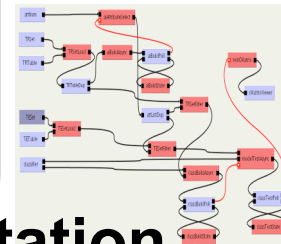
Virtual Learning Environment

Digital Libraries

Undergraduate Students

scientists

Graduate Students



experimentation



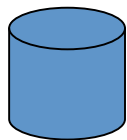
my experiment

Peer-Reviewed Journal & Conference Papers

Reprints

Preprints & Metadata

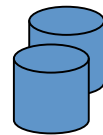
Technical Reports



Repositories



Local Web



Certified Experimental Results & Analyses

Data, Metadata, Provenance, Workflows, Services, Ontologies, ...



- “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 1800 registered users, 145 groups, 600 Taverna workflows plus 80 others, and 50 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

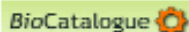
Share collections of items as individual packs – like all the digital items in an experiment. Include external items too.

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.



The screenshot shows the 'myexperiment' website interface. At the top, there are navigation tabs: Home, Users, Groups, Workflows, Files, Packs. The main content area displays a 'Workflow Entry: BioAID_DiseaseDiscovery' with details like 'Created at: 12/10/07 @ 22:28:54' and 'Last updated: 15/12/09 @ 22:41:51'. It includes a 'Taverna 1 workflow' section with an 'Original Uploader' profile for Marco Ricci. A central diagram shows the workflow steps: Document_index, searchHits, search_field, query_string, Retrieve_documents, Discover_proteins, Remove_and_tag, Link_problems_to_diseases, Filter_and_make_unique, discovered_diseases, discovered_problems, relevant_documents. The right sidebar contains a 'New Upload' section, a user profile for David De Roure, and various social features like 'My Profile', 'My Messages', 'My Members', 'My History', and 'My News'.



