BioTools at UMassMed

David S. Lapointe

University of Massachusetts Medical School
Biotools at UMassMed

David Lapointe, Ph.D.
Director Scientific Computing
University of Massachusetts Medical School
biotools.umassmed.edu
Bioinformatics has a large toolset
Bioinformatics?

• Bioinformatics covers a large territory
  – Sequence and Genome Analysis
  – Computational Biology
  – Databases
  – Visualization
  – Programming

• Informatics applied to Biology
Motivation

Biotools started 2001

First as a resource for the Bioinformatics Course

Later expanded access to UMass system, Worcester Colleges, and global.

Last month, 12000 visits from 73 countries.
Welcome to the BioTools site at the University of Massachusetts Medical School.

Restriction and Pattern Analysis
- Restriction mapping tool
- Rebase Query Tool
- Transcription Factor Site Scan

DNA Sequence Analysis
- ORF Plotting Tool
- Primer Selection Tool

Protein Sequence Analysis
- Signal Sequence Cleavage Tool
- Peptide/Protein Statistics
- Garnier Secondary Structure
- PRINTS protein motifs scan
- MHC Motif Predictor

Utilities
- PrettyPlot MSF files
- Translate Nucleic Acids

Links
- BioNetbook
- CoBRA (Biostatistics)
- HSLS Online
- BioGRID New!
- OregAnno New!
- PrimerBank
- Signaling Gateway
- Biinformatics.Org
- GeneCards

Last updated: Friday February 27, 2009
Comments and Suggestions welcome.

Research Computing/Information Services @ UMass Medical School
55 Lake Avenue N, Worcester MA 01655
BioTools

The BioTools site is a resource of tools for bioinformatics for the five schools of the UMass System. Some resources are licensed to the UMass Medical School and only usable at that site. Comments and Suggestions are welcome.

EMBOSS-WWW
  EmbossGUI
Restriction and Pattern Analysis
  Restriction mapping tool
  Rebase Query Tool
  Transcription Factor Site Scan
DNA Sequence Analysis
  ORF Plotting Tool
  Primer Selection Tool
Protein Sequence Analysis
  Signal Sequence Cleavage Tool
  Peptide/Protein Statistics
  Garnier Secondary Structure
  PRINTS protein motifs scan
  MHC Motif Predictor New!
Utilities
  PrettyPlot MSF files
  Translate Nucleic Acids
  ClustalW Multiple Alignment
  Matrix2PNG
  WebLogo New!
  Guide to Unix

Links
  BioNetbook
  CoBRA (Biostatistics)
  HSLS Online
  BioGRID New!
  OregAnno New!
  PrimerBank
  Signaling Gateway
  Bioinformatics.Org
  GeneCards

Last updated: Friday February 27, 2009
Comments and Suggestions welcome.
BioTools

The BioTools site is a resource of tools for bioinformatics for the five schools of the UMass System. Some resources are licensed to the UMass Medical School and only usable at that site. Comments and Suggestions are welcome.

EMBOSS-WWW
  EmbossGUI
Restriction and Pattern Analysis
  Restriction mapping tool
  Rebase Query Tool
  Transcription Factor Site Scan
DNA Sequence Analysis
  ORF Plotting Tool
  Primer Selection Tool
Protein Sequence Analysis
  Signal Sequence Cleavage Tool
  Peptide/Protein Statistics
  Garnier Secondary Structure
  PRINTS protein motifs scan
  MHC Motif Predictor
Utilities
  PrettyPlot MSF files
  Translate Nucleic Acids
  ClustalW Multiple Alignment
  Matrix2PNG
  WebLogo
  Guide to Unix

High Performance Computing
  UmassMed HPC Wiki

UMMS only
  BioTools Message Forum
  Statistics Message Forum
  TRANSFac [info]
  TRANSCompel [info]

Links
  BioNetbook
  CoBRA (Biostatistics)
  HSLS Online
  BioGRID [new]
  OregAnno [new]
  PrimerBank
  Signaling Gateway
  BioInformatics.Org
  GeneCards

Last updated: Friday February 27, 2009
Comments and Suggestions welcome.
BioTools

The BioTools site is a resource of tools for bioinformatics for the five schools of the UMass System. Some resources are licensed to the UMass Medical School and only usable at that site. Comments and Suggestions are welcome.

