myExperiment

Repository | VRE | Experiment

Jiten Bhagat

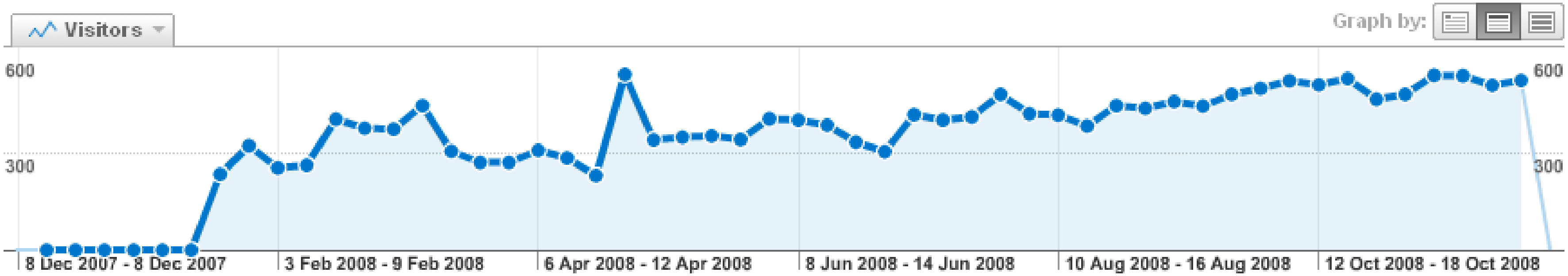
University of Manchester

DreSNet | 2009-07-14

myexperiment

Since its public launch in 2007, myExperiment has established the largest collection of scientific **workflows** publicly available.

Over 500 public workflows.



15,902 Absolute Unique Visitors

myexperiment

Social | Web 2.0 | VRE | Repository

… for Research Objects

myexperiment

Tailored to the needs of researchers

Making it really easy to...

Store | Share | Discover | Curate | Attribute

... Research Objects

myexperiment

Build communities | Form relationships

myexperiment

Share your workflows and files

Find people and make friends

Control access to your workflows and files

Build your profile and reputation

Create and join groups of similar interests

Find workflows and files that others have shared

Have discussions and collaborate

Maintain and use different versions of workflows

Execute workflows directly within myExperiment
(if you have access to a remote Taverna enactor)

Tag and rate workflows and files

Write reviews and comments

Build packs of related content

Reuse and repurpose workflows (and other files!)

Send messages to other people on myExperiment

myexperiment

- “Facebook for Scientists” ...but different to Facebook!
- A repository of research methods
- A community social network of people and things
- A Virtual Research Environment

- Open source (BSD) Ruby on Rails application with HTML, REST and SPARQL interfaces
- Project started March 2007
- Closed beta July 2007
- Open beta November 2007

myExperiment currently has over 1900 registered users, 150 groups, 700 workflows, 200 files and 60 packs.

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

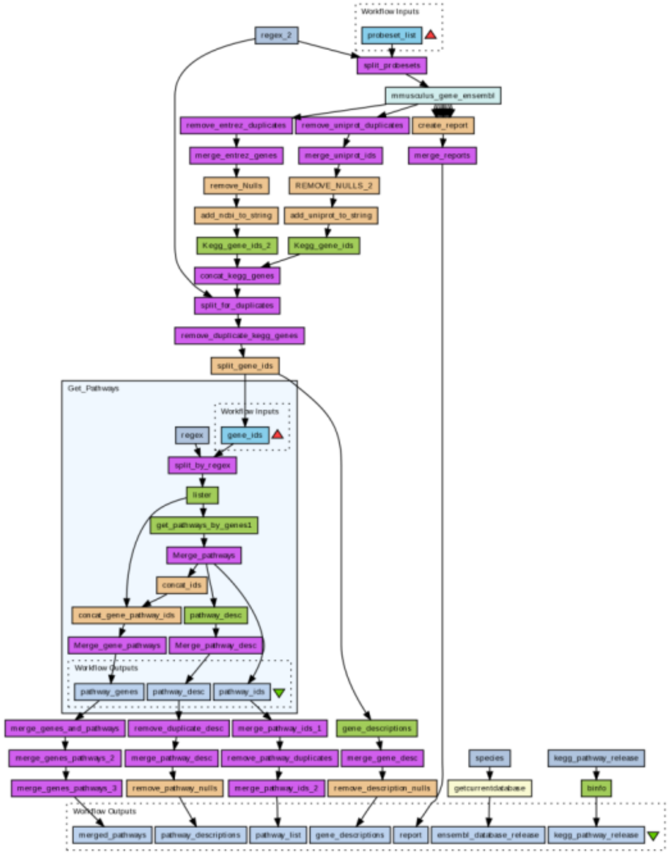
myexperiment

Why?

What was the motivation?

Scientific Workflows

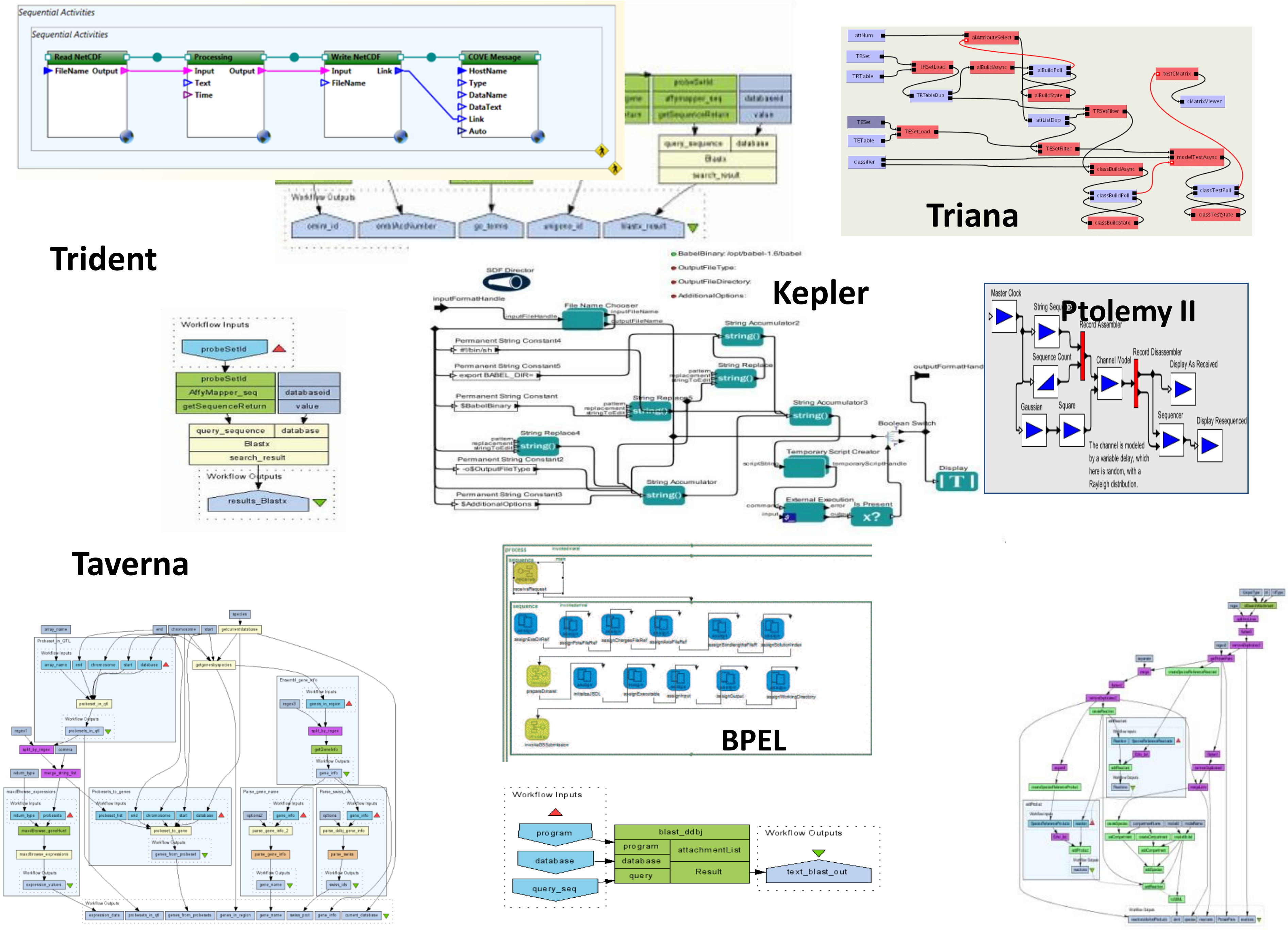
- Experimental protocols
- Automation of data flow
- Linking up data sets and iteration over large data sets
- Data gathering and annotation pipelines
- Data analysis from distributed tools
- Data mining and knowledge management
- Hypothesis generation and modelling
- Literature mining
- … and so on



"Pathways from Diff Expressed Genes"

Paul Fisher

http://www.myexperiment.org/workflows/19



Trident

Triana

Kepler

Ptolemy II

Taverna

BPEL

Experiments & Reuse

- Workflows are protocols and records.
- Workflows are know-how.
- Workflows are collaborations.