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

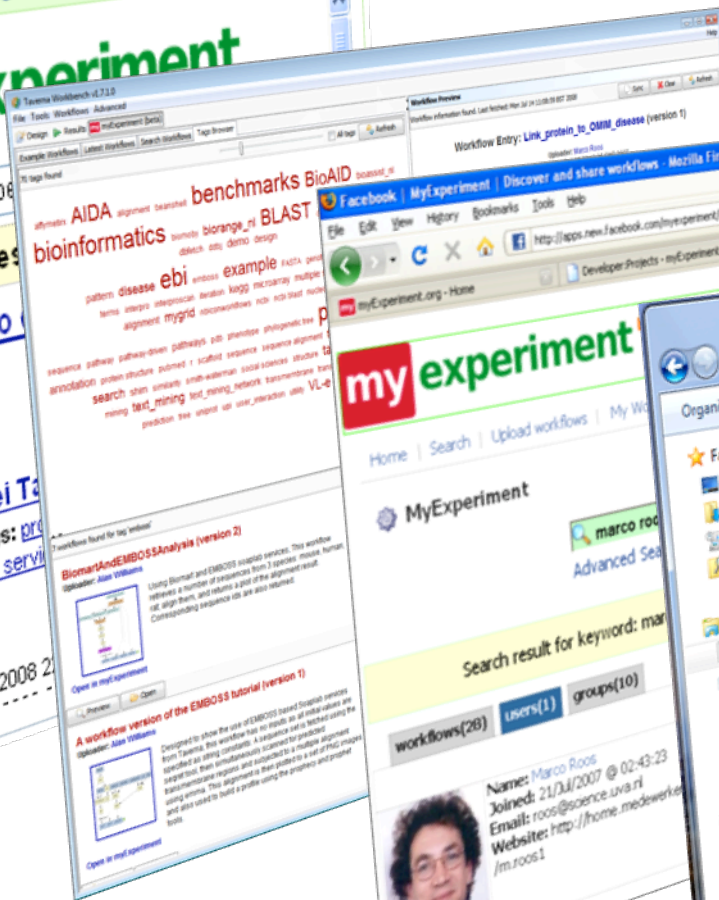
Distinctives



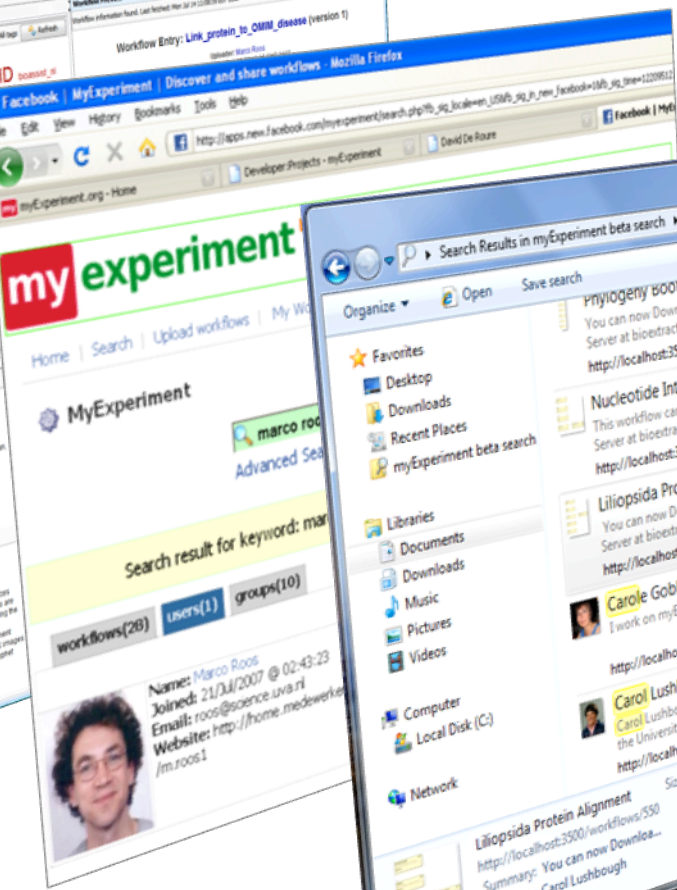
Bringing it to the user



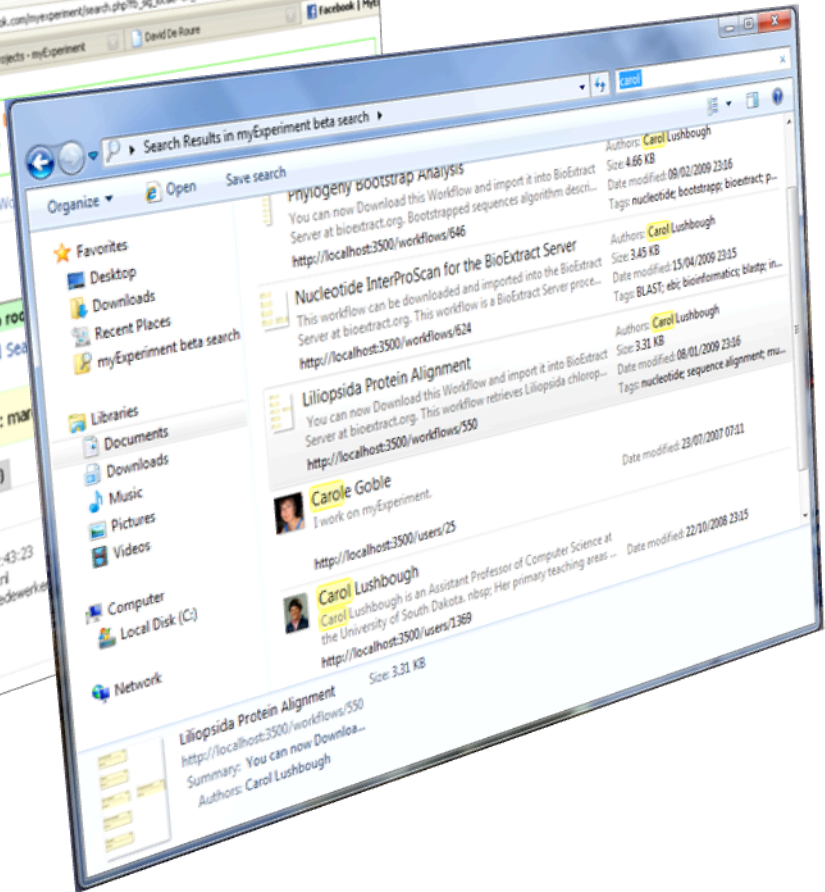
iGoogle



Taverna

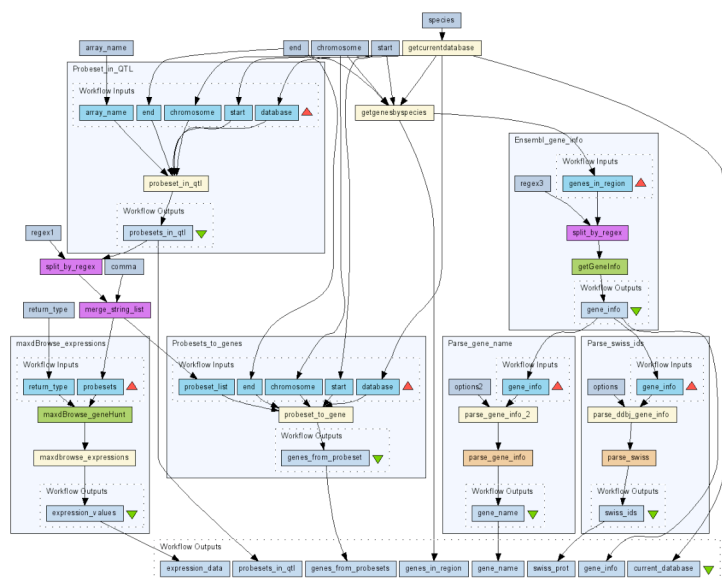


Facebook

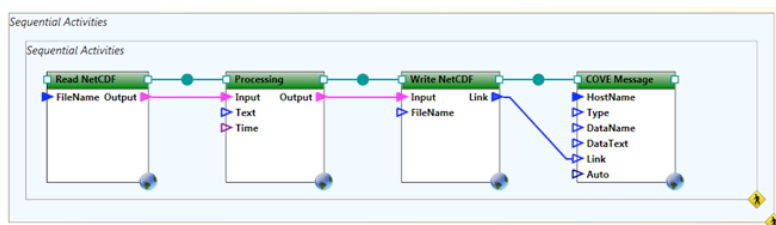


Windows 7

Sharing pieces of process



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



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

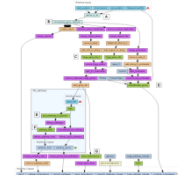
Monitor the formation of an aromatic imine by HMR and CMR in CDC13

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>

Reuse, Recycling, Repurposing

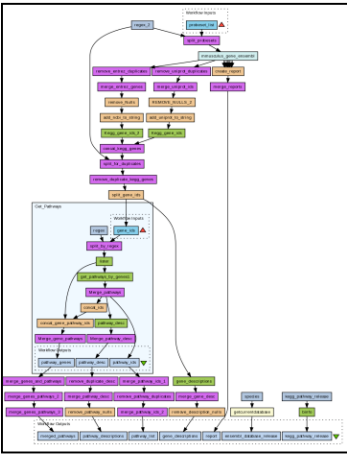
- Paul writes workflows for identifying biological pathways implicated in resistance to Trypanosomiasis in cattle
- Paul meets Jo. Jo is investigating Whipworm in mouse.
- Jo reuses one of Paul's workflow **without change**.
- Jo identifies the biological pathways involved in sex dependence in the mouse 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.



Logs

Results

Workflow 16



QTL

Analysis Protocol for Candidate Genes and Pathways

This protocol is aimed at providing a guide to the interpretation of the results obtained from both the QTL and microarray workflows. Each workflow provides a series of text files, which are to be used as a means of obtaining the pathways which relate to differentially expressed genes in the microarray study and genes located within the chosen QTL region.