Restriction and Pattern Analysis
- Restriction mapping tool
- Rebase Query Tool
- Transcription Factor Site Scan

DNA Sequence Analysis
- ORF Plotting Tool
- Primer Selection Tool

Protein Sequence Analysis
- Signal Sequence Cleavage Tool
- Peptide/Protein Statistics
- Garnier Secondary Structure
- PRINTS protein motifs scan
- MHC Motif Predictor

Utilities
- PrettyPlot MSF files
- Translate Nucleic Acids
- ClustalW Multiple Alignment
- Matrix2PNG
- WebLogo
- Guide to Unix

High Performance Computing
- UMassMed HPC Wiki

UMMS only
- BioTools Message Forum
- Statistics Message Forum
- TRANSFac [info]
- TRANSCompel [info]

Links
- BioNetbook
- CoBRA (Biostatistics)
- HSLS Online
- BioGRID [New]
- OregAnno [New]
- PrimerBank
- Signaling Gateway
- BioInformatics.Org
- GeneCards

Last updated: Friday February 27, 2009
Comments and Suggestions welcome.
Select a category to locate programs by function

<table>
<thead>
<tr>
<th>Alignment Consensus</th>
<th>Nucleic Motifs</th>
</tr>
</thead>
<tbody>
<tr>
<td>Alignment Differences</td>
<td>Nucleic Mutation</td>
</tr>
<tr>
<td>Alignment Dot Plots</td>
<td>Nucleic Primers</td>
</tr>
<tr>
<td>Alignment Global</td>
<td>Nucleic Profiles</td>
</tr>
<tr>
<td>Alignment Local</td>
<td>Nucleic Repeats</td>
</tr>
<tr>
<td>Alignment Multiple</td>
<td>Nucleic Restriction</td>
</tr>
<tr>
<td>Display</td>
<td>Nucleic Transcription</td>
</tr>
<tr>
<td>Edit</td>
<td>Nucleic Translation</td>
</tr>
<tr>
<td>Enzyme Kinetics</td>
<td>Phylogeny</td>
</tr>
<tr>
<td>Feature Tables</td>
<td>Protein 2D Structure</td>
</tr>
<tr>
<td>Nucleic 2D Structure</td>
<td>Protein Composition</td>
</tr>
<tr>
<td>Nucleic Codon Usage</td>
<td>Protein Motifs</td>
</tr>
<tr>
<td>Nucleic Composition</td>
<td>Protein Mutation</td>
</tr>
<tr>
<td>Nucleic CpG Islands</td>
<td>Protein Profiles</td>
</tr>
<tr>
<td>Nucleic Gene Finding</td>
<td></td>
</tr>
</tbody>
</table>

ALIGNMENT CONSENSUS

<table>
<thead>
<tr>
<th>Program name</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>cons</td>
<td>Creates a consensus from multiple alignments</td>
</tr>
<tr>
<td>megamerger</td>
<td>Merge two large overlapping nucleic acid sequences</td>
</tr>
<tr>
<td>merger</td>
<td>Merge two overlapping nucleic acid sequences</td>
</tr>
</tbody>
</table>
BioTools

The BioTools site is a resource of tools for bioinformatics for the five schools of the UMass System. Some resources are licensed to the UMass Medical School and only usable at that site. Comments and Suggestions are welcome.

EMBOSS-WWW
- EmbossGUI

Restriction and Pattern Analysis
- Restriction mapping tool
- Rebase Query Tool
- Transcription Factor Site Scan

DNA Sequence Analysis
- ORF Plotting Tool
- Primer Selection Tool

Protein Sequence Analysis
- Signal Sequence Cleavage Tool
- Peptide/Protein Statistics
- Garnier Secondary Structure
- PRINTS protein motifs scan
- MHC Motif Predictor

Utilities
- PrettyPlot MSF files
- Translate Nucleic Acids
- ClustalW Multiple Alignment
- Matrix2PNG
- WebLogo
- Guide to Unix

High Performance Computing
- UmassMed HPC Wiki

UMMS only
- BioTools Message Forum
- Statistics Message Forum
- TRANSFac [info]
- TRANSCompel [info]

Links
- BioNetbook
- CoBRA (Biostatistics)
- HSLS Online
- BioGRID [New]
- OregAnno [New]
- PrimerBank
- Signaling Gateway
- BioInformatics.Org
- GeneCards

Last updated: Friday February 27, 2009
Comments and Suggestions welcome.
Gateways to local resources

