

# Enabling Galaxy to access web services (accessing external resources with point and click)

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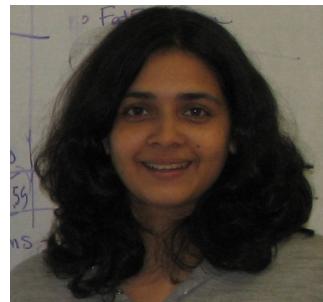
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Sumedha



Rui



Shefali



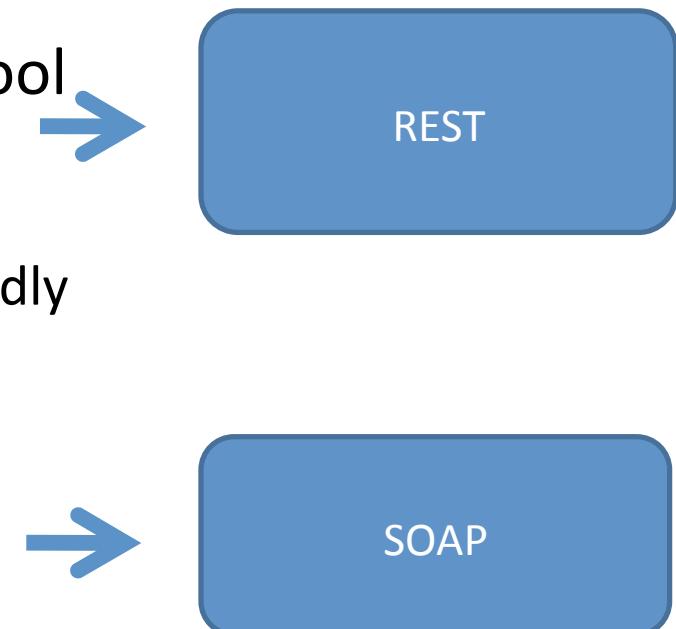
Maryam

# Why Web Service Support in Galaxy?

- Increases flexibility of interacting with any Web service provider
  - Data : may access sources beyond those that are currently registered with a Galaxy server.
  - Analysis : tools may be accessed remotely rather than being installed and registered on a Galaxy server.
- Greatly expands user options and workflow possibilities
- The number of available Web services has grown significantly ~1700 are available  
<http://www.biocatalogue.org/>

# Web Service Development for Galaxy

- There are two flavors of Web Services
  - RESTful and SOAP
- Our implementation in Galaxy
  - REST: Add universal client as a tool
    - Restrictions on tool's behavior
    - =>limitations in UI provisions
    - =>REST approach not so user-friendly
  - SOAP: Modify the source code
    - Difficult to maintain across newer versions of Galaxy



# REST: Our implementation

## (Minimal Change approach)

- Universal Client
  - Invokes any Web service accessible through Web using one universal client
- Parameters from WADL
  - If URL of the WADL provided by the Service provider is specified, parses it and displays the parameter names

# REST: Enter URL for WADL File

The screenshot shows a Mozilla Firefox browser window titled "Galaxy - Mozilla Firefox". The address bar contains the URL `http://localhost:8080`. The main content area displays the "Step 1 : WADL Information" page of the Galaxy interface. A red box highlights the "REST client" section in the left sidebar, which includes links for "Step 1 : WADL information", "WS information", and "Param information". The right sidebar shows a history entry for "Step 1 : WADL information". The bottom of the screen shows the standard Linux desktop taskbar with icons for the browser, file browser, terminal, and email.

Step 1 : WADL Information

Enter the WADL location:

`http://eupathdl`

Execute

Input the URL of the WADL of the REST webservice to be called, e.g. <http://eupathdb.org/webservices/GeneQuestions/GenesByMolecularWeight.wadl>, <http://eupathdb.org/eupathdb/webservices/GeneQuestions/GenesByTextSearch.wadl>

Execute this step and go to Step 2 : WS Information

Tools

- [Fetch Sequences](#)
- [Fetch Alignments](#)
- [Get Genomic Scores](#)
- [Operate on Genomic Intervals](#)
- [Statistics](#)
- [Graph/Display Data](#)
- [Regional Variation](#)
- [Multiple regression](#)
- [Multivariate Analysis](#)
- [Evolution](#)
- [Metagenomic analyses](#)
- [FASTA manipulation](#)
- [NGS: QC and manipulation](#)
- [NGS: Mapping](#)
- [NGS: SAM Tools](#)
- [NGS: Peak Calling](#)
- [Rg Data](#)
- [Rg Simulate](#)
- [Rg Visualise](#)
- [Rg Model Data](#)
- REST client**
- [Step 1 : WADL information](#)
- [WS information](#)
- [Param information](#)

History Options

Unnamed history

16: Step 1 : WADL information

Galaxy - Mozilla Firefox restclient - File Browser ganjoo@ganjoo:~/Des... [Gmail - Inbox - sumed...

