

# Introduction

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## What's **jORCA**?



**jORCA** is a Java desktop Client able to efficiently access different type of web services repositories mapping resources metadata over a general virtual definition to support scalable service discovery and achieving flexible tools inter-communication.

Right jORCA recognize and execute Moby-Central, INB (extended Moby) and ACGT repositories, we're working in another kind of repositories and web services technologies like WSDL or Taverna repositories.

### **Motivation**

This software is intended to facilitate the use of Web-Services offering a friendly tool able to execute BioMoby and general web-services, command line applications, R-scripts in easy and private way using their own data stored in its local file system.

Similar to MOWServ (Navas et.al 2006; <http://www.inab.org/MOWServ>) the interface is user friendly exploiting capabilities of desktop applications and with extended functionalities configurable by the users.

(1) Ismael Navas-Delgado, Maria del Mar Rojano-Muñoz, Sergio Ramírez, Antonio J. Pérez, Eduardo Andrés León; Jose F. Aldana-Montes, and Oswaldo Trelles; "Intelligent client for integrating bioinformatics services"; *Bioinformatics*, vol.22 no.1 2006 pages 106-111

### ***Acknowledgments***

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Several partners helped us to improve the software. We thank very much all those partners, specially all the people acting as tool tester and all the bitlab ([www.bitlab-es.com](http://www.bitlab-es.com)) team.

### ***Summary***

Diverse web-services repositories have been deployed to assist in the standardization and integration of appropriated tools for data processing in bioinformatics. One of the major advantages in using web-services is they are designed to support interoperable machine-to-machine interaction over a network or workflows (pre-defined invocations of web-services). However, in spite that at the end, tools are going to be used by human users web-services do not usually offer an interactive interface to deal with it, task that is generally delegated to the client processes who become in charge of invocation, input and output visualization, etc. To allow the development of clients for interactive and personalised use, the metadata containers use to offer a programmatic API in such a way that expert clients can offer user friendly, versatile and powerful interfaces to dynamically discover and use tools/algorithms.

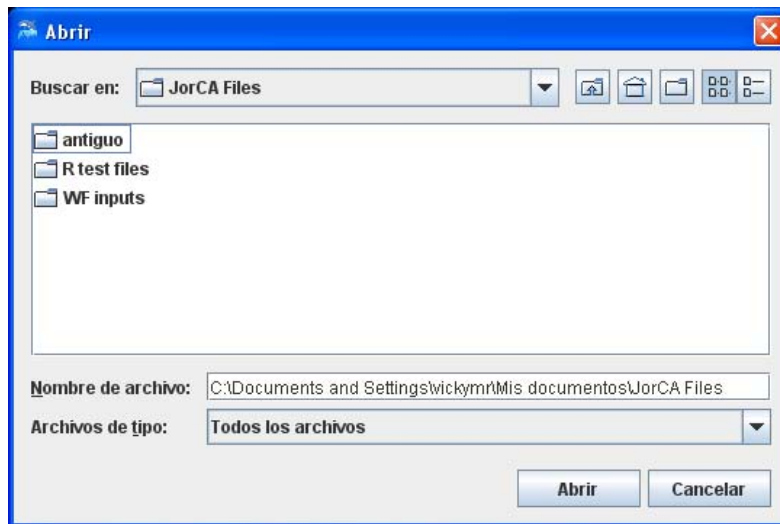
jORCA manages repositories heterogeneity supported by the Modular-API providing a uniform view of metadata by handling multiple repositories (e.g. GRID-based, native soap biomoby, R-bioconductor, and others), in a common way, independently of the access protocol and location of the metadata. JORCA is endowed with a functional plug-ins-API to extend its functionality by adding specific plug-ins.

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# Starting jORCA

To run jORCA double click on jORCA.bat (under MS-Windows) icon or jORCA.sh (under UNIX OS) .

jORCA is a Desktop application that uses the local file system in the user machine to manage data files. During the initial configuration, jORCA will request this “HOME” folder. Note: inputs can be in others folders



Once the user has selected the main folder for the application, program will start loading data from the default repository. This information can be changed at any time. Program will show you the loading progress in the following window:



jORCA is distributed with some caches files for different repositories to speed-up remote data retrieval. In computer sciences, a Cache is a collection of data duplicating original values stored elsewhere or computed earlier, where the original data is expensive to fetch (owing to longer access time) or to compute, compared to the cost of reading the cache. In other words, a cache is a temporary storage area where frequently accessed data can be stored for rapid access. Once the data is stored in the cache,

future use can be made by accessing the cached copy rather than re-fetching or re-computing the original data, so that the average access time is shorter. User can reload these caches at any time.

Once the loading step has finished, the user will see jORCA Graphic User interface with the default configuration and data from the default repository:

Search:   Filter

Options Configuration Help

My favorites

- Favorites
  - Blast services
    - getBestHitsFromBlast
    - runNCBIblastp1
    - parseMultipleAlignFromBLASTText
  - PDB Services
    - parseAminoAcidSequenceFromP

Data Types

- DataTypes
- ISO\_DateTime
- Object

Tools

- Tools
- Service

Namespaces

- Namespaces

Main

jORCA application will help you in the use of the available tools on the web (web services). You can connect to different available repositories and use their service with your data. See Online help for extended and useful information.

Useful Bioinformatics tools

**JorCA Web page**  
Follow this link to access full information about jORCA (documents, downloads etc..)

**MOWServ tool**  
Internet based client. Discovery of services based on data type ontology or on service type ontology. It allows to connect easily service outputs to service inputs. Interface helps to the Moby object construction.

**Cargo INB Platform**  
Currently, CARGO displays biological information only for human genes. Information for other species will be included. CARGO is involved in some projects as Cargo, BioSapiens, or as INB.

**IWWEIM**  
Interactive Web Workflow Enactor and Manager (IWWE and M) has been created to try tackling with web workflow management, workflow publishing and workflow execution problems, providing both an end user graphical interface and a programmatic API for those tasks.

**Bitlab group**  
BitLAB (Bioinformatics and Information Technologies Laboratory) is an internal group at AC-UMA focused in the application of advanced computing to solve management and data analysis in bioinformatics and biomedical fields; especially in Input/Output bounded applications. Bioinformatics, a data-driven science strongly featured by the high volume of heterogeneous data sets and the geographical dispersion of their services, is used as the benchmarking application domain in the research lines of Bitlab.

Name	Type	Size	Modified
AminoAcidSequence.xml	AminoAcidSequence	377B	31-ago-2007
GE-demo.dat	File	1 MB	08-ene-2009
getBestHitsFromBlast.2009-02-05.12-5...	Collection	1 KB	05-feb-2009
getBestHitsFromBlast.2009-02-05.13-1...	Collection	1 KB	05-feb-2009
getBestHitsFromBlast.2009-02-06.10-3...	Collection	1 KB	06-feb-2009
getBestHitsFromBlast.2009-02-06.10-4...	Collection	1 KB	06-feb-2009
getBestHitsFromBlast.2009-02-16.10-5...	Collection	1 KB	16-feb-2009
getPrositeAnnStructure.2009-02-05.13...	AnnotatedStructure	1 MB	05-feb-2009
holaWS.2009-02-06.10-24-1.xml	String	161B	06-feb-2009

jORCA: Easily integrating

# jORCA Areas

## Quick overview

jORCA interface is organized in four areas:

- ToolBar and Menu Area.
- Main Area.
- Control Area.
- File System area

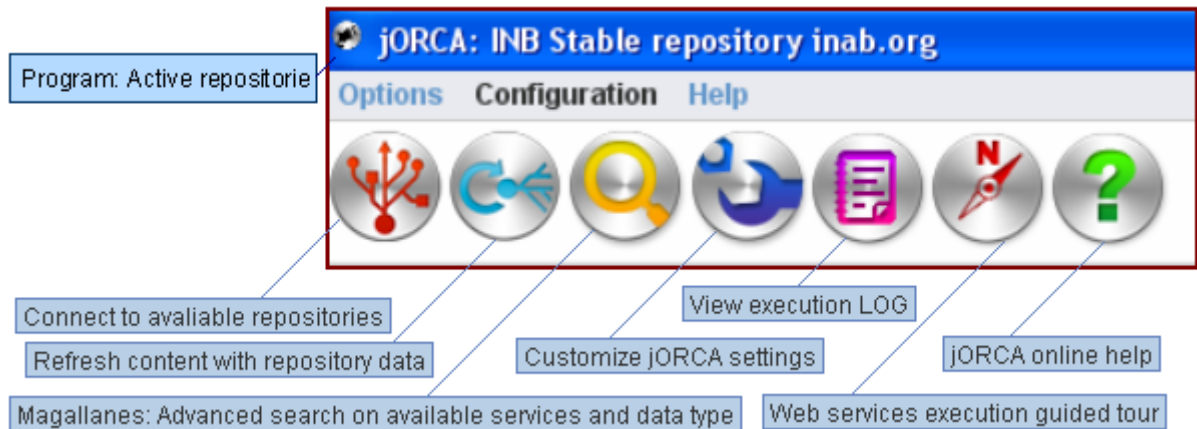
These areas will be explained in detail.