The output from each workflow consists of the following files:

- ensembl_database_release.txt
- pathway_descriptions.txt
- gene_descriptions.txt
- pathway_descriptions.txt
- merged_pathways.txt
- hpa_external_gene_reference.txt
- report.txt
- pathway_list.txt

[ensembl_database_release.txt](#)

The current release of the Ensembl dataset for the chosen species, e.g. *Mus musculus*. Although this uses the programmatic interface of Ensembl, it can be used to identify which release was used to generate the list of genes in the QTL region or mapping of Affymetrix probe IDs.

```

path:mmu04060 Cytokine-cytokine receptor interaction - Mus musculus (mouse)
path:mmu00970 Aminoacyl-tRNA biosynthesis - Mus musculus (mouse)
path:mmu00240 Pyrimidine metabolism - Mus musculus (mouse)
path:mmu03010 Ribosome - Mus musculus (mouse)
path:mmu04080 Neuroactive ligand-receptor interaction - Mus musculus (mouse)
path:mmu04210 Apoptosis - Mus musculus (mouse)
path:mmu05220 Chronic myeloid leukemia - Mus musculus (mouse)
path:mmu04612 Antigen processing and presentation - Mus musculus (mouse)
path:mmu00271 Methionine metabolism - Mus musculus (mouse)
path:mmu04912 GnRH signaling pathway - Mus musculus (mouse)
path:mmu04330 Notch signaling pathway - Mus musculus (mouse)
path:mmu04640 Hematopoietic cell lineage - Mus musculus (mouse)
path:mmu00561 Glycerolipid metabolism - Mus musculus (mouse)
path:mmu04110 Cell cycle - Mus musculus (mouse)
path:mmu04530 Tight junction - Mus musculus (mouse)
path:mmu02010 ABC transporters - General - Mus musculus (mouse)
  
