

MIRIAM Resources: robust cross-references in Systems Biology

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Introduction

Computational Systems Biology relies on developing large quantitative models of biological processes. In order to facilitate their exchange and reuse, as well as to improve their quality, a set of guidelines (suitable for use with any structured format) have been created: the Minimal Information Requested In the Annotation of biochemical Models (*MIRIAM*) [1].

An important part of *MIRIAM* consists in the controlled annotation of model components, based on Uniform Resource Identifiers (URI). To summarise, all the components of a model need to be unambiguously identified in a perennial and standard way. This annotation should be consistent across all the data types used to annotate a model. *MIRIAM URIs* have been introduced to bring reliable annotations (not dependent on physical locations). In order to support this annotation, we developed *MIRIAM Resources* (<http://www.ebi.ac.uk/miriam/>) [2], a set of on-line services.

Resources

Primarily, *MIRIAM Resources* is a catalogue of data types, their URIs and the corresponding physical URLs (or resources), whether the data types are controlled vocabularies or primary data resources.

Resolution and conversion services (such as generating a *MIRIAM URI* from a data type name and the identifier of a dataset, or resolving all the physical locations corresponding to a *MIRIAM URI*) are provided via SOAP and REST Web Services.

Use cases

Curator's point of view: For model curators, there is a need to put additional information on top of the model structure and mathematics. Whatever the format used to encode the model, all the components of the model must be unambiguously identified. One way to achieve that is to link, using *MIRIAM URIs*, the components to relevant entries in existing freely accessible resources. Therefore, the only thing needed is to use a model edition software to generate the appropriate URIs, such as SBMLEditor[3], based on the knowledge of a relevant accession for a given data type. Of course, this is possible using *MIRIAM Web Services*.

Developer's point of view: The developer of a software to be used in computational systems biology will have to import models already encoded. If an interface to display them is to be created, one would want to convert all the *MIRIAM URIs* for instance into physical addresses, which can be used to recover the knowledge stored in the entities pointed to by the annotations. This conversion is straightforward with *MIRIAM Web Services*.



- Browse
- Query
- Submit new
- Export
- Sign In

▪ Web Services

- WSDL
- Services available
- Library documentation

▪ Documents

- MIRIAM Standard
- FAQ
- Media
- News
- BioModels Qualifiers

▪ MIRIAM on SourceForge

▪ Contact



SOURCEFORGENET

EBI > Groups > Computational Neurobiology > Research > MIRIAM

Name		
Identifier	MIR:00000005	
Name	UniProt	
Synonyms	No synonym	
URIs		
Official URL	http://www.uniprot.org/	
Official URN	urn:lsid:uniprot.org:uniprot	
Deprecated	urn:lsid:uniprot.org	
Information		
Definition	UniProt (Universal Protein Resource) is the world's most comprehensive catalog of information on proteins. It is a central repository of protein sequence and function created by joining the information contained in Swiss-Prot, TrEMBL, and PIR.	
Identifier Pattern	^([OPQ][0-9][A-Z0-9][A-Z0-9][A-Z0-9][0-9]([dA-Z](1.5))?)\$	
Physical Locations		
Resource #1	Data Entry	http://www.ebi.uniprot.org/entry/\$id
	Data Resource	http://www.ebi.uniprot.org/
	Information	Universal Protein Resource
	Institution	European Bioinformatics Institute, United Kingdom
Resource #2	Data Entry	http://www.pir.uniprot.org/cgi-bin/upEntry?id=\$id
	Data Resource	http://www.pir.uniprot.org/
	Information	Universal Protein Resource
	Institution	Georgetown University, USA
Resource #3	Data Entry	http://us.expasy.org/uniprot/\$id
	Data Resource	http://www.expasy.uniprot.org/
	Information	Universal Protein Resource, ExPASy (Expert Protein Analysis System)
	Institution	Swiss Institute of Bioinformatics, Switzerland
Documentation		
URL(s)	http://srs.ebi.ac.uk/srsbin/cgi-bin/wgetz?-view+MedlineFull+[medline-PMID:16381842] http://www.ncbi.nlm.nih.gov/entrez/query.fcgi?cmd=Retrieve&db=pubmed&dopt=Abstract&list_uids=16381842 http://www.ebi.ac.uk/cite/Explore/citationDetails.do?dataSource=MED&externalId=16381842	
Miscellaneous		
Date of creation	2006-08-14 19:38:06 GMT	
Date of last modification	2007-07-17 11:06:35 GMT	

Figure 1: This example represents a data type (UniProt) stored in *MIRIAM Resources*. Notice the three alternative resources giving access to the dataset belonging to the same data type.

Implementation

The source code of the whole project is currently available, under the GNU General Public License, at: <http://sourceforge.net/projects/miriam/>.

Conclusions

MIRIAM Resources allows an easy access to *MIRIAM URIs* and the associated information, and is therefore crucial to foster a general use of *MIRIAM* annotations in computational models of biological processes. This in turn, should facilitate the identification, exchange, and integration of models.

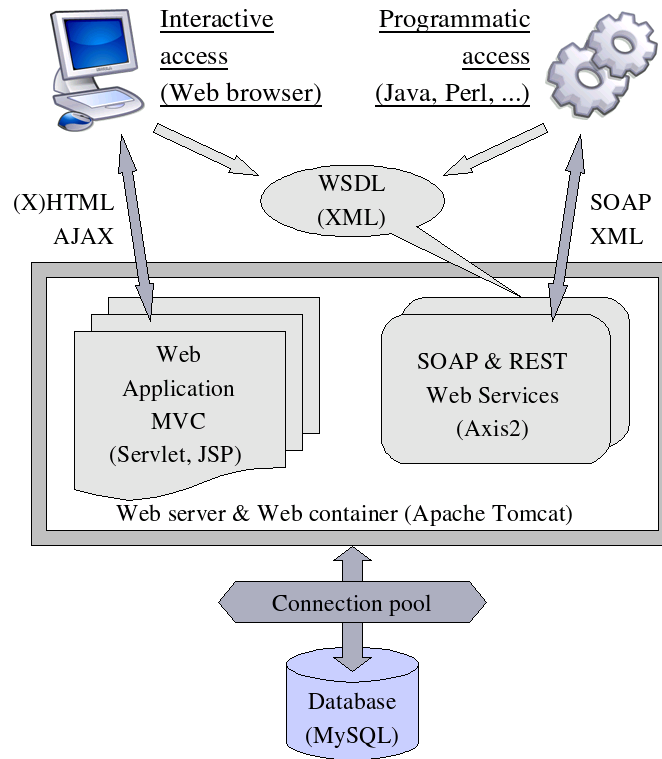


Figure 2: Diagram representing the different components of *MIRIAM Resources* and their interactions.

References

- [1] N. Le Novère, A. Finney, M. Hucka, U. Bhalla, F. Campagne, J. Collado-Vides, E.J. Crampin, M. Halstead, E. Klipp, P. Mendes, P. Nielsen, H. Sauro, B. Shapiro, J.L. Snoep, H.D. Spence, and B.L. Wanner. Minimum Information Requested In the Annotation of biochemical Models (MIRIAM). *Nature Biotechnology*, 23(12):1509–1515, 2005.
- [2] C. Laibe and N. Le Novère. MIRIAM Resources: tools to generate and resolve robust cross-references in Systems Biology. *BMC Systems Biology*, 2007, submitted.
- [3] N. Rodriguez, M. Donizelli, and N. Le Novère. SBMLeditor: effective creation of models in the Systems Biology Markup Language (SBML). *BMC Bioinformatics*, 8:79, 2007.