The screenshot shows the jORCA web application interface. The top navigation bar includes 'Options', 'Configuration', and 'Help'. Below this is a 'ToolBar and Menu Area' containing various icons. The main content area is divided into several sections: 'My Favorites', 'Data Types', 'Tools', and 'Namespaces' on the left; a central 'Main Area' with a search bar and a list of 'Useful Bioinformatics tools' (including JorCA Web page, MOWServ tool, Cargo INB Platform, Bitlab group, and INBProject); and a 'File System Area' at the bottom displaying a table of files.


Name	type	size	Modified
AminoAcidSequence.xml	AminoAcidSequence	377B	31-ago-2007
getBestHitFromEzst.2009.01.29.11.4...	Collection	1 KB	29-ene-2009
used.exercises.res.rar	File	670 KB	24-ene-2009
kobayashi.dat	File	1 MB	08-ene-2009
FDB-Text.xml	PCB-Text	1 MB	19-oct-2007
runNCBIblastp.1.2909-01-29.11-46-1.xml	BLAST-Text	43 KB	29-ene-2009
sequences.txt	File	136B	29-ene-2009

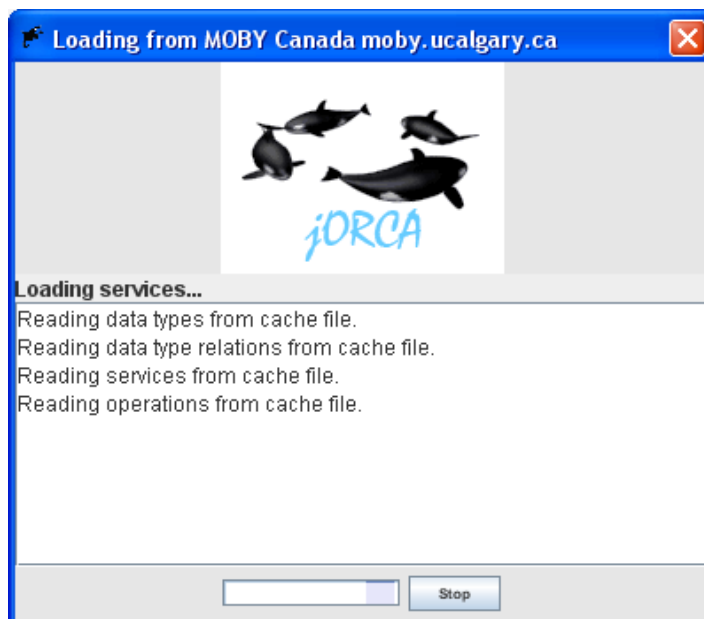
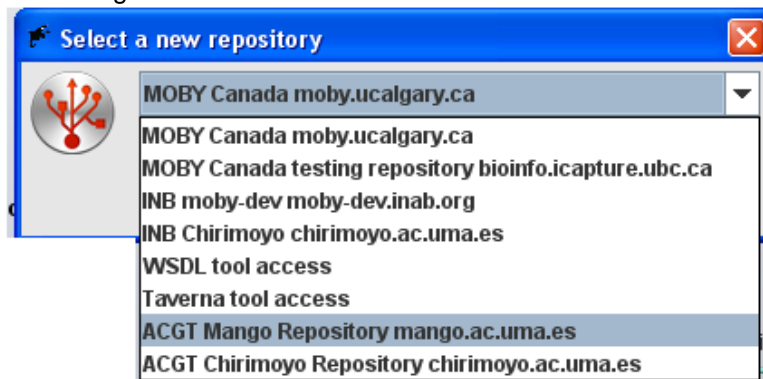
# Toolbar and Menu Area

This area is always visible and it's not configurable by the user. Contains the following controls:



The toolbar options are the following:

-  **Connect to a repository:** To change the current repository.
- jORCA will start loading the data from the cache if it is available or from the repository if not .






**Refresh repository data:** Re-load the active repository (this action can consume some minutes).

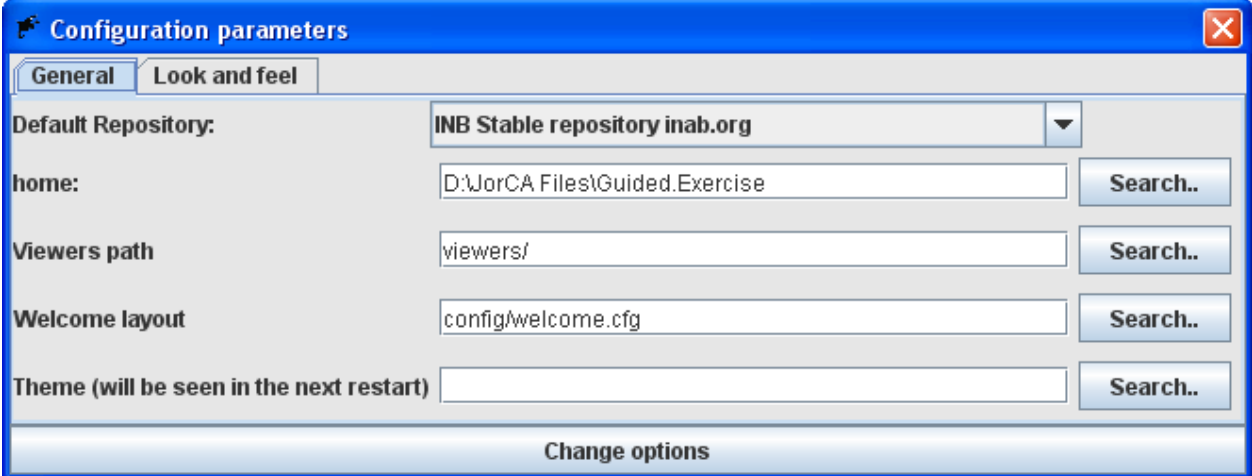


**Advanced Search** using Magallanes (<http://chirimoyo.ac.uma.es/magallanes>), this option will open a new tab with the search engine. The searching procedure and scoring system is based on the number of occurrences and relative word positions. Currently is endowed with AND, OR and regular expression operators. When no hits are found the Levenshtein distance is used to identify similar words in the repository, producing a ranked list of possible solutions available to the client (misspelling words cannot be detected). Finally, Magallanes also implements a discovering strategy base on services compatible with a given data-type (which services are able to process my data?). "Perfect match" and inheritance methods are implemented. Magallanes also allows searching a pipeline of services from a datatype to another.

The screenshot shows the Magallanes search interface with the following details:

- Search Interface:**
  - Find: phylo
  - Resource: All
  - Options:  Case Sensitive,  Follow Links
  - Type:  And,  Or,  Regular Expression
  - Results (27):
- Search Results:**
  - DataType:**
    - Repo: phylogenetic\_tree
    - Name: phylogenetic\_tree
    - Id: urn:lsid:biomoby.org/objectclass:phylogenetic\_tree
    - Description: phylogenetic tree
  - Compatible Services:**
    - urn:lsid:biomoby.org/serviceinstance:biomoby.renci.org.Consense
    - urn:lsid:biomoby.org/serviceinstance:biomoby.renci.org.Drawgram
    - urn:lsid:biomoby.org/serviceinstance:biomoby.renci.org.Drawgram
  - ServiceType:**
    - Repo: Phylogenetics
    - Name: Phylogenetics
    - Id: urn:lsid:biomoby.org/serviceinstance:Phylogenetics
    - Description: services related to the study of evolutionary relatedness among various groups of organisms.
  - DataType:**
    - Repo: GCP\_MolecularPhylogeny
    - Name: GCP\_MolecularPhylogeny
    - Id: urn:lsid:biomoby.org/objectclass:GCP\_MolecularPhylogeny
    - Description: A GCP\_MolecularPhylogeny inherits from GCP\_Entity to track molecular clades. This data type has 1 identified by GCP\_SimpleIdentifiers.
- Service Dependency Graph:**
  - Root node: phylogenetic\_tree
  - Intermediate nodes: Consense, Drawgram, Drawgram, Drawgram, Drawgram, Drawgram, Drawgram, Drawgram
  - Leaf nodes: SimpleKeyvaluePair, GCP\_MolecularPhylogeny, ArmsAcidSequence

-  **Advanced Configuration:** To change jORCA default parameters (the same effect is obtained by changing \$jorca/config/config.cfg file.) These changes won't be visible until the next restart.



**Configuration parameters**

**General** | Look and feel

Default Repository: INB Stable repository inab.org

home: D:\JorCA Files\Guided.Exercise Search..