- Workflow design is challenging and labour-intensive.
- Reuse is highly desirable.
- Reuse is a challenge.

Workflows are….

- explicit method
- blueprints
- protocols and records.
- know-how.

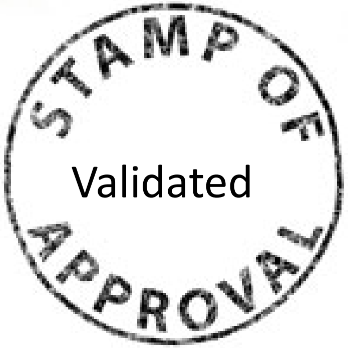
- asynchronous collaborations.
- promoters of cross-disciplinary collaborations.

- often complex.
- need explanations to use properly and safely.
- challenging to develop.
- can be good and can be bad.

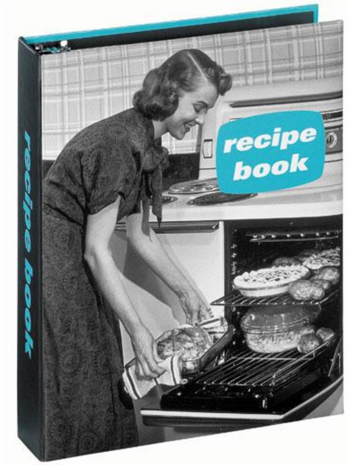
Carole Goble

- research assets.
- tradable commodities.
- publishable.
- combined with data and scholarly works.
- reproducible science.
- or at least transparent.
- and accountable.

Peer review

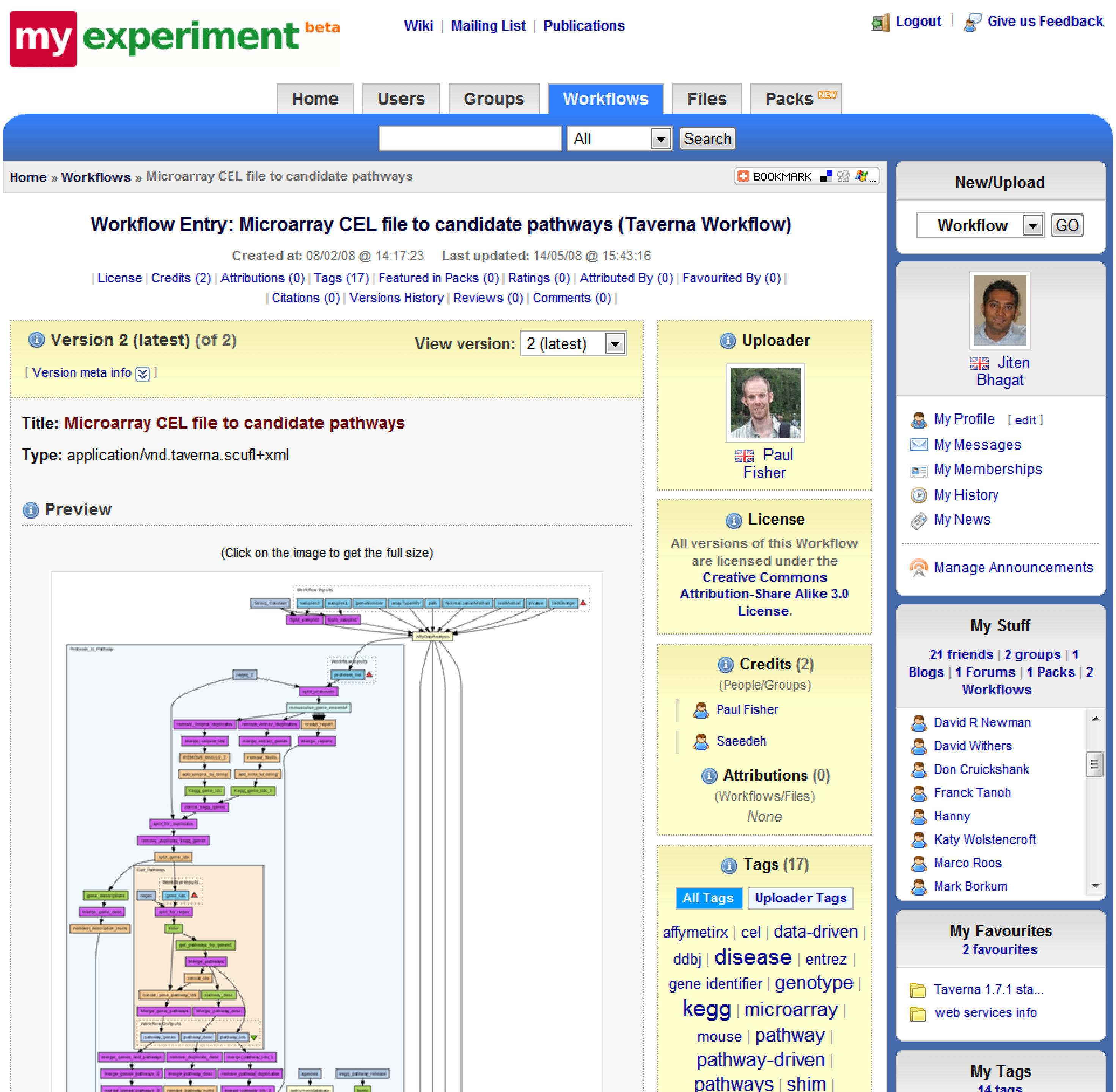


Validated



Carole Goble

my experiment



Home » Workflows » Microarray CEL file to candidate pathways

Workflow Entry: Microarray CEL file to candidate pathways (Taverna Workflow)

Created at: 08/02/08 @ 14:17:23 Last updated: 14/05/08 @ 15:43:16

| License | Credits (2) | Attributions (0) | Tags (17) | Featured in Packs (0) | Ratings (0) | Attributed By (0) | Favourited By (0) |
| Citations (0) | Versions History | Reviews (0) | Comments (0) |

Version 2 (latest) (of 2) View version: 2 (latest)

[Version meta info]

Title: Microarray CEL file to candidate pathways

Type: application/vnd.taverna.scufl+xml

Preview

(Click on the image to get the full size)

Uploader

Paul Fisher

License

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

Credits (2)

(People/Groups)

Paul Fisher

Saeedeh

Attributions (0)

(Workflows/Files)

None

Tags (17)

All Tags | Uploader Tags

affymetirx | cel | data-driven | ddbj | disease | entrez | gene identifier | genotype | kegg | microarray | mouse | pathway | pathway-driven | pathways | shim |

New/Upload

Workflow GO

Jiten Bhagat

My Profile [edit]
My Messages
My Memberships
My History
My News

Manage Announcements

My Stuff

21 friends | 2 groups | 1 Blogs | 1 Forums | 1 Packs | 2 Workflows

David R Newman
David Withers
Don Cruickshank
Franck Tanoh
Hanny
Katy Wolstencroft
Marco Roos
Mark Borkum