# REST: Verify the Web Service

The screenshot shows a Galaxy web interface running in Mozilla Firefox. The title bar indicates it's on a local host at port 8080. The main content area is titled "WS Information" and contains the following steps:

- Choose output from the previous step :** Step 1 : WADL information
- Verify the WADL selected is the one chosen:** http://eupathdb.org/webservices/Gene
- Select the method you want to invoke:** genesbymolecularweight
- Select the Resource url you want to work with:** http://eupathdb.org/webservices/Gene
- Execute**

Below these steps, there is explanatory text:

Once you have chosen the previous step's output and verified the WADL chosen, select the method you want to invoke from the given WADI e.g. genesbytextsearch,genesbymolecularweight.

Then select the resource you want to work with. e.g. <http://eupathdb.org/eupathdb/webservices/GeneQuestions/GenesByTextSearch.xml>, <http://eupathdb.org/eupathdb/webservices/GeneQuestions/GenesByTextSearch.json>.

Execute this step and go to Step 3 : Param Information

The left sidebar lists various tools and services, including "REST client" under "Tools". The "History" panel on the right shows a single entry: "16: Step 1 : WADL information".

# REST: Get Information on Parameters

The screenshot shows a Mozilla Firefox browser window with the title "Galaxy - Mozilla Firefox". The address bar displays "http://localhost:8080/". The main content area shows the "Param information" page of the Galaxy web interface. The left sidebar contains a "Tools" menu with various options like "Statistics", "Graph/Display Data", "Regional Variation", etc. The central panel has sections for "Param information", "Input Parameters", and a detailed description of how to add new input parameters. The right sidebar shows a "History" list with entries for "17: WS information on data 16" and "16: Step 1 : WADL Information". The bottom navigation bar includes tabs for "Galaxy - Mozilla Firefox", "[restclient - File Browser]", "[ganjoo@ganjoo:~/Des...]", and "[Gmail - Inbox - sumed...]".

**Param information**

Choose output from the previous step:  
17: WS information on data 16

Verify the Resource URL selected is the one chosen by you in the previous step:  
<http://eupathdb.org/webservices/Gene>

**Input Parameters**

Add new Input Parameters  
Execute

Once you have chosen the previous step's output and verified the Resource URL chosen, add new input parameters one by one by clicking on "Add new Inputs" button. For each parameter that you want to specify, select one from the dropdown list. You will see the type, default value, and if the parameter is required or not (if specified by the service provider)

e.g. If the method selected was genesbymolecularweight and from the WADL <http://eupathdb.org/webservices/GeneQuestions/GenesByMolecularWeight.wadl>. Once you have verified the Resource URL (e.g. <http://eupathdb.org/webservices/GeneQuestions/GenesByMolecularWeight.xml>) then click on "Add new Inputs" button for adding a parameter. A drop-down list of 4 parameters will be displayed, in this case organism min\_molecular\_weight max\_molecular\_weight o-fields o-tables

Select one of the above parameters. Say, you selected min\_molecular\_weight. The parameter type and default value will show up next. In this case it will be shown as "xsd:string" and "None". Next you enter the value for the parameter min\_molecular\_weight in the text box labeled, " Enter the parameter value". e.g. Enter 10000 for min\_molecular\_weight value.

NOTE: If the value contains a white space replace it with " character. e.g. In above case, if you want to enter the value of parameter organism as Entamoeba disparas, enter it as Entamoeba"dispar

Once you are done specifying all the parameters you want to specify (remember you need to specify all required parameters) Execute this step to see the result from the Web service operation.

# REST: Enter Parameters



Screenshot of a Galaxy web interface showing the 'Param information' step for a REST client. A red box highlights the 'Input Parameters 1' section.

**Param information**

Choose output from the previous step:  
17: WS information on data 16

Verify the Resource URL selected is the one chosen by you in the previous step:  
<http://eupathdb.org/webservices/Gene>

**Input Parameters 1**

Parameter name: organism

Parameter type: xsd:string

Parameter default value: None

Parameter Required?: false

Input the webservice parameter values:  
Entamoeba"dis"

Remove Input Parameters 1

**Input Parameters 2**

Parameter name:

**History**

Options

Unnamed history

17: WS information on data 16

16: Step 1 : WADL Information

Done

Galaxy - Mozilla Firefox [restclient - File Browser] [ganjoo@ganjoo:~/Des...] [Gmail - Inbox - sume...]

# REST: Enter More Parameters



Screenshot of the Galaxy web interface showing the REST client tool.

The interface includes a top menu bar with links like Applications, Places, System, etc., and a status bar showing the date and time (Wed May 12, 17:50). The main window has tabs for Analyze Data, Workflow, Data Libraries, Help, and User.