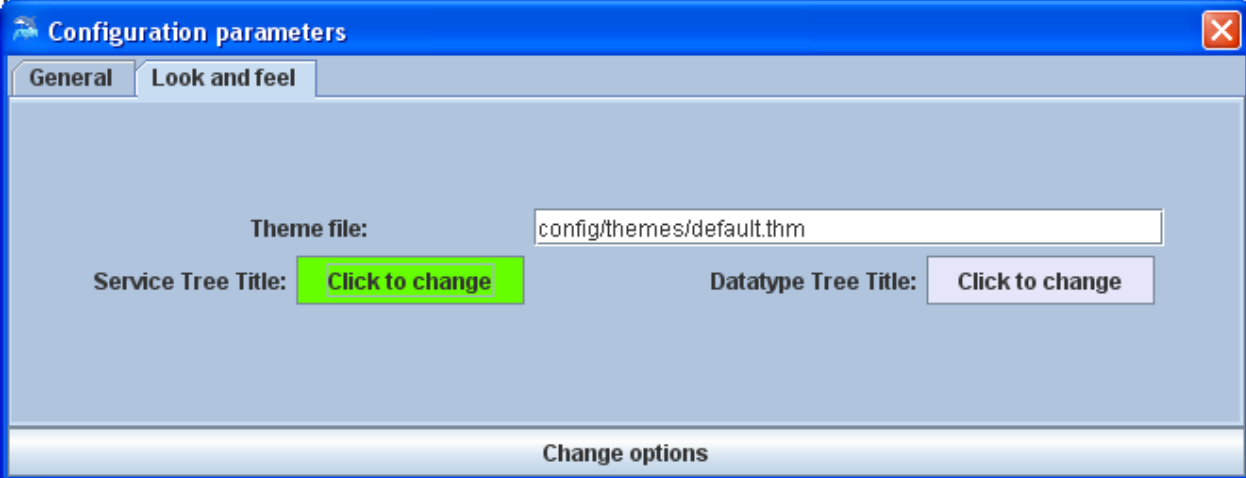
Viewers path: viewers/ Search..

Welcome layout: config/welcome.cfg Search..

Theme (will be seen in the next restart) Search..

Change options

- o General
  - Default repository is the repository that will be shown every time jORCA opens.
  - Viewer's path is the file path where the viewers will be stored.
  - Welcome layout: is the file that will be read in order to create the welcome toolbar.
  - Theme: is the look and feel parameters, colors, fonts icons that jORCA will use to create its interface



**Configuration parameters**

General | **Look and feel**

Theme file: config/themes/default.thm

Service Tree Title: Click to change

Datatype Tree Title: Click to change

Change options

- o Look and feel
  - This area is under development but in a new version of jORCA the user could create different themes for jORCA easily changing the parameters in this area.



- **Execution log:** Displays the log of executed actions (launched tasks, date, parameters etc). Services can be invoked even with new parameters.
- Log edition is also provided (delete tasks).

Tool	Date	Where	Repository	Parameters	Status
runFastf	4 Feb 2009 11:16:07 GMT	bioinfoinb.cnb.uam.es	INB Stable repository inab.org	[sequence,D:\JorCA Files\Guided.Exercise\AminoAcidSequence.xml]	FAILED
runPPSearchAgainstProsite	4 Feb 2009 11:16:14 GMT	inb.bsc.es	INB Stable repository inab.org	[abundantPatterns,no],[sequence,D:\JorCA Files\Guided.Exercise\AminoAcidSequence.xml]	FINISHED
runNCBIblastp_2Seqs	4 Feb 2009 11:15:53 GMT	inb.bsc.es	INB Stable repository inab.org	[database,D:\JorCA Files\Guided.Exercise\AminoAcidSequence.xml],[dropoff,15],[expect_threshold,10.0],[opengap,11],[word_size,3],[gap	FAILED
runEmbossAntigenicFromSequence	4 Feb 2009 11:28:40 GMT	inb.bsc.es	INB Stable repository inab.org	[to,2],[minlen,6],[sequence,D:\JorCA Files\Guided.Exercise\getBestHitsFromBlast.2009-02-02.12-55-4.xml],[from,8]	FAILED
runPhylipDnadist	4 Feb 2009 11:29:54 GMT	bioinfoinb.cnb.uam.es	INB Stable repository inab.org	[basefrequency,yes],[alignment,D:\JorCA Files\Guided.Exercise\fromGenericToNucleotideSequence.2009-02-03.11-09-1.xml],[ttratio,2.0],[matrix,square],[meth	FAILED



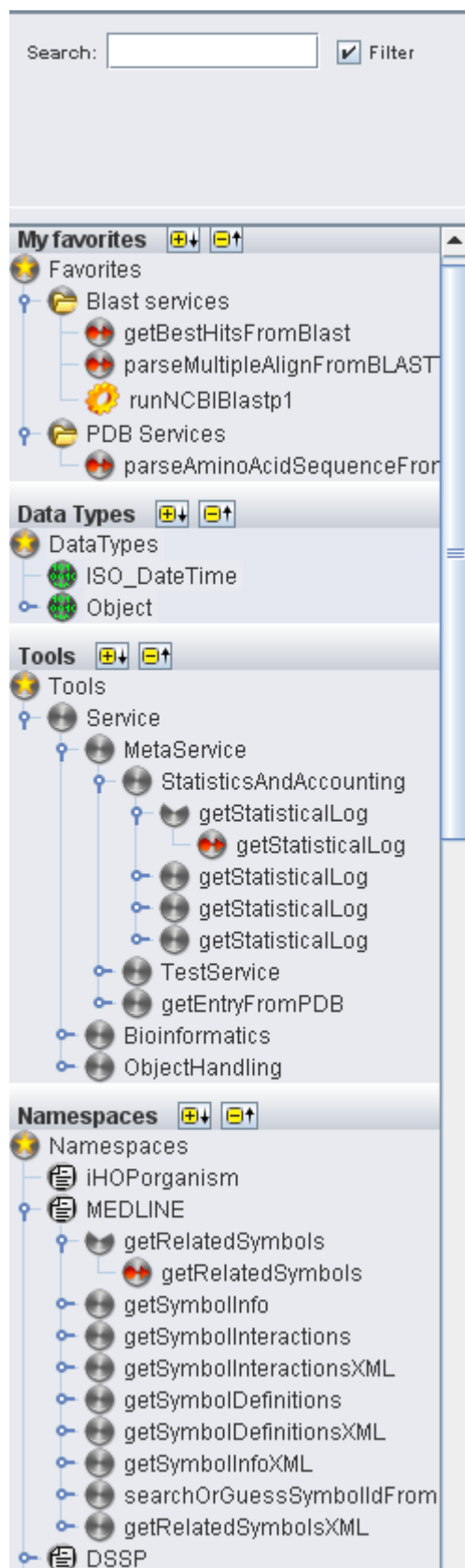
- **Guided tour:** Open a web browser with a guided tour on jORCA (some guided exercises).



- **Help:** Web access to full online jORCA help.

**Menú Options** are the same except for the “**Configuration**” Option, this option will be explained in the Main Area.

## Control Area



This area displays the active repository tools (web services), datatypes (data) and namespaces (if available) organized as a browseable tree, using the information about the repository ontology (Functional categories), ordered by authority or alphabetically. This order is configurable by the menu.

Favorite's section is also available in this panel.

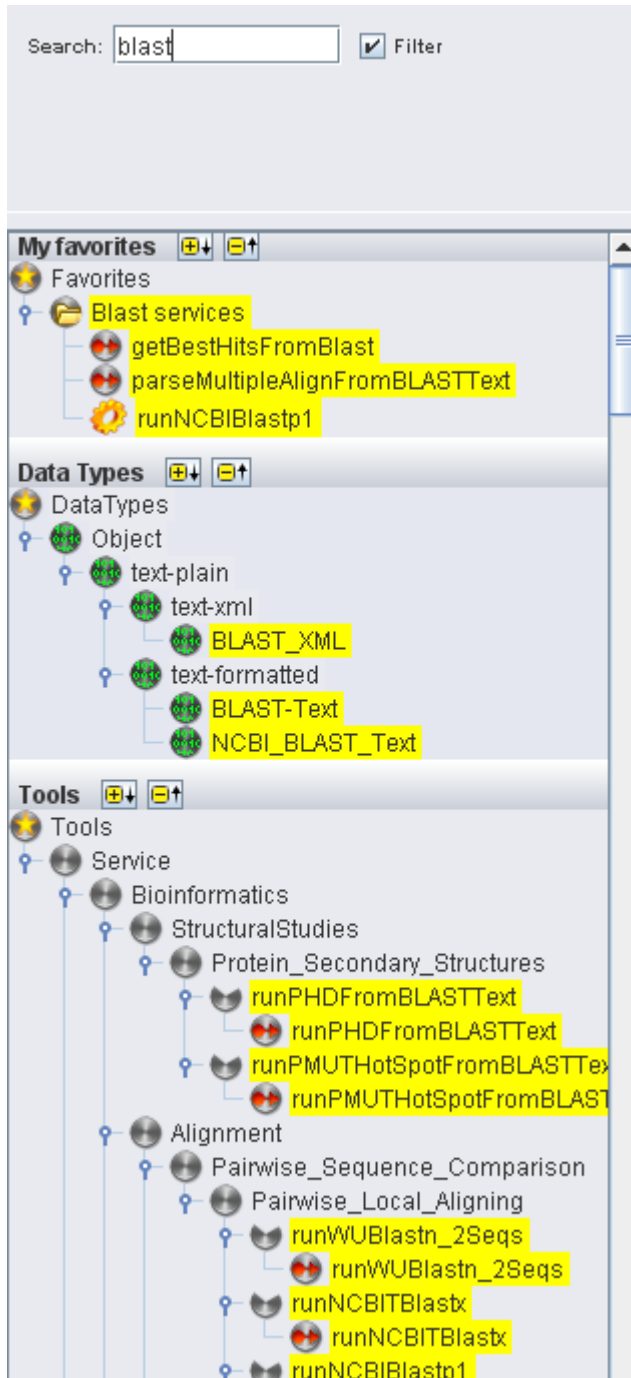
Content display can be configured in the Menu: hide trees, change configuration etc.