My Favourites

2 favourites

Taverna 1.7.1 sta...
web services info

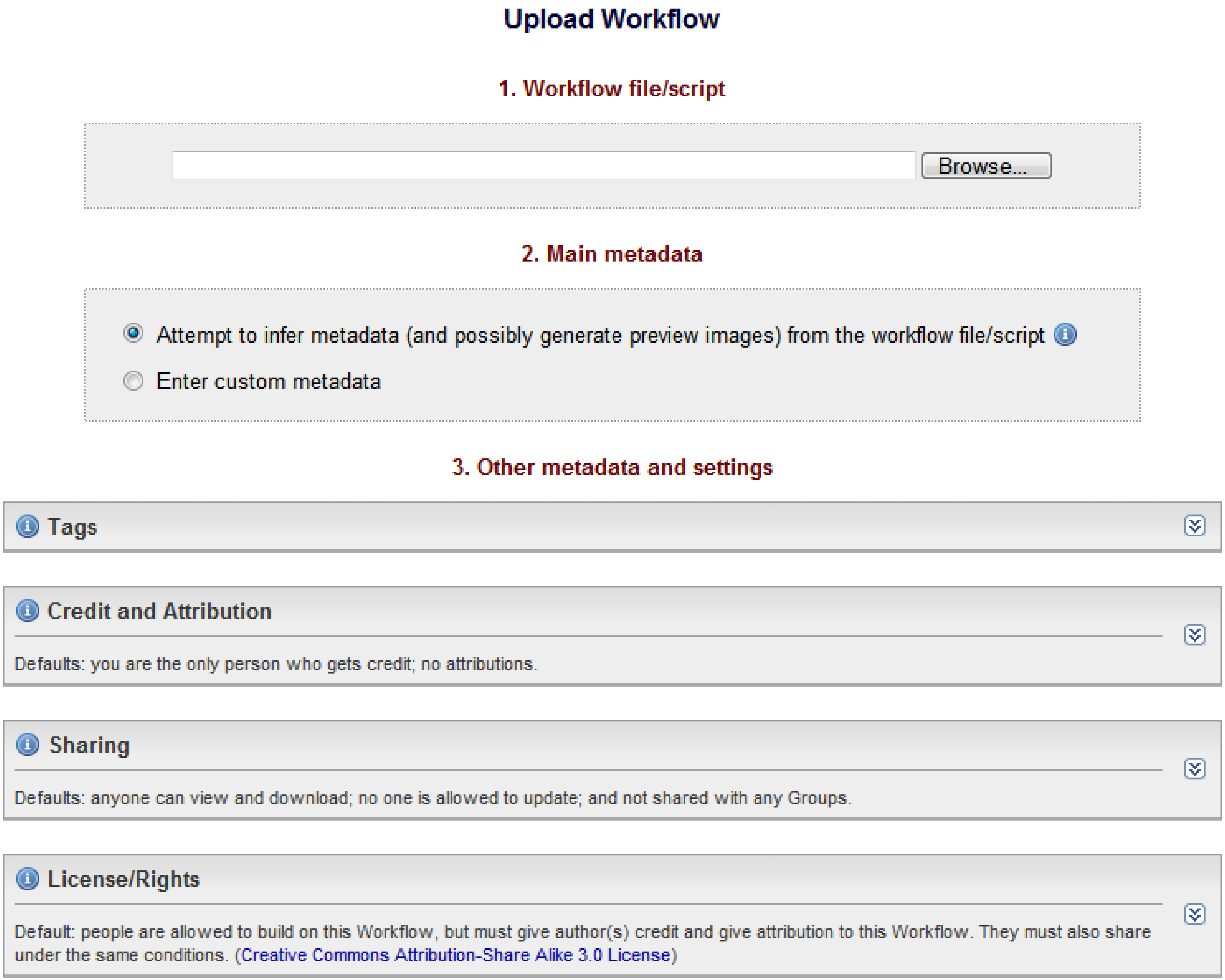
My Tags

14 tags

myexperiment

Emphasis on the special requirements of researchers...

Ownership | Credit | Attribution | Licensing | Visibility | Sharing |



Upload Workflow

1. Workflow file/script

2. Main metadata

● Attempt to infer metadata (and possibly generate preview images) from the workflow file/script

○ Enter custom metadata

3. Other metadata and settings

Tags

Credit and Attribution

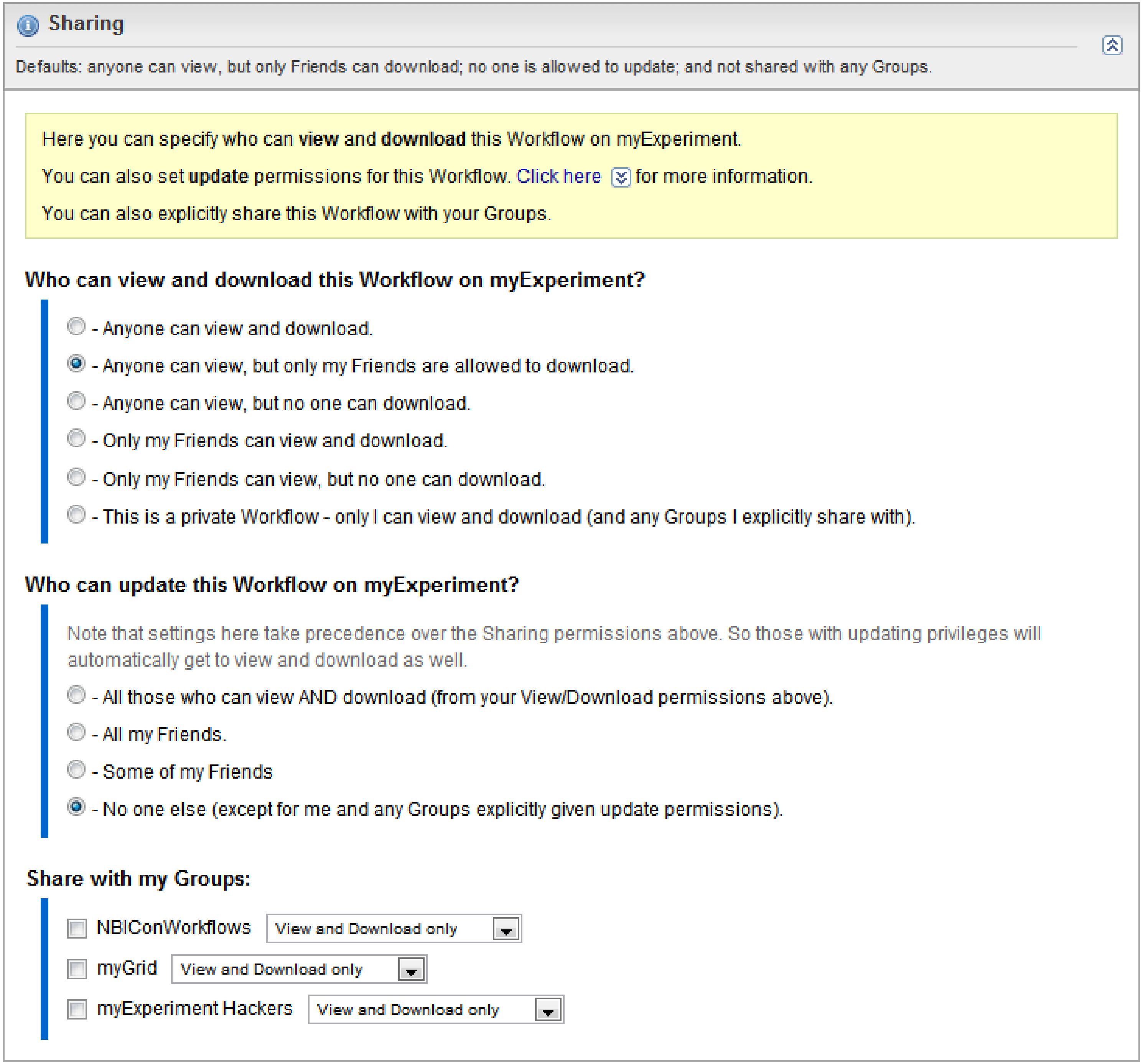
Defaults: you are the only person who gets credit; no attributions.

Sharing

Defaults: anyone can view and download; no one is allowed to update; and not shared with any Groups.

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)



Sharing

Defaults: anyone can view, but only Friends can download; no one is allowed to update; and not shared with any Groups.

Here you can specify who can **view** and **download** this Workflow on myExperiment.

You can also set **update** permissions for this Workflow. Click here for more information.

You can also explicitly share this Workflow with your Groups.

Who can view and download this Workflow on myExperiment?

○ - Anyone can view and download.
● - Anyone can view, but only my Friends are allowed to download.
○ - Anyone can view, but no one can download.
○ - Only my Friends can view and download.
○ - Only my Friends can view, but no one can download.
○ - This is a private Workflow - only I can view and download (and any Groups I explicitly share with).

Who can update this Workflow on myExperiment?

Note that settings here take precedence over the Sharing permissions above. So those with updating privileges will automatically get to view and download as well.

○ - All those who can view AND download (from your View/Download permissions above).
○ - All my Friends.
○ - Some of my Friends
● - No one else (except for me and any Groups explicitly given update permissions).