Lists

Wikis

Tools
<table>
<thead>
<tr>
<th>Date</th>
<th>Subject</th>
<th>Replies</th>
<th>Author</th>
</tr>
</thead>
<tbody>
<tr>
<td>2009-03-06 12:54:59</td>
<td>FW: Funding opportunities for construction/renovation and instrumentation</td>
<td>0</td>
<td>Lapointe, David</td>
</tr>
<tr>
<td>2009-03-05 12:40:33</td>
<td>FW: News on the ARRA Stimulus</td>
<td>0</td>
<td>Lapointe, David</td>
</tr>
<tr>
<td>2009-02-25 09:43:43</td>
<td>Desktop Sequence Software</td>
<td>2</td>
<td>Lapointe, David</td>
</tr>
<tr>
<td>2009-02-19 13:18:39</td>
<td>FW: Leveraging Data Pipelining for On-the-Fly Data Integration of Multiple Experiments</td>
<td>0</td>
<td>Kittler, Ellen Ph. D.</td>
</tr>
<tr>
<td>2009-02-15 09:53:30</td>
<td>Re: Ingenuity Software</td>
<td>3</td>
<td>Elizabeth Luna</td>
</tr>
<tr>
<td>2009-02-05 08:57:57</td>
<td>FW: [BioC] [JOB] National Cancer Institute, Bethesda, MD</td>
<td>0</td>
<td>Lapointe, David</td>
</tr>
<tr>
<td>2008-11-24 17:14:33</td>
<td>Mathworks Seminar Dec 3</td>
<td>0</td>
<td>Lapointe, David</td>
</tr>
<tr>
<td>2008-09-08 10:48:26</td>
<td>FW: [blast-announce] New BLAST 2 Sequences Interface</td>
<td>0</td>
<td>Lapointe, David</td>
</tr>
<tr>
<td>2008-08-27 09:55:46</td>
<td>Ingenuity Software</td>
<td>1</td>
<td>Elizabeth Luna</td>
</tr>
<tr>
<td>2008-08-12 16:16:00</td>
<td>Mathworks Seminar</td>
<td>0</td>
<td>Lapointe, David</td>
</tr>
<tr>
<td>2008-07-28 09:54:14</td>
<td>Simulation Tools/Software from Simbios</td>
<td>0</td>
<td>Lapointe, David</td>
</tr>
<tr>
<td>2008-07-22 09:23:50</td>
<td>FW: [blast-announce] Primer-BLAST now available - addendum</td>
<td>0</td>
<td>Lapointe, David</td>
</tr>
<tr>
<td>2008-07-21 11:36:31</td>
<td>FW: [Gene-announce] Enhancements to Entrez Gene</td>
<td>0</td>
<td>Lapointe, David</td>
</tr>
<tr>
<td>2008-06-16 22:01:10</td>
<td>FW: RECOMB Regulatory Genomics, Systems Biology, and DREAM3 2008 announcement</td>
<td>0</td>
<td>Lapointe, David</td>
</tr>
<tr>
<td>2008-06-10 16:27:57</td>
<td>FW: NIH Notices and Funding Opportunities</td>
<td>0</td>
<td>Lapointe, David</td>
</tr>
<tr>
<td>2008-06-06 14:35:20</td>
<td>FW: [Gene-announce] Entrez Gene removes links to GDB</td>
<td>0</td>
<td>Lapointe, David</td>
</tr>
<tr>
<td>2008-06-05 12:16:30</td>
<td>FW: Reminder: Webinar Invitation - Advances in GPCR Research, June 17</td>
<td>0</td>
<td>Lapointe, David</td>
</tr>
<tr>
<td>2008-06-02 13:32:18</td>
<td>FW: [Bioclusters] NCCR Summer Institute 2008 -- Cyberinfrastructure for Biomedicine</td>
<td>0</td>
<td>Lapointe, David</td>
</tr>
</tbody>
</table>
Main Page

High Performance Computing at UMassMed

The High Performance Wiki is maintained by Academic and Research Computing Services at the University of Massachusetts Medical School. If you would like to participate in this wiki contact us.

What is HPC?

High Performance Computing refers to the use of supercomputers and computer clusters to solve computationally intensive problems applied generally to scientific research. In the biomedical arena, high performance computing is used to solve problems of

- Medical Physics
- Protein Structure
- Molecular Dynamics
- Comparative Genomics
- Computational Biology

to name a few.