The user can select a new object or service by searching it in the tree or using the fast-search tool (text box in the upper position). When the user writes a word in the text box automatically the matching services/data types will be highlighted

A short description on each element in the tree is displayed into a tip when the mouse is over the name.

To use a web service o create a datatype double click on the tree name or drag and drop it into the main Area.

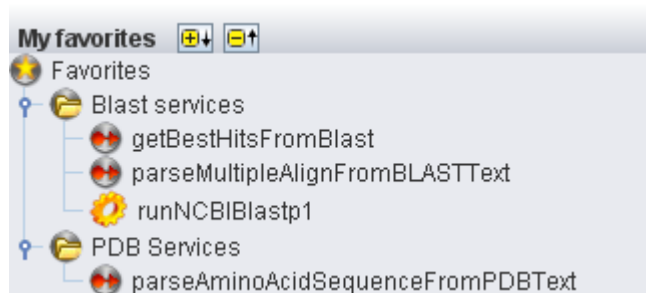
## The Fast Search tool



The **Fast search tool** is designed to search for information on the metadata associated to the different trees. Information may consist of the names of those favorites, tools, data types or namespaces.

- Perfect matching is used
- Matching elements will be highlighted.
- The on/off "filter" option display / hide no-matching elements

## Favorites



jORCA Favorites contains tools or datatypes often used by the user within easy reach. That way, the user doesn't have to remember or type anything. Just clicking the mouse twice—and there you are.

These tools are organized through their own categories/ icons/ name/ description.

A predefined set of tools is supplied with this installation (the user can modify this content).

To add a service or data-type to this area click on the star



next to the object or service name in the object creation tab or service tab.

A dialog window will be shown asking the user for some parameters, name of the favorite, description and icon.

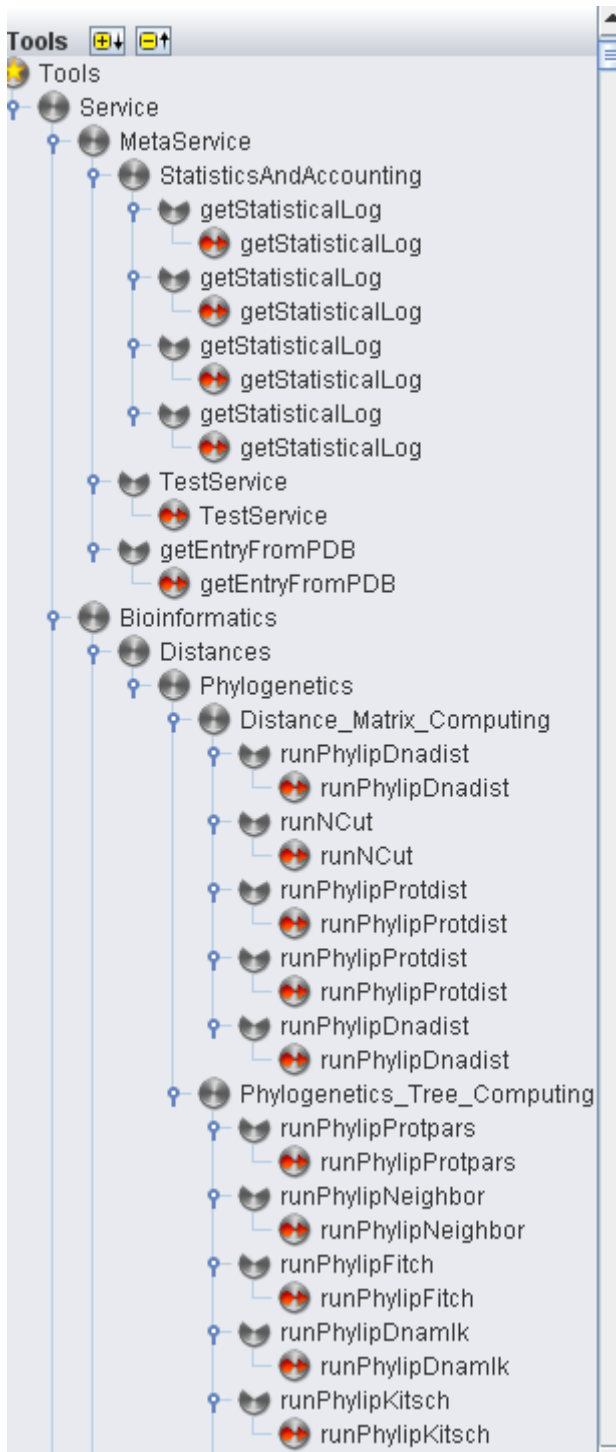


Favorites can be:

- deleted
- modified
- categorized

All these options are available right clicking on the favorites trees nodes, when the user add or modify a favorite category this dialog is displayed:





## Tools tree

A 'Web service' is defined by the W3C as "a software system designed to support interoperable machine-to-machine interaction over a network". Web services are frequently just Web APIs that can be accessed over a network, such as the Internet, and executed on a remote system hosting the requested services.

The W3C Web service definition encompasses many different systems, but in common usage the term refers to clients and servers that communicate over the HTTP protocol used on the Web.

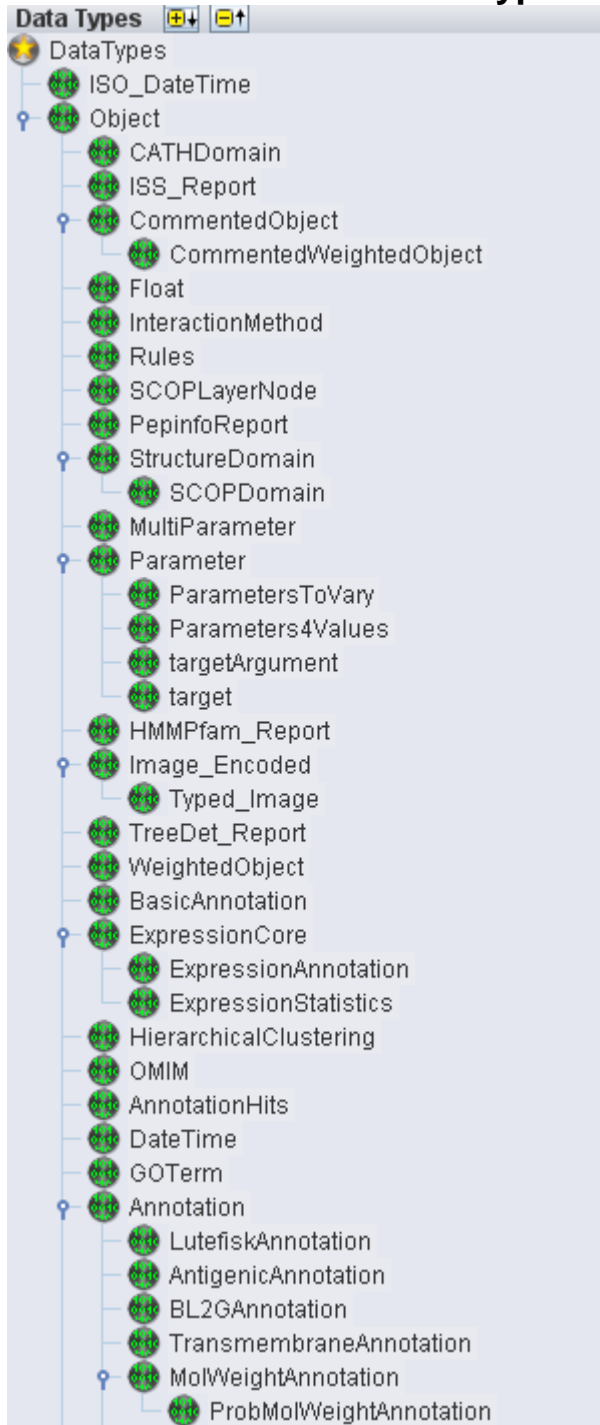
Web services normally are accessible through a centralized repository and organized using anthologies. All available web services in a selected repository are displayed in this tree.