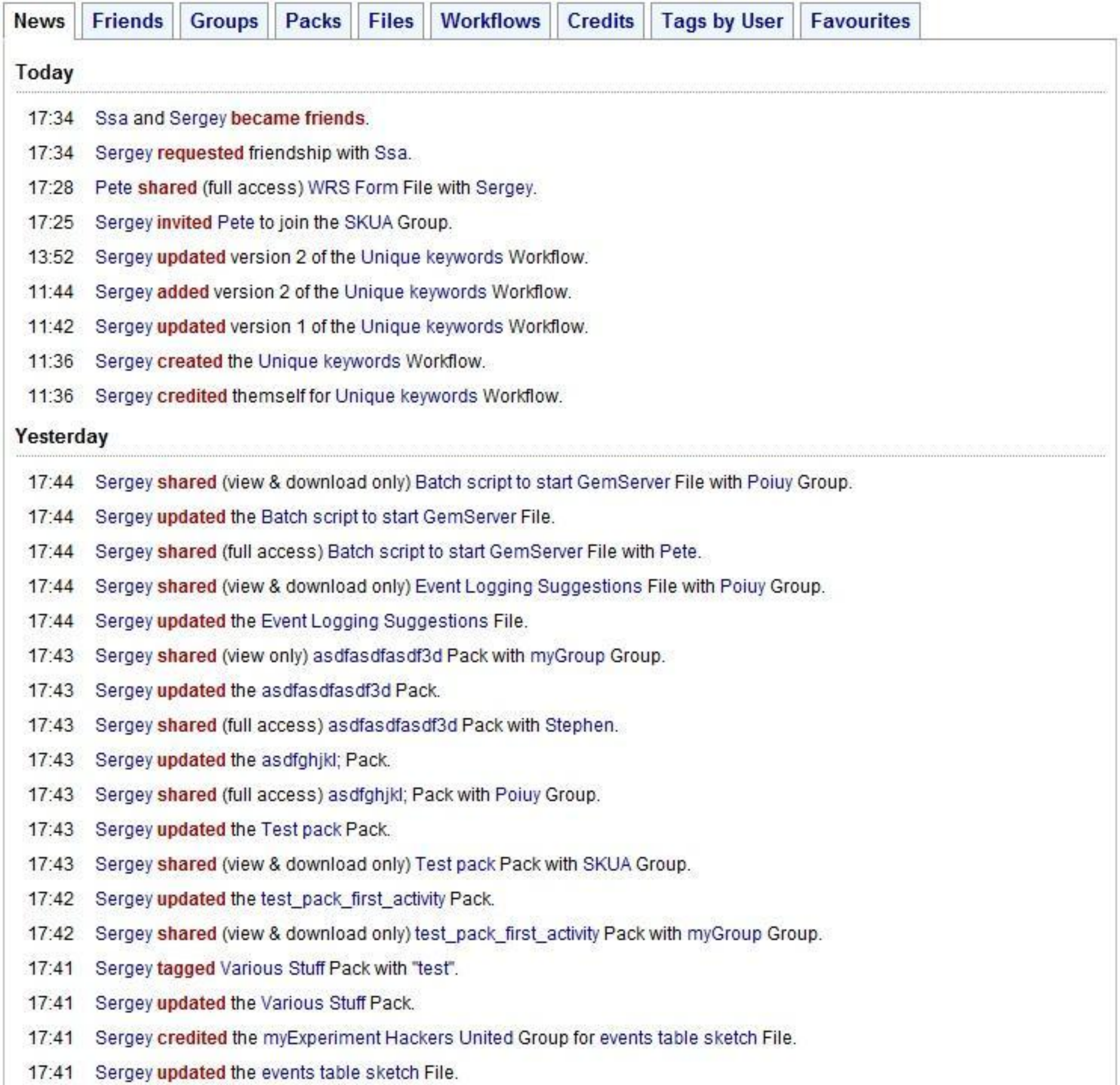
Share with my Groups:

☐ NBICon Workflows — View and Download only
☐ myGrid — View and Download only
☐ myExperiment Hackers — View and Download only

myexperiment

Keeping up with activity...

New | Tags | People | Friends | Items | Updates | Events



Today

17:34 Ssa and Sergey **became friends**.

17:34 Sergey **requested** friendship with Ssa.

17:28 Pete **shared** (full access) WRS Form File with Sergey.

17:25 Sergey **invited** Pete to join the SKUA Group.

13:52 Sergey **updated** version 2 of the Unique keywords Workflow.

11:44 Sergey **added** version 2 of the Unique keywords Workflow.

11:42 Sergey **updated** version 1 of the Unique keywords Workflow.

11:36 Sergey **created** the Unique keywords Workflow.

11:36 Sergey **credited** themself for Unique keywords Workflow.

Yesterday

17:44 Sergey **shared** (view & download only) Batch script to start GemServer File with Poiuy Group.

17:44 Sergey **updated** the Batch script to start GemServer File.

17:44 Sergey **shared** (full access) Batch script to start GemServer File with Pete.

17:44 Sergey **shared** (view & download only) Event Logging Suggestions File with Poiuy Group.

17:44 Sergey **updated** the Event Logging Suggestions File.

17:43 Sergey **shared** (view only) asdfasdfasdf3d Pack with myGroup Group.

17:43 Sergey **updated** the asdfasdfasdf3d Pack.

17:43 Sergey **shared** (full access) asdfasdfasdf3d Pack with Stephen.

17:43 Sergey **updated** the asdfghjkl; Pack.

17:43 Sergey **shared** (full access) asdfghjkl; Pack with Poiuy Group.

17:43 Sergey **updated** the Test pack Pack.

17:43 Sergey **shared** (view & download only) Test pack Pack with SKUA Group.

17:42 Sergey **updated** the test_pack_first_activity Pack.

17:42 Sergey **shared** (view & download only) test_pack_first_activity Pack with myGroup Group.

17:41 Sergey **tagged** Various Stuff Pack with "test".

17:41 Sergey **updated** the Various Stuff Pack.

17:41 Sergey **credited** the myExperiment Hackers United Group for events table sketch File.

17:41 Sergey **updated** the events table sketch File.

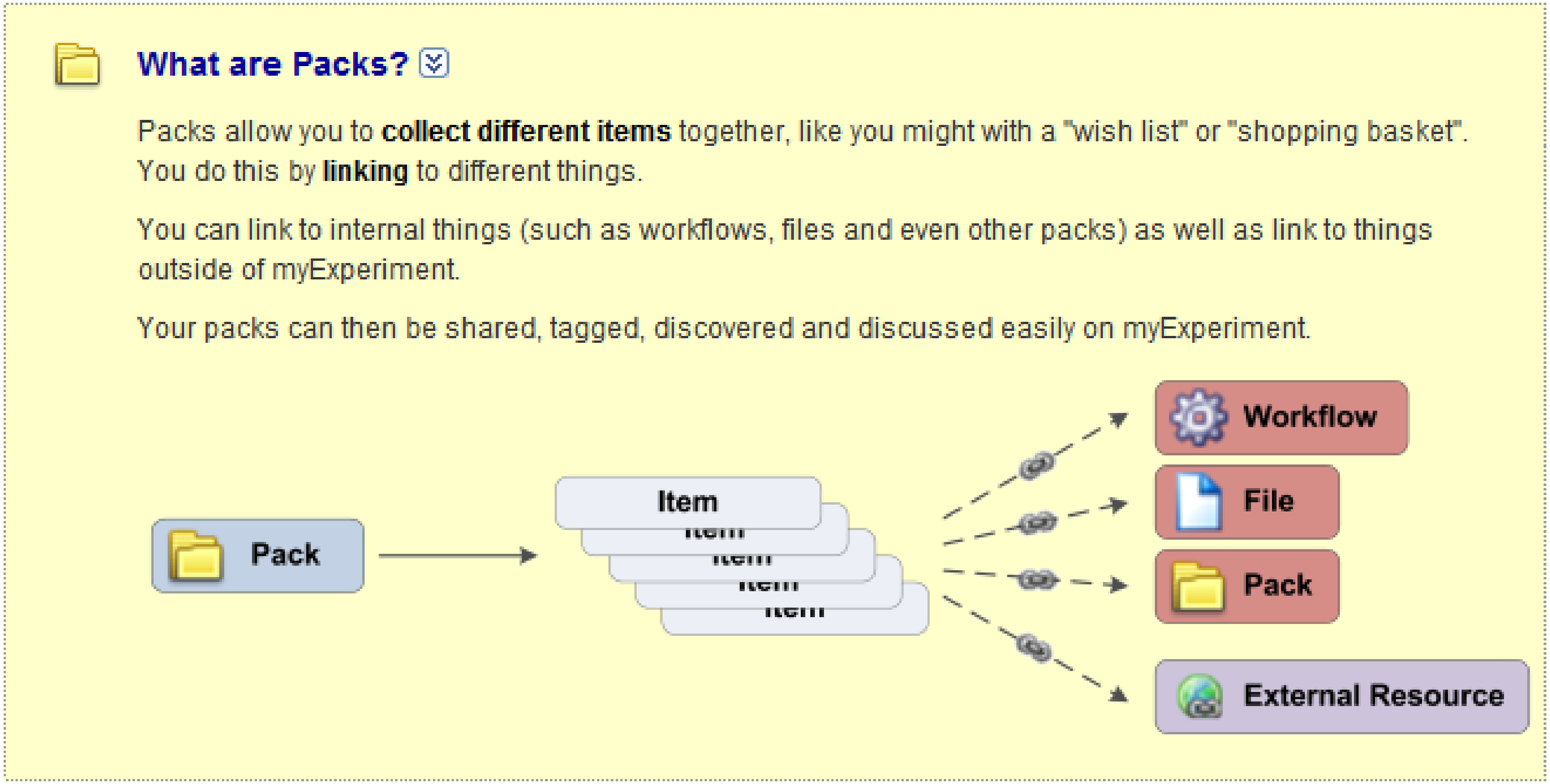
my experiment

Collecting together different types of research assets...