The left sidebar lists various tools under the "Tools" heading, including Fetch Sequences, Fetch Alignments, Get Genomic Scores, Operate on Genomic Intervals, Statistics, Graph/Display Data, Regional Variation, Multiple regression, Multivariate Analysis, Evolution, Metagenomic analyses, FASTA manipulation, NGS: QC and manipulation, NGS: Mapping, NGS: SAM Tools, NGS: Peak Calling, Rg Data, Rg Simulate, Rg Visualise, Rg Model Data, REST client, SOAP client, and Format convertors for Web services.

The central workspace shows a configuration form for a webservice parameter:

- Parameter name:** organism
- Parameter type:** xsd:string
- Parameter default value:** None
- Parameter Required?:** false
- Input the webservice parameter values:** Entamoeba"disj"
- Remove Input Parameters 1**

A red box highlights the second input section:

- Parameter name:** min\_molecular\_weight
- Parameter type:** xsd:string
- Parameter default value:** None
- Parameter Required?:** false
- Input the webservice parameter values:** 10000
- Remove Input Parameters 2**

The right sidebar displays the History panel, which contains two entries:

- 17: WS Information on data 16
- 16: Step 1 : WADL information

# REST: And More Parameters



Screenshot of a Galaxy web interface showing the REST client tool.

The interface includes a toolbar at the top with various icons, a menu bar (File, Edit, View, History, Delicious, Bookmarks, Tools, Help), and a status bar indicating the date and time (Wed May 12, 17:51).

The main area shows a list of recent URLs in the address bar:

- http://eupat...rWeight.xml
- http://eupa...Weight.wadl
- http://eup...s=EcNumber
- http://eupa...ba%20dispar
- http://eupat...Search.wadl
- Galaxy

The Galaxy logo is visible in the top left of the main content area.

The left sidebar contains a "Tools" section with many options, including:

- Fetch Sequences
- Fetch Alignments
- Get Genomic Scores
- Operate on Genomic Intervals
- Statistics
- Graph/Display Data
- Regional Variation
- Multiple regression
- Multivariate Analysis
- Evolution
- Metagenomic analyses
- FASTA manipulation
- NGS: QC and manipulation
- NGS: Mapping
- NGS: SAM Tools
- NGS: Peak Calling
- Rg Data
- Rg Simulate
- Rg Visualise
- Rg Model Data
- REST client
- Step 1 : WADL information
- WS information
- Param information
- REST client1

The "REST client" section is currently active, displaying the following form:

**Input the webservice parameter values:**  
10000  
**Remove Input Parameters 2**

**Input Parameters 3**

Parameter name:  
max\_molecular\_weight

Parameter type:  
xsd:string

Parameter default value:  
None

Parameter Required?:  
false

**Input the webservice parameter values:**  
50000  
**Remove Input Parameters 3**

Add new Input Parameters  
Execute

A red oval highlights the "Input Parameters 3" section and the "Execute" button.

At the bottom, a note says: Once you have chosen the previous step's output and verified the Resource URL chosen, add new input parameters one by one by

The bottom navigation bar shows other open tabs: restclient - File Browser, ganjoo@ganjoo:~/Des..., Gmail - Inbox - sume..., screenshots - File Bro..., and a Firefox icon.



# REST: Get Results

Sumedha    Wed May 12, 17:53

Galaxy - Mozilla Firefox

File Edit View History Delicious Bookmarks Tools Help

http://localhost:8080/

http://eupat...rWeight.xml http://eupa...Weight.wadl http://eup...s=EcNumber http://eupa...ba%20dispar http://eupat...Search.wadl Galaxy

Galaxy Analyze Data Workflow Data Libraries Help User

Tools

- Fetch Sequences
- Fetch Alignments
- Get Genomic Scores
- Operate on Genomic Intervals
- Statistics
- Graph/Display Data
- Regional Variation
- Multiple regression
- Multivariate Analysis
- Evolution
- Metagenomic analyses
- FASTA manipulation
- NGS: QC and manipulation
- NGS: Mapping
- NGS: SAM Tools
- NGS: Peak Calling
- Rg Data
- Rg Simulate
- Rg Visualise
- Rg Model Data
- REST client
  - Step 1 : WADL information
  - WS information
  - Param information
- REST client1

<?xml version='1.0' encoding='UTF-8'?>

<response>

<recordset id='773ca7f37cdcec7888b9b32b5daa4347' count='5886' type='Gene'>

<record id='EDI\_283340'>

</record>

<record id='EDI\_342250'>

</record>

<record id='EDI\_158260'>

</record>

<record id='EDI\_015980'>

</record>

<record id='EDI\_082780'>

</record>

<record id='EDI\_312860'>

</record>

<record id='EDI\_013030'>

</record>

<record id='EDI\_174910'>

</record>

<record id='EDI\_079350'>

</record>

<record id='EDI\_329340'>

</record>

<record id='EDI\_230235'>

History Options

Unnamed history

18: Param information on data 17

11,777 lines, 5,886 comments, format: tabular, database: ?