This tree can be displayed in several ways, configurable by the "Configuration" menu option:

- Ordered by functional categories.
- Plain list ordered alphabetically
- Plain list ordered by authority.
- Not displayed.

To get the selected web service launch interface just double click on it or drag and drop it to the main area.

## Data type tree



Web services use a message format to transmit data between the service and the client application that invokes the service. Most of the web services protocols use XML-based protocols, the user must use XML Schema notation to describe the structure of a data definition structure.

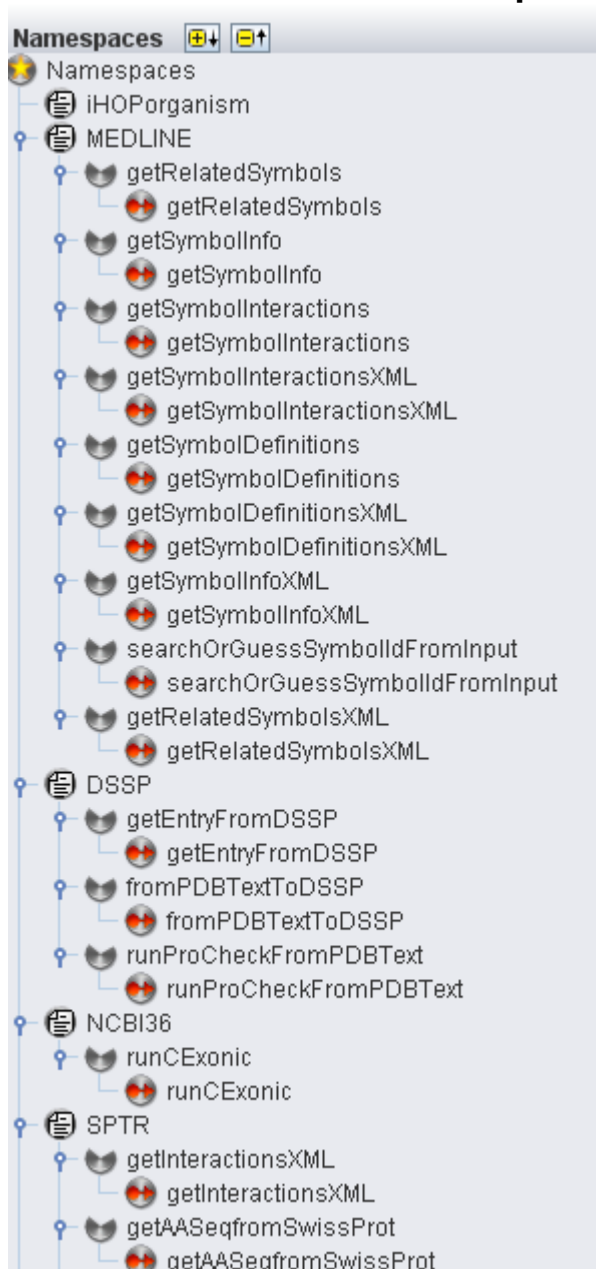
Using this tree the user can create complex data with user-friendly interfaces without any knowledge of XML.

This tree can be displayed in several ways, configurable by the "Configuration" menu option:

- Ordered hierarchically.
- Plain list ordered alphabetically
- Not displayed.

To get the selected data type creation interface just double click on it or drag and drop it to the main area.

## Namespaces tree



A namespace is an abstract container or environment created to hold a logical grouping of unique identifiers or symbols. An identifier defined in a namespace is associated with that namespace. The same identifier can be independently defined in multiple namespaces. That is, the meaning associated with an identifier defined in one namespace may or may not have the same meaning as the same identifier defined in another namespace.

Namespaces and tools related with those namespaces are shown in this tree.

This tree can be displayed in several ways, configurable by the "Configuration" menu option:

- Ordered hierarchically.
- Not displayed.

To get the selected web service launch interface just double click on it or drag and drop it to the main area.

## Trees' configuration

Tree display selection is done from the Configuration pop-up menu.

The tool tree can be displayed in these ways:

- Ordered by functional categories.
- Plain list ordered alphabetically
- Plain list ordered by authority.
- Not displayed.

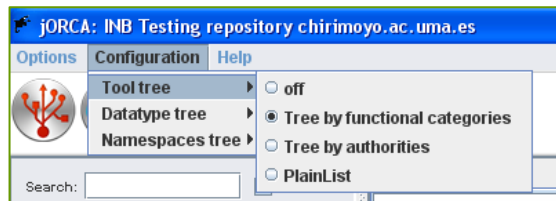
This tree can be displayed in these ways:

- Ordered hierarchically.
- Plain list ordered alphabetically
- Not displayed.

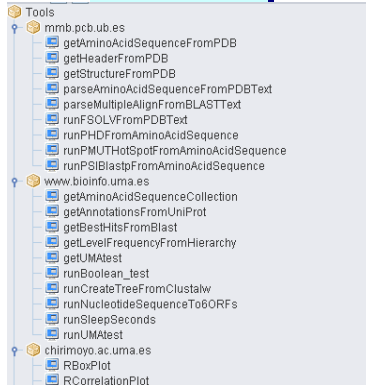
This tree can be displayed in these ways:

- Ordered hierarchically.
- Not displayed.

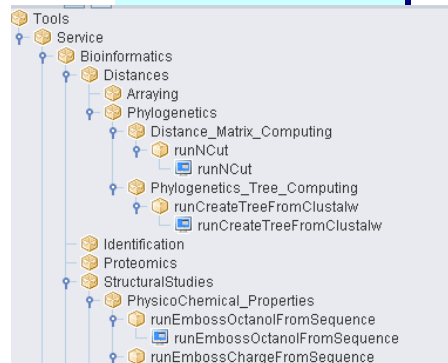
Each displayed tree can be switched on/off (using “display configuration”).



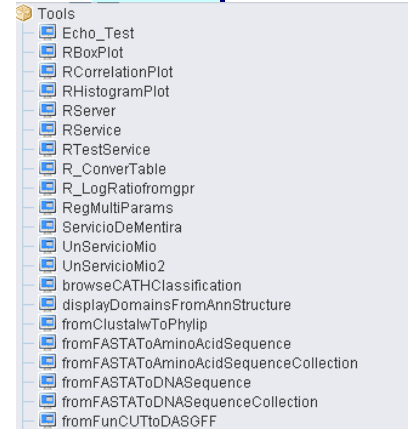
By authorities



By functional categories



Plain List









# Main Area

## Welcome tab or initial tab

jORCA application will help you in the use of the available tools on the web (web services).  
You can connect to different availables repositories and use their service with your data.  
See Online help for extended and useful information



### Useful Bioinformatics tools

	<b>JorCA Web page</b> Follow this link to access full information about jORCA (documents, downloads etc..)
	<b>MOWServ tool</b> Internet based client. Discovery of services based on data type ontology or on service type ontology. It allows to connect easily service outputs to service inputs. Interface helps to object construction
	<b>Cargo INB Platform</b> Currently, CARGO displays biological information only for human genes. Information for other species will be included. CARGO is involved in some projects as Cargo, BioSapie INB.
	<b>IWWE&amp;M</b> Interactive Web Workflow Enactor and Manager (IWWE and M) has been created to try tackling with web workflow management, workflow publishing and workflow enaction prob providing both an end user graphical interface and a programmatic API for those tasks.
	<b>Bitlab group</b> BitLAB (Bioinformatics and Information Technologies Laboratory) is an internal group at AC-UMA focused in the application of advanced computing to solve management and data analysis in bioinformatics and biomedical fields; especially in Input/Output bounded applications. Bioinformatics, a data-driven science strongly featured by the high volume of heterogeneous data sets and the geographical dispersion of their services, is used as the benchmarking application domain in the research lines of Bitlab.
	<b>INB Project</b> INB is a technological platform of Genoma España. A National Network for coordination, integration and development of Spanish Bioinformatics Resources in genomics and proteomics projects.

This tab is the first frame displayed when the user executes jORCA, this tab can't be closed. It is a configurable layout with quick links to useful bioinformatics tools.

To customize the frame, the user can edit this information adding or removing lines to a configuration file, this file is located in \$jorca/config/welcome.config.

In next Jorca releases it will be done by a configuration dialog.


An example of the content:

```
<Tool>
  <Title>JorCA Web page </Title>
  <Description> Follow this link to access full information about jORCA (documents,
downloads etc..)</Description>
  <URL>http://www.bitlab-es.com/jorca </URL>
  <Image>images/Welcome/jORCA.png </Image>
</Tool>
<Tool>
  <Title>MOWServ tool </Title>
  <Description>Internet based client. Discovery of services based on data type ontology
or on service type ontology. It allows to connect easily service outputs to service inputs.Interface helps
to the Moby object construction</Description>
  <URL>http://www.inab.org/MOWServ </URL>
  <Image>images/Welcome/MOWServ.png </Image>
</Tool>
```

Adding a new quick link is as simple as adding a new Tool tag element like this:

```
<Tool>  
  <Title>My tool </Title>  
  <Description>My description </Description>  
  <URL>Tool URL </URL>  
  <Image>Tool image directory</Image>  
</Tool
```

## Datatype creation tab

**Creating Data Type:AminoAcidSequence** 

---

Lightweight representation an amino acid sequence

**File Name:**

**id**

**namespace**  ▼

**SequenceStringString**

Web services use a message format to transmit data between the service and the client application that invokes the service. Most of the web services protocols use XML-based protocols, the user must use XML Schema notation to describe the structure of a data definition structure.