Workflows | Data | Results | Examples | Provenance | Tags | Documentation | Papers | Websites | Images

User X: “my experiment is not just a workflow!”

Packs



What are Packs?

Packs allow you to **collect different items** together, like you might with a "wish list" or "shopping basket". You do this by **linking** to different things.

You can link to internal things (such as workflows, files and even other packs) as well as link to things outside of myExperiment.

Your packs can then be shared, tagged, discovered and discussed easily on myExperiment.

myexperiment

Functionality can be accessed through simple RESTful APIs...

Wikis | Web apps | Desktop tools | Workbenches | Web services | Google gadgets | Facebook | Mashups | Other interfaces

Google Gadgets

All A B C D E F G H I J K L M N O P Q R S T U V W X Y Z

All (396 / 396)

AIDA BLAST BioAID DNA DNA sequence DailyDilbert
FASTA GO Kegg Pathways KeggID NE
ORF PSI-BLAST RNA SEG VL-e abstracts acces
accurate mass active address affmetrix affyme
affymetrix african trypanosomiasis aging agricola
alignment alternate analysis anim
annotation append term astrogrid-taverna astrono
astrophysics atmosphere automatic function prediction ba

20 results found for *"disease"*.

1. WORKFLOW
Gene annotation pipeline for the Graves disease scenario

WORKFLOW
ioAID ProteinToDiseases

WORKFLOW
nk protein to OMIM disease

WORKFLOW

blast simplifier.xml

Antoon Goderis

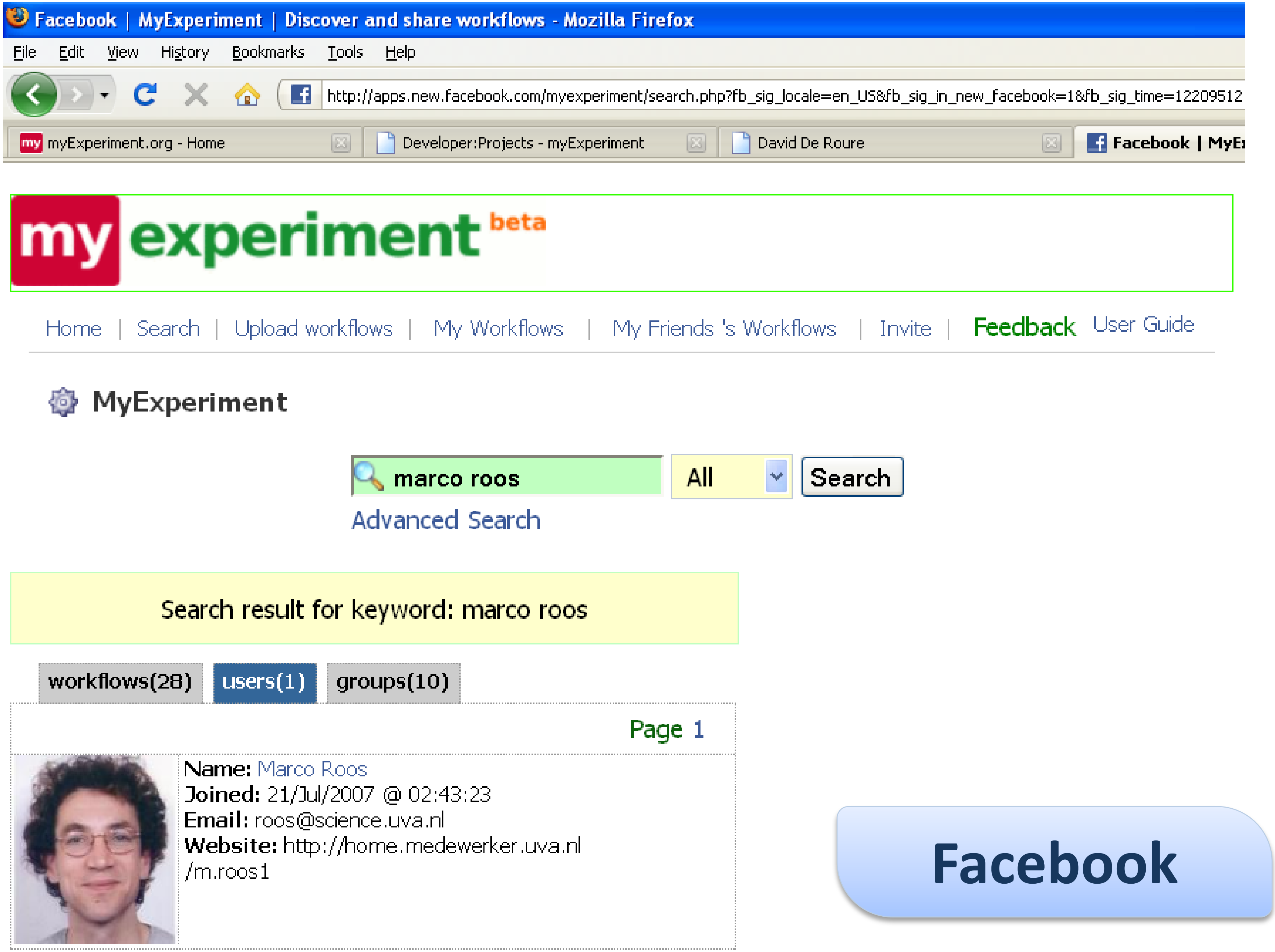
Tags: benchmarks

Created: 12 July 2008 09:17:40
Updated: 12 July 2008 20:20:20

Probeset id 2 Swissport id.xml

Antoon Goderis

Tags: benchmarks



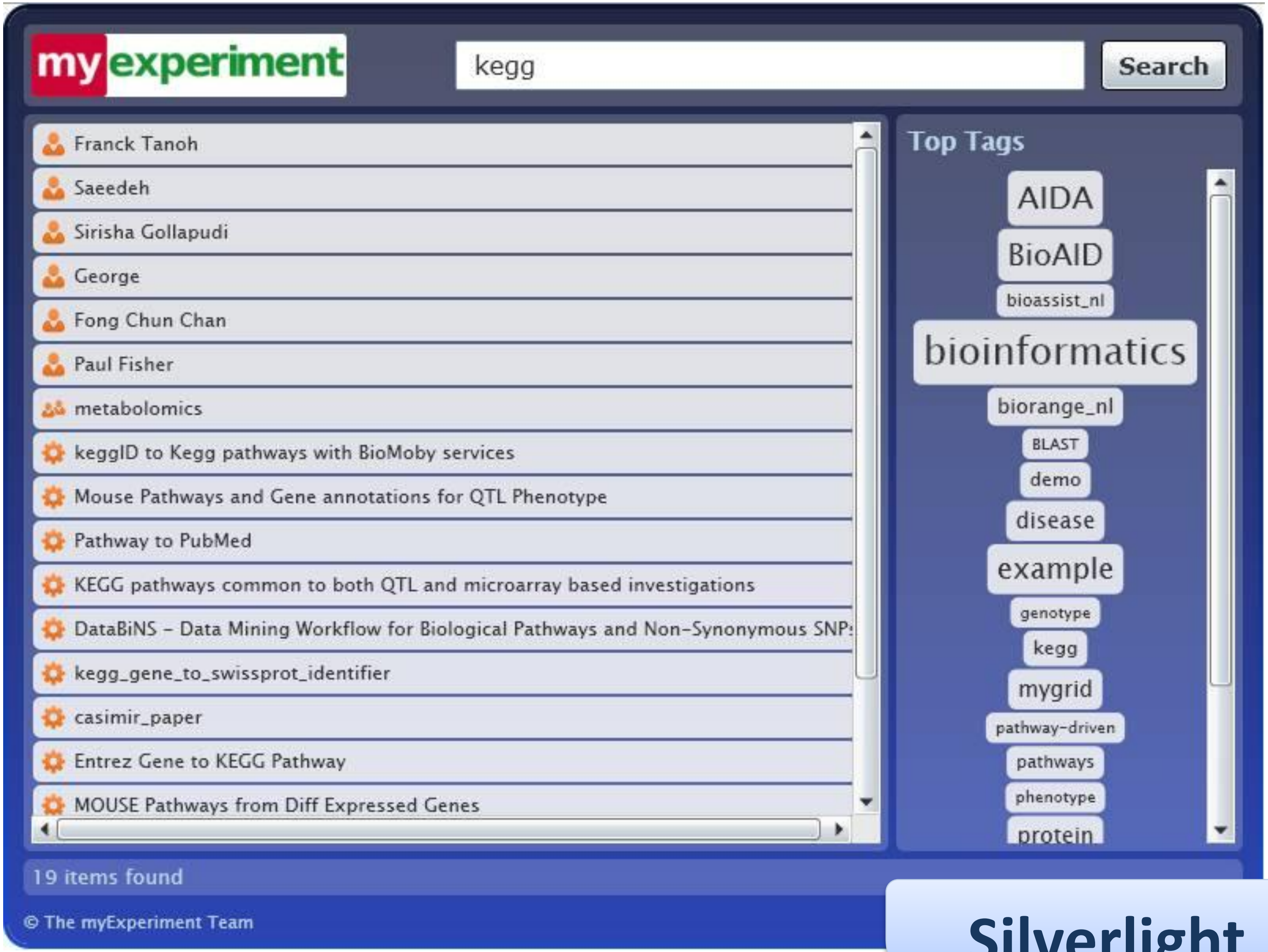
http://apps.new.facebook.com/myexperiment/search.php?fb_sig_locale=en_US&fb_sig_in_new_facebook=1&fb_sig_time=12209512