Topics

Overview

- Binar
- HPCC
- Getting Access
- Resources
- UNIX Related QA

Using Clusters

- Queues
- Software

This page was last modified on 3 March 2009, at 14:51. This page has been accessed 588 times. Privacy policy About HPCwiki Disclaimers
PMID Lookup to HTML

Here’s where to locate the pmid for a publication on PubMed. Just use the number on the form or create a text file of pmids to upload.


Enter PMIDs here (one pmid/line)
12036939
1769064
2501299

or upload file with PMIDS: 1 per line

Get Refs! Reset

Last updated: Tuesday November 18, 2008
Comments and Suggestions welcome.
References

Download zipped references


Last updated: Thursday April 02, 2009
Comments and Suggestions welcome.

Research Computing/Information Services @ UMass Medical School
55 Lake Avenue N, Worcester MA 01655
Links to External resources
BioTools

The BioTools site is a resource of tools for bioinformatics for the five schools of the UMass System. Some resources are licensed to the UMass Medical School and only usable at that site. Comments and Suggestions are welcome.

EMBOSS-WWW
- EmbossGUI

Restriction and Pattern Analysis
- Restriction mapping tool
- Rebase Query Tool
- Transcription Factor Site Scan

DNA Sequence Analysis
- ORF Plotting Tool
- Primer Selection Tool

Protein Sequence Analysis
- Signal Sequence Cleavage Tool
- Peptide/Protein Statistics
- Garnier Secondary Structure
- PRINTS protein motifs scan
- MHC Motif Predictor

Utilities
- PrettyPlot MSF files
- Translate Nucleic Acids
- ClustalW Multiple Alignment
- Matrix2PNG
- WebLogo
- Guide to Unix

High Performance Computing
- UmassMed HPC Wiki

UMMS only
- BioTools Message Forum
- Statistics Message Forum
- TRANSFac [info]
- TRANSCompel [info]

Links
- BioNetBook
- CoBRA (Biostatistics)
- HSLS Online
- BioGRID [New]
- OregAnno [New]
- PrimerBank
- Signaling Gateway
- BioInformatics.Org
- GeneCards

Last updated: Friday February 27, 2009
Comments and Suggestions welcome.
Browse COBRA by Subject

Categorical Data Analysis (71)
Clinical Epidemiology (55)
Clinical Trials (101)
Computation (120)
Computational Biology/Bioinformatics (218)
Design of Experiments and Sample Surveys (49)
Disease Modeling (89)
Epidemiology (187)
General Biostatistics (272)
Genetics (104)
Health Services Research (33)
Institutional and Historical (3)
Laboratory and Basic Science Research (19)
Longitudinal Data Analysis and Time Series (140)
Medical Specialties (27)
Microarrays (198)
Multivariate Analysis (132)
Statistical Models (372)
Statistical Theory and Methods (591)
Survival Analysis (269)
Vital and Health Statistics (11)

Peer-Reviewed Journals

Statistical Applications in Genetics and Molecular Biology*
The International Journal of Biostatistics*

Propose a journal

Browse COBRA by Institution

Bioconductor Project
Collection of Biostatistics Research Archive
Columbia University
Duke University
Harvard University
Johns Hopkins University
Memorial Sloan-Kettering Cancer Center
University of California, San Francisco
University of California, Berkeley
University of Michigan School of Public Health
University of North Carolina at Chapel Hill
University of Pennsylvania
University of Texas, MD Anderson Cancer Center
University of Washington

Create a new series

Paper counts as of 04/02/09
GeneCards® is a searchable, integrated database of human genes that provides concise genomic, proteomic, transcriptomic, genetic and functional information on all known and predicted human genes. Information featured in GeneCards includes orthologies, disease relationships, mutations and SNPs, gene expression, gene function, pathways, protein-protein interactions, related drugs & compounds and direct links to cutting edge research reagents and tools such as antibodies, recombinant proteins, clones, expression assays and RNAi reagents.

SAMPLE GENE: CASP3

[Gene Index] [Disease genes] [Hot genes] Random Gene From: ---GiFIS Group--- Go GiFIS improved

Search the GeneCards Human Gene Database

Search by:

- Keywords
- Gene Symbol only
- Symbol/alias
- GC id
- Symbol/External id

Examples:
tay sachs
dimerization AND diabetes
neurodegenerative OR smile

ESR1
wnt*
FRA1
GC17M03*
3395
7431
P12004
ENSG00000185515

Options:

- Show microcards only
- Show minicards also (slower)
- Sort microcards alphabetically (faster)
- Sort microcards by relevance

More search examples

The GeneCards search is case insensitive

GeneCards Gene Database statistics
Next Up

Provide links to local resources
Faculty developed applications
Portal to data storage

Develop applications for Web 3.0
Web 3.0?
Where is this going?