```

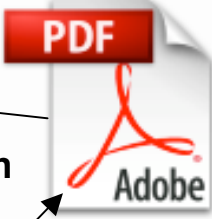
produces

Included in

Published in



complete.ppt



Included in

Paper

Feeds into

Included in

Slides

Published in

Results

produces

Metadata

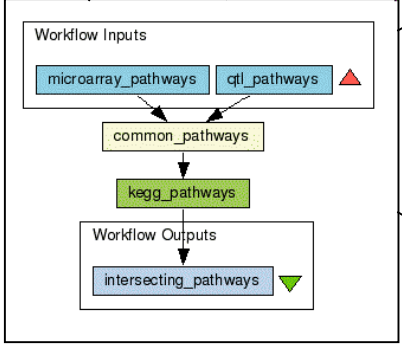
Tags (19)

Creator tags

affymetrix | african trypanosomiasis | cattle | data-driven | disease | entrez | genotype | Kegg Pathways | KeggID | link-integration | **microarray** | mouse | **pathway** | pathway-driven | phenotype | sleeping sickness | swissprot | uniprot | web services

[edit]

Add Tags

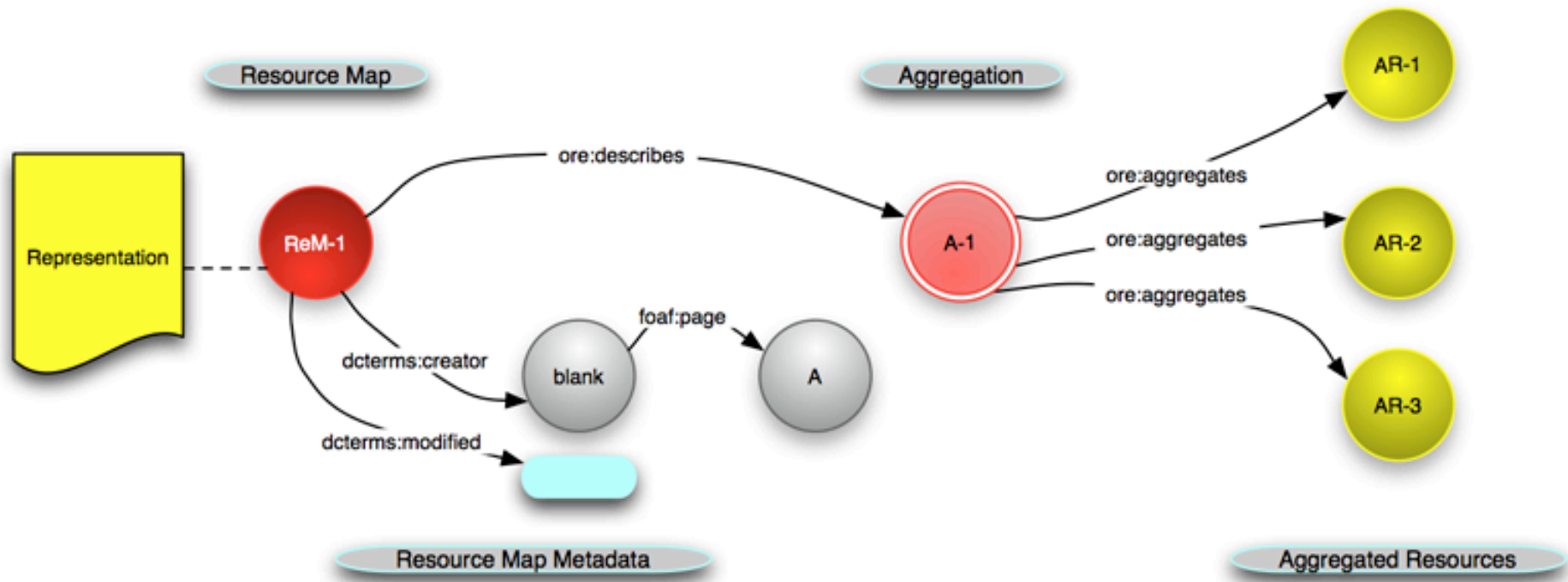


Common pathways

Workflow 13

Primer Name	Left Flank Nucleotide sequence	Right Flank Nucleotide sequence
DAXX_1274_1812	CAGGAGGAATGGCGAGTG	AGCTIAGTCTTCCCAAGCC
DAXX_140754_456_1070	CTTGATGATTGGGACTGGG	TCTCTCTCTCTCTCTCTC
DAXX_2270_2720	TGGCAGGAGAGATGGTTC	ATGGTCAAGGGAAGGGAAA
DAXX_2644_3187	TGTGTGATTGGCTGGTGTGT	GCAGAAACAGGAGAGCTGGG
DAXX_exon5	TCTCTCTCTACCAATCAA	AGCAGAACTAACCCACAAGG