marco roos

Search result for keyword: marco roos

Name: Marco Roos
Joined: 21/Jul/2007 @ 02:43:23
Email: roos@science.uva.nl
Website: http://home.medewerker.uva.nl/m.roos1

Facebook



Franck Tanoh
Saeedeh
Sirisha Gollapudi
George
Fong Chun Chan
Paul Fisher
metabolomics
keggID to Kegg pathways with BioMoby services
Mouse Pathways and Gene annotations for QTL Phenotype
Pathway to PubMed
KEGG pathways common to both QTL and microarray based investigations
DataBiNS - Data Mining Workflow for Biological Pathways and Non-Synonymous SNP
kegg_gene_to_swissprot_identifier
casimir_paper
Entrez Gene to KEGG Pathway
MOUSE Pathways from Diff Expressed Genes

Top Tags

AIDA
BioAID
bioassist_nl
bioinformatics
biorange_nl
BLAST
demo
disease
example
genotype
kegg
mygrid
pathway-driven
pathways
phenotype
protein

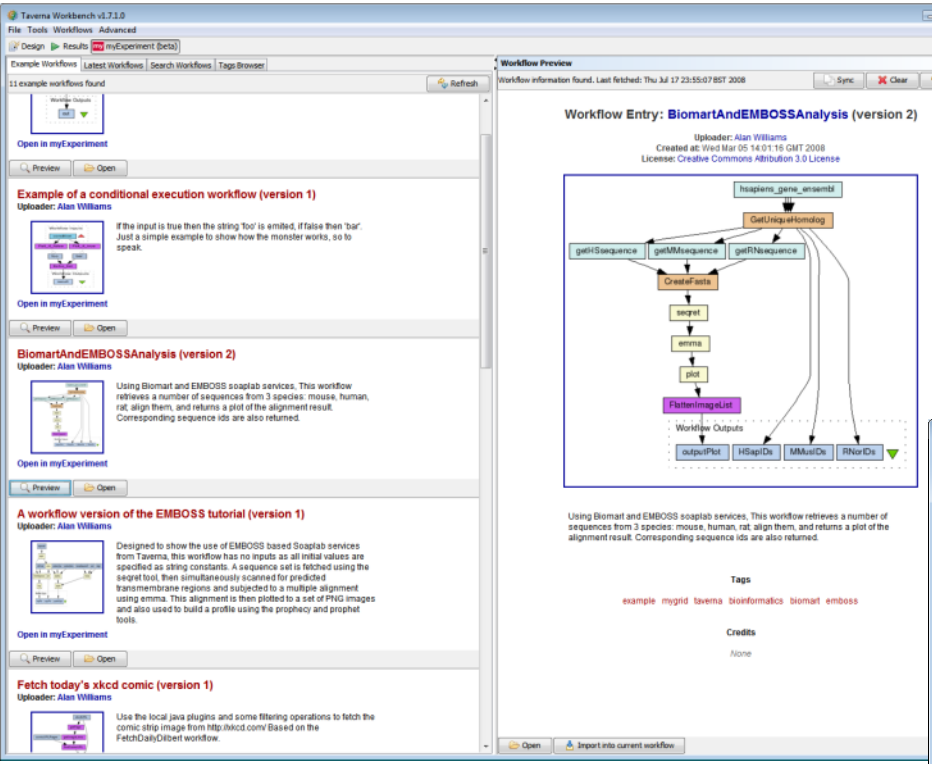
19 items found

© The myExperiment Team

Silverlight

Taverna Plugin

- One click' workflow launch from myExperiment to Taverna (using WHIP).
- Browse the example workflows mantained and curated by a member of the Taverna team (Alan Williams).
- Browse the latest workflows from myExperiment.
- Search for workflows from myExperiment.
- View a dynamic and resizeable tag cloud from myExperiment.
- Get workflows based on a tag.



11 example workflows found

Example of a conditional execution workflow (version 1)
Uploader: Alan Williams

If the input is true then the string 'foo' is emited, if false then 'bar'. Just a simple example to show how the monster works, so to speak.

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 prophecy and prophet tools.

Fetch today's xkcd comic (version 1)
Uploader: Alan Williams

Use the local java plugins and some filtering operations to fetch the comic strip image from http://xkcd.com/ Based on the FetchDailyDilbert workflow.

Workflow information found. Last fetched: Thu Jul 17 23:55:07 BST 2008

Workflow Entry: BiomartAndEMBOSSAnalysis (version 2)

Uploader: Alan Williams
Created at: Wed Mar 05 14:01:16 GMT 2008
License: Creative Commons Attribution 3.0 License

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.

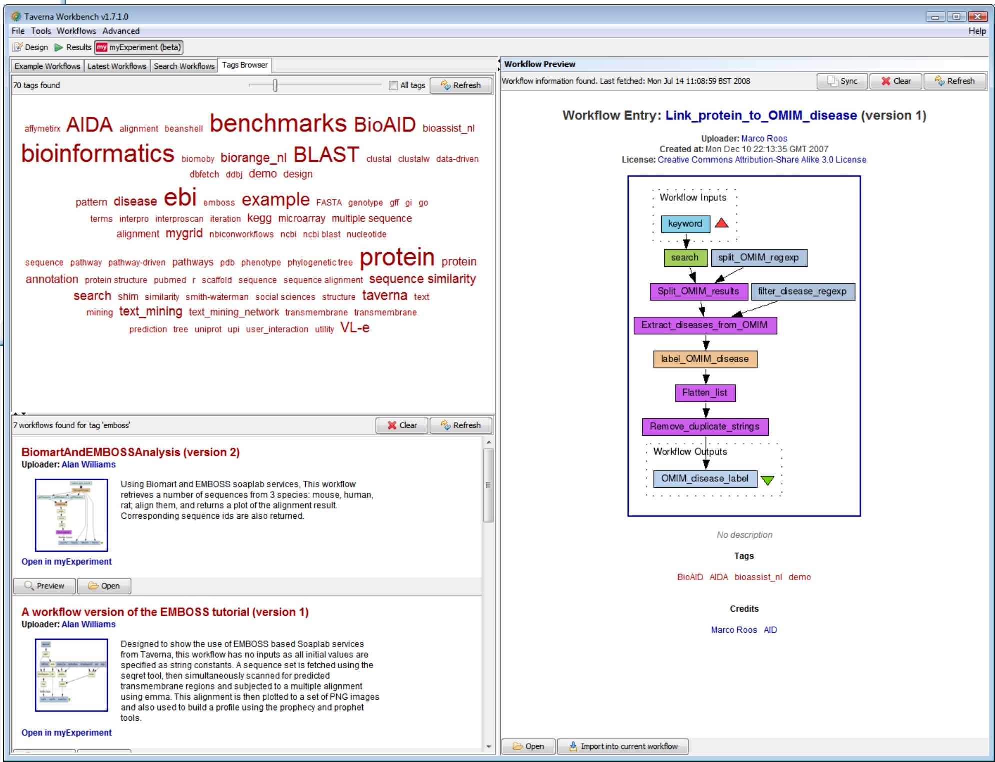
Tags

example mygrid taverna bioinformatics biomart emboss

Credits

None

- 'Preview' a workflow - get more information from myExperiment about a workflow.
- Open a workflow in design mode (when in the myExperiment section of the plugin).
- Import a workflow into a current workflow in design mode.