The web is a great vehicle for distributing information, creating resources.

The web, however, is human readable. It is difficult to harvest information from websites.

Resource creators are moving to semantic web along with web service models to allow machine harvest of information.
Pathguide is the pathway resource list.

Complete Listing of All Pathguide Resources

Pathguide contains information about 291 biological pathway resources. Click on a link to go to the resource home page or 'Details' for a description page. Databases that are free and those supporting BioPAX, CellML, PSI-MI or SBML standards are respectively indicated.

If you know of a pathway resource that is not listed here, or have other questions or comments, please send us an e-mail.

Protein-Protein Interactions

<table>
<thead>
<tr>
<th>Database Name (Order alphabetically)</th>
<th>Full Record</th>
<th>Availability</th>
<th>Standards</th>
</tr>
</thead>
<tbody>
<tr>
<td>3DID - 3D interacting domains</td>
<td>Details</td>
<td>Free</td>
<td></td>
</tr>
<tr>
<td>ABCdb - Archaea and Bacteria ABC transporter database</td>
<td>Details</td>
<td>Free</td>
<td></td>
</tr>
<tr>
<td>AfCS - Alliance for Cellular Signaling Molecule Pages Database</td>
<td>Details</td>
<td>Free</td>
<td></td>
</tr>
<tr>
<td>AllFun - Functional Associations of Proteins in Complete Genomes</td>
<td>Details</td>
<td>Free</td>
<td></td>
</tr>
<tr>
<td>aMAZE - Protein Function and Biochemical Pathways Project</td>
<td>Details</td>
<td>Free</td>
<td></td>
</tr>
<tr>
<td>ASEdb - Alanine Scanning Energetics Database</td>
<td>Details</td>
<td>Free</td>
<td></td>
</tr>
<tr>
<td>ASPD - Artificial Selected Proteins/Peptides Database</td>
<td>Details</td>
<td>Free</td>
<td></td>
</tr>
<tr>
<td>BID - Binding Interface Database</td>
<td>Details</td>
<td>Free</td>
<td></td>
</tr>
<tr>
<td>BIND - Biomolecular Interaction Network Database</td>
<td>Details</td>
<td>Free</td>
<td>PSI-MI</td>
</tr>
<tr>
<td>BioGRID - General Repository for Interaction Datasets</td>
<td>Details</td>
<td>Free</td>
<td>PSI-MI</td>
</tr>
<tr>
<td>BRITE - Biomolecular Relations in Information Transmission and Expression</td>
<td>Details</td>
<td>Free</td>
<td>BioPAX</td>
</tr>
<tr>
<td>CAINeuron - Pathways of the hippocampal CA1 neuron</td>
<td>Details</td>
<td>Free</td>
<td>BioPAX</td>
</tr>
<tr>
<td>Cancer Cell Map - The Cancer Cell Map</td>
<td>Details</td>
<td>Free</td>
<td></td>
</tr>
<tr>
<td>CEC - Cell Circuits</td>
<td>Details</td>
<td>Free</td>
<td></td>
</tr>
<tr>
<td>CPDB - ConsensusPathDB</td>
<td>Details</td>
<td>Free</td>
<td></td>
</tr>
<tr>
<td>CSP - Cytokine Signaling Pathway Database</td>
<td>Details</td>
<td>Free</td>
<td>BioPAX</td>
</tr>
<tr>
<td>CTB - Calmodulin Target Database</td>
<td>Details</td>
<td>Free</td>
<td></td>
</tr>
</tbody>
</table>
So a researcher might come to me or you and ask

I have 200 Entrez gene IDs.
What pathways do these genes belong to?

What resource would you direct them toward?
There is always Google!

Find workflows and Web services for bioinformatics

Pathways

Search

Creator

Name: Antoon Goderis
Member since: Nov 3, 2006

Contributors [Volunteer to contribute]

José M ... Anonymous ... Franck ... Duncan ... Paul Fish ...

Stian Soli ... Alan R Wi ...