The user can access this tab:

- Double clicking on the desired data type in the data type or favorites tree.
- Dragging an element from data type or favorites trees to the main Area.
- Clicking on edit object in the file system area.

This tab displays the interface to create a standardized object (file) from user data. The user must complete the data typing into the form fields or dropping files to these fields to dump the content to these fields.

All fields are mandatory. A name for the object is suggested but it can be easily changed. Once all fields are filled, click on create object and in the user file system the new object will appear. This panel is created by the Caronte application.

## Using tools

**runWUBlastn**  

---

**Authority:** www.cnb.uam.es  
It compares a nucleotide query sequence against a nucleotide sequence database using the Washington University BLAST algorithm.

**INPUT PARAMETERS**

<b>statistics</b>	String(Secondary)	sump			
<b>match</b>	Integer(Secondary)	5			
<b>expected_threshold</b>	Float(Secondary)	10.0			
<b>word_size</b>	Integer(Secondary)	11			
<b>nogaps</b>	String(Secondary)	false			
<b>filter</b>	String(Secondary)	none			
<b>gap_open</b>	Integer(Secondary)	10			
<b>scores</b>	Integer(Secondary)	25			
<b>sequence</b>	Nucleotide Sequence(Simple)				
<b>gap_extension</b>	Integer(Secondary)	10			
<b>database</b>	String(Secondary)	EMBL			
<b>alignments</b>	Integer(Secondary)	15			
<b>mismatch</b>	Integer(Secondary)	-4			

**OUTPUT PARAMETERS**

**wublast\_report** BLAST-Text(Simple) runWUBlastn.2009-02-16.11-47-13

**Launch Service**

---

**Advanced execution options:** 

*(These options will be available if the service has more than one mirror or if it is asynchronous)*

Mirror Selection	Execution
<input type="radio"/> bioinfoibn.cnb.uam.es	<input checked="" type="checkbox"/> Automatic Execution
	 Request Status
	 Get Results
	 Delete Results

To invoke a tool or service:

- Double clicking on the desired tool in the tool or favorites tree.
- Dragging an element from tool or favorites trees to the main Area.
- Clicking on compatible tool from the file system.
- Re-launching an executed task from the execution log.

This tab contains the information to be completed by the user to launch the selected tool. All fields are mandatory; most of the parameters will have a default value. A name for the output file object is suggested but it can be easily changed.

A web service usually needs a file input as an argument to be called, this file input must be standardized using XML tags, jORCA tries to facilitate this task to the user with different approaches:

- 1.- Look for a compatible file in the user file-system: jORCA uses an heuristic to search for a compatible standardized file in the user file system area.
- 2.- Create a new file of this data-type: this option display the data type creation tab to the user and when the user finishes editing it fills the parameter in the execution form.
- 3.- Get any file from the file system: this option allows the user to select any file from the file system.
- 4.- Drag and drop from the file system to the parameter input : the user can drag and drop a file from the file system to this area.

Once all fields are filled, to launch the service the user must click on the launch service button. The execution module will call to the tool; you can use jORCA while the service is running.

There are some advanced options for advanced users; these options are related to mirroring and asynchronism.

- Mirroring: if the service has more than one server to execute the user can choose where to execute it, otherwise this options will be disabled.
- Execution: If the service is asynchronous, the user can choose if he/she wants automatic (default) execution or using advanced features from the asynchronism.
  - o Request status: if the automatic execution is disabled, jORCA won't automatic inform the user about the service status, he/she must click on this button to get the information.
  - o Get results: when the service is asynchronous, you can decide to leave the results in the server where the service is being executed or to download them to your machine, this option download the service results to the user PC.
  - o Delete result: as said before, the user could need to leave the results in the results without downloading; this option is to ask the server to delete those results.

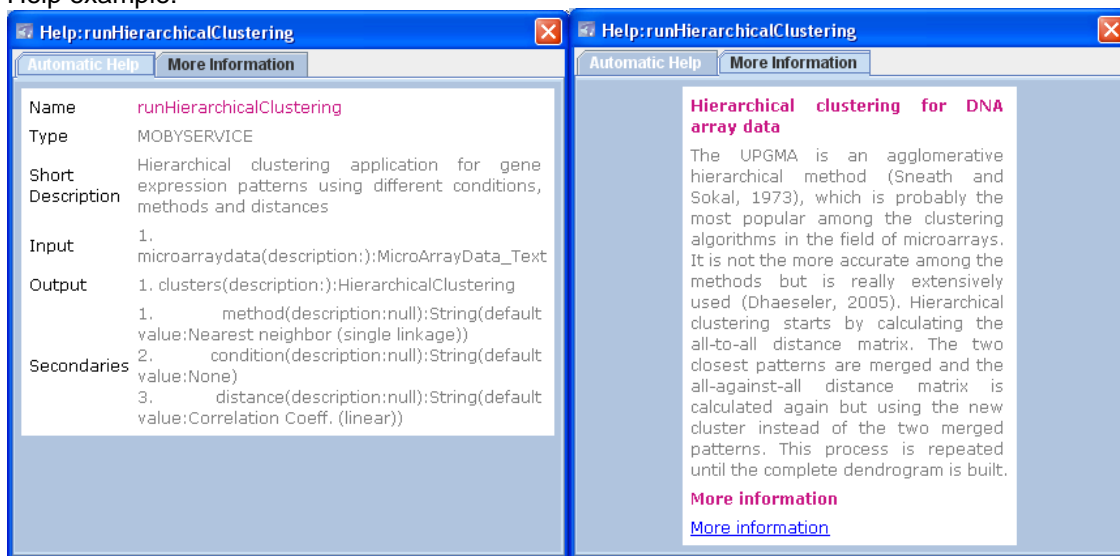
Automatic execution will, prompt the status automatically, inform the user about the status, get the results and delete the results from the server.

There are other options in this tab, the user can add the service to favorite (clicking on the star icon) or

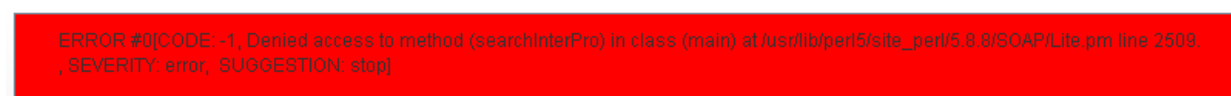
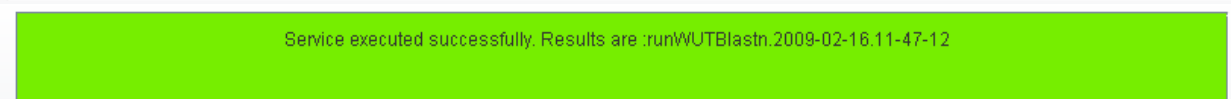


see the service help (clicking on the question mark icon).

Help example:



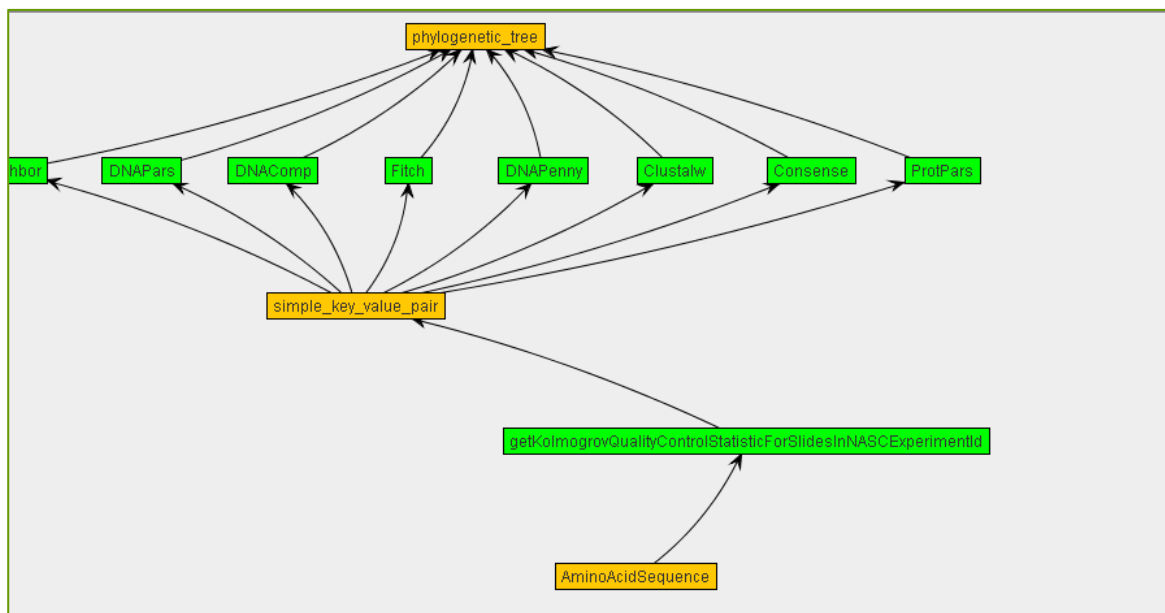
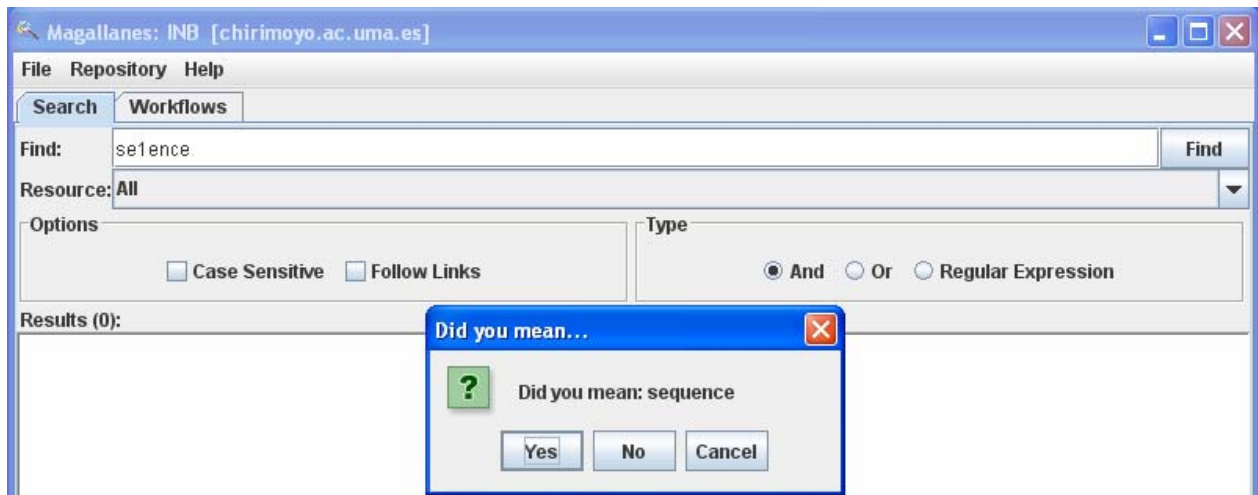
When the tool finishes the execution the user will be notified, the tab will turn red or green depending on the execution status and the result will be saved in the file system.



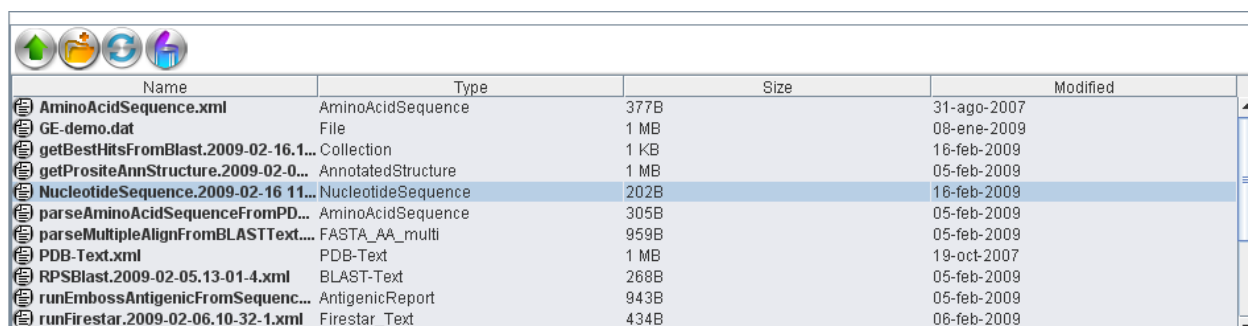
## Advanced search

The advanced search option is available through the search button in the toolbar, advanced search uses Magallanes search engine (<http://chirimoyo.ac.uma.es/magallanes>).

See <http://chirimoyo.ac.uma.es/magallanes/documents/Magallanes%20-%20Getting%20Started.pdf> for extended reference.



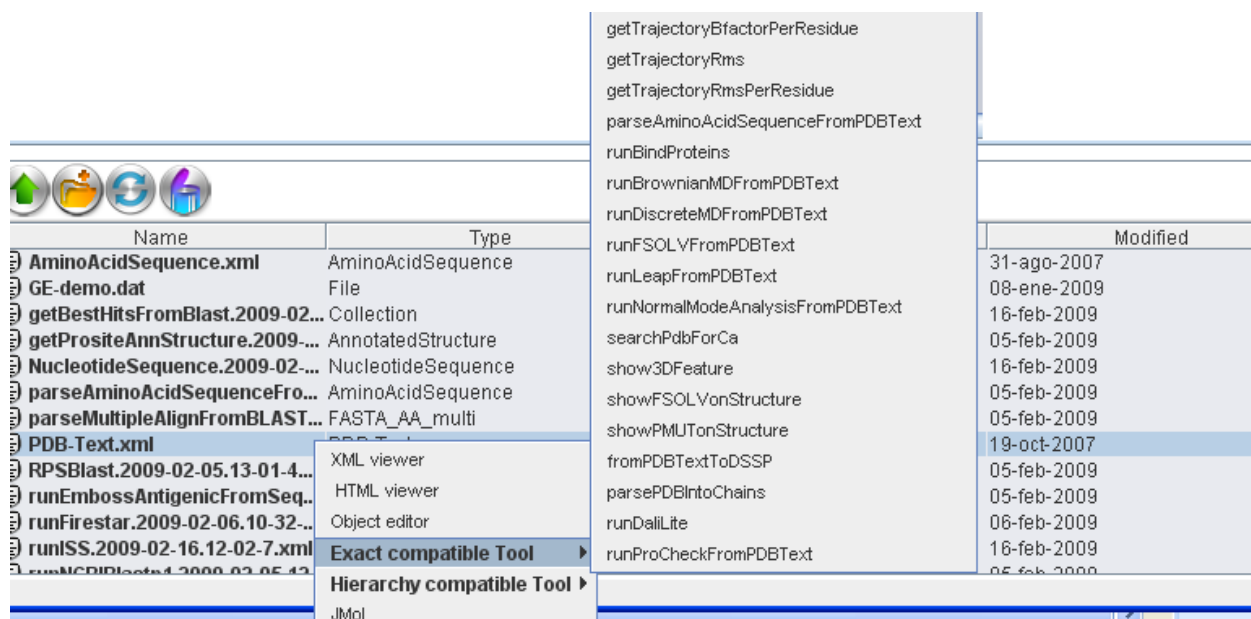
## User file system



Name	Type	Size	Modified
AminoAcidSequence.xml	AminoAcidSequence	377B	31-ago-2007
GE-demo.dat	File	1 MB	08-ene-2009
getBestHitsFromBlast.2009-02-16.1...	Collection	1 KB	16-feb-2009
getPrositeAnnStructure.2009-02-0...	AnnotatedStructure	1 MB	05-feb-2009
NucleotideSequence.2009-02-16 11...	NucleotideSequence	202B	16-feb-2009
parseAminoAcidSequenceFromPD...	AminoAcidSequence	305B	05-feb-2009
parseMultipleAlignFromBLASTText...	FASTA_AA_multi	959B	05-feb-2009
PDB-Text.xml	PDB-Text	1 MB	19-oct-2007
RPSBlast.2009-02-05.13-01-4.xml	BLAST-Text	268B	05-feb-2009
runEmbossAntigenicFromSequenc...	AntigenicReport	943B	05-feb-2009
runFirestar.2009-02-06.10-32-1.xml	Firestar_Text	434B	06-feb-2009

jORCA uses this area to display the user files (starting in the main directory). A heuristic approach is used to identify the data-type that matches the file content. When jORCA looks for a compatible object, it looks for in the home folder and all subfolders into it. jORCA heuristic detects if the file is a MOBY-object and shows the type to the user.

Some traditional file management abilities are available (creating new folder, refreshing data, navigation, and file deletion.)



When the user double clicks on a file the default file browser of the Operative System for that kind of file is opened. When the user right clicks on an object a pop-up menu is shown with several options:

- XML viewer: opens a viewer for XML files.
- HTML viewer: shows the content of the file in HTML style.
- Object editor: launch the object editor with the file information.
- Compatible web services: to launch a service with this file as parameter.