70 tags found

affymetirx AIDA alignment beanshell benchmarks BioAID bioassist_nl bioinformatics biomoby biorange_nl BLAST clustal clustalw data-driven dbfetch ddbj demo design pattern disease ebi emboss example FASTA genotype gff gi go terms interpro interproscan iteration kegg microarray multiple sequence alignment mygrid nbiconworkflows ncbi ncbi blast nucleotide sequence pathway pathway-driven pathways pdb phenotype phylogenetic tree protein protein annotation protein structure pubmed r scaffold sequence sequence alignment sequence similarity search shim similarity smith-waterman social sciences structure taverna text mining text_mining text_mining_network transmembrane transmembrane prediction tree uniprot upi user_interaction utility VL-e

7 workflows found for tag 'emboss'

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Uploader: Alan Williams

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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

No description

Tags

BioAID AIDA bioassist_nl demo

Credits

Marco Roos AID

Developer’s Perspective

- Completely user-driven design and development
- Constant interactions with users
- Being agile
- Being proactive AND reactive
- Understanding pros and cons
- Being practical!
- Building highly usable interfaces (HTML, REST, RDF, etc!)

BioCatalogue

"The Life Science Web Service Registry"

www.biocatalogue.org

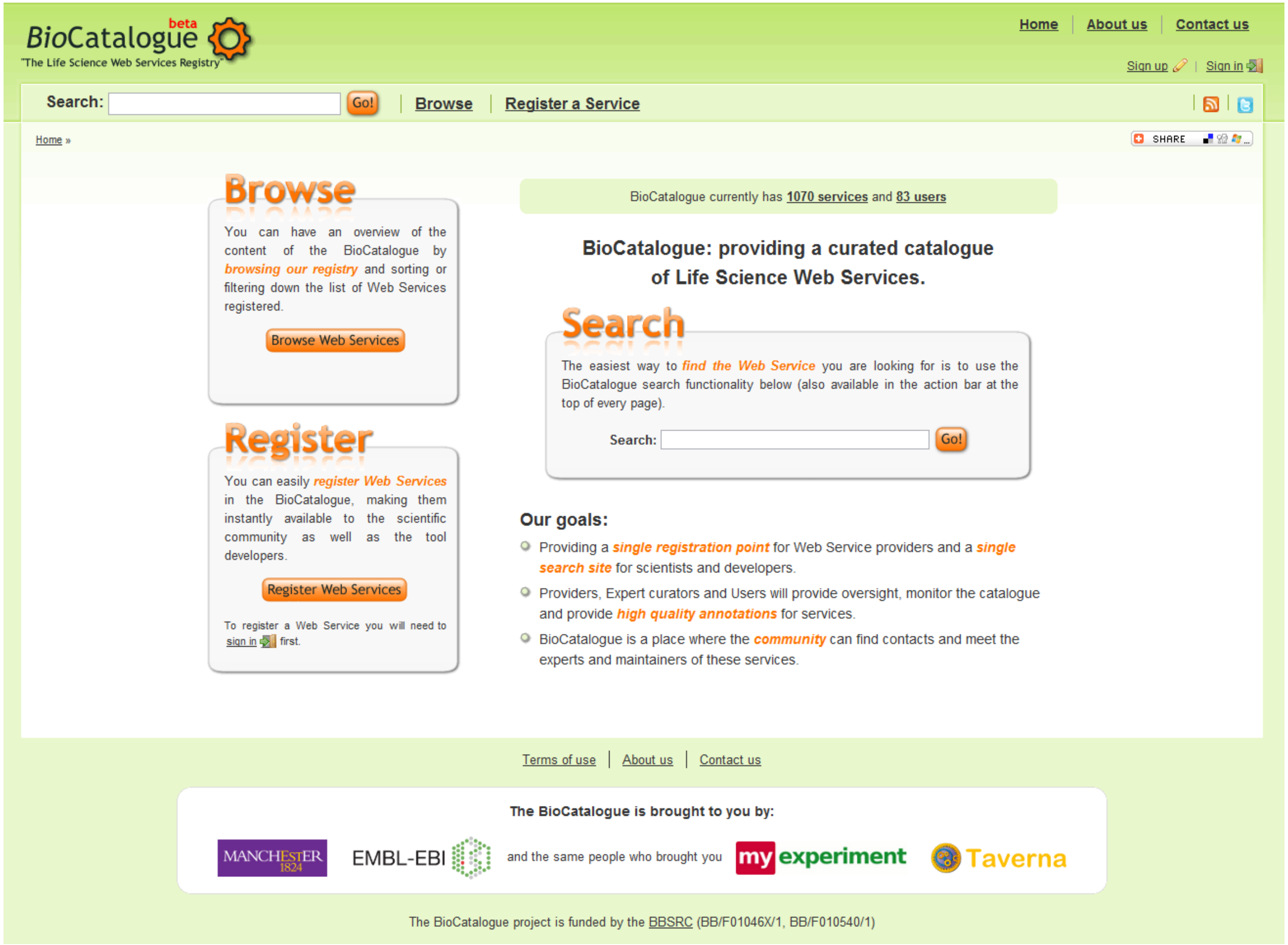
Sister project to myExperiment...

Web Services | Registry | Catalogue | Curated | Social | Web 2.0 | Search | Register | Browse | Annotations | Community | Awesome

BioCatalogue

"The Life Science Web Service Registry"

www.biocatalogue.org



BioCatalogue currently has 1070 services and 83 users

BioCatalogue: providing a curated catalogue of Life Science Web Services.

Browse

You can have an overview of the content of the BioCatalogue by *browsing our registry* and sorting or filtering down the list of Web Services registered.

Browse Web Services

Register

You can easily *register Web Services* in the BioCatalogue, making them instantly available to the scientific community as well as the tool developers.

Register Web Services

To register a Web Service you will need to sign in first.

Search

The easiest way to *find the Web Service* you are looking for is to use the BioCatalogue search functionality below (also available in the action bar at the top of every page).

Search: Go!

Our goals:

- Providing a *single registration point* for Web Service providers and a *single search site* for scientists and developers.
- Providers, Expert curators and Users will provide oversight, monitor the catalogue and provide *high quality annotations* for services.
- BioCatalogue is a place where the *community* can find contacts and meet the experts and maintainers of these services.

Terms of use | About us | Contact us

The BioCatalogue is brought to you by:

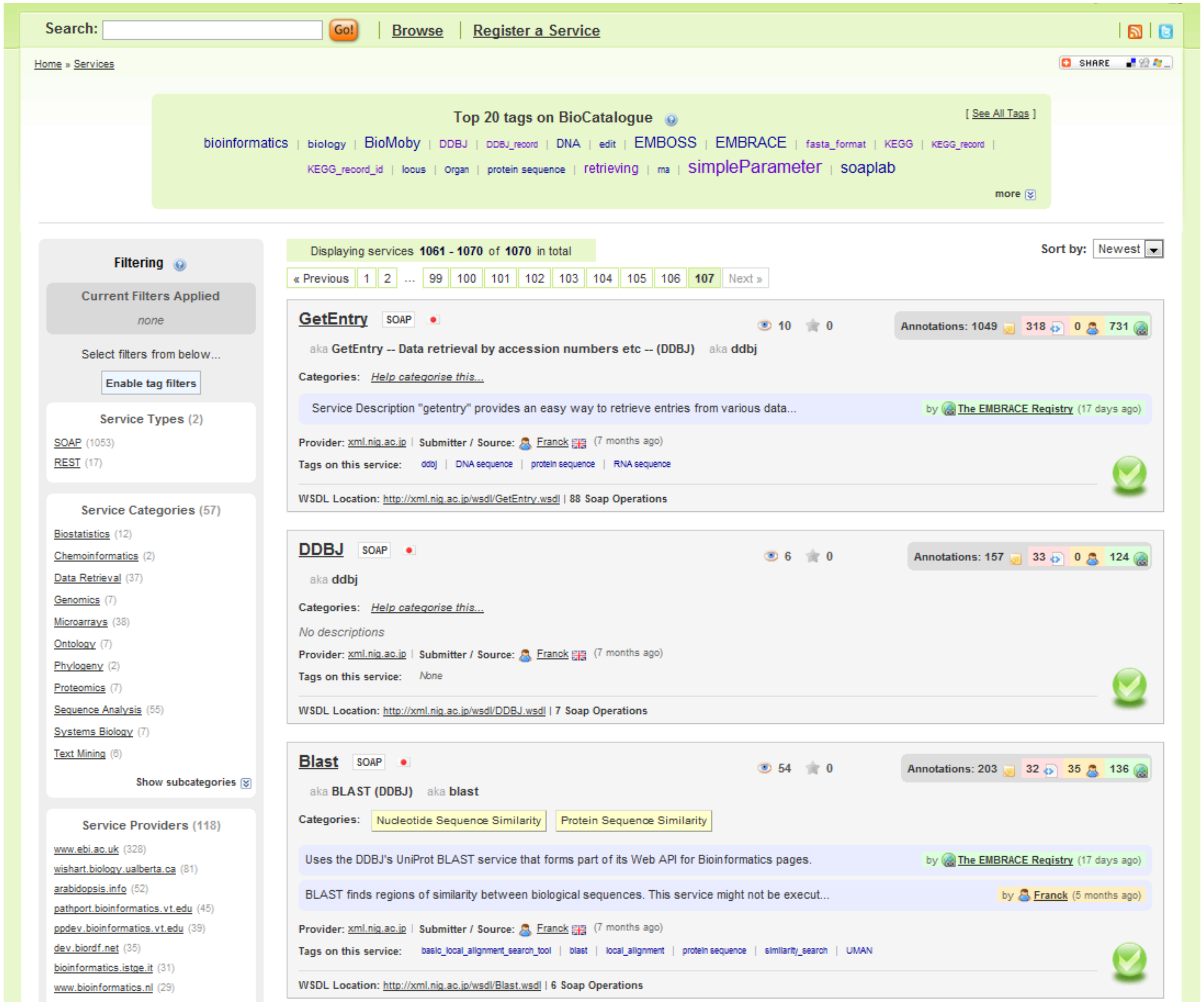
MANCHESTER 1824 EMBL-EBI and the same people who brought you myexperiment Taverna