Daxx_Upst_479_1104	CAGGCTTCTCATCAACACC	TGTCTATGGCTGTGCAGG

Exporting packs



Open Archives Initiative
Object Reuse and Exchange



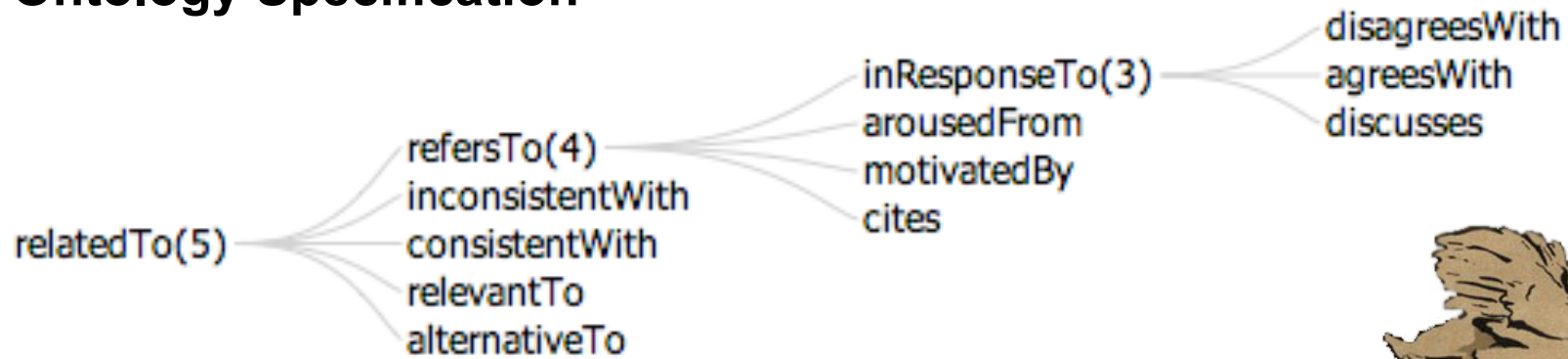
Mozilla Firefox

File Edit View History Bookmarks Tools Help

http://rdf.myexperiment.org/ResourceMap/Pack/56 semantic escience

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  <ore:describes rdf:resource="http://rdf.myexperiment.org/Pack/56"/>
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    <foaf:name>myExperiment Mothership RDF Generator</foaf:name>
    <foaf:page rdf:resource="http://rdf.myexperiment.org"/>
  </dcterms:creator>
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  - <dc:rights>
    This Resource Map is available under the Creative Commons Attribution-Noncommercial 2.5 Generic license
  </dc:rights>
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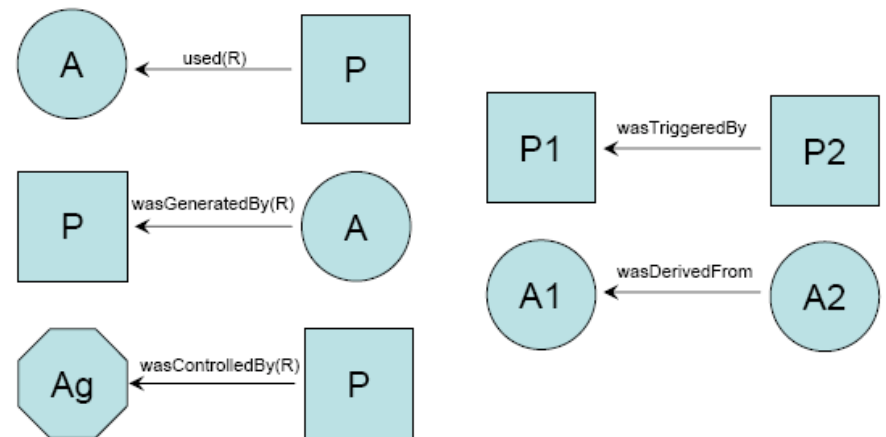
Scientific Discourse Relationships Ontology Specification