Info:

1

<?xml version='1.0' encoding='UTF-8'?>

<response>

<recordset id='773ca7f37cdcec7888b9b32b5daa4347' count='5886' type='Gene'>

<record id='EDI\_283340'>

</record>

17: WS information on data 16

16: Step 1 : WADL Information

Galaxy - Mozilla Firefox [restclient - File Browser] [ganjo@ganjo:~/Des...] [screenshots - File Bro...]

# SOAP Our Implementation

## (Maximal Functionality approach)

- Web Service Creator Tool
  - Permits the user register and add all operations of a SOAP Web service dynamically to Galaxy
- Clients for Web service operations
  - Creates individual clients specific for each operation of a Web service registered using a WSDL
  - Reads and displays parameter names from WSDL
- Semantic support
  - Works for semantically annotated Web services described using SAWSDL
  - Supports top-down data mediation

# SOAP: Enter URL for WSDL File

The screenshot shows the Galaxy web interface running in Mozilla Firefox. The main title bar says "Galaxy - Mozilla Firefox". The address bar shows the URL <http://walton.cs.uga.edu:8080/>. The page content is the "Web Service Tool Creator" tool. On the left sidebar under "Tools", the "WebServices" section is expanded, showing a bullet point about the "Web Service Tool Creator". The main panel has a "WSDL URL:" input field containing <http://www.cs.uga.edu/~wang/galaxy/WSWUBlast.wsdl>, and an "Execute" button below it. A large red box highlights this area. Below the input field is a descriptive text: "Take a WSDL URL and produce a set of Web Service Tools placed into the WebServices section. The WSDL URL must be accessible from the Internet. e.g., <http://www.ebi.ac.uk/Tools/webservices/wsdl/WSDbfetch.wsdl>". To the right of the main panel is a "History" section with a message: "Your history is empty. Click 'Get Data' on the left pane to start". A red arrow points from the top screenshot to the bottom one, indicating the step of entering the WSDL URL.

Galaxy - Mozilla Firefox  
File Edit View History Bookmarks Tools Help  
http://walton.cs.uga.edu:8080/  
Galaxy Galaxy Info: report bugs | wiki | screencasts | blog Account: create | login  
Tools  
WebServices  
▪ Web Service Tool Creator given a WSDL creates a Web Service Tools for all operations  
Get Data  
Get ENCODE Data  
Send Data  
ENCODE Tools  
Lift-over  
Text Manipulation  
Filter and Sort  
Join, Sub  
Convert  
Extract F  
Fetch Se  
Fetch Ali  
Get Geno  
Operate o  
Statistics  
Graph/D  
Regional  
Multiple r  
Evolution  
Taxonom  
Short Re  
FASTA m  
Short Re  
Workflow ro  
Get ENCODE Data  
Done  
Web Service Tool Creator  
WSDL URL:  
<http://www.ebi.ac.uk/Tools/webservices/wsdl/WSDbfetch.wsdl>  
Execute

# SOAP: Dynamically Add Services



Galaxy - Mozilla Firefox

File Edit View Bookmarks Tools Help

http://gws.eupathdb.org/

Galaxy

Tools

- getSensitivity
- getSort
- getStats
- getXML
- getXmlFormats
- poll
- poljob
- runWUblast

runWUblast

Select Parameters for Input 0:

Parameter Set One

Previous WS Data:  
Selection is Optional  
Data from a previously called W

Parameter Set Two  
*sensitivity*:

email: very@uga.edu

exp:

sort:

program: blastp

outformat:

matrix:

strand:

topcombon:

appxml:

echofilter:

filter:

database: swissprot

WebServices

- Web Service Tool Creator**  
given a WSDL creates a Web Service Tools for all operations
- fetchBatch** Get a set of database entries (see [http://www.ebi.ac.uk/Tools/webservices/services/dbfetch#fetchbatch\\_db\\_ids\\_form](http://www.ebi.ac.uk/Tools/webservices/services/dbfetch#fetchbatch_db_ids_form))
- fetchData** Get a database entry (see [http://www.ebi.ac.uk/Tools/webservices/services/dbfetch#fetchdata\\_query\\_format](http://www.ebi.ac.uk/Tools/webservices/services/dbfetch#fetchdata_query_format))
- getDbFormats** Get a list of formats for a given database (see [http://www.ebi.ac.uk/Tools/webservices/services/dbfetch#getdbformats\\_db](http://www.ebi.ac.uk/Tools/webservices/services/dbfetch#getdbformats_db))
- getFormatStyles** Get a list of available styles for a given database and format (see [http://www.ebi.ac.uk/Tools/webservices/services/dbfetch#getformatstyles\\_db\\_form](http://www.ebi.ac.uk/Tools/webservices/services/dbfetch#getformatstyles_db_form))
- getSupportedDBs** Get a list of available databases (see <http://www.ebi.ac.uk/Tools/webservices/services/dbfetch#getsupporteddbs>)