The BioCatalogue project is funded by the BBSRC (BB/F01046X/1, BB/F010540/1)

BioCatalogue

"The Life Science Web Service Registry"

www.biocatalogue.org



Home » Services

Top 20 tags on BioCatalogue [See All Tags]

bioinformatics | biology | BioMoby | DDBJ | DDBJ_record | DNA | edit | EMBOSS | EMBRACE | fasta_format | KEGG | KEGG_record | KEGG_record_id | locus | Organ | protein sequence | retrieving | rna | simpleParameter | soaplab

more

Filtering

Current Filters Applied

none

Select filters from below...

Enable tag filters

Service Types (2)

- SOAP (1053)
- REST (17)

Service Categories (57)

- Biostatistics (12)
- Chemoinformatics (2)
- Data Retrieval (37)
- Genomics (7)
- Microarrays (38)
- Ontology (7)
- Phylogeny (2)
- Proteomics (7)
- Sequence Analysis (55)
- Systems Biology (7)
- Text Mining (6)

Show subcategories

Service Providers (118)

- www.ebi.ac.uk (328)
- wishart.biology.ualberta.ca (81)
- arabidopsis.info (52)
- pathport.bioinformatics.vt.edu (45)
- ppdev.bioinformatics.vt.edu (39)
- dev.biordf.net (35)
- bioinformatics.istge.it (31)
- www.bioinformatics.nl (29)

Displaying services **1061 - 1070** of **1070** in total

Sort by: Newest

« Previous | 1 | 2 | ... | 99 | 100 | 101 | 102 | 103 | 104 | 105 | 106 | **107** | Next »

GetEntry SOAP ● 10 0 Annotations: 1049 318 0 731

aka **GetEntry -- Data retrieval by accession numbers etc -- (DDBJ)** aka **ddbj**

Categories: *Help categorise this...*

Service Description "getentry" provides an easy way to retrieve entries from various data... by The EMBRACE Registry (17 days ago)

Provider: xml.nig.ac.jp | **Submitter / Source:** Franck (7 months ago)

Tags on this service: ddbj | DNA sequence | protein sequence | RNA sequence

WSDL Location: http://xml.nig.ac.jp/wsdl/GetEntry.wsdl | **88 Soap Operations**

DDBJ SOAP ● 6 0 Annotations: 157 33 0 124

aka **ddbj**

Categories: *Help categorise this...*

No descriptions

Provider: xml.nig.ac.jp | **Submitter / Source:** Franck (7 months ago)

Tags on this service: *None*

WSDL Location: http://xml.nig.ac.jp/wsdl/DDBJ.wsdl | **7 Soap Operations**

Blast SOAP ● 54 0 Annotations: 203 32 35 136

aka **BLAST (DDBJ)** aka **blast**

Categories: Nucleotide Sequence Similarity | Protein Sequence Similarity

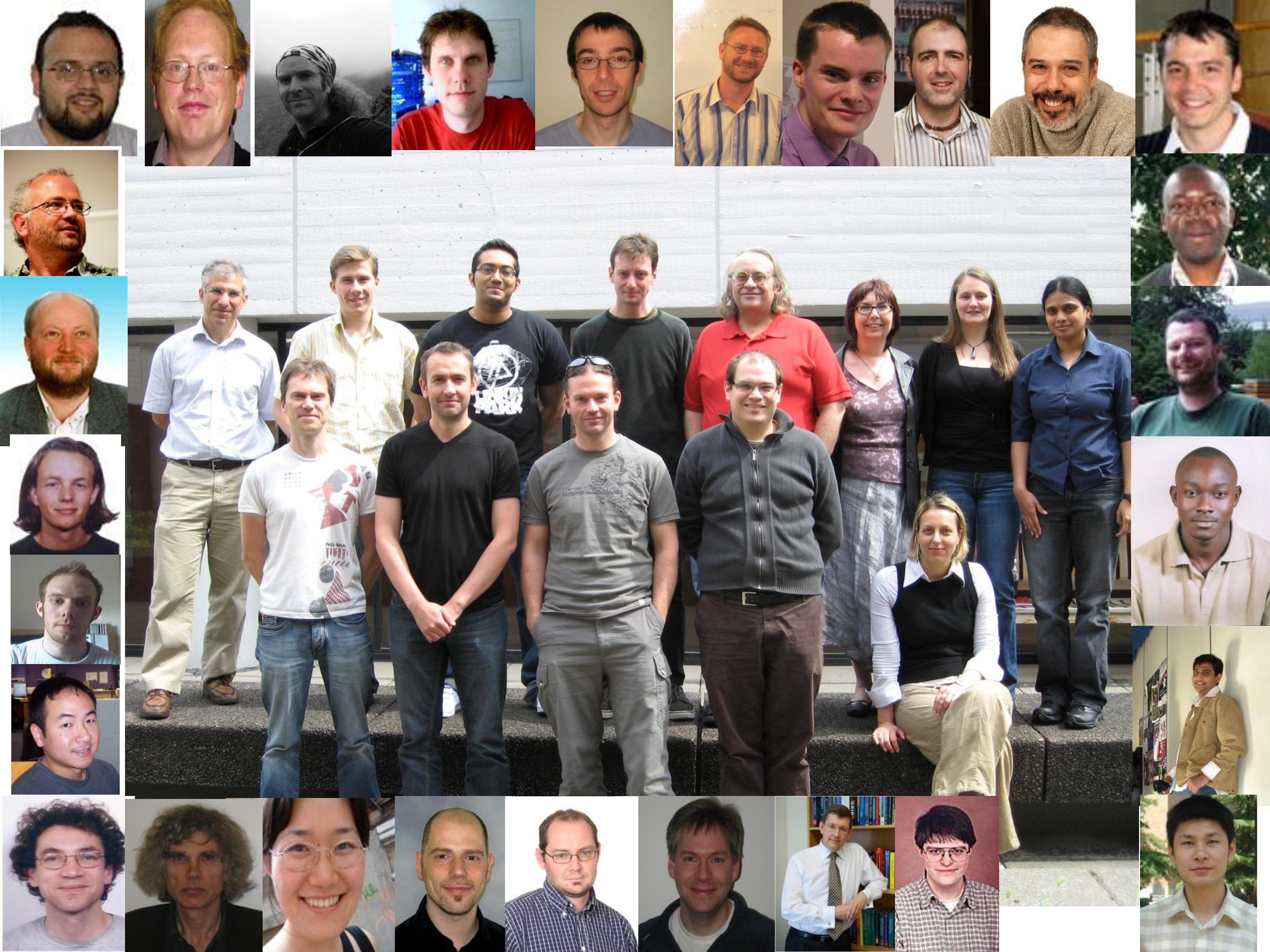
Uses the DDBJ's UniProt BLAST service that forms part of its Web API for Bioinformatics pages. by The EMBRACE Registry (17 days ago)

BLAST finds regions of similarity between biological sequences. This service might not be execut... by Franck (5 months ago)

Provider: xml.nig.ac.jp | **Submitter / Source:** Franck (7 months ago)

Tags on this service: basic_local_alignment_search_tool | blast | local_alignment | protein sequence | similarity_search | UMAN

WSDL Location: http://xml.nig.ac.jp/wsdl/Blast.wsdl | **6 Soap Operations**



Thank | You