Search engine details

Find Web services and workflows for bioinformatics applications, compatible with the open source Taverna workflow editor;
http://www.mygrid.org.uk/taverna

searches 136 sites, including:
http://www.mygrid.org.uk/wiki/Mygrid/BiologicalWebServices,
workflows.mygrid.org.uk, www.biojava.org/docs/
taverna.sourceforge.net/index.php?doc=services.html
bioweb.pasteur.fr/docs/EMBOSS/

Keywords: biology, bioinformatics, web services, workflows, Taverna, myGrid, registry, myExperiment

Last updated: Aug 14, 2007
Add this search engine to your Google homepage
Add this search engine to your blog or webpage »
Create your own Custom Search Engine »
Hmm, mostly journal articles. Let see Workflows only

Refine results for **Pathways:**

<table>
<thead>
<tr>
<th>No workflows</th>
<th>No local applications</th>
<th>Workflows only</th>
<th>WSDL only</th>
</tr>
</thead>
</table>

**BioMed Central | Full text | Systems biology for identifying liver ...**
Mar 10, 2009 ... The objective of this paper is to describe systems biology methods for identifying pathways involved in liver toxicity induced by free fatty ...
www.biomedcentral.com/1753-6561/3/S2/S2
by Z Li - 2009
Labeled No workflows WSDL only

**Genome Biology | Full text | Computational prediction of human ...**
PathoLogic predicts the metabolic pathways of the organism, providing new .... Current knowledge of human nutrition based on metabolic pathways is derived ...
genomebiology.com/2004/6/1/R2
by P Romero - 2004 - Cited by 80 - Related articles - All 13 versions
Labeled No workflows WSDL only

**Bioinformatics—from genes to pathways - Nature Methods**
Combined with the right computational tools, genomic data can uncover unknown pathways to cellular processes. Because few researchers have the resources to ...
www.nature.com/nmeth/journal/v1/n2/full/nmeth1104-159.html
by L Bonnetta - 2004 - Cited by 12 - Related articles
Labeled WSDL only No workflows

**Genome Biology | Full text | Reactome: a knowledgebase of ...**
Reactome: a knowledge base of biologic pathways and processes .... **Pathways** can be part of larger pathways. Reactome represents glycolysis and ...
genomebiology.com/2007/8/3/r39
by I Vastrik - 2007 - Cited by 101 - Related articles - All 7 versions
Labeled No workflows WSDL only

**PATIKAweb: a Web interface for analyzing biological pathways ...**
Summary: PATIKAweb provides a Web interface for retrieving and analyzing biological pathways in the PATIKA database, which contains data integrated from ...
bioinformatics.oxfordjournals.org/cgi/content/abstract/22/3/374
by U Dogrusoz - 2006 - Cited by 19 - Related articles - All 8 versions
Labeled No workflows WSDL only
This workflow takes in Entrez gene ids then adds the string "ncbi-geneid:" to the start of each gene id. These gene ids are then cross-referenced to KEGG gene ids. Each KEGG gene id is then sent to the KEGG pathway database and its relevant pathways returned.

BioCatalogue will provide a single registration point for Web Service providers and a single search site for scientists and developers.

BioCatalogue will also act as a place where the community can find contacts and meet the experts and maintainers of these services.

The BioCatalogue team is currently working with the Embrace team to merge their registries. In the meantime, if you are keen to register your web services, please use the Embrace Registry, the contents of which will be merged with BioCatalogue in due course.

The BioCatalogue team is currently working on its first release, the pilot BioCatalogue, which has been released for testing to our biocatalogue-friends mailing list.

More information about the pilot and current BioCatalogue activities can be found on the BioCatalogue public wiki.

"Web Services are hard to find..."
Scientist, tool developers, bioinformaticians will be able to find the right Web Service they were looking for, thanks to an easy and powerful search interface harvesting the information made available by the Web Services providers and the BioCatalogue community.

"My Web Services are not visible..."
Service providers will be able to easily register their Web Services in the BioCatalogue, making them instantly available to the scientific community as well as the tool developers.

"Web Services are poorly described..."
Expert curators will provide oversight, monitor the catalogue and provide high quality annotations for services. The wider community will also participate to this effort using social networking for recommending, tagging, commenting and rating the services.

"Web Services are volatile..."
Web Services are volatile. They change their location, capability and interaction or become outdated. BioCatalogue will allow agents to monitor the Web Services and automatically add information to the catalogue.
The end result is that we are approaching eScience (EU)/cyberinfrastructure(USA)

Genomics (NCBI, Ensembl, UCSC,GMOD)

meets System Biology (KEGG,BIND,GO)