Info: report bugs | wiki | screencasts | blog Account: create | login

History Options

refresh | collapse all

2: Output File 0

1: Output File 0

laxy200905... galaxy0627EK.... wublastInputs... EN 22:35

# Use Web Services in Workflow!



Galaxy Workflow Editor - Mozilla Firefox      Sumedha      Tue May 11, 11:37

File Edit View History Delicious Bookmarks Tools Help

http://walton.cs.uga.edu:8080/workflow/editor?id=cb6e11b662890a90#

Gmail - Inbox - sumedha.coe...    http://www.cs....SWUBlast.wsdl    Galaxy Workflow Editor    Web API for Biology

### Galaxy workflow editor

Workflow support is currently in beta

**Tools**  
**webservices**

- Web Service Tool Creator given a WSDL creates a Web Service Tools for all operations
- fetchBatch** Get a set of database entries (see [http://www.ebi.ac.uk/Tools/webservices/services/dbfetch#fetchbatch\\_db\\_ids\\_format](http://www.ebi.ac.uk/Tools/webservices/services/dbfetch#fetchbatch_db_ids_format))
- fetchData** Get a database entry (see [http://www.ebi.ac.uk/Tools/webservices/services/dbfetch#fetchdata\\_query\\_format](http://www.ebi.ac.uk/Tools/webservices/services/dbfetch#fetchdata_query_format))
- getDbFormats** Get a list of formats for a given database (see [http://www.ebi.ac.uk/Tools/webservices/services/dbfetch#getdbformats\\_db\\_format](http://www.ebi.ac.uk/Tools/webservices/services/dbfetch#getdbformats_db_format))
- getFormatStyles** Get a list of available styles for a given database and format (see [http://www.ebi.ac.uk/Tools/webservices/services/dbfetch#getformatstyles\\_db\\_form](http://www.ebi.ac.uk/Tools/webservices/services/dbfetch#getformatstyles_db_form))
- getSupportedDBs** Get a list of available databases (see <http://www.ebi.ac.uk/Tools/webservices/services/dbfetch#getsupporteddb>)

**Workflow canvas**

Get ID's

Run WUBLast

fetchBatch

Fetch Seqs By ID

**Details**

Tool: **fetchBatch**

Select Parameters for Input 0

Parameter Set One

Parameter Set One

Previous WS Data

Selection is Optional

Parameter Set Two

\_db

default

Select Parameters for Input 1

Parameter Set One

Parameter Set One

Previous WS Data

Selection is Optional

Parameter Set Two

\_ids

default

Select Parameters for Input 2

Parameter Set One

Parameter Set One

Previous WS Data

# New Features: Completed

	SOAP	REST
Parameter entry	<ul style="list-style-type: none"><li>The parameter names are read from WSDL and displayed in one shot</li><li>User can either enter values by hand or choose an output from a previous step in the workflow as a parameter value</li></ul>	<ul style="list-style-type: none"><li>The parameter names are read from WADL and displayed</li><li>Unfortunately user has to choose and add parameters one by one</li></ul>
Add Services	<ul style="list-style-type: none"><li>Services (each operation) can be added as tools in GUI dynamically</li></ul>	<ul style="list-style-type: none"><li>One universal Client for invoking all REST Web services</li><li>Unfortunately, REST services are not listed in the tool panel individually</li></ul>
Data Mediation	<ul style="list-style-type: none"><li>Top-down data mediation implemented</li></ul>	<ul style="list-style-type: none"><li>None presently</li></ul>
Code Maintenance	<ul style="list-style-type: none"><li>None presently</li></ul>	<ul style="list-style-type: none"><li>Not a major issue, code bases are largely independent</li></ul>

# New Features: Proposed

	SOAP	REST
Parameter entry	<ul style="list-style-type: none"> <li>Need a <i>data_ref</i> attribute of <i>param</i> tag to work with <i>type</i> textbox, to make the parameter entry more user-friendly</li> </ul>	<ul style="list-style-type: none"> <li>Provide parameter entry boxes in one shot, rather than looping through</li> </ul>
Add Services	<ul style="list-style-type: none"> <li>Test on a variety differently formatted WSDL files</li> </ul>	<ul style="list-style-type: none"> <li><b>Dynamic addition of services as tools in GUI</b></li> </ul>
Delete Services	<ul style="list-style-type: none"> <li><b>Organize and remove registered services from GUI</b></li> </ul>	<ul style="list-style-type: none"> <li>Remove registered services from GUI</li> </ul>
Discovery	<ul style="list-style-type: none"> <li>Allow services discovered with Lumina to be added to Galaxy</li> </ul>	<ul style="list-style-type: none"> <li>Allow services discovered with Lumina to be added to Galaxy</li> </ul>
Data Mediation	<ul style="list-style-type: none"> <li>Incorporate bottom-up and bidirectional capabilities</li> </ul>	<ul style="list-style-type: none"> <li>Introduce intermediate service, generated from SAWADL specs, for mediation</li> </ul>
Service Suggestion	<ul style="list-style-type: none"> <li>Migrate from research prototype</li> </ul>	<ul style="list-style-type: none"> <li>Migrate from research prototype</li> </ul>
Code Maintenance	<ul style="list-style-type: none"> <li>Instructions/ Tools for code merging</li> </ul>	<ul style="list-style-type: none"> <li>NA</li> </ul>