THE PROVENANCE OF ELECTRONIC DATA

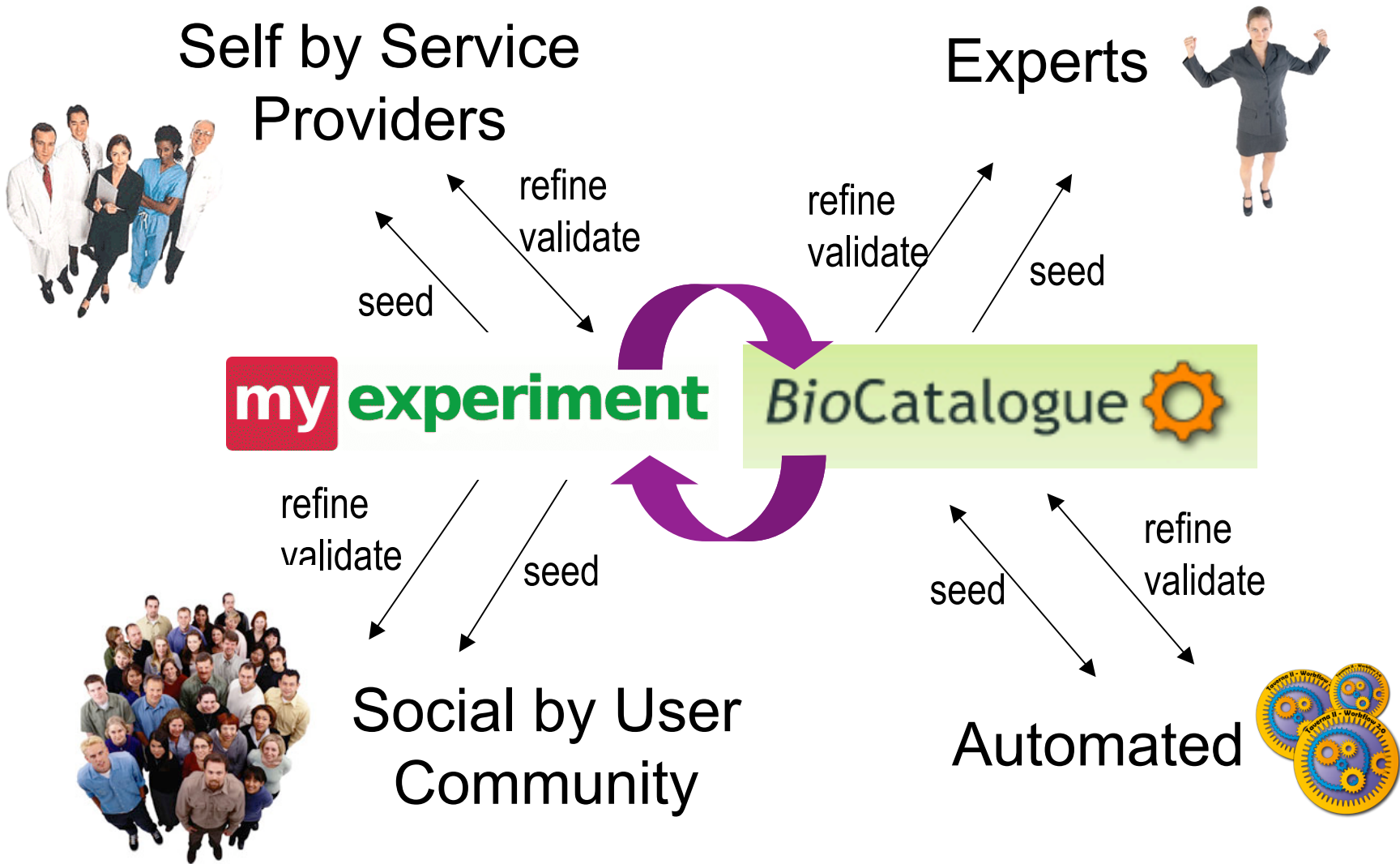
It would include details of the processes that produced electronic data as far back as the beginning of time or at least the epoch of provenance awareness.

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

Curation



Summary

- Understand the next generation of researchers
- Understand the changing nature of research practice
- Papers will be replaced by discoverable and shareable Research Objects that are:
 - Repeatable
 - Replayable
 - Reproducible
 - Repurposeable
 - Robust



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