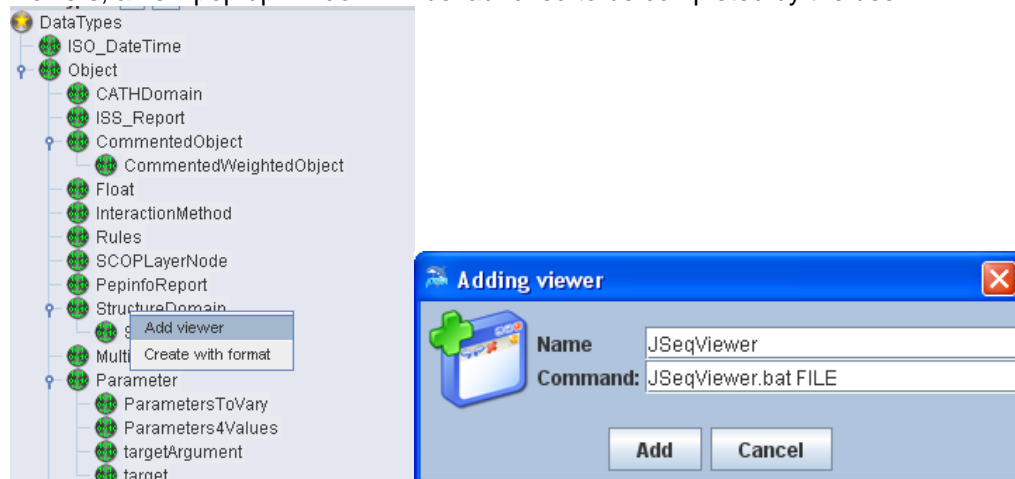
If the data type has a viewer associated, this viewer or viewers is also shown in this pop-up menu.

## Viewers

Some data types such as, PDB-text, Aminoacid Sequence etc could have specialized programs to view or manage its information.

jORCA allows the user associate programs with datatypes, these programs are called viewers, because most of them are able to visualize the data in the object in a special way.

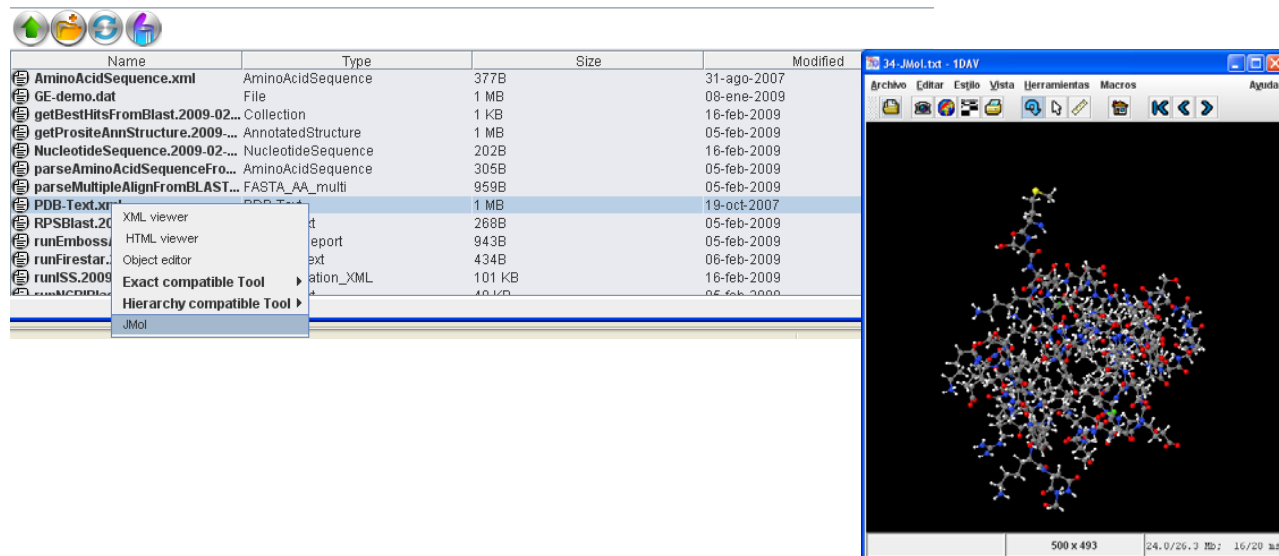
Adding a viewer is simple in jORCA, just right click on the datatypes tree and click on the option add viewers, a new pop up window will be launched to be completed by the user.



The user must specify a name for his object and also a command, the command must be like **“program FILE”**, FILE is a mandatory word that will match the data file selected in that command argument. The viewer is associated to the selected datatype and their children.

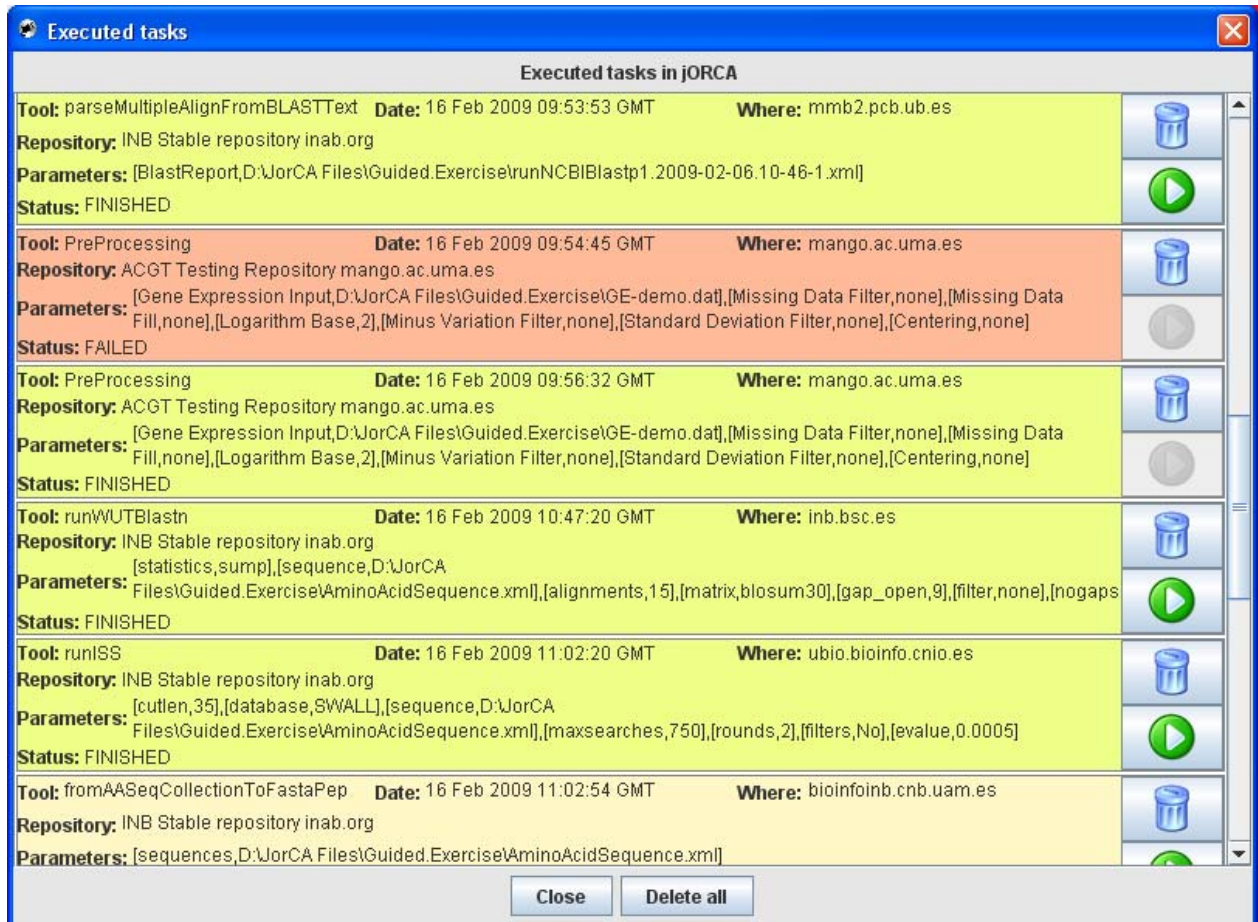
The viewer executable program must be placed at \$jorca/viewers.

Once a viewer is associated to a datatype, the user can use this viewer with his data:



## Execution Log

All executed tools are logged in jORCA. The user can view the executed task in the Log Dialog:



For each task, extended information is displayed:

- Date of execution
- Repository
- Parameter
- Server
- Execution status: FAILED/FINISHED/NOT FINISHED

The background is also coloured depending on the execution status. The user can delete all executed tasks or one by one.

If the user is in the same repository that the executed task he/she can relaunch the task with the same parameters clicking on the “play” button.

# Feedback



Any suggestions, bugs or feedback

- ***vickymr at uma.es***
- ***ortrelles at uma.es***
  
- Keep updated at: <http://www.bitlab-es.com/jorca>
- Guided tours at <http://www.bitlab-es.com/jorca/help>
- Videotutorials at: <http://www.bitlab-es.com/jorca>