# Questions?

# Goals

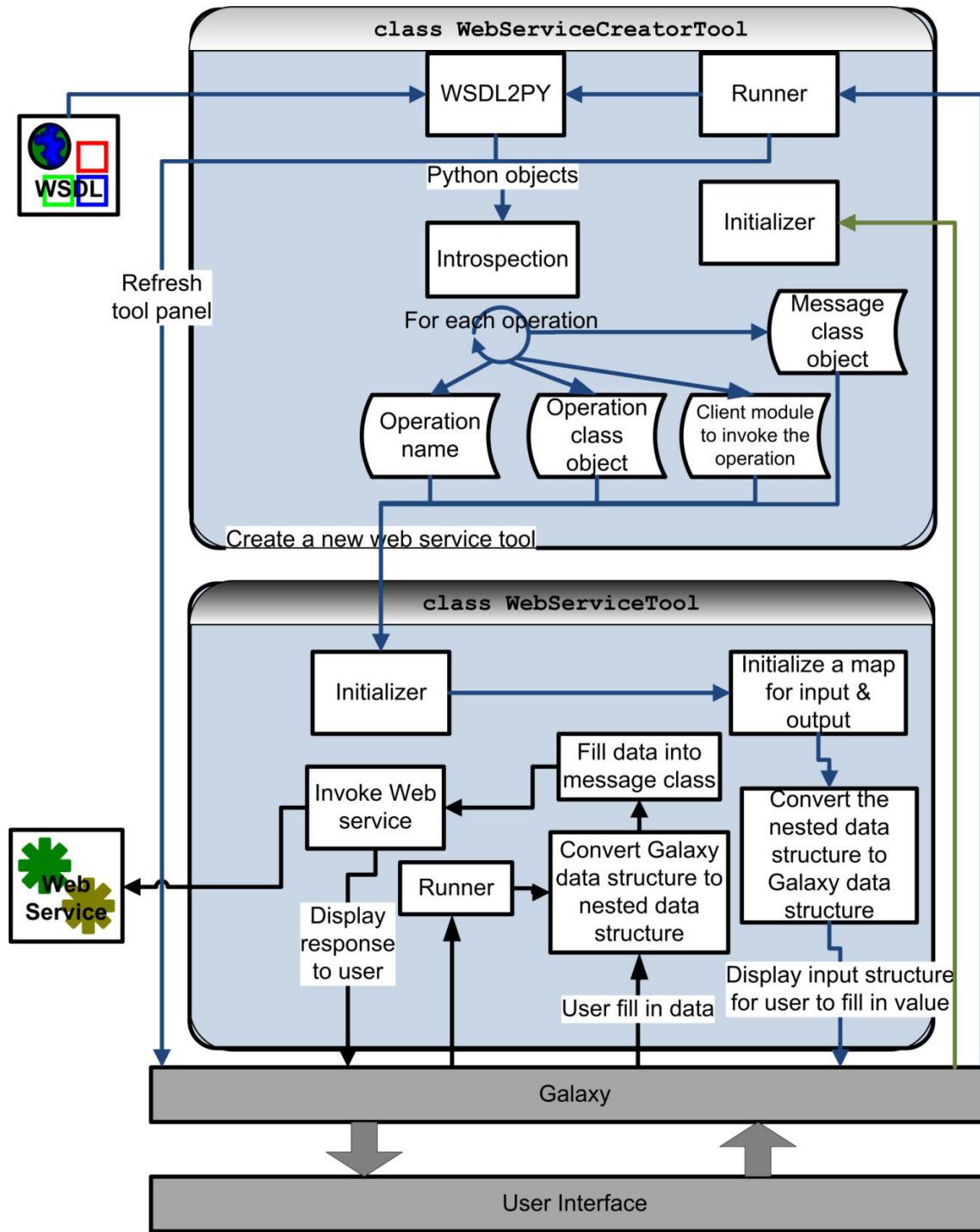
- ▶ Galaxy Web service development.
- ▶ Web Service access via tools in Galaxy.
- ▶ Support for both, REST and SOAP Web services.
- ▶ Support for semantically annotated Web services.

# Minimal Change Approach

- Add Web Services via a universal client tool
  - In keeping with the light-weight nature of **REST** Web services, we have chosen the minimal change approach
- Modify minimal source code to dynamically add tools
  - None so far
  - Unless dynamic addition of tools is provided, we will need to change 2 python packages (jobs, tools), add 1 additional python package for parser and client of Web service, change interface(mako)
- Currently all tools are static and server needs to be restarted on adding tools

# Maximal Functionality Approach

- ▶ Ability to add Web services directly into the core of Galaxy
  - In keeping with the heavy weight nature of **SOAP** services, we have integrated them into Galaxy
  - In order to provide more capabilities and improved user interface significant changes to the Galaxy code base are required
- ▶ Extensive development required
  - So far added 2000 lines of code: modified 9 packages, added 2 new packages(wstool , xmlconverter)
- ▶ Added code for dynamically added tools

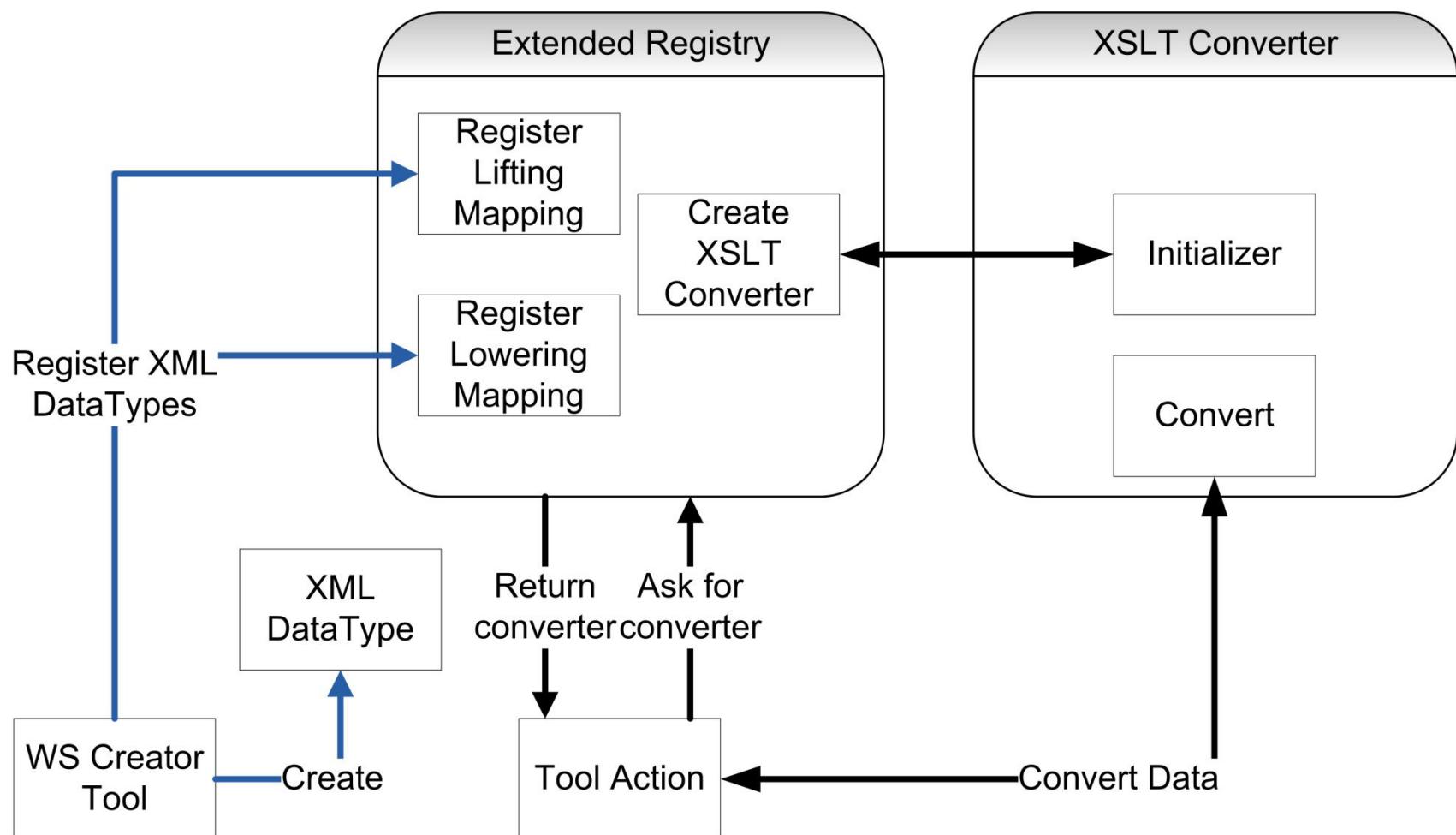


Code generator that creates an instance of a Web service client following the template below

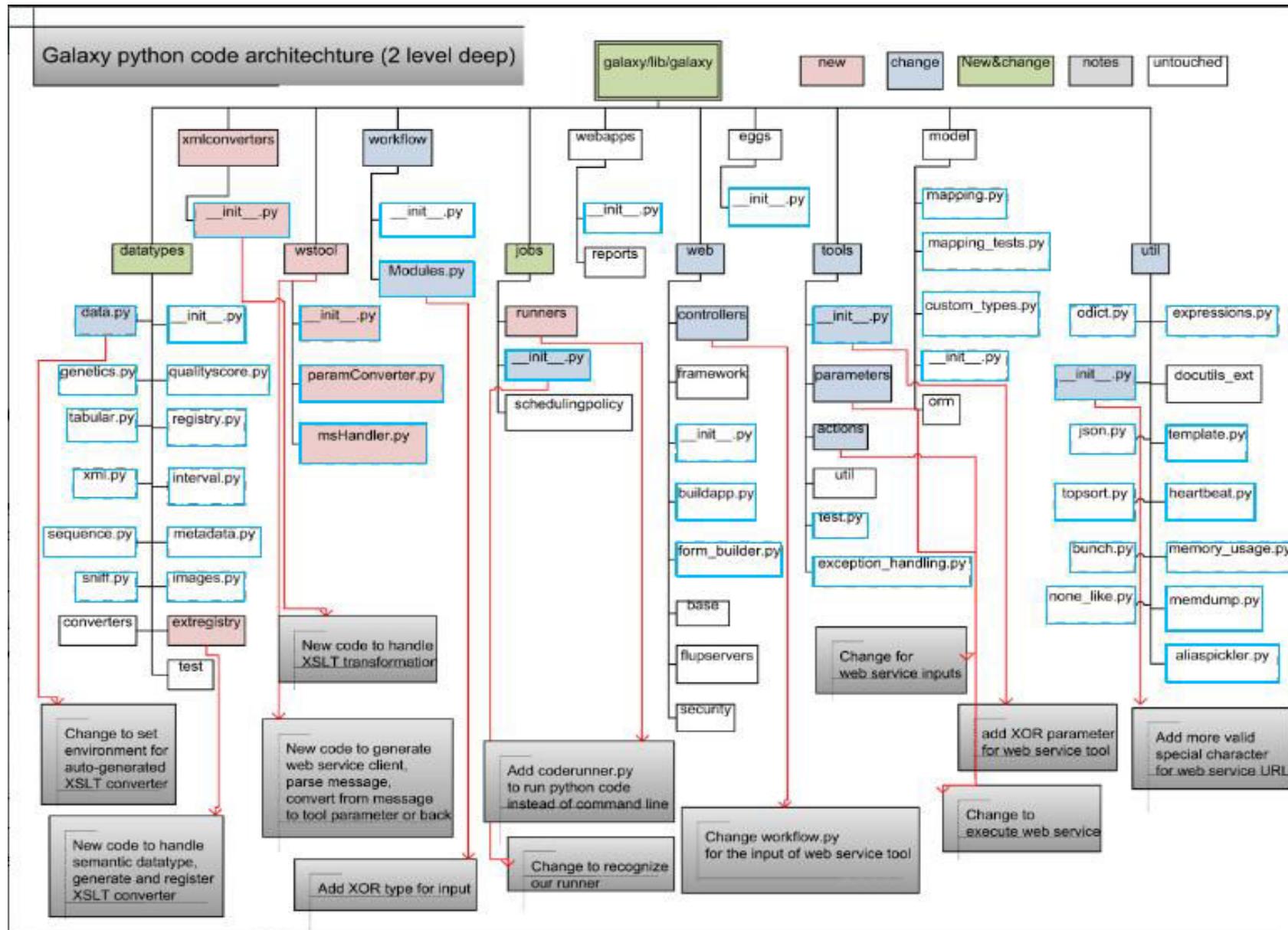
A template for Web service clients used to invoke Web services

**Green = System start**  
**Blue = Registration**  
**Black = Invocation**

# Semantic Web service datatype registry for Galaxy (Feb 19 '09)



# Changes to Galaxy for SOAP support



# Software Distribution Plan

- Galaxy server, with Web service extensions, at UGA
  - Galaxy server at Kissinger lab: gws.eupathdb.org
- Make REST universally available
  - Add REST support to the main Galaxy code base
    - Provide the main developer's team our tool (a zip file that contains 3 xml and 3 python files) : **ready now**
    - Provide a User's guide, Developer's guide : **end of May**
    - Galaxy developers to add the tool called REST client to main server

# Software Distribution Plan(contd..)

- Make SOAP universally available
  - Add SOAP support to the main Galaxy code base
    - Acquired a bitbucket account
    - Create a fork in galaxy-central on bitbucket
    - Provide a User's guide, Developer's guide
    - Get a server to run and test this branch (Meeting with James Taylor : In September)